
[1m

SqueezeMeta v1.6.2, March 2023 – (c) J. Tamames, F. Puente-Sánchez
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[0mRun started Fri Sep 29 19:59:11 2023 in coassembly mode
2 metagenomes found: SRR1927149 SRR1929485

Now creating directories

Reading configuration from /gpfs1/scratch/jonas/metasqueeze_test/
SqueezeMeta_conf.pl

[34m[0 seconds]: STEP1 -> RUNNING ASSEMBLY: 01.run_all_assemblies.pl
(megahit)

[0m Concatenating all samples: SRR1927149_1.fastq.gz

SRR1927149_2.fastq.gz SRR1929485_1.fastq.gz SRR1929485_2.fastq.gz

pair1: cat /gpfs1/scratch/jonas/test/raw/SRR1927149_1.fastq.gz /
gpfs1/scratch/jonas/test/raw/SRR1929485_1.fastq.gz > /gpfs1/scratch/
jonas/metasqueeze_test/data/raw_fastq/par1.fastq.gz

pair2: cat /gpfs1/scratch/jonas/test/raw/SRR1927149_2.fastq.gz /
gpfs1/scratch/jonas/test/raw/SRR1929485_2.fastq.gz > /gpfs1/scratch/
jonas/metasqueeze_test/data/raw_fastq/par2.fastq.gz

Running assembly with megahit: perl /home/jonas/miniconda3/envs/
SqueezeMeta_dev/SqueezeMeta/lib/SqueezeMeta/assembly_megahit.pl /
gpfs1/scratch/jonas/metasqueeze_test metasqueeze_test /gpfs1/
scratch/jonas/metasqueeze_test/data/raw_fastq/par1.fastq.gz /gpfs1/
scratch/jonas/metasqueeze_test/data/raw_fastq/par2.fastq.gz

Running prinseq (Schmieder et al 2011, *Bioinformatics* 27(6):863-4)
for selecting contigs longer than 200

-p destination: Broken pipe

Input and filter stats:

Input sequences: 241,008

Input bases: 212,125,857

Input mean length: 880.16

Good sequences: 241,008 (100.00%)

Good bases: 212,125,857

Good mean length: 880.16

Bad sequences: 0 (0.00%)

Sequences filtered by specified parameters:

none

Renaming contigs

Running prinseq for contig statistics: /home/jonas/miniconda3/envs/
SqueezeMeta_dev/SqueezeMeta/bin/prinseq-lite.pl -fasta /gpfs1/
scratch/jonas/metasqueeze_test/results/01.metasqueeze_test.fasta

-stats_len -stats_info -stats_assembly > /gpfs1/scratch/jonas/
metasqueeze_test/intermediate/01.metasqueeze_test.stats

-p destination: Broken pipe

Counting length of contigs

Contigs stored in /gpfs1/scratch/jonas/metasqueeze_test/results/
01.metasqueeze_test.fasta

