This article describes **glyphs** and **glyph configuration options** in GBrowse.

- *For the main GBrowse configuration article, see: GBrowse Configuration.*
- *See also: Glyphs and Glyph Options, a competing document.*
- *See also: The Glyph Gallery at webgbrowse.*

Glyphs and Glyph Options

A large variety of glyphs are available, and more are being added as the Bio::Graphics module grows.

A list of the common glyphs and their options is provided by the GBrowse itself. Click on the "[Help]" link in the section labeled "Upload your own annotations". This page also lists the valid foreground and background colors. Most of the glyphs are found in the BioPerl distribution, but a few are distributed directly with GBrowse.

Predefined glyphs are:

Glyph	Description
Glyph	Common options for all glyphs. (*Glyph* is the parent class of all the glyphs).
allele_tower	genotype found at a SNP position
anchored_arrow	a span with vertical bases |-----|. If one or the other end of the feature is off-screen, the base will be replaced by an arrow.
arrow	an arrow
box	another rectangle; doesn't show subparts of features
cds	shows the reading frame of spliced transcripts; used in conjunction with the "coding" aggregator (GFF2).
crossbox	
diamond	a point-like feature represented as a triangle
dna	DNA and GC content
dot	
ellipse	
extending_arrow	
generic	a rectangle
graded_segments	
heterogeneous_segments	a multi-segmented feature in which each segment can have a distinctive color. For Jim Kent's WABA features, this works with the waba_alignment aggregator.
idiogram	This takes specially-formatted feature data and turns it into an idiogram of a Giemsa-stained metaphase chromosome. (This is included in the GBrowse distribution, not in BioPerl.)
image	this embeds photographic images and/or diagrams on features processed_transcript multi-purpose representation of a spliced mRNA, including positions of UTRs
line	

primers	
processed_transcript	
rndrect	
ruler_arrow	
segments	a multi-segmented feature such as an alignment
span	like anchored_arrow, except that the ends are truncated at the edge of the panel, not turned into an arrow
toomany	
trace	reads an SCF trace file and draws a graphic representation
transcript	a gene model
transcript2	a slightly different representation of a gene model
translation	1-, 3- and 6-frame translations
triangle	a point-like feature represented as a diamond
wormbase_transcript	yet another gene model that can show UTR segments (for features that conform to the WormBase gene schema). Used in conjunction with the "wormbase_gene" aggregator (GFF2).
wiggle_density	Quantitative information from wiggle files (.wig) shown as color intensity. See GBrowse/Uploading Wiggle Tracks.
wiggle_xyplot	Quantitative information from wiggle files shown as an xyplot.
xyplot	histograms and line plots

A more definitive list of glyph options can be found in the Bio::Graphics manual pages. Consult the manual pages for the following modules:

The "perldoc" command is handy for reading the documentation from the Unix command line. For example:

```
perldoc Bio::Graphics::Glyph::primers
```

This will provide you with a summary of the options that apply to the "primers" glyph.

In the manual pages, the glyph options are presented the way they are called from Perl. For example, the documentation will tell you to use the -connect_color option to set the color to use when drawing the line that connects the two inward pointing arrows in the primer pair glyph. This translates to the configuration file as an option named "connect_color". For example:

```
[PCR Products]
glyph = primer
connect_color = blue
```

When referring to colors, you can use a variety of color names such as "blue" and "green". To get the full list, cut and paste the following magic incantation into the command line:

```
perl -MBio::Graphics::Panel -e 'print join "\n",Bio::Graphics::Panel->color_names'
```

or see this URL:

http://www.wormbase.org/db/seq/gbrowse?help=annotation

Alternatively, you can use the #RRGGBB notation to specify the red, green and blue components of the color. Refer to any book on HTML for the details on using the notation.