GFF2APLOT

USER'S MANUAL

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GFF2APLOT v2.0

Visualizing Pair-wise Alignments for Genomic Sequences in PostScript.

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Basic Concepts

In this chapter we would introduce you to GFF format definition as well as how GFF2APLOT handles your GFF files. The main goal is that you will learn which is the proper record structure for GFF files. So that, you will understand the program warnings when a record does not fit such structure and being not drawn. GFF2APLOT rejects all those records not conforming with the record structures described in the following sections.

2.1 GFF philosophy

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Chapter 3

Using GFF2APLOT

In this chapter it is explained how you can set system variables in order to start working with **GFF2APLOT**. This program was designed to work under UNIX and has been tested under Irix, Solaris and Linux. In table **??** you can see the program versions with which we have worked. **GFF2APLOT** has three inner modules: the shell script, the GNU awk script, and the PostScript prologue code. This prologue contains all procedure sets we have written to obtain the PostScript plots and it is embedded into '`gff2ps`'. This is a Bourne shell script —using *sh* or *bash* (systems under Linux have a link for *sh* to *bash*)–, that handles with command-line options, checks if given files exist and pass them to the GNU awk script. This loads data records and custom definitions generating the full PostScript output. You can visualize that with a PostScript viewer —like ghostview, xpsview— or send to a PostScript printer to obtain a hardcopy.

The main difference from older versions is that GNU awk script is now included within the shell script to facilitate installation of our program.

3.1 Installation

3.2 Command-Line

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Chapter 4

Customizing GFF2APLOT Output

4.1 Command-line Options Description

-h
--help

Shows command-line help.

--version

Shows current program version and exits.

-v
--verbose

By default, warnings and errors are sent to standard error. This option switches on process reporting messages to appear on standard error too.

-V <filename>
--logs-filename <filename>

If is possible to open <filename> then such file will contain all the messages and warnings produced by the program even though they were disabled from standard error with **quiet** option.

-q
--quiet

This option disables any message or warning from standard error. It does not disable error report because such errors are pointing a problem which can make GFF2APLOT produce unexpected results. Solve the cause of such problems before continuing to run the program in a silent mode.

-P <width,height>
--page-bbox <width,height> **page_bbox**=<width,height>

This option allows users to define an arbitrary page format, by defining the width and height for that page (GFF2APLOT assigns automatically a format name for this new page dimensions). See **page_bbox** customization variable on page 12 (section 4.2.1) for further info on this command-line option. It overrides any **page-size** command-line option (and any related variable passed through custom files). <width> and <height> are set to points if no unit is given, now you can use pt, mm, cm or in.

-p <format_name>
--page-size <format_name> **page_size**=<format_name>

<format_name> is a pre-defined page format from table A.3. By default is set to **a4**.

--margin-left <length> **margin_left**=<length>
--margin-right <length> **margin_right**=<length>
--margin-top <length> **margin_top**=<length>

--margin-bottom <length> **margin_bottom**=<length>

You can set page margin with those four variables. <length> can be given in points, milimeters, centimeters or inches (pt, mm, cm or in, respectively), but is set to points if no units are provided.

-B <color>
--background-color <color> **background_color**=<color>
-F <color>
--foreground-color <color> **foreground_color**=<color>

You can change background —say here page filling— and foreground —say here text, outlines and tickmarks— color for the page. Available colors are defined on table A.1, default values are **white** and **black**, for background and foreground respectively.

-T <string>
--title <string> **title**=<string>

Setting the main title to <string> for the current figure, by default showing **align_name** in the form of **sequence1_name** x **sequence2_name**.

-t <string>
--subtitle <string> **subtitle**=<string>

Setting <string> as the current figure subtitle, by default an empty string.

-X <string>
--x-label <string> **x_label**=<string>

TO BE DEFINED !!!

-Y <string>
--y-label <string> **y_label**=<string>

TO BE DEFINED !!!

-L <string>
--percent-box-label <string> **percent_box_label**=<string>

TO BE DEFINED !!!

-l <string>
--extra-box-label <string> **extra_box_label**=<string>

TO BE DEFINED !!!

-x <pos..pos>
--x-sequence-coords <pos..pos> **x_sequence_coords**=<pos..pos>

TO BE DEFINED !!!

-S <pos>
--start-x-sequence <pos> **x_sequence_start**=<pos>

TO BE DEFINED !!!

-E <pos>
--end-x-sequence <pos> **x_sequence_end**=<pos>

TO BE DEFINED !!!

-y <pos..pos>
--y-sequence-coords <pos..pos> **y_sequence_coords**=<pos..pos>

TO BE DEFINED !!!

-s <pos>
--start-y-sequence <pos> **y_sequence_start**=<pos>

TO BE DEFINED !!!

-e <pos>
--end-y-sequence <pos> **y_sequence_end**=<pos>

TO BE DEFINED !!!

--x-sequence-zoom <pos..pos> **x_sequence_zoom**=<pos..pos>
TO BE DEFINED !!!

--y-sequence-zoom <pos..pos> **y_sequence_zoom**=<pos..pos>
TO BE DEFINED !!!

-Z
--zoom **zoom**= **on**
TO BE DEFINED !!!

-z
--zoom-area **zoom_area**= **on**
TO BE DEFINED !!!

-A <seqXname:seqYname>
--alignment-name <seqXname:seqYname> **alignment_name**=<seqXname:seqYname>
When you are providing several alignments from input, you can select which one to be plotted. By default program uses first alignment found in the input stream if **x_sequence_name** and **y_sequence_name** were also not defined, else it will try combining those variables if they are set by user or relying on their default values. See **alignment_name** customization variable description on section 4.2.1, page 15, for further info. It is also explained there but remember that you should take care of unexpected side effects when setting different sequence names to this command-line option and its siblings, **x-sequence-name** and **y_sequence_name**, if you set one of them in a custom file and the others on command-line or viceversa.

-N <seqXname>
--x-sequence-name <seqXname> **x_sequence_name**=<seqXname>
You can choose the sequence that is going to be drawn along X-axis, or what is equivalent, which annotation will appear on that axis. See **alignment-name** description to know more about these variables.

-n <seqYname>
--y-sequence-name <seqYname> **y_sequence_name**=<seqYname>
Here you will define which sequence is drawn on Y-axis. Take a look to **alignment-name** to get more info about the interactions between these variables.

-r
--aplot-xy-noteq **aplot_xy_same_length**= **off**
TO BE DEFINED !!!

-R <X/Y ratio>
--xy-axes-scale <X/Y ratio> **aplot_xy_scale**=<X/Y ratio>
TO BE DEFINED !!!

-W
--aln-scale-width **alignment_scale_width**= **on**
TO BE DEFINED !!!

-w
--aln-scale-color **alignment_scale_color**= **on**
TO BE DEFINED !!!

-K <ribbon-type>
--show-ribbons <ribbon-type> **show_ribbons**=<ribbon-type>
TO BE DEFINED !!!

-G
--show-grid **show_grid**= **on**
TO BE DEFINED !!!

-I
--show-percent-box **show_percent_box**= **on**

TO BE DEFINED !!!

-i
--hide-percent-box **show_percent_box**= **off**

TO BE DEFINED !!!

-O
--show-extra-box **show_extra_box**=<on>

TO BE DEFINED !!!

-o
--hide-extra-box **show_extra_box**=<off>

TO BE DEFINED !!!

-D <color>
--aplot-box-color <color> **aplot_box_bgcolor**=<color>

TO BE DEFINED !!!

-d <color>
--percent-box-color <color> **percent_box_bgcolor**=<color>

TO BE DEFINED !!!

-b <color>
--extra-box-color <color> **extra_box_bgcolor**=<color>

TO BE DEFINED !!!

--nopswarnings **show_ps_warnings**= **off**

When input data is missing, regardless you do not provide X or Y sequence annotation, or even alignment records, GFF2APLOT will include a warning message in the final POSTSCRIPT output. This will help to identify what is missing from such input data, but sometimes it must be ignored and you may need to switch those warnings off. You can switch off on a single figure from command-line, or disable from a default customization file variable. The last choice it is not recommended unless you already know what you are doing and you are sure that you will get annotations along only for one of the axes or there are sequence pairs that do not have the corresponding alignment data.

-a
--hide-credits **hide_credits**= **on**

GFF2APLOT always displays a tiny copyright footer on the output POSTSCRIPT figures that users can remove using this command-line option for a single case, or the corresponding customization variable in a default customization file for all the figures.