Number of contigs: 241008

[34m[33 minutes, 16 seconds]: STEP2 -> RNA PREDICTION: 02.rnas.pl

[0m Running barrnap (Seeman 2014, Bioinformatics 30, 2068–9) for predicting RNAs: Bacteria Archaea Eukaryote Mitochondrial
Running RDP classifier (Wang et al 2007, Appl Environ Microbiol 73, 5261–7)
Running Aragorn (Laslett & Canback 2004, Nucleic Acids Res 31, 11–16) for tRNA/tmRNA prediction
[34m[34 minutes, 53 seconds]: STEP3 -> ORF PREDICTION:
03.run_prodigal.pl
[0m Running prodigal (Hyatt et al 2010, BMC Bioinformatics 11: 119) for predicting ORFs
ORFs predicted: 382155
[34m[48 minutes, 40 seconds]: STEP4 -> HOMOLOGY SEARCHES:
04.rundiamond.pl
[0m Setting block size for Diamond
AVAILABLE (free) RAM memory: 2853.28 Gb
We will set Diamond block size to 16 (Gb RAM/8, Max 16).
You can override this setting using the -b option when starting the project, or changing
the \$blocksize variable in SqueezeMeta_conf.pl
Working with taxonomy database in /gpfs1/db/squeeze_meta/v1.6.2/db/nr.dmd
taxa COGS Running Diamond (Buchfink et al 2015, Nat Methods 12, 59–60) for KEGG
[34m[2 hours, 5 minutes, 12 seconds]: STEP6 -> TAXONOMIC ASSIGNMENT:
06.lca.pl
[0m Splitting Diamond file
Starting multithread LCA in 60 threads
Creating /gpfs1/scratch/jonas/metasqueeze_test/results/06.metasqueeze_test.fun3.tax.wranks file
Creating /gpfs1/scratch/jonas/metasqueeze_test/results/06.metasqueeze_test.fun3.tax.noidfilter.wranks file
[34m[4 hours, 44 minutes, 48 seconds]: STEP7 -> FUNCTIONAL ASSIGNMENT: 07.fun3assign.pl
[0m Functional assignment for COGS KEGG
[34m[4 hours, 45 minutes, 3 seconds]: STEP9 -> CONTIG TAX ASSIGNMENT: 09.summarycontigs3.pl
[0m Reading /gpfs1/scratch/jonas/metasqueeze_test/results/06.metasqueeze_test.fun3.tax.wranks
Writing output to /gpfs1/scratch/jonas/metasqueeze_test/intermediate/09.metasqueeze_test.contiglog
Reading /gpfs1/scratch/jonas/metasqueeze_test/results/06.metasqueeze_test.fun3.tax.noidfilter.wranks
Writing output to /gpfs1/scratch/jonas/metasqueeze_test/intermediate/09.metasqueeze_test.contiglog.noidfilter
[34m[4 hours, 46 minutes, 7 seconds]: STEP10 -> MAPPING READS:
10.mapsamples.pl
[0m Reading samples from /gpfs1/scratch/jonas/metasqueeze_test/data/00.metasqueeze_test.samples
Metagenomes found: 2
Mapping with Bowtie2 (Langmead and Salzberg 2012, Nat Methods 9(4), 357–9)
Creating reference from contigs
Working with sample 1: SRR1927149

```
Getting raw reads
Aligning to reference with bowtie
[bam_sort_core] merging from 0 files and 60 in-memory blocks...
Calculating contig coverage
Reading contig length from /gpfs1/scratch/jonas/metasqueeze_test/
intermediate/01.metasqueeze_test.ln
Counting with sqm_counter: Opening 60 threads
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
494494 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
988987 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
1977973 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
1483480 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
2966959 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
2472466 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
3461452 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
3955945 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
4450438 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
5439424 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
4944931 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
6428410 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
5933917 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
6922903 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
7417396 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
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8406382 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
7911889 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
9395368 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
8900875 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
9889861 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
10384354 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
10878847 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
11867833 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
11373340 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
13351312 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
12362326 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
14834791 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
14340298 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
15329284 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
13845805 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
17307256 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
15823777 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
16812763 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1

16318270 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
18790735 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
17801749 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
12856819 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
18296242 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
19285228 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
19779721 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
20274214 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
20768707 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
21757693 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
22252186 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
21263200 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
24230158 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
25713637 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
22746679 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
25219144 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
23241172 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
27197116 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1

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24724651 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
26208130 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
23735665 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
28186102 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
28680595 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
26702623 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
27691609 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
29175088 reads counted
29669581 reads counted
Working with sample 2: SRR1929485
Getting raw reads
Aligning to reference with bowtie
[bam_sort_core] merging from 0 files and 60 in-memory blocks...
Calculating contig coverage
Reading contig length from /gpfs1/scratch/jonas/metasqueeze_test/
intermediate/01.metasqueeze_test.lon
Counting with sqm_counter: Opening 60 threads
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
158161 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
316321 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
474481 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
632641 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
790801 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
948961 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
1107121 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
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1265281 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
1423441 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
1581601 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
1739761 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
1897921 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
2056081 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
2214241 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
2372401 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
2530561 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
2688721 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
2846881 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
3005041 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
3163201 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
3321361 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
3479521 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
3637681 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
3795841 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
3954001 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1

4112161 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
4270321 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
4428481 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
4586641 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
4744801 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
4902961 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
5061121 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
5219281 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
5377441 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
5535601 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
5693761 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
5851921 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
6010081 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
6168241 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
6326401 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
6442721 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
6484561 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
6800881 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1


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6959041 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
7117201 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
7275361 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
7433521 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
7591681 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
7749841 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
7908001 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
8066161 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
8224321 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
8382481 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
8540641 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
8698801 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
8856961 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
9015121 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
9173281 reads counted
samtools view: writing to standard output failed: Broken pipe
samtools view: error closing standard output: -1
9331441 reads counted
9489601 reads counted
Output in /gpfs1/scratch/jonas/metasqueeze_test/intermediate/
10.metasqueeze_test.mapcount
[34m[5 hours, 0 minutes, 2 seconds]: STEP11 -> COUNTING TAX
ABUNDANCES: 11.mcount.pl
[0m[34m[5 hours, 0 minutes, 12 seconds]: STEP12 -> COUNTING FUNCTION
ABUNDANCES: 12.funcover.pl
[0m Calculating coverage for functions
```

```
Reading coverage in /gpfs1/scratch/jonas/metasqueeze_test/
intermediate/10.metasqueeze_test.mapcount
Reading rpkm in /gpfs1/scratch/jonas/metasqueeze_test/
intermediate/10.metasqueeze_test.mapcount
Now creating cog coverage output in /gpfs1/scratch/jonas/
metasqueeze_test/results/12.metasqueeze_test.cog.funcover
Now creating kegg coverage output in /gpfs1/scratch/jonas/
metasqueeze_test/results/12.metasqueeze_test.kegg.funcover
Now creating cog raw reads output in /gpfs1/scratch/jonas/
metasqueeze_test/ext_tables/12.metasqueeze_test.cog.stamp
Now creating kegg raw reads output in /gpfs1/scratch/jonas/
metasqueeze_test/ext_tables/12.metasqueeze_test.kegg.stamp
[34m[5 hours, 0 minutes, 31 seconds]: STEP13 -> CREATING GENE TABLE:
13.mergeannot2.pl
[0m Creating table in /gpfs1/scratch/jonas/metasqueeze_test/
results/13.metasqueeze_test.orftable
Reading GFF in /gpfs1/scratch/jonas/metasqueeze_test/results/
03.metasqueeze_test.gff
Reading Diamond hits
Reading COG list
Reading KEGG list
Reading aa sequences
Reading nt sequences
Reading rRNA sequences
Reading tRNA/tmRNA sequences
Reading ORF information
Calculating GC content for genes
Calculating GC content for RNAs
Reading contig information
Reading KEGG annotations
Reading COGs annotations
Reading RPKMs and Coverages
=====
GENE TABLE CREATED: /gpfs1/scratch/jonas/metasqueeze_test/results/
13.metasqueeze_test.orftable
=====

[34m[5 hours, 1 minutes, 35 seconds]: STEP14 -> BINNING:
14.runbinning.pl
[0m[34m[5 hours, 16 minutes, 11 seconds]: STEP15 -> DAS_TOOL
MERGING: 15.dastool.pl
[0m[34m[5 hours, 17 minutes, 20 seconds]: STEP16 -> BIN TAX
ASSIGNMENT: 16.addtax2.pl
[0m[34m[5 hours, 19 minutes, 33 seconds]: STEP17 -> CHECKING BINS:
17.checkM_batch.pl
[0m Evaluating bins with CheckM (Parks et al 2015, Genome Res 25,
1043-55)

Creating /gpfs1/scratch/jonas/metasqueeze_test/temp/checkm_batch
Reading /home/jonas/miniconda3/envs/SqueezeMeta_dev/SqueezeMeta/
data/alltaxlist.txt
Looking for DAS bins in /gpfs1/scratch/jonas/metasqueeze_test/
results/bins
64 bins found
```

