Reporte de Archivos de Texto

Tu Nombre

2024-06-18

Reporte de Archivos de Texto

report_annotation.txt

```
Resumen GENERAL de anotaciones:
El número de anotaciones finales es de: 0
```

report_spades.txt

```
Command line: /usr/libexec/spades/spades.py --careful   -o  /workspace/work/7d/ca90d7cb02d241f633da4588

System information:
  SPAdes version: 3.15.5
  Python version: 3.12.3
  OS: Linux-5.15.146.1-microsoft-standard-WSL2-x86_64-with-glibc2.39

Output dir: /workspace/work/7d/ca90d7cb02d241f633da4588d8a6bb/output_spades
Mode: read error correction and assembling
Debug mode is turned OFF

Dataset parameters:
  Standard mode
  For multi-cell/isolate data we recommend to use '--isolate' option; for single-cell MDA data use '--s
  Reads:
    Library number: 1, library type: paired-end
      orientation: fr
      left reads: ['/workspace/work/7d/ca90d7cb02d241f633da4588d8a6bb/_output_forward.fastq']
      right reads: ['/workspace/work/7d/ca90d7cb02d241f633da4588d8a6bb/_output_reverse.fastq']
      interlaced reads: not specified
      single reads: not specified
      merged reads: not specified
Read error correction parameters:
  Iterations: 1
  PHRED offset will be auto-detected
  Corrected reads will be compressed
Assembly parameters:
  k: automatic selection based on read length
  Repeat resolution is enabled
```

```
  Mismatch careful mode is turned ON
  MismatchCorrector will be used
  Coverage cutoff is turned OFF
Other parameters:
  Dir for temp files: /workspace/work/7d/ca90d7cb02d241f633da4588d8a6bb/output_spades/tmp
  Threads: 16
  Memory limit (in Gb): 6



=== Error correction and assembling warnings:
 * 0:00:01.341     1M / 1297M WARN    General                 (kmer_coverage_model.cpp   : 366)   Failed
 * 0:00:01.514     1M / 1297M WARN    General                 (simplification.cpp        : 504)   The de
 * 0:00:00.875     1M / 1319M WARN    General                 (kmer_coverage_model.cpp   : 366)   Failed
======= Warnings saved to /workspace/work/7d/ca90d7cb02d241f633da4588d8a6bb/output_spades/warnings.log
```

report_taxonomy.txt

```
 94.87  37  37  U   0   unclassified
  5.13  2   0       1   root
  5.13  2   0       10239     Viruses
  5.13  2   0   1   2731341     Duplodnaviria
  5.13  2   0   K   2731360       Heunggongvirae
  5.13  2   0   P   2731618         Uroviricota
  5.13  2   0   C   2731619           Caudoviricetes
  2.56  1   0   F   2946167             Peduoviridae
  2.56  1   0   G   2948951               Wadgaonvirus
  2.56  1   0   S   2956672                 Wadgaonvirus wv5004651
  2.56  1   1   S1  2716351                   Escherichia phage 500465-1
  2.56  1   0   G   2843442             Radostvirus
  2.56  1   0   S   2844247               Radostvirus ev099
  2.56  1   1   S1  2847061                 Escherichia phage ev099
```

report_trimmomatic.txt

```
Input Read Pairs: 500
Both Surviving Reads: 499
Both Surviving Read Percent: 99.80
Forward Only Surviving Reads: 0
Forward Only Surviving Read Percent: 0.00
Reverse Only Surviving Reads: 0
Reverse Only Surviving Read Percent: 0.00
Dropped Reads: 1
Dropped Read Percent: 0.20
```

report_variant_calling.txt

```
# This file was produced by bcftools stats (1.19+htslib-1.19) and can be plotted using plot-vcfstats.
# The command line was: bcftools stats  SNPs_only.recode.vcf
#
# Definition of sets:
# ID    [2]id   [3]tab-separated file names
ID  0   SNPs_only.recode.vcf
# SN, Summary numbers:
#   number of records   .. number of data rows in the VCF
#   number of no-ALTs   .. reference-only sites, ALT is either "." or identical to REF
#   number of SNPs      .. number of rows with a SNP
#   number of MNPs      .. number of rows with a MNP, such as CC>TT
#   number of indels    .. number of rows with an indel
#   number of others    .. number of rows with other type, for example a symbolic allele or
#                          a complex substitution, such as ACT>TCGA
#   number of multiallelic sites     .. number of rows with multiple alternate alleles
#   number of multiallelic SNP sites .. number of rows with multiple alternate alleles, all SNPs
#
#   Note that rows containing multiple types will be counted multiple times, in each
#   counter. For example, a row with a SNP and an indel increments both the SNP and
#   the indel counter.
#
# SN    [2]id   [3]key  [4]value
SN  0   number of samples:  1
SN  0   number of records:  90
SN  0   number of no-ALTs:  0
SN  0   number of SNPs: 90
SN  0   number of MNPs: 0
SN  0   number of indels:   0
SN  0   number of others:   0
SN  0   number of multiallelic sites:   0
SN  0   number of multiallelic SNP sites:   0
# TSTV, transitions/transversions:
# TSTV  [2]id   [3]ts   [4]tv   [5]ts/tv    [6]ts (1st ALT) [7]tv (1st ALT) [8]ts/tv (1st ALT)
TSTV    0   61  29  2.10    61  29  2.10
# SiS, Singleton stats:
# SiS   [2]id   [3]allele count [4]number of SNPs   [5]number of transitions    [6]number of transversi
SiS 0   1   90  61  29  0   0   0   0
# AF, Stats by non-reference allele frequency:
# AF    [2]id   [3]allele frequency [4]number of SNPs   [5]number of transitions    [6]number of transv
AF  0   0.000000    90  61  29  0   0   0   0
# QUAL, Stats by quality
# QUAL  [2]id   [3]Quality  [4]number of SNPs   [5]number of transitions (1st ALT)  [6]number of transv
QUAL    0   30.4    90  61  29  0
# IDD, InDel distribution:
# IDD   [2]id   [3]length (deletions negative)  [4]number of sites  [5]number of genotypes  [6]mean VAF
# ST, Substitution types:
# ST    [2]id   [3]type [4]count
ST  0   A>C 9
ST  0   A>G 13
ST  0   A>T 4
ST  0   C>A 1
```

```
ST  0   C>G 2
ST  0   C>T 17
ST  0   G>A 13
ST  0   G>C 2
ST  0   G>T 2
ST  0   T>A 6
ST  0   T>C 18
ST  0   T>G 3
# DP, Depth distribution
# DP    [2]id   [3]bin  [4]number of genotypes  [5]fraction of genotypes (%)    [6]number of sites  [7]
```