--layout-var '<variable=value>' **variable**= **value**
--sequence-var '<sequence::variable=value>' **sequence::variable**= **value**
--source-var '<source::variable=value>' **source::variable**= **value**
--strand-var '<strand::variable=value>' **strand::variable**= **value**
--group-var '<group::variable=value>' **group::variable**= **value**
--feature-var '<feature::variable=value>' **feature::variable**= **value**

Loading any of feature/group/strand/source/sequence/layout customization variables from command-line. You can set several variables by repeating any of these options, i.e.:

... --feature-var '/^cds.*/::feature_shape=box' --feature-var 'exon::feature_color=blue' ...

In the previous example, '/^**cds.***/' is a regular expression matching any GFF-feature which name starts with '**cds**', setting their shape to **box**. The second line sets GFF-feature color (filling the feature shape) only for those GFF-features that match exactly with '**exon**' (as if we passed the feature name as a regular expression, in this case as '/^**exon$**/').

These command-line options allow users to change on the fly any variable for the current GFF2APLOT execution. It is very useful for testing dinamically customizations before including them in the custom files. But it also lets users to keep a fixed customization file shared among several runs, while making small changes among them. Take care of protecting the parameters given to those command-line options by single-quoting them, just to avoid any undesirable side effect produced by shell-substitution of wild-chars (especially when passing regular expressions to match several elements to which set the same variable).

-C <filename>
--custom-filename <filename>

Loading customization parameters from <filename>. Now you can load several customization files by passing this option several times. The precedence is the input order in the command-line, so, for the common definitions, the last **custom_file** will override previous **custom_files** settings. If default customization file "`.gff2aplotrc`" does exist, it is the first customization that is loaded by the program.

-g
--hide-grid **show_grid**= **off**

TO BE DEFINED !!!

4.2 Customization Variables Description

4.2.1 Layout Attributes

page_bbox = <width,height> [***undef***]

This variable allows users to define an arbitrary page format, by defining the width and height for that page (GFF2APLOT assigns automatically a format name for this new page dimensions). Do not include this variable in your custom files if you are using standard page sizes which can be set using **page_size**, because **page_bbox** overrides any further page definition by that variable. If the variable is not set, default value forces the use of any settings given for **page_size**. <width> and <height> are set to points if no unit is given, now you can also use points, milimeters, centimeters or inches (pt, mm, cm or in, respectively). See table A.3 for a reference on already defined page sizes and their dimensions.

page_size = <format_name> [**a4**]

Setting a standard page size, available values for <format_name> are listed in table A.3. Page width and height values are coded for most common paper formats.

margin_left = <length> [**1cm**]
margin_right = <length> [**1cm**]
margin_top = <length> [**1cm**]
margin_bottom = <length> [**1cm**]

You can set page margin with those four variables. <length> can be given in points, milimeters, centimeters or inches (pt, mm, cm or in, respectively), but is set to points if no units are provided.

background_color = <color> [**white**]
foreground_color = <color> [**black**]

These two customization variables accept any <color> from those listed on table A.1. Default values are **white** and **black** for **background_color** and **foreground_color** respectively. These two variables also set the aliases **BGcolor** and **FGcolor**, so that you can use **bgcolor** and **bg**, or **fgcolor** and **fg**, to set any other color-related variable with the same colors you are defining as background/foreground colors.

title = <string> [***undef***]

title sets the main title to <string> for the current figure, by default showing **align_name** in the form of **sequence1_name** x **sequence2_name**.

show_title = <boolean> [**on**]

show_title switches on/off displaying the figure title. If you do not want to visualize the default title you can set this variable to **off**, but you are not able to reuse the area of plot where title appears (set **title_fontsize** to **0** if you want to remove that area from plot).

title_font = <font> [**helvetica-bold**]

TO BE DEFINED !!!

title_fontsize = <length> [**24pt**]

Sets title fontsize, <length> can be in pt, mm, cm or in (default is points if no units are given). Setting **title_fontsize** to **0** forces GFF2APLOT to remove title area from plot, so no space is left for it.

subtitle = <string> [***undef***]

subtitle sets the current figure subtitle to <string>, by default it is defined as an empty string.

show_subtitle = <boolean> [**on**]
show_subtitle switches on/off displaying the subtitle text. If you do not want to visualize the default subtitle you can set this variable to **off**, as with **show_title** you are not able to reuse the area of plot where subtitle appears (so set **subtitle_fontsize** to **0** if you want to remove that area from plot too).

subtitle_font = <font> [**helvetica**]
TO BE DEFINED !!!

subtitle_fontsize = <length> [**16pt**]
Sets subtitle fontsize, <length> can be in pt, mm, cm or in (default is points if no units are given). Setting **subtitle_fontsize** to **0** forces GFF2APLOT to remove subtitle area from plot, so no space is left for it.

x_label = <string> [***undef***]
TO BE DEFINED !!!

show_x_label = <boolean> [**on**]
show_x_label switches on/off displaying the subtitle text. If you do not want to visualize the default subtitle you can set this variable to **off**, as with **show_title** you are not able to reuse the area of plot where subtitle appears (so set **subtitle_fontsize** to **0** if you want to remove that area from plot too).

x_label_font = <font> [**helvetica-bold**]
TO BE DEFINED !!!

x_label_fontsize = <length> [**12pt**]
Sets X-label fontsize, <length> can be in pt, mm, cm or in (default is points if no units are given). Setting **subtitle_fontsize** to **0** forces GFF2APLOT to remove subtitle area from plot, so no space is left for it.

y_label = <string> [***undef***]
TO BE DEFINED !!!

show_y_label = <boolean> [**on**]
show_x_label switches on/off displaying the subtitle text. If you do not want to visualize the default subtitle you can set this variable to **off**, as with **show_title** you are not able to reuse the area of plot where subtitle appears (so set **subtitle_fontsize** to **0** if you want to remove that area from plot too).

y_label_font = <font> [**helvetica-bold**]
TO BE DEFINED !!!

y_label_fontsize = <length> [**12pt**]
Sets Y-label fontsize, <length> can be in pt, mm, cm or in (default is points if no units are given). Setting **subtitle_fontsize** to **0** forces GFF2APLOT to remove subtitle area from plot, so no space is left for it.

show_percent_box_label = <boolean> [**on**]
TO BE DEFINED !!!

percent_box_label = <string> [***undef***]
TO BE DEFINED !!!

percent_box_label_font = <font> [**helvetica-bold**]
TO BE DEFINED !!!

percent_box_label_fontsize = <length> [**12pt**]
TO BE DEFINED !!!

show_percent_box_sublabel = <boolean> [**on**]
TO BE DEFINED !!!

percent_box_sublabel = <string> [***undef***]
TO BE DEFINED !!!

percent_box_label_font = <font> [**helvetica**]
TO BE DEFINED !!!

percent_box_label_fontsize = <length> [**9pt**]
TO BE DEFINED !!!

show_extra_box_label = <boolean> [**on**]
TO BE DEFINED !!!

extra_box_label = <string> [***undef***]
TO BE DEFINED !!!

extra_box_label_font = <font> [**helvetica-bold**]
TO BE DEFINED !!!

extra_box_label_fontsize = <length> [**10pt**]
TO BE DEFINED !!!

show_extra_box_sublabel = <boolean> [**on**]
TO BE DEFINED !!!

extra_box_sublabel = <string> [***undef***]
TO BE DEFINED !!!

extra_box_sublabel_font = <font> [**helvetica**]
TO BE DEFINED !!!

extra_box_sublabel_fontsize = <length> [**9pt**]
TO BE DEFINED !!!

x_sequence_coords = <pos..pos> [***undef***]
TO BE DEFINED !!!

x_sequence_start = <pos> [***undef***]
TO BE DEFINED !!!

x_sequence_end = <pos> [***undef***]
TO BE DEFINED !!!

y_sequence_coords = <pos..pos> [***..***]
TO BE DEFINED !!!

y_sequence_start = <pos> [***undef***]
TO BE DEFINED !!!

y_sequence_end = <pos> [***undef***]
TO BE DEFINED !!!

x_sequence_zoom = <pos..pos> [***undef***]
TO BE DEFINED !!!

x_sequence_zoom_start = <pos> [***undef***]
TO BE DEFINED !!!

x_sequence_zoom_end = <pos> [***undef***]
TO BE DEFINED !!!

y_sequence_zoom = <pos..pos> [***undef***]
TO BE DEFINED !!!

y_sequence_zoom_start = <pos> [***undef***]
TO BE DEFINED !!!

y_sequence_zoom_end = <pos> [***undef***]
TO BE DEFINED !!!

