

# Environment setup

---

## Login to Hydra and install R libraries

```
$ ssh <username>@hydra-login01.si.edu
```

Now load the R module and open R

```
$ module load tools/R/3.2.1
```

```
$ R
```

Now we are going to install bioconductor packages that we will use during the differential expression portion of the analysis.

```
> source("http://bioconductor.org/biocLite.R")
```

```
> biocLite()
```

```
> biocLite('edgeR')
```

```
> biocLite('ctc')
```

```
> biocLite('Biobase')
```

```
> biocLite('ape')
```

```
> install.packages('gplots')
```

Exit R

```
> quit()
```

When prompted to save your workspace image, reply 'n' and press enter:

```
Save workspace image? [y/n/c]: n
```