Supplementary Information

The AnnotationSketch genome annotation drawing library

Sascha Steinbiss, Gordon Gremme, Christin Schärfer, Malte Mader and Stefan Kurtz

11/07/2012

Contents

1 AnnotationSketch

AnnotationSketch is a versatile and efficient C-based drawing library for GFF3-compatible genomic annotations. It is included in the *GenomeTools* distribution. In addition to the native C interface, bindings to the Lua, Python and Ruby programming languages are provided.

1.1 Overview

AnnotationSketch consists of several classes, which take part in three visualization *phases* (see Fig. 1.1).

1.1.1 Phase 1: Feature selection

The GFF3 input data are parsed into a directed acyclic graph (*annotation graph*, see Fig. 1.2 for an example) whose nodes correspond to single features (i.e. lines from the GFF3 file). Consequently, edges in the graph represent the *part-of* relationships between groups of genomic features according to the Sequence Ontology hierarchy. Note that GFF3 input files *must* be valid according to the GFF3 specification to ensure that they can be read for *AnnotationSketch* drawing or any other kind of manipulation using *GenomeTools*. A validating GFF3 parser is available in *GenomeTools* (and can be run using `gt gff3validator`).
Each top-level node (which is a node without a parent) is then registered into a persistent *FeatureIndex* object. The *FeatureIndex* holds a collection of the top-level nodes of all features in each sequence region in an interval tree data structure that can be efficiently queried for features in a genomic region of interest. All child nodes of the top-level node are then available by the use of traversal functions. Alternatively, annotation graphs can be built by the user by creating each node explicitly and then connecting the nodes in a way such that the relationships are reflected in the graph structure (see examples section for example annotation graph building code).

1.1.2 Phase 2: Layout

The next step consists of processing the features (given via a *FeatureIndex* or a simple array of top level nodes) into a *Diagram* object which represents a single view of the annotations of a genomic region. First, semantic units are formed from the annotation subgraphs. This is done by building *blocks* from connected features by grouping and overlaying them according to several user-defined collapsing options (see "Collapsing"). By default, a separate *track* is then created for each Sequence Ontology feature type. Alternatively, if more granularity in track assignment is desired, *track selector* functions can be used to create tracks and assign blocks to them based on arbitrary feature characteristics. This is simply done by creating a unique identifier string per track. The *Diagram* object can also be used to hold one or more *custom tracks*, which allow

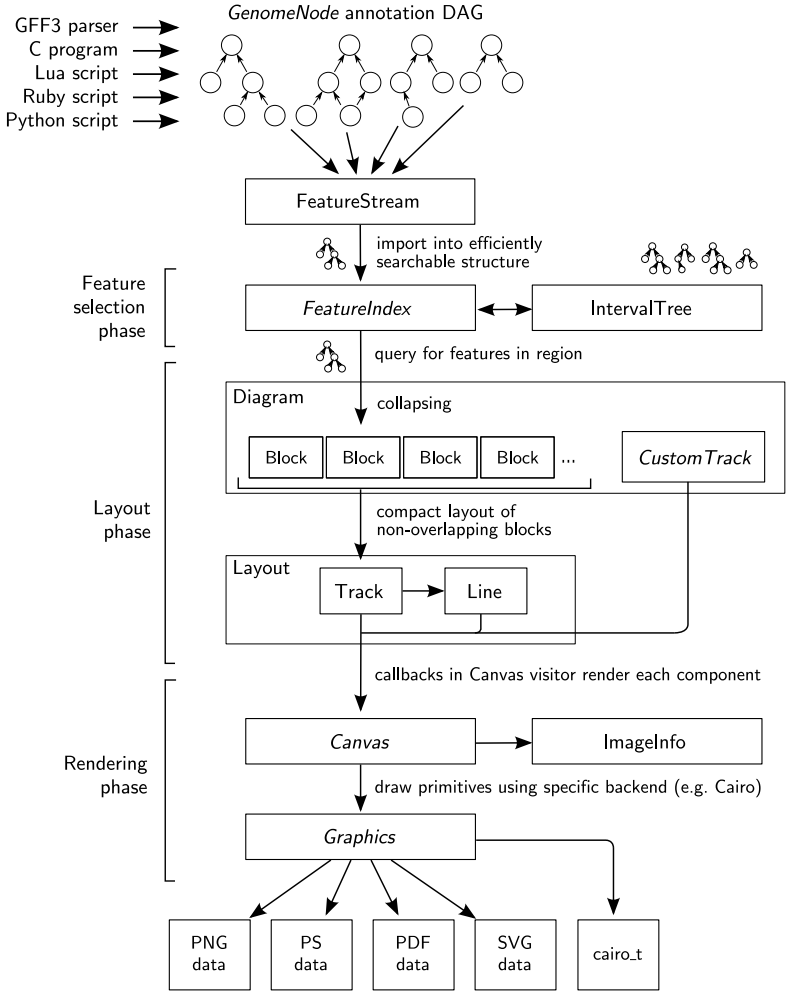


Figure 1.1: Schematic of the data flow through the classes involved in image creation.

users to develop their own graphical representations as plugins. The *Diagram* is then prepared for image output by calculating a compact *Layout* in which the *Block* objects in a track are distributed into *Line* objects, each containing non-overlapping blocks (see Fig. 1.3). The overall layout calculated this way tries to keep lines as compact as possible, minimising the amount of vertical space used. How new *Lines* are created depends on the chosen implementation of the *LineBreaker* interface, by default a *Block* is pushed into a new *Line* when either the *Block* or its caption overlaps with another one.

1.1.3 Phase 3: Rendering

In the final phase, the *Layout* object is used as a blueprint to create an image of a given type and size, considering user-defined options. The rendering process is invoked by calling the `sketch()` method of a *Layout* object. All rendering logic is implemented in classes implement-

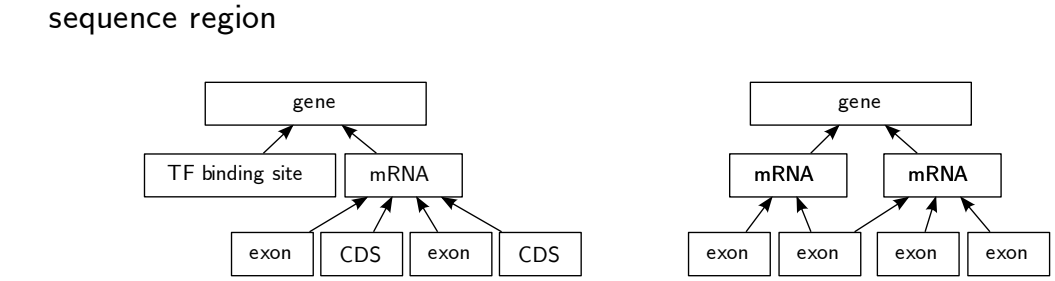


Figure 1.2: Example sequence region containing two genes in an annotation graph depicting the *part-of* relationships between their components.

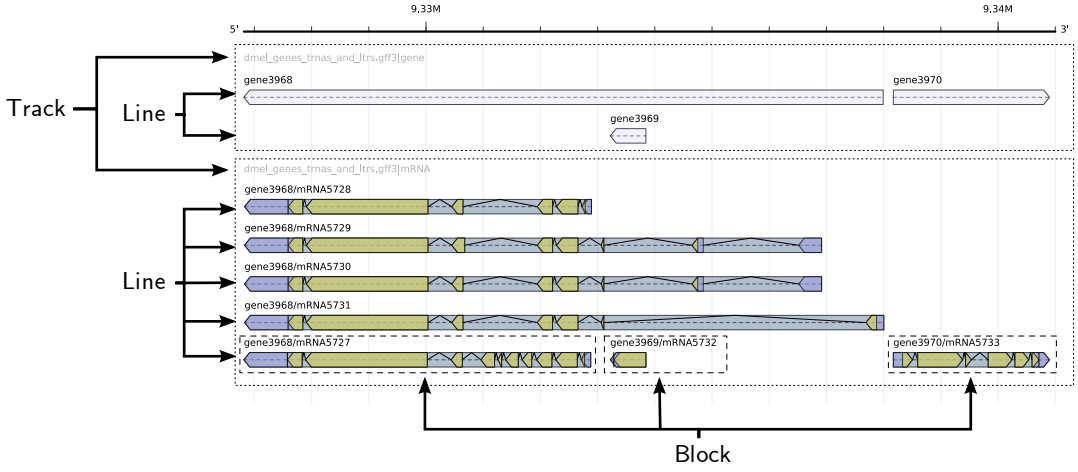


Figure 1.3: The components of the *Layout* class reflect sections of the resulting image.

ing the *Canvas* interface, whose methods are called during traversal of the *Layout* members. It encapsulates the state of a drawing and works independently of the chosen rendering back-end. Instead, rendering backend-dependent subclasses of *Canvas* are closely tied to a specific implementation of the *Graphics* interface, which provides methods to draw a number of primitives to a drawing surface abstraction. It wraps around the respective low-level graphics engine and allows for its easy extension or replacement. Currently, there is a *Graphics* implementation for the Cairo 2D graphics library (*GraphicsCairo*) and two *Canvas* subclasses providing access to the image file formats supported by Cairo (*CanvasCairoFile*) and to arbitrary Cairo contexts (*CanvasCairoContext*, which directly accesses a `cairo_t`). This class can be used, for example, to directly draw *AnnotationSketch* output in any graphical environment which is supported by Cairo (`http://www.cairographics.org/manual/cairo-surfaces.html`).

1.1.4 Collapsing

By default, *Lines* are grouped by the Sequence Ontology type associated with the top-level elements of their *Blocks*, resulting in one track per type. To obtain a shorter yet concise output,

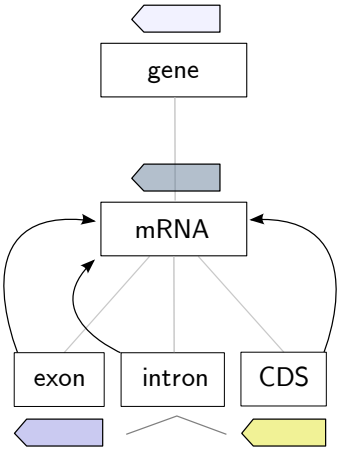


Figure 1.4: Schematic of the relationships between the *gene*, *mRNA*, *exon*, *intron* and *CDS* types and the colors of their representations in a diagram. The arrows illustrate how the relationships influence the collapsing process if collapsing is enabled for the *exon*, *intron* and *CDS* types. In this example, they will be drawn on top of their parent *mRNA* features.

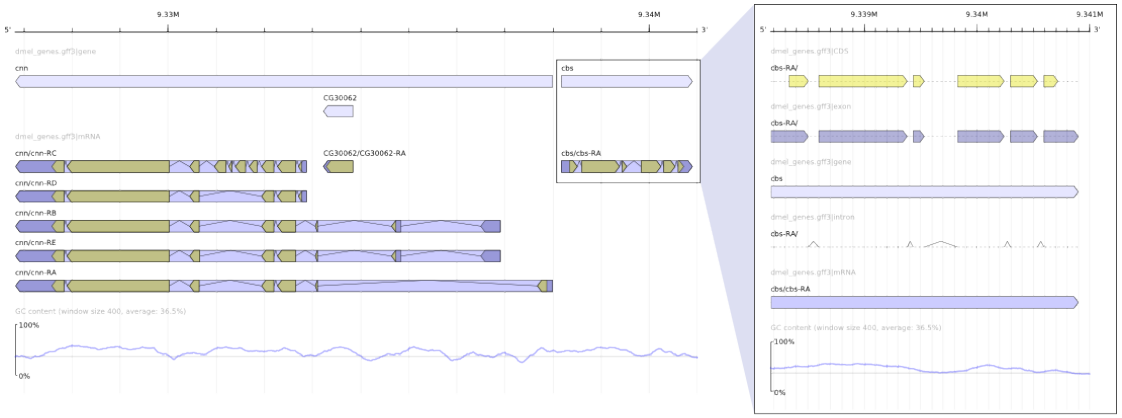
tracks for parent types in the feature graph can be enabled to contain all the features of their child types. The features with the given type are then drawn on top of their parent features (e.g. all *exon* and *intron* features are placed into their parent *mRNA* or *gene* track). This process is called *collapsing*. Collapsing can be enabled by setting the `collapse_to_parent` option for the respective child type to `true`, e.g. the following options:

```
config = {
  exon = {
    ...,
    collapse_to_parent = true,
    ...,
  },
  intron = {
    ...,
    collapse_to_parent = true,
    ...,
  },
  CDS = {
    ...,
    collapse_to_parent = true,
    ...,
  },
}
```

would lead to all features of the *exon*, *intron* and *CDS* types collapsing into the *mRNA* track (see Fig. 1.4 and 1.5).

1.1.5 Styles

The Lua scripting language is used to provide user-defined settings. Settings can be imported from a script that is executed when loaded, thus eliminating the need for another parser. The Lua configuration data are made accessible to C via the *Style* class. Configurable options in-



(a) collapsed view

(b) uncollapsed view

Figure 1.5: Example image of the *cnn* and *cbs* genes from *Drosophila melanogaster* (Ensembl release 51, positions 9326816–9341000 on chromosome arm 2R) as drawn by *AnnotationSketch*. At the bottom, the calculated GC content of the respective sequence is drawn via a custom track attached to the diagram. (a) shows a collapsed view in which all *exon*, *intron* and *CDS* types are collapsed into their parent type's track. In contrast, (b) shows the *cbs* gene with all collapsing options set to `false`, resulting in each type being drawn in its own track.

clude assignment of display styles to each feature type, spacer and margin sizes, and collapsing parameters.

Instead of giving direct values, callback Lua functions can be used in some options to generate feature-dependent configuration settings at run-time. During layout and/or rendering, the *GenomeNode* object for the feature to be rendered is passed to the callback function which can then be evaluated and the appropriate type can be returned.

For example, setting the following options in the style file (or via the Lua bindings):

```
config = {
  ...,
  mRNA = {
    block_caption       = function(gn)
                            rng = gn:get_range()
                            return string.format("%s/%s (%dbp, %d exons)",
                                  gn:get_attribute("Parent"),
                                  gn:get_attribute("ID"),
                                  rng:get_end() - rng:get_start() + 1,
                                  #(gn:get_exons()))
                          end,
    ...
  },

  exon = {
    -- Color definitions
    fill                = function(gn)
                            if gn:get_score() then
                              aval = gn:get_score()*1.0
                            else
                              aval = 0.0
                            end
                            return {red=1.0, green=0.0, blue=0.0, alpha=aval}
```

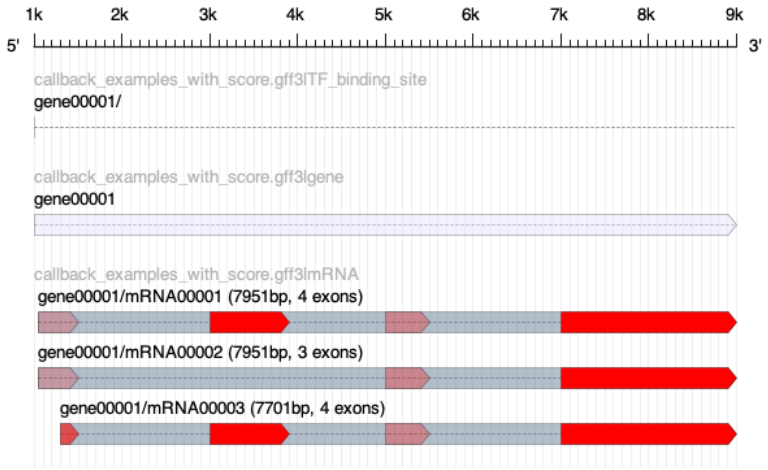


Figure 1.6: Example rendering using callback functions to enable custom block captions and score-dependent shading of exon features.

```
24                              end,
25       ...
26     },
27     ...
28   }
```

will result in a changed rendering (see Fig. 1.6). The `block_caption` function (line 4) overrides the default block naming scheme, allowing to set custom captions to each block depending on feature properties. Color definitions such as the `fill` setting (line 17) for a feature's fill color can also be individually styled using callbacks. In this case, the color intensity is shaded by the *exon* feature's score value (e.g. given in a GFF file).

1.2 The `gt sketch` tool

The *GenomeTools* `gt` executable provides a new tool which uses the *AnnotationSketch* library to create a drawing in PNG, PDF, PostScript or SVG format from GFF3 annotations. The annotations can be given by supplying one or more file names as command line arguments:

```
$ gt sketch output.png annotation.gff3
$
```

or by receiving GFF3 data via the standard input, here prepared by the `gt gff3` tool (here called with the `-addintrons` option to automatically add intron features between exons):

```
$ gt gff3 -addintrons annotation.gff3 | gt sketch output.png
$
```

The region to create a diagram for can be specified in detail by using the `-seqid`, `-start` and `-end` parameters. For example, if the *D. melanogaster* gene annotation is given in the `dmel_annotation.gff3` file, use

```
$ gt sketch -format pdf -seqid 2R -start 9326816 -end 9332879 output.pdf \
  dmel_annotation.gff3
$
```

to plot a graphical representation of the *cnn* and *cbs* gene region from the *FlyBase* default view in PDF format. The `-force` option can be used to force overwriting of an already existing output file. The `-pipe` option additionally allows passing the GFF3 input through the sketch tool via the standard output, allowing the intermediate visualisation of results in a longer pipeline of connected GFF3 tools. More command line options are available; their documentation can be viewed using the `-help` option.
If an input file is not plotted due to parsing errors, *GenomeTools* includes a strict GFF3 validator tool to check whether the input file is in valid GFF3 format. Simply run a command like the following:

```
$ gt gff3validator input_file.gff3
input is valid GFF3
$
```

This validator also allows one to check the SO types occurring in a GFF3 file against a given OBO ontology file. This checking can be enabled by specifying the file as an argument to the `-typecheck` option.
If the PDF, SVG and/or PostScript output format options are not available in the `gt` binary, the most likely cause is that PDF, SVG and/or PostScript support is disabled in your local *Cairo* headers and thus also not available in your local *Cairo* library. This issue is not directly related to *AnnotationSketch* and can be resolved by recompiling the *Cairo* library with the proper backend support enabled.

1.3 Dynamic track assignment

A special kind of function, called *track selector function*, can be used to customise the *AnnotationSketch* output by using arbitrary features of a block to assign blocks to tracks (and implicitly creating new tracks this way).

1.3.1 Default: Top level type decides track membership

By default, for each *Block* in a *Diagram*, its source filename and/or the type attribute of its top level element decides into which track the block is finally inserted during the layout phase. So by default, an annotation graph parsed from the GFF3 input file 'example.gff3' with *gene*, *mRNA* and *exon* type nodes will be rendered into two separate tracks (*exon→mRNA* collapsing enabled, see Fig. 1.7):

- `example.gff3|gene`, and
- `example.gff3|mRNA`.

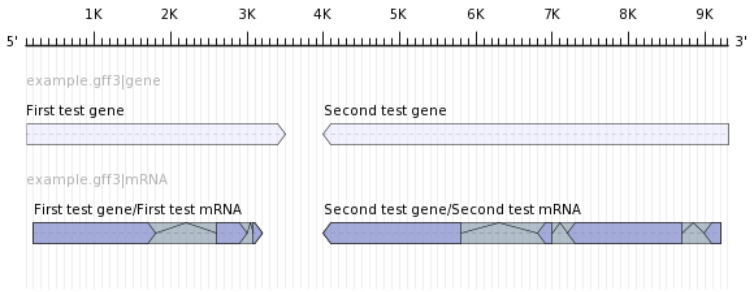


Figure 1.7: Default AnnotationSketch output for a simple GFF3 file with simple *exon→mRNA* collapsing.

We will call the second part (after the "|") of these track titles *track identifier strings* in the rest of this document.
While automatically determining tracks from the types actually present in the input annotations is convenient in many use cases, one could imagine cases in which more control about block handling may be desired. This leads to the question: How can one extract blocks with specific characteristics and assign them to a special track? The answer is simple: By overriding the default track identifier string, new tracks can be created and named on the fly as soon as a block satisfying user-defined rules is encountered.

1.3.2 Track selector functions

These rules take the form of *track selector functions*. Basically, a track selector function is a function which takes a block reference as an argument, and returns an appropriate track identifier string. For example, in Python the default track selector function would look like this:

```
def default_track_selector(block):
  return block.get_type()
```

This function simply returns a string representation of the type of a block's top level element, creating the tracks just like depicted in Fig. 1.7.
For a very simple example, let's assume that we want to create separate tracks for all mRNAs on the plus strand and for all mRNAs on the minus strand. The idea now is to change the strand identifier for blocks of the *mRNA* type to include the strand as additional information, thus creating different track identifiers for plus and minus strand features. In Python, this track selector function would construct a new string which contains both the type and the strand:

```
def strand_track_selector(block):
  if block.get_type() == "mRNA":
    return "%s (%s strand)" % (block.get_type(), block.get_strand())
  else:
    return block.get_type()
```

Using this track selector function would produce the desired result of separate tracks for the *mRNA* features for each strand (see Fig. 1.8).
A track selector function can be set for a *Diagram* object using the `diagram.set_track_selector_func()` method. In C, its argument is a pointer to a function of the signature

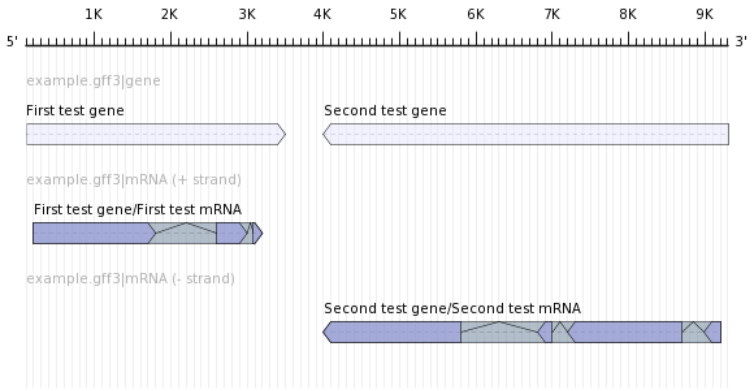


Figure 1.8: AnnotationSketch output with `strand_track_selector()` track selector function. This image now shows separate tracks for plus and minus strand features.

```
void (*GtTrackSelectorFunc)(GtBlock*, GtStr*, void*)
```

where arbitrary data can be passed via the third `void*` argument. The Python `set_track_selector_func()` method directly accepts a Python function as an argument, while the Ruby version takes a Proc object:

```
...
strand_track_selector = Proc.new { |block, data|
  "#{block.get_type} (#{block.get_strand} strand)"
}
...
diagram.set_track_selector_func(strand_track_selector)
...
```

Note that in Python and Ruby, it is also possible to reference data declared outside of the track selector function. For example, this can be used to filter blocks by pulling blocks whose description matches a pattern into a separate track:

```
...
interesting_genes = ["First test gene", "another gene"]

def filter_track_selector(block):
  if block.get_caption() in interesting_genes:
    return "interesting genes"
  else:
    return block.get_type()
...
diagram.set_track_selector_func(filter_track_selector)
...
```

This code results in the image shown in Fig. 1.9 :

1.4 Custom tracks

There are kinds of data which may be interesting to see together with annotation renderings, but that can not be expressed – or only in a complicated way – in GFF3 format. It may even be

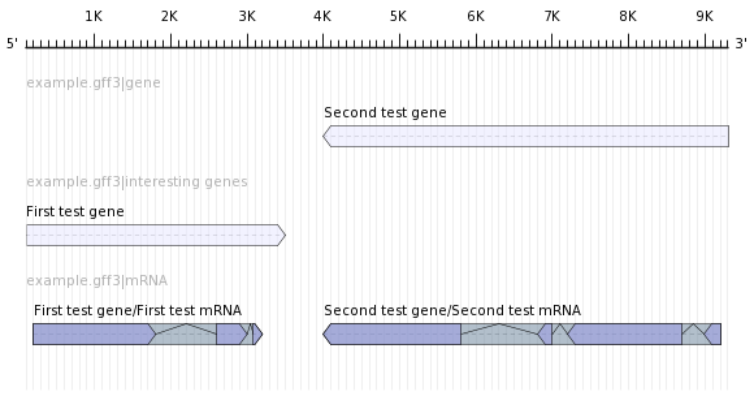


Figure 1.9: *AnnotationSketch* output with `filter_track_selector()` track selector function. This image now shows a separate track for features with a specific caption.

too difficult or counterintuitive to properly represent this data as typical *AnnotationSketch* box graphics. For example, this may be sequence data, numerical sequence analysis results, or other kinds of data which does not fit into the simple 'genomic feature' scheme. For an example, see Fig. 1.10.
With *custom tracks*, *AnnotationSketch* provides a mechanism to use the internal drawing functionality to create user-defined output which can be tailored to fit this kind of data. A custom track looks just like a normal *AnnotationSketch* track, but is completely in control of the developer. While native *AnnotationSketch* primitives such as boxes can of course be used, the author of a custom track is not restricted to the layout algorithm and can draw anything anywhere (as long as it is provided by the *Graphics* class), taking arbitrary external data into account.

1.4.1 Anatomy of a custom track class

Simply put, custom tracks are classes which are derived from a *CustomTrack* base class and must implement a set of mandatory methods:

- `get_height()`: Returns the amount of vertical space (in pixels or points) the custom track will occupy in the final image. Must return a numeric value.
- `get_title()`: Returns a title for the custom track which is displayed at the top of the track. Note that, unlike a track identifier string e.g. produced by a track selector function, the string returned by this function is not prepended by a file name.
- `render(graphics, ypos, range, style, error)`: Performs the actual rendering operations. As parameters, this function receives
  - a *Graphics* object to draw on,
  - the vertical offset *ypos* of the drawing area assigned to the custom track,
  - the *Range* of the sequence positions for which annotations are currently displayed,

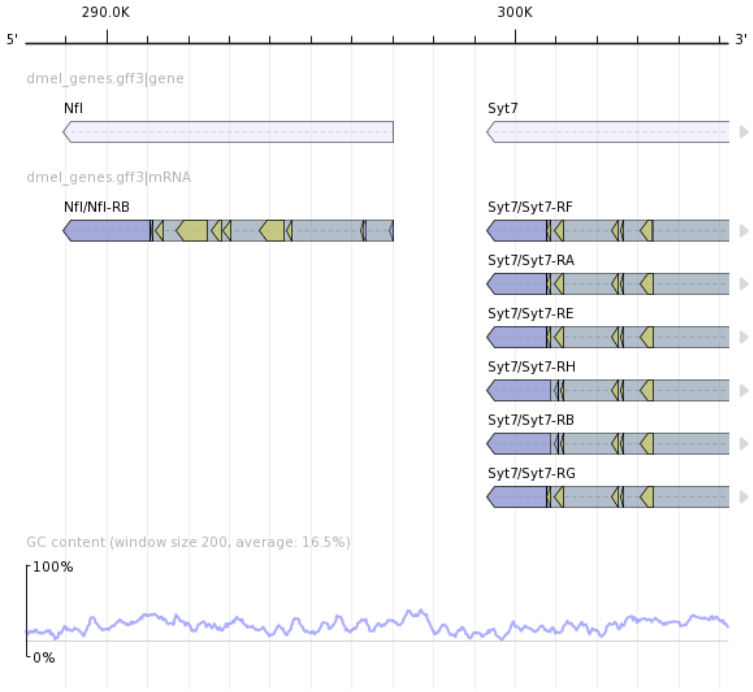


Figure 1.10: Example *AnnotationSketch* output with a custom track at the bottom, displaying the GC content over a window size of 200 bp.

- a *Style* object which can be used to obtain style information specific to this custom track, and
- an *Error* object which can be used to return an error message if the custom track needs to signal a problem.

The `render()` method must return 0 if drawing was successful, or a negative value if an error occurred.
Optionally, a `free()` method can be implemented if the subclass needs to clean up any private space allocated by itself. These methods are then called by the rendering code in AnnotationSketch when a Diagram containing a custom track is laid out and rendered. No other constraints apply on such a class besides that these methods are implemented (in the scripting language bindings, the parent classes' constructor must be called once).

1.4.2 Writing an example custom track

Let's suppose we are not satisfied with the display of single base features, such as transposable element insertion sites or SNPs. Instead of a single line denoting the feature location, we would like to have a small triangle pointing at the location. Suppose we also do not have this data in an annotation graph, so we cannot use the built-in rendering functions. It is straightforward to write

a small custom track class which does this for us. This tutorial uses Python code for simplicity, but the general approach is common to all supported languages.
First, we need to define a class inheriting from CustomTrack, call the parent constructor to register the functions and set instance variables for the triangle sidelength and a dictionary containing the feature positions and a description:

```
class CustomTrackInsertions(CustomTrack):
  def __init__(self, sidelength, data):
    super(CustomTrackInsertions, self).__init__()
    self.sidelength = sidelength
    self.data = data
```

We define the height to be 20 pixels:

```
  def get_height(self):
    return 20
```

As a track title, we set “Insertion site”:

```
  def get_title(self):
    return "Insertion site"
```

The rendering code then calculates the triangle coordinates and draws the respective lines:

```
  def render(self, graphics, ypos, rng, style, error):
    height = (self.sidelength*math.sqrt(3))/2
    margins = graphics.get_xmargins()
    red = Color(1, 0, 0, 0.7)
    for pos, desc in self.data.iteritems():
      drawpos = margins + (float(pos)-rng.start)/(rng.end-rng.start+1)          \
                * (graphics.get_image_width()-2*margins)
      graphics.draw_line(drawpos-self.sidelength/2, ypos + height,              \
                         drawpos, ypos,                                         \
                         red, 1)
      graphics.draw_line(drawpos, ypos,                                         \
                         drawpos+self.sidelength/2, ypos + height,              \
                         red, 1)
      graphics.draw_line(drawpos-self.sidelength/2, ypos + height,              \
                         drawpos+self.sidelength/2, ypos + height,              \
                         red, 1)
      graphics.draw_text_centered(drawpos, ypos + height + 13, str(desc))
    return 0
```

For a Python custom track, that’s it! No more code is necessary for this very simple custom track. We can now instantiate this class and attach the instance to a *Diagram* object:

```
...
diagram = Diagram(feature_index, seqid, range, style)
...
ctt = CustomTrackInsertions(15, {2000:"foo", 4400:"bar", 8000:"baz"})
diagram.add_custom_track(ctt)
...
```

Running layout and drawing functions on this diagram then produces the desired image (see Fig. 1.11

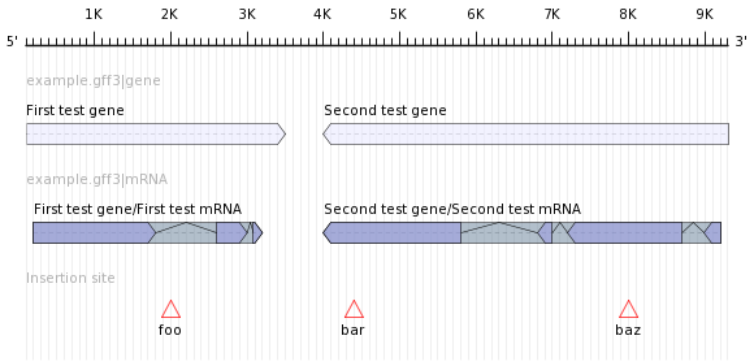


Figure 1.11: The example insertion site custom track (at the bottom), displaying three sample data points.

1.5 Examples

This section will show how to use the *AnnotationSketch* library in custom applications. As *AnnotationSketch* is distributed as a part of *GenomeTools*, its code is compiled into the `libgenometools.so` shared library. Please refer to the INSTALL file inside the *GenomeTools* distribution for installation instructions.
For a general idea about how to use the library, a simple implementation of the GFF3 validator is included in the source package (see `src/examples/gff3validator.c`) as an example showing how to create *GenomeTools*-based programs. In the same directory, there is also an appropriate `Makefile` to build and link this application against the installed shared library `libgenometools.so`.

1.5.1 Using AnnotationSketch to draw annotations from a file

The following code examples (in C and Lua) illustrate how to produce an image from a given GFF3 file using *AnnotationSketch*. The result is shown in Fig. 1.12. In essence, these code examples implement something like a simple version of the `gt sketch` tool from *GenomeTools* without most command-line options. The C-based examples mentioned below are compiled along with the *GenomeTools* library itself and available in the `bin/examples` directory.

C code

(See `src/examples/sketch_parsed.c` in the source distribution.)

```
1  #include "genometools.h"
2
3  static void handle_error(GtError *err)
4  {
5    fprintf(stderr, "error: %s\n", gt_error_get(err));
6    exit(EXIT_FAILURE);
7  }
8
9  int main(int argc, char *argv[])
10 {
```

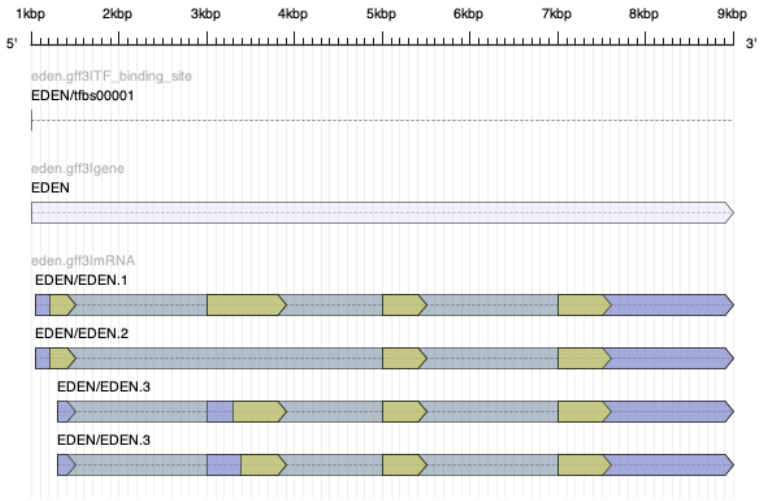


Figure 1.12: Example rendering of a GFF3 file with default style.

```
11  const char *style_file, *png_file, *gff3_file;
12  char *seqid;
13  GtStyle *style;
14  GtFeatureIndex *feature_index;
15  GtRange range;
16  GtDiagram *diagram;
17  GtLayout *layout;
18  GtCanvas *canvas;
19  GtUword height;
20  GtError *err;

22  if (argc != 4) {
23    fprintf(stderr, "Usage: %s style_file PNG_file GFF3_file\n", argv[0]);
24    return EXIT_FAILURE;
25  }

27  style_file = argv[1];
28  png_file = argv[2];
29  gff3_file = argv[3];

31  /* initialize */
32  gt_lib_init();

34  /* create error object */
35  err = gt_error_new();

37  /* create style */
38  if (!(style = gt_style_new(err)))
39    handle_error(err);

41  /* load style file */
42  if (gt_style_load_file(style, style_file, err))
43    handle_error(err);

45  /* create feature index */
46  feature_index = gt_feature_index_memory_new();
```

```
  /* add GFF3 file to index */
  if (gt_feature_index_add_gff3file(feature_index, gff3_file, err))
    handle_error(err);

  /* create diagram for first sequence ID in feature index */
  if (!(seqid = gt_feature_index_get_first_seqid(feature_index, err))) {
    if (gt_error_is_set(err))
      handle_error(err);
  }
  if (gt_feature_index_get_range_for_seqid(feature_index, &range, seqid, err))
    handle_error(err);
  diagram = gt_diagram_new(feature_index, seqid, &range, style, err);
  gt_free(seqid);
  if (gt_error_is_set(err))
    handle_error(err);

  /* create layout with given width, determine resulting image height */
  layout = gt_layout_new(diagram, 600, style, err);
  if (!layout)
    handle_error(err);
  if (gt_layout_get_height(layout, &height, err))
    handle_error(err);

  /* create PNG canvas */
  canvas = gt_canvas_cairo_file_new(style, GT_GRAPHICS_PNG, 600, height,
                                    NULL, err);
  if (!canvas)
    handle_error(err);

  /* sketch layout on canvas */
  if (gt_layout_sketch(layout, canvas, err))
    handle_error(err);

  /* write canvas to file */
  if (gt_canvas_cairo_file_to_file((GtCanvasCairoFile*) canvas, png_file, err))
    handle_error(err);

  /* free */
  gt_canvas_delete(canvas);
  gt_layout_delete(layout);
  gt_diagram_delete(diagram);
  gt_feature_index_delete(feature_index);
  gt_style_delete(style);
  gt_error_delete(err);
  /* perform static data cleanup */
  gt_lib_clean();
  return EXIT_SUCCESS;
}
```

Lua code

(See `gtscripts/sketch_parsed.lua` in the source distribution. This example can be run by the command line `gt gtscripts/sketch_parsed.lua <style_file> <PNG_file> <GFF3_file>`)

```
function usage()
  io.stderr:write(string.format("Usage: %s Style_file PNG_file GFF3_file\n",
      arg[0]))
  io.stderr:write("Create PNG representation of GFF3 annotation file.\n")
  os.exit(1)
end
```

```
if #arg == 3 then
  style_file = arg[1]
  png_file   = arg[2]
  gff3_file  = arg[3]
else
  usage()
end

-- load style file
dofile(style_file)

-- create feature index
feature_index = gt.feature_index_memory_new()

-- add GFF3 file to index
feature_index:add_gff3file(gff3_file)

-- create diagram for first sequence ID in feature index
seqid = feature_index:get_first_seqid()
range = feature_index:get_range_for_seqid(seqid)
diagram = gt.diagram_new(feature_index, seqid, range)

-- create layout
layout = gt.layout_new(diagram, 600)
height = layout:get_height()

-- create canvas
canvas = gt.canvas_cairo_file_new_png(600, height, nil)

-- sketch layout on canvas
layout:sketch(canvas)

-- write canvas to file
canvas:to_file(png_file)
```

Ruby code

(See `gtruby/sketch_parsed.rb` in the source distribution.)

```
require 'gtruby'

if ARGV.size != 3 then
  STDERR.puts "Usage: #{$0} style_file PNG_file GFF3_file"
  STDERR.puts "Create PNG representation of GFF3 annotation file."
  exit(1)
end

(stylefile, pngfile, gff3file) = ARGV

# load style file
style = GT::Style.new()
style.load_file(stylefile)

# create feature index
feature_index = GT::FeatureIndexMemory.new()

# add GFF3 file to index
feature_index.add_gff3file(gff3file)
```

```
# create diagram for first sequence ID in feature index
seqid = feature_index.get_first_seqid()
range = feature_index.get_range_for_seqid(seqid)
diagram = GT::Diagram.from_index(feature_index, seqid, range, style)

# create layout for given width
layout = GT::Layout.new(diagram, 800, style)

# create canvas with given width and computed height
canvas = GT::CanvasCairoFile.new(style, 800, layout.get_height, nil)

# sketch layout on canvas
layout.sketch(canvas)

# write canvas to file
canvas.to_file(pngfile)
```

Python code

(See gtpython/sketch_parsed.py in the source distribution.)

```
#!/usr/bin/python
# -*- coding: utf-8 -*-

from gt.annotationsketch import *
from gt.core.gtrange import Range
import sys

if __name__ == "__main__":
    if len(sys.argv) != 4:
        sys.stderr.write("Usage: " + (sys.argv)[0] +
                         " Style_file PNG_file GFF3_file\n")
        sys.stderr.write("Create PNG representation of GFF3 annotation file.")
        sys.exit(1)

    pngfile = (sys.argv)[2]

  # load style file

    style = Style()
    style.load_file((sys.argv)[1])

  # create feature index

    feature_index = FeatureIndexMemory()

  # add GFF3 file to index

    feature_index.add_gff3file((sys.argv)[3])

  # create diagram for first sequence ID in feature index

    seqid = feature_index.get_first_seqid()
    range = feature_index.get_range_for_seqid(seqid)
    diagram = Diagram.from_index(feature_index, seqid, range, style)

  # create layout

    layout = Layout(diagram, 600, style)
    height = layout.get_height()
```

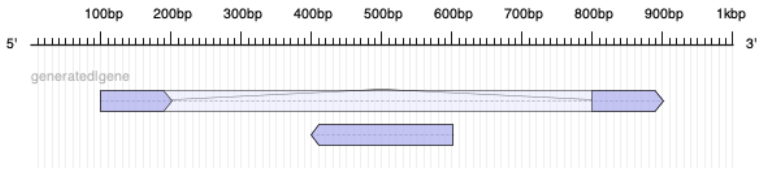


Figure 1.13: Example rendering of user-generated annotations with default style.

```
41    # create canvas

43      canvas = CanvasCairoFile(style, 600, height)

45    # sketch layout on canvas

47      layout.sketch(canvas)

49    # write canvas to file

51      canvas.to_file(pngfile)
```

1.5.2 Using AnnotationSketch to draw user-generated annotations

The following C code example illustrates how to produce an image from annotation graphs created by user code. The result is shown in Fig. 1.13.