zoom = <boolean> [**off**]
TO BE DEFINED !!!

zoom-area = <boolean> [**off**]
TO BE DEFINED !!!

zoom_marks = <boolean> [**off**]
TO BE DEFINED !!!

zoom_area_mark_width = <length> [**2pt**]
TO BE DEFINED !!!

zoom_area_mark_style = <line_style> [**solid**]
TO BE DEFINED !!!

zoom_area_mark_color = <color> [**lightred**]
TO BE DEFINED !!!

zoom_area_fill_color = <color> [***undef***]
TO BE DEFINED !!!

alignment_name = <seqXname:seqYname> [***undef***]
When you are providing several alignments from input, you can select which one to be plotted. By default program uses first alignment found in the input stream if **x_sequence_name** and **y_sequence_name** were also not defined, else it will try combining those variables if they are set by user or relying on their default values. The precedence of those variables is the following: <seqXname:seqYname> ≫ <seqXname>:<seqYname> ≫ <defaults>
Where <seqXname>:<seqYname> stands for the combination of the values set for **x_sequence_name** and **y_sequence_name** variables. If you set **alignment_name** and <seqXname:seqYname> is not found in the list of read alignments, program tries to find the reverse, <seqYname:seqXname>, else no alignment will be drawn.
Remember that if you set this variable on command-line and the other two in a customization file or viceversa, you will get a plot in which sequence annotation along the axes does not correlate to the alignment shown, so that make sure that you are using all three in a coordinated way (although you are looking for that uncorrelated effect, but then it will be your fault, do not blame on GFF2APLOT). This can seem a drawback, but think that it will be very useful if you are parsing GFF input and the alignment name was set with different sequence names: say here you have **SeqA** and **SeqB**, and the

alignment sequence name from filtered output after running those sequences through your alignment program was set to **my_a:my_b** instead of **SeqA:SeqB**, so you do not have to reformat the GFF records for the alignment or the annotation. Following with that example, if nothing else is defined, **SeqA** will be drawn on X-axis and **SeqB** on Y-axis. If happens that **my_a:my_b** (neither in case you already have **SeqA:SeqB**) does not appear on GFF input, but program finds an alignment named as **my_b:my_a**, then annotations will swap on axes, having **SeqA** along Y-axis and **SeqB** on X-axis.

x_sequence_name = <seqXname> [***undef***]
We define which sequence annotation is going to be drawn on X-axis, having two or more sequences from GFF input. By default, the program will use the first sequence id from that input (unless you have set something different on **alignment_name** or from command-line). <seqXname> will be the same as <seqYname> (but then you must define both variables, **x_sequence_name** and **y_sequence_name**), this is useful when comparing a sequence against itself to find repeated elements, but take care not doing that when you are trying to compare different sequences because the program cannot guess that you do not want to do that.

y_sequence_name = <seqYname> [***undef***]
This variable allows you to define which sequence is going to be drawn along the Y-axis. Take a look to **alignment_name** and **x_sequence_name** variables descriptions for a deeper explanation of their settings and behaviour.

aplot_xy_same_length = <boolean> [**on**]
TO BE DEFINED !!!

aplot_xy_scale = <X/Y ratio> [***undef***]
TO BE DEFINED !!!

alignment_scale_width = <boolean> [**off**]
TO BE DEFINED !!!

alignment_scale_color = <boolean> [**off**]
TO BE DEFINED !!!

show_ribbons = <boolean> [***undef***]
TO BE DEFINED !!!

show_grid = <boolean> [**off**]
TO BE DEFINED !!!

show_percent_box_grid = <boolean> [**on**]
TO BE DEFINED !!!

show_percent_box = <boolean> [**off**]
TO BE DEFINED !!!

show_extra_box = <boolean> [**off**]
TO BE DEFINED !!!

aplot_box_bgcolor = <color> [**bg**]
TO BE DEFINED !!!

percent_box_bgcolor = <color> [**bg**]
TO BE DEFINED !!!

extra_box_bgcolor = <color> [**bg**]
TO BE DEFINED !!!

percent_box_height = <length> [***undef***]
TO BE DEFINED !!!

extra_box_height = <length> [***undef***]
TO BE DEFINED !!!

show_tickmark_label = <boolean> [**on**]
TO BE DEFINED !!!

show_only_bottom_ticks = <boolean> [**off**]
TO BE DEFINED !!!

show_aplot_x_ticks = <boolean> [**on**]
TO BE DEFINED !!!

show_aplot_y_ticks = <boolean> [**on**]
TO BE DEFINED !!!

show_percent_x_ticks = <boolean> [**on**]
TO BE DEFINED !!!

show_percent_y_ticks = <boolean> [**on**]
TO BE DEFINED !!!

show_extrabox_x_ticks = <boolean> [**on**]
TO BE DEFINED !!!

show_extrabox_y_ticks = <boolean> [**on**]
TO BE DEFINED !!!

aplot_major_tickmark = <integer> [**2**]
TO BE DEFINED !!!

aplot_minor_tickmark = <integer> [**5**]
TO BE DEFINED !!!

aplot_score_range = <score..score> [***undef***]
TO BE DEFINED !!!

percent_major_tickmark = <integer> [***undef***]
TO BE DEFINED !!!

percent_minor_tickmark = <integer> [**4**]
TO BE DEFINED !!!

percent_box_score_range = <score..score> [***undef***]
TO BE DEFINED !!!

extra_major_tickmark = <integer> [**2**]
TO BE DEFINED !!!

extra_minor_tickmark = <integer> [**5**]
TO BE DEFINED !!!

extra_box_score_range = <score..score> [***undef***]
TO BE DEFINED !!!

major_tickmark_nucleotide = <nucleotides> [***undef***]
TO BE DEFINED !!!

minor_tickmark_nucleotide = <nucleotides> [***undef***]
TO BE DEFINED !!!

major_tickmark_score = <score-step> [***undef***]
TO BE DEFINED !!!

minor_tickmark_score = <score-step> [***undef***]
TO BE DEFINED !!!

show_feature_label = <boolean> [**on**]
feature_label_font = <font> [**helvetica**]
feature_label_fontsize = <length> [**6pt**]
TO BE DEFINED !!!

feature_x_label_length = <char-length> [***undef***]
feature_x_label_angle = <degrees> [$0°$]
feature_x_label_rotate = <boolean> [**off**]
TO BE DEFINED !!!

feature_y_label_length = <char-length> [***undef***]
feature_y_label_angle = <degrees> [$0°$]
feature_y_label_rotate = <boolean> [**on**]
TO BE DEFINED !!!

show_group_label = <boolean> [**on**]
group_label_font = <font> [**helvetica**]
group_label_fontsize = <length> [**8pt**]
TO BE DEFINED !!!

group_x_label_length = <char-length> [***undef***]
group_x_label_angle = <degrees> [$0°$]
group_x_label_rotate = <boolean> [**off**]
TO BE DEFINED !!!

group_y_label_length = <char-length> [***undef***]
group_y_label_angle = <degrees> [$0°$]
group_y_label_rotate = <boolean> [**on**]
TO BE DEFINED !!!

align_tag = <tag> [**target**]
align_tag holds the specific tag (for a grouping Tag-Value pair) to detect those GFF records coding for alignment data and having any of the three following group structures:

```
[ ... ] align_tag "group_name" <seq2_start> <seq2_end> \\
                    [ <seq2_strand> [ <seq2_frame> ] ] [ ; ... ]

[ ... ] align_tag "group_name" <seq2_start> <seq2_end> \\
                    [ ; strand_tag <seq2_strand> [ ; frame_tag <seq2_frame> ] ] [ ; ... ]

[ ... ] align_tag "group_name" ; start_tag <seq2_start> ; end_tag <seq2_end> \\
                    [ ; strand_tag <seq2_strand> [ ; frame_tag <seq2_frame> ] ] [ ; ... ]
```

The program can recover the coords for the target sequence from those grouping fields. If no strand or frame are given for the subject sequence then GFF2APLOT gets them from query sequence. Remember that tags are not case-sensitive and that the grouping fields separator is the semi-colon (';').

vector_tag = <tag> [**vector**]
vector_tag sets the specific tag (for a grouping Tag-Value pair) to detect scoring vector GFF records, which have the following group structure:

[. . .] vector_tag "group_name" [<vector_type>] [; Window <window_length> \\
[; Step <step_length>]] ; Scores <score_0> ... <score_n>

so the program can parse the list of single scores from the grouping fields. Remember that tags are not case-sensitive and that the grouping fields separator is the semi-colon (';').

