Transcriptomic and physiological responses to seasonal and diurnal cycles in Ostreococcus

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Load data and principal component analysis.

The matrix containing the gene expression data analyzed in this study can be downloaded from **this link to the GEO data base**. Make sure to uncompress this file and rename it to **gene_expression.tsv**. First, the gene expression data is loaded and the number of genes in the genome is determined.

```
gene.expression <- read.table(file ="gene_expression.tsv",sep="\t",header=T,as.is=T)
head(gene.expression[,1:6])
```

```
##              X  ld_zt00_1  ld_zt04_1 ld_zt08_1 ld_zt12_1 ld_zt16_1
## 1 ostta01g00010   9.664395  25.045279  30.81788  44.97020  32.61381
## 2 ostta01g00020  15.688867   9.913202  10.36669  14.64151  11.66096
## 3 ostta01g00030  16.108133  11.134813  13.85848  38.54982  24.16540
## 4 ostta01g00040  59.247765  32.837433  27.26293  42.82092  52.59695
## 5 ostta01g00050  27.909069  14.945981  12.04561  20.26003  28.25942
## 6 ostta01g00060 248.044205 145.486374  68.38238  66.96495 224.52632
```

```
number.genes <- nrow(gene.expression)
number.genes
```

```
## [1] 7668
```

The packages **FactoMineR** and **factoextra** are used to performed a **Principal components analysis** of the gene expression data.

```
library(FactoMineR)
library(factoextra)
```

```
## Loading required package: ggplot2
```

```
## Welcome! Want to learn more? See two factoextra-related books at https://goo.gl/ve3WBa
```

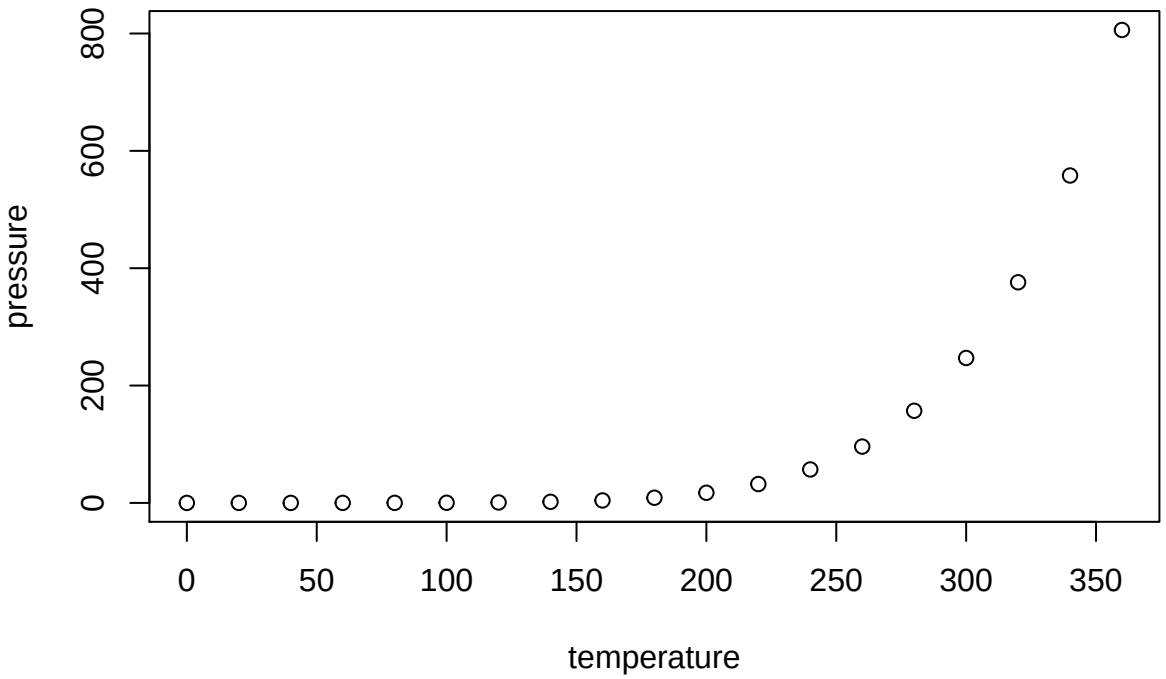
When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

```
summary(cars)
```

```
##      speed           dist
##  Min.   : 4.0   Min.   :  2.00
##  1st Qu.:12.0   1st Qu.: 26.00
##  Median :15.0   Median : 36.00
##  Mean   :15.4   Mean   : 42.98
##  3rd Qu.:19.0   3rd Qu.: 56.00
##  Max.   :25.0   Max.   :120.00
```

Including Plots

You can also embed plots, for example:



Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.