Bin 1/64: concoct.104.fa_sub.contigs.fa.tax
Using profile for family rank : Prevotellaceae
Bin 2/64: concoct.6.fa.contigs.fa.tax
Using profile for genus rank : Treponema
Bin 3/64: concoct.64.fa.contigs.fa.tax
Using profile for class rank : Lentisphaeria
Using profile for phylum rank : Lentisphaerae
Using profile for domain rank : Bacteria
Bin 4/64: concoct.77.fa.contigs.fa.tax
Using profile for order rank : Aeromonadales
Bin 5/64: metabat2.5.fa_sub.contigs.fa.tax
Using profile for genus rank : Prevotella
Bin 6/64: metabat2.13.fa_sub.contigs.fa.tax
Using profile for family rank : Rikenellaceae
Bin 7/64: concoct.31.fa.contigs.fa.tax
Using profile for class rank : Clostridia
Bin 8/64: concoct.9.fa_sub.contigs.fa.tax
Using profile for class rank : Clostridia
Bin 9/64: concoct.1.fa.contigs.fa.tax
Using profile for genus rank : Brachyspira
Bin 10/64: concoct.45.fa.contigs.fa.tax
Using profile for order rank : Bacteroidales
Bin 11/64: concoct.71.fa.contigs.fa.tax
Using profile for order rank : Spirochaetales
Bin 12/64: concoct.47.fa_sub.contigs.fa.tax
Using profile for class rank : Clostridia
Bin 13/64: concoct.20.fa_sub.contigs.fa.tax
Using profile for domain rank : Bacteria
Bin 14/64: concoct.25.fa.contigs.fa.tax
Using profile for family rank : Oscillospiraceae
Using profile for class rank : Clostridia
Bin 15/64: concoct.75.fa.contigs.fa.tax
Using profile for order rank : Bacteroidales
Bin 16/64: concoct.18.fa_sub.contigs.fa.tax
Using profile for genus rank : Prevotella
Bin 17/64: metabat2.8.fa.contigs.fa.tax
Using profile for class rank : Clostridia
Bin 18/64: concoct.81.fa.contigs.fa.tax
Using profile for order rank : Bacteroidales
Bin 19/64: concoct.103.fa_sub.contigs.fa.tax
Using profile for order rank : Bacteroidales
Bin 20/64: concoct.84.fa.contigs.fa.tax
Using profile for family rank : Succinivibrionaceae
Bin 21/64: metabat2.18.fa_sub.contigs.fa.tax
Using profile for genus rank : Alistipes
Bin 22/64: concoct.16.fa.contigs.fa.tax
Using profile for family rank : Elusimicrobiaceae
Using profile for order rank : Elusimicrobiales
Using profile for class rank : Elusimicrobia
Using profile for phylum rank : Elusimicrobia
Using profile for domain rank : Bacteria
Bin 23/64: metabat2.22.fa_sub.contigs.fa.tax
Using profile for genus rank : Prevotella

