

```
[root@tcmc_sandbox2 Test]# ./run_pipeline_test.sh
```

```
Warning: Newbler is not found, some functionality will not be available
```

```
Warning: SignalP+ is not found, some functionality will not be available
```

```
Warning: REAPR is not found, some functionality will not be available
```

```
Project dir /home/AnalysisTools/metAMOS-1.5rc3/Test/test1 successfully created!
```

```
Use runPipeline.py to start Pipeline
```

```
[Steps to be skipped]: set(['FunctionalAnnotation', 'FindRepeats'])
```

```
Starting Task = runpipeline.RUNPIPELINE
```

```
Starting metAMOS pipeline
```

```
Warning: Newbler is not found, some functionality will not be available
```

```
Warning: SignalP+ is not found, some functionality will not be available
```

```
Warning: REAPR is not found, some functionality will not be available
```

```
[Available RAM: 63 GB]
```

```
*ok
```

```
[Available CPUs: 32]
```

```
*ok
```

```
Tasks which will be run:
```

```
Task = preprocess.Preprocess
```

```
Task = assemble.SplitAssemblers
```

```
Task = assemble.Assemble
```

```
Task = assemble.CheckAsmResults
```

```
Task = assemble.SplitMappers
```

Task = mapreads.MapReads
Task = mapreads.CheckMapResults
Task = mapreads.SplitForORFs
Task = findorfs.FindORFS
Task = validate.Validate
Task = findreps.FindRepeats
Task = annotate.Annotate
Task = fannotate.FunctionalAnnotation
Task = scaffold.Scaffold
Task = findscforfs.FindScaffoldORFS
Task = abundance.Abandance
Task = propagate.Propagate
Task = classify.Classify
Task = postprocess.Postprocess

Warning: Graphviz is not found, some functionality will not be available

metAMOS configuration summary:

metAMOS Version:	v1.5rc3 "Praline Brownie"	workflows: core,optional,imetamos
Time and Date:	2016-09-28	
Working directory:	/home/AnalysisTools/metAMOS-1.5rc3/Test/test1	
Prefix:	proba	
K-Mer:	55	
Threads:	15	
Taxonomic level:	genus	
Verbose:	False	

Steps to skip: FunctionalAnnotation, Scaffold, Propagate, FindRepeats

Steps to force: Abundance, FindORFS, Annotate, Propagate, MapReads, Assemble, FindScaffoldORFS, Classify

[citation]

MetAMOS

Treangen, TJ & Koren, S, Sommer, DD, Liu, B, Astrovskaya, I, Ondov, B, Darling AE, Phillippy AM, Pop, M. MetAMOS: a modular and open source metagenomic assembly and analysis pipeline. *Genome biology*, 14(1), R2, 2013.

iMetAMOS

Koren, S, Treangen, TJ, Hill, CM, Pop, M, Phillippy, AM. Automated ensemble assembly and validation of microbial genomes. *BMC Bioinformatics* 15:126, 2014.

Step-specific configuration:

[abundance]

MetaPhyler

`/home/AnalysisTools/metAMOS-1.5rc3/Utilities/cpp/Linux-x86_64`

Liu B, Gibbons T, Ghodsi M, Treangen T, Pop M. Accurate and fast estimation of taxonomic profiles from metagenomic shotgun sequences. *BMC Genomics*. 2011;12 Suppl 2:S4. Epub 2011 Jul 27.

[multialign]

M-GCAT

`/home/AnalysisTools/metAMOS-1.5rc3/Utilities/cpp/Linux-x86_64`

Treangen TJ, Messeguer X. M-GCAT: interactively and efficiently constructing large-scale multiple genome comparison frameworks in closely related species. *BMC Bioinformatics*, 2006.

[fannotate]

BLAST

/home/AnalysisTools/metAMOS-1.5rc3/Utilities/cpp/Linux-x86_64

Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ. Basic local alignment search tool. *J Mol Biol.* 1990 Oct 5;215(3):403-10.

[scaffold]

Bambus 2

/home/AnalysisTools/metAMOS-1.5rc3/AMOS/Linux-x86_64/bin

Koren S, Treangen TJ, Pop M. Bambus 2: scaffolding metagenomes. *Bioinformatics* 27(21): 2964-2971 2011.

[findorfs]

Prokka

/home/AnalysisTools/metAMOS-1.5rc3/Utilities/cpp/Linux-x86_64/prokka/bin

Seemann, T. Prokka: rapid prokaryotic genome annotation. *Bioinformatics*, btu153. 2014.

