

Al respecto ver [http://www.perlmonks.org/?node\\_id=1015649](http://www.perlmonks.org/?node_id=1015649)

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use strict; use warnings;
use File::Slurp qw(read_file);
use Math::CDF qw(qnorm pnorm);
use List::MoreUtils qw(uniq);

my $ofile = "meta1.txt";
my @ifiles = @ARGV;
my %ipairs;
my @lpairs;

foreach my $ifile (@ifiles){
    (my $fk) = $ifile =~ /^(.*)\_sets./;
    my %ldata = reverse map {/^(.*(rs\d{1,20}\s+rs\d{1,20}).*)$/} grep
{/.*rs\d{1,20}\s+rs\d{1,20}.*/} read_file $ifile;
    foreach my $dline (sort keys %ldata){
        push @lpairs, $dline;
        ($ipairs{$fk}{$dline}{'head'}, $ipairs{$fk}{$dline}{'effect'},
        $ipairs{$fk}{$dline}{'pvalue'}) = $ldata{$dline} =~
/^(.*)\s+(\d\.\d+)\s+(\d\.\d+)\s+(\d\.\d+)/;
    }
}

@lpairs = uniq @lpairs;

open OF, ">$ofile";

my $head = "CHR1 CHR2 SNP1 SNP2 P N";
print OF "$head\n";

foreach my $pair (@lpairs) {
    my $n = 0;
    my $z = 0;
    my $hl;
    my $pvalue = 0;
    my $fk;
    foreach $fk (%ipairs) {
        my $pvt = 0;
        if (exists $ipairs{$fk} && exists $ipairs{$fk}{$pair} && exists
        $ipairs{$fk}{$pair}{'pvalue'}){
            #if($ipairs{$fk}{$pair}{'pvalue'}){
                $pvt = $ipairs{$fk}{$pair}{'pvalue'};
                if($pvt){
                    unless($hl){
                        $hl = $ipairs{$fk}{$pair}{'head'};
                    }
                    $n++;
                    $z+= qnorm($ipairs{$fk}{$pair}{'pvalue'});
                }
            }
        }
    }
}

```

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}  
if($n>2){  
    $z = $z/sqrt($n);  
    $pvalue = pnorm($z);  
}  
if ($pvalue) {  
    printf "$pair -> %.4f\n", $pvalue;  
    printf OF "$hl %.4f $n\n", $pvalue;  
}  
}  
  
close OF;
```

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