```
Mac version

Using ReadLine,Boost,HDF5,GSL
mothur v.1.47.0
Last updated: 1/21/22
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.file(inputdir=., type=fastq, prefix=stability)
Setting input directories to:
        /Users/natalieburkhard/bio-490/independentStudy/Lab9.3/


Output File Names:
/Users/natalieburkhard/bio-490/independentStudy/Lab9.3/stability.files


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 1 secs to assemble 7793 reads.

Group count:
F3D0   7793

Total of all groups is 7793

It took 1 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 > make.contigs(file=stability.files, maxambig=0, maxlength=275, maxhomop=8)

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:
F3D0    6638

Total of all groups is 6638

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 > get.current()

Current RAM usage: 0.137127 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
file=/Users/natalieburkhard/bio-490/independentStudy/Lab9.3/
stability.files

Current input directories saved by mothur:
        /Users/natalieburkhard/bio-490/independentStudy/Lab9.3/


Current default directories saved by mothur:
        mothur/


Current working directory: /Users/natalieburkhard/bio-490/
independentStudy/Lab9.3/

Output File Names:
current_files.summary


mothur > unique.seqs(fasta=stability.trim.contigs.good.fasta)
Unable to open stability.trim.contigs.good.fasta. Trying input
directory /Users/natalieburkhard/bio-490/independentStudy/Lab9.3/
stability.trim.contigs.good.fasta.
Unable to open /Users/natalieburkhard/bio-490/independentStudy/Lab9.3/
stability.trim.contigs.good.fasta. Trying MOTHUR_FILES directory
```

```
mothur/stability.trim.contigs.good.fasta.
Unable to open mothur/stability.trim.contigs.good.fasta. Trying
mothur's executable directory mothur/
stability.trim.contigs.good.fasta.
Unable to open mothur/stability.trim.contigs.good.fasta.
Unable to open stability.trim.contigs.good.fasta
[ERROR]: did not complete unique.seqs.

mothur > screen.seqs(fasta=stability.trim.contigs.fasta,
count=stability.contigs.count_table, maxambig=0, maxlength=275,
maxhomop=8)

Using 8 processors.

It took 0 secs to screen 6638 sequences, removed 0.

[NOTE]: no sequences were bad, removing
stability.trim.contigs.bad.accnos


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


It took 0 secs to screen 6638 sequences.

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 > unique.seqs(fasta=stability.trim.contigs.fasta,
count=stability.contigs.count_table)
6638    1533

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


mothur > ummary.seqs(count=stability.trim.contigs.count_table)
[ERROR]: Invalid command.
[ERROR]: did not complete ummary.seqs.

mothur > summary.seqs(count=stability.trim.contigs.count_table)
Using stability.trim.contigs.unique.fasta as input file for the fasta
parameter.
```

```
Using 8 processors.

                Start   End     NBases  Ambigs  Polymer NumSeqs
Minimum: 1      250     250     0       3       1
2.5%-tile:      1       252     252     0       4       166
25%-tile:       1       252     252     0       4       1660
Median:  1      252     252     0       4       3320
75%-tile:       1       253     253     0       5       4979
97.5%-tile:     1       253     253     0       6       6473
Maximum: 1      255     255     0       8       6638
Mean:   1       252     252     0       4
# of unique seqs:       1533
total # of seqs: 6638

It took 0 secs to summarize 6638 sequences.

Output File Names:
stability.trim.contigs.unique.summary


mothur > pcr.seqs(fasta=silva.bacteria.fasta, start=11894, end=25319,
keepdots=F)

Using 8 processors.
[NOTE]: no sequences were bad, removing silva.bacteria.bad.accnos

It took 8 secs to screen 14956 sequences.

Output File Names:
silva.bacteria.pcr.fasta



mothur > rename.file(input=silva.bacteria.pcr.fasta,
new=silva.v4.fasta)

Current files saved by mothur:
fasta=silva.bacteria.pcr.fasta
contigsreport=stability.contigs_report
count=stability.trim.contigs.count_table
processors=8
summary=stability.trim.contigs.unique.summary
file=/Users/natalieburkhard/bio-490/independentStudy/Lab9.3/
stability.files

mothur > summary.seqs(fasta=silva.v4.fasta)

Using 8 processors.
