

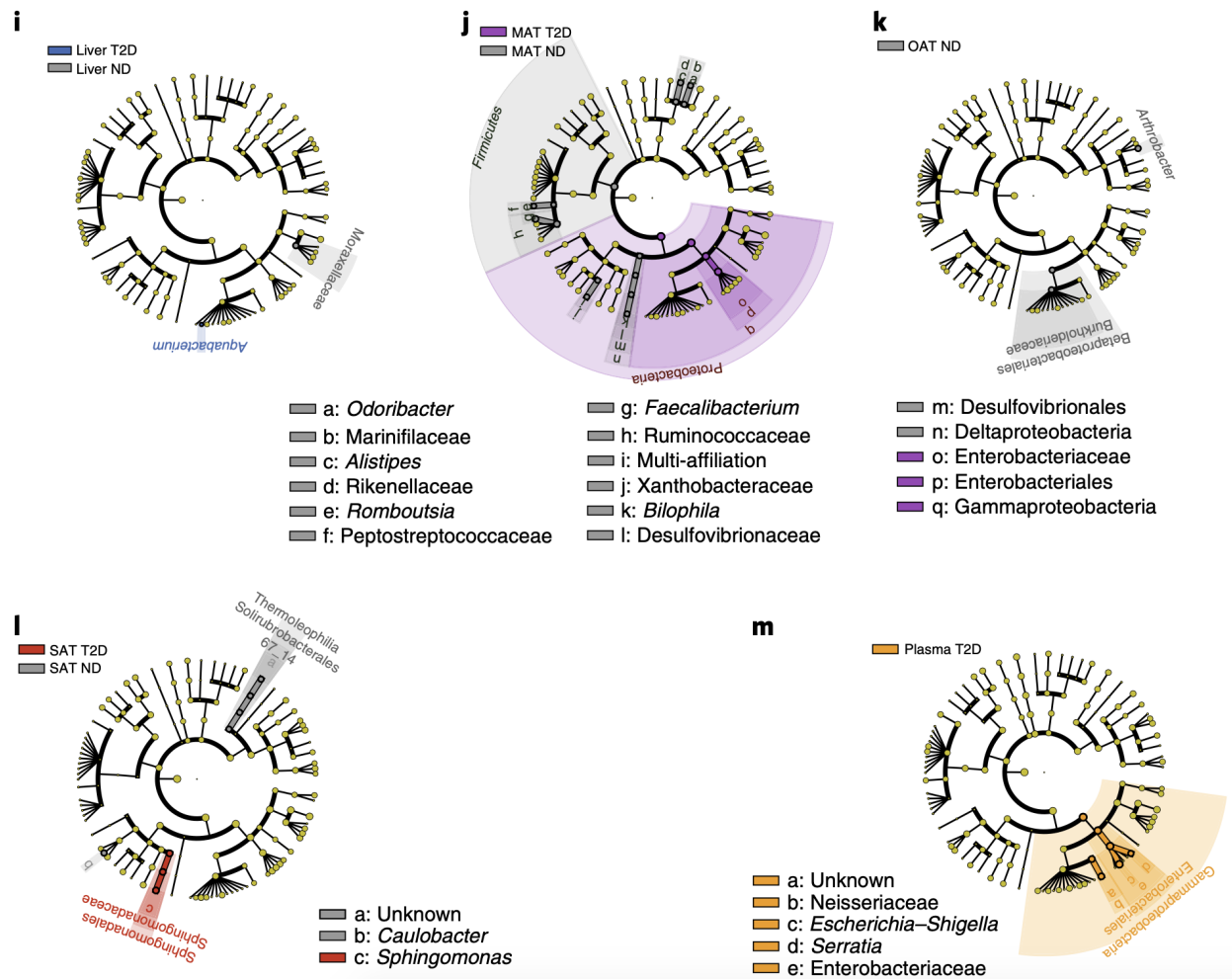
# Microbiome figures