[annotate]

Kraken

/home/AnalysisTools/metAMOS-1.5rc3/Utilities/cpp/Linux-x86_64/kraken/bin

Wood DE, Salzberg SL: Kraken: ultrafast metagenomic sequence classification using exact alignments. *Genome Biology* 2014, 15:R46.

[assemble]

Velvet

/home/AnalysisTools/metAMOS-1.5rc3/Utilities/cpp/Linux-x86_64/velvet

Zerbino DR, Birney E. Velvet: algorithms for de novo short read assembly using de Bruijn

graphs. Genome Res. 2008 May;18(5):821-9.

SOAPdenovo

/home/AnalysisTools/metAMOS-1.5rc3/Utilities/cpp/Linux-x86_64

Li Y, Hu Y, Bolund L, Wang J: State of the art de novo assembly of human genomes from massively parallel sequencing data. Human genomics 2010, 4:271-277.

[mapreads]

Bowtie

/home/AnalysisTools/metAMOS-1.5rc3/Utilities/cpp/Linux-x86_64

Langmead B, Trapnell C, Pop M, Salzberg SL. Ultrafast and memory-efficient alignment of short DNA sequences to the human genome. Genome Biol. 2009;10(3):R25. Epub 2009 Mar 4.

[preprocess]

metAMOS built-in filtering

N/A

[validate]

frc

UNKNOWN UNKNOWN

CGAL

/home/AnalysisTools/metAMOS-1.5rc3/Utilities/cpp/Linux-x86_64/cgal

Rahman, A, Pachter, L CGAL: computing genome assembly likelihoods. Genome biology, 14(1), R8, 2013.

ALE

/home/AnalysisTools/metAMOS-1.5rc3/Utilities/cpp/Linux-x86_64/ALE/src

Clark, SC, Egan, R, Frazier, PI, Wang, Z. ALE: a generic assembly likelihood evaluation framework for assessing the accuracy of genome and metagenome assemblies. *Bioinformatics*, 29(4) 435-443, 2013.

QUAST

/home/AnalysisTools/metAMOS-1.5rc3/quast

Gurevich, A, Saveliev, V, Vyahhi, N, Tesler, G. QUAST: quality assessment tool for genome assemblies. *Bioinformatics*, 29(8), 1072-1075, 2013.

Prokka

/home/AnalysisTools/metAMOS-1.5rc3/Utilities/cpp/Linux-x86_64/prokka/bin

Seemann, T. Prokka: rapid prokaryotic genome annotation. *Bioinformatics*, btu153. 2014.

FreeBayes

/home/AnalysisTools/metAMOS-1.5rc3/Utilities/cpp/Linux-x86_64/freebayes/bin

Garrison, E, Marth, G. Haplotype-based variant detection from short-read sequencing. *arXiv preprint arXiv:1207.3907*, 2012.

LAP

/home/AnalysisTools/metAMOS-1.5rc3/LAP

Ghods M, Hill CM, Astrovskaya I, Lin H, Sommer DD, Koren S, Pop M. De novo likelihood-based measures for comparing genome assemblies. *BMC research notes* 6:334, 2013.

REAPR

Hunt, M, Kikuchi, T, Sanders, M, Newbold, C, Berriman, M, & Otto, TD. REAPR: a universal tool for genome assembly evaluation. *Genome biology*, 14(5), R47, 2013.

[other]

Krona

/home/AnalysisTools/metAMOS-1.5rc3/KronaTools/bin

Ondov BD, Bergman NH, Phillippy AM. Interactive metagenomic visualization in a Web browser. BMC Bioinformatics. 2011 Sep 30;12:385.

Starting Task = preprocess.PREPROCESS

Job = [[carsonella_pe_filt.fna] -> preprocess.success] completed

Completed Task = preprocess.Preprocess

Starting Task = assemble.ASEMBLE

Job = [preprocess.success -> *.run] completed

Completed Task = assemble.SplitAssemblers

Job = [soapdenovo.55.run -> soapdenovo.55.asm.contig] completed

Job = [velvet.55.run -> velvet.55.asm.contig] completed

Completed Task = assemble.Assemble

Job = [[soapdenovo.55.asm.contig, velvet.55.asm.contig] -> [assemble.ok]] completed

