PROGRAM NAME: # multigeneplots.pl

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DESCRIPTION: From a table containing gene identifiers, start and end coords, and the strand,the program loops through a set of GFF files, making the plots for each single dataset using `gff2ps`. Once the PostScript figures have been obtained, it can convert them to a bitmap graphical format (say here JPEG or PNG). It must compute the width of every plot according to gene length.

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1 Introduction

1.1 Program description

1.2 Input

First input file must contain the gene information table which program will use to chop off the input GFF files for the single gene plots. Those GFF files may contain not only records corresponding to the genes listed in that table, other sources (vector support will be implemented later).

1.3 Output

Basic output will be a set of PostScript files containing a single gene each. It will save files for each gene GFF-records set.

1.4 To Do

- [*Section* 2.1, *page* 3]
  This is a first draft of the multigeneplots.pl.

- [*Section* 2.1, *page* 3]
  Using GetOPTS. New options:
  –save-gff to save GFF-records set for each gene.
  –jpeg to produce jpeg from PostScript output.
  –png to produce png from PostScript output.
  –pdf to produce pdf from PostScript output (can it be easily done???).
  –proportional-length
  –fixed-length
  –log-length
  –nucleotides-cm

2 Implementation

2a ⟨*Program Info* 2a⟩≡
```
my $PROGRAM = 'multigeneplots';
my $VERSION = '0.1_alpha';
```

2b ⟨*Prog USAGE* 2b⟩≡
```
$PROGRAM [options] < input_files > output_files
```

2c ⟨*Prog DESC* 2c⟩≡
```
A short description of what your program does.
```

2d ⟨*Program Description* 2d⟩≡
```
# #-----------------------------------------#
# #                          multigeneplots                          #
# #-----------------------------------------#
#
#  $PROGRAM [options] < input_files > output_files
#
#  Remember to put a short description of what your program does here...
#
#
#     Copyright (C) 2001 - Josep Francesc ABRIL FERRANDO
```

2.1 Program outline

2e ⟨*multigeneplots* 2e⟩≡
```
⟨PERL shebang 5a⟩
#
# MODULES
#
⟨Use Modules 2f⟩
#
# VARIABLES
#
⟨Global Vars 2g⟩
#
# MAIN LOOP
#
⟨Main Loop 2h⟩
#
# FUNCTIONS
#
⟨Functions 2i⟩
```

2f ⟨*Use Modules* 2f⟩≡

2g ⟨*Global Vars* 2g⟩≡

2h ⟨*Main Loop* 2h⟩≡
```
exit(0);
```

2i ⟨*Functions* 2i⟩≡
```
sub {
} #
```

TO DO

- This is a first draft of the multigeneplots.pl.

TO DO

- Using GetOPTS. New options:
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  –jpeg to produce jpeg from PostScript output.
  –png to produce png from PostScript output.
  –pdf to produce pdf from PostScript output (can it be easily done???).
  –proportional-length
  –fixed-length
  –log-length
  –nucleotides-cm

A empty appendix section

A.1 empty appendix subsection

B Common code blocks

B.1 PERL scripts

5a ⟨*PERL shebang* 5a⟩≡
```
#!/usr/bin/perl -w
# This is perl, version 5.005_03 built for i386-linux
#
⟨Program Description 2d⟩
#
⟨GNU License 7d⟩
#
⟨Version Control Id Tag 7c⟩
#
use strict;
#
⟨Program Info 2a⟩
my $DATE = localtime;
my $USER = defined($ENV{USER}) ? $ENV{USER} : 'Child Process';
my $host = `hostname`;
chomp($host);
#
```

5b ⟨*Global Constants - Boolean* 5b⟩≡
```
my ($T,$F) = (1,0); # for 'T'rue and 'F'alse
```

B.1.1 Timing our scripts

The '`Benchmark`' module encapsulates a number of routines to help to figure out how long it takes to execute a piece of code and the whole script.

5c ⟨*Use Modules - Benchmark* 5c⟩≡
```
use Benchmark;
  ⟨Timer ON 5d⟩
```

See '`man Benchmark`' for further info about this package. We set an array to keep record of timing for each section.

5d ⟨*Timer ON* 5d⟩≡
```
my @Timer = (new Benchmark);
```

5e ⟨*Common PERL subs - Benchmark* 5e⟩≡
```
sub timing() {
    push @Timer, (new Benchmark);
    # partial time
    $_[0] ||
        (return timestr(timediff($Timer[$#Timer],$Timer[($#Timer - 1)])));
    # total time
    return timestr(timediff($Timer[$#Timer],$Timer[0]));
} # timing
```

B.1.2 Printing complex Data Structures

With '`Data::Dumper`' we are able to pretty print complex data structures for debugging them.

