

Supplemental listings of commands

Removal of rRNA with SortMeRNA

```
sortmerna --ref \  
sortmerna/rRNA_databases/rfam-5s-database-id98.fasta,\  
sortmerna/index/rfam-5s-database-id98:\  
sortmerna/rRNA_databases/rfam-5.8s-database-id98.fasta,\  
sortmerna/index/rfam-5.8s-database-id98:\  
sortmerna/rRNA_databases/silva-arc-16s-id95.fasta,\  
sortmerna/index/silva-arc-16s-id95:\  
sortmerna/rRNA_databases/silva-bac-16s-id90.fasta,\  
sortmerna/index/silva-bac-16s-id90:\  
sortmerna/rRNA_databases/silva-euk-18s-id95.fasta,\  
sortmerna/index/silva-euk-18s-id95:\  
sortmerna/rRNA_databases/silva-arc-23s-id98.fasta,\  
sortmerna/index/silva-arc-23s-id98:\  
sortmerna/rRNA_databases/silva-bac-23s-id98.fasta,\  
sortmerna/index/silva-bac-23s-id98:\  
sortmerna/rRNA_databases/silva-euk-28s-id98.fasta,\  
sortmerna/index/silva-euk-28s-id98 \  
--reads totRNA-18_S32_L004_1 --other totRNA-18_S32_L004_sortmerna.fastq \  
fastq --paired_in --fastx -a 16 --sam --num_alignments 1 \  
--aligned totRNA-18_S32_L004_sortmerna_rRNA
```

Trimming of RNA-seq reads with Trimmomatic

```
java -jar \  
trimmomatic_dir/trimmomatic.jar PE -threads 16 -phred33 \  
totRNA-18_S32_L004_sortmerna_1.fq.gz totRNA-18_S32_L004_sortmerna_2.fq.gz \  
out_1.fq out_1.unpaired.fq out_2.fq out_2.unpaired.fq \  
ILLUMINACLIP:trimmomatic_dir/adapters/TruSeq3-PE-2.fa:2:30:10 \  
SLIDINGWINDOW:5:20 MINLEN:50
```

Graph traversal with Cortexpy

```
cortexpy traverse \  
TATGCAAAAATGTTGGAGAGGTATCAAAAGTATTCACAAGAAAGTG \  
--graphs input_graph.ctx \  
--max-nodes 20000 \  
--out - | \  

```

cortexpy view traversal - --to-json > output.json

Assembly with Trinity

```
Trinity --full_cleanup --KMER_SIZE 25 --seqType fq \  
--left totRNA-18_S32_L004_sortmerna_1.fq.gz \  
--right totRNA-18_S32_L004_sortmerna_2.fq.gz \  
--output trinity_output_dir
```

Assembly with Oases log

Fri Feb 9 22:08:10 2018

```
velveth /crex2/proj/sllstore2017083/nobackup/winni/proj/olof/spruce/results/2018-02-09_assembly/b2015052_nobackup/assembly/trimmomatic/oases 47 -shortPaired -fastq -separate /crex2/proj/sllstore2017083/nobackup/winni/proj/olof/spruce/results/2018-02-09_assembly/b2015052_nobackup/assembly/trimmomatic/pear/totRNA-18_S32_L004/pear.unassembled.forward.fq.gz /crex2/proj/sllstore2017083/nobackup/winni/proj/olof/spruce/results/2018-02-09_assembly/b2015052_nobackup/assembly/trimmomatic/pear/totRNA-18_S32_L004/pear.unassembled.reverse.fq.gz -short2 -fastq /crex2/proj/sllstore2017083/nobackup/winni/proj/olof/spruce/results/2018-02-09_assembly/b2015052_nobackup/assembly/trimmomatic/pear/totRNA-18_S32_L004/pear.assembled.fq.gz
```

Version 1.2.10

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Compilation settings:

CATEGORIES = 2

MAXKMERLENGTH = 64

OPENMP

Fri Feb 9 22:19:35 2018

```
velvetg /crex2/proj/sllstore2017083/nobackup/winni/proj/olof/spruce/results/2018-02-09_assembly/b2015052_nobackup/assembly/trimmomatic/oases -read_trkg yes
```

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Compilation settings:

CATEGORIES = 2

MAXKMERLENGTH = 64

OPENMP

Final graph has 364990 nodes and n50 of 248, max 5334, total 37418260, using
4654554/5941280 reads

Fri Feb 9 22:37:07 2018

oases /crex2/proj/sllstore2017083/nobackup/winni/proj/olof/spruce/results/2018-02-
09_assembly/b2015052_nobackup/assembly/trimmomatic/oases -ins_length2 500
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Compilation settings:

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MAXKMERLENGTH = 64

Finished extracting transcripts, used 5552009/5941280 reads on 22533 loci