At start of week 3:

47/300 cores

151 GB/ 1TB

Working through MarGen week3

-maybe rename week4 directory

- make sure they run fastqc in week4(named week3 now) dir

If they do exercise, they will get untrimmed in bam.file.list so have to either save exercise till end or rename that output

for filename in \*tiny\_70bp\_trimmed.fastq.gz; do

base=$(basename $filename .tiny\_70bp\_trimmed.fastq.gz)

echo=${base}

bowtie2 -x Ppar\_tinygenome -U ${base}.tiny\_70bp\_trimmed.fastq.gz -S ${base}.70trimmed.sam

done

for filename in \*.tiny\_70bp\_trimmed.fastq.gz

do

base=$(basename $filename .tiny\_70bp\_trimmed.fastq.gz)

echo ${base}

bowtie2 -x Ppar\_tinygenome -U ${base}.tiny\_70bp\_trimmed.fastq.gz -S ${base}.sam

done