C code

(See `src/examples/sketch_constructed.c` in the source distribution.)

```
1   #include "genometools.h"

3   static GtArray* create_example_features(void)
4   {
5     GtArray *features;
6     GtGenomeNode *gene, *exon, *intron; /* features */
7     GtStr *seqid; /* holds the sequence id the features refer to */

9     /* construct the example features */
10    features = gt_array_new(sizeof (GtGenomeNode*));
11    seqid = gt_str_new_cstr("chromosome_21");

13    /* construct a gene on the forward strand with two exons */
14    gene = gt_feature_node_new(seqid, "gene", 100, 900, GT_STRAND_FORWARD);
15    exon = gt_feature_node_new(seqid, "exon", 100, 200, GT_STRAND_FORWARD);
16    gt_feature_node_add_child((GtFeatureNode*) gene, (GtFeatureNode*) exon);
17    intron = gt_feature_node_new(seqid, "intron", 201, 799, GT_STRAND_FORWARD);
18    gt_feature_node_add_child((GtFeatureNode*) gene, (GtFeatureNode*) intron);
19    exon = gt_feature_node_new(seqid, "exon", 800, 900, GT_STRAND_FORWARD);
20    gt_feature_node_add_child((GtFeatureNode*) gene, (GtFeatureNode*) exon);

22    /* store forward gene in feature array */
23    gt_array_add(features, gene);
```

```
25    /* construct a single-exon gene on the reverse strand
26       (within the intron of the forward strand gene) */
27    gene = gt_feature_node_new(seqid, "gene", 400, 600, GT_STRAND_REVERSE);
28    exon = gt_feature_node_new(seqid, "exon", 400, 600, GT_STRAND_REVERSE);
29    gt_feature_node_add_child((GtFeatureNode*) gene, (GtFeatureNode*) exon);

31    /* store reverse gene in feature array */
32    gt_array_add(features, gene);

34    /* free */
35    gt_str_delete(seqid);

37    return features;
38  }

40  static void handle_error(GtError *err)
41  {
42    fprintf(stderr, "error writing canvas %s\n", gt_error_get(err));
43    exit(EXIT_FAILURE);
44  }

46  static void draw_example_features(GtArray *features, const char *style_file,
47                                    const char *output_file)
48  {
49    GtRange range = { 1, 1000 }; /* the genomic range to draw */
50    GtStyle *style;
51    GtDiagram *diagram;
52    GtLayout *layout;
53    GtCanvas *canvas;
54    GtUword height;
55    GtError *err = gt_error_new();

57    /* create style */
58    if (!(style = gt_style_new(err)))
59      handle_error(err);

61    /* load style file */
62    if (gt_style_load_file(style, style_file, err))
63      handle_error(err);

65    /* create diagram */
66    diagram = gt_diagram_new_from_array(features, &range, style);

68    /* create layout with given width, determine resulting image height */
69    layout = gt_layout_new(diagram, 600, style, err);
70    if (!layout)
71      handle_error(err);
72    if (gt_layout_get_height(layout, &height, err))
73      handle_error(err);

75    /* create PNG canvas */
76    canvas = gt_canvas_cairo_file_new(style, GT_GRAPHICS_PNG, 600, height,
77                                      NULL, err);
78    if (!canvas)
79      handle_error(err);

81    /* sketch layout on canvas */
82    if (gt_layout_sketch(layout, canvas, err))
83      handle_error(err);

85    /* write canvas to file */
86    if (gt_canvas_cairo_file_to_file((GtCanvasCairoFile*) canvas, output_file,
```

```
                                    err)) {
    handle_error(err);
  }

  /* free */
  gt_canvas_delete(canvas);
  gt_layout_delete(layout);
  gt_diagram_delete(diagram);
  gt_style_delete(style);
  gt_error_delete(err);
}

static void delete_example_features(GtArray *features)
{
  GtUword i;
  for (i = 0; i < gt_array_size(features); i++)
    gt_genome_node_delete(*(GtGenomeNode**) gt_array_get(features, i));
  gt_array_delete(features);
}

int main(int argc, char *argv[])
{
  GtArray *features; /* stores the created example features */

  if (argc != 3) {
    fprintf(stderr, "Usage: %s style_file output_file\n", argv[0]);
    return EXIT_FAILURE;
  }

  gt_lib_init();

  features = create_example_features();

  draw_example_features(features, argv[1], argv[2]);

  delete_example_features(features);

  gt_lib_clean();
  return EXIT_SUCCESS;
}
```

Lua code

(See gtscripts/sketch_constructed.lua in the source distribution. This example can be run by the command line gt gtscripts/sketch_constructed.lua <style_file> <PNG_file>)

```
function usage()
  io.stderr:write(string.format("Usage: %s Style_file PNG_file\n", arg[0]))
  os.exit(1)
end

if #arg == 2 then
  style_file = arg[1]
  png_file   = arg[2]
else
  usage()
end

-- load style file
dofile(style_file)
```

```
-- construct the example features
seqid = "chromosome_21"
nodes = {}

-- construct a gene on the forward strand with two exons
gene   = gt.feature_node_new(seqid, "gene", 100, 900, "+")
exon   = gt.feature_node_new(seqid, "exon", 100, 200, "+")
gene:add_child(exon)
intron = gt.feature_node_new(seqid, "intron", 201, 799, "+")
gene:add_child(intron)
exon   = gt.feature_node_new(seqid, "exon", 800, 900, "+")
gene:add_child(exon)
nodes[1] = gene

-- construct a single-exon gene on the reverse strand
-- (within the intron of the forward strand gene)
reverse_gene = gt.feature_node_new(seqid, "gene", 400, 600, "-")
reverse_exon = gt.feature_node_new(seqid, "exon", 400, 600, "-")
reverse_gene:add_child(reverse_exon)
nodes[2] = reverse_gene

-- create diagram
diagram = gt.diagram_new_from_array(nodes, 1, 1000)
layout = gt.layout_new(diagram, 600)
height = layout:get_height()

-- create canvas
canvas = gt.canvas_cairo_file_new_png(600, height, nil)

-- sketch layout on canvas
layout:sketch(canvas)

-- write canvas to file
canvas:to_file(png_file)
```

Ruby code

(See `gtruby/sketch_constructed.rb` in the source distribution.)

```
require 'gtruby'

if ARGV.size != 2 then
  STDERR.puts "Usage: #{$0} style_file PNG_file"
  exit(1)
end

seqid = "chromosome_21"

# construct a gene on the forward strand with two exons
gene   = GT::FeatureNode.create(seqid, "gene", 100, 900, "+")
exon   = GT::FeatureNode.create(seqid, "exon", 100, 200, "+")
gene.add_child(exon)
intron = GT::FeatureNode.create(seqid, "intron", 201, 799, "+")
gene.add_child(intron)
exon   = GT::FeatureNode.create(seqid, "exon", 800, 900, "+")
gene.add_child(exon)

# construct a single-exon gene on the reverse strand
# (within the intron of the forward strand gene)
```

```
reverse_gene = GT::FeatureNode.create(seqid, "gene", 400, 600, "-")
reverse_exon = GT::FeatureNode.create(seqid, "exon", 400, 600, "-")
reverse_gene.add_child(reverse_exon)

pngfile = ARGV[1]

style = GT::Style.new()
style.load_file(ARGV[0])

rng = GT::Range.new(1, 1000)

diagram = GT::Diagram.from_array([gene, reverse_gene], rng, style)

layout = GT::Layout.new(diagram, 600, style)
canvas = GT::CanvasCairoFile.new(style, 600, layout.get_height, nil)
layout.sketch(canvas)

canvas.to_file(pngfile)
```

Python code

(See gtpython/sketch_constructed.py in the source distribution.)

```
#!/usr/bin/python
# -*- coding: utf-8 -*-

from gt.core import *
from gt.extended import *
from gt.annotationsketch import *
from gt.annotationsketch.custom_track import CustomTrack
from gt.core.gtrange import Range
import sys

if __name__ == "__main__":
    if len(sys.argv) != 3:
        sys.stderr.write("Usage: " + (sys.argv)[0] +
                         " style_file PNG_file\n")
        sys.exit(1)

    seqid = "chromosome_21"
    nodes = []

  # construct a gene on the forward strand with two exons

    gene = FeatureNode.create_new(seqid, "gene", 100, 900, "+")
    exon = FeatureNode.create_new(seqid, "exon", 100, 200, "+")
    gene.add_child(exon)
    intron = FeatureNode.create_new(seqid, "intron", 201, 799, "+")
    gene.add_child(intron)
    exon = FeatureNode.create_new(seqid, "exon", 800, 900, "+")
    gene.add_child(exon)

  # construct a single-exon gene on the reverse strand
  # (within the intron of the forward strand gene)

    reverse_gene = FeatureNode.create_new(seqid, "gene", 400, 600, "-")
    reverse_exon = FeatureNode.create_new(seqid, "exon", 400, 600, "-")
    reverse_gene.add_child(reverse_exon)

    pngfile = (sys.argv)[2]
```

```
39      style = Style()
40      style.load_file((sys.argv)[1])
41
42      diagram = Diagram.from_array([gene, reverse_gene], Range(1, 1000),
43                                   style)
44
45      layout = Layout(diagram, 600, style)
46      height = layout.get_height()
47      canvas = CanvasCairoFile(style, 600, height)
48      layout.sketch(canvas)
49
50      canvas.to_file(pngfile)
```

API Reference

Table of Classes

Table of Modules

Sole functions

```
const char* GtGetSeqFunc(
                          void *seqs,
                          GtUword index)
```

Function used to retrieve a cleartext sequence for an index number.

```
GtUword GtGetSeqLenFunc(
                         void *seqs,
                         GtUword index)
```

Function used to retrieve a sequence length for an index number.

```
GtFile* gt_output_file_xopen_forcecheck(
          const char *path,
          const char *mode,
          bool force,
          GtError *err)
```

Helper function for (rare) tools which do not use the full GtOutputFileInfo (usually if directories are involved).

```
int gt_feature_index_gfflike_get_all_features(
      GtFeatureIndex *gfi,
      GtArray *results,
      GtError *err)
```

Retrieves all features contained in gfi into results. Returns 0 on success, a negative value otherwise. The message in err is set accordingly.

```
GtNodeStream* gt_dup_feature_stream_new(
                GtNodeStream*,
                const char *dest_type,
                const char *source_type)
```

Duplicate internal feature nodes of type source_type as features with type dest_type. The duplicated features does not inherit the children.

```
void GtTrackSelectorFunc(
                          GtBlock*,
                          GtStr*,
                          void*)
```

A `GtTrackSelectorFunc` is a callback function which sets a `GtStr` to a string to be used as a track identifier for assignment of a `GtBlock` to a given track.

```
int GtTrackOrderingFunc(
                         const char *s1,
                         const char *s2,
                         void *data)
```

A function describing the order of tracks based on their track identifier strings <s1> and <s2>. Must return a negative value if the track with ID <s1> should appear before the track with ID <s2> and a positive value if <s1> should appear after <s2>. Returning a value of 0 will result in an undefined ordering of <s1> and <s2>.

Class GtAddIntronsStream

Implements the `GtNodeStream` interface. A `GtAddIntronsStream` inserts new feature nodes with type *intron* between existing feature nodes with type *exon*. This is a special case of the `GtInterFeatureStream`.

Methods

```
GtNodeStream* gt_add_introns_stream_new(
                GtNodeStream *in_stream)
```

Create a `GtAddIntronsStream*` which inserts feature nodes of type *intron* between feature nodes of type *exon* it retrieves from `in_stream` and returns them.

Class GtAlphabet

The following type is for storing alphabets.

Methods

```
GtAlphabet* gt_alphabet_new_dna(
              void)
```

Return a `GtAlphabet` object which represents a DNA alphabet.

```
GtAlphabet* gt_alphabet_new_protein(
              void)
```

Return a `GtAlphabet` object which represents a protein alphabet.

```
GtAlphabet* gt_alphabet_new_empty(
              void)
```

Return an empty GtAlphabet object.

```
GtAlphabet* gt_alphabet_new_from_file(
              const char *filename,
              GtError *err)
```

Return a GtAlphabet object, as read from an .al1 file specified by filename (i.e. no al1 suffix necessary).

```
GtAlphabet* gt_alphabet_new_from_file_no_suffix(
              const char *filename,
              GtError *err)
```

Return a GtAlphabet object, as read from a file specified by filename.

```
GtAlphabet* gt_alphabet_new_from_string(
              const char *alphadef,
              GtUword len,
              GtError *err)
```

Return a GtAlphabet object, as read from a string of length len specified by alphadef.

```
GtAlphabet* gt_alphabet_new_from_sequence(
              const GtStrArray *filenametab,
              GtError *err)
```

Returns a new GtAlphabet object by scanning the sequence files in filenametab to determine whether they are DNA or protein sequences, and the appropriate alphabet will be used (see gt_alphabet_guess()). Returns NULL on error, see err for details.

```
GtAlphabet* gt_alphabet_guess(
              const char *sequence,
              GtUword seqlen)
```

Try to guess which type the given sequence with length has (DNA or protein) and return an according GtAlphabet* object.

```
GtAlphabet* gt_alphabet_clone(
              const GtAlphabet *alphabet)
```

Return a clone of alphabet.

```
bool gt_alphabet_equals(
       const GtAlphabet *a,
       const GtAlphabet *b)
```

Returns TRUE if a and b are equal (i.e. have the same symbol mapping), FALSE otherwise.

```
GtAlphabet* gt_alphabet_ref(
              GtAlphabet *alphabet)
```

Increase the reference count for `alphabet` and return it.

```
void gt_alphabet_add_mapping(
       GtAlphabet *alphabet,
       const char *characters)
```

Add the mapping of all given `characters` to the given `alphabet`. The first character is the result of subsequent `gt_alphabet_decode()` calls.

```
void gt_alphabet_add_wildcard(
       GtAlphabet *alphabet,
       char wildcard)
```

Add `wildcard` to the `alphabet`.

```
const GtUchar* gt_alphabet_symbolmap(
                 const GtAlphabet *alphabet)
```

Returns the array of symbols from `alphabet` such that the index of the character equals its encoding.

```
unsigned int gt_alphabet_num_of_chars(
               const GtAlphabet *alphabet)
```

Returns number of characters in `alphabet` (excluding wildcards).

```
unsigned int gt_alphabet_size(
               const GtAlphabet *alphabet)
```

Returns number of characters in `alphabet` (including wildcards).

```
const GtUchar* gt_alphabet_characters(
                 const GtAlphabet *alphabet)
```

Returns an array of the characters in `alphabet`.

```
GtUchar gt_alphabet_wildcard_show(
          const GtAlphabet *alphabet)
```

Returns the character used in `alphabet` to represent wildcards in output.

```
unsigned int gt_alphabet_bits_per_symbol(
               const GtAlphabet *alphabet)
```

Returns the required number of bits required to represent a symbol in `alphabet`.

```
void gt_alphabet_output(
       const GtAlphabet *alphabet,
       FILE *fpout)
```

Writes a representation of `alphabet` to the file pointer `fpout`.

```
int gt_alphabet_to_file(
      const GtAlphabet *alphabet,
      const char *indexname,
      GtError *err)
```

Writes a representation of `alphabet` to the .al1 output file as specified by `indexname` (i.e. without the .al1 suffix).

```
void gt_alphabet_to_str(
       const GtAlphabet *alphabet,
       GtStr *dest)
```

Writes a representation of `alphabet` to the `GtStr` as specified by `dest`.

```
GtUchar gt_alphabet_pretty_symbol(
          const GtAlphabet *alphabet,
          unsigned int currentchar)
```

Returns the printable character specified in `alphabet` for `currentchar`.

```
void gt_alphabet_echo_pretty_symbol(
       const GtAlphabet *alphabet,
       FILE *fpout,
       GtUchar currentchar)
```

Prints the printable character specified in `alphabet` for `currentchar` on `fpout`.

```
bool gt_alphabet_is_protein(
       const GtAlphabet *alphabet)
```

The following method checks if the given `alphabet` is the protein alphabet with the aminoacids A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y written in lower or upper case and returns `true`, if this is the case (`false` otherwise).

```
bool gt_alphabet_is_dna(
       const GtAlphabet *alphabet)
```

The following method checks if the given alphabet is the DNA alphabet with the bases A, C, G, T written in lower or upper case and returns `true`, if this is the case (`false` otherwise).

```
bool gt_alphabet_valid_input(
       const GtAlphabet *alphabet,
       char c)
```

Returns true if the character `c` is defined in `alphabet`.

```
GtUchar gt_alphabet_encode(
          const GtAlphabet *alphabet,
          char c)
```

Encode character `c` with given `alphabet`. Ensure that `c` is encodable with the given `alphabet`!

```
char gt_alphabet_decode(
       const GtAlphabet *alphabet,
       GtUchar c)
```

Decode character `c` with given `alphabet`.

```
void gt_alphabet_encode_seq(
       const GtAlphabet *alphabet,
       GtUchar *out,
       const char *in,
       GtUword length)
```

Encode sequence `in` of given `length` with `alphabet` and store the result in `out`. `in` has to be encodable with the given `alphabet`!

```
void gt_alphabet_decode_seq_to_fp(
       const GtAlphabet *alphabet,
       FILE *fpout,
       const GtUchar *src,
       GtUword len)
```

Suppose the string `src` of length `len` was transformed according to the `alphabet`. The following method shows each character in `src` as the printable character specified in the transformation. The output is written to the given file pointer `fpout`.

```
void gt_alphabet_decode_seq_to_cstr(
       const GtAlphabet *alphabet,
       char *dest,
       const GtUchar *src,
       GtUword len)
```

Suppose the string `src` of length `len` was transformed according to the `alphabet`. The following method shows each character in `src` as the printable character specified in the transformation. The output is written to the given string `dest` and terminated with '\0' at dest[len]. `dest` therefore has to be of at least `len` + 1 length.

```
GtStr* gt_alphabet_decode_seq_to_str(
         const GtAlphabet *alphabet,
         const GtUchar *src,
         GtUword len)
```

Analog to `gt_alphabet_decode_seq_to_fp()` writing the output to a new `GtStr`.

```
void gt_alphabet_delete(
       GtAlphabet *alphabet)
```

Decrease the reference count for `alphabet` or delete it, if this was the last reference.

Class GtAnnoDBGFFlike

The `GtAnnoDBGFFlike` class implements the `GtAnnoDBSchema` interface, using a database schema specifically tailored to store *GenomeTools* annotations.

Methods

```
GtAnnoDBSchema* gt_anno_db_gfflike_new(
                  void)
```

Creates a new `GtAnnoDBGFFlike` schema object.

Class GtAnnoDBSchema

The `GtAnnoDBSchema` interface for a database-backed abstract `GtFeatureIndex` factory.

Methods

```
GtFeatureIndex* gt_anno_db_schema_get_feature_index(
                  GtAnnoDBSchema *schema,
                  GtRDB *db,
                  GtError *err)
```

Returns a `GtFeatureIndex` object representing `GtRDB` object `db` interpreted as having schema `schema`. Returns NULL if an error occurred, `err` is set accordingly.

```
void gt_anno_db_schema_delete(
       GtAnnoDBSchema *schema)
```

Deletes `schema` and frees all associated memory.

Class GtArray

`GtArray` objects are generic arrays for elements of a certain size which grow on demand.

Methods

```
GtArray* gt_array_new(
           size_t size_of_elem)
```

Return a new GtArray object whose elements have the size size_of_elem.

```
GtArray* gt_array_ref(
           GtArray *array)
```

Increase the reference count for array and return it. If array is NULL, NULL is returned without any side effects.

```
GtArray* gt_array_clone(
           const GtArray *array)
```

Return a clone of array.

```
void* gt_array_get(
        const GtArray *array,
        GtUword index)
```

Return pointer to element number index of array. index has to be smaller than gt_array_size(array).

```
void* gt_array_get_first(
        const GtArray *array)
```

Return pointer to first element of array.

```
void* gt_array_get_last(
        const GtArray *array)
```

Return pointer to last element of array.

```
void* gt_array_pop(
        GtArray *array)
```

Return pointer to last element of array and remove it from array.

```
void* gt_array_get_space(
        const GtArray *array)
```

Return pointer to the internal space of array where the elements are stored.

```
#define gt_array_add(
          array,
          elem)
```

Add element elem to array. The size of elem must equal the given element size when the array was created and is determined automatically with the sizeof operator.

```
void gt_array_add_elem(
       GtArray *array,
       void *elem,
       size_t size_of_elem)
```

Add element `elem` with size `size_of_elem` to `array`. `size_of_elem` must equal the given element size when the `array` was created. Usually, this method is not used directly and the macro `gt_array_add()` is used instead.

```
void gt_array_add_array(
       GtArray *dest,
       const GtArray *src)
```

Add all elements of array `src` to the array `dest`. The element sizes of both arrays must be equal.

```
void gt_array_rem(
       GtArray *array,
       GtUword index)
```

Remove element with number `index` from `array` in O(`gt_array_size(array)`) time. `index` has to be smaller than `gt_array_size(array)`.

```
void gt_array_rem_span(
       GtArray *array,
       GtUword frompos,
       GtUword topos)
```

Remove elements starting with number `frompos` up to (and including) `topos` from `array` in O(`gt_array_size(array)`) time. `frompos` has to be smaller or equal than `topos` and both have to be smaller than `gt_array_size(array)`.

```
void gt_array_reverse(
       GtArray *array)
```

Reverse the order of the elements in `array`.

```
void gt_array_set_size(
       GtArray *array,
       GtUword size)
```

Set the size of `array` to `size`. `size` must be smaller or equal than `gt_array_size(array)`.

```
void gt_array_reset(
       GtArray *array)
```

Reset the `array`. That is, afterwards the array has size 0.

```
size_t gt_array_elem_size(
    const GtArray *array)
```

Return the size of the elements stored in `array`.

```
GtUword gt_array_size(
          const GtArray *array)
```

Return the number of elements in `array`. If `array` equals `NULL`, 0 is returned.

```
void gt_array_sort(
       GtArray *array,
       GtCompare compar)
```

Sort `array` with the given compare function `compar`.

```
void gt_array_sort_stable(
       GtArray *array,
       GtCompare compar)
```

Sort `array` in a stable way with the given compare function `compar`.

```
void gt_array_sort_with_data(
       GtArray *array,
       GtCompareWithData compar,
       void *data)
```

Sort `array` with the given compare function `compar`. Passes a pointer with userdata `data` to `compar`.

```
void gt_array_sort_stable_with_data(
       GtArray *array,
       GtCompareWithData compar,
       void *data)
```

Sort `array` in a stable way with the given compare function `compar`. Passes a pointer with userdata `data` to `compar`.

```
int gt_array_cmp(
      const GtArray *array_a,
      const GtArray *array_b)
```

Compare the content of `array_a` with the content of `array_b`. `array_a` and `array_b` must have the same `gt_array_size()` and `gt_array_elem_size()`.

```
void gt_array_prepend_array(
       GtArray *dest,
       const GtArray *src)
```

Prepend the items from `src` to `dest`.

```
void gt_array_delete(
       GtArray *array)
```

Decrease the reference count for `array` or delete it, if this was the last reference.

Class GtArrayInStream

Implements the `GtNodeStream` interface. `GtArrayOutStream` takes an array of `GtGenomeNodes` and delivers them when used as an input stream. This stream can be used to feed nodes from outside into a stream flow.

Methods

```
GtNodeStream* gt_array_in_stream_new(
                GtArray *nodes,
                GtUword *progress,
                GtError *err)
```

Creates a new `GtArrayInStream`, delivering nodes from `nodes`. Note that the array must contain pointers to `GtGenomeNodes`! For every node passed, the value pointed to by `progress` is incremented by 1.

Class GtArrayOutStream

The `GtArrayOutStream` class implements the `GtNodeStream` interface. `GtArrayOutStream` takes nodes from an input stream and adds them to a `GtArray`. This stream can be used to obtain nodes for processing outside of the usual stream flow.

Methods

```
GtNodeStream* gt_array_out_stream_new(
                GtNodeStream *in_stream,
                GtArray *nodes,
                GtError *err)
```

Creates a new `GtArrayInStream`, storing new references to `GtFeatureNodes` from `in_stream` in `nodes`. Note that the array must be set up to contain pointers to `GtGenomeNodes`!

```
GtNodeStream* gt_array_out_stream_all_new(
                GtNodeStream *in_stream,
                GtArray *nodes,
                GtError *err)
```

Like `gt_array_out_stream_new()`, but not restricted to feature nodes.

Class GtBEDInStream

Implements the GtNodeStream interface. A GtBEDInStream allows one to parse a BED file and return it as a stream of GtGenomeNode objects.

Methods

```
GtNodeStream* gt_bed_in_stream_new(
                const char *filename)
```

Return a GtBEDInStream object which subsequently reads the BED file with the given filename. If filename equals NULL, the BED data is read from stdin.

```
void gt_bed_in_stream_set_feature_type(
       GtBEDInStream *bed_in_stream,
       const char *type)
```

Create BED features parsed by bed_in_stream with given type (instead of the default "BED_feature").

```
void gt_bed_in_stream_set_thick_feature_type(
       GtBEDInStream
                                                  *bed_in_stream,
       const char *type)
```

Create thick BED features parsed by bed_in_stream with given type (instead of the default "BED_thick_feature").

```
void gt_bed_in_stream_set_block_type(
       GtBEDInStream *bed_in_stream,
       const char *type)
```

Create BED blocks parsed by bed_in_stream with given type (instead of the default "BED_block").

Class GtBioseq

GtBioseq represents a simple collection of biosequences.

Methods

```
GtBioseq* gt_bioseq_new(
            const char *sequence_file,
            GtError*)
```

Construct a new GtBioseq object (and create the bioseq files, if necessary).

```
GtBioseq* gt_bioseq_new_recreate(
            const char *sequence_file,
            GtError*)
```

Construct a new GtBioseq object (and always create the the bioseq files).

```
GtBioseq* gt_bioseq_new_str(
            GtStr* sequence_file,
            GtError*)
```

Construct a new GtBioseq object (and always create the the bioseq files, if necessary). Filename is given as a GtString.

```
void gt_bioseq_delete(
       GtBioseq *bioseq)
```

Delete the bioseq.

```
void gt_bioseq_delete_indices(
       GtBioseq *bioseq)
```

Delete the index files belonging to bioseq.

```
GtAlphabet* gt_bioseq_get_alphabet(
              GtBioseq *bioseq)
```

Return the GtAlphabet associated with bioseq.

```
GtSeq* gt_bioseq_get_seq(
         GtBioseq *bioseq,
         GtUword index)
```

Return sequence with given index as GtSeq.

```
GtSeq* gt_bioseq_get_seq_range(
         GtBioseq*,
         GtUword index,
         GtUword start,
         GtUword end)
```

Return subsequence within the boundaries start and end of the sequence with given index as GtSeq.

```
const char* gt_bioseq_get_description(
              GtBioseq*,
              GtUword)
```

Return description of the sequence with given `index`.

```
char gt_bioseq_get_char(
       const GtBioseq*,
       GtUword index,
       GtUword position)
```

Return character at position `position` of the sequence with given `index`.

```
bool gt_bioseq_seq_has_wildcards(
       const GtBioseq *bioseq,
       GtUword idx)
```

Return TRUE if sequence with given `index` contains wildcards.

```
char* gt_bioseq_get_sequence(
        const GtBioseq *bioseq,
        GtUword index)
```

Return sequence with given `index` (not '\0' terminated).

```
char* gt_bioseq_get_sequence_range(
        const GtBioseq *bioseq,
        GtUword index,
        GtUword start,
        GtUword end)
```

Return subsequence within the boundaries `start` and `end` of the sequence with given `index` (not '\0' terminated).

```
GtUchar gt_bioseq_get_encoded_char(
          const GtBioseq *bioseq,
          GtUword index,
          GtUword position)
```

Return character at position `position` of the sequence with given `index`. Character is encoded according to alphabet.

```
void gt_bioseq_get_encoded_sequence(
       const GtBioseq *bioseq,
       GtUchar *out,
       GtUword index)
```

Writes encoded sequence with given `index` as to `out`. The sequence is encoded according to alphabet.

```
void gt_bioseq_get_encoded_sequence_range(
       const GtBioseq *bioseq,
       GtUchar *out,
       GtUword index,
       GtUword start,
       GtUword end)
```

Return subsequence within the boundaries `start` and `end` of the sequence with given `index` (not '\0' terminated). The sequence is encoded according to the alphabet of `bioseq`.

```
const char* gt_bioseq_get_md5_fingerprint(
              GtBioseq *bioseq,
              GtUword index)
```

Return MD5 fingerprint of sequence with given `index`.

```
const char* gt_bioseq_filename(
              const GtBioseq *bioseq)
```

Return filename of sequence file underlying `bioseq`.

```
GtUword gt_bioseq_get_sequence_length(
          const GtBioseq *bioseq,
          GtUword index)
```

Return length of the sequence with given `index` in `bioseq`.

```
GtUword gt_bioseq_get_total_length(
          const GtBioseq *bioseq)
```

Return length of all sequences in `bioseq`.

```
GtUword gt_bioseq_number_of_sequences(
          GtBioseq *bioseq)
```

Return count of all sequences in `bioseq`.

```
GtUword gt_bioseq_md5_to_index(
          GtBioseq *bioseq,
          const char *MD5)
```

Return the index of the (first) sequence with given <MD5 > contained in `bioseq`, if it exists. Otherwise `GT_UNDEF_UWORD` is returned.

```
void gt_bioseq_show_as_fasta(
       GtBioseq *bioseq,
       GtUword width,
       GtFile *outfp)
```

Shows a `bioseq` on `outfp` (in fasta format). If `width` is != 0 the sequences are formatted accordingly.

```
void gt_bioseq_show_sequence_as_fasta(
       GtBioseq *bioseq,
       GtUword seqnum,
       GtUword width,
       GtFile *outfp)
```

Shows a sequence with number `seqnum` from a `bioseq` on `outfp` (in fasta format). If `width` is != 0 the sequences are formatted accordingly.

```
void gt_bioseq_show_gc_content(
       GtBioseq*,
       GtFile *outfp)
```

Shows GC-content on `outfp` (for DNA files).

```
void gt_bioseq_show_stat(
       GtBioseq *bioseq,
       GtFile *outfp)
```

Shows `bioseq` statistics (on `outfp`).

```
void gt_bioseq_show_seqlengthdistri(
       GtBioseq *bioseq,
       GtFile *outfp)
```

Shows `bioseq` sequence length distribution (on `outfp`).

Class GtBittab

Implements arbitrary-length bit arrays and various operations on them.

Methods

```
GtBittab* gt_bittab_new(
            GtUword num_of_bits)
```

Return a new `GtBittab` of length `num_of_bits`, initialised to 0. `num_of_bits` has to be > 0

```
void gt_bittab_set_bit(
       GtBittab *bittab,
       GtUword i)
```

Set bit `i` in `bittab` to 1.

```
void gt_bittab_unset_bit(
       GtBittab *bittab,
       GtUword i)
```

Set bit `i` in `bittab` to 0.

```
void gt_bittab_complement(
       GtBittab *bittab_a,
       const GtBittab *bittab_b)
```

Set bittab_a to be the complement of bittab_b.

```
void gt_bittab_equal(
       GtBittab *bittab_a,
       const GtBittab *bittab_b)
```

Set bittab_a to be equal to bittab_b.

```
void gt_bittab_and(
       GtBittab *bittab_a,
       const GtBittab *bittab_b,
       const GtBittab *bittab_c)
```

Set bittab_a to be the bitwise AND of bittab_b and bittab_c.

```
void gt_bittab_or(
       GtBittab *bittab_a,
       const GtBittab *bittab_b,
       const GtBittab *bittab_c)
```

Set bittab_a to be the bitwise OR of bittab_b and bittab_c.

```
void gt_bittab_nand(
       GtBittab *bittab_a,
       const GtBittab *bittab_b,
       const GtBittab *bittab_c)
```

Set bittab_a to be bittab_b NAND bittab_c.

```
void gt_bittab_and_equal(
       GtBittab *bittab_a,
       const GtBittab *bittab_b)
```

Set bittab_a to be the bitwise AND of bittab_a and bittab_b.

```
void gt_bittab_or_equal(
       GtBittab *bittab_a,
       const GtBittab *bittab_b)
```

Set bittab_a to be the bitwise OR of bittab_a and bittab_b.

```
void gt_bittab_shift_left_equal(
       GtBittab *bittab)
```

Shift bittab by one position to the left.

```
void gt_bittab_shift_right_equal(
       GtBittab *bittab)
```

Shift bittab by one position to the right.

```
void gt_bittab_unset(
       GtBittab *bittab)
```

Set all bits in bittab to 0.

```
void gt_bittab_show(
       const GtBittab *bittab,
       FILE *fp)
```

Output a representation of bittab to fp.

```
void gt_bittab_get_all_bitnums(
       const GtBittab *bittab,
       GtArray *array)
```

Fill array with the indices of all set bits in bittab.

```
bool gt_bittab_bit_is_set(
       const GtBittab *bittab,
       GtUword i)
```

Return true if bit i is set in bittab.

```
bool gt_bittab_cmp(
       const GtBittab *bittab_a,
       const GtBittab *bittab_b)
```

Return true if bittab_a and bittab_b are identical.

```
GtUword gt_bittab_get_first_bitnum(
          const GtBittab *bittab)
```

Return the index of the first set bit in bittab.

```
GtUword gt_bittab_get_last_bitnum(
          const GtBittab *bittab)
```

Return the index of the last set bit in bittab.

```
GtUword gt_bittab_get_next_bitnum(
          const GtBittab *bittab,
          GtUword i)
```

Return the index of the next set bit in bittab with an index greater than i.

```
GtUword gt_bittab_count_set_bits(
          const GtBittab *bittab)
```

Return the number of set bits in `bittab`.

```
GtUword gt_bittab_size(
          GtBittab *bittab)
```

Return the total number of bits of `bittab`.

```
void gt_bittab_delete(
       GtBittab *bittab)
```

Delete `bittab`.

Class GtBlock

The `GtBlock` class represents a portion of screen space which relates to a specific "top-level" feature (and maybe its collapsed child features). It is the smallest layoutable unit in Annotation-Sketch and has a caption (which may be displayed above the block rendering).

Methods

```
GtBlock* gt_block_new(
           void)
```

Creates a new `GtBlock` object.

```
GtBlock* gt_block_ref(
           GtBlock*)
```

Increases the reference count.

```
GtBlock* gt_block_new_from_node(
           GtFeatureNode *node)
```

Create a new GtBlock object, setting block parameters (such as strand, range) from a given `node` template.

```
GtRange gt_block_get_range(
          const GtBlock*)
```

Returns the base range of the `GtBlock`'s top level element.

```
GtRange* gt_block_get_range_ptr(
           const GtBlock *block)
```

Returns a pointer to the base range of the `GtBlock`'s top level element.

```
bool gt_block_has_only_one_fullsize_element(
       const GtBlock*)
```

Checks whether a `GtBlock` is occupied completely by a single element.

```
void gt_block_merge(
       GtBlock*,
       GtBlock*)
```

Merges the contents of two `GtBlock`s into the first one.

```
GtBlock* gt_block_clone(
           GtBlock*)
```

Returns an independent copy of a `GtBlock`.

```
void gt_block_set_caption_visibility(
       GtBlock*,
       bool)
```

Set whether a block caption should be displayed or not.

```
bool gt_block_caption_is_visible(
       const GtBlock*)
```

Returns whether a block caption should be displayed or not.

```
void gt_block_set_caption(
       GtBlock*,
       GtStr *caption)
```

Sets the `GtBlock`'s caption to `caption`.

```
GtStr* gt_block_get_caption(
         const GtBlock*)
```

Returns the `GtBlock`'s caption.

```
void gt_block_set_strand(
       GtBlock*,
       GtStrand strand)
```

Sets the `GtBlock`'s strand to `strand`.

```
GtStrand gt_block_get_strand(
           const GtBlock*)
```

Returns the `GtBlock`'s strand.

```
GtFeatureNode* gt_block_get_top_level_feature(
                 const GtBlock*)
```

Returns the `GtBlock`'s top level feature as a `GtFeatureNode` object.

```
GtUword gt_block_get_size(
          const GtBlock*)
```

Returns the number of elements in the `GtBlock`.

```
const char* gt_block_get_type(
              const GtBlock*)
```

Returns the feature type of the `GtBlock`.

```
void gt_block_delete(
       GtBlock*)
```

Deletes a `GtBlock`.

Class GtBoolMatrix

`GtBoolMatrix` implements a two-dimensional matrix containing boolean values.

Methods

```
GtBoolMatrix* gt_bool_matrix_new(
                void)
```

Create a new, empty `GtBoolMatrix`.

```
bool gt_bool_matrix_get(
       GtBoolMatrix *bm,
       GtUword firstdim,
       GtUword seconddim)
```

Returns the value at position `firstdim`, `seconddim` from `bm`.

```
void gt_bool_matrix_set(
       GtBoolMatrix *bm,
       GtUword firstdim,
       GtUword seconddim,
       bool b)
```

Sets the value at position `firstdim`, `seconddim` in `bm` to `b`.

```
GtUword gt_bool_matrix_get_first_column(
          const GtBoolMatrix *bm,
          GtUword firstdim)
```

Returns the first value from column position `firstdim` from `bm`.

```
GtUword gt_bool_matrix_get_last_column(
          const GtBoolMatrix *bm,
          GtUword firstdim)
```

Returns the last value from column position `firstdim` from `bm`.

```
GtUword gt_bool_matrix_get_next_column(
          const GtBoolMatrix *bm,
          GtUword firstdim,
          GtUword i)
```

Returns the next value from column position `firstdim` from `bm`, with `i` being the current position.

```
void gt_bool_matrix_delete(
       GtBoolMatrix *bm)
```

Deletes `bm`.

Class GtBufferStream

The `GtBufferStream` is a `GtNodeStream` that buffers `GtGenomeNodes`.

Methods

```
GtNodeStream* gt_buffer_stream_new(
                GtNodeStream *in_stream)
```

Create a new `GtBufferStream`, reading from `in_stream`. The stream is initially configured to buffer nodes read from the input until `gt_buffer_stream_dequeue()` switches it to dequeue mode. In this mode, calls to `gt_node_stream_next()` will deliver the stored nodes in FIFO order.

```
void gt_buffer_stream_dequeue(
       GtBufferStream *bs)
```

Switch stream `bs` to dequeue mode.

Class GtCDSStream

Implements the `GtNodeStream` interface. A `GtCDSStream` determines the coding sequence (CDS) for sequences determined by feature nodes of type *exon* and adds them as feature nodes of type *CDS*.

Methods

```
GtNodeStream* gt_cds_stream_new(
                GtNodeStream *in_stream,
                GtRegionMapping *region_mapping,
                unsigned int minorflen,
                const char *source,
                bool start_codon,
                bool final_stop_codon,
                bool generic_star_codons)
```

Create a `GtCDSStream*` which determines the coding sequence (CDS) for sequences determined by feature nodes of type *exon* it retrieves from `in_stream`, adds them as feature nodes of type *CDS* and returns all nodes. `region_mapping` is used to map the sequence IDs of the feature nodes to the regions of the actual sequences. `minorflen` is the minimum length an ORF must have in order to be added. The CDS features are created with the given `source`. If `start_codon` equals `true` an ORF must begin with a start codon, otherwise it can start at any position. If `final_stop_codon` equals `true` the final ORF must end with a stop codon. If `generic_start_codons` equals `true`, the start codons of the standard translation scheme are used as start codons (otherwise the amino acid 'M' is regarded as a start codon).

Class GtCDSVisitor

`GtCDSVisitor` is a `GtNodeVisitor` that adds CDS features for the longest ORFs in a `GtFeatureNode`.

Methods

```
GtNodeVisitor* gt_cds_visitor_new(
                  GtRegionMapping *region_mapping,
                  unsigned int minorflen,
                  GtStr *source,
                  bool start_codon,
                  bool final_stop_codon,
                  bool generic_start_codons)
```

Create a new `GtCDSVisitor` with the given `region_mapping` for sequence, `minorflen` minimum ORF length, `source` as the source string. If `start_codon` is `true` a frame has to start with a start codon, otherwise a frame can start everywhere (i.e., at the first amino acid or after a stop codon). If `final_stop_codon` is `true` the last ORF must end with a stop codon, otherwise it can be "open". Takes ownership of `region_mapping`.

```
void gt_cds_visitor_set_region_mapping(
       GtCDSVisitor
                                                          *cds_visitor,
       GtRegionMapping
                                                          *region_mapping)
```

Sets `region_mapping` to be the region mapping specifying the sequence for `cds_visitor`. Does not take ownership of `region_mapping`.

Class GtCSAStream

Implements the `GtNodeStream` interface. A `GtCSAStream` takes spliced alignments and transforms them into consensus spliced alignments.

Methods

```
GtNodeStream* gt_csa_stream_new(
                GtNodeStream *in_stream,
                GtUword join_length)
```

Create a `GtCSAStream*` which takes spliced alignments from its `in_stream` (which are at most `join_length` many bases apart), transforms them into consensus spliced alignments, and returns them.

Class GtCanvas

The `GtCanvas` class is an abstraction of a stateful drawing surface. Constructors must be implemented in subclasses as different arguments are required for drawing to specific graphics back-ends.

Methods

```
GtUword gt_canvas_get_height(
          GtCanvas *canvas)
```

Returns the height of the given `canvas`.

```
void gt_canvas_delete(
       GtCanvas *canvas)
```

Delete the given `canvas`.

Class GtCanvasCairoContext

Implements the `GtCanvas` interface using a Cairo context (`cairo_t`) as input. This Canvas uses the `GtGraphicsCairo` class.
Drawing to a `cairo_t` allows the use of the *AnnotationSketch* engine in any Cairo-based graphical application.

Methods

```
GtCanvas* gt_canvas_cairo_context_new(
            GtStyle *style,
            cairo_t *context,
            double offsetpos,
            GtUword width,
            GtUword height,
            GtImageInfo *image_info,
            GtError *err)
```

Create a new `GtCanvas` object tied to the cairo_t `context`, `width` and `height` using the given `style`. The optional `image_info` is filled when the created Canvas object is used to render a `GtDiagram` object. `offsetpos` determines where to start drawing on the surface.

Class GtCanvasCairoFile

Implements the `GtCanvas` interface. This Canvas uses the `GtGraphicsCairo` class.

Methods

```
GtCanvas* gt_canvas_cairo_file_new(
            GtStyle *style,
            GtGraphicsOutType output_type,
            GtUword width,
            GtUword height,
            GtImageInfo *image_info,
            GtError *err)
```

Create a new `GtCanvasCairoFile` object with given `output_type` and `width` using the configuration given in `style`. The optional `image_info` is filled when the created object is used to render a `GtDiagram` object. Possible `GtGraphicsOutType` values are `GRAPHICS_PNG`, `GRAPHICS_PS`, `GRAPHICS_PDF` and `GRAPHICS_SVG`. Dependent on the local Cairo installation, not all of them may be available.

```
int gt_canvas_cairo_file_to_file(
      GtCanvasCairoFile *canvas,
      const char *filename,
      GtError *err)
```

Write rendered `canvas` to the file with name `filename`. If this method returns a value other than 0, check `err` for an error message.

```
int gt_canvas_cairo_file_to_stream(
      GtCanvasCairoFile *canvas,
      GtStr *stream)
```

Append rendered `canvas` image data to given `stream`.

Class GtCheckBoundariesVisitor

Implements the `GtNodeVisitor` interface.

Methods

```
GtNodeVisitor* gt_check_boundaries_visitor_new(
                 void)
```

Creates a new `GtCheckBoundariesVisitor` object.