```

```
                Start   End     NBases  Ambigs  Polymer NumSeqs
Minimum:        2       13425   270     0       3       1
2.5%-tile:      2       13426   292     0       4       374
25%-tile:       2       13426   293     0       4       3740
Median:         2       13426   293     0       4       7479
75%-tile:       2       13426   293     0       5       11218
97.5%-tile:     2       13426   294     1       6       14583
Maximum:        4       13426   351     5       9       14956
Mean:   2       13425   292     0       4
# of Seqs:      14956

It took 2 secs to summarize 14956 sequences.

Output File Names:
silva.v4.summary


mothur > align.seqs(fasta=stability.trim.contigs.unique.fasta,
reference=silva.v4.fasta)

Using 8 processors.

Reading in the silva.v4.fasta template sequences...        DONE.
It took 5 to read  14956 sequences.

Aligning sequences from stability.trim.contigs.unique.fasta ...
It took 1 secs to align 1533 sequences.


It took 1 seconds to align 1533 sequences.

Output File Names:
stability.trim.contigs.unique.align
stability.trim.contigs.unique.align_report


mothur > summary.seqs(fasta=stability.trim.contigs.unique.align,
count=stability.trim.contigs.count_table)

Using 8 processors.

                Start   End     NBases  Ambigs  Polymer NumSeqs
Minimum:        1968    11550   250     0       3       1
2.5%-tile:      1969    11551   252     0       4       166
25%-tile:       1969    11551   252     0       4       1660
Median:         1969    11551   252     0       4       3320
75%-tile:       1969    11551   253     0       5       4979
97.5%-tile:     1969    11551   253     0       6       6473
Maximum:        1969    11553   255     0       8       6638
Mean:   1968    11550   252     0       4
```

```
# of unique seqs:        1533
total # of seqs: 6638

It took 0 secs to summarize 6638 sequences.

Output File Names:
stability.trim.contigs.unique.summary


mothur > screen.seqs(fasta=stability.trim.contigs.unique.align,
count=stability.trim.contigs.count_table, start=1969, end=11551)

Using 8 processors.

It took 0 secs to screen 1533 sequences, removed 10.

/******************************************/
Running command:
remove.seqs(accnos=stability.trim.contigs.unique.bad.accnos.temp,
count=stability.trim.contigs.count_table)
Removed 10 sequences from stability.trim.contigs.count_table.

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

/******************************************/

Output File Names:
stability.trim.contigs.unique.good.align
stability.trim.contigs.unique.bad.accnos
stability.trim.contigs.good.count_table


It took 1 secs to screen 1533 sequences.

mothur > summary.seqs(fasta=current, count=current)
Using stability.trim.contigs.good.count_table as input file for the
count parameter.
Using stability.trim.contigs.unique.good.align as input file for the
fasta parameter.

Using 8 processors.

                Start    End     NBases   Ambigs   Polymer  NumSeqs
Minimum: 1968   11551    250     0        3        1
2.5%-tile:      1969     11551   252      0        4        166
25%-tile:       1969     11551   252      0        4        1658
Median:  1969   11551    252     0        4        3315
75%-tile:       1969     11551   253      0        5        4972
97.5%-tile:     1969     11551   253      0        6        6463
```

```
Maximum: 1969    11553   255     0       8       6628
Mean:   1968    11551   252     0       4
# of unique seqs:        1523
total # of seqs: 6628

It took 1 secs to summarize 6628 sequences.

Output File Names:
stability.trim.contigs.unique.good.summary


mothur > filter.seqs(fasta=stability.trim.contigs.unique.good.align,
vertical=T, trump=.)

Using 8 processors.
Creating Filter...
It took 0 secs to create filter for 1523 sequences.


Running Filter...
It took 0 secs to filter 1523 sequences.



Length of filtered alignment: 297
Number of columns removed: 13129
Length of the original alignment: 13426
Number of sequences used to construct filter: 1523

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


mothur >
unique.seqs(fasta=stability.trim.contigs.unique.good.filter.fasta,
count=stability.trim.contigs.good.count_table)
1523    1523

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


mothur >
pre.cluster(fasta=stability.trim.contigs.unique.good.filter.unique.fas
ta, count=stability.trim.contigs.unique.good.filter.count_table,
diffs=2)

Using 8 processors.
```

```
/******************************************/
Running command: split.groups(groups=F3D0,
fasta=stability.trim.contigs.unique.good.filter.unique.fasta,
count=stability.trim.contigs.unique.good.filter.count_table)

Using 8 processors.