label_tag = <tag> [**id**]
label_tag sets the specific tag (for a grouping Tag-Value pair) that allows to identify a single record. The program looks for the grouping Tag-Value pair for which the tag matches **label_tag** and takes <value> as the specific record label. You must have an attribute like this within the grouping attribute list:

. . . ; label_tag "element_label" [. . . other sub-fields . . .] [; . . .]

if "other sub-fields" are present they are ignored by GFF2APLOT. Using this attribute makes easy to set specific properties for one or more records of your GFF dataset. Remember that tags are not case-sensitive.

start_tag = <tag> [**start**]
TO BE DEFINED !!!

end_tag = <tag> [**end**]
TO BE DEFINED !!!

score_tag = <tag> [**e_value**]
TO BE DEFINED !!!

strand_tag = <tag> [**strand**]
TO BE DEFINED !!!

frame_tag = <tag> [**frame**]
TO BE DEFINED !!!

scotype_tag = <tag> [**vectype**]
TO BE DEFINED !!!

window_tag = <tag> [**window**]
TO BE DEFINED !!!

step_tag = <tag> [**step**]
TO BE DEFINED !!!

scoary_tag = <tag> [**scores**]
TO BE DEFINED !!!

ribbon_color_merge = <boolean> [***undef***]
This property is device dependant, lower resolution devices (such as screen) will not show properly the color blending.

color_merge_factor = <alpha_factor> [**0.5**]
<alpha_factor> ranges from **0.07** up to **2**, default is set to **0.5**. If you plan to scale down your figures, it is advisable to increase it to **1** or **2**.

ribbon_style = <ribbon-type> [***undef***]
TO BE DEFINED !!!

ribbon_color = <color> [***undef***]
TO BE DEFINED !!!

4.2.2 GFF-Feature Attributes

hide = <boolean> [**off**]
TO BE DEFINED !!!

feature_color = <color> [**fg**]
TO BE DEFINED !!!

alignment_color = <color> [**fg**]
TO BE DEFINED !!!

ribbon_color = <color> [**verylightgrey**]
TO BE DEFINED !!!

feature_shape = <shape> [**box**]
TO BE DEFINED !!!

feature_label = <string> [***undef***]
TO BE DEFINED !!!

show_feature_label = <boolean> [**off**]
TO BE DEFINED !!!

show_ribbons = <boolean> [**off**]
TO BE DEFINED !!!

ribbon_style = <ribbon> [**none**]
TO BE DEFINED !!!

feature_scale_height = <boolean> [**on**]
When this variable is **on**, height of the feature shapes is proportional to the score, ranging from minimum to maximum score values of the sequence to which the feature belongs.

feature_scale_color = <boolean> [**off**]
Feature shape is color filled with a color gradient which depends on feature score and ranges from white to **feature_color** definition, mapped from minimum score to maximum score of the sequence to which that feature belongs.

alignment_scale_width = <boolean> [**off**]
TO BE DEFINED !!!

alignment_scale_color = <boolean> [**off**]
TO BE DEFINED !!!

feature_layer = <integer> [***undef***]

Setting layer on annotation tiers where to draw this feature shape. By default all features are drawn on layer 0, which represents the bottomest layer. Higher layer values move features forward, this allows users to visualize features that were hidden by others if they were overlapping. GFF2APLOT sorts features prior visualization by acceptor, but before that it sorts by layer, so features having smaller acceptor coords and are longer than others can be placed on top. What it actually happens is that feature layers are contained into their group layer, it migth be seen as those feature layers are sub-layers of the group ones.

Imagine you have "exons" and the "mrna" features for a gene, and would like to display the "mrna" (which contains all the "exons" between its starting and final coordinates), as a lower —than the "exons"— box. If all feature had same layer you will see fragments of the "mrna" rising between each consecutive "exons". Increasing layer number for "mrna" while preserving layer number for "exons" will make "mrna" box to be fully drawn on top of the exons.

4.2.3 GFF-Group Attributes

hide = <boolean> [**off**]

TO BE DEFINED !!!

group_color = <color> [**fg**]

TO BE DEFINED !!!

group_shape = <group_shape> [**bracket**]

TO BE DEFINED !!!

show_group_limits = <boolean> [**off**]

TO BE DEFINED !!!

group_label = <string> [***undef***]

TO BE DEFINED !!!

show_group_label = <boolean> [**on**]

TO BE DEFINED !!!

group_layer = <integer> [***undef***]

Setting layer on annotation tiers where to draw this group shape. By default all groups are drawn on layer 0, which represents the bottomest layer. Higher layer values move features forward, this allows users to visualize groups that were hidden by others if they were overlapping. GFF2APLOT sorts groups prior visualization by acceptor, but before that, it sorts by layer, so groups having smaller acceptor coords and are longer than others can be forced to appear on top. This is done before sorting by layer all the features, so that, features for the choosen group are raised to the group layer. This means that you actually have two layer levels, the group and the feature layer levels.

Imagine you have "exons" and the "mrna" features for a gene, and would like to display the "mrna" (which contains all the "exons" between its starting and final coordinates), as a lower —than the "exons"— box. If all feature had same layer you will see fragments of the "mrna" rising between each consecutive "exons". Increasing layer number for "mrna" while preserving layer number for "exons" will make "mrna" box to be fully drawn on top of the exons.

feature_color = <color> [***undef***]

TO BE DEFINED !!!

ribbon_color = <color> [***undef***]
TO BE DEFINED !!!

4.2.4 GFF-Strand Attributes

hide = <boolean> [**off**]
TO BE DEFINED !!!

strand_layer = <integer> [***undef***]
TO BE DEFINED !!!

feature_color = <color> [***undef***]
TO BE DEFINED !!!

ribbon_color = <color> [***undef***]
TO BE DEFINED !!!

4.2.5 GFF-Source Attributes

hide = <boolean> [**off**]
TO BE DEFINED !!!

source_layer = <integer> [***undef***]
TO BE DEFINED !!!

feature_color = <color> [***undef***]
TO BE DEFINED !!!

ribbon_color = <color> [***undef***]
TO BE DEFINED !!!

4.2.6 GFF-Sequence Attributes

feature_color = <color> [***undef***]
TO BE DEFINED !!!

ribbon_color = <color> [***undef***]
TO BE DEFINED !!!

4.2.7 Special Customization Features

font = <font-alias> <font-name> [***undef***]
Record format for font special features is the following: font font-alias font-name where font-alias will serve to call this font in other customization variables section. As example, having font-alias set as palatino for a font-name defined as Palatino-Roman in the printer, you have to recall it as my_palatino.

color = <color-alias> <cyan> <magenta> <yellow> <black> [***undef***]

Record format for color special features is the following: color <color-alias> <cyan> <magenta> <yellow> <black> <cyan>, <magenta>, <yellow> and <black> correspond to each color amount that is required to produce the desired CMYK color.

box = <Xori> <Xend> <Yori> <Yend> [L:<line_color>] [***undef***]

TO BE DEFINED !!!

circle = <Cx> <Cy> <Rx> <Ry> [A:<angle>] [L:<line_color>] [***undef***]

TO BE DEFINED !!!

arrow = <Cx> <Cy> <length> [A:<angle>] [L:<line_color>] [S:<line_style>] [***undef***]

TO BE DEFINED !!!

text = <Cx> <Cy> "<string>" [A:<angle>] [N:<font_name>] [Z:<font_size>] [***undef***]

TO BE DEFINED !!!