Class GtCodonIterator

The `GtCodonIterator` interface.

Methods

```
GtUword gt_codon_iterator_current_position(
          GtCodonIterator
                                                          *codon_iterator)
```

Return the current reading offset of `codin_iterator`, starting from the position in the sequence given at iterator instantiation time.

```
GtUword gt_codon_iterator_length(
          GtCodonIterator
                                                *codon_iterator)
```

Return the length of the substring to scan, given at instantiation time.

```
void gt_codon_iterator_rewind(
       GtCodonIterator
                                                *codon_iterator)
```

Rewind the `codon_iterator` to point again to the position in the sequence given at iterator instantiation time.

```
GtCodonIteratorStatus gt_codon_iterator_next(
                        GtCodonIterator *codon_iterator,
                        char *n1,
                        char *n2,
                        char *n3,
                        unsigned int *frame,
                        GtError *err)
```

Sets the values of <n1 >, <n2 > and <n3 > to the codon beginning at the current reading position of `codon_iterator` and then advances the reading position by one. The current reading frame shift (0, 1 or 2) is for the current codon is written to the position pointed to by `frame`. This function returns one of three status codes: GT_CODON_ITERATOR_OK : a codon was read successfully, GT_CODON_ITERATOR_END : no codon was read because the end of the scan region has been reached, GT_CODON_ITERATOR_ERROR : no codon was read because an error occurred during sequence access. See `err` for details.

```
void gt_codon_iterator_delete(
       GtCodonIterator
                                                *codon_iterator)
```

Delete `codon_iterator`.

Class GtCodonIteratorEncseq

```
GtCodonIterator* gt_codon_iterator_encseq_new(
                   GtEncseq *encseq,
                   GtUword startpos,
                   GtUword length,
                   GtError *err)
```

Creates a new `GtCodonIterator` traversing `encseq` over a length of `len` starting at concatenated position `startpos`. If an error occurs, NULL is returned and `err` is set accordingly.

```
GtCodonIterator* gt_codon_iterator_encseq_new_with_readmode(
                   GtEncseq *encseq,
                   GtUword startpos,
                   GtUword length,
                   GtReadmode readmode,
                   GtError *err)
```

Creates a new `GtCodonIterator` traversing `encseq` over a length of `len` starting at concatenated position `startpos`. `readmode` specified reading direction. If an error occurs, NULL is returned and `err` is set accordingly.

Class GtCodonIteratorSimple

```
GtCodonIterator* gt_codon_iterator_simple_new(
                   const char *seq,
                   GtUword len,
                   GtError *err)
```

Creates a new `GtCodonIterator` traversing `seq` over a length of `len`. If an error occurs, NULL is returned and `err` is set accordingly.

Class GtColor

The `GtColor` class holds a RGB color definition.

Methods

```
GtColor* gt_color_new(
           double red,
           double green,
           double blue,
           double alpha)
```

Create a new `GtColor` object with the color given by the `red`, `green`, and `blue` arguments. The value for each color channel must be between 0 and 1.

```
void gt_color_set(
       GtColor *color,
       double red,
       double green,
       double blue,
       double alpha)
```

Change the color of the `color` object to the color given by the `red`, `green`, and `blue` arguments. The value for each color channel must be between 0 and 1.

```
bool gt_color_equals(
       const GtColor *c1,
       const GtColor *c2)
```

Returns `true` if the colors <c1> and <c2> are equal.

```
void gt_color_delete(
       GtColor *color)
```

Delete the `color` object.

Class GtCommentNode

Implements the `GtGenomeNode` interface. Comment nodes correspond to comment lines in GFF3 files (i.e., lines which start with a single "<#>").

Methods

```
GtGenomeNode* gt_comment_node_new(
                const char *comment)
```

Return a new `GtCommentNode` object representing a `comment`. Please note that the single leading "<#>" which denotes comment lines in GFF3 files should not be part of `comment`.

```
const char* gt_comment_node_get_comment(
              const GtCommentNode
                                                    *comment_node)
```

Return the comment stored in `comment_node`.

```
GtCommentNode* gt_comment_node_try_cast(
                 GtGenomeNode *gn)
```

Test whether the given genome node is a comment node. If so, a pointer to the meta node is returned. If not, NULL is returned. Note that in most cases, one should implement a GtNodeVisitor to handle processing of different GtGenomeNode types.

```
GtCommentNode* gt_comment_node_cast(
                 GtGenomeNode *gn)
```

Test whether the given genome node is a comment node. If so, a pointer to the meta node is returned. If not, an assertion fails.

Class GtCstrTable

Implements a table of C strings.

Methods

```
GtCstrTable* gt_cstr_table_new(
               void)
```

Return a new `GtCstrTable` object.

```
void gt_cstr_table_add(
       GtCstrTable *table,
       const char *cstr)
```

Add `cstr` to `table`. `table` must not already contain `cstr`!

```
const char* gt_cstr_table_get(
              const GtCstrTable *table,
              const char *cstr)
```

If a C string equal to `cstr` is contained in `table`, it is returned. Otherwise `NULL` is returned.

```
GtStrArray* gt_cstr_table_get_all(
              const GtCstrTable *table)
```

Return a `GtStrArray*` which contains all `cstrs` added to `table` in alphabetical order. The caller is responsible to free it!

```
void gt_cstr_table_remove(
       GtCstrTable *table,
       const char *cstr)
```

Remove `cstr` from `table`.

```
void gt_cstr_table_reset(
       GtCstrTable *table)
```

Reset `table` (that is, remove all contained C strings).

```
void gt_cstr_table_delete(
       GtCstrTable *table)
```

Delete C string `table`.

Class GtCustomTrack

The `GtCustomTrack` interface allows the `GtCanvas` to call user-defined drawing functions on a `GtGraphics` object. Please refer to the specific implementations' documentation for more information on a particular custom track.

Methods

```
GtCustomTrack* gt_custom_track_ref(
                 GtCustomTrack *ctrack)
```

Increase the reference count for `ctrack`.

```
void gt_custom_track_delete(
       GtCustomTrack *ctrack)
```

Delete the given `ctrack`.

Class GtCustomTrackGcContent

Implements the `GtCustomTrack` interface. This custom track draws a plot of the GC content of a given sequence in the displayed range. As a window size for GC content calculation, `windowsize` is used.

Methods

```
GtCustomTrack* gt_custom_track_gc_content_new(
                  const char *seq,
                  GtUword seqlen,
                  GtUword windowsize,
                  GtUword height,
                  double avg,
                  bool show_scale)
```

Creates a new `GtCustomTrackGcContent` for sequence `seq` with length `seqlen` of height `height` with windowsize `windowsize`. A horizontal line is drawn for the percentage value `avg`, with `avg` between 0 and 1. If `show_scale` is set to true, then a vertical scale rule is drawn at the left end of the curve.

Class GtCustomTrackScriptWrapper

Implements the `GtCustomTrack` interface. This custom track is only used to store pointers to external callbacks, e.g. written in a scripting language. This class does not store any state, relying on the developer of the external custom track class to do so.

Methods

```
GtCustomTrack* gt_custom_track_script_wrapper_new(
                  GtCtScriptRenderFunc
                                                      render_func,
                  GtCtScriptGetHeightFunc
                                                      get_height_func,
                  GtCtScriptGetTitleFunc
                                                      get_title_func,
                  GtCtScriptFreeFunc
                                                      free_func)
```

Creates a new `GtCustomTrackScriptWrapper` object.

Class GtDiagram

The `GtDiagram` class acts as a representation of a sequence annotation diagram independent of any output format. Besides annotation features as annotation graphs, it can contain one or more custom tracks. A individual graphical representation of the `GtDiagram` contents is created by

creating a GtLayout object using the GtDiagram and then calling gt_layout_sketch() with an appropriate GtCanvas object.

Methods

```
GtDiagram* gt_diagram_new(
             GtFeatureIndex *feature_index,
             const char *seqid,
             const GtRange *range,
             GtStyle *style,
             GtError*)
```

Create a new GtDiagram object representing the feature nodes in feature_index in region seqid overlapping with range. The GtStyle object style will be used to determine collapsing options during the layout process.

```
GtDiagram* gt_diagram_new_from_array(
             GtArray *features,
             const GtRange *range,
             GtStyle *style)
```

Create a new GtDiagram object representing the feature nodes in features. The features must overlap with range. The GtStyle object style will be used to determine collapsing options during the layout process.

```
GtRange gt_diagram_get_range(
          const GtDiagram *diagram)
```

Returns the sequence position range represented by the diagram.

```
void gt_diagram_set_track_selector_func(
       GtDiagram*,
       GtTrackSelectorFunc,
       void*)
```

Assigns a GtTrackSelectorFunc to use to assign blocks to tracks. If none is set, or set to NULL, then track types are used as track keys (default behavior).

```
void gt_diagram_reset_track_selector_func(
       GtDiagram *diagram)
```

Resets the track selection behavior of this GtDiagram back to the default.

```
void gt_diagram_add_custom_track(
       GtDiagram*,
       GtCustomTrack*)
```

Registers a new custom track in the diagram.

```
void gt_diagram_delete(
       GtDiagram*)
```

Delete the `diagram` and all its components.

Class GtDiscDistri

The `GtDiscDistri` class represents a discrete distribution of integer values.

Methods

```
void GtDiscDistriIterFunc(
                          GtUword key,
                          GtUint64 value,
                          void *data)
```

Callback function called during iteration over each item of the distribution, where `key` is the counted value and `value` is the count.

```
GtDiscDistri* gt_disc_distri_new(
                 void)
```

Creates a new, empty `GtDiscDistri`.

```
void gt_disc_distri_add(
       GtDiscDistri *d,
       GtUword key)
```

Adds one count of `key` to `d`.

```
void gt_disc_distri_add_multi(
       GtDiscDistri *d,
       GtUword key,
       GtUint64 occurrences)
```

Adds `occurrences` counts of `key` to `d`.

```
GtUint64 gt_disc_distri_get(
           const GtDiscDistri *d,
           GtUword key)
```

Return the current count of `key` as stored in `d`.

```
void gt_disc_distri_show(
       const GtDiscDistri *d,
       GtFile *outfp)
```

Prints the current state of `d` to `outfile`. If `outfp` is NULL, stdout will be used for output.

```
void gt_disc_distri_foreach(
       const GtDiscDistri *d,
       GtDiscDistriIterFunc func,
       void *data)
```

Iterate over all non-empty entries in `d`, calling `func` for each one, from the smallest to the largest key. The `data` pointer can be used to pass arbitrary data to `func`.

```
void gt_disc_distri_foreach_in_reverse_order(
       const GtDiscDistri *d,
       GtDiscDistriIterFunc func,
       void *data)
```

Same as foreach, but from the longest to the smallest key.

Class GtDlist

A double-linked list which is sorted according to a `GtCompare` compare function (<qsort(3)>-like, only if one was supplied to the constructor).

Methods

```
GtDlist* gt_dlist_new(
           GtCompare compar)
```

Return a new `GtDlist` object sorted according to `compar` function. If `compar` equals `NULL`, no sorting is enforced.

```
GtDlist* gt_dlist_new_with_data(
           GtCompareWithData compar,
           void *data)
```

Return a new `GtDlist` object sorted according to `compar` function. If `compar` equals `NULL`, no sorting is enforced. Use `data` to supply additional data to the comparator function.

```
GtDlistelem* gt_dlist_first(
               const GtDlist *dlist)
```

Return the first `GtDlistelem` object in `dlist`.

```
GtDlistelem* gt_dlist_last(
               const GtDlist *dlist)
```

Return the last `GtDlistelem` object in `dlist`.

```
GtDlistelem* gt_dlist_find(
                const GtDlist *dlist,
                void *data)
```

Return the first `GtDlistelem` object in `dlist` which contains data identical to `data`. Takes O(n) time.

```
GtUword gt_dlist_size(
          const GtDlist *dlist)
```

Return the number of `GtDlistelem` objects in `dlist`.

```
void gt_dlist_add(
       GtDlist *dlist,
       void *data)
```

Add a new `GtDlistelem` object containing `data` to `dlist`. Usually O(n), but O(1) if data is added in sorted order.

```
void gt_dlist_remove(
       GtDlist *dlist,
       GtDlistelem *dlistelem)
```

Remove `dlistelem` from `dlist` and free it.

```
int gt_dlist_example(
      GtError *err)
```

Example for usage of the `GtDlist` class.

```
void gt_dlist_delete(
       GtDlist *dlist)
```

Delete `dlist`.

Class GtDlistelem

```
GtDlistelem* gt_dlistelem_next(
                const GtDlistelem *dlistelem)
```

Return the successor of `dlistelem`, or `NULL` if the element is the last one in the `GtDlist`.

```
GtDlistelem* gt_dlistelem_previous(
                const GtDlistelem *dlistelem)
```

Return the predecessor of `dlistelem`, or `NULL` if the element is the first one in the `GtDlist`.

```
void* gt_dlistelem_get_data(
        const GtDlistelem *dlistelem)
```

Return the data pointer attached to `dlistelem`.

Class GtEOFNode

Implements the `GtGenomeNode` interface. EOF nodes mark the barrier between separate input files in an GFF3 stream.

Methods

```
GtGenomeNode* gt_eof_node_new(
                void)
```

Create a new `GtEOFNode*` representing an EOF marker.

```
GtEOFNode* gt_eof_node_try_cast(
             GtGenomeNode *gn)
```

Test whether the given genome node is an EOF node. If so, a pointer to the EOF node is returned. If not, NULL is returned. Note that in most cases, one should implement a GtNodeVisitor to handle processing of different GtGenomeNode types.

Class GtEncseq

The `GtEncseq` class represents a concatenated collection of sequences from one or more input files in a bit-compressed encoding. It is stored in a number of `mmap()`able files, depending on which features it is meant to support. The main compressed sequence information is stored in an *encoded sequence* table, with the file suffix '.esq'. This table is the minimum requirement for the `GtEncseq` structure and must always be present. In addition, if support for multiple sequences is desired, a *sequence separator position* table with the '.ssp' suffix is required. If support for sequence descriptions is required, two additional tables are needed: a *description* table with the suffix '.des' and a *description separator* table with the file suffix '.sds'. Creation and requirement of these tables can be switched on and off using API functions as outlined below. The `GtEncseq` represents the stored sequences as one concatenated string. It allows access to the sequences by providing start positions and lengths for each sequence, making it possible to extract encoded substrings into a given buffer, as well as accessing single characters both in a random and a sequential fashion.

Methods

```
const char* gt_encseq_indexname(
              const GtEncseq *encseq)
```

Returns the indexname (as given at loading time) of encseq or the string ”generated” if the GtEncseq was build in memory only.

```
GtUword gt_encseq_total_length(
          const GtEncseq *encseq)
```

Returns the total number of characters in all sequences of encseq, including separators and wildcards.

```
GtUword gt_encseq_num_of_sequences(
          const GtEncseq *encseq)
```

Returns the total number of sequences contained in encseq.

```
GtUchar gt_encseq_get_encoded_char(
          const GtEncseq *encseq,
          GtUword pos,
          GtReadmode readmode)
```

Returns the encoded representation of the character at position pos of encseq read in the direction as indicated by readmode.

```
char gt_encseq_get_decoded_char(
       const GtEncseq *encseq,
       GtUword pos,
       GtReadmode readmode)
```

Returns the decoded representation of the character at position pos of encseq read in the direction as indicated by readmode.

```
bool gt_encseq_position_is_separator(
       const GtEncseq *encseq,
       GtUword pos,
       GtReadmode readmode)
```

Returns true iff pos is a separator position of encseq read in the direction as indicated by readmode.

```
bool gt_encseq_position_is_wildcard(
       const GtEncseq *encseq,
       GtUword pos,
       GtReadmode readmode)
```

Returns true iff pos is a wildcard in encseq read in the direction as indicated by readmode.

```
GtEncseq* gt_encseq_ref(
            GtEncseq *encseq)
```

Increases the reference count of encseq.

```
GtEncseqReader* gt_encseq_create_reader_with_readmode(
                  const GtEncseq *encseq,
                  GtReadmode readmode,
                  GtUword startpos)
```

Returns a new GtEncseqReader for encseq, starting from position startpos. Also supports reading the sequence from the reverse and delivering (reverse) complement characters on DNA alphabets using the readmode option. Please make sure that the GT_READMODE_COMPL and GT_READMODE_REVCOMPL readmodes are only used on DNA alphabets.

```
void gt_encseq_extract_encoded(
       const GtEncseq *encseq,
       GtUchar *buffer,
       GtUword frompos,
       GtUword topos)
```

Stores the encoded representation of the substring from 0-based position frompos to position topos of encseq. The result is written to the location pointed to by buffer, which must be large enough to hold the result.

```
void gt_encseq_extract_decoded(
       const GtEncseq *encseq,
       char *buffer,
       GtUword frompos,
       GtUword topos)
```

Stores the decoded version of the substring from 0-based position frompos to position topos of encseq. If the extracted region contains a separator character, it will be represented by non-printable GT_SEPARATOR constant. The caller is responsible to handle this case. The result of the extraction is written to the location pointed to by buffer, which must be sufficiently large to hold the result.

```
GtUword gt_encseq_seqlength(
          const GtEncseq *encseq,
          GtUword seqnum)
```

Returns the length of the seqnum-th sequence in the encseq. Requires multiple sequence support enabled in encseq.

```
GtUword gt_encseq_min_seq_length(
          const GtEncseq *encseq)
```

Returns the length of the shortest sequence in the encseq.

```
GtUword gt_encseq_max_seq_length(
          const GtEncseq *encseq)
```

Returns the length of the longest sequence in the encseq.

```
bool gt_encseq_has_multiseq_support(
       const GtEncseq *encseq)
```

Returns true if encseq has multiple sequence support.

```
bool gt_encseq_has_description_support(
       const GtEncseq *encseq)
```

Returns true if encseq has description support.

```
bool gt_encseq_has_md5_support(
       const GtEncseq *encseq)
```

Returns true if encseq has MD5 support.

```
GtUword gt_encseq_seqstartpos(
          const GtEncseq *encseq,
          GtUword seqnum)
```

Returns the start position of the seqnum-th sequence in the encseq. Requires multiple sequence support enabled in encseq.

```
GtUword gt_encseq_seqnum(
          const GtEncseq *encseq,
          GtUword position)
```

Returns the sequence number from the given position for a given GtEncseq encseq.

```
const char* gt_encseq_description(
              const GtEncseq *encseq,
              GtUword *desclen,
              GtUword seqnum)
```

Returns a pointer to the description of the seqnum-th sequence in the encseq. The length of the returned string is written to the location pointed at by desclen. The returned description pointer is not $<\backslash 0>$-terminated! Requires description support enabled in encseq.

```
const GtStrArray* gt_encseq_filenames(
                    const GtEncseq *encseq)
```

Returns a GtStrArray of the names of the original sequence files contained in encseq.

```
GtUword gt_encseq_num_of_files(
          const GtEncseq *encseq)
```

Returns the number of files contained in encseq.

```
GtUint64 gt_encseq_effective_filelength(
           const GtEncseq *encseq,
           GtUword filenum)
```

Returns the effective length (sum of sequence lengths and separators between them) of the filenum-th file contained in encseq.

```
GtUword gt_encseq_filestartpos(
          const GtEncseq *encseq,
          GtUword filenum)
```

Returns the start position of the sequences of the filenum-th file in the encseq. Requires multiple file support enabled in encseq.

```
GtUword gt_encseq_filenum(
          const GtEncseq *encseq,
          GtUword position)
```

Returns the file number from the given position for a given GtEncseq encseq.

```
GtUword gt_encseq_filenum_first_seqnum(
          const GtEncseq *encseq,
          GtUword filenum)
```

Returns the first sequence number of the sequences in file filenum for a given GtEncseq encseq.

```
GtAlphabet* gt_encseq_alphabet(
              const GtEncseq *encseq)
```

Returns the GtAlphabet associated with encseq.

```
int gt_encseq_mirror(
      GtEncseq *encseq,
      GtError *err)
```

Extends encseq by virtual reverse complement sequences. Returns 0 if mirroring has been successfully enabled, otherwise -1. err is set accordingly.

```
void gt_encseq_unmirror(
       GtEncseq *encseq)
```

Removes virtual reverse complement sequences added by gt_encseq_mirror().

```
bool gt_encseq_is_mirrored(
       const GtEncseq *encseq)
```

Returns `true` if `encseq` contains virtual reverse complement sequences as added by `gt_encseq_mirror()`.

```
GtUword gt_encseq_version(
          const GtEncseq *encseq)
```

Returns the version number of the file representation of `encseq` if it exists, or 0 if it was not mapped from a file.

```
bool gt_encseq_is_64_bit(
       const GtEncseq *encseq)
```

Returns TRUE if `encseq` was created on a 64-bit system.

```
void gt_encseq_delete(
       GtEncseq *encseq)
```

Deletes `encseq` and frees all associated space.

Class GtEncseqBuilder

The `GtEncseqBuilder` class creates `GtEncseq` objects by constructing uncompressed, encoded string copies in memory.

Methods

```
GtEncseqBuilder* gt_encseq_builder_new(
                   GtAlphabet *alpha)
```

Creates a new `GtEncseqBuilder` using the alphabet `alpha` as a basis for on-the-fly encoding of sequences in memory.

```
void gt_encseq_builder_enable_description_support(
       GtEncseqBuilder *eb)
```

Enables support for retrieving descriptions from the encoded sequence to be built by `eb`. Requires additional memory to hold the descriptions and a position index. Activated by default.

```
void gt_encseq_builder_disable_description_support(
       GtEncseqBuilder *eb)
```

Disables support for retrieving descriptions from the encoded sequence to be built by `eb`. Disabling this support will result in an error when trying to call the method `gt_encseq_description()` on the `GtEncseq` object created by `eb`.

```
void gt_encseq_builder_enable_multiseq_support(
       GtEncseqBuilder *eb)
```

Enables support for random access to multiple sequences in the encoded sequence to be built by `eb`. Requires additional memory for an index of starting positions. Activated by default.

```
void gt_encseq_builder_disable_multiseq_support(
       GtEncseqBuilder *eb)
```

Disables support for random access to multiple sequences in the encoded sequence to be built by `eb`. Disabling this support will result in an error when trying to call the method `gt_encseq_seqlength()` or `gt_encseq_seqstartpos()` on the `GtEncseq` object created by `eb`.

```
void gt_encseq_builder_create_esq_tab(
       GtEncseqBuilder *eb)
```

Enables creation of the .esq table containing the encoded sequence itself. Naturally, enabled by default.

```
void gt_encseq_builder_do_not_create_esq_tab(
       GtEncseqBuilder *eb)
```

Disables creation of the .esq table.

```
void gt_encseq_builder_create_des_tab(
       GtEncseqBuilder *eb)
```

Enables creation of the .des table containing sequence descriptions.

```
void gt_encseq_builder_do_not_create_des_tab(
       GtEncseqBuilder *eb)
```

Disables creation of the .des table.

```
void gt_encseq_builder_create_ssp_tab(
       GtEncseqBuilder *eb)
```

Enables creation of the .ssp table containing indexes for multiple sequences.

```
void gt_encseq_builder_do_not_create_ssp_tab(
       GtEncseqBuilder *eb)
```

Disables creation of the .ssp table.

```
void gt_encseq_builder_create_sds_tab(
       GtEncseqBuilder *eb)
```

Enables creation of the .sds table containing indexes for sequence descriptions.

```
void gt_encseq_builder_do_not_create_sds_tab(
       GtEncseqBuilder *eb)
```

Disables creation of the .sds table.

```
void gt_encseq_builder_add_cstr(
       GtEncseqBuilder *eb,
       const char *str,
       GtUword strlen,
       const char *desc)
```

Adds a sequence given as a C string `str` of length `strlen` to the encoded sequence to be built by `eb`. Additionally, a description can be given (`desc`). If description support is enabled, this must not be `NULL`. A copy will be made during the addition process and the sequence will be encoded using the alphabet set at the construction time of `eb`. Thus it must only contain symbols compatible with the alphabet.

```
void gt_encseq_builder_add_str(
       GtEncseqBuilder *eb,
       GtStr *str,
       const char *desc)
```

Adds a sequence given as a GtStr `str` to the encoded sequence to be built by `eb`. Additionally, a description can be given. If description support is enabled, `desc` must not be `NULL`. A copy will be made during the addition process and the sequence will be encoded using the alphabet set at the construction time of `eb`. Thus it must only contain symbols compatible with the alphabet.

```
void gt_encseq_builder_add_encoded(
       GtEncseqBuilder *eb,
       const GtUchar *str,
       GtUword strlen,
       const char *desc)
```

Adds a sequence given as a pre-encoded string `str` of length `strlen` to the encoded sequence to be built by `eb`. `str` must be encoded using the alphabet set at the construction time of `eb`. `str` is not allowed to include sequence separators. Does not take ownership of `str`. Additionally, a description `desc` can be given. If description support is enabled, this must not be `NULL`.

```
void gt_encseq_builder_add_encoded_own(
       GtEncseqBuilder *eb,
       const GtUchar *str,
       GtUword strlen,
       const char *desc)
```

Adds a sequence given as a pre-encoded string `str` of length `strlen` to the encoded sequence to be built by `eb`. `str` must be encoded using the alphabet set at the construction time of `eb`. Always creates a copy of `str`, so it can be used with memory that is to be freed immediately after adding. Additionally, a description `desc` can be given. If description support is enabled, this must not be `NULL`.

```
void gt_encseq_builder_add_multiple_encoded(
       GtEncseqBuilder *eb,
       const GtUchar *str,
       GtUword strlen)
```

Adds a sequence given as a pre-encoded string `str` of length `strlen` to the encoded sequence to be built by `eb`. `str` must be encoded using the alphabet set at the construction time of `eb`. `str` may include sequence separators. Does not take ownership of `str`.

```
void gt_encseq_builder_set_logger(
       GtEncseqBuilder*,
       GtLogger *l)
```

Sets the logger to use by `ee` during encoding to `l`. Default is `NULL` (no logging).

```
GtEncseq* gt_encseq_builder_build(
            GtEncseqBuilder *eb,
            GtError *err)
```

Creates a new `GtEncseq` from the sequences added to `eb`. Returns a `GtEncseq` instance on success, or `NULL` on error. If an error occurred, `err` is set accordingly. The state of `eb` is reset to empty after successful creation of a new `GtEncseq` (like having called `gt_encseq_builder_reset()`).

```
void gt_encseq_builder_reset(
       GtEncseqBuilder *eb)
```

Clears all added sequences and descriptions, resetting `eb` to a state similar to the state immediately after its initial creation.

```
void gt_encseq_builder_delete(
       GtEncseqBuilder *eb)
```

Deletes `eb`.

Class GtEncseqEncoder

The GtEncseqEncoder class creates objects encapsulating a parameter set for conversion from sequence files into encoded sequence files on secondary storage.

Methods

```
GtEncseqEncoder* gt_encseq_encoder_new(
                    void)
```

Creates a new GtEncseqEncoder.

```
void gt_encseq_encoder_set_timer(
       GtEncseqEncoder *ee,
       GtTimer *t)
```

Sets t to be the timer for ee. Default is NULL (no progress reporting).

```
GtTimer* gt_encseq_encoder_get_timer(
           const GtEncseqEncoder *ee)
```

Returns the timer set for ee.

```
int gt_encseq_encoder_use_representation(
      GtEncseqEncoder *ee,
      const char *sat,
      GtError *err)
```

Sets the representation of ee to sat which must be one of 'direct', 'bytecompress', 'bit', 'uchar', 'ushort' or 'uint32'. Returns 0 on success, and a negative value on error (err is set accordingly).

```
GtStr* gt_encseq_encoder_representation(
         const GtEncseqEncoder *ee)
```

Returns the representation requested for ee.

```
int gt_encseq_encoder_use_symbolmap_file(
      GtEncseqEncoder *ee,
      const char *smap,
      GtError *err)
```

Sets the symbol map file to use in ee to smap which must a valid alphabet description file. Returns 0 on success, and a negative value on error (err is set accordingly). Default is NULL (no alphabet transformation).

```
const char* gt_encseq_encoder_symbolmap_file(
              const GtEncseqEncoder *ee)
```

Returns the symbol map file requested for ee.

```
void gt_encseq_encoder_set_logger(
       GtEncseqEncoder *ee,
       GtLogger *l)
```

Sets the logger to use by `ee` during encoding to `l`. Default is `NULL` (no logging).

```
void gt_encseq_encoder_enable_description_support(
       GtEncseqEncoder *ee)
```

Enables support for retrieving descriptions from the encoded sequence encoded by `ee`. That is, the .des and .sds tables are created. This is a prerequisite for being able to activate description support in `gt_encseq_loader_require_description_support()`. Activated by default.

```
void gt_encseq_encoder_disable_description_support(
       GtEncseqEncoder *ee)
```

Disables support for retrieving descriptions from the encoded sequence encoded by `ee`. That is, the .des and .sds tables are not created. Encoded sequences created without this support will not be able to be loaded via a `GtEncseqLoader` with `gt_encseq_loader_require_description_support()` enabled.

```
void gt_encseq_encoder_enable_multiseq_support(
       GtEncseqEncoder *ee)
```

Enables support for random access to multiple sequences in the encoded sequence encoded by `ee`. That is, the .ssp table is created. This is a prerequisite for being able to activate description support in `gt_encseq_loader_require_multiseq_support()`. Activated by default.

```
void gt_encseq_encoder_disable_multiseq_support(
       GtEncseqEncoder *ee)
```

Disables support for random access to multiple sequences in the encoded sequence encoded by `ee`. That is, the .ssp table is not created. Encoded sequences created without this support will not be able to be loaded via a `GtEncseqLoader` with `gt_encseq_loader_require_multiseq_support()` enabled.

```
void gt_encseq_encoder_enable_lossless_support(
       GtEncseqEncoder *ee)
```

Enables support for lossless reproduction of the original sequence, regardless of alphabet transformations that may apply. Deactivated by default.

```
void gt_encseq_encoder_disable_lossless_support(
       GtEncseqEncoder *ee)
```

Enables support for lossless reproduction of the original sequence, regardless of alphabet transformations that may apply. Encoded sequences created without this support will not be able to be loaded via a `GtEncseqLoader` with `gt_encseq_loader_require_lossless_support()` enabled.

```
void gt_encseq_encoder_enable_md5_support(
       GtEncseqEncoder *ee)
```

Enables support for quick MD5 indexing of the sequences in `ee`. Activated by default.

```
void gt_encseq_encoder_disable_md5_support(
       GtEncseqEncoder *ee)
```

Enables support for quick MD5 indexing of the sequences in `ee`. Encoded sequences created without this support will not be able to be loaded via a `GtEncseqLoader` with <gt_encseq_loader_require_md5_support()> enabled.

```
void gt_encseq_encoder_create_des_tab(
       GtEncseqEncoder *ee)
```

Enables creation of the .des table containing sequence descriptions. Enabled by default.

```
void gt_encseq_encoder_do_not_create_des_tab(
       GtEncseqEncoder *ee)
```

Disables creation of the .des table.

```
bool gt_encseq_encoder_des_tab_requested(
       const GtEncseqEncoder *ee)
```

Returns `true` if the creation of the .des table has been requested, `false` otherwise.

```
void gt_encseq_encoder_create_ssp_tab(
       GtEncseqEncoder *ee)
```

Enables creation of the .ssp table containing indexes for multiple sequences. Enabled by default.

```
void gt_encseq_encoder_do_not_create_ssp_tab(
       GtEncseqEncoder *ee)
```

Disables creation of the .ssp table.

```
bool gt_encseq_encoder_ssp_tab_requested(
       const GtEncseqEncoder *ee)
```

Returns `true` if the creation of the .ssp table has been requested, `false` otherwise.

```
void gt_encseq_encoder_create_sds_tab(
       GtEncseqEncoder *ee)
```

Enables creation of the .sds table containing indexes for sequence descriptions. Enabled by default.

```
void gt_encseq_encoder_do_not_create_sds_tab(
       GtEncseqEncoder *ee)
```

Disables creation of the .sds table.

```
bool gt_encseq_encoder_sds_tab_requested(
       const GtEncseqEncoder *ee)
```

Returns `true` if the creation of the .sds table has been requested, `false` otherwise.

```
void gt_encseq_encoder_create_md5_tab(
       GtEncseqEncoder *ee)
```

Enables creation of the .md5 table containing MD5 sums. Enabled by default.

```
void gt_encseq_encoder_do_not_create_md5_tab(
       GtEncseqEncoder *ee)
```

Disables creation of the .md5 table.

```
bool gt_encseq_encoder_md5_tab_requested(
       const GtEncseqEncoder *ee)
```

Returns `true` if the creation of the .md5 table has been requested, `false` otherwise.

```
void gt_encseq_encoder_set_input_dna(
       GtEncseqEncoder *ee)
```

Sets the sequence input type for `ee` to DNA.

```
bool gt_encseq_encoder_is_input_dna(
       GtEncseqEncoder *ee)
```

Returns `true` if the input sequence has been defined as being DNA.

```
void gt_encseq_encoder_set_input_protein(
       GtEncseqEncoder *ee)
```

Sets the sequence input type for `ee` to protein/amino acids.

```
bool gt_encseq_encoder_is_input_protein(
       GtEncseqEncoder *ee)
```

Returns `true` if the input sequence has been defined as being protein.

```
void gt_encseq_encoder_clip_desc(
       GtEncseqEncoder *ee)
```

Makes ee ignore all description suffixes after the first whitespace character per description (as defined via isspace(3)).

```
bool gt_encseq_encoder_are_descs_clipped(
       GtEncseqEncoder *ee)
```

Returns true if ee clips all descriptions after the first whitespace.

```
void gt_encseq_encoder_enable_dust(
       GtEncseqEncoder *ee,
       bool echo,
       GtUword ws,
       double thresh,
       GtUword linker)
```

Enables masking of low-complexity regions according to the dust algorithm.

```
int gt_encseq_encoder_encode(
      GtEncseqEncoder *ee,
      GtStrArray *seqfiles,
      const char *indexname,
      GtError *err)
```

Encodes the sequence files given in seqfiles using the settings in ee and indexname as the prefix for the index tables. Returns 0 on success, or a negative value on error (err is set accordingly).

```
void gt_encseq_encoder_delete(
       GtEncseqEncoder *ee)
```

Deletes ee.

Class GtEncseqLoader

The GtEncseqLoader class creates GtEncseq objects by mapping index files from secondary storage into memory.

Methods

```
GtEncseqLoader* gt_encseq_loader_new(
                  void)
```

Creates a new GtEncseqLoader.

```
void gt_encseq_loader_enable_autosupport(
       GtEncseqLoader *el)
```

Enables auto-discovery of supported features when loading an encoded sequence. That is, if a file with indexname.suffix exists which is named like a table file, it is loaded automatically. Use gt_encseq_has_multiseq_support() etc. to query for these capabilities.

```
void gt_encseq_loader_disable_autosupport(
       GtEncseqLoader *el)
```

Disables auto-discovery of supported features.

```
void gt_encseq_loader_require_description_support(
       GtEncseqLoader *el)
```

Enables support for retrieving descriptions from the encoded sequence to be loaded by el. That is, the .des and .sds tables must be present. For example, these tables are created by having enabled the gt_encseq_encoder_enable_description_support() option when encoding. Activated by default.

```
void gt_encseq_loader_drop_description_support(
       GtEncseqLoader *el)
```

Disables support for retrieving descriptions from the encoded sequence to be loaded by el. That is, the .des and .sds tables need not be present. However, disabling this support will result in an error when trying to call the method gt_encseq_description() on the GtEncseq object created by el.

```
void gt_encseq_loader_require_multiseq_support(
       GtEncseqLoader *el)
```

Enables support for random access to multiple sequences in the encoded sequence to be loaded by el. That is, the .ssp table must be present. For example, this table is created by having enabled the gt_encseq_encoder_enable_multiseq_support() option when encoding. Activated by default.

```
void gt_encseq_loader_drop_multiseq_support(
       GtEncseqLoader *el)
```

Disables support for random access to multiple sequences in the encoded sequence to be loaded by `el`. That is, the .ssp table needs not be present. However, disabling this support will result in an error when trying to call the method `gt_encseq_seqlength()` and `gt_encseq_seqstartpos()` on the `GtEncseq` object created by `el`.

```
void gt_encseq_loader_require_lossless_support(
       GtEncseqLoader *el)
```

Enables support for lossless reproduction of the original sequence in the encoded sequence to be loaded by `el`. That is, the .ois table must be present. For example, this table is created by having enabled the `gt_encseq_encoder_enable_lossless_support()` option when encoding. Deactivated by default.

```
void gt_encseq_loader_drop_lossless_support(
       GtEncseqLoader *el)
```

Disables support for lossless reproduction of the original sequence in the encoded sequence to be loaded by `el`. That is, the .ois table needs not be present. However, disabling this support may result in a reduced alphabet representation when accessing decoded characters.

```
void gt_encseq_loader_require_md5_support(
       GtEncseqLoader *el)
```

Enables support for quick retrieval of the MD5 sums for the sequences in the encoded sequence to be loaded by `el`. That is, the .md5 table must be present. For example, this table is created by having enabled the <gt_encseq_encoder_enable_md5_support()> option when encoding. Activated by default.

```
void gt_encseq_loader_drop_md5_support(
       GtEncseqLoader *el)
```

Disables support for quick retrieval of the MD5 sums for the sequences in the encoded sequence to be loaded by `el`. That is, the .md5 table needs not be present.

```
void gt_encseq_loader_require_des_tab(
       GtEncseqLoader *el)
```

Requires presence of the .des table containing sequence descriptions. Enabled by default.

```
void gt_encseq_loader_do_not_require_des_tab(
       GtEncseqLoader *el)
```

Disables requirement of the .des table for loading a `GtEncseq` using `el`.

```
bool gt_encseq_loader_des_tab_required(
       const GtEncseqLoader *el)
```

Returns `true` if a .des table must be present for loading to succeed.

```
void gt_encseq_loader_require_ssp_tab(
       GtEncseqLoader *el)
```

Requires presence of the .ssp table containing indexes for multiple sequences. Enabled by default.

```
void gt_encseq_loader_do_not_require_ssp_tab(
       GtEncseqLoader *el)
```

Disables requirement of the .ssp table for loading a `GtEncseq` using `el`.

```
bool gt_encseq_loader_ssp_tab_required(
       const GtEncseqLoader *el)
```

Returns `true` if a .ssp table must be present for loading to succeed.

```
void gt_encseq_loader_require_sds_tab(
       GtEncseqLoader *el)
```

Requires presence of the .sds table containing indexes for sequence descriptions. Enabled by default.

```
void gt_encseq_loader_do_not_require_sds_tab(
       GtEncseqLoader *el)
```

Disables requirement of the .sds table for loading a `GtEncseq` using `el`.

```
bool gt_encseq_loader_sds_tab_required(
       const GtEncseqLoader *el)
```

Returns `true` if a .sds table must be present for loading to succeed.

```
void gt_encseq_loader_set_logger(
       GtEncseqLoader *el,
       GtLogger *l)
```

Sets the logger to use by `ee` during encoding to `l`. Default is `NULL` (no logging).

```
void gt_encseq_loader_mirror(
       GtEncseqLoader *el)
```

Enables loading of a sequence using `el` with mirroring enabled from the start. Identical to invoking `gt_encseq_mirror()` directly after loading.

```
void gt_encseq_loader_do_not_mirror(
       GtEncseqLoader *el)
```

Disables loading of a sequence using `el` with mirroring enabled right from the start.

```
GtEncseq* gt_encseq_loader_load(
            GtEncseqLoader *el,
            const char *indexname,
            GtError *err)
```

Attempts to map the index files as specified by `indexname` using the options set in `el` using this interface. Returns a `GtEncseq` instance on success, or `NULL` on error. If an error occurred, `err` is set accordingly.

```
void gt_encseq_loader_delete(
       GtEncseqLoader *el)
```

Deletes `el`.

Class GtEncseqReader

The `GtEncseqReader` class represents the current state of a sequential scan of a `GtEncseq` region as an iterator.

Methods

```
void gt_encseq_reader_reinit_with_readmode(
       GtEncseqReader *esr,
       const GtEncseq *encseq,
       GtReadmode readmode,
       GtUword startpos)
```

Reinitializes the given `esr` with the values as described in `gt_encseq_create_reader_with_readmode()`.

```
GtUchar gt_encseq_reader_next_encoded_char(
          GtEncseqReader *esr)
```

Returns the next encoded character from current position of `esr`, advancing the iterator by one position.

```
char gt_encseq_reader_next_decoded_char(
       GtEncseqReader *esr)
```

Returns the next decoded character from current position of `esr`, advancing the iterator by one position.

```
void gt_encseq_reader_delete(
       GtEncseqReader *esr)
```

Deletes esr, freeing all associated space.

Class GtError

This class is used for the handling of **user errors** in *GenomeTools*. Thereby, the actual GtError object is used to store the *error message* while it is signaled by the return value of the called function, if an error occurred.
By convention in *GenomeTools*, the GtError object is always passed into a function as the last parameter and -1 (or NULL for constructors) is used as return value to indicate that an error occurred. Success is usually indicated by 0 as return value or via a non-NULL object pointer for constructors.
It is possible to use NULL as an GtError object, if one is not interested in the actual error message.
Functions which do not get an GtError object cannot fail due to a user error and it is not necessary to check their return code for an error condition.

Methods

```
GtError* gt_error_new(
           void)
```

Return a new GtError object

```
#define gt_error_check(
          err)
```

Insert an assertion to check that the error err is not set or is NULL. This macro should be used at the beginning of every routine which has an GtError* argument to make sure the error propagation has been coded correctly.

```
void gt_error_set(
       GtError *err,
       const char *format,
       ...)
```

Set the error message stored in err according to format (as in <printf(3)>).

```
void gt_error_vset(
       GtError *err,
       const char *format,
       va_list ap)
```

Set the error message stored in err according to format (as in <vprintf(3)>).

```
void gt_error_set_nonvariadic(
       GtError *err,
       const char *msg)
```

Set the error message stored in `err` to `msg`.

```
bool gt_error_is_set(
       const GtError *err)
```

Return `true` if the error `err` is set, `false` otherwise.

```
void gt_error_unset(
       GtError *err)
```

Unset the error `err`.

```
const char* gt_error_get(
              const GtError *err)
```

Return the error string stored in `err` (the error must be set).

```
void gt_error_set_progname(
       GtError *err,
       const char *progname)
```

Sets the program name assigned to `err` to `progname`.

```
const char* gt_error_get_progname(
              const GtError *err)
```

Returns the program name assigned to `err`.

```
void gt_error_delete(
       GtError *err)
```

Delete the error object `err`.