Bin 24/64: concoct.7.fa.contigs.fa.tax
Using profile for family rank : Lachnospiraceae
Bin 25/64: concoct.54.fa.contigs.fa.tax
Using profile for phylum rank : Firmicutes
Bin 26/64: metabat2.14.fa.contigs.fa.tax
Using profile for class rank : Clostridia
Bin 27/64: concoct.111.fa.contigs.fa.tax
Using profile for class rank : Clostridia
Bin 28/64: concoct.98.fa.contigs.fa.tax
Using profile for family rank : Lachnospiraceae
Bin 29/64: concoct.102.fa.contigs.fa.tax
Using profile for family rank : Oscillospiraceae
Using profile for class rank : Clostridia
Bin 30/64: concoct.43.fa.contigs.fa.tax
Using profile for family rank : Lachnospiraceae
Bin 31/64: concoct.69.fa.contigs.fa.tax
Using profile for class rank : Clostridia
Bin 32/64: concoct.10.fa.contigs.fa.tax
Using profile for phylum rank : Spirochaetes
Bin 33/64: concoct.34.fa_sub.contigs.fa.tax
Using profile for genus rank : Alistipes
Bin 34/64: concoct.99.fa.contigs.fa.tax
Bin 35/64: concoct.109.fa_sub.contigs.fa.tax
Using profile for genus rank : Prevotella
Bin 36/64: concoct.94.fa.contigs.fa.tax
Using profile for genus rank : Campylobacter
Bin 37/64: concoct.95.fa.contigs.fa.tax
Using profile for family rank : Prevotellaceae
Bin 38/64: concoct.110.fa.contigs.fa.tax
Using profile for class rank : Clostridia
Bin 39/64: metabat2.32.fa_sub.contigs.fa.tax
Using profile for genus rank : Prevotella
Bin 40/64: concoct.32.fa.contigs.fa.tax
Using profile for genus rank : Escherichia
Bin 41/64: concoct.106.fa.contigs.fa.tax
Using profile for class rank : Alphaproteobacteria
Bin 42/64: concoct.36.fa.contigs.fa.tax
Using profile for domain rank : Bacteria
Bin 43/64: concoct.13.fa.contigs.fa.tax
Using profile for domain rank : Bacteria
Bin 44/64: concoct.27.fa.contigs.fa.tax
Using profile for class rank : Negativicutes
Bin 45/64: concoct.49.fa.contigs.fa.tax
Using profile for genus rank : Phascolarctobacterium
Using profile for family rank : Acidaminococcaceae
Bin 46/64: concoct.12.fa.contigs.fa.tax
Using profile for family rank : Oscillospiraceae
Using profile for class rank : Clostridia
Bin 47/64: concoct.74.fa.contigs.fa.tax
Using profile for class rank : Alphaproteobacteria
Bin 48/64: concoct.60.fa_sub.contigs.fa.tax
Using profile for genus rank : Alistipes
Bin 49/64: concoct.46.fa.contigs.fa.tax
Using profile for genus rank : Dialister