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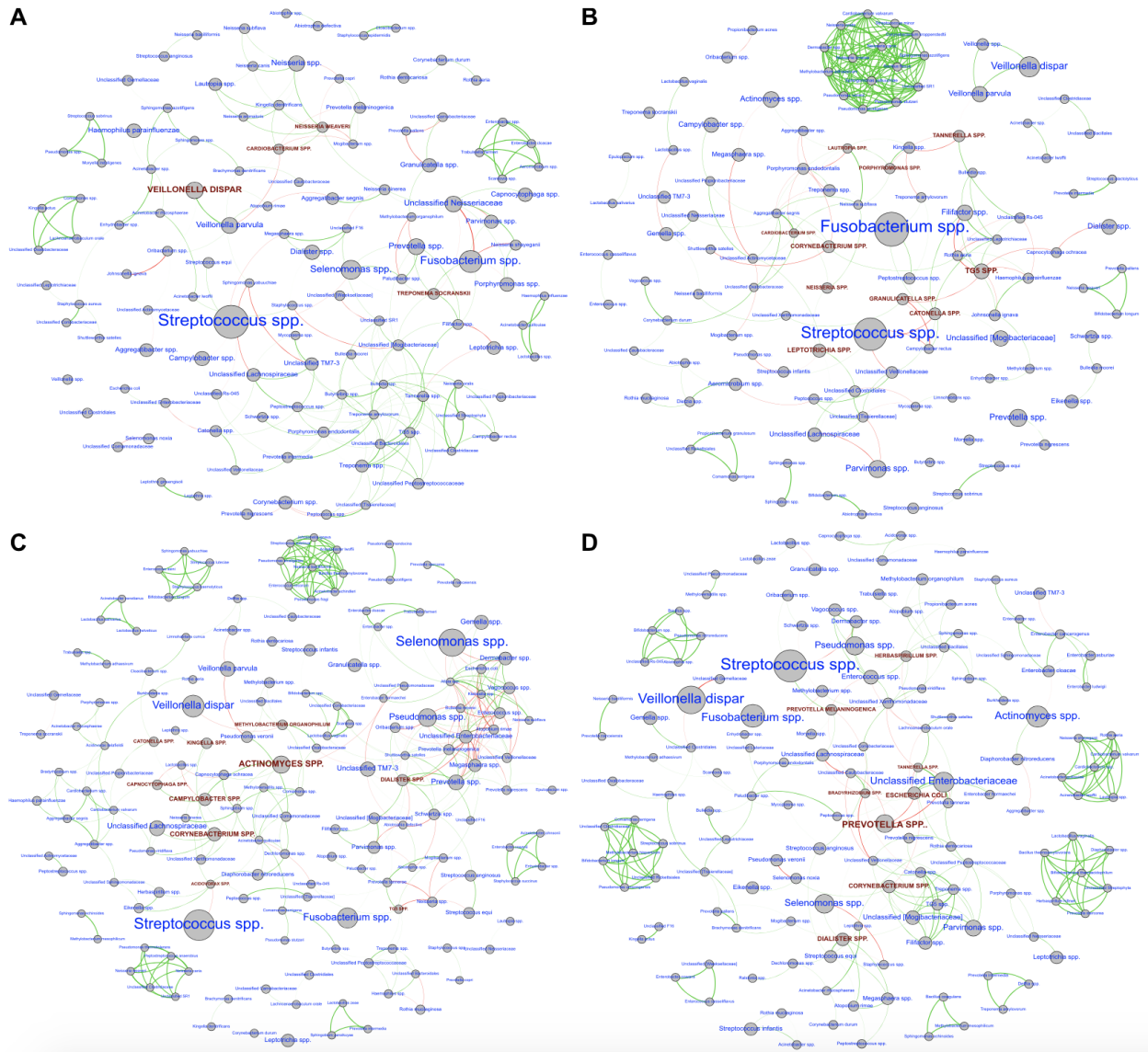
## Cladogram