Class GtExtractFeatureStream

Implements the `GtNodeStream` interface. A `GtExtractFeatureStream` extracts the corresponding sequences of features.

Methods

```
GtNodeStream* gt_extract_feature_stream_new(
                GtNodeStream *in_stream,
                GtRegionMapping *region_Mapping,
                const char *type,
                bool join,
                bool translate,
                bool seqid,
                bool target,
                GtUword width,
                GtFile *outfp)
```

Create a `GtExtractFeatureStream*` which extracts the corresponding sequences of feature nodes (of the given `type`) it retrieves from `in_stream` and writes them in FASTA format (with the given `width`) to `outfp`. If `join` is `true`, features of the given `type` are joined together before the sequence is extracted. If `translate` is `true`, the sequences are translated into amino acid sequences before they are written to `outfp`. If `seqid` is `true` the sequence IDs of the extracted features are added to the FASTA header. If `target` is `true` the target IDs of the extracted features are added to the FASTA header. Takes ownership of `region_mapping`!

Class GtFastaReader

`GtFastaReader` is an interface to iteratively process the sequences in a FASTA file, with multiple implementations.

Methods

```
int GtFastaReaderProcDescription(
                                  const char *description,
                                  GtUword length,
                                  void *data,
                                  GtError*)
```

Gets called for each description (the start of a fasta entry).

```
int GtFastaReaderProcSequencePart(
                                   const char *seqpart,
                                   GtUword length,
                                   void *data,
                                   GtError*)
```

Gets called for each sequence part of a fasta entry.

```
int GtFastaReaderProcSequenceLength(
                                      GtUword,
                                      void *data,
                                      GtError*)
```

Gets called after a fasta entry has been read.

```
int gt_fasta_reader_run(
      GtFastaReader *fr,
      GtFastaReaderProcDescription,
      GtFastaReaderProcSequencePart,
      GtFastaReaderProcSequenceLength,
      void *data,
      GtError*)
```

Run `fr` with the given handler functions and `data` for common storage. A value less than zero is returned on error and `err` is set accordingly.

```
void gt_fasta_reader_delete(
       GtFastaReader *fr)
```

Delete `fr`.

Class GtFeatureInStream

```
GtNodeStream* gt_feature_in_stream_new(
                GtFeatureIndex *fi)
```

Create a new `GtFeatureInStream` using the given `GtFeatureIndex` as the source of a node stream.

```
void gt_feature_in_stream_use_orig_ranges(
       GtFeatureInStream *stream)
```

Instruct `stream` to deliver GtRegionNode objects whose ranges are specified such as with <##sequence-region> pragmas, rather than those inferred from the features. Specifically, use `gt_feature_index_get_orig_range_for_seqid` on the underlying feature index rather than the default `gt_feature_index_get_range_for_seqid`.

Class GtFeatureIndex

This interface represents a searchable container for `GtFeatureNode` objects, typically root nodes of larger structures. How storage and searching takes place is left to the discretion of the implementing class.
Output from a `gt_feature_index_get_features_*()` method should always be sorted by feature start position.

Methods

```
int gt_feature_index_add_region_node(
      GtFeatureIndex *feature_index,
      GtRegionNode *region_node,
      GtError *err)
```

Add `region_node` to `feature_index`.

```
int gt_feature_index_add_feature_node(
      GtFeatureIndex *feature_index,
      GtFeatureNode *feature_node,
      GtError *err)
```

Add `feature_node` to `feature_index`, associating it with a sequence region denoted by its identifier string.

```
int gt_feature_index_remove_node(
      GtFeatureIndex *feature_index,
      GtFeatureNode *node,
      GtError *err)
```

Removes node `genome_node` from `feature_index`.

```
int gt_feature_index_add_gff3file(
      GtFeatureIndex *feature_index,
      const char *gff3file,
      GtError *err)
```

Add all features contained in <gff3file> to `feature_index`, if <gff3file> is valid. Otherwise, `feature_index` is not changed and `err` is set.

```
GtArray* gt_feature_index_get_features_for_seqid(
           GtFeatureIndex*,
           const char *seqid,
           GtError *err)
```

Returns an array of `GtFeatureNodes` associated with a given sequence region identifier `seqid`.

```
int gt_feature_index_get_features_for_range(
      GtFeatureIndex
                                                  *feature_index,
      GtArray *results,
      const char *seqid,
      const GtRange *range,
      GtError*)
```

Look up genome features in `feature_index` for sequence region `seqid` in `range` and store them in `results`.

```
char* gt_feature_index_get_first_seqid(
        const GtFeatureIndex
                                                *feature_index,
        GtError *err)
```

Returns the first sequence region identifier added to `feature_index`.

```
GtStrArray* gt_feature_index_get_seqids(
              const GtFeatureIndex *feature_index,
              GtError *err)
```

Returns a `GtStrArray` of all sequence region identifiers contained in `feature_index` (in alphabetical order).

```
int gt_feature_index_get_range_for_seqid(
      GtFeatureIndex *feature_index,
      GtRange *range,
      const char *seqid,
      GtError *err)
```

Writes the range of all features contained in the `feature_index` for region identifier `seqid` to the `GtRange` pointer `range`.

```
int gt_feature_index_get_orig_range_for_seqid(
      GtFeatureIndex
                                                                    *feature_index,
      GtRange *range,
      const char *seqid,
      GtError *err)
```

Writes the range of the whole sequence region contained in the `feature_index` for region identifier `seqid` to the `GtRange` pointer `range`.

```
int gt_feature_index_has_seqid(
      const GtFeatureIndex *feature_index,
      bool *has_seqid,
      const char *seqid,
      GtError *err)
```

Returns `has_seqid` to true if the sequence region identified by `seqid` has been registered in the `feature_index`.

```
int gt_feature_index_save(
      GtFeatureIndex *feature_index,
      GtError *err)
```

Calls the save function for the given `feature_index`. The save functions must be defined, otherwise the method fails with an assertion (for example, the memory based feature index does not have a save function) .

```
void gt_feature_index_delete(
       GtFeatureIndex*)
```

Deletes the `feature_index` and all its referenced features.

Class GtFeatureIndexMemory

The `GtFeatureIndexMemory` class implements a `GtFeatureIndex` in memory. Features are organized by region node. Each region node collects its feature nodes in an interval tree structure, which allows for efficient range queries.

Methods

```
GtFeatureIndex* gt_feature_index_memory_new(
                  void)
```

Creates a new `GtFeatureIndexMemory` object.

```
GtFeatureNode* gt_feature_index_memory_get_node_by_ptr(
                 GtFeatureIndexMemory*,
                 GtFeatureNode *ptr,
                 GtError *err)
```

Returns `ptr` if it is a valid node indexed in `GtFeatureIndexMemory`. Otherwise NULL is returned and `err` is set accordingly.

Class GtFeatureNode

Implements the `GtGenomeNode` interface. A single feature node corresponds to a GFF3 feature line (i.e., a line which does not start with <#>). Part-of relationships (which are realized in GFF3 with the `Parent` and `ID` attributes) are realized in the C API with the `gt_feature_node_add_child()` method.
Besides the "mere" feature nodes two "special" feature nodes exist: multi-features and pseudo-features.
Multi-features represent features which span multiple lines (it is indicated in GFF3 files by the fact, that each line has the same ID attribute).
To check if a feature is a multi-feature use the method `gt_feature_node_is_multi()`. Multi-features are connected via a "representative". That is, two features are part of the same multi-feature if they have the same representative. The feature node representative can be be retrieved via the `gt_feature_node_get_multi_representative()` method.
Pseudo-features became a technical necessity to be able to pass related top-level features as a single entity through the streaming machinery. There are two cases in which a pseudo-feature has to be introduced.
First, if a multi-feature has no parent. In this case all features which comprise the multi-feature become the children of a pseudo-feature.

Second, if two or more top-level features have the same children (and are thereby connected). In this case all these top-level features become the children of a pseudo-feature.
It should be clear from the explanation above that pseudo-features make only sense as top-level features (a fact which is enforced in the code).
Pseudo-features are typically ignored during a traversal to give the illusion that they do not exist.

Methods

```
GtGenomeNode* gt_feature_node_new(
                GtStr *seqid,
                const char *type,
                GtUword start,
                GtUword end,
                GtStrand strand)
```

Return an new `GtFeatureNode` object on sequence with ID `seqid` and type `type` which lies from `start` to `end` on strand `strand`. The `GtFeatureNode*` stores a new reference to `seqid`, so make sure you do not modify the original `seqid` afterwards! `start` and `end` always refer to the forward strand, therefore `start` has to be smaller or equal than `end`.

```
GtGenomeNode* gt_feature_node_new_pseudo(
                GtStr *seqid,
                GtUword start,
                GtUword end,
                GtStrand strand)
```

Return a new pseudo-`GtFeatureNode` object on sequence with ID `seqid` which lies from `start` to `end` on strand `strand`. Pseudo-features do not have a type. The <GtFeatureNode > stores a new reference to `seqid`, so make sure you do not modify the original `seqid` afterwards. `start` and `end` always refer to the forward strand, therefore `start` has to be smaller or equal than `end`.

```
GtGenomeNode* gt_feature_node_new_pseudo_template(
                GtFeatureNode *feature_node)
```

Return a new pseudo-`GtFeatureNode` object which uses `feature_node` as template. That is, the sequence ID, range, strand, and source are taken from `feature_node`.

```
GtGenomeNode* gt_feature_node_new_standard_gene(
                void)
```

Return the "standard gene" (mainly for testing purposes).

```
void gt_feature_node_add_child(
       GtFeatureNode *parent,
       GtFeatureNode *child)
```

Add `child` feature node to `parent` feature node. `parent` takes ownership of `child`.

```
const char* gt_feature_node_get_source(
              const GtFeatureNode *feature_node)
```

Return the source of `feature_node`. If no source has been set, "." is returned. Corresponds to column 2 of GFF3 feature lines.

```
void gt_feature_node_set_source(
       GtFeatureNode *feature_node,
       GtStr *source)
```

Set the `source` of `feature_node`. Stores a new reference to `source`. Corresponds to column 2 of GFF3 feature lines.

```
bool gt_feature_node_has_source(
       const GtFeatureNode *feature_node)
```

Return `true` if `feature_node` has a defined source (i.e., on different from "."). `false` otherwise.

```
const char* gt_feature_node_get_type(
              const GtFeatureNode *feature_node)
```

Return the type of `feature_node`. Corresponds to column 3 of GFF3 feature lines.

```
void gt_feature_node_set_type(
       GtFeatureNode *feature_node,
       const char *type)
```

Set the type of `feature_node` to `type`.

```
bool gt_feature_node_has_type(
       GtFeatureNode *feature_node,
       const char *type)
```

Return `true` if `feature_node` has given `type`, `false` otherwise.

```
GtUword gt_feature_node_number_of_children(
          const GtFeatureNode
                                                *feature_node)
```

Return the number of children for given `feature_node`.

```
GtUword gt_feature_node_number_of_children_of_type(
          const GtFeatureNode
                                                      *parent,
          const GtFeatureNode
                                                      *node)
```

Return the number of children of type `node` for given GtFeatureNode `parent`.

```
bool gt_feature_node_score_is_defined(
       const GtFeatureNode
                                                    *feature_node)
```

Return `true` if the score of `feature_node` is defined, `false` otherwise.

```
float gt_feature_node_get_score(
        const GtFeatureNode *feature_node)
```

Return the score of `feature_node`. The score has to be defined. Corresponds to column 6 of GFF3 feature lines.

```
void gt_feature_node_set_score(
       GtFeatureNode *feature_node,
       float score)
```

Set the score of `feature_node` to `score`.

```
void gt_feature_node_unset_score(
       GtFeatureNode *feature_node)
```

Unset the score of `feature_node`.

```
GtStrand gt_feature_node_get_strand(
          const GtFeatureNode *feature_node)
```

Return the strand of `feature_node`. Corresponds to column 7 of GFF3 feature lines.

```
void gt_feature_node_set_strand(
       GtFeatureNode *feature_node,
       GtStrand strand)
```

Set the strand of `feature_node` to `strand`.

```
GtPhase gt_feature_node_get_phase(
          const GtFeatureNode *feature_node)
```

Return the phase of `feature_node`. Corresponds to column 8 of GFF3 feature lines.

```
void gt_feature_node_set_phase(
       GtFeatureNode *feature_node,
       GtPhase phase)
```

Set the phase of `feature_node` to `phase`.

```
const char* gt_feature_node_get_attribute(
              const GtFeatureNode *feature_node,
              const char *name)
```

Return the attribute of `feature_node` with the given `name`. If no such attribute has been added, `NULL` is returned. The attributes are stored in column 9 of GFF3 feature lines.

```
GtStrArray* gt_feature_node_get_attribute_list(
              const GtFeatureNode
                                                    *feature_node)
```

Return a string array containing the used attribute names of `feature_node`. The caller is responsible to free the returned `GtStrArray*`.

```
void gt_feature_node_add_attribute(
       GtFeatureNode *feature_node,
       const char *tag,
       const char *value)
```

Add attribute `tag=value` to `feature_node`. `tag` and `value` must at least have length 1. `feature_node` must not contain an attribute with the given `tag` already. You should not add Parent and ID attributes, use `gt_feature_node_add_child()` to denote part-of relationships.

```
void gt_feature_node_set_attribute(
       GtFeatureNode* feature_node,
       const char *tag,
       const char *value)
```

Set attribute `tag` to new `value` in `feature_node`, if it exists already. Otherwise the attribute `tag=value` is added to `feature_node`. `tag` and `value` must at least have length 1. You should not set Parent and ID attributes, use `gt_feature_node_add_child()` to denote part-of relationships.

```
void gt_feature_node_remove_attribute(
       GtFeatureNode* feature_node,
       const char *tag)
```

Remove attribute `tag` from `feature_node`. `feature_node` must contain an attribute with the given `tag` already! You should not remove Parent and ID attributes.

```
void GtFeatureNodeAttributeIterFunc(
                                    const char *attr_name,
                                    const char *attr_value,
                                    void *data)
```

Delivers the key (in `attr_name`)and value (in `attr_value`) of an attribute. The `data` parameter carries over arbitrary user data from the `gt_feature_node_foreach_attribute` call.

```
void gt_feature_node_foreach_attribute(
       GtFeatureNode *feature_node,
       GtFeatureNodeAttributeIterFunc func,
       void *data)
```

Calls `func` for each attribute in `feature_node`. Use `data` to forward arbitrary data during traversal.

```
bool gt_feature_node_is_multi(
       const GtFeatureNode *feature_node)
```

Return `true` if `feature_node` is a multi-feature, `false` otherwise.

```
bool gt_feature_node_is_pseudo(
       const GtFeatureNode *feature_node)
```

Return `true` if `feature_node` is a pseudo-feature, `false` otherwise.

```
void gt_feature_node_make_multi_representative(
       GtFeatureNode
                                                          *feature_node)
```

Make `feature_node` the representative of a multi-feature. Thereby `feature_node` becomes a multi-feature.

```
void gt_feature_node_set_multi_representative(
       GtFeatureNode
                                                        *feature_node,
       GtFeatureNode
                                                        *representative)
```

Set the multi-feature representative of `feature_node` to `representative`. Thereby `feature_node` becomes a multi-feature.

```
void gt_feature_node_unset_multi(
       GtFeatureNode *feature_node)
```

Unset the multi-feature status of `feature_node` and remove its multi-feature representative.

```
GtFeatureNode* gt_feature_node_get_multi_representative(
                 GtFeatureNode
                                                        *feature_node)
```

Return the representative of the multi-feature `feature_node`.

```
bool gt_feature_node_is_similar(
       const GtFeatureNode *feature_node_a,
       const GtFeatureNode *feature_node_b)
```

Returns `true`, if the given `feature_node_a` has the same seqid, feature type, range, strand, and phase as `feature_node_b`. Returns `false` otherwise.

```
void gt_feature_node_mark(
       GtFeatureNode*)
```

Marks the given `feature_node`.

```
void gt_feature_node_unmark(
       GtFeatureNode*)
```

If the given `feature_node` is marked it will be unmarked.

```
bool gt_feature_node_contains_marked(
       GtFeatureNode *feature_node)
```

Returns `true` if the given `feature_node` graph contains a marked node.

```
bool gt_feature_node_is_marked(
       const GtFeatureNode *feature_node)
```

Returns `true` if the (top-level) `feature_node` is marked.

```
void gt_feature_node_remove_leaf(
       GtFeatureNode *tree,
       GtFeatureNode *leafn)
```

Removes the parent-child relationship between the leaf node `leafn` and a parent node `tree`. `tree` needs not be the direct parent of the `leafn`. Note that `leafn` is freed, use `gt_genome_node_ref()` to increase the reference count if deletion is not wanted. As a side effect, the tree property of `tree` is set back to an undefined state.

```
GtFeatureNode* gt_feature_node_try_cast(
                 GtGenomeNode *gn)
```

Test whether the given genome node is a feature node. If so, a pointer to the feature node is returned. If not, NULL is returned. Note that in most cases, one should implement a GtNodeVisitor to handle processing of different GtGenomeNode types.

```
GtFeatureNode* gt_feature_node_cast(
                 GtGenomeNode *gn)
```

Test whether the given genome node is a feature node. If so, a pointer to the feature node is returned. If not, an assertion fails.

Class GtFeatureNodeIterator

```
GtFeatureNodeIterator* gt_feature_node_iterator_new(
                          const GtFeatureNode
                                                  *feature_node)
```

Return a new `GtFeatureNodeIterator*` which performs a depth-first traversal of `feature_node` (including `feature_node` itself). It ignores pseudo-features.

```
GtFeatureNodeIterator* gt_feature_node_iterator_new_direct(
                          const GtFeatureNode
                                                      *feature_node)
```

Return a new `GtFeatureNodeIterator*` which iterates over all direct children of `feature_node` (without `feature_node` itself).

```
GtFeatureNode* gt_feature_node_iterator_next(
                  GtFeatureNodeIterator
                                                    *feature_node_iterator)
```

Return the next `GtFeatureNode*` in `feature_node_iterator` or `NULL` if none exists.

```
void gt_feature_node_iterator_delete(
       GtFeatureNodeIterator
                                                      *feature_node_iterator)
```

Delete `feature_node_iterator`.

Class GtFeatureOutStream

```
GtNodeStream* gt_feature_out_stream_new(
                GtNodeStream*,
                GtFeatureIndex *fi)
```

Create a new `GtFeatureOutStream` which writes all passed nodes to `GtFeatureIndex fi`.

Class GtFeatureStream

```
GtNodeStream* gt_feature_stream_new(
                GtNodeStream*,
                GtFeatureIndex *fi)
```

Create a new `GtFeatureStream` which writes all passed nodes to `GtFeatureIndex fi`. Note: The `GtFeatureStream` class is now deprecated. Please use the `GtFeatureOutStream` class instead.

Class GtFile

This class defines (generic) files in *GenomeTools*. A generic file is is a file which either uncompressed or compressed (with gzip or bzip2). A `NULL`-pointer as generic file implies `stdout`.

Methods

```
GtFile* gt_file_new(
          const char *path,
          const char *mode,
          GtError *err)
```

Return a new `GtFile` object for the given `path` and open the underlying file handle with given `mode`. Returns `NULL` and sets `err` accordingly, if the file `path` could not be opened. The compression mode is determined by the ending of `path` (gzip compression if it ends with '.gz', bzip2 compression if it ends with '.bz2', and uncompressed otherwise).

```
GtFile* gt_file_ref(
          GtFile *file)
```

Increments the reference count of `file`.

```
GtFile* gt_file_new_from_fileptr(
          FILE *fp)
```

Create a new `GtFile` object from a normal file pointer `fp`.

```
void gt_file_xprintf(
       GtFile *file,
       const char *format,
       ...)
```

<printf(3)> for generic `file`.

```
void gt_file_xfputs(
       const char *cstr,
       GtFile *file)
```

Write <\0 >-terminated C string `cstr` to `file`. Similar to <fputs(3)>, but terminates on error.

```
void gt_file_xfputc(
       int c,
       GtFile *file)
```

Write single character `c` to `file`. Similar to <fputc(3)>, but terminates on error.

```
int gt_file_xfgetc(
      GtFile *file)
```

Return next character from `file` or `EOF`, if end-of-file is reached.

```
int gt_file_xread(
      GtFile *file,
      void *buf,
      size_t nbytes)
```

Read up to `nbytes` from generic `file` and store result in `buf`, returns bytes read.

```
void gt_file_xwrite(
       GtFile *file,
       void *buf,
       size_t nbytes)
```

Write `nbytes` from `buf` to given generic `file`.

```
void gt_file_xrewind(
       GtFile *file)
```

Rewind the generic `file`.

```
GtFileMode gt_file_mode_determine(
             const char *path)
```

Returns `GT_FILE_MODE_GZIP` if file with `path` ends with '.gz', <GT_FILE_MODE_BZIP2 > if it ends with '.bz2', and `GT_FILE_MODE_UNCOMPRESSED` otherwise.

```
const char* gt_file_mode_suffix(
              GtFileMode mode)
```

Returns ".gz" if `mode` is GFM_GZIP, ".bz2" if `mode` is GFM_BZIP2, and "" otherwise.

```
size_t gt_file_basename_length(
    const char *path)
```

Returns the length of the "basename" of `path`. That is, the length of path without '.gz' or '.bz2' suffixes.

```
GtFile* gt_file_open(
          GtFileMode,
          const char *path,
          const char *mode,
          GtError*)
```

Create a new GtFile object and open the underlying file handle, returns NULL and sets `err` if the file `path` could not be opened.

```
GtFile* gt_file_xopen_file_mode(
          GtFileMode file_mode,
          const char *path,
          const char *mode)
```

Create a new GtFile object and open the underlying file handle, abort if the file `path` does not exist. The `file_mode` has to be given explicitly.

```
GtFile* gt_file_xopen(
          const char *path,
          const char *mode)
```

Create a new GtFile object and open the underlying file handle. Aborts if the file `path` could not be opened. The GtFileMode is determined automatically via gt_file_mode_determine(path).

```
GtFileMode gt_file_mode(
             const GtFile *file)
```

Returns the mode of the given `file`.

```
void gt_file_unget_char(
       GtFile *file,
       char c)
```

Unget character `c` to `file` (which obviously cannot be `NULL`). Can only be used once at a time.

```
void gt_file_delete(
       GtFile *file)
```

Close the underlying file handle and destroy the `file` object.

```
void gt_file_delete_without_handle(
       GtFile*)
```

Destroy the file handle object, but do not close the underlying handle.

Class GtGFF3InStream

Implements the `GtNodeStream` interface. A <GtGFF3InStream> parses GFF3 files and returns them as a stream of `GtGenomeNode` objects.

Methods

```
GtNodeStream* gt_gff3_in_stream_new_unsorted(
                int num_of_files,
                const char **filenames)
```

Return a <GtGFF3InStream> object which subsequently reads the `num_of_files` many GFF3 files denoted in `filenames`. The GFF3 files do not have to be sorted. If `num_of_files` is 0 or a file name is "-", it is read from `stdin`. The memory footprint is O(file size) in the worst-case.

```
GtNodeStream* gt_gff3_in_stream_new_sorted(
                const char *filename)
```

Create a <GtGFF3InStream*> which reads the sorted GFF3 file denoted by `filename`. If filename is `NULL`, it is read from `stdin`. The memory footprint is O(1) on average.

```
void gt_gff3_in_stream_check_id_attributes(
       GtGFF3InStream
                                                          *gff3_in_stream)
```

Make sure all ID attributes which are parsed by <gff3_in_stream> are correct. Increases the memory footprint to O(file size).

```
void gt_gff3_in_stream_enable_tidy_mode(
       GtGFF3InStream
                                                          *gff3_in_stream)
```

Enable tidy mode for <gff3_in_stream>. That is, the GFF3 parser tries to tidy up features which would normally lead to an error.

```
void gt_gff3_in_stream_enable_strict_mode(
       GtGFF3InStream
                                                          *gff3_in_stream)
```

Enable strict mode for <gff3_in_stream>.

```
void gt_gff3_in_stream_show_progress_bar(
       GtGFF3InStream
                                                          *gff3_in_stream)
```

Show progress bar on `stdout` to convey the progress of parsing the GFF3 files underlying <gff3_in_stream>.

```
GtStrArray* gt_gff3_in_stream_get_used_types(
              GtNodeStream *gff3_in_stream)
```

Returns a `GtStrArray*` which contains all type names in alphabetical order which have been parsed by <gff3_in_stream>. The caller is responsible to free it!

```
void gt_gff3_in_stream_set_type_checker(
       GtNodeStream *gff3_in_stream,
       GtTypeChecker *type_checker)
```

Sets `type_checker` to be the type checker used in <gff3_in_stream>. That is, it will be queried when the validity of SO types is to be determined.

Class GtGFF3OutStream

Implements the `GtNodeStream` interface. A <GtGFF3OutStream> produces GFF3 output. It automatically inserts termination lines at the appropriate places.

Methods

```
GtNodeStream* gt_gff3_out_stream_new(
                GtNodeStream *in_stream,
                GtFile *outfp)
```

Create a <GtGFF3OutStream*> which uses `in_stream` as input. It shows the nodes passed through it as GFF3 on `outfp`.

```
void gt_gff3_out_stream_set_fasta_width(
       GtGFF3OutStream
                                              *gff3_out_stream,
       GtUword fasta_width)
```

Set the width with which the FASTA sequences of `GtSequenceNodes` passed through <gff3_out_stream> are shown to `fasta_width`. Per default, each FASTA entry is shown on a single line.

```
void gt_gff3_out_stream_retain_id_attributes(
       GtGFF3OutStream
                                                    *gff3_out_stream)
```

If this method is called upon <gff3_out_stream>, use the original ID attributes provided in the input (instead of creating new ones, which is the default). Memory consumption for <gff3_out_stream> is raised from O(1) to O(`input_size`), because bookkeeping of used IDs becomes necessary to avoid ID collisions.

Class GtGFF3Parser

A <GtGFF3Parser> can be used to parse GFF3 files and convert them into `GtGenomeNode` objects. If the GFF3 files do not contain the encouraged sequence-region meta directives, the GFF3 parser introduces the corresponding region nodes automatically. This is a low-level class and it is usually not used directly. Normally, a <GtGFF3InStream> is used to parse GFF3 files.

Methods

```
GtGFF3Parser* gt_gff3_parser_new(
                GtTypeChecker *type_checker)
```

Return a new <GtGFF3Parser> object with optional `type_checker`. If a `type_checker` was given, the <GtGFF3Parser> stores a new reference to it internally and uses the `type_checker` to check types during parsing.

```
void gt_gff3_parser_check_id_attributes(
       GtGFF3Parser *gff3_parser)
```

Enable ID attribute checking in <gff3_parser>. Thereby, the memory consumption of the <gff3_parser> becomes proportional to the input file size(s).

```
void gt_gff3_parser_check_region_boundaries(
       GtGFF3Parser *gff3_parser)
```

Enable sequence region boundary checking in <gff3_parser>. That is, encountering features outside the sequence region boundaries will result in an error.

```
void gt_gff3_parser_do_not_check_region_boundaries(
       GtGFF3Parser
                                                  *gff3_parser)
```

Disable sequence region boundary checking in <gff3_parser>. That is, features outside the sequence region boundaries will be permitted.

```
void gt_gff3_parser_set_offset(
       GtGFF3Parser *gff3_parser,
       GtWord offset)
```

Transform all features parsed by <gff3_parser> by the given `offset`.

```
void gt_gff3_parser_set_type_checker(
       GtGFF3Parser *gff3_parser,
       GtTypeChecker *type_checker)
```

Set `type_checker` used by <gff3_parser>.

```
void gt_gff3_parser_set_xrf_checker(
       GtGFF3Parser *gff3_parser,
       GtXRFChecker *xrf_checker)
```

Set `xrf_checker` used by <gff3_parser>.

```
void gt_gff3_parser_enable_tidy_mode(
       GtGFF3Parser *gff3_parser)
```

Enable the tidy mode in <gff3_parser>. In tidy mode the <gff3_parser> parser tries to tidy up features which would normally lead to a parse error.

```
int gt_gff3_parser_parse_genome_nodes(
      GtGFF3Parser *gff3_parser,
      int *status_code,
      GtQueue *genome_nodes,
      GtCstrTable *used_types,
      GtStr *filenamestr,
      GtUint64 *line_number,
      GtFile *fpin,
      GtError *err)
```

Use <gff3_parser> to parse genome nodes from file pointer `fpin`. `status_code` is set to 0 if at least one genome node was created (and stored in `genome_nodes`) and to `EOF` if no further genome nodes could be parsed from `fpin`. Every encountered (genome feature) type is recorded in the C string table `used_types`. The parser uses the given `filenamestr` to store the file name of `fpin` in the created genome nodes or to give the correct filename in error messages, if necessary. `line_number` is increased accordingly during parsing and has to be set to 0 before parsing a new `fpin`. If an error occurs during parsing this method returns -1 and sets `err` accordingly.

```
void gt_gff3_parser_reset(
       GtGFF3Parser *gff3_parser)
```

Reset the <gff3_parser> (necessary if the input file is switched).

```
void gt_gff3_parser_delete(
       GtGFF3Parser *gff3_parser)
```

Delete the <gff3_parser>.

Class GtGFF3Visitor

Implements the `GtNodeVisitor` interface with a visitor that produces GFF3 output. This is a low-level class and it is usually not used directly. Normally, a <GtGFF3OutStream> is used to produce GFF3 output.

Methods

```
GtNodeVisitor* gt_gff3_visitor_new(
                  GtFile *outfp)
```

Create a new `GtNodeVisitor*` which writes the output it produces to the given output file pointer `outfp`. If `outfp` is `NULL`, the output is written to `stdout`.

```
void gt_gff3_visitor_set_fasta_width(
       GtGFF3Visitor *gff3_visitor,
       GtUword fasta_width)
```

Set the width with which the FASTA sequences of `GtSequenceNodes` visited by <gff3_visitor> are shown to `fasta_width`. Per default, each FASTA entry is shown on a single line.

```
void gt_gff3_visitor_retain_id_attributes(
       GtGFF3Visitor
                                                  *gff3_visitor)
```

Retain the original ID attributes (instead of creating new ones), if possible. Memory consumption for <gff3_visitor> is raised from O(1) to O(`input_size`), because bookkeeping of used IDs becomes necessary to avoid ID collisions.

Class GtGTFInStream

Implements the `GtNodeStream` interface. A `GtGTFInStream` parses a GTF2.2 file and returns it as a stream of `GtGenomeNode` objects.

Methods

```
GtNodeStream* gt_gtf_in_stream_new(
                 const char *filename)
```

Create a `GtGTFInStream*` which subsequently reads the GTF file with the given `filename`. If `filename` equals `NULL`, the GTF data is read from `stdin`.

Class GtGTFOutStream

Implements the `GtNodeStream` interface. A `GtGTFOutStream` produces GTF2.2 output.

Methods

```
GtNodeStream* gt_gtf_out_stream_new(
                GtNodeStream *in_stream,
                GtFile *outfp)
```

Create a `GtNodeStream*` which uses `in_stream` as input. It shows the nodes passed through it as GTF2.2 on `outfp`.

Class GtGenomeNode

The `GtGenomeNode` interface. The different implementation of the `GtGenomeNode` interface represent different parts of genome annotations (as they are usually found in GFF3 files).

Methods

```
GtGenomeNode* gt_genome_node_ref(
                GtGenomeNode *genome_node)
```

Increase the reference count for `genome_node` and return it. `genome_node` must not be `NULL`.

```
GtStr* gt_genome_node_get_seqid(
          GtGenomeNode *genome_node)
```

Return the sequence ID of `genome_node`. Corresponds to column 1 of GFF3 feature lines.

```
GtRange gt_genome_node_get_range(
           GtGenomeNode *genome_node)
```

Return the genomic range of of `genome_node`. Corresponds to columns 4 and 5 of GFF3 feature lines.

```
GtUword gt_genome_node_get_start(
           GtGenomeNode *genome_node)
```

Return the start of `genome_node`. Corresponds to column 4 of GFF3 feature lines.

```
GtUword gt_genome_node_get_end(
           GtGenomeNode *genome_node)
```

Return the end of `genome_node`. Corresponds to column 5 of GFF3 feature lines.

```
GtUword gt_genome_node_get_length(
           GtGenomeNode *genome_node)
```

Return the length of `genome_node`. Computed from column 4 and 5 of GFF3 feature lines.

```
const char* gt_genome_node_get_filename(
              const GtGenomeNode* genome_node)
```

Return the filename the genome_node was read from. If the node did not originate from a file, an appropriate string is returned.

```
unsigned int gt_genome_node_get_line_number(
               const GtGenomeNode*)
```

Return the line of the source file the genome_node was encountered on (if the node was read from a file, otherwise 0 is returned).

```
void gt_genome_node_set_range(
       GtGenomeNode *genome_node,
       const GtRange *range)
```

Set the genomic range of genome_node to given range.

```
void gt_genome_node_add_user_data(
       GtGenomeNode *genome_node,
       const char *key,
       void *data,
       GtFree free_func)
```

Attach a pointer to data to the genome_node using a given string as key. free_func is the optional destructor for data.

```
void* gt_genome_node_get_user_data(
        const GtGenomeNode *genome_node,
        const char *key)
```

Return the pointer attached to the genome_node for a given key.

```
void gt_genome_node_release_user_data(
       GtGenomeNode *genome_node,
       const char *key)
```

Call the destructor function associated with the user data attached to genome_node under the key on the attached data.

```
int gt_genome_node_cmp(
      GtGenomeNode *genome_node_a,
      GtGenomeNode *genome_node_b)
```

Compare genome_node_a with genome_node_b and return the result (similar to <strcmp(3)>). This method is the criterion used to sort genome nodes.

```
void gt_genome_nodes_sort(
       GtArray *nodes)
```

Sort node array nodes

```
void gt_genome_nodes_sort_stable(
       GtArray *nodes)
```

Sort node array nodes in a stable way

```
int gt_genome_node_accept(
      GtGenomeNode *genome_node,
      GtNodeVisitor *node_visitor,
      GtError *err)
```

Let genome_node accept the node_visitor. In the case of an error, -1 is returned and err is set accordingly.

```
void gt_genome_nodes_show(
       GtArray *nodes,
       GtFile *outfp)
```

Outputs the nodes nodes to the output outfp.

```
void gt_genome_node_delete(
       GtGenomeNode *genome_node)
```

Decrease the reference count for genome_node or delete it, if this was the last reference.

Class GtGraphics

The GtGraphics interface acts as a low-level abstraction of a drawing surface. It is used as a common drawing object in GtCanvas and GtCustomTrack implementations and supports a variety of drawing operations for both text and basic primitive shapes.

Methods

```
void gt_graphics_draw_text(
       GtGraphics*,
       double x,
       double y,
       const char*)
```

Draws text in black to the right of (x,y). The coordinate y is used as a baseline.

```
void gt_graphics_draw_text_clip(
       GtGraphics*,
       double x,
       double y,
       const char*)
```

Draws text in black to the right of (x,y). The coordinate y is used as a baseline. If the text exceeds the margins, it is clipped.

```
#define gt_graphics_draw_text_left(
          g,x,y,t)
```

Synonym to gt_graphics_draw_text()

```
void gt_graphics_draw_text_centered(
       GtGraphics*,
       double x,
       double y,
       const char*)
```

Draws text in black centered at (x,y). The coordinate y is used as a baseline.

```
void gt_graphics_draw_text_right(
       GtGraphics*,
       double x,
       double y,
       const char*)
```

Draws text in black to the left of (x,y). The coordinate y is used as a baseline.

```
void gt_graphics_draw_colored_text(
       GtGraphics*,
       double x,
       double y,
       GtColor,
       const char*)
```

Draws text in a given GtColor to the right of (x,y). The coordinate y is used as a baseline.

```
double gt_graphics_get_text_height(
         GtGraphics*)
```

Returns the height of a capital letter in pixels/points.

```
int gt_graphics_set_background_color(
      GtGraphics*,
      GtColor)
```

Sets the background color of the GtGraphics to a specific color. Note that this may only be supported for bitmap output formats.

```
double gt_graphics_get_text_width(
         GtGraphics*,
         const char *text)
```

Returns the width of the given string in pixels/points.

```
void gt_graphics_set_font(
       GtGraphics *g,
       const char *family,
       FontSlant slant,
       FontWeight weight,
       double size)
```

Sets basic font family, slant and weight options. Font families are implementation-specific, e.g. in Cairo there is no operation to list available family names on the system, but the standard CSS2 generic family names, (”serif”, ”sans-serif”, ”cursive”, ”fantasy”, ”monospace”), are likely to work as expected.

```
double gt_graphics_get_image_width(
         GtGraphics*)
```

Returns the width of the image in pixels/points.

```
double gt_graphics_get_image_height(
         GtGraphics*)
```

Returns the height of the image in pixels/points.

```
void gt_graphics_set_margins(
       GtGraphics*,
       double margin_x,
       double margin_y)
```

Set margins (space to the image boundaries that are clear of elements) in the graphics. `margin_x` denotes the Margin to the left and right, in pixels. `margin_y` denotes the Margin to the top and bottom, in pixels.

```
double gt_graphics_get_xmargins(
         GtGraphics*)
```

Returns the horizontal margins in pixels/points.

```
double gt_graphics_get_ymargins(
         GtGraphics*)
```

Returns the vertical margins in pixels/points.

```
void gt_graphics_draw_horizontal_line(
       GtGraphics *g,
       double x,
       double y,
       GtColor color,
       double width,
       double stroke_width)
```

Draws a horizontal line of length `width` beginning at the given coordinates to the right in the color `color` with stroke width `stroke_width`.

```
void gt_graphics_draw_vertical_line(
       GtGraphics *g,
       double x,
       double y,
       GtColor color,
       double length,
       double stroke_width)
```

Draws a vertical line of length `length` beginning at the given coordinates downwards in the color `color` with stroke width `stroke_width`.

```
void gt_graphics_draw_line(
       GtGraphics *g,
       double x,
       double y,
       double xto,
       double yto,
       GtColor color,
       double stroke_width)
```

Draws a line beginning at (x,y) to (`xto`,`yto`) in the color `color` with stroke width `stroke_width`.

```
void gt_graphics_draw_box(
       GtGraphics*,
       double x,
       double y,
       double width,
       double height,
       GtColor fill_color,
       ArrowStatus arrow_status,
       double arrow_width,
       double stroke_width,
       GtColor stroke_color,
       bool dashed)
```

Draws a arrow-like box glyph at (x,y) where these are the top left coordinates. The box extends `width` pixels (incl. arrowhead) into the x direction and `height` pixels into the y direction. It will be filled with `fill_color` and stroked with width `stroke_width` and color `stroke_color`. The width of the arrowhead is given by the `arrow_width` parameter. The `arrow_status` parameter determines whether an arrowhead will be drawn at the left or right end, both ends, or none. If `dashed` is set to true, then the outline will be dashed instead of solid.

```
void gt_graphics_draw_dashes(
       GtGraphics*,
       double x,
       double y,
       double width,
       double height,
       ArrowStatus arrow_status,
       double arrow_width,
       double stroke_width,
       GtColor stroke_color)
```

Draws a transparent box with a dashed line at the center at (x,y) (where these are the top left coordinates). The box extends `width` pixels (incl. arrowhead) into the x direction and `height` pixels into the y direction. It will be stroked with width `stroke_width` and color `stroke_color`. The width of the arrowhead is given by the `arrow_width` parameter. The `arrow_status` parameter determines whether an arrowhead will be drawn at the left or right end, both ends, or none.

```
void gt_graphics_draw_caret(
       GtGraphics*,
       double x,
       double y,
       double width,
       double height,
       ArrowStatus arrow_status,
       double arrow_width,
       double stroke_width,
       GtColor stroke_color)
```

Draws a caret ("hat") style glyph at (x,y) (where these are the top left coordinates). The box extends `width` pixels (incl. arrowhead) into the x direction and `height` pixels into the y direction. It will be stroked with width `stroke_width` and color `stroke_color`. The width of the arrowhead is given by the `arrow_width` parameter. The `arrow_status` parameter determines whether an arrowhead will be drawn at the left or right end, both ends, or none.

```
void gt_graphics_draw_rectangle(
       GtGraphics*,
       double x,
       double y,
       bool filled,
       GtColor fill_color,
       bool stroked,
       GtColor stroke_color,
       double stroke_width,
       double width,
       double height)
```

Draws a rectangle at (x,y) where these are the top left coordinates. The rectangle extends `width` pixels (incl. arrowhead) into the x direction and `height` pixels into the y direction. It will be filled with `fill_color` if `filled` is set to true and stroked with width `stroke_width` and color `stroke_color` if `stroked` is set to true.

```
void gt_graphics_draw_arrowhead(
       GtGraphics*,
       double x,
       double y,
       GtColor,
       ArrowStatus arrow_status)
```

Draws an arrowhead at (x,y) where these are the top left coordinates. The direction is determined by the `arrow_status` parameter.

```
void gt_graphics_draw_curve_data(
       GtGraphics *g,
       double x,
       double y,
       GtColor color,
       double data[],
       GtUword ndata,
       GtRange valrange,
       GtUword height)
```

Draws a curve over the full visible image width (without margins) at (x,y) where these are the top left coordinates. As input, the array of double values `data` with `ndata` data points is used. The `valrange` gives the minimum and maximum value of the displayed data. If a value outside the data range is encountered, the drawing will be stopped at this data point.

```
int gt_graphics_save_to_file(
      const GtGraphics*,
      const char *filename,
      GtError*)
```

Write out the `GtGraphics` object to the given file with `filename`.

```
void gt_graphics_save_to_stream(
       const GtGraphics*,
       GtStr *stream)
```

Write out the GtGraphics object to the given stream.

```
void gt_graphics_delete(
       GtGraphics*)
```

Deletes the the GtGraphics object.

