

# METAmock\_v0.1

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## METAmock usage:

```
uzi@quince-srv2 ~/METAmock]$ ./METAmock
Usage: METAmock [options] filename
```

### Options:

```
--version          show program's version number and exit
-h, --help         show this help message and exit
-q QUERY_READS, --query_reads=QUERY_READS
                   specify single or paired-end reads in fastq format.
                   For each file, use -q, e.g., -q R1.fastq -q R2.fastq
-d REFERENCE_DATABASE, --reference_database=REFERENCE_DATABASE
                   reference database
-o OUTPUT_NAME, --output_name=OUTPUT_NAME
                   name under which the files are stored
-t BWA_THREADS, --threads=BWA_THREADS
                   number of threads to use in bwa
```

## METAmock example run (running bwa on 20 threads):

```
[uzi@quince-srv2 ~/METAmock/test]$ ~/METAmock/METAmock -q
/home/shared1/TSB/Metagenomes/Mircea_Mock/Nextera_even_50ng_AGGCAGAA-CTCTCTAT/Raw/50ng_even_AGGCAGAA-
CTCTCTAT_L003_R1_001.fastq -q /home/shared1/TSB/Metagenomes/Mircea_Mock/Nextera_even_50ng_AGGCAGAA-
CTCTCTAT/Raw/50ng_even_AGGCAGAA-CTCTCTAT_L003_R2_001.fastq -d ~/TSB_METAGENOMES/prob_genomes/even/Mercier_New.fasta
-o 50ng_even -t 20
This is METAmock v0.1. Copyright (c) 2013 Computational Microbial Genomics Group, University of Glasgow, UK
Checking for 'bwa': found /home/opt/bwa-0.7.3a/bwa
Checking for 'samtools': found /usr/bin/samtools
Checking for 'bedtools': found /usr/bin/bedtools
[2013-08-15 22:24:40] Aligning 50ng_even_AGGCAGAA-CTCTCTAT_L003_R1_001.fastq and 50ng_even_AGGCAGAA-
CTCTCTAT_L003_R2_001.fastq against Mercier_New.fasta using bwa on 20 threads
```

```
[2013-08-15 22:28:04] Generated 50ng_even.sam successfully!
[2013-08-15 22:28:04] Converting 50ng_even.sam to 50ng_even.bam
[2013-08-15 22:35:41] Generated 50ng_even.bam successfully!
[2013-08-15 22:35:41] Extracting mapped reads from bam file
[2013-08-15 22:42:42] Generated 50ng_even_mapped.bam successfully!
[2013-08-15 22:42:42] Extracting length of reference genomes
[2013-08-15 22:42:42] Generated lengths.genome successfully!
[2013-08-15 22:42:42] Sorting mapped bam file
[2013-08-15 22:51:26] Generated 50ng_even_mapped_sorted.bam successfully!
[2013-08-15 22:51:26] Generating per-base coverage for each reference genome
[2013-08-15 23:04:14] Generated 50ng_even_perbasecoverage.tsv successfully!
[2013-08-15 23:04:14] Generating pipeline statistics
[2013-08-15 23:16:22] Following files were generated successfully:
50ng_even_MEAN-GENOME-COVERAGE.tsv
50ng_even_PROPORTION-GENOME-COVERED.tsv
50ng_even_PROPORTION-GENOME-READS.tsv
```

**The pipeline took 42 minutes to process Illumina MISEQ dataset and produced three tab-delimited files (their first few entries shown):**

```
[uzi@quince-srv2 ~/METAmock/test]$ head 50ng_even_MEAN-GENOME-COVERAGE.tsv
Clostridium_thermocellum_ATCC_27405 12.6496058987
Caldisaccharolyticus_DSM_8903 16.6704086322
gi|55979969|ref|NC_006461.1| 7.57585490301
Leptothrix_cholodnii_SP-6 6.29279181196
Thermotoga_sp._RQ2 21.4120519169
Nanoarchaeum_equitans_Kin4-M 6.0231194679
Bacteroides_vulgatus_ATCC_8482 12.7609489019
Rhodopirellula_baltica_SH_1_complete_genome 13.7021065901
Chlorobiumphaeovibrioides_DSM_265 10.8044322468
Chlorobiumphaeobacteroides_DSM_266 11.6570084195
```

```
[uzi@quince-srv2 ~/METAmock/test]$ head 50ng_even_MEAN-GENOME-COVERAGE.tsv
Clostridium_thermocellum_ATCC_27405 12.6496058987
Caldisaccharolyticus_DSM_8903 16.6704086322
gi|55979969|ref|NC_006461.1| 7.57585490301
```

```
Leptothrix_cholodnii_SP-6      6.29279181196
Thermotoga_sp._RQ2             21.4120519169
Nanoarchaeum_equitans_Kin4-M   6.0231194679
Bacteroides_vulgatus_ATCC_8482 12.7609489019
Rhodopirellula_baltica_SH_1_complete_genome 13.7021065901
Chlorobiumphaeovibrioides_DSM_265 10.8044322468
Chlorobiumphaeobacteroides_DSM_266 11.6570084195
```

```
[uzi@quince-srv2 ~/METAmock/test]$ head 50ng_even_PROPORTION-GENOME-READS.tsv
```

```
Clostridium_thermocellum_ATCC_27405 0.0217448610085
Caldisaccharolyticus_DSM_8903 0.0221088084707
Treponema_vincentii_ATCC_35580_NZACYH00000000.1 0.0303996116472
Leptothrix_cholodnii_SP-6      0.0153027687381
Thermotoga_sp._RQ2             0.0180099779374
Nanoarchaeum_equitans_Kin4-M   0.00132483097551
Bacteroides_vulgatus_ATCC_8482 0.0295224493815
Rhodopirellula_baltica_SH_1_complete_genome 0.0446545316481
Chlorobiumphaeovibrioides_DSM_265 0.00964256359793
Chlorobiumphaeobacteroides_DSM_266 0.0164579797547
```