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#!/usr/local/bin/perl -w

use strict;
use warnings;

use lib '/project/rodent/medaka_anja/pscripte';
use ClusterFunc;

my($USAGE) = "$0 ***Datei***\n";

unless (@ARGV) {
    print $USAGE;
    exit;}

my $filename = $ARGV[0];#medgastrula.res.lib

unless (open(GET_DATA,$filename)) {
    print STDERR "Cannot open file\"$filename\"\n\n";
    exit;}

#outputfile
#my $outputfilename =$filename.".temp";
#open(OUTPUT,">$outputfilename");

#alle Cluster, die keinen sequenzierten Klon enthalten, werden in
*.temp geschrieben

my $data='';
my @cluster;
my $copy = 0;

#while ($data = <GET_DATA>){
#   $data =~ s/\n//g;
#   if ($data =~ /^d/){
#       if ($copy){print OUTPUT "$cluster[0]\n";}
#       $copy = 1;
#       @cluster = split(/\s+/, $data);}
#   if ($data =~ /OldCoord/){$copy = 0;}
#}

#close(GET_DATA);
#close(OUTPUT);

#*.temp wird durchlaufen und Klon rausgezogen, aber kein OL-Klon;
Singletons getrennt betrachten
#unless (open(GET_DATA,$outputfilename)) {
#   print STDERR "Cannot open file\"$outputfilename\"\n\n";
#   exit;}

#outputfile
my $outputfile = 'Rearray_Jul2003_2nd';
open(OUTPUT_REARRAY,">$outputfile");

my @temp;
my $clone='';
my $file='';
my $singl='';
my $los=0;
my $found=0;
my $trace='';

while ($data = <GET_DATA>){
    $data =~ s/\n//g;
    @temp = split(/\s+/, $data);#0 - ClusterID; 1 - Clustersize

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$data = $temp[0];
$clone = getClone($data);print OUTPUT_REARRAY "$clone\n";
# else {#Singletons; in 'medgastrula.res' Singletonliste durchgehen
#   $file='medgastrula.res';
#   #$file = 'test.res';
#   unless (open(GET_SINGL,$file)) {
#     print STDERR "Cannot open file\"$file\"\n\n";
#     exit;}
#   while ($singl = <GET_SINGL>){
#     if ($los){
#       @temp = split(/\s+/, $singl);
#       $singl = $temp[4];
#       if ($singl =~ /MedGastrula_/){
#         ($found,$trace) = clone_seq($singl);
#         if ($found == 0){$singl =~ s/Gastrula//; print
OUTPUT_REARRAY "$singl\n";}}
#       else {
#         if ($singl !~ /MedGastrula2000_/){
#           $singl =~ s/Gastrula//;print OUTPUT_REARRAY "$singl\n";}}}
#       if ($singl =~ /^#\ 4690/){$los=1;}}
#     }
#   }
}
close(GET_DATA);
close(OUTPUT_REARRAY);

exit;

sub getClone{
  my ($ID) = @_ ;

  my $clust='';
  my $new = 0;
  my @temp;

  my $filename_clust = 'my1A.res';
  #my $filename_clust = 'test.res';
  unless (open(GET_CLUST,$filename_clust)) {
    print STDERR "Cannot open file\"$filename_clust\"\n\n";
    exit;}

  while ($clust = <GET_CLUST>){
    if ($clust =~ /^#\ 7/){
      if ($new){close(GET_CLUST);return 'Med2000 only';}
      @temp = split(/\s+/, $clust);#0 - #; 1 - ID; ...
      if ($temp[1] eq $ID){$new=1;}}
    if ($clust =~ /MedGastrula/){
      if ($new){if ($clust !~ /MedGastrula2000_/){
        @temp = split (\s+/, $clust);#4 - MedGastrula...
        $clust = $temp[4];
        $clust =~ s/Gastrula//;
        close(GET_CLUST);
        return $clust;}}}}}}

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