Class GtGraphicsCairo

Implements the GtGraphics interface. This implementation uses the Cairo 2D vector graphics library as a drawing back-end.

Methods

```
GtGraphics* gt_graphics_cairo_new(
              GtGraphicsOutType type,
              unsigned int width,
              unsigned int height)
```

Creates a new GtGraphics object using the Cairo backend. The object is meant for writing a new image of width width and height height to a file or stream. Use type to define the output format.

```
GtGraphics* gt_graphics_cairo_new_from_context(
              cairo_t *context,
              unsigned int width,
              unsigned int height)
```

Creates a new GtGraphics object using the Cairo backend. The object is meant for writing on an existing cairo_t context within the boundaries of width width and height height.

```
void gt_graphics_cairo_draw_curve_data(
       GtGraphics *gg,
       double x,
       double y,
       GtColor color,
       double data[],
       GtUword ndata,
       GtRange valrange,
       GtUword height)
```

Draws a curve in gg at the position x,y for ndata data points as given in data. The data points must be in the range valrange and the resulting graph has the height height in type-dependent units (e.g. pixels).

Class GtHashmap

A hashmap allowing to index any kind of pointer (as a value). As keys, strings or any other pointer can be used.

Methods

```
int GtHashmapVisitFunc(
                        void *key,
                        void *value,
                        void *data,
                        GtError *err)
```

Callback function when using the gt_hashmap_foreach*() functions. Must return a status code (0 = continue iteration, 1 = stop iteration, 2 = deleted element, 3 = modified key, 4 = redo iteration). Gets called with the key and value of the current hashmap member, and the `err` object given in the original gt_hashmap_foreach*() call.

```
GtHashmap* gt_hashmap_new(
             GtHashType keyhashtype,
             GtFree keyfree,
             GtFree valuefree)
```

Creates a new `GtHashmap` object of type `keyhashtype`. If `keyfree` and/or `valuefree` are given, they will be used to free the hashmap members when the `GtHashmap` is deleted. `keyhashtype` defines how to hash the keys given when using the `GtHashmap`. `GT_HASH_DIRECT` uses the key pointer as a basis for the hash function. Equal pointers will refer to the same value. If `GT_HASH_STRING` is used, the keys will be evaluated as strings and keys will be considered equal if the strings are identical, regardless of their address in memory

```
GtHashmap* gt_hashmap_new_no_ma(
             GtHashType keyhashtype,
             GtFree keyfree,
             GtFree valuefree)
```

Like `gt_hashmap_new()`, but without using GenomeTools' memory allocator.

```
GtHashmap* gt_hashmap_ref(
             GtHashmap *hm)
```

Increase the reference count of `hm`.

```
void* gt_hashmap_get(
        GtHashmap *hashmap,
        const void *key)
```

Return the value stored in `hashmap` for `key` or `NULL` if no such key exists.

```
void* gt_hashmap_get_key(
        GtHashmap *hm,
        const void *key)
```

Returns the key stored in `hm` for `key` or NULL if no such key exists.

```
void gt_hashmap_add(
       GtHashmap *hashmap,
       void *key,
       void *value)
```

Set the value stored in `hashmap` for `key` to `value`, overwriting the prior value for that key if present.

```
void gt_hashmap_remove(
       GtHashmap *hashmap,
       const void *key)
```

Remove the member with key `key` from `hashmap`.

```
int gt_hashmap_foreach_ordered(
      GtHashmap *hashmap,
      GtHashmapVisitFunc func,
      void *data,
      GtCompare cmp,
      GtError *err)
```

Iterate over `hashmap` in order given by compare function `cmp`. For each member, `func` is called (see interface).

```
int gt_hashmap_foreach(
      GtHashmap *hashmap,
      GtHashmapVisitFunc func,
      void *data,
      GtError *err)
```

Iterate over `hashmap` in arbitrary order. For each member, `func` is called (see interface).

```
int gt_hashmap_foreach_in_key_order(
      GtHashmap *hashmap,
      GtHashmapVisitFunc func,
      void *data,
      GtError *err)
```

Iterate over `hashmap` in either alphabetical order (if `GtHashType` was specified as `GT_HASH_STRING`) or numerical order (if `GtHashType` was specified as `GT_HASH_DIRECT`).

```
void gt_hashmap_reset(
       GtHashmap *hashmap)
```

Reset `hashmap` by unsetting values for all keys, calling the free function if necessary.

```
void gt_hashmap_delete(
       GtHashmap *hashmap)
```

Delete hashmap, calling the free function if necessary.

Class GtIDToMD5Stream

Implements the GtNodeStream interface. A <GtIDToMD5Stream> converts "regular" sequence IDs to MD5 fingerprints.

Methods

```
GtNodeStream* gt_id_to_md5_stream_new(
                GtNodeStream *in_stream,
                GtRegionMapping *region_mapping,
                bool substitute_target_ids)
```

Create a <GtIDToMD5Stream> object which converts "regular" sequence IDs from nodes it retrieves from its in_stream to MD5 fingerprints (with the help of the given region_mapping). If substitute_target_ids is true, the IDs of Target attributes are also converted to MD5 fingerprints. Takes ownership of region_mapping!

Class GtImageInfo

The GtImageInfo class is a container for 2D coordinate to GtFeatureNode mappings which could, for example, be used to associate sections of a rendered image with GUI widgets or HTML imagemap areas. This information is given in the form of GtRecMap objects. They are created during the image rendering process and stored inside a GtImageInfo object for later retrieval. Additionally, the rendered width of an image can be obtained via a GtImageInfo method.

Methods

```
GtImageInfo* gt_image_info_new(
               void)
```

Creates a new GtImageInfo object.

```
unsigned int gt_image_info_get_height(
               GtImageInfo *image_info)
```

Returns the height of the rendered image (in pixels or points).

```
GtUword gt_image_info_num_of_rec_maps(
          GtImageInfo *image_info)
```

Returns the total number of mappings in image_info.

```
const GtRecMap* gt_image_info_get_rec_map(
                  GtImageInfo *image_info,
                  GtUword i)
```

Returns the `i`-th `GtRecMap` mapping in `image_info`.

```
void gt_image_info_delete(
       GtImageInfo *image_info)
```

Deletes `image_info` and all the `GtRecMap` objects created by it.

Class GtInterFeatureStream

Implements the `GtNodeStream` interface. A `GtInterFeatureStream` inserts new feature nodes between existing feature nodes of a certain type.

Methods

```
GtNodeStream* gt_inter_feature_stream_new(
                GtNodeStream *in_stream,
                const char *outside_type,
                const char *inter_type)
```

Create a `GtInterFeatureStream*` which inserts feature nodes of type `inter_type` between the feature nodes of type `outside_type` it retrieves from `in_stream` and returns them.

Class GtIntervalTree

This is an interval tree data structure, implemented according to Cormen et al., Introduction to Algorithms, 2nd edition, MIT Press, Cambridge, MA, USA, 2001

Methods

```
GtIntervalTree* gt_interval_tree_new(
                  GtFree)
```

Creates a new `GtIntervalTree`. If a `GtFree` function is given as an argument, it is applied on the data pointers in all inserted nodes when the `GtIntervalTree` is deleted.

```
GtUword gt_interval_tree_size(
          GtIntervalTree*)
```

Returns the number of elements in the `GtIntervalTree`.

```
GtIntervalTreeNode* gt_interval_tree_find_first_overlapping(
                      GtIntervalTree*,
                      GtUword start,
                      GtUword end)
```

Returns the first node in the GtIntervalTree which overlaps the given range (from start to end).

```
void gt_interval_tree_insert(
       GtIntervalTree *tree,
       GtIntervalTreeNode *node)
```

Inserts node node into tree.

```
void gt_interval_tree_find_all_overlapping(
       GtIntervalTree*,
       GtUword start,
       GtUword end,
       GtArray*)
```

Collects data pointers of all GtIntervalTreeNodes in the tree which overlap with the query range (from start to end) in a GtArray.

```
void gt_interval_tree_iterate_overlapping(
       GtIntervalTree *it,
       GtIntervalTreeIteratorFunc func,
       GtUword start,
       GtUword end,
       void *data)
```

Call func for all GtIntervalTreeNodes in the tree which overlap with the query range (from start to end). Use data to pass in arbitrary user data.

```
int gt_interval_tree_traverse(
      GtIntervalTree*,
      GtIntervalTreeIteratorFunc func,
      void *data)
```

Traverses the GtIntervalTree in a depth-first fashion, applying func to each node encountered. The data pointer can be used to reference arbitrary data needed in the GtIntervalTreeIteratorFunc.

```
void gt_interval_tree_remove(
       GtIntervalTree*,
       GtIntervalTreeNode *node)
```

Removes the entry referenced by node from the GtIntervalTree. The data attached to node is freed according to the free function defined in the tree. Note that the memory pointed to by node can be re-used internally, referencing other data in the tree. Make sure to handle this pointer as expired after calling gt_interval_tree_remove()!

```
void gt_interval_tree_delete(
       GtIntervalTree*)
```

Deletes a GtIntervalTree. If a GtFree function was set in the tree constructor, data pointers specified in the nodes are freed using the given GtFree function.

Class GtIntervalTreeNode

```
GtIntervalTreeNode* gt_interval_tree_node_new(
                      void *data,
                      GtUword low,
                      GtUword high)
```

Creates a new GtIntervalTreeNode. Transfers ownership of data to interval tree if inserted into a GtIntervalTree in which a GtIntervalTreeDataFreeFunc is set.

```
void* gt_interval_tree_node_get_data(
        GtIntervalTreeNode* node)
```

Returns a pointer to the data associated with node node.

Class GtLayout

The GtLayout class represents contents (tracks) of a GtDiagram broken up into lines such that a given horizontal space allotment given in pixels or points is used up most efficiently. This is done using the GtLineBreaker and GtTextWidthCalculator classes. As defaults, Cairo-based instances of these classes are used but can be specified separately.
A GtLayout can be queried for the height of the laid out representation and finally be rendered to a GtCanvas.

Methods

```
GtLayout* gt_layout_new(
            GtDiagram *diagram,
            unsigned int width,
            GtStyle*,
            GtError*)
```

Creates a new `GtLayout` object for the contents of `diagram`. The layout is done for a target image width of `width` and using the rules in `GtStyle` object `style`.

```
GtLayout* gt_layout_new_with_twc(
            GtDiagram*,
            unsigned int width,
            GtStyle*,
            GtTextWidthCalculator*,
            GtError*)
```

Like `gt_layout_new()`, but allows use of a different `GtTextWidthCalculator` implementation.

```
void gt_layout_set_track_ordering_func(
       GtLayout *layout,
       GtTrackOrderingFunc func,
       void *data)
```

Sets the `GtTrackOrderingFunc` comparator function `func` which defines an order on the tracks contained in `layout`. This determines the order in which the tracks are drawn vertically. Additional data necessary in the comparator function can be given in `data`, the caller is responsible to free it.

```
int gt_layout_get_height(
      GtLayout *layout,
      GtUword *result,
      GtError *err)
```

Calculates the height of `layout` in pixels. The height value is written to the location pointed to by `result`. If an error occurs during the calculation, this function returns -1 and `err` is set accordingly. Returns 0 on success.

```
int gt_layout_sketch(
      GtLayout *layout,
      GtCanvas *target_canvas,
      GtError*)
```

Renders `layout` on the `target_canvas`.

```
void gt_layout_delete(
       GtLayout*)
```

Destroys a layout.

Class GtLogger

```
GtLogger* gt_logger_new(
            bool enabled,
            const char *prefix,
            FILE *target)
```

Creates a new `GtLogger`, with logging `enabled` or not, and prefixing all log entries with `prefix` (e.g. "debug"). The log output is terminated by a newline. All log output will be written to `target`.

```
void gt_logger_enable(
       GtLogger *logger)
```

Enable logging on `logger`.

```
void gt_logger_disable(
       GtLogger *logger)
```

Disable logging on `logger`.

```
bool gt_logger_enabled(
       GtLogger *logger)
```

Return `true` if logging is enabled on `logger`, false otherwise.

```
FILE* gt_logger_target(
        GtLogger *logger)
```

Return logging target of `logger`.

```
void gt_logger_set_target(
       GtLogger *logger,
       FILE *fp)
```

Set logging target of `logger` to `fp`.

```
void gt_logger_log_force(
       GtLogger *logger,
       const char *format,
       ...)
```

Log to target regardless of logging status.

```
void gt_logger_log(
       GtLogger *logger,
       const char *format,
       ...)
```

Log to target depending on logging status.

```
void gt_logger_log_va_force(
       GtLogger *logger,
       const char *format,
       va_list)
```

Log to target regardless of logging status, using a va_list argument.

```
void gt_logger_log_va(
       GtLogger *logger,
       const char *format,
       va_list)
```

Log to target depending on logging status, using a va_list argument.

```
void gt_logger_delete(
       GtLogger *logger)
```

Delete `logger`.

Class GtMD5Encoder

The <GtMD5Encoder> class implements a stateful encoder for MD5 hashes for strings build by iterative addition of blocks.

Methods

```
GtMD5Encoder* gt_md5_encoder_new(
                void)
```

Returns a new <GtMD5Encoder> object.

```
void gt_md5_encoder_add_block(
       GtMD5Encoder *enc,
       const char *message,
       GtUword len)
```

Processes `message` of length `len` (max. block length 64 bytes) to be incorporated in the hash currently represented by `enc`.

```
void gt_md5_encoder_finish(
       GtMD5Encoder *enc,
       unsigned char *output,
       char *outstr)
```

Finishes `enc` to produce the final MD5 value, written to the 16-byte array `output`. If `outstr` is not NULL, a \0-terminated string representation of the hash will be written to the 32-byte string buffer it points to.

```
void gt_md5_encoder_reset(
       GtMD5Encoder *enc)
```

Discards the current state of enc and resets it to represent the MD5 hash of the empty string.

```
void gt_md5_encoder_delete(
       GtMD5Encoder *enc)
```

Deletes enc and frees all associated space.

Class GtMD5Tab

<GtMd5Tab> is a table referencing sequences in a sequence collection.

Methods

```
GtMD5Tab* gt_md5_tab_new(
            const char *sequence_file,
            void *seqs,
            GtGetSeqFunc get_seq,
            GtGetSeqLenFunc get_seq_len,
            GtUword num_of_seqs,
            bool use_cache_file,
            bool use_file_locking)
```

Create a new MD5 table object for sequences contained in sequence_file. The sequences have to be stored in seqs (num_of_seqs many) and have to be accessible via the functions get_seq and get_seq_len. If use_cache_file is true, the MD5 sums are read from a cache file (named "sequence_file<GT_MD5TAB_FILE_SUFFIX>"), if it exists or written to it, if it doesn't exist. If use_cache_file is false, no cache file is read or written. If use_file_locking is true, file locking is used to access the cache file (recommended).

```
GtMD5Tab* gt_md5_tab_new_from_cache_file(
            const char *cache_file,
            GtUword num_of_seqs,
            bool use_file_locking,
            GtError *err)
```

Create a new MD5 table object for sequences directly from a cache_file, containing MD5 sums for num_of_seqs many sequences. If use_file_locking is true, file locking is used to access the cache file (recommended). Returns NULL if an error occurred opening the cache file, err is set accordingly.

```
GtMD5Tab* gt_md5_tab_ref(
            GtMD5Tab *md5_tab)
```

Increment reference count for <md5_tab>.

```
void gt_md5_tab_disable_file_locking(
       GtMD5Tab *md5_tab)
```

Do not use file locking for <md5_tab>.

```
const char* gt_md5_tab_get(
              const GtMD5Tab*,
              GtUword index)
```

Return the MD5 sum for sequence `index`.

```
GtUword gt_md5_tab_map(
          GtMD5Tab*,
          const char *md5)
```

Map <md5 > back to sequence index.

```
GtUword gt_md5_tab_size(
          const GtMD5Tab *md5_tab)
```

Return the size of the <md5_tab>.

```
void gt_md5_tab_delete(
       GtMD5Tab *md5_tab)
```

Decrement reference count for or delete <md5_tab>.

Class GtMD5ToIDStream

Implements the `GtNodeStream` interface. A <GtMD5ToIDStream> converts MD5 fingerprints used as sequence IDs to "regular" ones.

Methods

```
GtNodeStream* gt_md5_to_id_stream_new(
                GtNodeStream *in_stream,
                GtRegionMapping *region_mapping)
```

Create a <GtMD5toIDStream*> which converts MD5 sequence IDs from nodes it retrieves from its `in_stream` to "regular" ones (with the help of the given `region_mapping`). Takes ownership of `region_mapping`!

Class GtMatch

The `GtMatch` interface defines a generic set of functions for a data structure designed to hold matches, that is, two similar locations on two sequences which are further described by additional data specific to the matching engine. Matches have a direction, e.g. direct or reverse (palindromic).

Methods

```
void gt_match_set_seqid1(
       GtMatch *match,
       const char *seqid)
```

Sets the sequence ID of the first sequence involved in the match `match` to `seqid`. The string `seqid` must be null-terminated.

```
void gt_match_set_seqid1_nt(
       GtMatch *match,
       const char *seqid,
       GtUword len)
```

Sets the sequence ID of the first sequence involved in the match `match` to `seqid`. The string `seqid` needs not be null-terminated, its length is given by `len`.

```
void gt_match_set_seqid2(
       GtMatch *match,
       const char *seqid)
```

Sets the sequence ID of the second sequence involved in the match `match` to `seqid`. The string `seqid` must be null-terminated.

```
void gt_match_set_seqid2_nt(
       GtMatch *match,
       const char *seqid,
       GtUword len)
```

Sets the sequence ID of the second sequence involved in the match `match` to `seqid`. The string `seqid` needs not be null-terminated, its length is given by `len`.

```
const char* gt_match_get_seqid1(
              const GtMatch *match)
```

Returns the sequence ID of the first sequence involved in the match `match`.

```
const char* gt_match_get_seqid2(
              const GtMatch *match)
```

Returns the sequence ID of the second sequence involved in the match `match`.

```
void gt_match_set_range_seq1(
       GtMatch *match,
       GtUword start,
       GtUword end)
```

Sets the range of the first sequence involved in the match `match` to `start-end`.

```
void gt_match_set_range_seq2(
       GtMatch *match,
       GtUword start,
       GtUword end)
```

Sets the range of the second sequence involved in the match `match` to `start-end`.

```
void gt_match_get_range_seq1(
       const GtMatch *match,
       GtRange *range)
```

Writes the range of the first sequence involved in the match `match` to the location pointed to by `range`. Note: depending on how the matches were produced the resulting range might differ. e.g. Blast hit ranges are 1-Based, not zero based and inclusive i.e. `range`.end is the last position that is part of the match.

```
void gt_match_get_range_seq2(
       const GtMatch *match,
       GtRange *range)
```

Writes the range of the second sequence involved in the match `match` to the location pointed to by `range`. Note: depending on how the matches were produced the resulting range might differ. e.g. Blast hit ranges are 1-Based, not zero based and inclusive i.e. `range`.end is the last position that is part of the match.

```
GtMatchDirection gt_match_get_direction(
                   const GtMatch *match)
```

Returns the match direction of `match`.

```
void gt_match_delete(
       GtMatch *match)
```

Deletes the match `match`, freeing all associated memory.

Class GtMatchBlast

```
GtMatch* gt_match_blast_new(
            char *seqid1,
            char *seqid2,
            GtUword start_seq1,
            GtUword start_seq2,
            GtUword end_seq1,
            GtUword end_seq2,
            double evalue,
            float bitscore,
            GtUword ali_l,
            double similarity,
            GtMatchDirection dir)
```

Creates a new `GtMatch` object meant to store results in the BLAST format. That is, it stores double values `evalue` for match E-values, `bitscores` and the alignment length `ali_l` in addition to the generic match contents <seqid1 >, <seqid2 >, <start_seq1 >, <start_seq2 >, <end_seq1 >, and <end_seq2 >.

```
GtMatch* gt_match_blast_new_extended(
            char *seqid1,
            char *seqid2,
            GtUword start_seq1,
            GtUword end_seq1,
            GtUword start_seq2,
            GtUword end_seq2,
            double evalue,
            float bitscore,
            GtUword length,
            double similarity,
            GtUword mm_num,
            GtUword gap_open_num,
            GtMatchDirection dir)
```

Creates a new `GtMatch` object meant to store results in the BLAST format. That is, it stores double values `evalue` for match E-values, `bitscores` and the alignment length `ali_l` in addition to the generic match contents <seqid1 >, <seqid2 >, <start_seq1 >, <start_seq2 >, <end_seq1 >, and <end_seq2 >. In addition to `gt_match_blast_new` it also stores the number of mismatches and the number of gap

```
void gt_match_blast_set_evalue(
       GtMatchBlast *mb,
       double evalue)
```

Sets `evalue` to be the E-value in `mb`.

```
void gt_match_blast_set_bitscore(
       GtMatchBlast *mb,
       float bits)
```

Sets `bits` to be the bit-score in `mb`.

```
void gt_match_blast_set_align_length(
       GtMatchBlast *mb,
       GtUword length)
```

Sets `length` to be the alignment length in `mb`.

```
void gt_match_blast_set_similarity(
       GtMatchBlast *mb,
       double similarity)
```

Sets `similarity` to be the match similarity in `mb`.

```
void gt_match_blast_set_mismatches(
       GtMatchBlast *mb,
       GtUword mm_num)
```

Sets `num` to be the number of mismatches in `mb`.

```
void gt_match_blast_set_gapopen(
       GtMatchBlast *mb,
       GtUword gap_open_num)
```

Sets `num` to be the number of gap openings in `mb`.

```
double gt_match_blast_get_evalue(
         GtMatchBlast *mb)
```

Returns the E-value stored in `mb`.

```
float gt_match_blast_get_bitscore(
        GtMatchBlast *mb)
```

Returns the bit-score value stored in `mb`.

```
GtUword gt_match_blast_get_align_length(
          GtMatchBlast *mb)
```

Returns the alignment length stored in `mb`.

```
double gt_match_blast_get_similarity(
         GtMatchBlast *mb)
```

Returns the alignment similarity stored in `mb`.

```
GtUword gt_match_blast_get_mismatches(
          GtMatchBlast *mb)
```

Returns the number of mismatches stored in `mb`.

```
GtUword gt_match_blast_get_gapopen(
          GtMatchBlast *mb)
```

Returns the number of gap openings stored in `mb`.

Class GtMatchIterator

```
GtMatchIteratorStatus gt_match_iterator_next(
                        GtMatchIterator *mp,
                        GtMatch **match,
                        GtError *err)
```

Advances `mp` by one, returning the next match. Writes a pointer to the next match to the position pointed to by `match`. Returns GT_MATCHER_STATUS_OK when the match could be delivered and there are more matches to come, GT_MATCHER_STATUS_END when no more matches are available, and GT_MATCHER_STATUS_ERROR if an error occurred. `err` is set accordingly.

```
void gt_match_iterator_delete(
       GtMatchIterator *mp)
```

Deletes `mp`, freeing all associated space.

Class GtMatchLAST

The `GtMatchLAST` class, implementing the `GtMatch` interface, is meant to store results given in the format as output by LAST.

Methods

```
GtMatch* gt_match_last_new(
           const char *seqid1,
           const char *seqid2,
           GtUword score,
           GtUword seqno1,
           GtUword seqno2,
           GtUword start_seq1,
           GtUword start_seq2,
           GtUword end_seq1,
           GtUword end_seq2,
           GtMatchDirection dir)
```

Creates a new `GtMatch` object meant to store results from the LAST software.

```
GtUword gt_match_last_get_seqno1(
          const GtMatchLAST *ml)
```

Returns the sequence number of the match `ms` in the first sequence set.

```
GtUword gt_match_last_get_seqno2(
          const GtMatchLAST *ml)
```

Returns the sequence number of the match `ms` in the second sequence set.

```
GtUword gt_match_last_get_score(
          const GtMatchLAST *ml)
```

Returns the LAST score of the match `ms`.

Class GtMatchOpen

The `GtMatchOpen` class, implementing the `GtMatch` interface, is meant to store results in the OpenMatch format, e.g. as output by Vmatch.

Methods

```
GtMatch* gt_match_open_new(
           char *seqid1,
           char *seqid2,
           GtUword start_seq1,
           GtUword start_seq2,
           GtUword end_seq1,
           GtUword end_seq2,
           GtWord weight,
           GtMatchDirection dir)
```

Creates a new `GtMatchOpen` object, storing long values `weight` in addition to the generic match contents <seqid1 >, <seqid2 >, <start_seq1 >, <start_seq2 >, <end_seq1 >, and <end_seq2 >.

```
void gt_match_open_set_weight(
       GtMatchOpen *mo,
       GtWord weight)
```

Sets `weight` to be the weight value in `mo`.

```
GtWord gt_match_open_get_weight(
         GtMatchOpen *mo)
```

Returns the weight value stored in `mo`.

Class GtMatchSW

The `GtMatchSW` class, implementing the `GtMatch` interface, is meant to store results from Smith-Waterman matching (using the `swalign` module).

Methods

```
GtMatch* gt_match_sw_new(
           const char *seqid1,
           const char *seqid2,
           GtUword seqno1,
           GtUword seqno2,
           GtUword length,
           GtUword edist,
           GtUword start_seq1,
           GtUword start_seq2,
           GtUword end_seq1,
           GtUword end_seq2,
           GtMatchDirection dir)
```

Creates a new `GtMatch` object, storing the alignment length `length`, the edit distance `edist` and the sequence numbers in the sequence collections in addition to the generic match contents <seqid1 >, <seqid2 >, <start_seq1 >, <start_seq2 >, <end_seq1 > and <end_seq2 >.

```
GtUword gt_match_sw_get_seqno1(
          const GtMatchSW *ms)
```

Returns the sequence number of the match `ms` in the first sequence set.

```
GtUword gt_match_sw_get_seqno2(
          const GtMatchSW *ms)
```

Returns the sequence number of the match `ms` in the second sequence set.

```
GtUword gt_match_sw_get_alignment_length(
          const GtMatchSW *ms)
```

Returns the alignment length of the match `ms`.

```
GtUword gt_match_sw_get_edist(
          const GtMatchSW *ms)
```

Returns the edit distance of the match `ms`.

Class GtMatchVisitor

The `GtMatchVisitor` class allows one to distinguish a `GtMatch` implementation, e.g. BLAST or OpenMatch, and to call different code for each implementation.

Methods

```
int gt_match_visitor_visit_match_blast(
      GtMatchVisitor *match_visitor,
      GtMatchBlast *match_blast,
      GtError *err)
```

Visit `match_blast` with `match_visitor`.

```
int gt_match_visitor_visit_match_open(
      GtMatchVisitor *match_visitor,
      GtMatchOpen *match_open,
      GtError *err)
```

Visit `match_open` with `match_visitor`.

```
void gt_match_visitor_delete(
       GtMatchVisitor *match_visitor)
```

Deletes `match_visitor` freeing all associated space.

Class GtMergeFeatureStream

Implements the `GtNodeStream` interface. A `GtMergeFeatureStream` merges adjacent features of the same type.

Methods

```
GtNodeStream* gt_merge_feature_stream_new(
                GtNodeStream *in_stream)
```

Create a `GtMergeFeatureStream*` which merges adjacent features of the same type it retrieves from `in_stream` and returns them (and all other unmodified features).

Class GtMergeStream

Implements the `GtNodeStream` interface. A `GtMergeStream` allows one to merge a set of sorted streams in a sorted fashion.

Methods

```
GtNodeStream* gt_merge_stream_new(
                const GtArray *node_streams)
```

Create a `GtMergeStream*` which merges the given (sorted) `node_streams` in a sorted fashion.

Class GtMetaNode

Implements the GtGenomeNode interface. Meta nodes correspond to meta lines in GFF3 files (i.e., lines which start with "<##>") which are not sequence-region lines.

Methods

```
GtGenomeNode* gt_meta_node_new(
                const char *meta_directive,
                const char *meta_data)
```

Return a new GtMetaNode object representing a meta_directive with the corresponding meta_data. Please note that the leading "<##>" which denotes meta lines in GFF3 files should not be part of the meta_directive. The meta_directive must not be NULL, the meta_data can be NULL.

```
const char* gt_meta_node_get_directive(
              const GtMetaNode
                                                    *meta_node)
```

Return the meta directive stored in meta_node.

```
const char* gt_meta_node_get_data(
              const GtMetaNode *meta_node)
```

Return the meta data stored in meta_node. Can return NULL!

```
GtMetaNode* gt_meta_node_try_cast(
              GtGenomeNode *gn)
```

Test whether the given genome node is a meta node. If so, a pointer to the meta node is returned. If not, NULL is returned. Note that in most cases, one should implement a GtNodeVisitor to handle processing of different GtGenomeNode types.

```
GtMetaNode* gt_meta_node_cast(
              GtGenomeNode *gn)
```

Test whether the given genome node is a meta node. If so, a pointer to the meta node is returned. If not, an assertion fails.

Class GtMutex

The GtMutex class represents a simple mutex structure.

Methods

```
GtMutex* gt_mutex_new(
           void)
```

Return a new `GtMutex*` object.

```
void gt_mutex_delete(
       GtMutex *mutex)
```

Delete the given `mutex`.

```
#define gt_mutex_lock(
          mutex)
```

Lock the given `mutex`.

```
#define gt_mutex_unlock(
          mutex)
```

Unlock the given `mutex`.

Class GtNodeStream

The `GtNodeStream` interface. `GtNodeStream` objects process `GtGenomeNode` objects in a pull-based architecture and can be chained together.

Methods

```
GtNodeStream* gt_node_stream_ref(
                GtNodeStream *node_stream)
```

Increase the reference count for `node_stream` and return it.

```
int gt_node_stream_next(
      GtNodeStream *node_stream,
      GtGenomeNode **genome_node,
      GtError *err)
```

Try to get the the next `GtGenomeNode` from `node_stream` and store it in `genome_node` (transfers ownership to `genome_node`). If no error occurs, 0 is returned and `genome_node` contains either the next `GtGenomeNode` or `NULL`, if the `node_stream` is exhausted. If an error occurs, -1 is returned and `err` is set accordingly (the status of `genome_node` is undefined, but no ownership transfer occurred).

```
int gt_node_stream_pull(
      GtNodeStream *node_stream,
      GtError *err)
```

Calls gt_node_stream_next() on node_stream repeatedly until the node_stream is exhausted (0 is returned) or an error occurs (-1 is returned and err is set). All retrieved GtGenomeNodes are deleted automatically with calls to gt_genome_node_delete(). This method is basically a convenience method which simplifies calls to gt_node_stream_next() in a loop where the retrieved GtGenomeNode objects are not processed any further.

```
bool gt_node_stream_is_sorted(
       GtNodeStream *node_stream)
```

Return true if node_stream is a sorted stream, false otherwise.

```
void gt_node_stream_delete(
       GtNodeStream *node_stream)
```

Decrease the reference count for node_stream or delete it, if this was the last reference.

```
void GtNodeStreamFreeFunc(
                          GtNodeStream*)
```

Callback function. Performs the necessary steps to delete implementation-specific memory in the stream implementation.

```
int GtNodeStreamNextFunc(
                         GtNodeStream*,
                         GtGenomeNode**,
                         GtError*)
```

Callback function. May receive a GtGenomeNode from its predecessor and must write a node reference or NULL to the node pointer.

```
GtNodeStream* gt_node_stream_create(
                const GtNodeStreamClass
                                        *node_stream_class,
                bool ensure_sorting)
```

Create a new object of the given node_stream_class. If ensure_sorting is true, it is enforced that all genome node objects pulled from this class are sorted. That is, for consecutive nodes a and b obtained from the given node_stream_class the return code of <gt_genome_node_compare(a,b)> has to be smaller or equal than 0. If this condition is not met, an assertion fails.

```
void* gt_node_stream_cast(
        const GtNodeStreamClass
                                          *node_stream_class,
        GtNodeStream *node_stream)
```

Cast node_stream to the given node_stream_class. That is, if node_stream is not from the given node_stream_class, an assertion will fail.

Class GtNodeStreamClass

```
const
GtNodeStreamClass* gt_node_stream_class_new(
                           size_t size,
                           GtNodeStreamFreeFunc free,
                           GtNodeStreamNextFunc next)
```

Create a new node stream class (that is, a class which implements the node stream interface). size denotes the size of objects of the new node stream class. The optional free method is called once, if an object of the new class is deleted. The mandatory next method has to implement the gt_node_stream_next() semantic for the new class.

Class GtNodeVisitor

The GtNodeVisitor interface, a visitor for GtGenomeNode objects.

Methods

```
int gt_node_visitor_visit_comment_node(
      GtNodeVisitor *node_visitor,
      GtCommentNode *comment_node,
      GtError *err)
```

Visit comment_node with node_visitor.

```
int gt_node_visitor_visit_feature_node(
      GtNodeVisitor *node_visitor,
      GtFeatureNode *feature_node,
      GtError *err)
```

Visit feature_node with node_visitor.

```
int gt_node_visitor_visit_meta_node(
      GtNodeVisitor *node_visitor,
      GtMetaNode *meta_node,
      GtError *err)
```

Visit meta_node with node_visitor.

```
int gt_node_visitor_visit_region_node(
      GtNodeVisitor *node_visitor,
      GtRegionNode *region_node,
      GtError *err)
```

Visit region_node with node_visitor.

```
int gt_node_visitor_visit_sequence_node(
      GtNodeVisitor *node_visitor,
      GtSequenceNode *sequence_node,
      GtError *err)
```

Visit sequence_node with node_visitor.

```
void gt_node_visitor_delete(
       GtNodeVisitor *node_visitor)
```

Delete node_visitor.

Class GtORFIterator

The GtORFIterator class is used to enumerate open reading frames (ORFs) in codon streams as delivered by a GtCodonIterator using a translation process as defined by a GtTranslator.

Methods

```
GtORFIterator* gt_orf_iterator_new(
                 GtCodonIterator *ci,
                 GtTranslator *translator)
```

Return a new GtORFIterator* using the codons delivered by ci and translated by translator.

```
GtORFIteratorStatus gt_orf_iterator_next(
                      GtORFIterator *orf_iterator,
                      GtRange *orf_rng,
                      unsigned int *orf_frame,
                      GtError *err)
```

Sets the values of <orf_rng.start>, <orf_rng.end> and orf_frame to the current reading position of ci if a START/STOP codon is found. The frame in which the ORF is located is written to the position pointed to by orf_frame. This function returns one of three status codes: GT_ORF_ITERATOR_OK if an ORF was detected successfully(START/STOP AA pair), GT_ORF_ITERATOR_END if no ORF was detected because the end of the scan region has been reached, or GT_ORF_ITERATOR_ERROR if no ORF was detected because an error occurred during sequence access. See err for details.

```
void gt_orf_iterator_delete(
       GtORFIterator *orf_iterator)
```

Delete `orf_iterator` and frees all associated memory.

Class GtOption

`GtOption` objects represent command line options (which are used in a `GtOptionParser`). Option descriptions are automatically formatted to `GT_OPTION_PARSER_TERMINAL_WIDTH`, but it is possible to embed newlines into the descriptions to manually affect the formatting.

Methods

```
GtOption* gt_option_new_bool(
            const char *option_string,
            const char *description,
            bool *value,
            bool default_value)
```

Return a new `GtOption` with the given `option_string`, `description`, and `default_value`. The result of the option parsing is stored in `value`.

```
GtOption* gt_option_new_double(
            const char *option_string,
            const char *description,
            double *value,
            double default_value)
```

Return a new `GtOption` with the given `option_string`, `description`, and `default_value`. The result of the option parsing is stored in `value`.

```
GtOption* gt_option_new_double_min(
            const char *option_string,
            const char *description,
            double *value,
            double default_value,
            double minimum_value)
```

Return a new `GtOption` with the given `option_string`, `description`, and `default_value`. The result of the option parsing is stored in `value`. The argument to this option must at least have the `minimum_value`.

```
GtOption* gt_option_new_double_min_max(
            const char *option_string,
            const char *description,
            double *value,
            double default_value,
            double minimum_value,
            double maximum_value)
```

Return a new `GtOption` with the given `option_string`, `description`, and `default_value`. The result of the option parsing is stored in `value`. The argument to this option must at least have the `minimum_value` and at most the `maximum_value`.

```
GtOption* gt_option_new_probability(
            const char *option_string,
            const char *description,
            double *value,
            double default_value)
```

Return a new `GtOption` with the given `option_string`, `description`, and `default_value`. The result of the option parsing is stored in `value`. The argument to this option must at larger or equal than 0.0 and smaller or equal than 1.0.

```
GtOption* gt_option_new_int(
            const char *option_string,
            const char *description,
            int *value,
            int default_value)
```

Return a new `GtOption` with the given `option_string`, `description`, and `default_value`. The result of the option parsing is stored in `value`.

```
GtOption* gt_option_new_int_min(
            const char *option_string,
            const char *description,
            int *value,
            int default_value,
            int minimum_value)
```

Return a new `GtOption` with the given `option_string`, `description`, and `default_value`. The result of the option parsing is stored in `value`. The argument to this option must at least have the `minimum_value`.

```
GtOption* gt_option_new_int_max(
            const char *option_string,
            const char *description,
            int *value,
            int default_value,
            int maximum_value)
```

Return a new `GtOption` with the given `option_string`, `description`, and `default_value`. The result of the option parsing is stored in `value`. The argument to this option must at most have the `maximum_value`.

```
GtOption* gt_option_new_int_min_max(
            const char *option_string,
            const char *description,
            int *value,
            int default_value,
            int minimum_value,
            int maximum_value)
```

Return a new `GtOption` with the given `option_string`, `description`, and `default_value`. The result of the option parsing is stored in `value`. The argument to this option must at least have the `minimum_value` and at most the `maximum_value`.

```
GtOption* gt_option_new_uint(
            const char *option_string,
            const char *description,
            unsigned int *value,
            unsigned int default_value)
```

Return a new `GtOption` with the given `option_string`, `description`, and `default_value`. The result of the option parsing is stored in `value`.

```
GtOption* gt_option_new_uint_min(
            const char *option_string,
            const char *description,
            unsigned int *value,
            unsigned int default_value,
            unsigned int minimum_value)
```

Return a new `GtOption` with the given `option_string`, `description`, and `default_value`. The result of the option parsing is stored in `value`. The argument to this option must at least have the `minimum_value`.

```
GtOption* gt_option_new_uint_max(
            const char *option_string,
            const char *description,
            unsigned int *value,
            unsigned int default_value,
            unsigned int maximum_value)
```

Return a new `GtOption` with the given `option_string`, `description`, and `default_value`. The result of the option parsing is stored in `value`. The argument to this option must at most have the `maximum_value`.

```
GtOption* gt_option_new_uint_min_max(
            const char *option_string,
            const char *description,
            unsigned int *value,
            unsigned int default_value,
            unsigned int minimum_value,
            unsigned int maximum_value)
```

Return a new `GtOption` with the given `option_string`, `description`, and `default_value`. The result of the option parsing is stored in `value`. The argument to this option must at least have the `minimum_value` and at most the `maximum_value`.

```
GtOption* gt_option_new_word(
            const char *option_string,
            const char *description,
            GtWord *value,
            GtWord default_value)
```

Return a new `GtOption` with the given `option_string`, `description`, and `default_value`. The result of the option parsing is stored in `value`.

```
GtOption* gt_option_new_uword(
            const char *option_string,
            const char *description,
            GtUword *value,
            GtUword default_value)
```

Return a new `GtOption` with the given `option_string`, `description`, and `default_value`. The result of the option parsing is stored in `value`.

```
GtOption* gt_option_new_uword_min(
            const char *option_string,
            const char *description,
            GtUword *value,
            GtUword default_value,
            GtUword minimum_value)
```

Return a new `GtOption` with the given `option_string`, `description`, and `default_value`. The result of the option parsing is stored in `value`. The argument to this option must at least have the `minimum_value`.

```
GtOption* gt_option_new_uword_min_max(
            const char *option_string,
            const char *description,
            GtUword *value,
            GtUword default_value,
            GtUword minimum_value,
            GtUword maximum_value)
```

Return a new `GtOption` with the given `option_string`, `description`, and `default_value`. The result of the option parsing is stored in `value`. The argument to this option must at least have the `minimum_value` and at most the `maximum_value`.

```
GtOption* gt_option_new_long(
            const char *option_string,
            const char *description,
            GtWord *value,
            GtWord default_value)
```

Deprecated. Usage identical to `gt_option_new_word`.

```
GtOption* gt_option_new_ulong(
            const char *option_string,
            const char *description,
            GtUword *value,
            GtUword default_value)
```

Deprecated. Usage identical to `gt_option_new_uword`.

```
GtOption* gt_option_new_ulong_min(
            const char *option_string,
            const char *description,
            GtUword *value,
            GtUword default_value,
            GtUword minimum_value)
```

Deprecated. Usage identical to `gt_option_new_uword_min`.

```
GtOption* gt_option_new_ulong_min_max(
            const char *option_string,
            const char *description,
            GtUword *value,
            GtUword default_value,
            GtUword minimum_value,
            GtUword maximum_value)
```

Deprecated. Usage identical to `gt_option_new_uword_min_max`.

```
GtOption* gt_option_new_range(
            const char *option_string,
            const char *description,
            GtRange *value,
            GtRange *default_value)
```

Return a new GtOption with the given option_string, description, and default_value. The result of the option parsing is stored in value. If default_value equals NULL, GT_UNDEF_WORD will be used as the default start and end point of value.

```
GtOption* gt_option_new_range_min_max(
            const char *option_string,
            const char *description,
            GtRange *value,
            GtRange *default_value,
            GtUword minimum_value,
            GtUword maximum_value)
```

Return a new GtOption with the given option_string, description, and default_value. The result of the option parsing is stored in value. The first argument to this option (which will be used as the start) must at least have the minimum_value and the second argument (which will be used as the end) at most the maximum_value.

```
GtOption* gt_option_new_string(
            const char *option_string,
            const char *description,
            GtStr *value,
            const char *default_value)
```

Return a new GtOption with the given option_string, description, and default_value. The result of the option parsing is stored in value.

```
GtOption* gt_option_new_string_array(
            const char *option_string,
            const char *description,
            GtStrArray *value)
```

Return a new GtOption with the given option_string, description, and default_value. The result of the option parsing are stored in value.

```
GtOption* gt_option_new_choice(
            const char *option_string,
            const char *description,
            GtStr *value,
            const char *default_value,
            const char **domain)
```

Return a GtOption with the given option_string, description, and default_value which allows only arguments given in the NULL-terminated domain (default_value must be an entry of domain or NULL).

```
GtOption* gt_option_new_filename(
            const char *option_string,
            const char *description,
            GtStr *filename)
```

Return a new `GtOption` with the given `option_string`, `description`. The result of the option parsing is stored in the `GtStr` object `filename`. `filename` may not be NULL!

```
GtOption* gt_option_new_filename_array(
            const char *option_string,
            const char *description,
            GtStrArray *filename_array)
```

Return a new `GtOption` with the given `option_string`, `description`, and `default_value`. The results of the option parsing are stored in `value`.

```
GtOption* gt_option_new_debug(
            bool *value)
```

Return a new debug `GtOption` object: ←debug>, ”enable debugging output”, default is `false`. The result of the option parsing is stored in `value`

```
GtOption* gt_option_new_verbose(
            bool *value)
```

Return a new verbose `GtOption` object: ←v>, ”be verbose”, default is `false`. The result of the option parsing is stored in `value`

```
GtOption* gt_option_new_width(
            GtUword *value)
```

Return a new width `GtOption` object: ←width>, ”set output width for FASTA sequence printing (0 disables formatting)”, default is 0. The result of the option parsing is stored in `value`

```
GtOption* gt_option_ref(
            GtOption *option)
```

Increase the reference count for `option` and return it.

```
const char* gt_option_get_name(
              const GtOption * option)
```

Return the name of `option`

```
void gt_option_is_mandatory(
       GtOption *option)
```

Make `option` mandatory.

```
void gt_option_is_mandatory_either(
       GtOption *option_a,
       const GtOption *option_b)
```

Make it mandatory, that either option_a or option_b is used.

```
void gt_option_is_mandatory_either_3(
       GtOption *option_a,
       const GtOption *option_b,
       const GtOption *option_c)
```

Make it mandatory, that one of the options option_a, option_b, or option_c is used.

```
void gt_option_is_mandatory_either_4(
       GtOption *option_a,
       const GtOption *option_b,
       const GtOption *option_c,
       const GtOption *option_d)
```

Make it mandatory, that one of the options option_a, option_b, option_c or option_d is used.

```
void gt_option_is_extended_option(
       GtOption *option)
```

Set that option is only shown in the output of ←help+>.

```
void gt_option_is_development_option(
       GtOption *option)
```

Set that option is only shown in the output of ←helpdev>.

```
void gt_option_imply(
       GtOption *option_a,
       const GtOption *option_b)
```

Make option_a imply option_b.

```
void gt_option_imply_either_2(
       GtOption *option_a,
       const GtOption *option_b,
       const GtOption *option_c)
```

Make option_a imply either option_b or option_c

```
void gt_option_imply_either_3(
       GtOption *option_a,
       const GtOption *option_b,
       const GtOption *option_c,
       const GtOption *option_d)
```

Make option_a imply either option_b, option_c or option_d

```
void gt_option_exclude(
       GtOption *option_a,
       GtOption *option_b)
```

Set that the options option_a and option_b exclude each other.

```
void gt_option_hide_default(
       GtOption *option)
```

Hide the default value of option in ←help> output.

```
void gt_option_argument_is_optional(
       GtOption *option)
```

Set that the argument to option is optional

```
bool gt_option_is_set(
       const GtOption *option)
```

Return true if option was set, false otherwise.

```
void gt_option_delete(
       GtOption*)
```

Delete option.

```
int gt_option_parse_spacespec(
      GtUword *maximumspace,
      const char *optname,
      const GtStr *memlimit,
      GtError *err)
```

Parse the argument to option -memlimit. Could be made into a special parser, but I do not know how. SK. 2011-09-19

Class GtOptionParser

GtOptionParser objects can be used to parse command line options.