Reducing processors to 1.
/******************************************/
Selecting sequences for group F3D0

Selected 1523 sequences from
stability.trim.contigs.unique.good.filter.unique.fasta0_1.
/******************************************/


Output File Names:
stability.trim.contigs.unique.good.filter.F3D0.count_table
stability.trim.contigs.unique.good.filter.unique.F3D0.fasta

/******************************************/
Reducing processors to 1.

Processing group F3D0:
F3D0    1523    617     906
Total number of sequences before pre.cluster was 1523.
pre.cluster removed 906 sequences.

It took 0 secs to cluster 1523 sequences.

Deconvoluting count table results...
It took 0 secs to merge 617 sequences group data.
/******************************************/
Running command:
get.seqs(fasta=stability.trim.contigs.unique.good.filter.unique.fasta,
accnos=stability.trim.contigs.unique.good.filter.unique.precluster.cou
nt_table.temp)
Selected 617 sequences from
stability.trim.contigs.unique.good.filter.unique.fasta.

Output File Names:
stability.trim.contigs.unique.good.filter.unique.pick.fasta

/******************************************/
It took 0 secs to run pre.cluster.

Using 8 processors.

Output File Names:
stability.trim.contigs.unique.good.filter.unique.precluster.fasta
```

```
stability.trim.contigs.unique.good.filter.unique.precluster.count_tabl
e
stability.trim.contigs.unique.good.filter.unique.precluster.F3D0.map


mothur >
chimera.vsearch(fasta=stability.trim.contigs.unique.good.filter.unique
.precluster.fasta,
count=stability.trim.contigs.unique.good.filter.unique.precluster.coun
t_table, dereplicate=t)

Using 8 processors.
Using vsearch version v2.16.0.
Checking sequences from
stability.trim.contigs.unique.good.filter.unique.precluster.fasta ...

/******************************************/
Running command: split.groups(groups=F3D0,
fasta=stability.trim.contigs.unique.good.filter.unique.precluster.fast
a,
count=stability.trim.contigs.unique.good.filter.unique.precluster.coun
t_table)

Using 8 processors.
Reducing processors to 1.
/******************************************/
Selecting sequences for group F3D0

Selected 617 sequences from
stability.trim.contigs.unique.good.filter.unique.precluster.fasta0_1.
/******************************************/


Output File Names:
stability.trim.contigs.unique.good.filter.unique.precluster.F3D0.count
_table
stability.trim.contigs.unique.good.filter.unique.precluster.F3D0.fasta

/******************************************/
Reducing processors to 1.

It took 1 secs to check 617 sequences from group F3D0.
It took 1 secs to check 617 sequences.


Removing chimeras from your input files:
/******************************************/
Running command:
remove.seqs(fasta=stability.trim.contigs.unique.good.filter.unique.pre
cluster.fasta,
```

```
accnos=stability.trim.contigs.unique.good.filter.unique.precluster.den
ovo.vsearch.accnos)
Removed 304 sequences from
stability.trim.contigs.unique.good.filter.unique.precluster.fasta.

Output File Names:
stability.trim.contigs.unique.good.filter.unique.precluster.pick.fasta

/******************************************/

Output File Names:
stability.trim.contigs.unique.good.filter.unique.precluster.denovo.vse
arch.count_table
stability.trim.contigs.unique.good.filter.unique.precluster.denovo.vse
arch.chimeras
stability.trim.contigs.unique.good.filter.unique.precluster.denovo.vse
arch.accnos
stability.trim.contigs.unique.good.filter.unique.precluster.denovo.vse
arch.fasta


mothur >
remove.seqs(fasta=stability.trim.contigs.good.unique.good.filter.uniqu
e.precluster.fasta,
accnos=stability.trim.contigs.good.unique.good.filter.unique.precluste
r.denovo.vsearch.accnos)
Unable to open
stability.trim.contigs.good.unique.good.filter.unique.precluster.denov
o.vsearch.accnos. Trying input directory /Users/natalieburkhard/
bio-490/independentStudy/Lab9.3/
stability.trim.contigs.good.unique.good.filter.unique.precluster.denov
o.vsearch.accnos.
Unable to open /Users/natalieburkhard/bio-490/independentStudy/Lab9.3/
stability.trim.contigs.good.unique.good.filter.unique.precluster.denov
o.vsearch.accnos. Trying MOTHUR_FILES directory mothur/
stability.trim.contigs.good.unique.good.filter.unique.precluster.denov
o.vsearch.accnos.
