

matrix

data.frame

matrix

OTU Abundance
class: **otuTable**
slots: **.Data**,
speciesAreRows

Sample Variables
sampleMap
slots: **.Data**,
names,
row.names,
.S3Class

Taxonomy Table
taxonomyTable
slots: **.Data**

Phylogen. Tree
class: **phylo**
slots: see
phylobase, *ape*
packages

phyloseq
slots:
otuTable
sampleMap
taxTab
tre

