

Microbial_interactions

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R Markdown

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see <http://rmarkdown.rstudio.com>.

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:

```
library(compositions)
```

```
## Loading required package: tensorA
```

```
##
```

```
## Attaching package: 'tensorA'
```

```
## The following object is masked from 'package:base':
```

```
##
```

```
##      norm
```

```
## Loading required package: robustbase
```

```
## Loading required package: energy
```

```
## Loading required package: bayesm
```

```
## Welcome to compositions, a package for compositional data analysis.
```

```
## Find an intro with "? compositions"
```

```
##
```

```
## Attaching package: 'compositions'
```

```
## The following objects are masked from 'package:stats':
```

```
##
```

```
##      cor, cov, dist, var
```

```
## The following objects are masked from 'package:base':
```

```
##
```

```
##      %*%, scale, scale.default
```

```
genus_table <- read.table("~/Dropbox/controlled_metagenomics/metagenome_data/German_192/totalReads_bact
```

```
genus_table$percent_bac <- genus_table$Bacteria_reads/genus_table$Total_reads*100
```

```
#predict_bac <- 10~log10(genus_table$percent_bac) * beta + inter
```

```
g_t <- apply(t(genus_table), 2, as.numeric)
```

```
rownames(g_t) = colnames(genus_table)
```

```
#colnames(g_t) = t(genus_table)[1,]
```

```
met_table <- read.table("~/Dropbox/controlled_metagenomics/metagenome_data/German_192/genus_counts.txt"
```

```
gen_met <- rbind(met_table, g_t)
```

```
gen_met['plant',] <- gen_met['Total_reads',]-gen_met['Bacteria_reads',]
```

```
gen_met <- gen_met[order(rowSums(gen_met), decreasing=TRUE),]
```

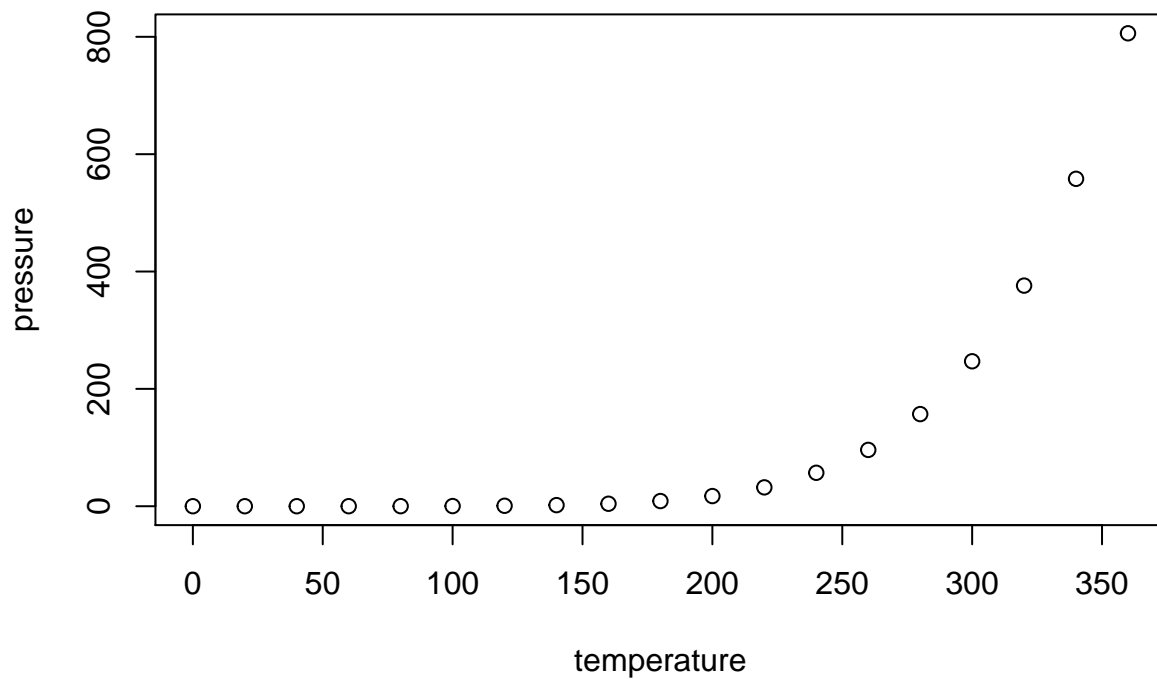
```
gen_met_rotate <- t(gen_met)[,c(2,4:8)]
```

```
pdf("~/Dropbox/controlled_metagenomics/results_figures/clr_relations_192.pdf")
pairs(clr(gen_met_rotate), pch='.')
my_clr <- clr(gen_met_rotate)
dev.off()
```

```
## pdf
## 2
```

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.