

Modernizing the GB on-line docs

[RM: 18504](#)

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Why ?

UCSC Genome Bioinformatics

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Configuring VCF tracks

Genome Browser VCF tracks may be configured in a variety of ways to highlight different aspects of the displayed information. Click [here](#) for more information on VCF custom track creation.

If the VCF file contains genotype columns for at least two samples (four haplotypes), then a haplotype sorting display can be configured:

- **Enable Haplotype sorting display:** If checked, then each sample's phased and/or homozygous genotypes are split into haplotypes, clustered by similarity around a central variant, and sorted for display by their position in the clustering tree. The tree (or as much of the tree as space allows) is drawn in the label area next to the track image. Leaf clusters, in which all haplotypes are identical (at least for the span of variants used in clustering), are colored purple. Each variant is drawn as a vertical column, using color to distinguish between reference alleles and alternate alleles of the horizontally running haplotypes. If unchecked, then the display is the same as for VCF without genotypes: a stacked bar graph of the top two alleles, showing the proportion of alleles if allele counts are available. This is checked (enabled) by default. The following options are applicable only when enabled.
 - **Haplotype sorting order:** Haplotypes are sorted using a distance function that uses a central variant; differences between haplotypes are penalized with weights that decrease for each successive variant away from the central variant. By default, the median variant in the window is used. By clicking on a variant in the display, you will get the option to always use that variant when it is in the current view.
 - **Haplotype coloring scheme:** There are three ways that reference and alternate alleles can be colored:
 - By default, the reference allele is invisible and the alternate allele is black. When multiple haplotypes must be combined into the same pixel row, grayscale is used to shade according to the proportions of reference and alternate alleles. The central variant has a thin purple outline. Extra pixel rows at the top and bottom show the locations of

Before

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Configuring the haplotype sorting display

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The following options are applicable only when the haplotype sorting display is enabled:

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After

Why (more detail)

- Achieve a more modern look
- Maintain consistency with new Home page and hgGateway
- Simplify page HTML source
- Adhere better to current HTML standards and style recommendations
- Review and update help content
- Improve organization of help docs

How

1) Update infrastructure

- Create include files for boilerplate
- Create new static page stylesheet
- Create new template with examples

2) Whack the pages!

- Tidy pages
- Remove wrapper tables
- Remove hard-coded styling
- Add new includes (and variables they need)

What

- Include files:

- gbPageStart.html stylesheets, top menu, wrapper div
- gbPageEnd.html footer, end wrapper

- CSS files:

- bootstrap.min.css subset of capabilities, responsive grid layout
- gb.css new UI look from Jeff West. Used by CGI's too
- staticStyle/gbStatic.css new UI look, file used only by static pages

- Tools:

- tidy lower case tags, fix white-space, report errors

HTML tags for GB static pages

`<p>` paragraph

`<h1>` page header (title)

`<h2>` section header

`<h3>` subsection header

`<h6>` paragraph title

`<table><th><tr><td>` table

`<pre>` preformatted section

`<code>` code

`` unordered (bulleted) list

`` ordered (numbered) list

`<dl><dt><dd>` definition list

`` image

Classes for GB static pages

- `<div class="row">` define a row for multi-column layout
- `<div class="col-md-6">` define a column for multi-column layout (12-col grid)
- `<ul class="gbsNoBullet">` unordered list without bullets
- `<table class="gbsNoBorder">` table with border suppressed
- `` right-align image
- `<p class="gbsCaption">` caption for image

Sample Genome Browser Static Page (h1)

This is a standard paragraph ('p' tag) of explanatory text. The next part of the page demonstrates how to create a multi-column layout using the grid layout feature of bootstrap.css, a widely used stylesheet which is now included in the browser static pages.

Page section (h2)

This is one of two subsections, formatted as equal-sized columns. The bootstrap grid contains 12 columns; column widths are specified using classes 'col-md-1' through 'col-md-12'. This example contains two divs, each assigned class 'col-md-6', within a 'row' div.

NOTE: The two columns are displayed only on wide screens. On small screens, the sections will be stacked vertically (a feature of bootstrap responsive layout).

Subsection (h3)

This is the next level, a subsection. Use an 'h3' tag for this. To structure content below this level use a list, table, or titled paragraph:

Titled paragraph

Use the 'h6' tag at any level in the section hierarchy to precede a paragraph with a bolded title.

Lists

The description of lists below is formatted as an HTML definition list. Use this format when defining terms or phrases. (You will not see this much in our current pages -- instead, this type of text was usually styled ad-hoc using 'strong' and 'br' tags).

Definition list

Use the 'dl' tag to enclose the full list, then 'dt' for each item term, and 'dd' for each item definition.

Bulleted list

Use the 'ul' (unordered list tag) to enclose the full list, then 'li' for each list item.

Numbered list

Use the 'ol' (ordered list) tag to enclose the full list, then 'li' for each list item.

Another section

List Examples

Here is a bulleted list ('ul' and 'li' elements). To suppress the 'bullet' add the class 'gbsNoBullet' to the 'ul' tag.

- red
- white
- blue

Here is a numbered list ('ol' and 'li' elements):

- chrom** - The name of the chromosome (e.g. chr3, chrY, chr2_random) or scaffold (e.g. scaffold10671).
- chromStart** - The starting position of the feature in the chromosome or scaffold. The first base in a chromosome is numbered 0.
- chromEnd** - The ending position of the feature in the chromosome or scaffold. The *chromEnd* base is not included in the display of the feature. For example, the first 100 bases of a chromosome are defined as *chromStart=0*, *chromEnd=100*, and span the bases numbered 0-99.

Tables

Here is a table ('table', 'tr', 'th', and 'td' elements):

| Type | Total |
|---------------------|-------|
| Chromosomes | 261 |
| Haplotypes | 261 |
| Unlocalized contigs | 1270 |

Code

Here is some code in a preformatted section ('pre' and 'code' tags):

```
sudo -i
bash browserSetup.sh install
```

And here is some text with a `bit of code` embedded (just the 'code' tag)..

Template:

Shows examples and explains how to use tags to take advantage of new styles

<http://hgwdev-demo7.soe.ucsc.edu/template.html>

When

Phase 1: New look and cleanup

Tasks: Remove old cruft. Use new styles.

Release: 1) Merge branch 2) Resolve conflicts with work-in-progress
3) Broad & shallow QA of htdocs 4) Push

Timeline: ASAP, as we have a soft freeze currently on the docs. Feb 7 latest ?

Phase 2: Content and organization improvement.

Target: On-going