Bin 50/64: concoct.113.fa_sub.contigs.fa.tax
Using profile for domain rank : Bacteria
Bin 51/64: concoct.57.fa.contigs.fa.tax
Using profile for class rank : Alphaproteobacteria
Bin 52/64: concoct.40.fa.contigs.fa.tax
Using profile for family rank : Prevotellaceae
Bin 53/64: metabat2.15.fa_sub.contigs.fa.tax
Using profile for genus rank : Prevotella
Bin 54/64: concoct.82.fa.contigs.fa.tax
Using profile for class rank : Clostridia
Bin 55/64: concoct.66.fa.contigs.fa.tax
Using profile for genus rank : Treponema
Bin 56/64: concoct.100.fa.contigs.fa.tax
Using profile for genus rank : Prevotella
Bin 57/64: concoct.19.fa.contigs.fa.tax
Using profile for genus rank : Escherichia
Bin 58/64: concoct.115.fa_sub.contigs.fa.tax
Using profile for class rank : Clostridia
Bin 59/64: concoct.55.fa_sub.contigs.fa.tax
Using profile for class rank : Clostridia
Bin 60/64: concoct.96.fa.contigs.fa.tax
Using profile for genus rank : Treponema
Bin 61/64: concoct.92.fa.contigs.fa.tax
Using profile for domain rank : Bacteria
Bin 62/64: concoct.114.fa.contigs.fa.tax
Using profile for family rank : Oscillospiraceae
Using profile for class rank : Clostridia
Bin 63/64: concoct.76.fa.contigs.fa.tax
Using profile for domain rank : Bacteria
Bin 64/64: concoct.56.fa.contigs.fa.tax
Using profile for genus rank : Prevotella

Storing results for DAS in /gpfs1/scratch/jonas/metasqueeze_test/
intermediate/17.metasqueeze_test.checkM
[34m[6 hours, 20 minutes, 43 seconds]: STEP18 -> CREATING BIN TABLE:
18.getbins.pl
[0m Method:DAS

Reading checkM results in /gpfs1/scratch/jonas/metasqueeze_test/
intermediate/17.metasqueeze_test.checkM

Looking for bins in /gpfs1/scratch/jonas/metasqueeze_test/results/
bins

Reading data for bin concoct.104.fa_sub.contigs
Reading data for bin concoct.6.fa.contigs
Reading data for bin concoct.64.fa.contigs
Reading data for bin concoct.77.fa.contigs
Reading data for bin metabat2.5.fa_sub.contigs
Reading data for bin metabat2.13.fa_sub.contigs
Reading data for bin concoct.31.fa.contigs
Reading data for bin concoct.9.fa_sub.contigs
Reading data for bin concoct.1.fa.contigs
Reading data for bin concoct.45.fa.contigs
Reading data for bin concoct.71.fa.contigs
Reading data for bin concoct.47.fa_sub.contigs
Reading data for bin concoct.20.fa_sub.contigs