Chapter 5

A Practical Approach to GFF2APLOT

This chapter is intended to show how to use GFF2APLOT to visualize

Further tutorials will be find at:

`http://genome.imim.es/software/gfftools/`

Appendix A

GFF2APLOT Reference Guide

-h, **--help**	Showing the command-line help (and exit).
--version	Shows current version and exits from program.
-v, **--verbose**	Verbose mode, a full report is sent to standard error.
-V, **--logs-filename** <filename>	Report is written to a log file.
-q, **--quiet**	Quiet mode, messages/warnings disabled (only ERRORS shown).
-P, **--page-bbox** <width,height>	Defining arbitrary page formats.
-p, **--page-size** <format_name>	Setting a page size (see table A.3).
--margin-left <length> **--margin-right** <length> **--margin-top** <length> **--margin-bottom** <length>	Setting page margins (default is 1cm each).
-B, **--background-color** <color>	Setting background color for the page (default is **white**).
-F, **--foreground-color** <color>	Setting foreground color for the page (default is **black**).
-T, **--title** <string>	Setting figure title to <string>.
-t, **--subtitle** <string>	Setting subtitle to <string>.
-X, **--x-label** <string>	<string>.
-Y, **--y-label** <string>	<string>.
-L, **--percent-box-label** <string>	<string>.
-l, **--extra-box-label** <string>	<string>.
-x, **--x-sequence-coords** <pos..pos>	**TO BE DEFINED !!!**
-S, **--start-x-sequence** <pos>	**TO BE DEFINED !!!**
-E, **--end-x-sequence** <pos>	**TO BE DEFINED !!!**
-y, **--y-sequence-coords** <pos..pos>	**TO BE DEFINED !!!**
-s, **--start-y-sequence** <pos>	**TO BE DEFINED !!!**
-e, **--end-y-sequence** <pos>	**TO BE DEFINED !!!**
--x-sequence-zoom <pos..pos>	**TO BE DEFINED !!!**
--y-sequence-zoom <pos..pos>	**TO BE DEFINED !!!**
-Z, **--zoom**	**TO BE DEFINED !!!**
-z, **--zoom-area**	**TO BE DEFINED !!!**
-A, **--alignment-name** <seqXname:seqYname>	Selects <seqXname:seqYname> alignment.
-N, **--x-sequence-name** <seqXname>	Selects which sequence to plot on X-axis.
-n, **--y-sequence-name** <seqYname>	Selects which sequence to plot on Y-axis.
-r, **--aplot-xy-noteq**	**TO BE DEFINED !!!**
-R, **--xy-axes-scale** <X/Y ratio>	**TO BE DEFINED !!!**
-W, **--aln-scale-width**	**TO BE DEFINED !!!**
-w, **--aln-scale-color**	**TO BE DEFINED !!!**
-K, **--show-ribbons** <ribbon-type>	**TO BE DEFINED !!!**
-G, **--show-grid**	**TO BE DEFINED !!!**
-I, **--show-percent-box**	**TO BE DEFINED !!!**
-i, **--hide-percent-box**	**TO BE DEFINED !!!**
-O, **--show-extra-box**	**TO BE DEFINED !!!**
-o, **--hide-extra-box**	**TO BE DEFINED !!!**
-D, **--aplot-box-color** <color>	**TO BE DEFINED !!!**
-d, **--percent-box-color** <color>	**TO BE DEFINED !!!**
-b, **--extra-box-color** <color>	**TO BE DEFINED !!!**
--nopswarnings	Switch off warnings on final PS figure.
-a, **--hide-credits**	Switch off program credits line on plot.
--layout-var '<variable=value>' **--sequence-var** '<sequence::variable=value>' **--source-var** '<source::variable=value>' **--strand-var** '<strand::variable=value>' **--group-var** '<group::variable=value>' **--feature-var** '<feature::variable=value>'	Set a GFF-element customization variable from command-line.
-C, **--custom-filename** <filename>	Read customization parameters from file.
-g, **--hide-grid**	**TO BE DEFINED !!!**

NOTE:	**When a parameter is required, it applies for both short and long options.**
<int>	An integer value.
<float>	A float value.
<string>	A free text string, single or double-quoted if special chars or white-spaces/tabs are present respectively.
<format>	Page format, see available values on Appendix **??** table.
<color>	A color name chosen from table on Appendix **??**.
<file>	A valid file name (including path if necessary).

PAGE LAYOUT

page_bbox	***undef***	Defining arbitrary page formats. Overrides any setting for **page_size**.
page_size	**a4**	Sets a standard page size, available format names are listed in table A.3.
margin_left	**1cm**	
margin_right	**1cm**	
margin_top	**1cm**	
margin_bottom	**1cm**	Setting page margins (default is 1cm each).
background_color	**white**	Setting background color for the page. Available colors are listed on table A.1.
foreground_color	**black**	Setting foreground color for the page. Find available colors on table A.1.

ZOOM OPTIONS

x_sequence_coords	***undef***	**TO BE DEFINED !!!**
x_sequence_start	***undef***	**TO BE DEFINED !!!**
x_sequence_end	***undef***	**TO BE DEFINED !!!**
y_sequence_coords	***..***	**TO BE DEFINED !!!**
y_sequence_start	***undef***	**TO BE DEFINED !!!**
y_sequence_end	***undef***	**TO BE DEFINED !!!**
x_sequence_zoom	***undef***	**TO BE DEFINED !!!**
x_sequence_zoom_start	***undef***	**TO BE DEFINED !!!**
x_sequence_zoom_end	***undef***	**TO BE DEFINED !!!**
y_sequence_zoom	***undef***	**TO BE DEFINED !!!**
y_sequence_zoom_start	***undef***	**TO BE DEFINED !!!**
y_sequence_zoom_end	***undef***	**TO BE DEFINED !!!**
zoom	**off**	**TO BE DEFINED !!!**
zoom-area	**off**	**TO BE DEFINED !!!**
zoom_marks	**off**	**TO BE DEFINED !!!**
zoom_area_mark_width	**2pt**	**TO BE DEFINED !!!**
zoom_area_mark_style	**solid**	**TO BE DEFINED !!!**
zoom_area_mark_color	**lightred**	**TO BE DEFINED !!!**
zoom_area_fill_color	***undef***	**TO BE DEFINED !!!**

title	***undef***	Setting figure title to <string>.
show_title	**on**	Switching on/off title from plot.
title_font	**helvetica-bold**	Sets title font, see available fonts at **??**.
title_fontsize	**24pt**	Sets title fontsize, <length> can be in pt, mm, cm or in (default is points if no units are given).
subtitle	***undef***	Setting subtitle to <string>.
show_subtitle	**on**	Switching on/off subtitle from plot.
subtitle_font	**helvetica**	Sets subtitle font, see available fonts at **??**.
subtitle_fontsize	**16pt**	Sets subtitle fontsize, <length> can be in pt, mm, cm or in (default is points if no units are given).
x_label	***undef***	<string>.
show_x_label	**on**	Switching on/off subtitle from plot.
x_label_font	**helvetica-bold**	Sets X-label font, see available fonts at **??**.
x_label_fontsize	**12pt**	Sets X-label fontsize, <length> can be in pt, mm, cm or in (default is points if no units are given).
y_label	***undef***	<string>.
show_y_label	**on**	Switching on/off subtitle from plot.
y_label_font	**helvetica-bold**	Sets Y-label font, see available fonts at **??**.
y_label_fontsize	**12pt**	Sets Y-label fontsize, <length> can be in pt, mm, cm or in (default is points if no units are given).
show_percent_box_label	**on**	**TO BE DEFINED !!!**
percent_box_label	***undef***	**TO BE DEFINED !!!**
percent_box_label_font	**helvetica-bold**	Sets percent-box main label font.
percent_box_label_fontsize	**12pt**	Sets percent-box main label fontsize.
show_percent_box_sublabel	**on**	**TO BE DEFINED !!!**
percent_box_sublabel	***undef***	**TO BE DEFINED !!!**
percent_box_label_font	**helvetica**	Sets percent-box sublabel font.
percent_box_label_fontsize	**9pt**	Sets percent-box sublabel fontsize.
show_extra_box_label	**on**	**TO BE DEFINED !!!**
extra_box_label	***undef***	**TO BE DEFINED !!!**
extra_box_label_font	**helvetica-bold**	Sets extra-box main label font.
extra_box_label_fontsize	**10pt**	Sets extra-box main label fontsize.
show_extra_box_sublabel	**on**	**TO BE DEFINED !!!**
extra_box_sublabel	***undef***	**TO BE DEFINED !!!**
extra_box_sublabel_font	**helvetica**	Sets extra-box sublabel font.
extra_box_sublabel_fontsize	**9pt**	Sets extra-box sublabel fontsize.