From <https://doi.org/10.1038/s42255-020-0178-9>



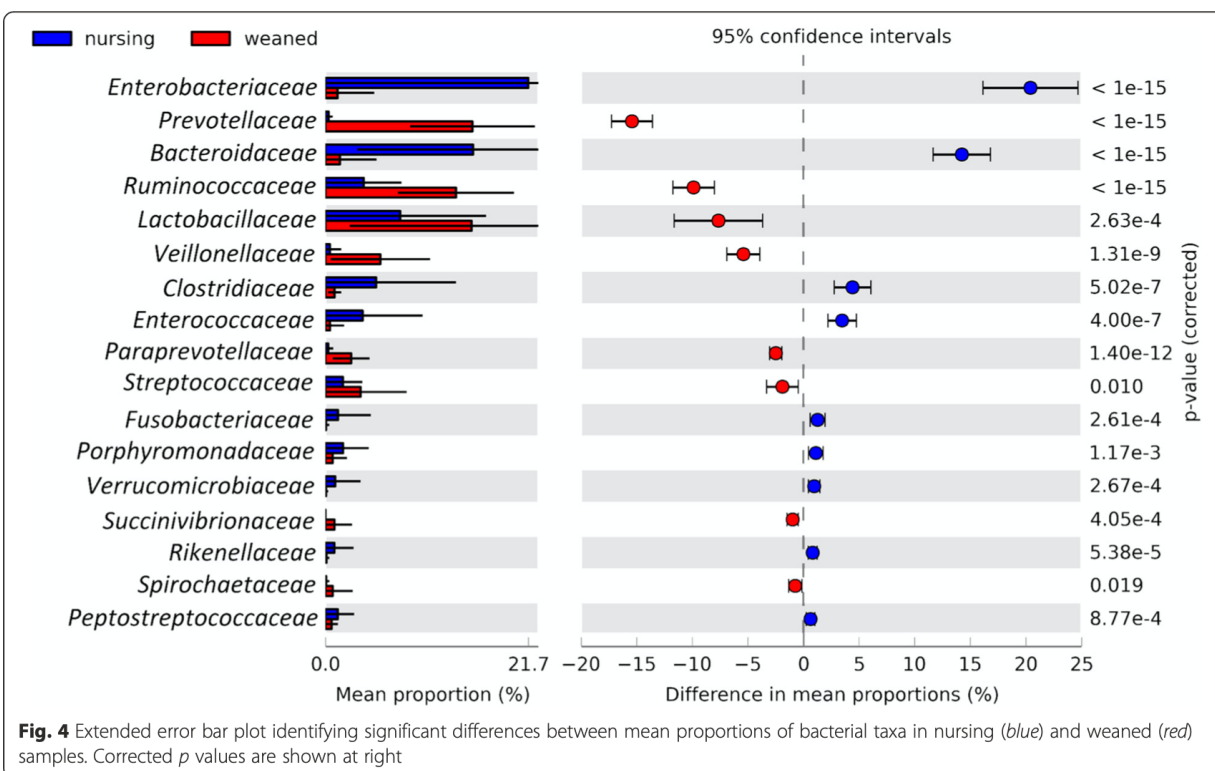
# Co-occurrence network

From <https://www.nature.com/articles/srep30388>