Unable to open mothur/
stability.trim.contigs.good.unique.good.filter.unique.precluster.denov
o.vsearch.accnos. Trying mothur's executable directory mothur/
stability.trim.contigs.good.unique.good.filter.unique.precluster.denov
o.vsearch.accnos.
Unable to open mothur/
stability.trim.contigs.good.unique.good.filter.unique.precluster.denov
o.vsearch.accnos.
Unable to open
stability.trim.contigs.good.unique.good.filter.unique.precluster.denov
o.vsearch.accnos
Unable to open
stability.trim.contigs.good.unique.good.filter.unique.precluster.fasta
```

```
. Trying input directory /Users/natalieburkhard/bio-490/
independentStudy/Lab9.3/
stability.trim.contigs.good.unique.good.filter.unique.precluster.fasta
.
Unable to open /Users/natalieburkhard/bio-490/independentStudy/Lab9.3/
stability.trim.contigs.good.unique.good.filter.unique.precluster.fasta
. Trying MOTHUR_FILES directory mothur/
stability.trim.contigs.good.unique.good.filter.unique.precluster.fasta
.
Unable to open mothur/
stability.trim.contigs.good.unique.good.filter.unique.precluster.fasta
. Trying mothur's executable directory mothur/
stability.trim.contigs.good.unique.good.filter.unique.precluster.fasta
.
Unable to open mothur/
stability.trim.contigs.good.unique.good.filter.unique.precluster.fasta
.
Unable to open mothur/
stability.trim.contigs.good.unique.good.filter.unique.precluster.fasta
, skipping.
[ERROR]: did not complete remove.seqs.

mothur >
remove.seqs(fasta=stability.trim.contigs.unique.good.filter.unique.pre
cluster.fasta,
accnos=stability.trim.contigs.unique.good.filter.unique.precluster.den
ovo.vsearch.accnos)
Removed 304 sequences from
stability.trim.contigs.unique.good.filter.unique.precluster.fasta.

Output File Names:
stability.trim.contigs.unique.good.filter.unique.precluster.pick.fasta


mothur > summary.seqs(fasta=current, count=current)
Using
stability.trim.contigs.unique.good.filter.unique.precluster.denovo.vse
arch.count_table as input file for the count parameter.
Using
stability.trim.contigs.unique.good.filter.unique.precluster.pick.fasta
as input file for the fasta parameter.

Using 8 processors.

                Start   End     NBases  Ambigs  Polymer NumSeqs
Minimum: 1      297     250     0       3       1
2.5%-tile:      1       297     252     0       4       155
25%-tile:       1       297     252     0       4       1550
Median:  1      297     252     0       4       3099
75%-tile:       1       297     253     0       5       4648
```

```
97.5%-tile:     1       297     253     0       6       6042
Maximum: 1      297     255     0       8       6196
Mean:   1       297     252     0       4
# of unique seqs:       313
total # of seqs: 6196

It took 0 secs to summarize 6196 sequences.

Output File Names:
stability.trim.contigs.unique.good.filter.unique.precluster.pick.summa
ry


mothur >
classify.seqs(fasta=stability.trim.contigs.unique.good.filter.unique.p
recluster.denovo.vsearch.fasta,
count=stability.trim.contigs.unique.good.filter.unique.precluster.deno
vo.vsearch.count_table, reference=trainset9_032012.pds.fasta,
taxonomy=trainset9_032012.pds.tax)

Using 8 processors.
Unable to open trainset9_032012.pds.fasta. Trying input directory /
Users/natalieburkhard/bio-490/independentStudy/Lab9.3/
trainset9_032012.pds.fasta.
Unable to open /Users/natalieburkhard/bio-490/independentStudy/Lab9.3/
trainset9_032012.pds.fasta. Trying MOTHUR_FILES directory mothur/
trainset9_032012.pds.fasta.
Unable to open mothur/trainset9_032012.pds.fasta. Trying mothur's
executable directory mothur/trainset9_032012.pds.fasta.
Unable to open mothur/trainset9_032012.pds.fasta.
Unable to open trainset9_032012.pds.fasta
Unable to open trainset9_032012.pds.tax. Trying input directory /
Users/natalieburkhard/bio-490/independentStudy/Lab9.3/
trainset9_032012.pds.tax.
Unable to open /Users/natalieburkhard/bio-490/independentStudy/Lab9.3/
trainset9_032012.pds.tax. Trying MOTHUR_FILES directory mothur/
trainset9_032012.pds.tax.
