

iv) *mothur* Diversity Analysis

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22/11/2019

The following shell script is the pipeline that was used to run the *mothur* portion of the analysis from the command line as a job on the HPC cluster.

```
#!/bin/bash
#$ -cwd
#$ -V
#$ -M lmpugh@dundee.ac.uk
#$ -m e
#$ -m a

cp /homes/lmpugh/cluster_home/raw_data/16S_samples/trimmed/files/16S.shared $TMPDIR
cp /homes/lmpugh/cluster_home/raw_data/16S_samples/trimmed/16S.taxonomy $TMPDIR

mothur "#dist.shared(shared=16S.shared, calc=thetayc-jclass, subsample=t);
        nmds(phylip=16S.thetayc.0.03.lt.ave.dist, mindim=3, maxdim=3);
        amova(phylip=16S.thetayc.0.03.lt.ave.dist, design=16S.metadata);
        homova(phylip=16S.thetayc.0.03.lt.ave.dist, design=16S.metadata)
        "

cp /$TMPDIR/16S.* /homes/lmpugh/cluster_home/raw_data/16S_samples/trimmed/files/diversity
```