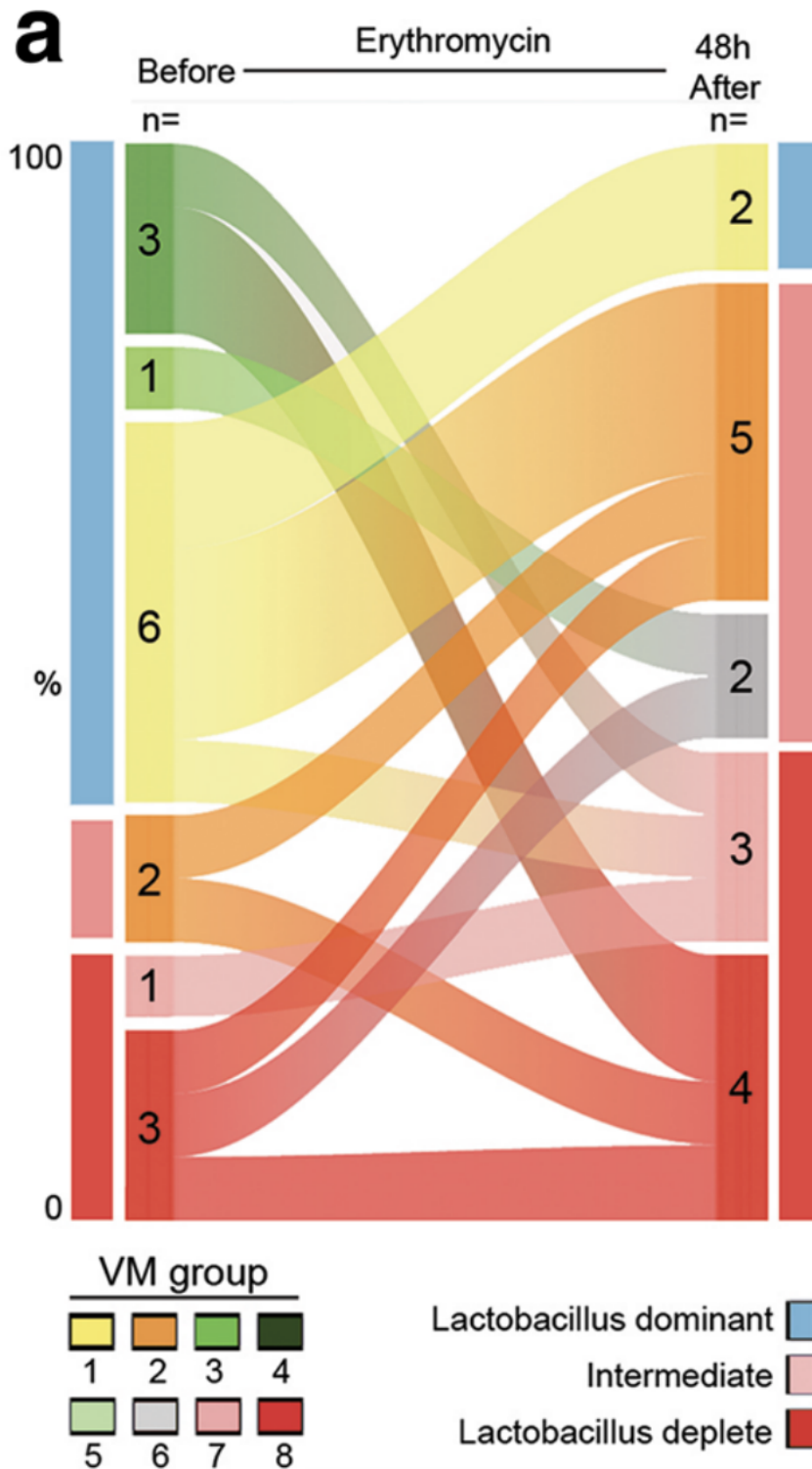
## Extended error bars

From <https://microbiomejournal.biomedcentral.com/articles/10.1186/s40168-015-0091-8>



