Importing data from FROGS with `import_frogs`

To import directly from FROGS formatted biom, you can use `import_frogs`. Works as `import_biom` with one extra `taxMethod` parameter to choose either the blast (default) or the rdp taxonomy (phyloseq is not designed to deal with both).

```
frogsBiom <- "data/frogs/frogs-data.biom"
frogs.data <- import_frogs(frogsBiom, taxMethod = "blast")
```

For *standard* biom, use `import_biom` and change the taxonomic ranks

```
frogsStandardBiom <- "data/frogs/frogs-data-standard.biom"
frogs.data <- import_biom(frogsStandardBiom)
rank_names(frogs.data)
```

```
## [1] "Rank1" "Rank2" "Rank3" "Rank4" "Rank5" "Rank6" "Rank7"
```

```
colnames(tax_table(frogs.data)) <- c("Kingdom", "Phylum", "Class",
                                     "Order", "Family", "Genus", "Species")
rank_names(frogs.data)
```

```
## [1] "Kingdom" "Phylum"  "Class"   "Order"   "Family"  "Genus"   "Species"
```

Importing data from FROGS (II)

In both instances, `frogs.data` has no `sample_data`. You can add metadata simply like this

```
metadata <- read.table("data/frogs/frogs-data-standard-metadata.tsv")
head(metadata, 2)
```

```
##                                     Error  Type Rep
## 500taxas_With_Error_Power_Law-01-reads  TRUE Power   1
## 500taxas_With_Error_Power_Law-02-reads  TRUE Power   2
```

```
sample_data(frogs.data) <- metadata
frogs.data
```

```
## phyloseq-class experiment-level object
## otu_table()    OTU Table:         [ 507 taxa and 10 samples ]
## sample_data() Sample Data:        [ 10 samples by 3 sample variables ]
## tax_table()    Taxonomy Table:    [ 507 taxa by 7 taxonomic ranks ]
```