Unable to open mothur/trainset9_032012.pds.tax. Trying mothur's
executable directory mothur/trainset9_032012.pds.tax.
Unable to open mothur/trainset9_032012.pds.tax.
Unable to open trainset9_032012.pds.tax
[ERROR]: did not complete classify.seqs.

mothur >
classify.seqs(fasta=stability.trim.contigs.good.unique.good.filter.uni
que.precluster.pick.fasta,
count=stability.trim.contigs.good.unique.good.filter.unique.precluster
.count_table, reference=trainset9_032012.pds/
trainset9_032012.pds.fasta, taxonomy=trainset9_032012.pds/
trainset9_032012.pds.tax, cutoff=80)
```

```
Unable to open
stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.
fasta. Trying input directory /Users/natalieburkhard/bio-490/
independentStudy/Lab9.3/
stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.
fasta.
Unable to open /Users/natalieburkhard/bio-490/independentStudy/Lab9.3/
stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.
fasta. Trying MOTHUR_FILES directory mothur/
stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.
fasta.
Unable to open mothur/
stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.
fasta. Trying mothur's executable directory mothur/
stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.
fasta.
Unable to open mothur/
stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.
fasta.
Unable to open
stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.
fasta
Unable to open
stability.trim.contigs.good.unique.good.filter.unique.precluster.count
_table. Trying input directory /Users/natalieburkhard/bio-490/
independentStudy/Lab9.3/
stability.trim.contigs.good.unique.good.filter.unique.precluster.count
_table.
Unable to open /Users/natalieburkhard/bio-490/independentStudy/Lab9.3/
stability.trim.contigs.good.unique.good.filter.unique.precluster.count
_table. Trying MOTHUR_FILES directory mothur/
stability.trim.contigs.good.unique.good.filter.unique.precluster.count
_table.
Unable to open mothur/
stability.trim.contigs.good.unique.good.filter.unique.precluster.count
_table. Trying mothur's executable directory mothur/
stability.trim.contigs.good.unique.good.filter.unique.precluster.count
_table.
Unable to open mothur/
stability.trim.contigs.good.unique.good.filter.unique.precluster.count
_table.
Unable to open
stability.trim.contigs.good.unique.good.filter.unique.precluster.count
_table

Using 8 processors.
[ERROR]: did not complete classify.seqs.

mothur >
classify.seqs(fasta=stability.trim.contigs.good.unique.good.filter.uni
```

```
que.precluster.pick.fasta,
count=stability.trim.contigs.good.unique.good.filter.unique.precluster
.count_table, reference=trainset9_032012.pds/
trainset9_032012.pds.fasta, taxonomy=trainset9_032012.pds/
trainset9_032012.pds.tax, cutoff=80)
Unable to open
stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.
fasta. Trying input directory /Users/natalieburkhard/bio-490/
independentStudy/Lab9.3/
stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.
fasta.
Unable to open /Users/natalieburkhard/bio-490/independentStudy/Lab9.3/
stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.
fasta. Trying MOTHUR_FILES directory mothur/
stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.
fasta.
Unable to open mothur/
stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.
fasta. Trying mothur's executable directory mothur/
stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.
fasta.
Unable to open mothur/
stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.
fasta.
Unable to open
stability.trim.contigs.good.unique.good.filter.unique.precluster.pick.
fasta
Unable to open
stability.trim.contigs.good.unique.good.filter.unique.precluster.count
_table. Trying input directory /Users/natalieburkhard/bio-490/
independentStudy/Lab9.3/
stability.trim.contigs.good.unique.good.filter.unique.precluster.count
_table.
Unable to open /Users/natalieburkhard/bio-490/independentStudy/Lab9.3/
stability.trim.contigs.good.unique.good.filter.unique.precluster.count
_table. Trying MOTHUR_FILES directory mothur/
stability.trim.contigs.good.unique.good.filter.unique.precluster.count
_table.
Unable to open mothur/
stability.trim.contigs.good.unique.good.filter.unique.precluster.count
_table. Trying mothur's executable directory mothur/
stability.trim.contigs.good.unique.good.filter.unique.precluster.count
_table.
Unable to open mothur/
stability.trim.contigs.good.unique.good.filter.unique.precluster.count
_table.
Unable to open
stability.trim.contigs.good.unique.good.filter.unique.precluster.count
_table
```

```
Using 8 processors.
[ERROR]: did not complete classify.seqs.