Completed Task = assemble.CheckAsmResults

Uptodate Task = assemble.SplitMappers

Starting Task = mapreads.MAPREADS

Job = [soapdenovo.55.asm.contig -> soapdenovo.55.contig.cvg] completed

Job = [velvet.55.asm.contig -> velvet.55.contig.cvg] completed

Completed Task = mapreads.MapReads

Job = [[soapdenovo.55.contig.cvg, velvet.55.contig.cvg] -> [mapreads.ok]] completed

Completed Task = mapreads.CheckMapResults

Uptodate Task = mapreads.SplitForORFs

Starting Task = findorfs.FINDORFS

[91m*****

*****ERROR*****

During findorfs, the following command failed with return code 2:

```
>> /home/AnalysisTools/metAMOS-1.5rc3/Utilities/cpp/Linux-x86_64/prokka/bin/prokka --fast --outdir
/home/AnalysisTools/metAMOS-1.5rc3/Test/test1/FindORFS/out/soapdenovo.55.prokka --prefix
soapdenovo.55 --force
/home/AnalysisTools/metAMOS-1.5rc3/Test/test1/FindORFS/in/soapdenovo.55.asm.contig
```

*****DETAILS*****

Last 10 commands run before the error

(/home/AnalysisTools/metAMOS-1.5rc3/Test/test1/Logs/COMMANDS.log)

|2016-09-28 11:24:50| cat

```
/home/AnalysisTools/metAMOS-1.5rc3/Test/test1/Assemble/out/soapdenovo.55.lib1.mappedmates >>
/home/AnalysisTools/metAMOS-1.5rc3/Test/test1/Assemble/out/soapdenovo.55.lib1.hdr
```

|2016-09-28 11:24:50| cp

```
/home/AnalysisTools/metAMOS-1.5rc3/Test/test1/Assemble/out/soapdenovo.55.lib1.hdr
/home/AnalysisTools/metAMOS-1.5rc3/Test/test1/Assemble/out/soapdenovo.55.lib1.mappedmates
```

```
|2016-09-28 11:24:51| /home/AnalysisTools/metAMOS-1.5rc3/Utilities/cpp/Linux-x86_64/bowtie-build
-o 2 /home/AnalysisTools/metAMOS-1.5rc3/Test/test1/Assemble/out/velvet.55.asm.contig
/home/AnalysisTools/metAMOS-1.5rc3/Test/test1/Assemble/out/velvet.55.IDX
```

```
|2016-09-28 11:24:51| /home/AnalysisTools/metAMOS-1.5rc3/Utilities/cpp/Linux-x86_64/bowtie -p 15
-f -l 25 -e 140 --best --strata -m 10 -k 1 --un
```

```
/home/AnalysisTools/metAMOS-1.5rc3/Test/test1/Assemble/out/velvet.55.lib1.unaligned.fasta
/home/AnalysisTools/metAMOS-1.5rc3/Test/test1/Assemble/out/velvet.55.IDX
/home/AnalysisTools/metAMOS-1.5rc3/Test/test1/Preprocess/out/lib1.seq >
/home/AnalysisTools/metAMOS-1.5rc3/Test/test1/Assemble/out/lib1.bout
```

|2016-09-28 11:24:53| cat

```
/home/AnalysisTools/metAMOS-1.5rc3/Test/test1/Assemble/out/velvet.55.lib1.mappedmates >>
/home/AnalysisTools/metAMOS-1.5rc3/Test/test1/Assemble/out/velvet.55.lib1.hdr
```



```
|2016-09-28 11:24:53| cp
/home/AnalysisTools/metAMOS-1.5rc3/Test/test1/Assemble/out/velvet.55.lib1.hdr
/home/AnalysisTools/metAMOS-1.5rc3/Test/test1/Assemble/out/velvet.55.lib1.mappedmates
```

```
|2016-09-28 11:24:55|# [FINDORFS]
```

```
|2016-09-28 11:24:55| unlink
/home/AnalysisTools/metAMOS-1.5rc3/Test/test1/FindORFS/in/soapdenovo.55.asm.contig
```

```
|2016-09-28 11:24:55| ln
/home/AnalysisTools/metAMOS-1.5rc3/Test/test1/Assemble/out/soapdenovo.55.asm.contig
/home/AnalysisTools/metAMOS-1.5rc3/Test/test1/FindORFS/in/soapdenovo.55.asm.contig
```

```
|2016-09-28 11:24:58|
/home/AnalysisTools/metAMOS-1.5rc3/Utilities/cpp/Linux-x86_64/prokka/bin/prokka --fast --outdir
/home/AnalysisTools/metAMOS-1.5rc3/Test/test1/FindORFS/out/soapdenovo.55.prokka --prefix
soapdenovo.55 --force
/home/AnalysisTools/metAMOS-1.5rc3/Test/test1/FindORFS/in/soapdenovo.55.asm.contig
```