5f ⟨*Use Modules - Dumper* 5f⟩≡
```
use Data::Dumper;
local $Data::Dumper::Purity = 0;
local $Data::Dumper::Deepcopy = 1;
```

B.1.3 Common functions

6a ⟨*Skip comments and empty records* 6a⟩≡
```
next if /^\#/o;
next if /^\s*$/o;
chomp;
```

6b ⟨*Common PERL subs - Min Max* 6b⟩≡
```
#
sub max() {
    my $z = shift @_;
    foreach my $l (@_) { $z = $l if $l > $z };
    return $z;
} # max
sub min() {
    my $z = shift @_;
    foreach my $l (@_) { $z = $l if $l < $z };
    return $z;
} # min
```

6c ⟨*Common PERL subs - Text fill* 6c⟩≡
```
#
sub fill_right() { $_[0].($_[2] x ($_[1] - length($_[0]))) }
sub fill_left()  { ($_[2] x ($_[1] - length($_[0]))).$_[0] }
sub fill_mid()   {
    my $l = length($_[0]);
    my $k = int(($_[1] - $l)/2);
    ($_[2] x $k).$_[0].($_[2] x ($_[1] - ($l+$k)));
} # fill_mid
```

These functions are used to report to STDERR a single char for each record processed (useful for reporting parsed records).

6d ⟨*Common PERL subs - Counter* 6d⟩≡
```
#
sub counter { # $_[0]~current_pos++ $_[1]~char
    print STDERR "$_[1]";
    (($_[0] % 50) == 0) && (print STDERR "[".&fill_left($_[0],6,"0")."]\n");
} # counter
#
sub counter_end { # $_[0]~current_pos   $_[1]~char
    (($_[0] % 50) != 0) && (print STDERR "[".&fill_left($_[0],6,"0")."]\n");
} # counter_end
```

6e ⟨*Global Vars - Counter* 6e⟩≡
```
my ($n,$c); # counter and char (for &counter function)
```

B.1.4 Common functions for reporting program processes

Function '`report`' requires that a hash variable '`%MessageList`' has been set, such hash contains the strings for each report message we will need. The first parameter for '`report`' is a key for that hash, in order to retrieve the message string, the other parameters passed are processed by the `sprintf` function on that string.

6f ⟨*Common PERL subs - STDERR* 6f⟩≡
```
sub report() { print STDERR sprintf($MessageList{ shift @_ },@_) }
```

The same happens to '`warn`' function which also requires a hash variable '`%ErrorList`' containing the error messages.

6g ⟨*Common PERL subs - STDERR* 6f⟩+≡
```
sub warn() { print STDERR sprintf($ErrorList{ shift @_ }, @_) }
```

B.2 BASH scripts

7a ⟨*BASH shebang* 7a⟩≡
```
#!/usr/bin/bash
# GNU bash, version 2.03.6(1)-release (i386-redhat-linux-gnu)
⟨Version Control Id Tag 7c⟩
#
SECONDS=0 # Reset Timing
# Which script are we running...
L="####################"
{ echo "$L$L$L$L";
  echo "### RUNNING [$0]";
  echo "### Current date:‘date‘";
  echo "###"; } 1>&2;
```

7b ⟨*BASH script end* 7b⟩≡
```
{ echo "###"; echo "### Execution time for [$0] : $SECONDS secs";
  echo "$L$L$L$L";
  echo ""; } 1>&2;
#
exit 0
```

B.3 Version control tags

This document is under Revision Control System (RCS). The version you are currently reading is the following:

7c ⟨*Version Control Id Tag* 7c⟩≡
```
# $Id: deploy.nw,v 1.12 2001/10/05 18:30:33 jabril Exp $
```

B.4 GNU General Public License

7d ⟨*GNU License* 7d⟩≡
```
# This program is free software; you can redistribute it and/or modify
# it under the terms of the GNU General Public License as published by
# the Free Software Foundation; either version 2 of the License, or
# (at your option) any later version.
#
# This program is distributed in the hope that it will be useful,
# but WITHOUT ANY WARRANTY; without even the implied warranty of
# MERCHANTABILITY or FITNESS FOR A PARTICULAR PURPOSE.  See the
# GNU General Public License for more details.
#
# You should have received a copy of the GNU General Public License
# along with this program; if not, write to the Free Software
# Foundation, Inc., 675 Mass Ave, Cambridge, MA 02139, USA.
#
# #-----------------------------------------#
```

C Extracting code blocks from this document

From this file we can obtain both the code and the documentation. The following instructions are needed:

C.1 Extracts Script code chunks from the NOWEB file

Remember when tangling that '-L' option allows you to include program line-numbering relative to original NOWEB file. Then the first line of the executable files is a comment, not a shebang, and must be removed to make scripts runnable.

