

humangenome

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Abstract

Short description of your program here !!!

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2 Working on data

2.1 Command-line

1 $\langle BASH\ commands\ 1 \rangle \equiv$

#

A empty appendix section

A.1 empty appendix subsection

B Common code blocks

B.1 PERL scripts

```

3a  <PERL shebang 3a>≡
    #!/usr/bin/perl -w
    # This is perl, version 5.005_03 built for i386-linux
    #
    <Program Description (never defined)>
    #
    <GNU License (never defined)>
    #
    <Version Control Id Tag 5d>
    #
    use strict;
    #
    <Program Info (never defined)>
    my $DATE = localtime;
    my $USER = defined($ENV{USER}) ? $ENV{USER} : 'Child Process';
    my $host = `hostname`;
    chomp($host);
    #

3b  <Global Constants - Boolean 3b>≡
    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.

```

3c  <Use Modules - Benchmark 3c>≡
    use Benchmark;
    <Timer ON 3d>

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

3d  <Timer ON 3d>≡
    my @Timer = (new Benchmark);

3e  <Common PERL subs - Benchmark 3e>≡
    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.

```

3f  <Use Modules - Dumper 3f>≡
    use Data::Dumper;
    local $Data::Dumper::Purity = 0;
    local $Data::Dumper::Deepcopy = 1;

```

B.1.3 Common functions

- 4a *<Skip comments and empty records 4a>*≡
- ```
next if /^#\o;
next if /^\$*\o;
chomp;
```
- 4b *<Common PERL subs - Min Max 4b>*≡
- ```
#
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
```
- 4c *<Common PERL subs - Text fill 4c>*≡
- ```
#
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).

- 4d *<Common PERL subs - Counter 4d>*≡
- ```
#
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($_[0],6,"0")."]\n");
} # counter_end
```
- 4e *<Global Vars - Counter 4e>*≡
- ```
my ($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.

- 4f *<Common PERL subs - STDERR 4f>*≡
- ```
sub report() { print STDERR sprintf($MessageList{ shift @_ },@_) }
```

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

- 4g *<Common PERL subs - STDERR 4f>*+≡
- ```
sub warn() { print STDERR sprintf($ErrorList{ shift @_ }, @_) }
```

## B.2 AWK scripts

5a *<GAWK shebang 5a>*≡  
 #!/usr/bin/gawk -f  
 # GNU Awk 3.0.4  
*<Version Control Id Tag 5d>*

## B.3 BASH scripts

5b *<BASH shebang 5b>*≡  
 #!/usr/bin/bash  
 # GNU bash, version 2.03.6(1)-release (i386-redhat-linux-gnu)  
*<Version Control Id Tag 5d>*  
 #  
 SECONDS=0 # Reset Timing  
 # Which script are we running...  
 L="#####"  
 { echo "\$L\$L\$L\$L\$L";  
 echo "### RUNNING [\$0]";  
 echo "### Current date:`date`";  
 echo "###"; } 1>&2;

5c *<BASH script end 5c>*≡  
 { echo "###"; echo "### Execution time for [\$0] : \$SECONDS secs";  
 echo "\$L\$L\$L\$L\$L";  
 echo "; } 1>&2;  
 #  
 exit 0

## B.4 Version control tags

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

5d *<Version Control Id Tag 5d>*≡  
 # \$Id: deploy.nw,v 1.9 2001/09/25 17:45:07 jabril Exp \$

## 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.

```
6a <tangling 6a>≡
 # showing line numbering comments in program
 notangle -L -R"humangenome" $WORK/$nwfile.nw | \
 perl -ne '$.>1 && print' | cpif $BIN/humangenome ;
 chmod a+x $BIN/humangenome ;

6b <tangling 6a>+≡
 # reformatting program with perltidy
 notangle -R"humangenome" $WORK/$nwfile.nw | \
 perltidy - | cpif $BIN/humangenome ;
 # html pretty-printing program with perltidy
 notangle -R"humangenome" $WORK/$nwfile.nw | \
 perltidy -html - | cpif $DOCS/html/humangenome.html ;
 #
```

### C.2 Extracting different Config Files

```
6c <tangling 6a>+≡
 notangle -R"root" $WORK/$nwfile.nw | \
 cpif $DATA/root_config ;
```

### C.3 Extracting documentation and L<sup>A</sup>T<sub>E</sub>X'ing it

```
6d <tangling 6a>+≡
 notangle -Rweaving $WORK/$nwfile.nw | cpif $WORK/nw2tex ;
 notangle -RLaTeXing $WORK/$nwfile.nw | cpif $WORK/ltx ;
 chmod a+x $WORK/nw2tex $WORK/ltx;

6e <tangling complementary LaTeX files 6e>≡
 notangle -R"HIDE: LaTeX new definitions" $WORK/$nwfile.nw | cpif $DOCS/defs.tex ;
 notangle -R"HIDE: TODO" $WORK/$nwfile.nw | cpif $DOCS/todo.tex ;

6f <weaving 6f>≡
 <BASH shebang 5b>
 # weaving and LaTeXing
 <BASH Environment Variables 7b>
 <tangling complementary LaTeX files 6e>
 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 5c>
```



```

7a <LaTeXing 7a>≡
 <BASH shebang 5b>
 # only LaTeXing
 <BASH Environment Variables 7b>
 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 5c>

```

## C.4 Defining working shell variables for the current project

```

7b <BASH Environment Variables 7b>≡
 #
 # Setting Global Variables
 WORK="/home/ug/jabril/development/projects/sgp/humangenome" ;
 BIN="$WORK/bin" ;
 PARAM="$BIN/param" ;
 DOCS="$WORK/docs" ;
 DATA="$WORK/data" ;
 nwfile="humangenome" ;
 export WORK BIN PARAM DOCS DATA nwfile ;
 #

7c <tangling 6a>+≡
 #
 # BASH Environment Variables
 notangle -R'BASH Environment Variables' $WORK/$nwfile.nw | \
 cpif $WORK/.bash_VARS ;
 source $WORK/.bash_VARS ;
 #

```