Reading data for bin concoct.25.fa.contigs
Reading data for bin concoct.75.fa.contigs
Reading data for bin concoct.18.fa_sub.contigs
Reading data for bin metabat2.8.fa.contigs
Reading data for bin concoct.81.fa.contigs
Reading data for bin concoct.103.fa_sub.contigs
Reading data for bin concoct.84.fa.contigs
Reading data for bin metabat2.18.fa_sub.contigs
Reading data for bin concoct.16.fa.contigs
Reading data for bin metabat2.22.fa_sub.contigs
Reading data for bin concoct.7.fa.contigs
Reading data for bin concoct.54.fa.contigs
Reading data for bin metabat2.14.fa.contigs
Reading data for bin concoct.111.fa.contigs
Reading data for bin concoct.98.fa.contigs
Reading data for bin concoct.102.fa.contigs
Reading data for bin concoct.43.fa.contigs
Reading data for bin concoct.69.fa.contigs
Reading data for bin concoct.10.fa.contigs
Reading data for bin concoct.34.fa_sub.contigs
Reading data for bin concoct.99.fa.contigs
Reading data for bin concoct.109.fa_sub.contigs
Reading data for bin concoct.94.fa.contigs
Reading data for bin concoct.95.fa.contigs
Reading data for bin concoct.110.fa.contigs
Reading data for bin metabat2.32.fa_sub.contigs
Reading data for bin concoct.32.fa.contigs
Reading data for bin concoct.106.fa.contigs
Reading data for bin concoct.36.fa.contigs
Reading data for bin concoct.13.fa.contigs
Reading data for bin concoct.27.fa.contigs
Reading data for bin concoct.49.fa.contigs
Reading data for bin concoct.12.fa.contigs
Reading data for bin concoct.74.fa.contigs
Reading data for bin concoct.60.fa_sub.contigs
Reading data for bin concoct.46.fa.contigs
Reading data for bin concoct.113.fa_sub.contigs
Reading data for bin concoct.57.fa.contigs
Reading data for bin concoct.40.fa.contigs
Reading data for bin metabat2.15.fa_sub.contigs
Reading data for bin concoct.82.fa.contigs
Reading data for bin concoct.66.fa.contigs
Reading data for bin concoct.100.fa.contigs
Reading data for bin concoct.19.fa.contigs
Reading data for bin concoct.115.fa_sub.contigs
Reading data for bin concoct.55.fa_sub.contigs
Reading data for bin concoct.96.fa.contigs
Reading data for bin concoct.92.fa.contigs
Reading data for bin concoct.114.fa.contigs
Reading data for bin concoct.76.fa.contigs
Reading data for bin concoct.56.fa.contigs
Calculating coverages
Creating table in /gpfs1/scratch/jonas/metasqueeze_test/results/
18.metasqueeze_test.bintable

Done!

=====

BIN TABLE CREATED: /gpfs1/scratch/jonas/metasqueeze_test/results/
18.metasqueeze_test.bintable

=====

[34m[6 hours, 21 minutes, 3 seconds]: STEP19 -> CREATING CONTIG

TABLE: 19.getcontigs.pl

[0m Reading taxa for contigs information...done!

Reading GC & length... done!

Reading number of genes... done!

Reading coverages... done!

Reading bins... done!

Creating contig table...done!

=====

CONTIG TABLE CREATED: /gpfs1/scratch/jonas/metasqueeze_test/results/
19.metasqueeze_test.contigtable

=====

[34m[6 hours, 21 minutes, 47 seconds]: STEP20 -> CREATING TABLE OF

PATHWAYS IN BINS: 20.minpath.pl

[0m Running MinPath (Ye and Doak 2009, PLoS Comput Biol 5(8),
e1000465)

Running MinPath for kegg: concoct.1.fa.contigs

Running MinPath for kegg: concoct.10.fa.contigs

Running MinPath for kegg: concoct.100.fa.contigs

Running MinPath for kegg: concoct.102.fa.contigs

Running MinPath for kegg: concoct.103.fa_sub.contigs

Running MinPath for kegg: concoct.104.fa_sub.contigs

Running MinPath for kegg: concoct.106.fa.contigs

Running MinPath for kegg: concoct.109.fa_sub.contigs

Running MinPath for kegg: concoct.110.fa.contigs

Running MinPath for kegg: concoct.111.fa.contigs

Running MinPath for kegg: concoct.113.fa_sub.contigs

Running MinPath for kegg: concoct.114.fa.contigs

Running MinPath for kegg: concoct.115.fa_sub.contigs

Running MinPath for kegg: concoct.12.fa.contigs

Running MinPath for kegg: concoct.13.fa.contigs

Running MinPath for kegg: concoct.16.fa.contigs

Running MinPath for kegg: concoct.18.fa_sub.contigs

Running MinPath for kegg: concoct.19.fa.contigs

Running MinPath for kegg: concoct.20.fa_sub.contigs

Running MinPath for kegg: concoct.25.fa.contigs

Running MinPath for kegg: concoct.27.fa.contigs

Running MinPath for kegg: concoct.31.fa.contigs

Running MinPath for kegg: concoct.32.fa.contigs

Running MinPath for kegg: concoct.34.fa_sub.contigs

Running MinPath for kegg: concoct.36.fa.contigs

Running MinPath for kegg: concoct.40.fa.contigs

Running MinPath for kegg: concoct.43.fa.contigs

Running MinPath for kegg: concoct.45.fa.contigs

Running MinPath for kegg: concoct.46.fa.contigs

Running MinPath for kegg: concoct.47.fa_sub.contigs

Running MinPath for kegg: concoct.49.fa.contigs

Running MinPath for kegg: concoct.54.fa.contigs
Running MinPath for kegg: concoct.55.fa_sub.contigs
Running MinPath for kegg: concoct.56.fa.contigs
Running MinPath for kegg: concoct.57.fa.contigs
Running MinPath for kegg: concoct.6.fa.contigs
Running MinPath for kegg: concoct.60.fa_sub.contigs
Running MinPath for kegg: concoct.64.fa.contigs
Running MinPath for kegg: concoct.66.fa.contigs
Running MinPath for kegg: concoct.69.fa.contigs
Running MinPath for kegg: concoct.7.fa.contigs
Running MinPath for kegg: concoct.71.fa.contigs
Running MinPath for kegg: concoct.74.fa.contigs
Running MinPath for kegg: concoct.75.fa.contigs
Running MinPath for kegg: concoct.76.fa.contigs
Running MinPath for kegg: concoct.77.fa.contigs
Running MinPath for kegg: concoct.81.fa.contigs
Running MinPath for kegg: concoct.82.fa.contigs
Running MinPath for kegg: concoct.84.fa.contigs
Running MinPath for kegg: concoct.9.fa_sub.contigs
Running MinPath for kegg: concoct.92.fa.contigs
Running MinPath for kegg: concoct.94.fa.contigs
Running MinPath for kegg: concoct.95.fa.contigs
Running MinPath for kegg: concoct.96.fa.contigs
Running MinPath for kegg: concoct.98.fa.contigs
Running MinPath for kegg: concoct.99.fa.contigs
Running MinPath for kegg: metabat2.13.fa_sub.contigs
Running MinPath for kegg: metabat2.14.fa.contigs
Running MinPath for kegg: metabat2.15.fa_sub.contigs
Running MinPath for kegg: metabat2.18.fa_sub.contigs
Running MinPath for kegg: metabat2.22.fa_sub.contigs
Running MinPath for kegg: metabat2.32.fa_sub.contigs
Running MinPath for kegg: metabat2.5.fa_sub.contigs
Running MinPath for kegg: metabat2.8.fa.contigs
Running MinPath for metacyc: concoct.1.fa.contigs
Running MinPath for metacyc: concoct.10.fa.contigs
Running MinPath for metacyc: concoct.100.fa.contigs
Running MinPath for metacyc: concoct.102.fa.contigs
Running MinPath for metacyc: concoct.103.fa_sub.contigs
Running MinPath for metacyc: concoct.104.fa_sub.contigs
Running MinPath for metacyc: concoct.106.fa.contigs
Running MinPath for metacyc: concoct.109.fa_sub.contigs
Running MinPath for metacyc: concoct.110.fa.contigs
Running MinPath for metacyc: concoct.111.fa.contigs
Running MinPath for metacyc: concoct.113.fa_sub.contigs
Running MinPath for metacyc: concoct.114.fa.contigs
Running MinPath for metacyc: concoct.115.fa_sub.contigs