show_feature_label	**on**	**TO BE DEFINED !!!**
feature_label_font	**helvetica**	**TO BE DEFINED !!!**
feature_label_fontsize	**6pt**	**TO BE DEFINED !!!**
feature_x_label_length	***undef***	**TO BE DEFINED !!!**
feature_x_label_angle	0°	**TO BE DEFINED !!!**
feature_x_label_rotate	**off**	**TO BE DEFINED !!!**
feature_y_label_length	***undef***	**TO BE DEFINED !!!**
feature_y_label_angle	0°	**TO BE DEFINED !!!**
feature_y_label_rotate	**on**	**TO BE DEFINED !!!**
show_group_label	**on**	**TO BE DEFINED !!!**
group_label_font	**helvetica**	**TO BE DEFINED !!!**
group_label_fontsize	**8pt**	**TO BE DEFINED !!!**
group_x_label_length	***undef***	**TO BE DEFINED !!!**
group_x_label_angle	0°	**TO BE DEFINED !!!**
group_x_label_rotate	**off**	**TO BE DEFINED !!!**
group_y_label_length	***undef***	**TO BE DEFINED !!!**
group_y_label_angle	0°	**TO BE DEFINED !!!**
group_y_label_rotate	**on**	**TO BE DEFINED !!!**

show_tickmark_label	on	TO BE DEFINED !!!
show_only_bottom_ticks	off	TO BE DEFINED !!!
show_aplot_x_ticks	on	TO BE DEFINED !!!
show_aplot_y_ticks	on	TO BE DEFINED !!!
show_percent_x_ticks	on	TO BE DEFINED !!!
show_percent_y_ticks	on	TO BE DEFINED !!!
show_extrabox_x_ticks	on	TO BE DEFINED !!!
show_extrabox_y_ticks	on	TO BE DEFINED !!!
aplot_major_tickmark	2	TO BE DEFINED !!!
aplot_minor_tickmark	5	TO BE DEFINED !!!
aplot_score_range	*undef*	TO BE DEFINED !!!
percent_major_tickmark	*undef*	TO BE DEFINED !!!
percent_minor_tickmark	4	TO BE DEFINED !!!
percent_box_score_range	*undef*	TO BE DEFINED !!!
extra_major_tickmark	2	TO BE DEFINED !!!
extra_minor_tickmark	5	TO BE DEFINED !!!
extra_box_score_range	*undef*	TO BE DEFINED !!!
major_tickmark_nucleotide	*undef*	TO BE DEFINED !!!
minor_tickmark_nucleotide	*undef*	TO BE DEFINED !!!
major_tickmark_score	*undef*	TO BE DEFINED !!!
minor_tickmark_score	*undef*	TO BE DEFINED !!!

Aplot Layout

alignment_name	***undef***	Selects <seqXname:seqYname> alignment (useful when input contain many alignments).
x_sequence_name	***undef***	Selects which sequence annotation is going to be plotted on X-axis.
y_sequence_name	***undef***	Selects which sequence annotation is going to be plotted on Y-axis.
aplot_xy_same_length	**on**	**TO BE DEFINED !!!**
aplot_xy_scale	***undef***	**TO BE DEFINED !!!**
alignment_scale_width	**off**	**TO BE DEFINED !!!**
alignment_scale_color	**off**	**TO BE DEFINED !!!**
show_ribbons	***undef***	**TO BE DEFINED !!!**
show_grid	**off**	**TO BE DEFINED !!!**
show_percent_box_grid	**on**	**TO BE DEFINED !!!**
show_percent_box	**off**	**TO BE DEFINED !!!**
show_extra_box	**off**	**TO BE DEFINED !!!**
aplot_box_bgcolor	**bg**	**TO BE DEFINED !!!**
percent_box_bgcolor	**bg**	**TO BE DEFINED !!!**
extra_box_bgcolor	**bg**	**TO BE DEFINED !!!**
percent_box_height	***undef***	**TO BE DEFINED !!!**
extra_box_height	***undef***	**TO BE DEFINED !!!**
ribbon_color_merge	***undef***	Enabling pattern color fill for projection ribbons to emulate color blending when horizontal and vertical ribbons overlap.
color_merge_factor	**0.5**	Setting the pattern point size for the color blend emulation.
ribbon_style	***undef***	**TO BE DEFINED !!!**
ribbon_color	***undef***	**TO BE DEFINED !!!**

General Definitions

align_tag	**target**	**TO BE DEFINED !!!**
vector_tag	**vector**	**TO BE DEFINED !!!**
label_tag	**id**	**TO BE DEFINED !!!**
start_tag	**start**	**TO BE DEFINED !!!**
end_tag	**end**	**TO BE DEFINED !!!**
score_tag	**e_value**	**TO BE DEFINED !!!**
strand_tag	**strand**	**TO BE DEFINED !!!**
frame_tag	**frame**	**TO BE DEFINED !!!**
scotype_tag	**vectype**	**TO BE DEFINED !!!**
window_tag	**window**	**TO BE DEFINED !!!**
step_tag	**step**	**TO BE DEFINED !!!**
scoary_tag	**scores**	**TO BE DEFINED !!!**

GFF-Feature Attributes

hide	**off**	Hide the given GFF feature, does not plot it in the current figure.
feature_color	**fg**	Fill feature shape with this color.
alignment_color	**fg**	Use this color for drawing the alignment lines defined by such GFF feature.
ribbon_color	**verylightgrey**	Fill feature ribbon with this color if they are shown in the current plot.
feature_shape	**box**	Choose current feature shape.
feature_label	***undef***	**TO BE DEFINED !!!**
show_feature_label	**off**	**TO BE DEFINED !!!**
show_ribbons	**off**	**TO BE DEFINED !!!**
ribbon_style	**none**	**TO BE DEFINED !!!**
feature_scale_height	**on**	Feature shape height depends on score by default.
feature_scale_color	**off**	Feature shape is color filled with a color gradient.
alignment_scale_width	**off**	Drawing alignment lines while making their width score dependent.
alignment_scale_color	**off**	Drawing alignment lines while painting with its color as a score dependent gradient.
feature_layer	***undef***	Setting layer on annotation tiers where to draw this feature shape.

GFF-Group Attributes

hide	**off**	Hide the given group, does not plot it in the current figure.
group_color	**fg**	**TO BE DEFINED !!!**
group_shape	**bracket**	**TO BE DEFINED !!!**
show_group_limits	**off**	**TO BE DEFINED !!!**
group_label	***undef***	**TO BE DEFINED !!!**
show_group_label	**on**	**TO BE DEFINED !!!**
group_layer	***undef***	Setting layer on annotation tiers where to draw the given group.
feature_color	***undef***	Fill shapes for all elements of that group with this color.
ribbon_color	***undef***	Setting fill color of aplot ribbons for all the features of that group showing them.

GFF-Strand Attributes

hide	**off**	Hide the given strand, does not plot it in the current figure.
strand_layer	***undef***	Setting layer on annotation tiers where to draw the given strand.
feature_color	***undef***	Fill shapes for all elements of that strand with the given color.
ribbon_color	***undef***	Setting fill color of aplot ribbons for all features of that strand showing them.

GFF-SOURCE ATTRIBUTES

hide	**off**	Hide the given source, does not plot it in the current figure.
source_layer	***undef***	Setting layer on annotation tiers where to draw the given source.
feature_color	***undef***	Fill shapes for all elements of the selected source with that color.
ribbon_color	***undef***	Setting fill color of aplot ribbons for all the features within the given source that show them.

GFF-SEQUENCE ATTRIBUTES

feature_color	***undef***	Fill shapes for all elements of the given sequence with that color.
ribbon_color	***undef***	Setting fill color of aplot ribbons for all the sequence features that show them.

SPECIAL CUSTOMIZATION FEATURES

font	***undef***	**TO BE DEFINED !!!**
color	***undef***	**TO BE DEFINED !!!**
box	***undef***	**TO BE DEFINED !!!**
circle	***undef***	**TO BE DEFINED !!!**
arrow	***undef***	**TO BE DEFINED !!!**
text	***undef***	**TO BE DEFINED !!!**

