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

use strict;
use warnings;

my($USAGE) = "$0 ***filename***\n";#fofn_group

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

my $filename = $ARGV[0];

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

#outputfile
#my $outputfilename = '';
#$outputfilename='Ace_out_seqsfasta';
#open(OUTPUT,">$outputfilename");

my $ace = '';
my $data = '';

while ($ace = <GET_ACE>){
    $ace =~ s/\s+//g;
    $ace= $ace.".cap.ace";
    unless (open(GET_DATA,$ace)) {
        print STDERR "Cannot open file\"$ace\"\n\n";
        exit;}
    print "\n$ace\n";

    while ($data = <GET_DATA>){
        if ($data =~ /^CO/){print "$data";}
        if ($data =~ /^RD/){print "$data";}
        if ($data =~ /^QA/){print "$data";}
    }
    close(GET_DATA);
}
close(GET_ACE);

#Qualität des Alignment beurteilen, indem Länge der im Contig
enthaltenen
#Stücke berechnet wird
#$filename = $outputfilename;
#unless (open(GET_ACE,$filename)) {
#    print STDERR "Cannot open file\"$filename\"\n\n";
#    exit;}

#my $temp = 'fofn_temp';
#unless (open(GET_TEMP,$temp)) {
#    print STDERR "Cannot open file\"$temp\"\n\n";
#    exit;}

#$outputfilename='CAP3_out_seqsfasta';
#open(OUTPUT,">$outputfilename");

#my @contig;
#my @qual;
#my $quality = 0;

#while ($ace = <GET_ACE>) {

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# $ace =~ s/\n//g;
# if ($ace =~ /group.cap.ace/) {print OUTPUT "$ace\n";}
# if ($ace =~ /^CO/) {
#   @contig = split (/s/, $ace); #0 - CO; 1 - Contig1; 2 - Länge des
Contigs in bp
#   print OUTPUT "$ace\n";}
# if ($ace =~ /^RD/){print OUTPUT "$ace\n";}
# if ($ace =~ /^QA/){
#   @qual = split (/s/, $ace); #0 - QA; 1 - firstbp; 2 - lastbp
#   $quality = (($qual[2] - $qual[1])/$scontig[2])*100;
#   print OUTPUT ("Quality: " . ("."$qual[2]".-" . "$qual
[1]".") / "."$scontig[2]". "\n");
# }
# }
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exit;
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