8a ⟨*tangling* 8a⟩≡
```
# showing line numbering comments in program
notangle -L -R"multigeneplots" $WORK/$nwfile.nw | \
    perl -ne '$.>1 && print' | cpif $BIN/multigeneplots ;
chmod a+x $BIN/multigeneplots ;
```

8b ⟨*tangling* 8a⟩+≡
```
# reformating program with perltidy
notangle -R"multigeneplots" $WORK/$nwfile.nw | \
    perltidy - | cpif $BIN/multigeneplots ;
# html pretty-printing program with perltidy
notangle -R"multigeneplots" $WORK/$nwfile.nw | \
    perltidy -html - | cpif $DOCS/html/multigeneplots.html ;
#
```

C.2 Extracting different Config Files

8c ⟨*tangling* 8a⟩+≡
```
notangle -R"root" $WORK/$nwfile.nw | \
         cpif $DATA/root_config ;
```

C.3 Extracting documentation and LaTeX'ing it

8d ⟨*tangling* 8a⟩+≡
```
notangle -Rweaving  $WORK/$nwfile.nw | cpif $WORK/nw2tex ;
notangle -RLaTeXing $WORK/$nwfile.nw | cpif $WORK/ltx ;
chmod a+x $WORK/nw2tex $WORK/ltx;
```

8e ⟨*tangling complementary LaTeX files* 8e⟩≡
```
notangle -R"HIDE: LaTeX new definitions" $WORK/$nwfile.nw | cpif $DOCS/defs.tex ;
notangle -R"HIDE: TODO" $WORK/$nwfile.nw | cpif $DOCS/todo.tex ;
```

8f ⟨*weaving* 8f⟩≡
```
⟨BASH shebang 7a⟩
# weaving and LaTeXing
⟨BASH Environment Variables 9b⟩
⟨tangling complementary LaTeX files 8e⟩
noweave -v -t4 -delay -x -filter 'elide "HIDE: *"' \
        $WORK/$nwfile.nw | cpif $DOCS/$nwfile.tex ;
# noweave -t4 -delay -index $WORK/$nwfile.nw > $DOCS/$nwfile.tex
pushd $DOCS/ ;
#
latex $nwfile.tex ;
dvips $nwfile.dvi -o $nwfile.ps -t a4 ;
#
popd;
⟨BASH script end 7b⟩
```

9a ⟨*LaTeXing* 9a⟩≡
```
⟨BASH shebang 7a⟩
# only LaTeXing
⟨BASH Environment Variables 9b⟩
pushd $DOCS/ ;
#
echo "### RUNNING LaTeX on $nwfile.tex" 1>&2 ;
latex $nwfile.tex ;
latex $nwfile.tex ;
latex $nwfile.tex ;
dvips $nwfile.dvi -o $nwfile.ps -t a4 ;
#
# pdflatex $nwfile.tex ;
echo "### CONVERTING PS to PDF: $nwfile" 1>&2 ;
ps2pdf $nwfile.ps $nwfile.pdf ;
#
popd ;
⟨BASH script end 7b⟩
```

C.4 Defining working shell variables for the current project

9b ⟨*BASH Environment Variables* 9b⟩≡
```
#
# Setting Global Variables
WORK="/home/ug/jabril/development/softjabril/multigeneplots" ;
BIN="$WORK/bin" ;
PARAM="$BIN/param" ;
SRC="$WORK/src" ; # where to put the distributable files
DOCS="$WORK/docs" ;
DATA="$WORK/data" ;
TEST="$WORK/tests" ;
nwfile="multigeneplots" ;
export WORK BIN PARAM DOCS DATA nwfile ;
#
```

9c ⟨*tangling* 8a⟩+≡
```
#
# BASH Environment Variables
notangle -R'BASH Environment Variables' $WORK/$nwfile.nw | \
         cpif $WORK/.bash_VARS ;
source $WORK/.bash_VARS ;
#
```