Methods

```
#define GT_OPTION_PARSER_TERMINAL_WIDTH
```

The default terminal width used in the output of the GtOptionParser.

```
GtOptionParser* gt_option_parser_new(
                  const char *synopsis,
                  const char *one_liner)
```

Return a new GtOptionParser object. The synopsis should summarize the command line arguments and mandatory arguments in a single line. The one_liner should describe the program for which the GtOptionParser is used in a single line and must have an upper case letter at the start and a '.' at the end.

```
void gt_option_parser_add_option(
       GtOptionParser *option_parser,
       GtOption *option)
```

Add option to option_parser. Takes ownership of option.

```
GtOption* gt_option_parser_get_option(
            GtOptionParser *option_parser,
            const char *option_string)
```

Return the GtOption object if an option named option_string is present in option_parser, and NULL if no such option exists.

```
void gt_option_parser_refer_to_manual(
       GtOptionParser *option_parser)
```

Refer to manual at the end of ←help> output of opion_parser.

```
void gt_option_parser_set_comment_func(
       GtOptionParser *option_parser,
       GtShowCommentFunc
                                                  comment_func,
       void *data)
```

Set comment_func in option_parser (data is passed along).

```
void gt_option_parser_set_version_func(
       GtOptionParser *option_parser,
       GtShowVersionFunc
                                                  version_func)
```

Set the version function used by option_parser to version_func. This version function takes precedence to the one supplied to gt_option_parser_parse().

```
void gt_option_parser_set_mail_address(
       GtOptionParser*,
       const char *mail_address)
```

Set the mail_address used in the final "Report bugs to" line of the ←help> output. It should be of the form <<bill@microsoft.com>> (email address enclosed in one pair of angle brackets).

```
void gt_option_parser_register_hook(
       GtOptionParser *option_parser,
       GtOptionParserHookFunc
                                                hook_function,
       void *data)
```

Register a hook_function with option_parser. All registered hook functions are called at the end of gt_option_parser_parse(). This allows one to have a module which registers a bunch of options in the option parser and automatically performs necessary postprocessing after the option parsing has been done via the hook function.

```
void gt_option_parser_set_min_args(
       GtOptionParser *option_parser,
       unsigned int minimum)
```

The minimum number of additional command line arguments option_parser must parse in order to succeed.

```
void gt_option_parser_set_max_args(
       GtOptionParser *option_parser,
       unsigned int maximum)
```

The maximum number of additional command line arguments option_parser must parse in order to succeed.

```
void gt_option_parser_set_min_max_args(
       GtOptionParser *option_parser,
       unsigned int minimum,
       unsigned int maximum)
```

The minimum and maximum number of additional command line arguments option_parser must parse in order to succeed.

```
GtOPrval gt_option_parser_parse(
           GtOptionParser *option_parser,
           int *parsed_args,
           int argc,
           const char **argv,
           GtShowVersionFunc version_func,
           GtError *err)
```

Use option_parser to parse options given in argument vector argv (with argc many arguments). The number of parsed arguments is stored in parsed_args. version_func is used for the output of option ←version>. In case of error, GT_OPTION_PARSER_ERROR is returned and err is set accordingly.

```
void gt_option_parser_reset(
       GtOptionParser *op)
```

Reset all options set in op to the default values specified at option parser creation time.

```
void gt_option_parser_delete(
       GtOptionParser *option_parser)
```

Delete option_parser.

Class GtOutputFileInfo

The GtOutputFileInfo class encapsulates output options.

Methods

```
GtOutputFileInfo* gt_output_file_info_new(
                    void)
```

Create a new GtOutputFileInfo object.

```
void gt_output_file_info_register_options(
       GtOutputFileInfo *output_file_info,
       GtOptionParser *option_parser,
       GtFile **outfp)
```

Registers the options '-o', '-gzip', '-bzip2' and '-force' in option_parser. Options chosen during option parsing will be stored in output_file_info and the output file will be accessible using *outfp. If no option is given, default *outfp will use stdout. Caller retains ownership of *outfp.

```
void gt_output_file_info_delete(
       GtOutputFileInfo *output_file_info)
```

Deletes output_file_info and frees all associated memory.

Class GtPhase

This enum type defines the possible phases. The following phases are defined: GT_PHASE_ZERO, GT_PHASE_ONE, GT_PHASE_TWO, and GT_PHASE_UNDEFINED.

Methods

```
#define GT_PHASE_CHARS
```

Use this string to map phase enum types to their corresponding character.

```
GtPhase gt_phase_get(
          char phase_char)
```

Map phase_char to the corresponding phase enum type. An assertion will fail if phase_char is not a valid one.

Class GtQueue

GtQueue objects are generic queues which can be used to process objects of any type in an First-In-First-Out (FIFO) fashion.

Methods

```
GtQueue* gt_queue_new(
           void)
```

Return a new GtQueue object.

```
void gt_queue_add(
       GtQueue *queue,
       void *elem)
```

Add elem to queue (*enqueue* in computer science terminology).

```
void* gt_queue_get(
        GtQueue *queue)
```

Remove the first element from non-empty queue and return it (*dequeue* in computer science terminology).

```
void* gt_queue_head(
        GtQueue *queue)
```

Return the first element in non-empty queue without removing it.

```
void gt_queue_remove(
       GtQueue *queue,
       void *elem)
```

Remove elem from queue (elem has to be in queue). Thereby queue is traversed in reverse order, leading to O(gt_queue_size(queue)) worst-case running time.

```
GtUword gt_queue_size(
          const GtQueue *queue)
```

Return the number of elements in queue.

```
void gt_queue_delete(
       GtQueue *queue)
```

Delete queue. Elements contained in queue are not freed!

Class GtRBTree

The GtRBTree class. Fast logarithmic data structure. This implementation does not allow storage of duplicates.

Methods

```
GtRBTree* gt_rbtree_new(
            GtCompareWithData cmp,
            GtRBTreeFreeFunc free,
            void *info)
```

Returns a new GtRBTree object. free might be NULL and will be used to free key-object otherwise. info is the data for the cmp-function.

```
void gt_rbtree_clear(
       GtRBTree *tree)
```

Deletes all tree elements

```
void* gt_rbtree_find(
        const GtRBTree *tree,
        void *key)
```

Returns key if element was found in tree and NULL if not

```
void gt_rbtree_insert(
       GtRBTree *tree,
       void *key)
```

inserts key into tree. If key is already present in tree, it will not be changed.

```
void* gt_rbtree_search(
        GtRBTree *tree,
        void *key,
        bool *nodecreated)
```

Returns `key`, if `key` is not present in `tree` it will be inserted and `nodecreated` set accordingly

```
int gt_rbtree_erase(
      GtRBTree *tree,
      void *key)
```

Remove `key` from `tree`, returns -1 if no such key exists and 0 on success

Class GtRBTreeIter

```
GtRBTreeIter* gt_rbtree_iter_new_from_first(
                const GtRBTree *tree)
```

Creates an iterator from the first (smallest) element.

```
GtRBTreeIter* gt_rbtree_iter_new_from_last(
                const GtRBTree *tree)
```

Creates an iterator from the last (largest) element

```
void gt_rbtree_iter_reset_from_first(
       GtRBTreeIter *trav)
```

Resets the iterator to the first (smallest) element.

```
void gt_rbtree_iter_reset_from_last(
       GtRBTreeIter *trav)
```

Resets the iterator to the last (largest) element.

```
void* gt_rbtree_iter_next(
        GtRBTreeIter *trav)
```

Return next (larger) key, NULL if iterator reached end.

```
void* gt_rbtree_iter_prev(
        GtRBTreeIter *trav)
```

Return previous (smaller) key, NULL if iterator reached end.

```
void gt_rbtree_iter_delete(
       GtRBTreeIter *trav)
```

free all memory of `trav`

Class GtRDBMySQL

The GtRDBMySQL class implements the GtRDB interface using the MySQL client backend. This implementation is only available if compiled with the option “with-mysql=yes”.

Methods

```
GtRDB* gt_rdb_mysql_new(
          const char *server,
          unsigned int port,
          const char *database,
          const char *username,
          const char *password,
          GtError *err)
```

Creates a new GtRDBSqlite object from the database accessible on server port port, selecting the database database using the credentials given by username and password. Returns NULL on error, err is set accordingly.

Class GtRDBSqlite

The GtRDBSqlite class implements the GtRDB interface using the SQLite embedded database backend. This implementation is only available if compiled with the option “with-sqlite=yes”.

Methods

```
GtRDB* gt_rdb_sqlite_new(
          const char *dbpath,
          GtError *err)
```

Creates a new GtRDBSqlite object from the database file located at dbpath. Returns NULL on error, err is set accordingly.

Class GtRDBVisitor

The GtRDBVisitor interface, a visitor for GtRDB objects.

Methods

```
int gt_rdb_visitor_visit_sqlite(
      GtRDBVisitor *rdbv,
      GtRDBSqlite *rdbs,
      GtError *err)
```

Visit a SQLite database `rdbs` with `rdbv`. Returns 0 on success, a negative value otherwise, and `err` is set accordingly.

```
int gt_rdb_visitor_visit_mysql(
      GtRDBVisitor *rdbv,
      GtRDBMySQL *rdbm,
      GtError *err)
```

Visit a MySQL database `rdbm` with `rdbv`. Returns 0 on success, a negative value otherwise, and `err` is set accordingly.

```
void gt_rdb_visitor_delete(
       GtRDBVisitor *rdbv)
```

Delete `rdbv`.

Class GtRWLock

The `GtRWLock` class represents a read/write lock.

Methods

```
GtRWLock* gt_rwlock_new(
            void)
```

Return a new `GtRWLock*` object.

```
void gt_rwlock_delete(
       GtRWLock *rwlock)
```

Delete the given `rwlock`.

```
#define gt_rwlock_rdlock(
          rwlock)
```

Acquire a read lock for `rwlock`.

```
#define gt_rwlock_wrlock(
          rwlock)
```

Acquire a write lock for `rwlock`.

```
#define gt_rwlock_unlock(
          rwlock)
```

Unlock the given `rwlock`.

Class GtRange

The `GtRange` class is used to represent genomic ranges in *GenomeTools*. Thereby, the `start` must **always** be smaller or equal than the `end`.

Methods

```
int gt_range_compare(
      const GtRange *range_a,
      const GtRange *range_b)
```

Compare `range_a` and `range_b`. Returns 0 if `range_a` equals `range_b`, -1 if `range_a` starts before `range_b` or (for equal starts) `range_a` ends before `range_b`, and 1 else.

```
int gt_range_compare_with_delta(
      const GtRange *range_a,
      const GtRange *range_b,
      GtUword delta)
```

Compare `range_a` and `range_b` with given `delta`. Returns 0 if `range_a` equals `range_b` modulo `delta` (i.e., the start and end points of `range_a` and `range_b` are at most `delta` bases apart), -1 if `range_a` starts before `range_b` or (for equal starts) `range_a` ends before `range_b`, and 1 else.

```
bool gt_range_overlap(
       const GtRange *range_a,
       const GtRange *range_b)
```

Returns `true` if `range_a` and `range_b` overlap, `false` otherwise.

```
bool gt_range_overlap_delta(
       const GtRange *range_a,
       const GtRange *range_b,
       GtUword delta)
```

Returns `true` if `range_a` and `range_b` overlap **at least** `delta` many positions, `false` otherwise.

```
bool gt_range_contains(
       const GtRange *range_a,
       const GtRange *range_b)
```

Returns `true` if `range_b` is contained in `range_a`, `false` otherwise.

```
bool gt_range_within(
       const GtRange *range,
       GtUword point)
```

Returns `true` if `point` lies within `range`, `false` otherwise.

```
GtRange gt_range_join(
          const GtRange *range_a,
          const GtRange *range_b)
```

Join `range_a` and `range_b` and return the result.

```
GtRange gt_range_offset(
          const GtRange *range,
          GtWord offset)
```

Transform start and end of `range` by `offset` and return the result.

```
GtUword gt_range_length(
          const GtRange *range)
```

Returns the length of the given `range`.

```
GtRange gt_range_reorder(
          GtRange range)
```

Reorder `range`.

```
void gt_ranges_sort(
       GtArray *ranges)
```

Sort an array `ranges` of ranges.

```
void gt_ranges_sort_by_length_stable(
       GtArray *ranges)
```

Sort an array `ranges` of ranges by length.

```
bool gt_ranges_are_sorted(
       const GtArray *ranges)
```

RetuUE if the ranges in `ranges` are sorted.

```
bool gt_ranges_do_not_overlap(
       const GtArray *ranges)
```

Returns TRUE if the ranges in `ranges` do not overlap.

```
bool gt_ranges_are_sorted_and_do_not_overlap(
       const GtArray *ranges)
```

Retuns TRUE if the ranges in `ranges` are sorted and do not overlap.

```
bool gt_ranges_are_equal(
       const GtArray *ranges_a,
       const GtArray *ranges_b)
```

Returns TRUE if the ranges in `ranges_a` and `ranges_b` are equal.

```
void gt_ranges_uniq(
       GtArray*,
       const GtArray*)
```

Takes a sorted array of ranges and runs the equivalent of uniq on it.

```
void gt_ranges_uniq_in_place(
       GtArray*)
```

Similar to the previous function, just in place.

```
GtArray* gt_ranges_uniq_count(
           GtArray*,
           const GtArray*)
```

Similar to `gt_ranges_uniq()`, additionally returns an array which contains the counts of the occurrences of each elem in the original array.

```
GtArray* gt_ranges_uniq_in_place_count(
           GtArray*)
```

Similar to the previous function, just in place.S

```
bool gt_ranges_are_consecutive(
       const GtArray *ranges)
```

Returns TRUE if the ranges in `ranges` are consecutive.

```
GtUword gt_ranges_total_length(
          const GtArray *ranges)
```

Returns the sum of the length of the ranges in `ranges`.

```
GtUword gt_ranges_spanned_length(
          const GtArray *ranges)
```

Returns the length of the boundaries of the ranges in `ranges`.

```
void gt_ranges_copy_to_opposite_strand(
       GtArray *outranges,
       const GtArray *inranges,
       GtUword gen_total_length,
       GtUword gen_offset)
```

Copies ranges `inranges` to the 'opposite' strand, the result being in `outranges`.

```
bool gt_ranges_borders_are_in_region(
       GtArray *ranges,
       const GtRange *region)
```

Returns TRUE if all ranges in `ranges` are within the `region`.

```
void gt_ranges_show(
       GtArray *ranges,
       GtFile *outfp)
```

Prints a representation of the ranges `ranges` to `outfp`.

Class GtReadmode

This enum type defines the possible reamodes, namely `GT_READMODE_FORWARD`, `GT_READMODE_REVERSE`, `GT_READMODE_COMPL`, and `GT_READMODE_REVCOMPL`.

Methods

```
const char* gt_readmode_show(
              GtReadmode readmode)
```

Returns the descriptive string for `readmode`.

```
int gt_readmode_parse(
      const char *string,
      GtError *err)
```

Returns the `GtReadmode` for the description `string`, which must be one of "fwd","rev","cpl" or "rcl". If `string` does not equal any of them, -1 is returned and `err` is set accordingly.

```
GtReadmode gt_readmode_inverse_dir(
             GtReadmode readmode)
```

invert the direction of a readmode: fwd => rev, rev => fwd, cpl => rcl, rcl => cpl

Class GtRecMap

A `GtRecMap` object contains a mapping from a 2D coordinate pair which identifies a rectangle in a rendered image to the `GtFeatureNode` it represents. The rectangle is defined by the coordinates of its upper left ("northwest") and lower right ("southeast") points.
`GtRecMap` objects are created by an `GtImageInfo` object which is filled during the generation of an image by *AnnotationSketch*.

Methods

```
GtRecMap* gt_rec_map_new(
            double nw_x,
            double nw_y,
            double se_x,
            double se_y,
            GtFeatureNode *f)
```

Creates a new `GtRecMap` for feature `f` with the given coordinates.

```
GtRecMap* gt_rec_map_ref(
            GtRecMap *rm)
```

Increases the reference count of `rm`.

```
double gt_rec_map_get_northwest_x(
         const GtRecMap*)
```

Retrieve *x* value of the the upper left point of the rectangle.

```
double gt_rec_map_get_northwest_y(
         const GtRecMap*)
```

Retrieve *y* value of the the upper left point of the rectangle.

```
double gt_rec_map_get_southeast_x(
         const GtRecMap*)
```

Retrieve *x* value of the the lower right point of the rectangle.

```
double gt_rec_map_get_southeast_y(
         const GtRecMap*)
```

Retrieve *y* value of the the lower right point of the rectangle.

```
const GtFeatureNode* gt_rec_map_get_genome_feature(
                       const GtRecMap*)
```

Retrieve `GtFeatureNode` associated with this rectangle.

```
bool gt_rec_map_has_omitted_children(
       const GtRecMap*)
```

Returns `true` if the rectangle represents a block root whose elements have not been drawn due to size restrictions.

```
void gt_rec_map_delete(
       GtRecMap*)
```

Deletes a `GtRecMap` and frees all associated memory.

Class GtRegionMapping

A GtRegionMapping objects maps sequence-regions to the corresponding entries of sequence files.

Methods

```
GtRegionMapping* gt_region_mapping_new_mapping(
                   GtStr *mapping_filename,
                   GtError *err)
```

Return a new GtRegionMapping object for the mapping file with the given mapping_filename. In the case of an error, NULL is returned and err is set accordingly.

```
GtRegionMapping* gt_region_mapping_new_seqfiles(
                   GtStrArray *sequence_filenames,
                   bool matchdesc,
                   bool usedesc)
```

Return a new GtRegionMapping object for the sequence files given in sequence_filenames. If matchdesc is true, the sequence descriptions from the input files are matched for the desired sequence IDs (in GFF3).
If usedesc is true, the sequence descriptions are used to map the sequence IDs (in GFF3) to actual sequence entries. If a description contains a sequence range (e.g., III:1000001..2000000), the first part is used as sequence ID ('III') and the first range position as offset ('1000001').
matchdesc and usedesc cannot be true at the same time.

```
GtRegionMapping* gt_region_mapping_new_encseq(
                   GtEncseq *encseq,
                   bool matchdesc,
                   bool usedesc)
```

Like gt_region_mapping_new_seqfiles(), but using encseq as a sequence source.

```
GtRegionMapping* gt_region_mapping_new_rawseq(
                   const char *rawseq,
                   GtUword length,
                   GtUword offset)
```

Return a new GtRegionMapping object which maps to the given sequence rawseq with the corresponding length and offset.

```
GtRegionMapping* gt_region_mapping_ref(
                   GtRegionMapping *region_mapping)
```

Increase the reference count for region_mapping and return it.

```
int gt_region_mapping_get_sequence(
      GtRegionMapping *region_mapping,
      char **seq,
      GtStr *seqid,
      GtUword start,
      GtUword end,
      GtError *err)
```

Use `region_mapping` to extract the sequence from `start` to `end` of the given sequence ID `seqid` into a buffer written to `seq` (the caller is responsible to free it). In the case of an error, -1 is returned and `err` is set accordingly.

```
int gt_region_mapping_get_sequence_length(
      GtRegionMapping
                                                    *region_mapping,
      GtUword *length,
      GtStr *seqid,
      GtError *err)
```

Use `region_mapping` to retrieve the sequence length of the given sequence ID `seqid` and store the result in `length`. In the case of an error, -1 is returned and `err` is set accordingly.

```
int gt_region_mapping_get_description(
      GtRegionMapping
                                                *region_mapping,
      GtStr *desc,
      GtStr *seqid,
      GtError *err)
```

Use `region_mapping` to get the description of the MD5 sequence ID `seqid`. The description is appended to `desc`. In the case of an error, -1 is returned and `err` is set accordingly.

```
const char* gt_region_mapping_get_md5_fingerprint(
              GtRegionMapping
                                                    *region_mapping,
              GtStr *seqid,
              const GtRange *range,
              GtUword *offset,
              GtError *err)
```

Use `region_mapping` to return the MD5 fingerprint of the sequence with the sequence ID `seqid` and its corresponding `range`. The offset of the sequence is stored in `offset`. In the case of an error, `NULL` is returned and `err` is set accordingly.

```
void gt_region_mapping_delete(
       GtRegionMapping *region_mapping)
```

Delete `region_mapping`.

Class GtRegionNode

Implements the GtGenomeNode interface. Region nodes correspond to the <##sequence-region> lines in GFF3 files.

Methods

```
GtGenomeNode* gt_region_node_new(
                GtStr *seqid,
                GtUword start,
                GtUword end)
```

Create a new GtRegionNode* representing sequence with ID seqid from base position start to base position end (1-based). start has to be smaller or equal than end. The GtRegionNode* stores a new reference to seqid, so make sure you do not modify the original seqid afterwards!

```
GtRegionNode* gt_region_node_try_cast(
                GtGenomeNode *gn)
```

Test whether the given genome node is a region node. If so, a pointer to the region node is returned. If not, NULL is returned. Note that in most cases, one should implement a GtNodeVisitor to handle processing of different GtGenomeNode types.

```
GtRegionNode* gt_region_node_cast(
                GtGenomeNode *gn)
```

Test whether the given genome node is a region node. If so, a pointer to the region node is returned. If not, an assertion fails.

Class GtScoreMatrix

GtScoreMatrix represents a matrix of signed integer values, for example for scoring alphabet symbols against each other.

Methods

```
GtScoreMatrix* gt_score_matrix_new(
                 GtAlphabet *alphabet)
```

A score matrix is always defined over a given alphabet.

```
GtScoreMatrix* gt_score_matrix_clone_empty(
                 const GtScoreMatrix *scorematrix)
```

Create empty score matrix with same dimension as scorematrix.

```
GtScoreMatrix* gt_score_matrix_new_read_protein(
                  const char *path,
                  GtError *err)
```

Read in a protein score matrix from the given `path` and return it.

```
GtScoreMatrix* gt_score_matrix_new_read(
                  const char *path,
                  GtAlphabet *alphabet,
                  GtError *err)
```

Read in score matrix from `path` over given `alphabet` and return it.

```
unsigned int gt_score_matrix_get_dimension(
                const GtScoreMatrix *scorematrix)
```

Return the dimension of `scorematrix`.

```
int gt_score_matrix_get_score(
      const GtScoreMatrix *scorematrix,
      unsigned int idx1,
      unsigned int idx2)
```

Return the score value in `scorematrix` at positions (<idx1 >,<idx2 >).

```
void gt_score_matrix_set_score(
       GtScoreMatrix *scorematrix,
       unsigned int idx1,
       unsigned int idx2,
       int score)
```

Set the score value in `scorematrix` at positions (<idx1 >,<idx2 >) to `score`.

```
const int** gt_score_matrix_get_scores(
               const GtScoreMatrix *scorematrix)
```

Return the score values in `scorematrix` as a two-dimensional array.

```
void gt_score_matrix_show(
       const GtScoreMatrix *scorematrix,
       FILE *fp)
```

Print `scorematrix` to output `fp`.

```
void gt_score_matrix_delete(
       GtScoreMatrix *scorematrix)
```

Delete `scorematrix`.

Class GtScriptWrapperStream

Implements the `GtScriptWrapperStream` interface. This stream is only used to store pointers to external callbacks, e.g. written in a scripting language. This class does not store any state or logic, relying on the developer of the external custom stream class to do so.

Methods

```
GtNodeStream* gt_script_wrapper_stream_new(
                GtScriptWrapperStreamNextFunc,
                GtScriptWrapperStreamFreeFunc)
```

Creates a new `GtScriptWrapperStream` given a next and a free function.

Class GtScriptWrapperVisitor

Implements the `GtNodeVisitor` interface.

Methods

```
GtNodeVisitor* gt_script_wrapper_visitor_new(
                 GtScriptWrapperVisitorCommentNodeFunc,
                 GtScriptWrapperVisitorFeatureNodeFunc,
                 GtScriptWrapperVisitorRegionNodeFunc,
                 GtScriptWrapperVisitorSequenceNodeFunc,
                 GtScriptWrapperVisitorMetaNodeFunc,
                 GtScriptWrapperVisitorEOFNodeFunc,
                 GtScriptWrapperVisitorFreeFunc)
```

Creates a new `GtScriptWrapperVisitor` for a number of callback functions.

Class GtSelectStream

Implements the `GtNodeStream` interface. A `GtSelectStream` selects certain nodes it retrieves from its node source and passes them along.

Methods

```
GtNodeStream* gt_select_stream_new(
                GtNodeStream *in_stream,
                GtStr *seqid,
                GtStr *source,
                const GtRange *contain_range,
                const GtRange *overlap_range,
                GtStrand strand,
                GtStrand targetstrand,
                bool has_CDS,
                GtUword max_gene_length,
                GtUword max_gene_num,
                double min_gene_score,
                double max_gene_score,
                double min_average_splice_site_prob,
                GtUword feature_num,
                GtStrArray *select_files,
                GtStr *select_logic,
                GtError *err)
```

Create a `GtSelectStream` object which selects genome nodes it retrieves from its `in_stream` and passes them along if they meet the criteria defined by the other arguments. All comment nodes are selected. If `seqid` is defined, a genome node must have it to be selected. If `source` is defined, a genome node must have it to be selected. If `contain_range` is defined, a genome node must be contained in it to be selected. If `overlap_range` is defined, a genome node must overlap it to be selected. If `strand` is defined, a (top-level) genome node must have it to be selected. If `targetstrand` is defined, a feature with a target attribute must have exactly one of it and its strand must equal `targetstrand`. If `had_cds` is `true`, all top-level features are selected which have a child with type *CDS*. If `max_gene_length` is defined, only genes up to the this length are selected. If `max_gene_num` is defined, only so many genes are selected. If `min_gene_score` is defined, only genes with at least this score are selected. If `max_gene_score` is defined, only genes with at most this score are selected. If `min_average_splice_site_prob` is defined, feature nodes which have splice sites must have at least this average splice site score to be selected. If `feature_num` is defined, just the `feature_num`th feature node occurring in the `in_stream` is selected. If `select_files` is defined and has at least one entry, the entries are evaluated as Lua scripts containing functions taking `GtGenomeNodes` that are evaluated to boolean values to determine selection. `select_logic` can be "OR" or "AND", defining how the results from the select scripts are combined. Returns a pointer to a new `GtSelectStream` or NULL on error (`err` is set accordingly).

```
void gt_select_stream_set_drophandler(
       GtSelectStream *sstr,
       GtSelectNodeFunc fp,
       void *data)
```

Sets `fp` as a handler function to be called for every `GtGenomeNode` not selected by `sstr`. The void pointer `data` can be used for arbitrary user data.

Class GtSeq

GtSeq is a container for a sequence plus metadata.

Methods

```
GtSeq* gt_seq_new(
          const char *seq,
          GtUword seqlen,
          GtAlphabet *seqalpha)
```

Create and return a new GtSeq, storing the pointer for seq (of length seqlen and with alphabet seqalpha).

```
GtSeq* gt_seq_new_own(
          char *seq,
          GtUword seqlen,
          GtAlphabet *seqalpha)
```

Like gt_seq_new(), but tkes ownership of seq.

```
void gt_seq_set_description(
        GtSeq *s,
        const char *desc)
```

Associates s with description desc, storing its pointer.

```
void gt_seq_set_description_own(
        GtSeq *s,
        char *desc)
```

Like gt_seq_set_description(), but takes ownership of desc.

```
const char* gt_seq_get_description(
              GtSeq *s)
```

Return the description string for s.

```
const char* gt_seq_get_orig(
              const GtSeq *s)
```

Return the underlying sequence memory for s, not guaranteed to be '\0' terminated.

```
const GtUchar* gt_seq_get_encoded(
                 GtSeq *s)
```

Return the sequence for s, encoded using the defined alphabet.

```
const GtAlphabet* gt_seq_get_alphabet(
                    const GtSeq*)
```

Return the alphabet associated with `s`.

```
GtUword gt_seq_length(
          const GtSeq *s)
```

Return the length of the sequence in `s`.

```
void gt_seq_delete(
       GtSeq *s)
```

Delete `s` and free all associated memory.

Class GtSeqIterator

```
void gt_seq_iterator_set_symbolmap(
       GtSeqIterator*,
       const GtUchar *symbolmap)
```

Sets a symbol map for the `GtSeqIterator`. If a `symbolmap` is given, all read in sequences are transformed with it. Set to NULL to disable alphabet transformation.

```
void gt_seq_iterator_set_sequence_output(
       GtSeqIterator*,
       bool)
```

If set to `true`, sequences and descriptions are processed (otherwise only the descriptions). By default, sequences are processed.

```
int gt_seq_iterator_next(
      GtSeqIterator *seqit,
      const GtUchar **sequence,
      GtUword *len,
      char **description,
      GtError *err)
```

Get next `sequence` (of length `len`) and `description` from `seqit`. Note that `seqit` retains ownership of the `sequence` and `description`. Returns 1 if another sequence could be parsed, 0 if all given sequence files are exhausted, And -1 if an error occurred (`err` is set accordingly).

```
const GtUint64* gt_seq_iterator_getcurrentcounter(
                  GtSeqIterator*,
                  GtUint64)
```

Returns a pointer to the current total number of read characters.

```
bool gt_seq_iterator_has_qualities(
       GtSeqIterator *seqit)
```

Returns TRUE if `seqit` supports setting of a quality buffer.

```
void gt_seq_iterator_set_quality_buffer(
       GtSeqIterator *seqit,
       const GtUchar **qualities)
```

Turns on reporting of sequence qualities to the location pointed to by `qualities`. That pointer will be set to a string containing the quality data (which must then be processed into scores).

```
void gt_seq_iterator_delete(
       GtSeqIterator *seqit)
```

Deletes `seqit` and frees associated memory.

Class GtSeqIteratorFastQ

```
GtSeqIterator* gt_seq_iterator_fastq_new(
                 const GtStrArray *filenametab,
                 GtError *err)
```

Create a new `GtSeqIteratorFastQ` for all sequence files in `filenametab`.

```
GtSeqIterator* gt_seq_iterator_fastq_new_colorspace(
                 const GtStrArray
                                                  *filenametab,
                 GtError *err)
```

Create a new `GtSeqIteratorFastQ` for all sequence files in `filenametab` containing color space reads.

```
GtUword gt_seq_iterator_fastq_get_file_index(
          GtSeqIteratorFastQ *seqit)
```

Returns the number of the file in the file name array which `seqit` is currently reading.

```
void gt_seq_iterator_fastq_relax_check_of_quality_description(
       GtSeqIteratorFastQ *seqit)
```

Disable checking if quality description is equal to read description in `seqit` (it should be, but it is not in output of some tools, e.g. Coral).

Class GtSeqIteratorSequenceBuffer

```
GtSeqIterator* gt_seq_iterator_sequence_buffer_new(
                  const GtStrArray
                                                     *filenametab,
                  GtError *err)
```

Create a new `GtSeqIterator` for all sequence files in `filenametab`. All files have to be of the same format, which will be guessed by examining the beginning of the first file. If an error occurs, NULL is returned (see the `err` object for details).

Class GtSeqid2FileInfo

The <GtSeqid2FileInfo> class represents the state of a sequence source statement as given by the -seqfile, -seqfiles, -matchdesc, -usedesc and -regionmapping options.

Methods

```
GtSeqid2FileInfo* gt_seqid2file_info_new(
                    void)
```

Create a new <GtSeqid2FileInfo> object.

```
void gt_seqid2file_info_delete(
       GtSeqid2FileInfo *)
```

Create a new <GtSeqid2FileInfo> object.

Class GtSequenceNode

Implements the `GtGenomeNode` interface. Sequence nodes correspond to singular embedded FASTA sequences in GFF3 files.

Methods

```
GtGenomeNode* gt_sequence_node_new(
                const char *description,
                GtStr *sequence)
```

Create a new GtSequenceNode* representing a FASTA entry with the given description and sequence. Takes ownership of sequence.

```
const char* gt_sequence_node_get_description(
              const
                                                    GtSequenceNode
                                                    *sequence_node)
```

Return the description of sequence_node.

```
const char* gt_sequence_node_get_sequence(
              const GtSequenceNode
                                                *sequence_node)
```

Return the sequence of sequence_node.

```
GtUword gt_sequence_node_get_sequence_length(
          const
                                                      GtSequenceNode
                                                      *sequence_node)
```

Return the sequence length of sequence_node.

```
GtSequenceNode* gt_sequence_node_try_cast(
                  GtGenomeNode *gn)
```

Test whether the given genome node is a sequence node. If so, a pointer to the sequence node is returned. If not, NULL is returned. Note that in most cases, one should implement a GtNodeVisitor to handle processing of different GtGenomeNode types.

```
GtSequenceNode* gt_sequence_node_cast(
                  GtGenomeNode *gn)
```

Test whether the given genome node is a sequence node. If so, a pointer to the sequence node is returned. If not, an assertion fails.

Class GtSetSourceVisitor

Implements the GtNodeVisitor interface. Used with the GtVisitorStream class, a GtSetSourceVisitor resets the source value for GtFeatureNode objects.

Methods

```
GtNodeVisitor* gt_set_source_visitor_new(
                  GtStr *newsource)
```

Create a node visitor object which will reset the source value of all `GtFeatureNode` objects it processes to `newsource`.

Class GtSortStream

Implements the `GtNodeStream` interface. A `GtSortStream` sorts the `GtGenomeNode` objects it retrieves from its node source.

Methods

```
GtNodeStream* gt_sort_stream_new(
                 GtNodeStream *in_stream)
```

Create a `GtSortStream*` which sorts the genome nodes it retrieves from `in_stream` and returns them unmodified, but in sorted order.

Class GtSpliceSiteInfoStream

The `GtSpliceSiteInfoStream` is a `GtNodeStream` that gathers splice site information from `GtFeatureNodes`.

Methods

```
GtNodeStream* gt_splice_site_info_stream_new(
                 GtNodeStream *in_stream,
                 GtRegionMapping *region_mapping)
```

Create a GtSpliceSiteInfoStream, takes ownership of `region_mapping`.

```
bool gt_splice_site_info_stream_show(
       GtNodeStream *ns,
       GtFile *outfp)
```

Prints splice site information gathered in `ns` to `outfp`.

```
bool gt_splice_site_info_stream_intron_processed(
       GtNodeStream *ns)
```

Returns `true` if an intron has been processed in `ns`, `false` otherwise

```
bool gt_splice_site_info_stream_show_canonical(
       GtNodeStream *ns,
       bool show_gc)
```

Print information for canonical splice sites as stored in `ns`.

Class GtSplitter

The `GtSplitter` class defines objects which can split given strings into tokens delimited by a given character, allowing for convenient access to each token.

Methods

```
GtSplitter* gt_splitter_new(
              void)
```

Create a new `GtSplitter` object.

```
void gt_splitter_split(
       GtSplitter *splitter,
       char *string,
       GtUword length,
       char delimiter)
```

Use `splitter` to split `string` of given `length` into tokens delimited by `delimiter`. Note that `string` is modified in the splitting process!

```
void gt_splitter_split_non_empty(
       GtSplitter *s,
       char *string,
       GtUword length,
       char delimiter)
```

Use `splitter` to split `string` of given `length` into tokens delimited by `delimiter`. Empty tokens will be ignored. Note that `string` is modified in the splitting process!

```
char** gt_splitter_get_tokens(
         GtSplitter *splitter)
```

Return all tokens split by `splitter` in an array.

```
char* gt_splitter_get_token(
        GtSplitter *splitter,
        GtUword token_num)
```

Return token with number `token_num` from `splitter`.

```
void gt_splitter_reset(
       GtSplitter *splitter)
```

Reset the splitter.

```
GtUword gt_splitter_size(
          GtSplitter *splitter)
```

Return the number of tokens in splitter.

```
void gt_splitter_delete(
       GtSplitter *splitter)
```

Delete the splitter.

Class GtStatStream

Implements the GtNodeStream interface. A GtStatStream gathers statistics about the GtGenomeNode objects it retrieves from its node source and passes them along unmodified.

Methods

```
GtNodeStream* gt_stat_stream_new(
                GtNodeStream *in_stream,
                bool gene_length_distribution,
                bool gene_score_distribution,
                bool exon_length_distribution,
                bool exon_number_distribution,
                bool intron_length_distribution,
                bool cds_length_distribution,
                bool used_sources)
```

Create a GtStatStream object which gathers statistics about the GtGenomeNode objects it retrieves from its in_stream and returns them unmodified. Besides the basic statistics, statistics about the following distributions can be gathered, if the corresponding argument equals true: gene_length_distribution, gene_score_distribution, exon_length_distribution, exon_number_distribution, intron_length_distribution, cds_length_distribution.
If used_sources equals true, it is recorded which source tags have been encountered.

```
void gt_stat_stream_show_stats(
       GtStatStream *stat_stream,
       GtFile *outfp)
```

Write the statistics gathered by stat_stream to outfp.

Class GtStr

Objects of the `GtStr` class are strings which grow on demand.

