

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:

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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.

Unable to open Mock\_S280\_L001\_R1\_001.fastq. Trying MOTHUR\_FILES

directory mothur/Mock\_S280\_L001\_R1\_001.fastq.

Unable to open mothur/Mock\_S280\_L001\_R1\_001.fastq. Trying mothur's executable directory mothur/Mock\_S280\_L001\_R1\_001.fastq.

Unable to open mothur/Mock\_S280\_L001\_R1\_001.fastq.

[WARNING]: can't find mothur/Mock\_S280\_L001\_R1\_001.fastq, ignoring pair.

Unable to open Mock\_S280\_L001\_R2\_001.fastq. Trying MOTHUR\_FILES

directory mothur/Mock\_S280\_L001\_R2\_001.fastq.

Unable to open mothur/Mock\_S280\_L001\_R2\_001.fastq. Trying mothur's executable directory mothur/Mock\_S280\_L001\_R2\_001.fastq.

Unable to open mothur/Mock\_S280\_L001\_R2\_001.fastq.

[WARNING]: can't find mothur/Mock\_S280\_L001\_R2\_001.fastq, ignoring pair.

```
>>>>> Processing file pair F3D0_S188_L001_R1_001.fastq -
F3D0_S188_L001_R2_001.fastq (files 1 of 3) <<<<<
Making contigs...
Done.
```

It took 1 secs to assemble 7793 reads.

```
>>>>> Processing file pair F3D144_S210_L001_R1_001.fastq -
F3D144_S210_L001_R2_001.fastq (files 2 of 3) <<<<<
Making contigs...
Done.
```

It took 1 secs to assemble 4827 reads.

```
>>>>> Processing file pair F3D7_S195_L001_R1_001.fastq -
F3D7_S195_L001_R2_001.fastq (files 3 of 3) <<<<<
Making contigs...
Done.
```

It took 1 secs to assemble 5129 reads.

```
Group count:
F3D0      7793
F3D144    4827
F3D7      5129
```

Total of all groups is 17749

It took 3 secs to process 17749 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	3	444
25%-tile:	1	252	252	0	4	4438
Median: 1	252	252	0	4	8875	

75%-tile:	1	253	253	0	5	13312
97.5%-tile:	1	253	253	6	6	17306
Maximum: 1	502	502	246	243	17749	
Mean: 1	252	252	0	4		
# of Seqs:	17749					

It took 0 secs to summarize 17749 sequences.

Output File Names:  
stability.trim.contigs.summary

mothur > get.current()

Current RAM usage: 0.138233 Gigabytes. Total Ram: 8 Gigabytes.

Current files saved by mothur:  
fasta=stability.trim.contigs.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/Lab10.3/

Output File Names:  
current\_files.summary

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

Using 8 processors.

It took 0 secs to screen 17749 sequences, removed 2871.

Output File Names:  
stability.trim.contigs.good.fasta  
stability.trim.contigs.bad.accnos

It took 0 secs to screen 17749 sequences.

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

14878    2831

Output File Names:

stability.trim.contigs.good.unique.fasta

stability.trim.contigs.good.count\_table

```
mothur > count.seqs(name=stability.trim.contigs.good.unique.fasta)
[ERROR]: Your count table contains more than 1 sequence named
ee=0.161021, sequence names must be unique. Please correct.
```

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

14878    2831

Output File Names:

stability.trim.contigs.good.unique.fasta

stability.trim.contigs.good.count\_table

```
mothur > count.seqs(name=stability.trim.contigs.good.unique.fasta)
[ERROR]: Your count table contains more than 1 sequence named
ee=0.161021, sequence names must be unique. Please correct.
```

```
mothur > unique.seqs(fasta=stability.trim.contigs.good.count_table)
[WARNING]: We found more than 25% of the bases in sequence
epresentative_Sequence to be ambiguous. Mothur is not setup to process
protein sequences.
1            1
```

Output File Names:

stability.trim.contigs.good.unique.count\_table

stability.trim.contigs.good.count\_table