

Examples and Figures from Microbiome Recursive Partitioning 2019

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First we need to load the **HMP** package and data:

```
> library(HMP)
> library(rpart)
> data(dmrp_data)
> data(dmrp_covars)
>
```

The data consists of 128 subjects and 29 taxa at the Genus level. The taxon labeled "Other" is the rarest 139 taxa collapsed into one and combined they make up less than 5 percent of the total reads. This was done by the function `Data.filter` in the HMP package.

The covariate file consists of the same 128 subjects in the same order and 11 cytokines.

II Figure 2

The barcharts below show the taxa composition for each terminal node from the above rpart tree plot.

```
> # Split the data by terminal nodes
> nodeNums <- bestTree$frame$yval[bestTree$frame$var == "<leaf>"]
> nodeList <- split(dmrp_data, f=bestTree$where)
> names(nodeList) <- paste("Node", nodeNums)
> # Get the PI for each terminal node
> myEst <- Est.PI(nodeList)
> myPI <- myEst$MLE$params
> # Plot the PI for each terminal node
> myColr <- rainbow(ncol(dmrp_data))
> lattice::barchart(PI ~ Group, data=myPI, groups=Taxa, stack=TRUE, col=myColr,
+                   ylab="Fractional Abundance", xlab="Terminal Node",
+                   auto.key=list(space="top", columns=3, cex=.65, rectangles=FALSE,
+                               col=myColr, title="", cex.title=1))
>
```