Methods

```
GtStr* gt_str_new(
         void)
```

Return an empty `GtStr` object.

```
GtStr* gt_str_new_cstr(
         const char *cstr)
```

Return a new `GtStr` object whose content is set to `cstr`.

```
GtStr* gt_str_clone(
         const GtStr *str)
```

Return a clone of `str`.

```
GtStr* gt_str_ref(
         GtStr *str)
```

Increase the reference count for `str` and return it. If `str` is `NULL`, `NULL` is returned without any side effects.

```
char* gt_str_get(
        const GtStr *str)
```

Return the content of `str`. Never returns NULL, and the content is always $<\backslash 0>$-terminated

```
void gt_str_set(
       GtStr *str,
       const char *cstr)
```

Set the content of `str` to `cstr`.

```
void gt_str_append_str(
       GtStr *dest,
       const GtStr *src)
```

Append the string `src` to `dest`.

```
void gt_str_append_cstr(
       GtStr *str,
       const char *cstr)
```

Append the $<\backslash 0>$-terminated `cstr` to `str`.

```
void gt_str_append_cstr_nt(
       GtStr *str,
       const char *cstr,
       GtUword length)
```

Append the (not necessarily $<\backslash 0>$-terminated) `cstr` with given `length` to `str`.

```
void gt_str_append_char(
       GtStr *str,
       char c)
```

Append character `c` to `str`.

```
void gt_str_append_double(
       GtStr *str,
       double d,
       int precision)
```

Append double `d` to `str` with given `precision`.

```
void gt_str_append_sci_double(
       GtStr *dest,
       double d,
       int precision)
```

Append double `d` to `str` in scientific notation e.g. 0.52e10, with given `precision`.

```
void gt_str_append_uword(
       GtStr *str,
       GtUword uword)
```

Append `ulong` to `str`.

```
void gt_str_append_int(
       GtStr *str,
       int intval)
```

Append `intval` to `str`.

```
void gt_str_append_uint(
       GtStr *str,
       unsigned int uint)
```

Append `uint` to `str`.

```
void gt_str_set_length(
       GtStr *str,
       GtUword length)
```

Set length of `str` to `length`. `length` must be smaller or equal than `gt_str_length(str)`.

```
void gt_str_reset(
       GtStr *str)
```

Reset `str` to length 0.

```
int gt_str_cmp(
      const GtStr *str1,
      const GtStr *str2)
```

Compare <str1 > and <str2 > and return the result (similar to <strcmp(3)>).

```
GtUword gt_str_length(
          const GtStr *str)
```

Return the length of `str`. If `str` is `NULL`, 0 is returned.

```
void* gt_str_get_mem(
        const GtStr *str)
```

Return the memory pointed to by *str. Never returns NULL, not always '\0' terminated.

```
void gt_str_clip_suffix(
       GtStr *s,
       char c)
```

Remove end of `s` beginning with first occurrence of `c`

```
int gt_str_read_next_line(
      GtStr *str,
      FILE *fpin)
```

Read the next line from file pointer `fpin` and store the result in `str` (without the terminal newline). If the end of file `fpin` is reached, `EOF` is returned, otherwise 0. `str` should be empty, or the next line will be concatenated to its content.

```
int gt_str_read_next_line_generic(
      GtStr*,
      GtFile*)
```

Read the next line via a `GtFile`-object, but otherwise behave as the previous function.

```
void gt_str_delete(
       GtStr *str)
```

Decrease the reference count for `str` or delete it, if this was the last reference.

```
GtStr* GtStrConstructorFunc(
                            void *str_source,
                            GtUword index)
```

Function to obtain a `GtStr` from a `str_source`, given an `index`.

Class GtStrArray

`GtStrArray*` objects are arrays of string which grow on demand.

Methods

```
GtStrArray* gt_str_array_new(
              void)
```

Return a new `GtStrArray` object.

```
GtStrArray* gt_str_array_ref(
              GtStrArray*)
```

Increases the reference to a GtStrArray.

```
void gt_str_array_add_cstr(
       GtStrArray *str_array,
       const char *cstr)
```

Add `cstr` to `str_array`. Thereby, an internal copy of `cstr` is created.

```
void gt_str_array_add_cstr_nt(
       GtStrArray *str_array,
       const char *cstr,
       GtUword length)
```

Add the non $<\backslash 0>$-terminated `cstr` with given `length` to `str_array`. Thereby, an internal copy of `cstr` is created.

```
void gt_str_array_add(
       GtStrArray *str_array,
       const GtStr *str)
```

Add `str` to `str_array`. Thereby, an internal copy of `str` is created.

```
const char* gt_str_array_get(
              const GtStrArray *str_array,
              GtUword strnum)
```

Return pointer to internal string with number `strnum` of `str_array`. `strnum` must be smaller than `gt_str_array_size(str_array)`.

```
void gt_str_array_set_cstr(
       GtStrArray *str_array,
       GtUword strnum,
       const char *cstr)
```

Set the string with number `strnum` in `str_array` to `cstr`.

```
void gt_str_array_set(
       GtStrArray *str_array,
       GtUword strnum,
       const GtStr *str)
```

Set the string with number `strnum` in `str_array` to `str`.

```
void gt_str_array_set_size(
       GtStrArray *str_array,
       GtUword size)
```

Set the size of `str_array` to `size`. `size` must be smaller or equal than `gt_str_array_size(str_array)`.

```
void gt_str_array_reset(
       GtStrArray *str_array)
```

Set the size of `str_array` to 0.

```
GtUword gt_str_array_size(
          const GtStrArray *str_array)
```

Return the number of strings stored in `str_array`.

```
void gt_str_array_delete(
       GtStrArray *str_array)
```

Delete `str_array`.

Class GtStrCache

`GtStrCache` is a string cache. That is, the first time a certain string is requested with the method `gt_str_cache_get()`, a new string object is created via `str_constructor` and then cached and returned. Subsequent calls to `gt_str_cache_get()` for the same string return a new reference made from the cached string.

Methods

```
GtStrCache* gt_str_cache_new(
              void *str_source,
              GtStrConstructorFunc str_constructor,
              GtUword num_of_strings)
```

Create a new string cache object for `num_of_strings` many strings creatable from `str_source` with the function `str_constructor`.

```
GtStr* gt_str_cache_get(
         GtStrCache *str_cache,
         GtUword index)
```

Return a new (i.e., the caller is responsible to free it) `GtStr*` object from `str_cache` for string with given `index`. The mechanics of the cache are described in detail in the documentation of `GtStrCache`.

```
void gt_str_cache_delete(
       GtStrCache *str_cache)
```

Delete `str_cache`.

Class GtStrand

This enum type defines the possible strands. The following strands are defined: `GT_STRAND_FORWARD`, `GT_STRAND_REVERSE`, `GT_STRAND_BOTH`, and `GT_STRAND_UNKNOWN`.

Methods

```
#define GT_STRAND_CHARS
```

Use this string to map strand enum types to their corresponding character.

```
GtStrand gt_strand_get(
           char strand_char)
```

Map `strand_char` to the corresponding strand enum type. Returns `GT_NUM_OF_STRAND_TYPES` if `strand_char` is not a valid one.

Class GtStyle

Objects of the `GtStyle` class hold *AnnotationSketch* style information like colors, margins, collapsing options, and others. The class provides methods to set values of various types. Each value is organized into a *section* and is identified by a *key*. That is, a *section*, *key* pair must uniquely identify a value.

Methods

```
GtStyle* gt_style_new(
           GtError*)
```

Creates a new `GtStyle` object.

```
GtStyle* gt_style_ref(
           GtStyle*)
```

Increments the reference count of the given `GtStyle`.

```
void gt_style_unsafe_mode(
       GtStyle*)
```

Enables unsafe mode ("io" and "os" libraries loaded).

```
void gt_style_safe_mode(
       GtStyle*)
```

Enables safe mode ("io" and "os" libraries not accessible).

```
bool gt_style_is_unsafe(
       GtStyle *sty)
```

Returns true if `sty` is in unsafe mode.

```
GtStyle* gt_style_clone(
           const GtStyle*,
           GtError*)
```

Creates a independent ("deep") copy of the given `GtStyle` object.

```
int gt_style_load_file(
      GtStyle*,
      const char *filename,
      GtError*)
```

Loads and executes Lua style file with given `filename`. This file must define a global table called *style*.

```
int gt_style_load_str(
      GtStyle*,
      GtStr *instr,
      GtError*)
```

Loads and executes Lua style code from the given `GtStr instr`. This code must define a global table called *style*.

```
int gt_style_to_str(
      const GtStyle*,
      GtStr *outstr,
      GtError*)
```

Generates Lua code which represents the given `GtStyle` object and writes it into the `GtStr` object `outstr`.

```
void gt_style_reload(
       GtStyle*)
```

Reloads the Lua style file.

```
void gt_style_set_color(
       GtStyle*,
       const char *section,
       const char *key,
       const GtColor *color)
```

Sets a color value in the `GtStyle` for section `section` and `key` to a certain `color`.

```
GtStyleQueryStatus gt_style_get_color(
                     const GtStyle *style,
                     const char *section,
                     const char *key,
                     GtColor *result,
                     GtFeatureNode *fn,
                     GtError *err)
```

Retrieves a color value from `style` for key `key` in section `section`. The color is written to the location pointed to by `result`. Optionally, a feature node pointer `fn` can be specified for handling in node-specific callbacks. Because color definitions can be functions, `gt_style_get_color()` can fail at runtime. In this case, this function returns GT_STYLE_QUERY_ERROR and `err` is set accordingly. If the color was not specified in `style`, a grey default color is written to `result` and GT_STYLE_QUERY_NOT_SET is returned so the caller can provide a custom default. In case of successful retrieval of an existing color, GT_STYLE_QUERY_OK is returned.

```
GtStyleQueryStatus gt_style_get_color_with_track(
                     const GtStyle *style,
                     const char *section,
                     const char *key,
                     GtColor *result,
                     GtFeatureNode *fn,
                     const GtStr *track_id,
                     GtError *err)
```

Identical to `gt_style_get_color()`, except that it also takes a `track_id` which is passed to a potential callback function in the style file.

```
void gt_style_set_str(
       GtStyle*,
       const char *section,
       const char *key,
       GtStr *value)
```

Set string with key `key` in `section` to `value`.

```
GtStyleQueryStatus gt_style_get_str(
                     const GtStyle *style,
                     const char *section,
                     const char *key,
                     GtStr *result,
                     GtFeatureNode *fn,
                     GtError *err)
```

Retrieves a string value from `style` for key `key` in section `section`. The string is written to the `GtStr` object `result`, overwriting its prior contents. Optionally, a feature node pointer `fn` can be specified for handling in node-specific callbacks. Because color definitions can be functions, `gt_style_get_str()` can fail at runtime. In this case, this function returns GT_STYLE_QUERY_ERROR and `err` is set accordingly. If the string was not specified in `style`, `result` is left untouched and GT_STYLE_QUERY_NOT_SET is returned so the caller can handle this case. In case of successful retrieval of an existing string, GT_STYLE_QUERY_OK is returned.

```
GtStyleQueryStatus gt_style_get_str_with_track(
                     const GtStyle *style,
                     const char *section,
                     const char *key,
                     GtStr *result,
                     GtFeatureNode *fn,
                     const GtStr *track_id,
                     GtError *err)
```

Identical to `gt_style_get_str()`, except that it also takes a `track_id` which is passed to a potential callback function in the style file.

```
void gt_style_set_num(
       GtStyle*,
       const char *section,
       const char *key,
       double number)
```

Set numeric value of key `key` in `section` to `number`.

```
GtStyleQueryStatus gt_style_get_num(
                     const GtStyle *style,
                     const char *section,
                     const char *key,
                     double *result,
                     GtFeatureNode *fn,
                     GtError *err)
```

Retrieves a numeric value from `style` for key `key` in section `section`. The value is written to the location pointed to by `result`. Optionally, a feature node pointer `fn` can be specified for handling in node-specific callbacks. Because the definitions can be functions, `gt_style_get_num()` can fail at runtime. In this case, this function returns GT_STYLE_QUERY_ERROR and `err` is set accordingly. If the number was not specified in `style`, `result` is left untouched and GT_STYLE_QUERY_NOT_SET is returned so the caller can handle this case. In case of successful retrieval of an existing number, GT_STYLE_QUERY_OK is returned.

```
GtStyleQueryStatus gt_style_get_num_with_track(
                     const GtStyle *style,
                     const char *section,
                     const char *key,
                     double *result,
                     GtFeatureNode *fn,
                     const GtStr *track_id,
                     GtError *err)
```

Identical to `gt_style_get_num()`, except that it also takes a `track_id` which is passed to a potential callback function in the style file.

```
void gt_style_set_bool(
       GtStyle*,
       const char *section,
       const char *key,
       bool val)
```

Set boolean value of key `key` in `section` to `val`.

```
GtStyleQueryStatus gt_style_get_bool(
                     const GtStyle *style,
                     const char *section,
                     const char *key,
                     bool *result,
                     GtFeatureNode *fn,
                     GtError *err)
```

Retrieves a boolean value from `style` for key `key` in section `section`. The value is written to the location pointed to by `result`. Optionally, a feature node pointer `fn` can be specified for handling in node-specific callbacks. Because the definitions can be functions, `gt_style_get_bool()` can fail at runtime. In this case, this function returns GT_STYLE_QUERY_ERROR and `err` is set accordingly. If the value was not specified in `style`, `result` is left untouched and GT_STYLE_QUERY_NOT_SET is returned so the caller can handle this case. In case of successful retrieval of an existing boolean, GT_STYLE_QUERY_OK is returned.

```
GtStyleQueryStatus gt_style_get_bool_with_track(
                     const GtStyle *style,
                     const char *section,
                     const char *key,
                     bool *result,
                     GtFeatureNode *fn,
                     const GtStr *track_id,
                     GtError *err)
```

Identical to `gt_style_get_bool()`, except that it also takes a `track_id` which is passed to a potential callback function in the style file.

```
void gt_style_unset(
       GtStyle*,
       const char *section,
       const char *key)
```

Unset value of key `key` in `section`.

```
void gt_style_delete(
       GtStyle *style)
```

Deletes this `style`.

Class GtTagValueMap

A very simple tag/value map absolutely optimized for space (i.e., memory consumption) on the cost of time. Basically, each read/write access costs O(n) time, whereas n denotes the accumulated length of all tags and values contained in the map. Tags and values cannot have length 0. The implementation as a char* shines through (also to save one additional memory allocation), therefore the usage is a little bit different compared to other *GenomeTools* classes. See the implementation of `gt_tag_value_map_example()` for an ussage example.

Methods

```
void GtTagValueMapIteratorFunc(
                                const char *tag,
                                const char *value,
                                void *data)
```

Iterator function used to iterate over tag/value maps. A `tag`/`value` pair and user `data` are given as arguments.

```
GtTagValueMap gt_tag_value_map_new(
                const char *tag,
                const char *value)
```

Return a new `GtTagValueMap` object which stores the given `tag`/`value` pair.

```
void gt_tag_value_map_add(
       GtTagValueMap *tag_value_map,
       const char *tag,
       const char *value)
```

Add `tag`/`value` pair to `tag_value_map`. `tag_value_map` must not contain the given `tag` already!

```
void gt_tag_value_map_set(
       GtTagValueMap *tag_value_map,
       const char *tag,
       const char *value)
```

Set the given `tag` in `tag_value_map` to `value`.

```
const char* gt_tag_value_map_get(
              const GtTagValueMap tag_value_map,
              const char *tag)
```

Return value corresponding to `tag` from `tag_value_map`. If `tag_value_map` does not contain such a value, `NULL` is returned.

```
GtUword gt_tag_value_map_size(
          const GtTagValueMap tag_value_map)
```

Return the number of tag-value pairs in `tag_value_map`.

```
void gt_tag_value_map_remove(
       GtTagValueMap *tag_value_map,
       const char *tag)
```

Removes the given `tag` from `tag_value_map`. `tag_value_map` must contain the given `tag` already! Also, at least one tag-value pair must remain in the map.

```
void gt_tag_value_map_foreach(
       const GtTagValueMap tag_value_map,
       GtTagValueMapIteratorFunc iterator_func,
       void *data)
```

Apply `iterator_func` to each tag/value pair contained in `tag_value_map` and pass `data` along.

```
int gt_tag_value_map_example(
      GtError *err)
```

Implements an example useage of a tag/value map.

```
void gt_tag_value_map_delete(
       GtTagValueMap tag_value_map)
```

Delete `tag_value_map`.

Class GtTextWidthCalculator

The GtTextWidthCalculator interface answers queries w.r.t. text width in a specific drawing backend. This interface is needed to do proper line breaking in a `GtLayout` even if there is no `GtCanvas` or `GtGraphics` created yet.

Methods

```
GtTextWidthCalculator* gt_text_width_calculator_ref(
                         GtTextWidthCalculator*)
```

Increases the reference count of the `GtTextWidthCalculator`.

```
double gt_text_width_calculator_get_text_width(
         GtTextWidthCalculator*,
         const char *text,
         GtError *err)
```

Requests the width of `text` from the `GtTextWidthCalculator`. If the returned value is negative, an error occurred. Otherwise, a positive double value is returned.

```
void gt_text_width_calculator_delete(
       GtTextWidthCalculator*)
```

Deletes a `GtTextWidthCalculator` instance.

Class GtTextWidthCalculatorCairo

Implements the GtTextWidthCalculator interface with Cairo as the drawing backend. If text width is to be calculated with regard to a specific transformation etc. which is in effect in a

cairo_t and which should be used later via a GtCanvasCairoContext, create a GtTextWidthCalculatorCairo object and pass it to the GtLayout via gt_layout_new_with_twc().

Methods

```
GtTextWidthCalculator* gt_text_width_calculator_cairo_new(
                         cairo_t*,
                         GtStyle*,
                         GtError*)
```

Creates a new GtTextWidthCalculatorCairo object for the given context using the text size options given in the GtStyle. If the GtStyle is NULL, the current font settings in the cairo_t will be used for all text width calculations.

Class GtThread

The GtThread class represents a handle to a single thread of execution.

Methods

```
void* GtThreadFunc(
                    void *data)
```

A function to be multithreaded.

```
GtThread* gt_thread_new(
            GtThreadFunc function,
            void *data,
            GtError *err)
```

Create a new thread which executes the given function (with data passed to it). Returns a GtThread* handle to the newly created thread, if successful. Returns NULL and sets err accordingly upon failure.

```
void gt_thread_delete(
       GtThread *thread)
```

Delete the given thread handle. Does not stop the thread itself!

```
void gt_thread_join(
       GtThread *thread)
```

Wait for thread to terminate before continuing execution of the current thread.

Class GtTimer

The GtTimer class encapsulates a timer which can be used for run-time measurements.

Methods

```
GtTimer* gt_timer_new(
           void)
```

Return a new GtTimer object.

```
GtTimer* gt_timer_new_with_progress_description(
           const char* description)
```

Return a new GtTimer object with the first description.

```
void gt_timer_start(
       GtTimer *timer)
```

Start the time measurement on timer.

```
void gt_timer_stop(
       GtTimer *timer)
```

Stop the time measurement on timer.

```
void gt_timer_show(
       GtTimer *timer,
       FILE *fp)
```

Output the current state of timer in the format ””GT_WD”.pointer fp (see gt_timer_show_formatted). The timer is then stopped.

```
void gt_timer_show_formatted(
       GtTimer *timer,
       const char *fmt,
       FILE *fp)
```

Output the current state of timer in a user-defined format given by fmt. fmt must be a format string for four ”GT_WD” numbers, which are filled with: elapsed seconds, elapsed microseconds, used usertime in seconds, system time in seconds. The output is written to fp. The timer is then stopped.

```
GtWord gt_timer_elapsed_usec(
         GtTimer *t)
```

return usec of time from start to stop of giben timer. The timer is then stopped.

```
void gt_timer_get_formatted(
       GtTimer *t,
       const char *fmt,
       GtStr *str)
```

Like gt_timer_show_formatted(), but appends the output to str.

```
void gt_timer_show_progress(
       GtTimer *timer,
       const char *desc,
       FILE *fp)
```

Output the current state of `timer` on `fp` since the last call of `gt_timer_show_progress()` or the last start of `timer`, along with the current description. The timer is not stopped, but updated with `desc` to be the next description.

```
void gt_timer_show_progress_formatted(
       GtTimer *timer,
       FILE *fp,
       const char *desc,
       ...)
```

Like `gt_timer_show_progress()`, but allows one to format the description in a `printf()`-like fashion.

```
void gt_timer_show_progress_va(
       GtTimer *timer,
       FILE *fp,
       const char *desc,
       va_list ap)
```

Like `gt_timer_show_progress()`, but allows one to format the description in a `vprintf()`-like fashion using a va_list argument `ap`.

```
void gt_timer_show_progress_final(
       GtTimer *timer,
       FILE *fp)
```

Output the overall time measured with `timer` from start to now on `fp`.

```
void gt_timer_show_cpu_time_by_progress(
       GtTimer *timer)
```

Show also user and sys time in output of `gt_timer_show_progress[_final]()`.

```
void gt_timer_omit_last_stage(
       GtTimer *timer)
```

Hide output of last stage time in `gt_timer_show_progress_final()`.

```
void gt_timer_delete(
       GtTimer *timer)
```

Delete `timer`.

Class GtTool

The `GtTool` class encapsulates a single *GenomeTools* tool. Can also be used in external applications based on `libgenometools`.

Methods

```
void* GtToolArgumentsNew(
                           void)
```

Callback function. Must return memory to be used as a storage space for tool arguments.

```
void GtToolArgumentsDelete(
                             void *tool_arguments)
```

Callback function. Must free up all memory reserved by the `GtToolArgumentsNew` function in `tool_arguments`.

```
GtOptionParser* GtToolOptionParserNew(
                                        void *tool_arguments)
```

Callback function. Must return a new `GtOptionParser` filling `tool_arguments` with content.

```
int GtToolArgumentsCheck(
                           int rest_argc,
                           void *tool_arguments,
                           GtError *err)
```

Callback function. Checks the validity of `tool_arguments` when `rest_argc` additional parameters are given to the tool command line. Must return zero if checks are successful, and a negative value otherwise. In that case `err` should be set accordingly.

```
int GtToolRunner(
                  int argc,
                  const char **argv,
                  int parsed_args,
                  void *tool_arguments,
                  GtError*)
```

Callback function. Acts as a main entry point for the tool logic. Parameters `argc` and `argv` are similar to a regular `main()` function. The `parsed_args` parameter gives the number of parameters already parsed by the option parser before additional parameters start. Use `tool_arguments` to access options set by the option parser and write errors to `err`. This function should return the error status of the tool (i.e. 0 for success). If the return value is not equal to 0, errors written to `err` will be printed on stderr.

```
GtTool* GtToolConstructor(
                            void)
```

Returns a new self-contained `GtTool`.

```
GtTool* gt_tool_new(
          GtToolArgumentsNew tool_arguments_new,
          GtToolArgumentsDelete tool_arguments_delete,
          GtToolOptionParserNew tool_option_parser_new,
          GtToolArgumentsCheck tool_arguments_check,
          GtToolRunner tool_runner)
```

Create a new tool object, with a tool argument constructor `gt_tool_arguments_new` (optional), a tool argument destructor `gt_tool_arguments_delete` (optional). a tool option parser constructor `gt_tool_option_parser_new` (required), a tool argument checker `gt_tool_arguments_check` (optional), a tool runner `gt_tool_runner` (required), and `tool_arguments_new` and `tool_arguments_delete` imply each other. Returns a new GtTool object.

```
int gt_tool_run(
      GtTool*,
      int argc,
      const char **argv,
      GtError *err)
```

Run the given `tool` as follows: 1. Create a tool arguments object, if necessary. 2. Create a new option parser and pass the tool arguments along. 3. Parse the options (`argc` and `argv`) with the created option parser. Return upon error, continue otherwise. 4. Check the tool arguments, if necessary. Return upon error, continue otherwise. 5. Run the actual tool with the given arguments (the tool arguments object is passed along). 6. Delete the tool arguments object, if one was created. Returns -1 and sets `err` on error, returns 0 otherwise.

```
void gt_tool_delete(
       GtTool*)
```

Delete the given `tool`.

Class GtToolbox

The `GtToolbox` class groups several tools into one and can be used to structure *GenomeTools* into sensible sets of subtools.

Methods

```
GtToolbox* gt_toolbox_new(
             void)
```

Return a new empty `GtToolbox`.

```
void gt_toolbox_add_tool(
       GtToolbox *toolbox,
       const char *toolname,
       GtTool *tool)
```

Add `tool` with name `toolname` to `toolbox`. Takes ownership of `tool`.

```
void gt_toolbox_add_hidden_tool(
       GtToolbox *toolbox,
       const char *toolname,
       GtTool *tool)
```

Add (hidden) `tool` with name `toolname` to `toolbox`. Hidden tools are not shown in the output of `gt_toolbox_show()`. Takes ownership of `tool`.

```
GtTool* gt_toolbox_get_tool(
          GtToolbox *toolbox,
          const char *toolname)
```

Get `GtTool` with name `toolname` from `toolbox`. Returns NULL if tool does not exist in `toolbox`.

```
int gt_toolbox_show(
      const char *progname,
      void *toolbox,
      GtError*)
```

Show all tools in `toolbox` except the hidden ones. Intended to be used as an argument to `gt_option_parser_set_comment_func()`.

```
void gt_toolbox_delete(
       GtToolbox *toolbox)
```

Deletes `toolbox`.

Class GtTransTable

The `GtTransTable` represents a *translation table*, i.e. a mapping between codons and amino acids, as well as associated metadata.

Methods

```
GtStrArray* gt_trans_table_get_scheme_descriptions(
              void)
```

Returns a GtStrArray of translation scheme descriptions, each of the format "in gt_translator_set_translation_scheme()) and the string is the scheme name.

```
GtTransTable* gt_trans_table_new(
                unsigned int scheme,
                GtError *err)
```

Returns a translation table as given by scheme which refers to the numbers as reported by gt_translator_get_translation_table_descriptions() or the list given at the NCBI web site *http://www.ncbi.nlm.nih.gov/Taxonomy/Utils/wprintgc.cgi*. Returns NULL if an error occurred, see err for details.

```
GtTransTable* gt_trans_table_new_standard(
                GtError *err)
```

Returns the standard translation table.

```
const char* gt_trans_table_description(
              const GtTransTable *tt)
```

Returns the description of tt.

```
int gt_trans_table_translate_codon(
      const GtTransTable *tt,
      char c1,
      char c2,
      char c3,
      char *amino,
      GtError *err)
```

Writes the translation for the codon <c1 >,<c2 >,<c3 > to the position pointed to by amino. The current translation scheme set in translator is used. Returns a negative value if an error occurred, see err for details. Otherwise, 0 is returned.

```
bool gt_trans_table_is_start_codon(
       const GtTransTable *tt,
       char c1,
       char c2,
       char c3)
```

Returns TRUE if the codon <c1 >,<c2 >,<c3 > is a start codon in tt.

```
bool gt_trans_table_is_stop_codon(
       const GtTransTable *tt,
       char c1,
       char c2,
       char c3)
```

Returns TRUE if the codon <c1 >,<c2 >,<c3 > is a stop codon in `tt`.

```
void gt_trans_table_delete(
       GtTransTable *tt)
```

Deletes `tt`.

Class GtTranslator

The `GtTranslator` can be used to produce 3-frame translations of DNA sequences via an iterator interface.

Methods

```
GtTranslator* gt_translator_new_with_table(
                GtTransTable *tt,
                GtCodonIterator *ci)
```

Creates a new `GtTranslator`, starting its translation at the current position of `ci`. The current reading frame is also taken from the state of `ci`. The translation table `tt` is used.

```
GtTranslator* gt_translator_new(
                GtCodonIterator *ci)
```

Creates a new `GtTranslator`, starting its translation at the current position of `ci`. The current reading frame is also taken from the state of `ci`. The standard translation table is used.

```
void gt_translator_set_codon_iterator(
       GtTranslator *translator,
       GtCodonIterator *ci)
```

Reinitializes `translator` with the position and frame status as given in `ci`.

```
void gt_translator_set_translation_table(
       GtTranslator *translator,
       GtTransTable *tt)
```

Selects the translation scheme in `translator` to the one identified by translation table `tt`.

```
GtTranslatorStatus gt_translator_next(
                     GtTranslator *translator,
                     char *translated,
                     unsigned int *frame,
                     GtError *err)
```

Returns the translation of the next codon. The currently translated character is put in `translated` while the current reading frame is put in `frame`. Returns GT_TRANSLATOR_ERROR if an error occurred, see `err` for details. If the end of the sequence region to translate has been reached, GT_TRANSLATOR_END is returned. Otherwise, GT_TRANSLATOR_OK (equal to 0) is returned.

```
GtTranslatorStatus gt_translator_find_startcodon(
                     GtTranslator *translator,
                     GtUword *pos,
                     GtError *err)
```

Moves the `translator` to the beginning of the first codon in `dnaseq` (of length `dnalen`) which is a start codon according to the selected translation scheme in `translator`. The offset is written to the location pointed to by `pos`. Returns GT_TRANSLATOR_ERROR if an error occurred, see `err` for details. If the end of the sequence region to scan has been reached without finding a start codon, GT_TRANSLATOR_END is returned. Otherwise, GT_TRANSLATOR_OK (equal to 0) is returned.

```
GtTranslatorStatus gt_translator_find_stopcodon(
                     GtTranslator *translator,
                     GtUword *pos,
                     GtError *err)
```

Moves the `translator` to the beginning of the first codon in `dnaseq` (of length `dnalen`) which is a stop codon according to the selected translation scheme in `translator`. The offset is written to the location pointed to by `pos`. Returns GT_TRANSLATOR_ERROR if an error occurred, see `err` for details. If the end of the sequence region to scan has been reached without finding a stop codon, GT_TRANSLATOR_END is returned. Otherwise, GT_TRANSLATOR_OK (equal to 0) is returned.

```
GtTranslatorStatus gt_translator_find_codon(
                     GtTranslator *translator,
                     GtStrArray *codons,
                     GtUword *pos,
                     GtError *err)
```

Moves the `translator` to the beginning of the first codon in `dnaseq` (of length `dnalen`) which belongs to the set of codons specified in `codons`. The offset is written to the location pointed to by `pos`. Returns GT_TRANSLATOR_ERROR if an error occurred, see `err` for details. If the end of the sequence region to scan has been reached without finding one of the codons, GT_TRANSLATOR_END is returned. Otherwise, GT_TRANSLATOR_OK (equal to 0) is returned.

```
void gt_translator_delete(
       GtTranslator *translator)
```

Delete `translator`.

Class GtTypeChecker

The `GtTypeChecker` interface, allows one to check the validity of (genome feature) types.

Methods

```
GtTypeChecker* gt_type_checker_ref(
                  GtTypeChecker *type_checker)
```

Increase the reference count for `type_checker` and return it.

```
const char* gt_type_checker_description(
              GtTypeChecker *type_checker)
```

Return description of `type_checker`.

```
bool gt_type_checker_is_valid(
       GtTypeChecker *type_checker,
       const char *type)
```

Return `true` if `type` is a valid type for the given `type_checker`, `false` otherwise.

```
bool gt_type_checker_is_partof(
       GtTypeChecker *type_checker,
       const char *parent_type,
       const char *child_type)
```

Return `true` if `child_type` is partof `parent_type`, `false` otherwise.

```
bool gt_type_checker_is_a(
       GtTypeChecker *type_checker,
       const char *parent_type,
       const char *child_type)
```

Return `true` if `child_type` is a `parent_type`, `false` otherwise.

```
void gt_type_checker_delete(
       GtTypeChecker *type_checker)
```

Decrease the reference count for `type_checker` or delete it, if this was the last reference.

Class GtTypeCheckerOBO

Implements the `GtTypeChecker` interface with types from an OBO file.

Methods

```
GtTypeChecker* gt_type_checker_obo_new(
                  const char *obo_file_path,
                  GtError *err)
```

Create a new `GtTypeChecker*` for OBO file with given `obo_file_path`. If the OBO file cannot be parsed correctly, `NULL` is returned and `err` is set correspondingly.

Class GtUniqStream

Implements the `GtNodeStream` interface. A `GtUniqStream` filters out repeated features it retrieves from its node source.

Methods

```
GtNodeStream* gt_uniq_stream_new(
                GtNodeStream*)
```

Create a `GtUniqStream` object which filters out repeated feature node graphs it retrieves from the sorted `in_stream` and return all other nodes. Two feature node graphs are considered to be *repeated* if they have the same depth-first traversal and each corresponding feature node pair is similar according to the `gt_feature_node_is_similar()` method. For such a repeated feature node graph the one with the higher score (of the top-level feature) is kept. If only one of the feature node graphs has a defined score, this one is kept.

Class GtVisitorStream

Implements the `GtNodeStream` interface.

Methods

```
GtNodeStream* gt_visitor_stream_new(
                GtNodeStream *in_stream,
                GtNodeVisitor *node_visitor)
```

Create a new `GtVisitorStream*`, takes ownership of `node_visitor`. This stream applies `node_visitor` to each node which passes through it. Can be used to implement all streams with such a functionality.

Class GtXRFChecker

The `GtXRFChecker` interface, allows one to check the validity of Dbxref and Ontology_type attributes.

Methods

```
GtXRFChecker* gt_xrf_checker_new(
                const char *file_path,
                GtError *err)
```

Create a new `GtXRFChecker` from the definitions found in `file_path`. Returns NULL on error, and `err` is set accordingly.

```
GtXRFChecker* gt_xrf_checker_ref(
                GtXRFChecker *xrf_checker)
```

Increase reference count for `xrf_checker`

```
bool gt_xrf_checker_is_valid(
       GtXRFChecker *xrf_checker,
       const char *value,
       GtError *err)
```

Return `true` if `value` is valid for the given `xrf_checker`, `false` otherwise. In case of `value` being invalid, `err` is set accordingly.

```
void gt_xrf_checker_delete(
       GtXRFChecker *xrf_checker)
```

Decrease the reference count for `xrf_checker` or delete it.

Module Array2dim

```
#define gt_array2dim_malloc(
          ARRAY2DIM,
          ROWS,
          COLUMNS)
```

Allocates a new 2-dimensional array with dimensions `ROWS` x `COLUMNS` and assigns a pointer to the newly allocated space to <ARRAY2DIM>. The size of each element is determined automatically from the type of the <ARRAY2DIM> pointer.

```
#define gt_array2dim_calloc(
          ARRAY2DIM,
          ROWS,
          COLUMNS)
```

Allocates a new 2-dimensional array with dimensions `ROWS` x `COLUMNS` and assigns a pointer to the newly allocated space to <ARRAY2DIM>. The allocated space is initialized to be filled with zeroes. The size of each element is determined automatically from the type of the <ARRAY2DIM> pointer.

```
int gt_array2dim_example(
      GtError*)
```

An example for usage of the <Array2dim> module.

```
#define gt_array2dim_delete(
          ARRAY2DIM)
```

Frees the space allocated for the 2-dimensional array pointed to by <ARRAY2DIM>.

```
#define gt_array2dim_sparse_calloc(
          ARRAY2DIM,
          ROWS,
          SIZE,
          ROWINFO)
```

Allocates a new 2-dimensional sparse array with the given number of `ROWS` and a total `SIZE`. Each row starts at the corresponding offset given in `ROWINFO` and has the corresponding length. It assigns a pointer to the newly allocated space to <ARRAY2DIM>. The size of each element is determined automatically from the type of the <ARRAY2DIM> pointer.

Module Array3dim

```
#define gt_array3dim_malloc(
          ARRAY3DIM,
          X_SIZE,
          Y_SIZE,
          Z_SIZE)
```

Allocates a new 3-dimensional array with dimensions `X_SIZE` x `Y_SIZE` x `Z_SIZE` and assigns a pointer to the newly allocated space to <ARRAY3DIM>. The size of each element is determined automatically from the type of the <ARRAY3DIM> pointer.

```
#define gt_array3dim_calloc(
          ARRAY3DIM,
          X_SIZE,
          Y_SIZE,
          Z_SIZE)
```

Allocates a new 3-dimensional array with dimensions `X_SIZE` x `Y_SIZE` and assigns a pointer to the newly allocated space to <ARRAY3DIM>. The allocated space is initialized to be filled with zeroes. The size of each element is determined automatically from the type of the <ARRAY3DIM> pointer.

```
int gt_array3dim_example(
      GtError*)
```

An example for usage of the <Array3dim> module.

```
#define gt_array3dim_delete(
          ARRAY3DIM)
```

Frees the space allocated for the 3-dimensional array pointed to by <ARRAY3DIM>.

Module Arraydef

```
#define GT_DECLAREARRAYSTRUCT(
          TYPE)
```

GT_DECLAREARRAYSTRUCT expands to a corresponding type definition over some given type.

```
#define GT_INITARRAY(
          A,TYPE)
```

GT_INITARRAY initializes an empty array.

```
#define GT_COPYARRAY(
          A,B)
```

GT_COPYARRAY copies an array.

```
#define GT_CHECKARRAYSPACE_GENERIC(
          A,TYPE,L,ADD)
```

GT_CHECKARRAYSPACE checks if the next (L) cells in the array have been allocated. If this is not the case, then the number of cells allocated is incremented by ADD, which must not be smaller than (L). The contents of the previously filled array elements is of course.

```
#define GT_CHECKARRAYSPACE(
          A,TYPE,L)
```

GT_CHECKARRAYSPACE checks if the integer nextfree##T points to an index for which the space is not allocated yet. If this is the case, the number of cells allocated is incremented by L. The contents of the previously filled array elements is of course maintained.

```
#define GT_CHECKARRAYSPACEMULTI(
          A,TYPE,L)
```

The next macro is a variation of GT_CHECKARRAYSPACE, which checks if the next L cells have been allocated. If not, then this is done.

```
#define GT_GETNEXTFREEINARRAY(
          P,A,TYPE,L)
```

This macro checks the space and delivers a pointer P to the next free element in the array.

```
#define GT_STOREINARRAY(
          A,TYPE,L,VAL)
```

This macro checks the space and stores V in the nextfree-component of the array. nextfree is incremented.

```
#define GT_FREEARRAY(
          A,TYPE)
```

This macro frees the space for an array if it is not NULL.

Module Assert

```
#define gt_assert(
          expression)
```

The `gt_assert()` macro tests the given `expression` and if it is false, the calling process is terminated. A diagnostic message is written to `stderr` and the <abort(3)> function is called, effectively terminating the program. If `expression` is true, the `gt_assert()` macro does nothing.

Module Bsearch

```
void* gt_bsearch_data(
        const void *key,
        const void *base,
        size_t nmemb,
        size_t size,
        GtCompareWithData,
        void *data)
```

Similar interface to <bsearch(3)>, except that the `GtCompareWithData` function gets an additional `data` pointer.

```
void gt_bsearch_all(
       GtArray *members,
       const void *key,
       const void *base,
       size_t nmemb,
       size_t size,
       GtCompareWithData,
       void *data)
```

Similar interface to `gt_bsearch_data()`, except that all members which compare as equal are stored in the `members` array. The order in which the elements are added is undefined.

```
void gt_bsearch_all_mark(
       GtArray *members,
       const void *key,
       const void *base,
       size_t nmemb,
       size_t size,
       GtCompareWithData,
       void *data,
       GtBittab*)
```

Similar interface to `gt_bsearch_all()`. Additionally, if a bittab is given (which must be of size `nmemb`), the bits corresponding to the found elements are marked (i.e., set).

Module BytePopcount

`extern const unsigned char gt_byte_popcount[256]`

Lookup table containing the popcount (number of set bits). Entry at `i` equals popcount(`i`).

Module ByteSelect

`extern const unsigned char gt_byte_select[2048]`

Contains 256 * 8 select values, Entry at index 256 * `j` + `i` equals the position of the (`j` + 1)-th set bit in byte `i`. Positions lie in the range [0..7]. Returns 8 if byte `i` contains less than `j` set bits.

Module ClassAlloc

```
void* gt_class_alloc(
        size_t size)
```

Allocates space for a class with size `size`.

```
void gt_class_alloc_clean(
       void)
```

Frees static memory allocated for classes.

Module Compat

```
int gt_mkstemp(
      char *templ)
```

Return (read-write) handle of temporary file, with template `templ`.

```
GtUword gt_pagesize(
          void)
```

Returns the page size of the current platform.

Module ConsensusSplicedAlignment

```
GtRange GtGetGenomicRangeFunc(
                                const void *sa)
```

Function to obtain the genomic range from spliced alignment `sa`.

```
GtStrand GtGetStrandFunc(
                           const void *sa)
```

Function to obtain the strand from spliced alignment `sa`.

```
void GtGetExonsFunc(
                     GtArray *exon_ranges,
                     const void *sa)
```

Function to obtain exon ranges from spliced alignment `sa`.

```
void GtProcessSpliceFormFunc(
                               GtArray *spliced_alignments_in_form,
                               const void *set_of_sas,
                               GtUword number_of_sas,
                               size_t size_of_sa,
                               void *userdata)
```

Function to process the generated from the consensus spliced alignment process.

```
void gt_consensus_sa(
       const void *set_of_sas,
       GtUword number_of_sas,
       size_t size_of_sa,
       GtGetGenomicRangeFunc,
       GtGetStrandFunc,
       GtGetExonsFunc,
       GtProcessSpliceFormFunc,
       void *userdata)
```

Construct consensus spliced alignments according to:
B.J. Haas, A.L. Delcher, S.M. Mount, J.R. Wortman, R.K. Smith Jr, L.I. Hannick, R. Maiti, C.M. Ronning, D.B. Rusch, C.D. Town, S.L. Salzberg, and O. White. Improving the Arabidopsis genome annotation using maximal transcript alignment assemblies. Nucleic Acids Res., 31(19):5654-5666, 2003.
following the description on page 972 and 973 of the paper:
G. Gremme, V. Brendel, M.E. Sparks, and S. Kurtz. Engineering a Software Tool for Gene Structure Prediction in Higher Organisms. Information and Software Technology, 47(15):965-978, 2005.

Module Countingsort

```
void gt_countingsort(
       void *out,
       const void *in,
       size_t elem_size,
       GtUword size,
       GtUword max_elemvalue,
       void *data,
       GtGetElemvalue get_elemvalue)
```

Sort the array of elements pointed to by `in` containing `size` many elements of size `elem_size` and store the result in the array `out` of the same size. `max_elemvalue` denotes the maximum value an element can have. `get_elemvalue` should return an integer value for the given element `elem`.
Implements the counting sort algorithm. For a description see for example page 175 to page 177 of the book:
T.H. Cormen, C.E. Leiserson and R.L. Rivest. *Introduction to Algorithms*. MIT Press: Cambridge, MA, 1990.

```
GtUword gt_countingsort_get_max(
          const void *in,
          size_t elem_size,
          GtUword size,
          void *data,
          GtGetElemvalue get_elemvalue)
```

If `max_elemvalue` is not known, it can be determined with this function.

Module Cstr

```
char* gt_cstr_dup(
        const char *cstr)
```

Creates a duplicate of string `cstr` using the *GenomeTools* memory allocator.

```
char** gt_cstr_split(
         const char *cstr,
         char sep)
```

Splits the \0-terminated `cstr` at all positions where `sep` occurs and returns a C string array in which each element is a separate string between the occurrences of `sep`. The string array is terminated by NULL. The caller is responsible to free the result.

```
char* gt_cstr_dup_nt(
        const char *cstr,
        GtUword length)
```

Creates a duplicate of string `cstr` using the *GenomeTools* memory allocator. The string needs not be \0-terminated, instead its `length` must be given.

```
void gt_cstr_rep(
       char *cstr,
       char f,
       char t)
```

Replace each occurrence of `f` in `cstr` to `t`.

```
void gt_cstr_show(
       const char *cstr,
       GtUword length,
       FILE *outfp)
```

Outputs the first `length` characters of the string `cstr` to file pointer `outfp`.

```
GtUword gt_cstr_length_up_to_char(
          const char *cstr,
          char c)
```

Returns the length of the prefix of `cstr` ending just before `c`, if `cstr` does not contain `c`, strlen(cstr) is returned.

```
char* gt_cstr_rtrim(
        char* cstr,
        char remove)
```

Removes all occurrences of `remove` from the right end of `cstr`.

