

DHA and Microbiome

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This mini-project provides visualization of the microbiome (genus level) influenced by DHA intake in human subjects.

```
d <- read.csv("DHA and Microbiome.csv")
library(tm)
```

```
## Loading required package: NLP
```

```
library(quanteda)
```

```
## Package version: 2.0.1
```

```
## Parallel computing: 2 of 8 threads used.
```

```
## See https://quanteda.io for tutorials and examples.
```

```
##
```

```
## Attaching package: 'quanteda'
```

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

```
##
```

```
##   as.DocumentTermMatrix, stopwords
```

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

```
##
```

```
##   meta, meta<-
```

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

```
##
```

```
##   View
```

```
dc <- corpus(d, docid_field = "ID",
             text_field = "Text",
             unique_docnames = TRUE)
dc <- Corpus(VectorSource(dc))
```

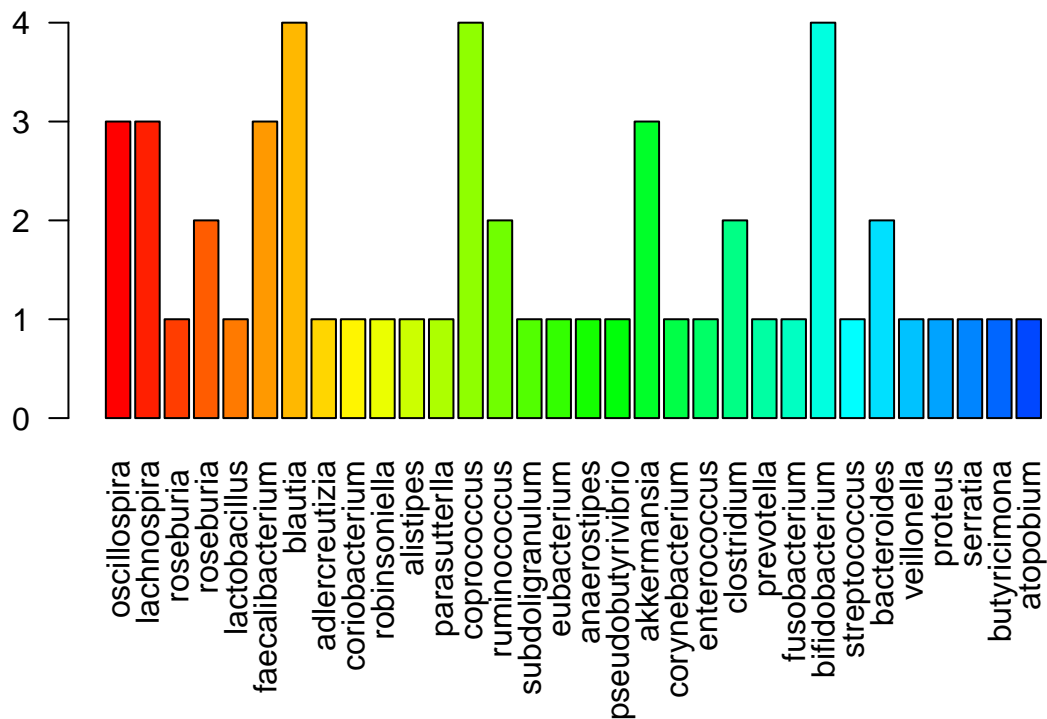
```
# check word frequency
```

```

fdc <- TermDocumentMatrix(dc)
fdcf <- as.data.frame(as.matrix(fdc))

f2 <- rowSums(fdcf)
par(mar=c(8, 4.1, 4.1, 2.1))
barplot(f2,
        las=2,
        col = rainbow(50))

```



```
library(wordcloud)
```

```
## Loading required package: RColorBrewer
```

```

f3 <- sort(rowSums(fdcf), decreasing = TRUE)
par(mar=c(0.1, 0.1, 0.1, 0.1))
wordcloud(words = names(f3),
          freq = f3,
          max.words = 60,
          random.order = F,
          min.freq = 1,
          colors = brewer.pal(8, 'Dark2'), scale = c(2, 0.05) )

```