black	0.00	0.00	0.00	1.00
verydeepgrey	0.00	0.00	0.00	0.90
deepgrey	0.00	0.00	0.00	0.80
verydarkgrey	0.00	0.00	0.00	0.70
darkgrey	0.00	0.00	0.00	0.60
grey	0.00	0.00	0.00	0.50
lightgrey	0.00	0.00	0.00	0.40
verylightgrey	0.00	0.00	0.00	0.30
palegrey	0.00	0.00	0.00	0.20
verypalegrey	0.00	0.00	0.00	0.10
white	0.00	0.00	0.00	0.00
verydeeppink	0.00	0.60	0.15	0.35
deeppink	0.00	0.75	0.20	0.15
verydarkpink	0.00	0.90	0.25	0.00
darkpink	0.00	0.75	0.30	0.00
pink	0.00	0.60	0.25	0.00
lightpink	0.00	0.45	0.20	0.00
verylightpink	0.00	0.30	0.15	0.00
palepink	0.00	0.20	0.10	0.00
verypalepink	0.00	0.10	0.05	0.00
verydeepmagenta	0.00	0.60	0.00	0.40
deepmagenta	0.00	0.75	0.00	0.20
verydarkmagenta	0.00	0.90	0.00	0.00
darkmagenta	0.00	0.75	0.00	0.00
magenta	0.00	0.60	0.00	0.00
lightmagenta	0.00	0.45	0.00	0.00
verylightmagenta	0.00	0.30	0.00	0.00
palemagenta	0.00	0.20	0.00	0.00
verypalemagenta	0.00	0.10	0.00	0.00
verydeepviolet	0.30	0.60	0.00	0.40
deepviolet	0.35	0.75	0.00	0.20
verydarkviolet	0.45	0.90	0.00	0.00
darkviolet	0.35	0.75	0.00	0.00
violet	0.30	0.60	0.00	0.00
lightviolet	0.22	0.45	0.00	0.00
verylightviolet	0.15	0.30	0.00	0.00
paleviolet	0.10	0.20	0.00	0.00
verypaleviolet	0.05	0.10	0.00	0.00
verydeepblue	0.60	0.60	0.00	0.40
deepblue	0.75	0.75	0.00	0.20
verydarkblue	0.90	0.90	0.00	0.00
darkblue	0.75	0.75	0.00	0.00
blue	0.60	0.60	0.00	0.00
lightblue	0.45	0.45	0.00	0.00
verylightblue	0.30	0.30	0.00	0.00
paleblue	0.20	0.20	0.00	0.00
verypaleblue	0.10	0.10	0.00	0.00
verydeepskyblue	0.60	0.40	0.00	0.40
deepskyblue	0.75	0.50	0.00	0.20
verydarkskyblue	0.90	0.60	0.00	0.00
darkskyblue	0.75	0.50	0.00	0.00
skyblue	0.60	0.40	0.00	0.00
lightskyblue	0.45	0.30	0.00	0.00
verylightskyblue	0.30	0.22	0.00	0.00
paleskyblue	0.20	0.14	0.00	0.00
verypaleskyblue	0.10	0.07	0.00	0.00
verydeepcyan	0.60	0.00	0.00	0.40
deepcyan	0.75	0.00	0.00	0.20
verydarkcyan	0.90	0.00	0.00	0.00
darkcyan	0.75	0.00	0.00	0.00
cyan	0.60	0.00	0.00	0.00
lightcyan	0.45	0.00	0.00	0.00
verylightcyan	0.30	0.00	0.00	0.00
palecyan	0.20	0.00	0.00	0.00
verypalecyan	0.10	0.00	0.00	0.00

Table A.1: GFF2APLOT CMYK color definition table and Color Names (continues on next page).

verydeepseagreen	0.60	0.00	0.15	0.40
deepseagreen	0.75	0.00	0.20	0.20
verydarkseagreen	0.90	0.00	0.25	0.00
darkseagreen	0.75	0.00	0.30	0.00
seagreen	0.60	0.00	0.25	0.00
lightseagreen	0.45	0.00	0.20	0.00
verylightseagreen	0.30	0.00	0.15	0.00
paleseagreen	0.20	0.00	0.10	0.00
verypaleseagreen	0.10	0.00	0.05	0.00
verydeepgreen	0.60	0.00	0.60	0.40
deepgreen	0.75	0.00	0.75	0.20
verydarkgreen	0.90	0.00	0.90	0.00
darkgreen	0.75	0.00	0.75	0.00
green	0.60	0.00	0.60	0.00
lightgreen	0.45	0.00	0.45	0.00
verylightgreen	0.30	0.00	0.30	0.00
palegreen	0.20	0.00	0.20	0.00
verypalegreen	0.10	0.00	0.10	0.00
verydeeplimegreen	0.15	0.00	0.60	0.40
deeplimegreen	0.20	0.00	0.75	0.20
verydarklimegreen	0.25	0.00	0.90	0.00
darklimegreen	0.30	0.00	0.75	0.00
limegreen	0.25	0.00	0.60	0.00
lightlimegreen	0.20	0.00	0.45	0.00
verylightlimegreen	0.15	0.00	0.30	0.00
palelimegreen	0.10	0.00	0.20	0.00
verypalelimegreen	0.05	0.00	0.10	0.00

verydeepyellow	0.00	0.00	0.60	0.40
deepyellow	0.00	0.00	0.75	0.20
verydarkyellow	0.00	0.00	0.90	0.00
darkyellow	0.00	0.00	0.75	0.00
yellow	0.00	0.00	0.60	0.00
lightyellow	0.00	0.00	0.45	0.00
verylightyellow	0.00	0.00	0.30	0.00
paleyellow	0.00	0.00	0.20	0.00
verypaleyellow	0.00	0.00	0.10	0.00
verydeeporange	0.00	0.30	0.80	0.40
deeporange	0.00	0.32	0.85	0.20
verydarkorange	0.00	0.35	0.90	0.00
darkorange	0.00	0.30	0.75	0.00
orange	0.00	0.25	0.60	0.00
lightorange	0.00	0.20	0.45	0.00
verylightorange	0.00	0.15	0.30	0.00
paleorange	0.00	0.10	0.20	0.00
verypaleorange	0.00	0.05	0.10	0.00
verydeepred	0.00	0.60	0.60	0.40
deepred	0.00	0.75	0.75	0.20
verydarkred	0.00	0.90	0.90	0.00
darkred	0.00	0.75	0.75	0.00
red	0.00	0.60	0.60	0.00
lightred	0.00	0.45	0.45	0.00
verylightred	0.00	0.30	0.30	0.00
palered	0.00	0.20	0.20	0.00
verypalered	0.00	0.10	0.10	0.00
verydeepbrown	0.35	0.85	0.90	0.35
deepbrown	0.30	0.75	0.90	0.25
verydarkbrown	0.25	0.70	0.90	0.15
darkbrown	0.20	0.60	0.75	0.05
brown	0.17	0.50	0.65	0.00
lightbrown	0.15	0.40	0.55	0.00
verylightbrown	0.12	0.28	0.45	0.00
palebrown	0.10	0.18	0.30	0.00
verypalebrown	0.05	0.10	0.20	0.00

Table A.2: GFF2APLOT CMYK color definition table and Color Names (continued from previous page).

PAGE FORMAT	PAGE SIZE (in points)		(in cms)		(in inches)	
a0	2384	3370	84.1	118.9	33.1	46.8
a1	1684	2384	59.4	84.1	23.4	33.1
a2	1190	1684	42.0	59.4	16.5	23.4
a3	842	1190	29.7	42.0	11.7	16.5
a4	595	842	21.0	29.7	8.3	11.7
a5	420	595	14.8	21.0	5.8	8.3
a6	297	420	10.5	14.8	4.1	5.8
a7	210	297	7.4	10.5	2.9	4.1
a8	148	210	5.2	7.4	2.1	2.9
a9	105	148	3.7	5.2	1.5	2.1
a10	73	105	2.6	3.7	1.0	1.5
b0	2920	4127	103.0	145.6	40.6	57.3
b1	2064	2920	72.8	103.0	28.7	40.6
b2	1460	2064	51.5	72.8	20.3	28.7
b3	1032	1460	36.4	51.5	14.3	20.3
b4	729	1032	25.7	36.4	10.1	14.3
b5	516	729	18.2	25.7	7.2	10.1
b6	363	516	12.8	18.2	5.0	7.2
b7	258	363	9.1	12.8	3.6	5.0
b8	181	258	6.4	9.1	2.5	3.6
b9	127	181	4.5	6.4	1.8	2.5
b10	91	127	3.2	4.5	1.3	1.8
executive	540	720	19.0	25.4	7.5	10.0
folio	612	936	21.6	33.0	8.5	13.0
legal	612	1008	21.6	35.6	8.5	14.0
letter	612	792	21.6	27.9	8.5	11.0
quarto	610	780	21.5	27.5	8.5	10.8
statement	396	612	14.0	21.6	5.5	8.5
10x14	720	1008	25.4	35.6	10.0	14.0
ledger	1224	792	43.2	27.9	17.0	11.0
tabloid	792	1224	27.9	43.2	11.0	17.0

Table A.3: Page Sizes defined in GFF2APLOT.

