synDss Tutorial
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Objective: This is a tutorial to illustrate the use of the synDss package in `R`.

- First, read the installation instructions at `http://evolmod.r-forge.r-project.org/synDss`. Once these steps are completed, run `R` and then load the package:

```
> library(synDss)
```

- Now, let us try to calculate the original and synonymous Dss statistics from a DNA sequence alignment. First, we will read in the fasta file for a sequence alignment of 18 salmonella sequences included in the package:

```
> salmonella<-fasta.to.alignment(system.file("seqdata/Salmonella_fimH_aligned-18alleles.txt",package="
>
```

- Now, let us calculate the Dss statistic for this dataset, with a window size of 105 nucleotides, and step size of 9 nucleotides:

```
> dss.stat<-calc.Dss(salmonella, l=270, m=9)
>
```

- We can also calculate the synonymous Dss statistic (for a dataset of this size, this will take about 5 minutes):

```
> syn.stat<-calc.Dss.syn(salmonella, l=270, m=9,syn.matrix=regist.synonym())
>
```

- To look at our statistic landscapes, we can plot them:

```
> m<-9
> l<-270
> length<-dim(as.matrix.alignment(salmonella))[2]
> n.windows<-((length-(2*l))/m+1)
> index<-c(1:n.windows)
> max<-max(c(dss.stat,syn.stat),na.rm=T)
> plot(dss.stat~index,type="l",xlab="window number",ylab="",ylim=c(0,max),lty=2)
> lines(syn.stat~index,type="l")
> legend("topright",c("Original Dss","Synonymous Dss"),lty=c(2,1))
>
>
```

Here is the landscape plot, with a window size of 540 and step size of 9: