

Mac version

Using ReadLine, Boost, HDF5, GSL
mothur v.1.47.0

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by

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<http://www.mothur.org>

When using, please cite:

Schloss, P.D., et al., Introducing mothur: Open-source, platform-independent, community-supported software for describing and comparing microbial communities. *Appl Environ Microbiol*, 2009. 75(23):7537-41.

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Type 'help()' for information on the commands that are available

For questions and analysis support, please visit our forum at <https://forum.mothur.org>

Type 'quit()' to exit program

[NOTE]: Setting random seed to 19760620.

Interactive Mode

```
mothur > make.contigs(file=stability.files)
```

Using 8 processors.

```
>>>> Processing file pair F3D0_S188_L001_R1_001.fastq -  
F3D0_S188_L001_R2_001.fastq (files 1 of 1)<<<<  
Making contigs...  
Done.
```

It took 2 secs to assemble 7793 reads.

Group count:

```
FD30      7793
```

Total of all groups is 7793

It took 2 secs to process 7793 sequences.

Output File Names:

stability.trim.contigs.fasta
stability.scrap.contigs.fasta
stability.contigs_report
stability.contigs.count_table

```
mothur > summary.seqs(fasta=stability.trim.contigs.fasta)
```

Using 8 processors.

	Start	End	NBases	Ambigs	Polymer	NumSeqs
Minimum: 1	249	249	0	3	1	
2.5%-tile:	1	252	252	0	4	195
25%-tile:	1	252	252	0	4	1949
Median: 1	252	252	0	4	3897	
75%-tile:	1	253	253	0	5	5845
97.5%-tile:	1	253	253	5	6	7599
Maximum: 1	502	502	241	188	7793	
Mean: 1	252	252	0	4		
# of Seqs:	7793					

It took 0 secs to summarize 7793 sequences.

Output File Names:

stability.trim.contigs.summary

```
mothur > screen.seqs(fasta=stability.trim.contigs.fasta, maxambig=0,  
maxlength=275)
```

Using 8 processors.

It took 0 secs to screen 7793 sequences, removed 1155.

Output File Names:

stability.trim.contigs.good.fasta
stability.trim.contigs.bad.accnos

It took 0 secs to screen 7793 sequences.

```
mothur > get.current()
```

Current RAM usage: 0.130989 Gigabytes. Total Ram: 8 Gigabytes.

Current files saved by mothur:

```
accnos=stability.trim.contigs.bad.accnos
fasta=stability.trim.contigs.good.fasta
contigsreport=stability.contigs_report
count=stability.contigs.count_table
processors=8
summary=stability.trim.contigs.summary
```

Current default directories saved by mothur:
mothur/

Current working directory: /Users/natalieburkhard/bio-490/
independentStudy/Lab9.2/

Output File Names:
current_files.summary

```
mothur > unique.seqs(fasta=stability.trim.contigs.good.fasta)
6638      1533
```

Output File Names:
stability.trim.contigs.good.unique.fasta
stability.trim.contigs.good.count_table

```
mothur > count.seqs(name=stability.trim.contigs.good.count_table)
```

It took 0 secs to create a table for 1534 sequences.

Total number of sequences: 1534

Output File Names:
stability.trim.contigs.good.count_table