28.35 pt	≡	1 cm
72.00 pt	≡	1 inch

Font	Sample
`Times-Roman`	ABCDEFGHIJKLMNOPQRSTUVWXYZ abcdefghijklmnopqrstuvwxyz 1234567890 @#$%&_-+*?!\/|[]{}<>()
`Times-Italic`	*ABCDEFGHIJKLMNOPQRSTUVWXYZ* *abcdefghijklmnopqrstuvwxyz* *1234567890 @#$%&_-+*?!\/|[]{}<>()*
`Times-Bold`	**ABCDEFGHIJKLMNOPQRSTUVWXYZ** **abcdefghijklmnopqrstuvwxyz** **1234567890 @#$%&_-+*?!\/|[]{}<>()**
`Times-BoldItalic`	***ABCDEFGHIJKLMNOPQRSTUVWXYZ*** ***abcdefghijklmnopqrstuvwxyz*** ***1234567890 @#$%&_-+*?!\/|[]{}<>()***
`Helvetica`	ABCDEFGHIJKLMNOPQRSTUVWXYZ abcdefghijklmnopqrstuvwxyz 1234567890 @#$%&_-+*?!\/|[]{}<>()
`Helvetica-Oblique`	*ABCDEFGHIJKLMNOPQRSTUVWXYZ* *abcdefghijklmnopqrstuvwxyz* *1234567890 @#$%&_-+*?!\/|[]{}<>()*
`Helvetica-Bold`	**ABCDEFGHIJKLMNOPQRSTUVWXYZ** **abcdefghijklmnopqrstuvwxyz** **1234567890 @#$%&_-+*?!\/|[]{}<>()**
`Helvetica-BoldOblique`	***ABCDEFGHIJKLMNOPQRSTUVWXYZ*** ***abcdefghijklmnopqrstuvwxyz*** ***1234567890 @#$%&_-+*?!\/|[]{}<>()***
`Courier`	`ABCDEFGHIJKLMNOPQRSTUVWXYZ` `abcdefghijklmnopqrstuvwxyz` `1234567890 @#$%&_-+*?!\/|[]{}<>()`
`Courier-Oblique`	*ABCDEFGHIJKLMNOPQRSTUVWXYZ* *abcdefghijklmnopqrstuvwxyz* *1234567890 @#$%&_-+*?!\/|[]{}<>()*
`Courier-Bold`	**ABCDEFGHIJKLMNOPQRSTUVWXYZ** **abcdefghijklmnopqrstuvwxyz** **1234567890 @#$%&_-+*?!\/|[]{}<>()**
`Courier-BoldOblique`	***ABCDEFGHIJKLMNOPQRSTUVWXYZ*** ***abcdefghijklmnopqrstuvwxyz*** ***1234567890 @#$%&_-+*?!\/|[]{}<>()***

Figure A.1: GFF2APLOT only provides the default POSTSCRIPT fonts, those font names are available for variables which set labels font. Font size was set to 10 points for the samples shown above. **default** is an alias for **Times-Roman** font, and all font names are case-insensitive. These settings apply to all the variables ending up with the **_font** suffix.

1 pt
ABCDEFGHIJKLMNOPQRSTUVWXYZ
abcdefghijklmnopqrstuvwxyz
1234567890 @#$%&_-+*?!\/|[]{}<>()

2 pt
ABCDEFGHIJKLMNOPQRSTUVWXYZ
abcdefghijklmnopqrstuvwxyz
1234567890 @#$%&_-+*?!\/|[]{}<>()

4 pt
ABCDEFGHIJKLMNOPQRSTUVWXYZ
abcdefghijklmnopqrstuvwxyz
1234567890 @#$%&_-+*?!\/|[]{}<>()

6 pt
ABCDEFGHIJKLMNOPQRSTUVWXYZ
abcdefghijklmnopqrstuvwxyz
1234567890 @#$%&_-+*?!\/|[]{}<>()

8 pt
ABCDEFGHIJKLMNOPQRSTUVWXYZ
abcdefghijklmnopqrstuvwxyz
1234567890 @#$%&_-+*?!\/|[]{}<>()

10 pt
ABCDEFGHIJKLMNOPQRSTUVWXYZ
abcdefghijklmnopqrstuvwxyz
1234567890 @#$%&_-+*?!\/|[]{}<>()

12 pt
ABCDEFGHIJKLMNOPQRSTUVWXYZ
abcdefghijklmnopqrstuvwxyz
1234567890 @#$%&_-+*?!\/|[]{}<>()

14 pt
ABCDEFGHIJKLMNOPQRSTUVWXYZ
abcdefghijklmnopqrstuvwxyz
1234567890 @#$%&_-+*?!\/|[]{}<>()

16 pt
ABCDEFGHIJKLMNOPQRSTUVWXYZ
abcdefghijklmnopqrstuvwxyz
1234567890 @#$%&_-+*?!\/|[]{}<>()

18 pt
ABCDEFGHIJKLMNOPQRSTUVWXYZ
abcdefghijklmnopqrstuvwxyz
1234567890 @#$%&_-+*?!\/|[]{}<>()

20 pt
ABCDEFGHIJKLMNOPQRSTUVWXYZ
abcdefghijklmnopqrstuvwxyz
1234567890 @#$%&_-+*?!\/|[]{}<>()

25 pt
ABCDEFGHIJKLMNOPQRSTUVWX
abcdefghijklmnopqrstuvwxyz
1234567890 @#$%&_-+*?!\/|[]{}<>()

Figure A.2: **Helvetica** font scaled at diferent font sizes. Those values can be applied to any of the variables ending with the suffix **_fontsize**.

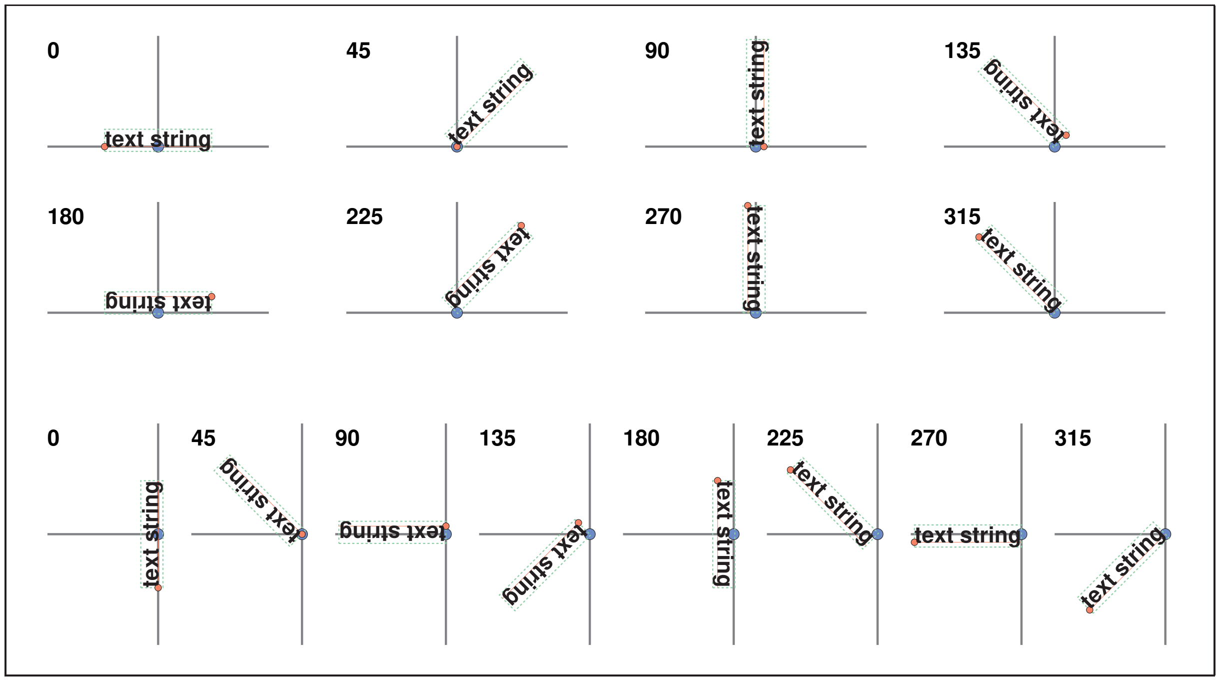

Figure A.3: Group and feature labels string alignment depends on angle. The upper two rows show examples for horizontal axes labels (**feature_x_label_angle** and **group_x_label_angle**), while the lower one visualizes same angles for vertical axes labels (**feature_y_label_angle** and **group_y_label_angle**).
The angle, in degrees, used is shown on the left upper corner of each plot. The blue dot represents the insertion point for the label on the annotation axes. As it can be seen here, we cannot print the labels below the main reference line, the grey axes, because we do not want to invade the alignment box area. The bounding box for the label string is delimited as a green dotted line, the string baseline is shown as a red straight line underlining the label and, finally, the insertion point (used by the POSTSCRIPT `show` function) is shown as a red dot at the begining of the label.