Module CstrArray

```
char** gt_cstr_array_dup(
         const char **cstr_array)
```

Return copy of cstr_array.

```
char** gt_cstr_array_prefix_first(
         const char **cstr_array,
         const char *p)
```

Use p and a blank as prefix for <cstr_array[0]> and return the result.

```
char** gt_cstr_array_prepend(
         const char **cstr_array,
         const char *p)
```

Use p as prefix for <cstr_array[0]> and return the result.

```
void gt_cstr_array_show(
       char **cstr_array,
       FILE *fp)
```

Print cstr_array to fp, separated b newlines.

```
void gt_cstr_array_show_genfile(
       const char **cstr_array,
       GtFile *fp)
```

Print cstr_array to fp, separated b newlines.

```
GtUword gt_cstr_array_size(
          const char **cstr_array)
```

Return the count of strings in cstr_array. O(n).

```
void gt_cstr_array_delete(
       char **cstr_array)
```

Delete cstr_array.

Module Deprecated

```
#define GT_DEPRECATED(
          msg)
```

Deprecated functions, typedefs and structs in API headers should be annotated with this macro to get warnings when the gcc or clang compiler is used. msg should inform about an alternative API.

Module Divmodmul

```
#define GT_DIV2(
          N)
```

Division by 2.

```
#define GT_DIV4(
          N)
```

Division by 4.

```
#define GT_DIV8(
          N)
```

Division by 8.

```
#define GT_DIV16(
          N)
```

Division by 16.

```
#define GT_DIV32(
          N)
```

Division by 32.

```
#define GT_DIV64(
          N)
```

Division by 64.

```
#define GT_MOD2(
          N)
```

Modulo 2.

```
#define GT_MOD4(
          N)
```

Modulo 4.

```
#define GT_MOD8(
          N)
```

Modulo 8.

```
#define GT_MOD16(
          N)
```

Modulo 16.

```
#define GT_MOD32(
          N)
```

Modulo 32.

```
#define GT_MOD64(
          N)
```

Modulo 64.

```
#define GT_MULT2(
          N)
```

Multiplication by 2.

```
#define GT_MULT4(
          N)
```

Multiplication by 4.

```
#define GT_MULT8(
          N)
```

Multiplication by 8.

```
#define GT_MULT16(
          N)
```

Multiplication by 16.

```
#define GT_MULT32(
          N)
```

Multiplication by 32.

```
#define GT_MULT64(
          N)
```

Multiplication by 64.

```
#define GT_POW2(
          N)
```

Power of 2 to the N-th.

```
#define GT_LOG2(
          v)
```

Binary logarithm of v.

Module Endianess

```
bool gt_is_little_endian(
       void)
```

Returns `true` if host CPU is little-endian, `false` otherwise.

Module Ensure

```
#define gt_ensure(
          expr)
```

The ensure macro used for unit tests. If the expression `expr` evaluates to FALSE, the `GtError err` will be set and `had_err` will be set to -1. These variables are expected to exist when using this macro.

Module FASTA

```
void gt_fasta_show_entry(
       const char *description,
       const char *sequence,
       GtUword sequence_length,
       GtUword width,
       GtFile *outfp)
```

Print a fasta entry with optional `description` and mandatory `sequence` to `outfp`. If `width` is != 0 the sequence is formatted accordingly.

```
void gt_fasta_show_entry_nt(
       const char *description,
       GtUword description_length,
       const char *sequence,
       GtUword sequence_length,
       GtUword width,
       GtFile *outfp)
```

Print a fasta entry with optional `description` and mandatory `sequence` to `outfp`. If `width` is != 0 the sequence is formatted accordingly. Will print at most `sequence_length` characters from `sequence` if no '\0'-byte is encountered. `description` and `description_length` are handled accordingly if present.

```
void gt_fasta_show_entry_str(
       const char *description,
       const char *sequence,
       GtUword sequence_length,
       GtUword width,
       GtStr *outstr)
```

Append a fasta entry with optional `description` and mandatory `sequence` to `outstr`. If `width` is != 0 the sequence is formatted accordingly.

```
void gt_fasta_show_entry_nt_str(
       const char *description,
       GtUword description_length,
       const char *sequence,
       GtUword sequence_length,
       GtUword width,
       GtStr *outstr)
```

Print a fasta entry with optional `description` and mandatory `sequence` to `outstr`. If `width` is != 0 the sequence is formatted accordingly. Will print at most `sequence_length` characters from `sequence` if no '\0'-byte is encountered. `description` and `description_length` are handled accordingly if present.

```
void gt_fasta_show_entry_with_suffix(
       const char *description,
       const char *sequence,
       GtUword sequence_length,
       const char *suffix,
       GtUword width,
       GtFile *outfp)
```

Print a fasta entry with optional `description` and `suffix` plus mandatory `sequence` to `outfp`. If `width` is != 0 the sequence is formatted accordingly.

```
void gt_fasta_show_entry_nt_with_suffix(
       const char *description,
       GtUword description_length,
       const char *sequence,
       GtUword sequence_length,
       const char *suffix,
       GtUword width,
       GtFile *outfp)
```

Print a fasta entry with optional `description` and `suffix` plus mandatory `sequence` to `outfp`. If `width` is != 0 the sequence is formatted accordingly. Will print at most `sequence_length` characters from `sequence` and at most `description_length` characters from `description` if present.

```
void gt_fasta_show_entry_with_suffix_str(
       const char *description,
       const char *sequence,
       GtUword sequence_length,
       const char *suffix,
       GtUword width,
       GtStr *outstr)
```

Print a fasta entry with optional `description` and `suffix` plus mandatory `sequence` to `outstr`. If `width` is != 0 the sequence is formatted accordingly.

```
void gt_fasta_show_entry_nt_with_suffix_str(
       const char *description,
       GtUword description_length,
       const char *sequence,
       GtUword sequence_length,
       const char *suffix,
       GtUword width,
       GtStr *outstr)
```

Print a fasta entry with optional `description` and `suffix` plus mandatory `sequence` to `outstr`. If `width` is != 0 the sequence is formatted accordingly. Will print at most `sequence_length` characters from `sequence` and at most `description_length` characters from `description` if present.

Module FileAllocator

```
void gt_fa_init(
       void)
```

Initialize file allocator. Only needs to be called once per process.

```
#define gt_fa_fopen(
          path,
          mode,
          err)
```

Returns a FILE pointer after opening the file at `path` with `mode`. If an error occurs, NULL is returned and `err` is set accordingly.

```
#define gt_fa_xfopen(
          path,
          mode)
```

Returns a FILE pointer after opening the file at `path` with `mode`. If an error occurs, the program is terminated.

```
#define gt_fa_fopen_with_suffix(
          path,
          suffix,
          mode,
          err)
```

Returns a FILE pointer after opening the file at `path` with suffix `suffix` and mode `mode`. If an error occurs, NULL is returned and `err` is set accordingly.

```
void gt_fa_fclose(
       FILE *stream)
```

Closes the file `stream`.

```
void gt_fa_xfclose(
       FILE *stream)
```

Closes the file `stream`, terminating on error.

```
void gt_fa_lock_shared(
       FILE *stream)
```

Obtain a shared lock on `stream`.

```
void gt_fa_lock_exclusive(
       FILE *stream)
```

Obtain an exclusive lock on `stream`.

```
void gt_fa_unlock(
       FILE *stream)
```

Unlock `stream`.

```
#define gt_fa_gzopen(
          path,
          mode,
          err)
```

Returns a FILE pointer after opening the gzipped file at `path` with `mode`. If an error occurs, NULL is returned and `err` is set accordingly.

```
#define gt_fa_xgzopen(
          path,
          mode)
```

Returns a FILE pointer after opening the gzipped file at `path` with `mode`. If an error occurs, the program is terminated.

```
void gt_fa_gzclose(
       gzFile stream)
```

Closes the gzipped file `stream`.

```
void gt_fa_xgzclose(
       gzFile stream)
```

Closes the gzipped file `stream`, terminating on error.

```
#define gt_fa_bzopen(
          path,
          mode,
          err)
```

Returns a FILE pointer after opening the bzipped file at `path` with `mode`. If an error occurs, NULL is returned and `err` is set accordingly.

```
#define gt_fa_xbzopen(
          path,
          mode)
```

Returns a FILE pointer after opening the bzipped file at `path` with `mode`. If an error occurs, the program is terminated.

```
void gt_fa_bzclose(
       BZFILE *stream)
```

Closes the bzipped file `stream`.

```
void gt_fa_xbzclose(
       BZFILE *stream)
```

Closes the bzipped file `stream`, terminating on error.

```
#define gt_xtmpfp_generic(
          template_code,
          flags)
```

Create a temp file optionally using template analogous to mkstemp(3).

```
#define gt_xtmpfp(
          template_code)
```

Create a temp file optionally using template analogous to mkstemp(3), with default flags.

```
#define gt_fa_mmap_read(
          path,
          len,
          err)
```

Map file `path` with len `len` into memory for reading and returns a pointer to the mapped region. `err` is set on error.

```
#define gt_fa_mmap_read_range(
          path,
          len,
          offset,
          err)
```

Map file `path` with len `len` starting from `offset` into memory for reading and returns a pointer to the mapped region. `err` is set on error.

```
#define gt_fa_mmap_write(
          path,
          len,
          err)
```

Map file `path` with len `len` into memory for writing and returns a pointer to the mapped region. `err` is set on error.

```
#define gt_fa_mmap_write_range(
          path,
          len,
          offset,
          err)
```

Map file `path` with len `len` starting from `offset` into memory for writing and returns a pointer to the mapped region. `err` is set on error.

```
#define gt_fa_xmmap_read(
          path,
          len)
```

Map file `path` with len `len` into memory for reading and returns a pointer to the mapped region. Terminates on error.

```
#define gt_fa_xmmap_read_range(
          path,
          len,
          offset)
```

Map file `path` with len `len` starting from `offset` into memory for reading and returns a pointer to the mapped region. Terminates on error.

```
#define gt_fa_xmmap_write(
          path,
          len)
```

Map file `path` with len `len` into memory for writing and returns a pointer to the mapped region. Terminates on error.

```
#define gt_fa_xmmap_write_range(
          path,
          len,
          offset)
```

Map file `path` with len `len` starting from `offset` into memory for writing and returns a pointer to the mapped region. Terminates on error.

```
void gt_fa_xmunmap(
       void *addr)
```

Unmap mmapped file at address `addr`.

```
int gt_fa_check_fptr_leak(
      void)
```

Check if all allocated file pointer have been released, prints to stderr.

```
int gt_fa_check_mmap_leak(
      void)
```

Check if all allocated memory maps have been freed, prints to stderr.

```
void gt_fa_enable_global_spacepeak(
       void)
```

Enable bookkeeping for global space peak.

```
GtUword gt_fa_get_space_peak(
          void)
```

Return current global space peak, in bytes.

```
GtUword gt_fa_get_space_current(
          void)
```

Return current space usage, in bytes.

```
void gt_fa_show_space_peak(
       FILE *fp)
```

Print statistics about current space peak to `fp`.

```
void gt_fa_clean(
       void)
```

Finalize and free static data held by file allocator.

Module Fileutils

```
const char* gt_file_suffix(
              const char *path)
```

Returns the suffix of `path`, if there is any. Returns "" otherwise. The suffix is the part after and including the last '.' but after the last '/' (or '\' on Windows). Except if `path` ends with ".gz" or ".bz2", then the suffix is the part after and including the second last '.'.

```
bool gt_file_exists(
       const char *path)
```

Returns true if the file with the given `path` exists, false otherwise.

```
bool gt_file_exists_with_suffix(
       const char *path,
       const char *suffix)
```

Returns true if the file with the name composed of the concatenation of `path` and `suffix` exists, false otherwise.

```
bool gt_file_is_newer(
       const char *a,
       const char *b)
```

Returns true if the file with path `a` has a later modification time than the file with path `b`, false otherwise.

```
GtUword gt_file_number_of_lines(
          const char*)
```

Returns the number of lines in a file.

```
void gt_file_dirname(
       GtStr *path,
       const char *file)
```

Set `path` to the dirname of `file`, if it has one, to "" otherwise.

```
int gt_file_find_in_path(
      GtStr *path,
      const char *file,
      GtError*)
```

Find `file` in *PATH*, *if it has no dirname*; *set* `path` *to dirname otherwise. Sets* `path` *to the empty string if* `file` *coula*

```
int gt_file_find_in_env(
      GtStr *path,
      const char *file,
      const char *env,
      GtError*)
```

Find `file` in the ':'-separated directory list (on Windows ';'-separated) specified in environment variable `env`, *if it has no dirname*; *set* `path` *to dirname otherwise. Sets* `path` *to the empty string if* `file` *could not be found in e*

```
off_t gt_file_estimate_size(
   const char *file)
```

Return the (estimated) size of `file`. If `file` is uncompressed, the exact size is returned. If `file` is compressed, an estimation which assumes that `file` contains a DNA sequence is returned.

```
off_t gt_files_estimate_total_size(
   const GtStrArray *filenames)
```

Return the (estimated) total size of all files given in `filenames`. Uses `gt_file_estimate_size()`.

```
int gt_files_guess_if_protein_sequences(
      const GtStrArray *filenames,
      GtError *err)
```

Guesse if the sequences contained in the files given in `filenames` are protein sequences. Returns 1 if the guess is that the files contain protein sequences. Returns 0 if the guess is that the files contain DNA sequences. Returns -1 if an error occurs while reading the files (`err` is set accordingly).

```
int gt_file_find_exec_in_path(
      GtStr *path,
      const char *file,
      GtError *err)
```

Find regular executable `file` in *PATH*, *if it has no dirname*; *set* `path` *to dirname otherwise. Sets* `path` *to the empty*

```
off_t gt_file_size(
   const char *file)
```

Return the size of `file` in bytes. `file` must exist.

```
off_t gt_file_size_with_suffix(
   const char *path,
   const char *suffix)
```

Returns the size of the file whose name is composed of the concatenation of `path` and `suffix`. `file` must exist.

```
bool gt_file_exists_and_is_dir(
       const char *path)
```

Returns true if the file with the given `path` exists and is a directory, false otherwise.

```
void gt_xfile_cmp(
       const char *file1,
       const char *file2)
```

Compare two files bytewise, fails hard with exit(1) if files differ.

Module FunctionPointer

```
int GtCompare(
              const void *a,
              const void *b)
```

Functions of this type return less than 0 if `a` is *smaller* than `b`, 0 if `a` is *equal* to `b`, and greater 0 if `a` is *larger* than `b`. Thereby, the operators *smaller*, *equal*, and *larger* are implementation dependent. Do not count on these functions to return -1, 0, or 1!

```
int GtCompareWithData(
                      const void*,
                      const void*,
                      void *data)
```

Similar to `GtCompare`, but with an additional `data` pointer.

```
void GtFree(
            void*)
```

The generic free function pointer type.

Module GFF3Escaping

```
void gt_gff3_escape(
       GtStr *escaped_seq,
       const char *unescaped_seq,
       GtUword length)
```

Escape unescaped_seq of given length for GFF3 format and append the result to escaped_seq.

```
int gt_gff3_unescape(
      GtStr *unescaped_seq,
      const char *escaped_seq,
      GtUword length,
      GtError *err)
```

Unescape GFF3 format escaped_seq of given length and append the result to unescaped_seq. Returns a value less than zero on error. err is set accordingly.

Module GlobalChaining

```
void GtChainProc(
                 GtChain *c,
                 GtFragment *frags,
                 GtUword num_of_fragments,
                 GtUword max_gap_width,
                 void *cpinfo)
```

Function to process a chain. frags is an array of GtFragments, of size num_of_fragments. max_gap_width and cpinfo are passed from the gt_globalchaining_*() calls.

```
void gt_globalchaining_max(
       GtFragment *fragments,
       GtUword num_of_fragments,
       GtUword max_gap_width,
       GtChainProc,
       void *cpinfo)
```

Perform global chaining with overlaps of num_of_fragments many fragments in quadratic time w.r.t. num_of_fragments. Two fragments can maximally be max_gap_width many bases away. For all global chains of maximal score, the GtChainProc function is called. Thereby, GtChainProc does not get the ownership of the GtChain.

```
void gt_globalchaining_coverage(
       GtFragment *fragments,
       GtUword num_of_fragments,
       GtUword max_gap_width,
       GtUword seqlen1,
       double mincoverage,
       GtChainProc,
       void *cpinfo)
```

Perform global chaining with overlaps of `num_of_fragments` many `fragments` in quadratic time w.r.t. `num_of_fragments`. Two fragments can maximally be `max_gap_width` many bases away. For all non-overlapping global chains with a coverage of more then `mincoverage` of the sequence in dimension 1 (with length <seqlen1 >), the GtChainProc function is called. Thereby, GtChainProc does not get the ownership of the GtChain.

Module Grep

```
int gt_grep(
      bool *match,
      const char *pattern,
      const char *line,
      GtError*)
```

Set `match` to `true` if `pattern` matches `line`, to `false` otherwise.

```
int gt_grep_nt(
      bool *match,
      const char *pattern,
      const char *line,
      size_t len,
      GtError *err)
```

Set `match` to `true` if `pattern` matches `line` up to `len`, to `false` otherwise.

Module Init

```
void gt_lib_init(
       void)
```

Initialize this *GenomeTools* library instance. This has to be called before the library is used!

```
void gt_lib_reg_atexit_func(
       void)
```

Registers exit function which calls `gt_lib_clean()` at exit.

```
int gt_lib_clean(
      void)
```

Frees all static data associated with the library. Returns 0 if no memory map, file pointer, or memory has been leaked and a value != 0 otherwise.

Module Log

```
void gt_log_enable(
       void)
```

Enable logging.

```
bool gt_log_enabled(
       void)
```

Returns true if logging is enabled, false otherwise

```
void gt_log_log(
       const char *format,
       ...)
```

Prints the log message obtained from format and following parameters according if logging is enabled. The logging output is prefixed with the string ”debug: ” and finished by a newline.

```
void gt_log_vlog(
       const char *format,
       va_list)
```

Prints the log message obtained from format and following parameter according to if logging is enabled analog to `gt_log_log()`. But in contrast to `gt_log_log()` `gt_log_vlog()` does not accept individual arguments but a single va_list argument instead.

```
FILE* gt_log_fp(
        void)
```

Return logging file pointer.

```
void gt_log_set_fp(
       FILE *fp)
```

Set logging file pointer to `fp`.

Module MD5Fingerprint

```
char* gt_md5_fingerprint(
        const char *sequence,
        GtUword seqlen)
```

Returns an MD5 fingerprint of `sequence` with length `seqlen` transformed to upper case letters (with toupper(3)). It is the responsibility of the caller to free the returned string.

Module MD5Seqid

```
bool gt_md5_seqid_has_prefix(
       const char *seqid)
```

Returns `true` if `seqid` has the prefix used to denote MD5 sequence IDs, `false` otherwise.

```
int gt_md5_seqid_cmp_seqids(
      const char *id_a,
      const char *id_b)
```

Compares \0-terminated seqid strings `id_a` and `id_b` (similarly to strcmp(3)), but is aware of MD5 prefixes. That is, if both seqids have MD5 prefixes, only the MD5 prefixes will be compared. If at least one seqid has no MD5 prefix, the sequd without the prefix will sort before the other one.

Module Mathsupport

```
double gt_logsum(
         double p1,
         double p2)
```

Returns the log of the sum of two log probabilities.

```
bool gt_double_equals_one(
       double)
```

Returns TRUE if the passed double value equals 1.

```
bool gt_double_equals_double(
       double,
       double)
```

Returns TRUE if <d1 > equals <d2 >.

```
int gt_double_compare(
      double d1,
      double d2)
```

Compares two doubles with standard comparator semantics.

```
bool gt_double_smaller_double(
       double d1,
       double d2)
```

Returns TRUE if <d1 > is smaller than <d2 >.

```
bool gt_double_larger_double(
       double d1,
       double d2)
```

Returns TRUE if <d1 > is larger than <d2 >.

```
GtUword gt_rand_max(
          GtUword maximal_value)
```

Returns a random number between 0 and maximal_value.

```
double gt_rand_max_double(
         double maximal_value)
```

Returns a random double between 0.0 and maximal_value.

```
double gt_rand_0_to_1(
         void)
```

Returns a random double between 0.0 and 1.0.

```
char gt_rand_char(
       void)
```

Returns a random character from 'a' to 'z'.

```
unsigned int gt_determinebitspervalue(
               GtUword maxvalue)
```

Retuns the log base 2 of an integer `maxvalue` in *O(wordsize)* operations

```
GtUword gt_power_for_small_exponents(
          unsigned int base,
          unsigned int exponent)
```

Determine pow(base,exponent) for small values of exponent

```
GtWord gt_round_to_long(
         double x)
```

Return `x` rounded to the nearest long integer, similar to `lrint()` which may not be available on older glibc versions.

```
unsigned int gt_gcd_uint(
               unsigned int m,
               unsigned int n)
```

Compute the greatest common divisor of two unsigned integers

```
unsigned int gt_lcm_uint(
               unsigned int m,
               unsigned int n)
```

Compute the least common multiplier of two unsigned integers

```
double gt_log_base(
         double x,
         double b)
```

Compute the logarithm of `x` to the base `b`

Module MemoryAllocation

```
void gt_ma_init(
       bool bookkeeping)
```

Initialize the memory allocator. Only needs to be done once per process.

```
void gt_ma_enable_global_spacepeak(
       void)
```

Enable bookkeeping for global space peak.

```
void gt_ma_disable_global_spacepeak(
       void)
```

Disable bookkeeping for global space peak.

```
GtUword gt_ma_get_space_peak(
          void)
```

Return current global space peak, in bytes.

```
GtUword gt_ma_get_space_current(
          void)
```

Return current space usage, in bytes.

```
void gt_ma_show_space_peak(
       FILE *fp)
```

Print statistics about current space peak to `fp`.

```
void gt_ma_show_allocations(
       FILE *fp)
```

Print statistics about allocations to `fp`.

```
bool gt_ma_bookkeeping_enabled(
       void)
```

Returns TRUE if any bookeeping is enabled.

```
int gt_ma_check_space_leak(
      void)
```

Check if all allocated memory has been freed, prints result to stderr.

```
void gt_ma_clean(
       void)
```

Finalize and free static data held by memory allocator.

```
#define gt_malloc(
          size)
```

Allocate **uninitialized** space for an object whose size is specified by `size` and return it. Besides the fact that it never returns `NULL` analog to <malloc(3)>.

```
#define gt_calloc(
          nmemb,
          size)
```

Allocate contiguous space for an array of `nmemb` objects, each of whose size is `size`. The space is initialized to zero. Besides the fact that it never returns `NULL` analog to <calloc(3)>.

```
#define gt_realloc(
          ptr,
          size)
```

Change the size of the object pointed to by `ptr` to `size` bytes and return a pointer to the (possibly moved) object. Besides the fact that it never returns `NULL` analog to <realloc(3)>.

```
#define gt_free(
          ptr)
```

Free the space pointed to by `ptr`. If `ptr` equals `NULL`, no action occurs. Analog to <free(3)>.

```
void gt_free_func(
       void *ptr)
```

Analog to `gt_free()`, but usable as a function pointer.

Module Msort

```
void gt_msort(
       void *base,
       size_t nmemb,
       size_t size,
       GtCompare compar)
```

Sorts an array of `nmemb` elements, each of size `size`, according to compare function `compar`. Uses the merge sort algorithm, the interface equals <qsort(3)>.

```
void gt_msort_r(
       void *base,
       size_t nmemb,
       size_t size,
       void *comparinfo,
       GtCompareWithData compar)
```

Identical to `gt_msort()` except that the compare function is of `GtCompareWithData` type accepting `comparinfo` as arbitrary data.

Module Multithread

```
int gt_multithread(
      GtThreadFunc function,
      void *data,
      GtError *err)
```

Execute `function` (with `data` passed to it) in `gt_jobs` many parallel threads, if threading is enabled. Otherwise `function` is executed `gt_jobs` many times sequentially. `gt_jobs` is a global <unsigned int> variable.

Module ORF

```
void GtORFProcessor(
                    void *data,
                    GtRange *orf,
                    GtUword framenum,
                    const char *frame,
                    bool ends_with_stop_codon)
```

Function to handle ORFs produced by `gt_determine_ORFs()`.

```
void gt_determine_ORFs(
       GtORFProcessor orf_processor,
       void *data,
       unsigned int framenum,
       const char *frame,
       GtUword framelen,
       bool start_codon,
       bool final_stop_codon,
       bool framepos,
       const char *start_codons)
```

Determine all ORFs in the given `frame` of length `framelength` and frame number `framenum` (0, 1, or 2). If `start_codon` is `true` a frame has to start with a start codon, otherwise a frame can start everywhere (i.e., at the first amino acid or after a stop codon). If `final_stop_codon` is `true` the last ORF must end with a stop codon, otherwise it can be "open". For each ORF the `orf_processor` function is called and `data`, `framenum` and `frame` is passed along. If `framepos` is true, the ORF range is reported in the coordinate system of the frame (i.e., the amino acids). Otherwise the coordinate system of the original sequence is used (i.e., the nucleotides). The correct `framenum` is needed for the conversion.

Module POSIX

```
char* gt_basename(
        const char *path)
```

This module implements the function `gt_basename()` according to the specifications in http://www.unix-systems.org/onlinepubs/7908799/xsh/basename.html and http://www.opengroup.org/onlinepubs/009695399/
`gt_basename()` is equivalent to the function basename(3) which is available on most unix systems, but in different libraries and with slightly different functionality.
`gt_basename()` takes the pathname pointed to by `path` and returns a pointer to the final component of the pathname, deleting any trailing '/' characters.
If `path` consists entirely of the '/' character, then `gt_basename()` returns a pointer to the string "/".
On Windows '\' is used instead of '/'.
If `path` is a null pointer or points to an empty string, `gt_basename()` returns a pointer to the string ".".
See the implementation of `gt_basename_unit_test()` for additional examples.
The caller is responsible for freeing the received pointer!

Module Parseutils

```
int gt_parse_int(
      int *out,
      const char *nptr)
```

Parse integer from `nptr` and store result in `out`. Returns 0 upon success and -1 upon failure.

```
int gt_parse_uint(
      unsigned int *out,
      const char *nptr)
```

Parse unsigned integer from `nptr` and store result in `out`. Returns 0 upon success and -1 upon failure.

```
int gt_parse_long(
      GtWord *out,
      const char *nptr)
```

Parse long from `nptr` and store result in `out`. Returns 0 upon success and -1 upon failure.

```
int gt_parse_word(
      GtWord *out,
      const char *nptr)
```

Parse GtWord from `nptr` and store result in `out`. Returns 0 upon success and -1 upon failure.

```
int gt_parse_ulong(
      GtUword *out,
      const char *nptr)
```

Parse ulong from `nptr` and store result in `out`. Returns 0 upon success and -1 upon failure. Deprecated, use `gt_parse_uword()` instead.

```
int gt_parse_uword(
      GtUword *out,
      const char *nptr)
```

Parse GtUword from `nptr` and store result in `out`. Returns 0 upon success and -1 upon failure.

```
int gt_parse_double(
      double *out,
      const char *nptr)
```

Parse double from `nptr` and store result in `out`. Returns 0 upon success and -1 upon failure.

```
int gt_parse_range(
      GtRange *rng,
      const char *start,
      const char *end,
      unsigned int line_number,
      const char *filename,
      GtError*)
```

Parse a range given by `start` and `end`, writing the result into `rng`. Enforces that `start` is smaller or equal than `end`. Give `filename` and `line_number` for error reporting. Returns 0 upon success and -1 upon failure.

```
int gt_parse_description_range(
      const char *description,
      GtRange *range)
```

Parse the range description in the given `description` and store it in `range`. Range descriptions have the folowing format: III:1000001..2000000 That is, the part between ':' and '..' denotes the range start and the part after '..' the end. Returns 0 upon success and -1 upon failure.

```
int gt_parse_range_tidy(
      GtRange *rng,
      const char *start,
      const char *end,
      unsigned int line_number,
      const char *filename,
      GtError*)
```

Like gt_parse_range, but issues a warning if start is larger then end and swaps both values. It also issues a warning, if start and/or end is not-positive and sets the corresponding value to 1.

Module Qsort

```
void gt_qsort_r(
       void *a,
       size_t n,
       size_t es,
       void *data,
       GtCompareWithData cmp)
```

Like <qsort(3)>, but allows an additional data pointer passed to the GtCompareWithData comparison function cmp.

Module RegularSeqID

```
void gt_regular_seqid_save(
       GtStr *seqid,
       GtStr *description)
```

Parse "regular" sequence ID from description and save it in seqid.

Module Reverse

```
int gt_reverse_complement(
      char *dna_seq,
      GtUword seqlen,
      GtError*)
```

Reverse dna_seq of length seqlen in place.

Module Safearith

`void (GtOverflowHandlerFunc)(const char *src_file, int src_line, void *data)`

Function called when an integer overflow occurs.

```
#define gt_safearith_assign(
          dest,
          src)
```

Safely assign `src` to `dest`, returns false on success, true otherwise.

```
#define gt_safearith_add_of(
          c,
          a,
          b)
```

Safely add `a` to `b` and assign the result to `c`, returns false on success, true otherwise.

```
#define gt_safearith_sub_of(
          c,
          a,
          b)
```

Safely subtract `b` from `a` and assign the result to `c`, returns false on success, true otherwise.

```
#define gt_safe_assign(
          dest,
          src)
```

Assign `src` to `dest` or exit upon overflow.

```
#define gt_safe_add(
          c,
          a,
          b)
```

Add `a` to `b` and assign the result to `c` or exit upon overflow.

```
#define gt_safe_sub(
          c,
          a,
          b)
```

Subtract `b` from `a` and assign the result to `c` or exit upon overflow. Warning: this will result in an overflow if c is signed and a and b are unsigned values, as integer promotion will garble the tests.

```
#define gt_safe_abs(
          j)
```

Overflow-safe version of `abs()`.

```
#define gt_safe_labs(
          j)
```

Overflow-safe version of `labs()`.

```
#define gt_safe_llabs(
          j)
```

Overflow-safe version of `llabs()`.

```
#define gt_safe_mult_u32(
          i,
          j)
```

Overflow-safe multiplication of two unsigned 32-bit integers.

```
#define gt_safe_mult_u64(
          i,
          j)
```

Overflow-safe multiplication of two unsigned 64-bit integers.

```
#define gt_safe_mult_ulong(
          i,
          j)
```

Overflow-safe multiplication of two ulong integers.

```
#define gt_safe_cast2long(
          j)
```

Overflow-safe typecast to long.

```
#define gt_safe_cast2ulong(
          j)
```

Overflow-safe typecast to unsigned long.

```
#define gt_safe_cast2ulong_64(
          j)
```

Overflow-safe typecast to ulong64.

Module SeqID2File

```
void gt_seqid2file_register_options(
       GtOptionParser *option_parser,
       GtSeqid2FileInfo *s2fi)
```

Add the options -seqfile, -seqfiles, -matchdesc, -usedesc and -regionmapping to the given `option_parser`.

```
void gt_seqid2file_register_options_ext(
       GtOptionParser
                                                    *option_parser,
       GtSeqid2FileInfo *s2fi,
       bool mandatory,
       bool debug)
```

Add the options -seqfile, -seqfiles, -matchdesc, -usedesc and -regionmapping to the given `option_parser`. If `mandatory` is set, either option -seqfile, -seqfiles or -regionmapping is mandatory. If `debug` is set, then the options are marked as development options.

```
bool gt_seqid2file_option_used(
       GtSeqid2FileInfo *s2fi)
```

Returns TRUE if any of the options -seqfile, -seqfiles, -matchdesc, -usedesc or -regionmapping stored in <s2fi> has been specified and given a parameter.

```
GtRegionMapping* gt_seqid2file_region_mapping_new(
                   GtSeqid2FileInfo *s2fi,
                   GtError *err)
```

Returns a `GtRegionMapping` based on the <s2fi>. `NULL` will be returned on error, and `err` will be set accordingly.

Module Strcmp

```
int gt_strcmp(
      const char *s1,
      const char *s2)
```

Returns 0 if <s1 > == <s2 >, otherwise the equivalent of <strcmp(s1,s2)>. Useful as a performance improvement in some cases (for example, to compare symbols).

Module Symbol

```
const char* gt_symbol(
              const char *cstr)
```

Return a symbol (a canonical representation) for `cstr`. An advantage of symbols is that they can be compared for equality by a simple pointer comparison, rather than using `strcmp()` (as it is done in `gt_strcmp()`). Furthermore, a symbol is stored only once in memory for equal `cstr`s, but keep in mind that this memory can never be freed safely during the lifetime of the calling program. Therefore, it should only be used for a small set of `cstr`s.

Module Threads

`extern unsigned int gt_jobs`

Number of parallel threads to be used.

Module Tooldriver

```
int GtToolFunc(
               int argc,
               const char **argv,
               GtError *err)
```

The prototype of a tool function.

```
int gt_tooldriver(
      GtToolFunc tool,
      int argc,
      char *argv[])
```

The tool driver module allows one to compile a tool into a separate binary. This is mostly useful for stand-alone applications like GenomeThreader. The tool driver creates an GtError object, calls `tool`, and reports errors.

```
int gt_toolobjdriver(
      GtToolConstructor,
      GtShowVersionFunc version_func,
      int argc,
      char *argv[])
```

Optional `version_func` to override the default one.

Module Undef

`#define GT_UNDEF_BOOL`

The undefined `bool` value.

`#define GT_UNDEF_CHAR`

The undefined `char` value.

`#define GT_UNDEF_DOUBLE`

The undefined `double` value.

`#define GT_UNDEF_FLOAT`

The undefined `float` value.

`#define GT_UNDEF_INT`

The undefined `int` value.

`#define GT_UNDEF_WORD`

The undefined `GtWord` value.

`#define GT_UNDEF_LONG`

The undefined `long` value. deprecated

`#define GT_UNDEF_UCHAR`

The undefined <unsigned char> value.

`#define GT_UNDEF_UINT`

The undefined <unsigned int> value.

`#define GT_UNDEF_UWORD`

The undefined `GtUword` value.

`#define GT_UNDEF_ULONG`

The undefined <unsigned long> value. deprecated

Module UnitTest

```
int GtUnitTestFunc(
                   GtError*)
```

A unit test function. It is assumed to return 0 on successful test completion, otherwise `err` should be set accordingly.

```
int gt_unit_test_run(
      void *key,
      void *value,
      void *data,
      GtError *err)
```

Run unit test. `key` is expected to be a C string, `value` a `GtUnitTestFunc`. `data` is assumed to be a pointer to an int, containing the test return code. `err` should not be touched.

Module Unused

```
#define GT_UNUSED
```

Unused function arguments should be annotated with this macro to get rid of compiler warnings.

Module Version

```
const char* gt_version_check(
              unsigned int required_major,
              unsigned int required_minor,
              unsigned int required_micro)
```

Check that the *GenomeTools* library in use is compatible with the given version. Generally you would pass in the constants `GT_MAJOR_VERSION`, `GT_MINOR_VERSION`, and `GT_MICRO_VERSION` as the three arguments to this function.
Returns `NULL` if the *GenomeTools* library is compatible with the given version, or a string describing the version mismatch, if the library is not compatible.

```
const char* gt_version(
              void)
```

Return the version of the *GenomeTools* library in use as a string.

Module VersionFunc

```
void gt_versionfunc(
       const char *progname)
```

Prints the GenomeTools version header with `progname` being the name of the tool where it is called from.

```
void gt_showshortversion(
       const char *progname)
```

Prints the short GenomeTools version header with `progname` being the name of the tool where it is called from.

Module Warning

```
void GtWarningHandler(
                      void *data,
                      const char *format,
                      va_list ap)
```

Handler type used to process warnings.

```
void gt_warning(
       const char *format,
       ...)
```

Print a warning according to `format` and $<\ldots>$, if a handler is set.

```
void gt_warning_disable(
       void)
```

Disable that warnings are shown. That is, subsequent `gt_warning()` calls have no effect.

```
void gt_warning_set_handler(
       GtWarningHandler warn_handler,
       void *data)
```

Set `warn_handler` to handle all warnings issued with `gt_warning()`. The `data` is passed to `warning_handler` on each invocation.

```
void gt_warning_default_handler(
       void *data,
       const char *format,
       va_list ap)
```

The default warning handler which prints on `stderr`. ”warning: ” is prepended and a newline is appended to the message defined by `format` and `ap`. Does not use `data`.

```
GtWarningHandler gt_warning_get_handler(
                   void)
```

Return currently used `GtWarningHandler`.

```
void* gt_warning_get_data(
        void)
```

Return currently used `data` which is passed to the currently used `GtWarningHandler`.

Module XANSI

```
void gt_xatexit(
       void (*function)
```

Similar to <atexit(3)>, terminates on error.

```
void gt_xfclose(
       FILE*)
```

Similar to <fclose(3)>, terminates on error.

```
void gt_xfflush(
       FILE*)
```

Similar to <fflush(3)>, terminates on error.

```
int gt_xfgetc(
      FILE*)
```

Similar to <fgetc(3)>, terminates on error.

```
char* gt_xfgets(
        char *s,
        int size,
        FILE *stream)
```

Similar to <fgets(3)>, terminates on error.

```
void gt_xfgetpos(
       FILE*,
       fpos_t*)
```

Similar to <fgetpos(3)>, terminates on error.

```
FILE* gt_xfopen(
        const char *path,
        const char *mode)
```

Similar to <fopen(3)>, terminates on error.

```
void gt_xfputc(
       int,
       FILE*)
```

Similar to <fputc(3)>, terminates on error.

```
void gt_xfputs(
       const char*,
       FILE*)
```

Similar to <fputs(3)>, terminates on error.

```
size_t gt_xfread(
    void *ptr,
    size_t size,
    size_t nmemb,
    FILE *fp)
```

Similar to <fread(3)>, terminates on error.

```
#define gt_xfread_one(
          ptr,
          fp)
```

Shortcut to `gt_xfread()` which reads a single element of data (of size <sizeof (*ptr)>) from `fp` and stores the result in `ptr`.

```
void gt_xfseek(
       FILE*,
       GtWord offset,
       int whence)
```

Similar to <fseek(3)>, terminates on error.

```
void gt_xfsetpos(
       FILE*,
       const fpos_t*)
```

Similar to <fsetpos(3)>, terminates on error.

```
void gt_xfwrite(
       const void *ptr,
       size_t size,
       size_t nmemb,
       FILE *fp)
```

Similar to <fwrite(3)>, terminates on error.

```
#define gt_xfwrite_one(
          ptr,
          fp)
```

Shortcut to `gt_xfwrite()` which writes a single element of data (of size <sizeof (*ptr)>) from `ptr` to `fp`.

```
void gt_xputchar(
       int)
```

Similar to <putchar(3)>, terminates on error.

```
void gt_xputs(
       const char*)
```

Similar to <puts(3)>, terminates on error.

```
void gt_xremove(
       const char*)
```

Similar to <remove(3)>, terminates on error.

```
void gt_xungetc(
       int,
       FILE*)
```

Similar to <ungetc(3)>, terminates on error.

```
void gt_xvfprintf(
       FILE *stream,
       const char *format,
       va_list ap)
```

Similar to <vfprintf(3)>, terminates on error.

```
int gt_xvsnprintf(
      char *str,
      size_t size,
      const char *format,
      va_list ap)
```

Similar to <vsnprintf(3)>, terminates on error.

Module XPOSIX

```
void gt_xclose(
       int d)
```

Wrapper around `close()`, terminating on error.

```
FILE* gt_xfdopen(
        int filedes,
        const char *mode)
```

Wrapper around `fdopen()`, terminating on error.

```
void gt_xfstat(
       int fd,
       struct stat *sb)
```

Wrapper around `fstat()`, terminating on error.

```
void gt_xgetrusage(
       int who,
       struct rusage *rusage)
```

Wrapper around `getrusage()`, terminating on error.

```
void gt_xglob(
       const char *pattern,
       int flags,
       int (*errfunc)
```

Wrapper around `glob()`, terminating on error.

```
int gt_xopen(
      const char *path,
      int flags,
      mode_t mode)
```

Wrapper around `open()`, terminating on error.

```
void gt_xmkdir(
       const char *path)
```

Wrapper around `mkdir()`, terminating on error.

```
int gt_xmkstemp(
      char *temp)
```

Wrapper around `mkstemp()`, terminating on error.

```
void* gt_xmmap(
        void *addr,
        size_t len,
        int prot,
        int flags,
        int fd,
        off_t offset)
```

Low-level wrapper for the `mmap()` routine, terminating on error.

```
void gt_xmunmap(
       void *addr,
       size_t len)
```

Generic unmapping routine, terminating on error.

```
void gt_xraise(
       int sig)
```

Wrapper around `raise()`, terminating on error.

```
void gt_xstat(
       const char *path,
       struct stat *sb)
```

Wrapper around `stat()`, terminating on error.

```
time_t gt_xtime(
    time_t *tloc)
```

Wrapper around `time()`, terminating on error.

```
void gt_xunlink(
       const char *path)
```

Wrapper around `unlink()`, terminating on error.

```
void gt_xwrite(
       int d,
       const void *buf,
       size_t nbytes)
```

Wrapper around `write()`, terminating on error.

Module Yarandom

```
unsigned int gt_ya_random(
                void)
```

Return a random number.

```
unsigned int gt_ya_rand_init(
                unsigned int)
```

Initialize random number generator using given seed.

```
void gt_ya_rand_clean(
       void)
```

Clean up static data for random number generator.

```
#define GT_RAND_MAX
```

Maximum random number (2147483647)

```
#define random()
```

Return random number up to RAND_MAX.