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#!/usr/bin/perl

use strict;
use warnings;
use Data::Dumper;

my $SAM_file = $ARGV[0];
my $deg_list = $ARGV[1];
my $usage = "./convert_TRINITY_DEG_list.pl input.SAM
input.DEG_list";

unless (defined $SAM_file) {
    die "ERROR: Either a SAM file wasn't specified or it can't
be found. Usage: $usage";
}
unless (defined $deg_list) {
    die "ERROR: Either a DEG list wasn't specified or it could
not be found. Usage: $usage";
}

my @splitline;
my @splitread;
my %readnames;
my ( $readname, $gene, $trinityname );

# Store our read names from the SAM file into a hash
# Assumes a non-header SAM file
open SAMFILE, $SAM_file or die "ERROR: Unable to open $SAM_file\n";

while (my $alignment = <SAMFILE>) {

    chomp $alignment;
    @splitline = split(/\t/, $alignment);
    $readname = $splitline[0];
    # Alter the readname since the DEG list leaves off the
    "_i#"
    $readname =~ s/_i[0-9]*$//g;
    $trinityname = $readname;
    @splitread = split(/_/, $readname);
    $gene = $splitread[0];
    $trinityname =~ s/$gene/TRINITY/;
    ## There might already be a sequence ID with this name if
the read aligned to more than one gene,
    ## so treat this as a hash of arrays
    ## Since the DEG format is less specific for its Trinity
names, make sure we do exclude if we have this exact gene/TRINITY
name combo already
    unless (exists $readnames{$trinityname} && (grep /$gene/,
@{$readnames{$trinityname}})) {
        push @{$readnames{$trinityname} }, $gene;
    }
}
}
close SAMFILE;

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my $genename;

# Loop through the DEG list IDs and change any target names that
# were in the SAM file
open DEG, $deg_list or die "ERROR: Unable to open $deg_list\n";

while (my $line = <DEG>) {
    foreach my $key (keys %readnames) {
        if ( $line =~ /$key\s/ ) {
            my $newtarget;
            foreach $genename ( @{$readnames{$key}} )
            {
                $newtarget .= $genename . "_";
            }
            $line =~ s/TRINITY_/$newtarget/g;
            last;
        }
    }
    print $line;
}

close DEG;

```