For the fourth NGS class, you will need to perform the following actions. As before, these links are also present on the course web site:
http://physiology.med.cornell.edu/faculty/mason/lab/data/NGS/

1. ChIP-Seq
Download the ChIPseeqer package:
http://physiology.med.cornell.edu/faculty/elemento/lab/files/ChIPseeqer-1.0.zip

Unzip the package and move into the directory
```
]unzip ChIPseeqer-1.0.zip
]cd ChIPseeqer-1.0/
```

Move into the directory "libmd" and compile the library
```
]cd libmd/
]perl Makefile.PL
]make
```

Move back into the ChIPseeqer directory and compile chip-seeqer
```
]cd ..
]make
```
(OR, on Linux, type cd ../ ; make –f Makefile.linux)

Set environmental variable (make sure to use back-ticks! cmd substituion)
export CHIPSEEQERDIR=`pwd`

Make a new directory for data analysis and move into that directory
```
]cd ..
]mkdir CHIP
]cd CHIP
```

Download raw data into the CHIP directory, taken from
ftp://ftp.ncbi.nih.gov/pub/geo/DATA/supplementary/samples/GSM327nnn/GSM327662/GSM327662_hES.H3K4me3.aligned.txt.gz
Then unzip the chip data
```
]gunzip GSM327662_hES.H3K4me3.aligned.txt.gz
```

2. Prepare a genome assembler
Download Velvet
http://www.ebi.ac.uk/~zerbino/velvet/velvet_0.7.62.tgz

Gunzip and Untar the tarball
```
]gunzip velvet_0.7.62.tgz
]tar –xvf velvet_0.7.62.tar
```

Compile the program
```
]make
```