Running MinPath for metacyc: concoct.12.fa.contigs
Running MinPath for metacyc: concoct.13.fa.contigs
Running MinPath for metacyc: concoct.16.fa.contigs
Running MinPath for metacyc: concoct.18.fa_sub.contigs
Running MinPath for metacyc: concoct.19.fa.contigs
Running MinPath for metacyc: concoct.20.fa_sub.contigs
Running MinPath for metacyc: concoct.25.fa.contigs
Running MinPath for metacyc: concoct.27.fa.contigs


```
Running MinPath for metacyc: concoct.31.fa.contigs
Running MinPath for metacyc: concoct.32.fa.contigs
Running MinPath for metacyc: concoct.34.fa_sub.contigs
Running MinPath for metacyc: concoct.36.fa.contigs
Running MinPath for metacyc: concoct.40.fa.contigs
Running MinPath for metacyc: concoct.43.fa.contigs
Running MinPath for metacyc: concoct.45.fa.contigs
Running MinPath for metacyc: concoct.46.fa.contigs
Running MinPath for metacyc: concoct.47.fa_sub.contigs
Running MinPath for metacyc: concoct.49.fa.contigs
Running MinPath for metacyc: concoct.54.fa.contigs
Running MinPath for metacyc: concoct.55.fa_sub.contigs
Running MinPath for metacyc: concoct.56.fa.contigs
Running MinPath for metacyc: concoct.57.fa.contigs
Running MinPath for metacyc: concoct.6.fa.contigs
Running MinPath for metacyc: concoct.60.fa_sub.contigs
Running MinPath for metacyc: concoct.64.fa.contigs
Running MinPath for metacyc: concoct.66.fa.contigs
Running MinPath for metacyc: concoct.69.fa.contigs
Running MinPath for metacyc: concoct.7.fa.contigs
Running MinPath for metacyc: concoct.71.fa.contigs
Running MinPath for metacyc: concoct.74.fa.contigs
Running MinPath for metacyc: concoct.75.fa.contigs
Running MinPath for metacyc: concoct.76.fa.contigs
Running MinPath for metacyc: concoct.77.fa.contigs
Running MinPath for metacyc: concoct.81.fa.contigs
Running MinPath for metacyc: concoct.82.fa.contigs
Running MinPath for metacyc: concoct.84.fa.contigs
Running MinPath for metacyc: concoct.9.fa_sub.contigs
Running MinPath for metacyc: concoct.92.fa.contigs
Running MinPath for metacyc: concoct.94.fa.contigs
Running MinPath for metacyc: concoct.95.fa.contigs
Running MinPath for metacyc: concoct.96.fa.contigs
Running MinPath for metacyc: concoct.98.fa.contigs
Running MinPath for metacyc: concoct.99.fa.contigs
Running MinPath for metacyc: metabat2.13.fa_sub.contigs
Running MinPath for metacyc: metabat2.14.fa.contigs
Running MinPath for metacyc: metabat2.15.fa_sub.contigs
Running MinPath for metacyc: metabat2.18.fa_sub.contigs
Running MinPath for metacyc: metabat2.22.fa_sub.contigs
Running MinPath for metacyc: metabat2.32.fa_sub.contigs
Running MinPath for metacyc: metabat2.5.fa_sub.contigs
Running MinPath for metacyc: metabat2.8.fa.contigs
[34m[6 hours, 23 minutes, 58 seconds]: STEP21 -> MAKING FINAL
STATISTICS: 21.stats.pl
[0m-p destination: Broken pipe
Output in /gpfs1/scratch/jonas/metasqueeze_test/results/
21.metasqueeze_test.stats

Deleting temporary files in /gpfs1/scratch/jonas/metasqueeze_test/
temp
[34m[6 hours, 24 minutes, 13 seconds]: FINISHED -> Have fun!
[0mFor citation purposes, you can find a summary of methods in the
file /gpfs1/scratch/jonas/metasqueeze_test/methods.txt
```

You can analyze your results using the SQMTools R library (see <https://github.com/jtamames/SqueezeMeta/wiki/Using-R-to-analyze-your-SQM-results>)

```
=====
=====
Resource Usage on 2023-09-30 02:23:44.914470:
JobId: 139192.pbs01                               Project:
_pbs_project_default
Submission Host: ln-0001.scelse.sg
Exit Status: 0
NCPUs Requested: 72                               NCPUs Used:
72
Memory Requested: None                            Memory
Used: 58555332kb
Vmem Used: 62231612kb
CPU Time Used: 98:12:10
Walltime requested: None                           Walltime Used:
06:24:16
Start Time: Fri Sep 29 19:59:07 2023
End Time: Sat Sep 30 02:23:44 2023
Execution Nodes Used: (hmn-0003:ncpus=72)
=====
=====
```