Last 10 lines of output (/home/AnalysisTools/metAMOS-1.5rc3/Test/test1/Logs/FINDORFS.log)

```
[11:24:55] 16 tRNA-Glu c[40105,40175] 33 (ttc)
```

```
[11:24:55] 17 tRNA-Ile c[61482,61557] 36 (gat)
```

```
[11:24:55] 18 tRNA-Tyr [88050,88131] 35 (gta)
```

```
[11:24:55] 19 tRNA-Gly [88134,88206] 34 (tcc)
```

```
[11:24:55] 20 tRNA-Trp [88228,88298] 33 (cca)
```

```
[11:24:55] Found 28 tRNAs
```

```
[11:24:55] Predicting Ribosomal RNAs
```

```
[11:24:55] Running RNAmmer
```

```
[11:24:55] Running: rnammer -S bac -multi -xml
/home/AnalysisTools/metAMOS-1.5rc3/Test/test1/FindORFS/out/soapdenovo.55.prokka/rnammer.xml
/home/AnalysisTools/metAMOS-1.5rc3/Test/test1/FindORFS/out/soapdenovo.55.prokka/soapdenovo.5
5.fna
```

```
[11:24:58] Could not run command: rnammer -S bac -multi -xml
/home/AnalysisTools/metAMOS-1.5rc3/Test/test1/FindORFS/out/soapdenovo.55.prokka/rnammer.xml
/home/AnalysisTools/metAMOS-1.5rc3/Test/test1/FindORFS/out/soapdenovo.55.prokka/soapdenovo.5
```

5.fna

Please verify input data and restart MetAMOS. If the problem persists please contact the MetAMOS development team.

*****ERROR*****

rm: cannot remove â/home/AnalysisTools/metAMOS-1.5rc3/Test/test1/Logs/findorfs.okâ: No such file or directory

Oops, MetAMOS finished with errors! see text in red above for details.

[root@tcmc_sandbox2 Test]# ls -l /home/AnalysisTools/metAMOS-1.5rc3/Test/test1/FindORFS/out

total 180

-rw-r--r--. 1 root root 591 Sep 28 11:24 6837.lsu.cf
-rw-r--r--. 1 root root 591 Sep 28 11:24 6837.ssu.cf
-rw-r--r--. 1 root root 588 Sep 28 11:24 6837.tsu.cf
drwxr-xr-x. 2 root root 4096 Sep 28 11:24 soapdenovo.55.prokka
-rw-r--r--. 1 root root 162469 Sep 28 11:24 temp.6837.fsa
-rw-r--r--. 1 root root 380 Sep 28 11:24 temp.6837.xml

[root@tcmc_sandbox2 Test]# ls -l /home/AnalysisTools/metAMOS-1.5rc3/Test/test1/Logs

total 64

-rw-r--r--. 1 root root 12167 Sep 28 11:24 ASSEMBLE.log
-rw-r--r--. 1 root root 0 Sep 28 11:24 assemble.ok
-rw-r--r--. 1 root root 0 Sep 28 11:24 assemble.started
-rw-r--r--. 1 root root 11357 Sep 28 11:24 COMMANDS.log
-rw-r--r--. 1 root root 5039 Sep 28 11:24 FINDORFS.log

-rw-r--r--. 1 root root 0 Sep 28 11:24 findorfs.started
-rw-r--r--. 1 root root 22514 Sep 28 11:24 MAPREADS.log
-rw-r--r--. 1 root root 0 Sep 28 11:24 mapreads.ok
-rw-r--r--. 1 root root 0 Sep 28 11:24 mapreads.started
-rw-r--r--. 1 root root 1294 Sep 28 11:24 PREPROCESS.log
-rw-r--r--. 1 root root 0 Sep 28 11:24 preprocess.ok
-rw-r--r--. 1 root root 0 Sep 28 11:24 preprocess.started
-rw-r--r--. 1 root root 1305 Sep 28 11:24 RUNPIPELINE.log
-rw-r--r--. 1 root root 0 Sep 28 11:24 runpipeline.started