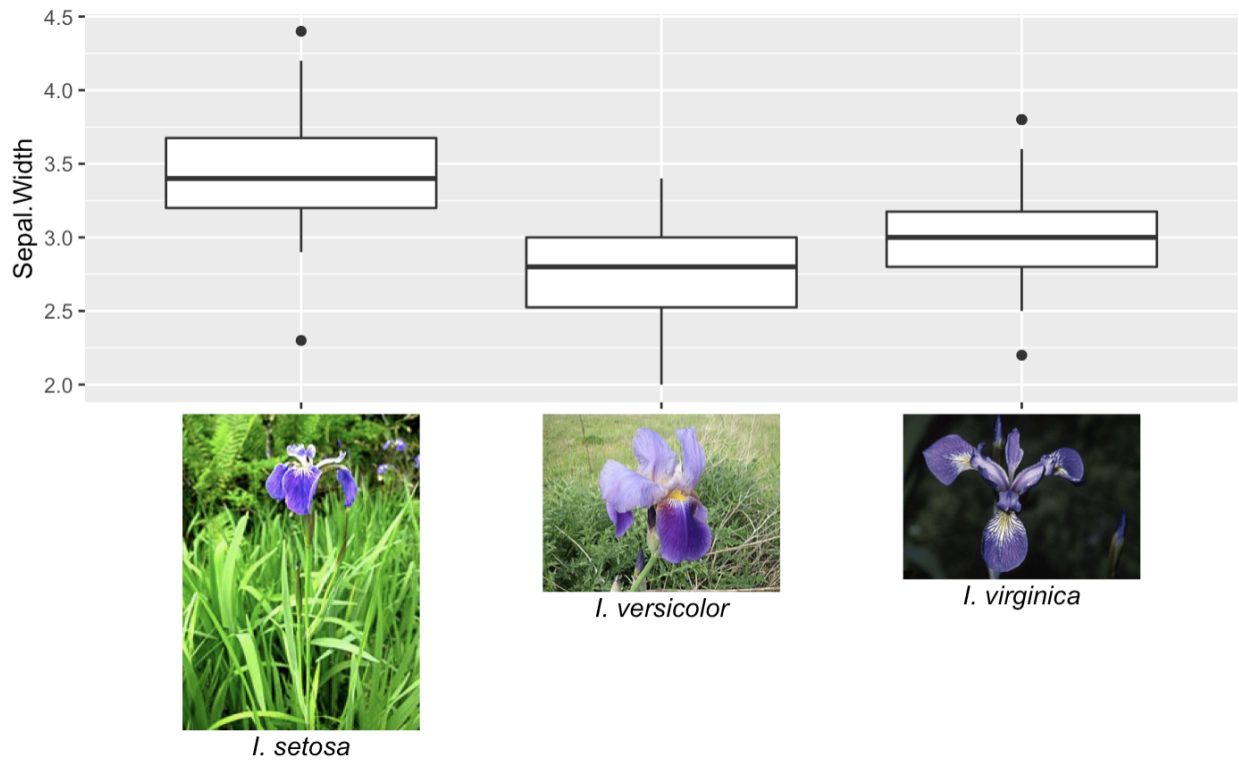
## Sankey diagram – change of composition

From <https://bmcmicrobiome.biomedcentral.com/articles/10.1186/s12916-017-0999-x>



# Introduction to ggtext

From <https://wilkelab.org/ggtext/>



```
library(ggplot2)
library(ggtext)

labels <- c(
  setosa = "<img src='https://upload.wikimedia.org/wikipedia/commons/thumb/8/86/Iris_setosa.JPG/180px-I-  
width='100' /><br>*I. setosa*",
  virginica = "<img src='https://upload.wikimedia.org/wikipedia/commons/thumb/3/38/Iris_virginica_-_NRC  
width='100' /><br>*I. virginica*",
  versicolor = "<img src='https://upload.wikimedia.org/wikipedia/commons/thumb/2/27/20140427Iris_versic  
width='100' /><br>*I. versicolor*"
)

ggplot(iris, aes(Species, Sepal.Width)) +
  geom_boxplot() +
  scale_x_discrete(
    name = NULL,
    labels = labels
  ) +
  theme(
    axis.text.x = element_markdown(color = "black", size = 11)
  )
```