mothur > get.current()

Current RAM usage: 0.339287 Gigabytes. Total Ram: 8 Gigabytes.

Current files saved by mothur:
accnos=stability.trim.contigs.unique.good.filter.unique.precluster.den
ovo.vsearch.accnos
fasta=stability.trim.contigs.unique.good.filter.unique.precluster.deno
vo.vsearch.fasta
contigsreport=stability.contigs_report
count=stability.trim.contigs.unique.good.filter.unique.precluster.deno
vo.vsearch.count_table
processors=8
summary=stability.trim.contigs.unique.good.filter.unique.precluster.pi
ck.summary
file=/Users/natalieburkhard/bio-490/independentStudy/Lab9.3/
stability.files

Current input directories saved by mothur:
        /Users/natalieburkhard/bio-490/independentStudy/Lab9.3/


Current default directories saved by mothur:
        mothur/


Current working directory: /Users/natalieburkhard/bio-490/
independentStudy/Lab9.3/

Output File Names:
current_files.summary


mothur > clearcut(fasta=<current, DNA=T)
Unable to open <current. Trying input directory /Users/
natalieburkhard/bio-490/independentStudy/Lab9.3/<current.
Unable to open /Users/natalieburkhard/bio-490/independentStudy/Lab9.3/
<current. Trying MOTHUR_FILES directory mothur/<current.
Unable to open mothur/<current. Trying mothur's executable directory
mothur/<current.
Unable to open mothur/<current.
Unable to open <current
Using
stability.trim.contigs.unique.good.filter.unique.precluster.denovo.vse
arch.fasta as input file for the fasta parameter.
[ERROR]: did not complete clearcut.
```

```
mothur > clearcut(fasta=current, DNA=T)
Using
stability.trim.contigs.unique.good.filter.unique.precluster.denovo.vse
arch.fasta as input file for the fasta parameter.

Output File Names:
stability.trim.contigs.unique.good.filter.unique.precluster.denovo.vse
arch.tre


mothur > system(ls)
F3D0_S188_L001_R1_001.fastq
F3D0_S188_L001_R2_001.fastq
MiSeq_SOP
commandScreen.output
current_files.summary
mothur
mothur.1647400807.logfile
silva.bacteria
silva.bacteria.fasta
silva.v4.8mer
silva.v4.fasta
silva.v4.summary
stability.contigs.count_table
stability.contigs_report
stability.files
stability.filter
stability.scrap.contigs.fasta
stability.trim.contigs.count_table
stability.trim.contigs.fasta
stability.trim.contigs.good.count_table
stability.trim.contigs.good.fasta
stability.trim.contigs.good.unique.fasta
stability.trim.contigs.summary
stability.trim.contigs.unique.align
stability.trim.contigs.unique.align_report
stability.trim.contigs.unique.bad.accnos
stability.trim.contigs.unique.fasta
stability.trim.contigs.unique.good.align
stability.trim.contigs.unique.good.filter.count_table
stability.trim.contigs.unique.good.filter.fasta
stability.trim.contigs.unique.good.filter.unique.fasta
stability.trim.contigs.unique.good.filter.unique.precluster.F3D0.count
_table
stability.trim.contigs.unique.good.filter.unique.precluster.F3D0.fasta
stability.trim.contigs.unique.good.filter.unique.precluster.F3D0.map
stability.trim.contigs.unique.good.filter.unique.precluster.count_tabl
e
stability.trim.contigs.unique.good.filter.unique.precluster.denovo.vse
arch.accnos
```

```
stability.trim.contigs.unique.good.filter.unique.precluster.denovo.vse
arch.chimeras
stability.trim.contigs.unique.good.filter.unique.precluster.denovo.vse
arch.count_table
stability.trim.contigs.unique.good.filter.unique.precluster.denovo.vse
arch.fasta
stability.trim.contigs.unique.good.filter.unique.precluster.denovo.vse
arch.tre
stability.trim.contigs.unique.good.filter.unique.precluster.fasta
stability.trim.contigs.unique.good.filter.unique.precluster.pick.fasta
stability.trim.contigs.unique.good.filter.unique.precluster.pick.summa
ry
stability.trim.contigs.unique.good.summary
stability.trim.contigs.unique.summary
trainset9_032012.pds


mothur > quit
Logfile : mothur.1647400807.logfile



**************************************************************
**************************************************************
**************************************************************
Detected 8 [ERROR] messages, please review.
**************************************************************
**************************************************************
**************************************************************
```