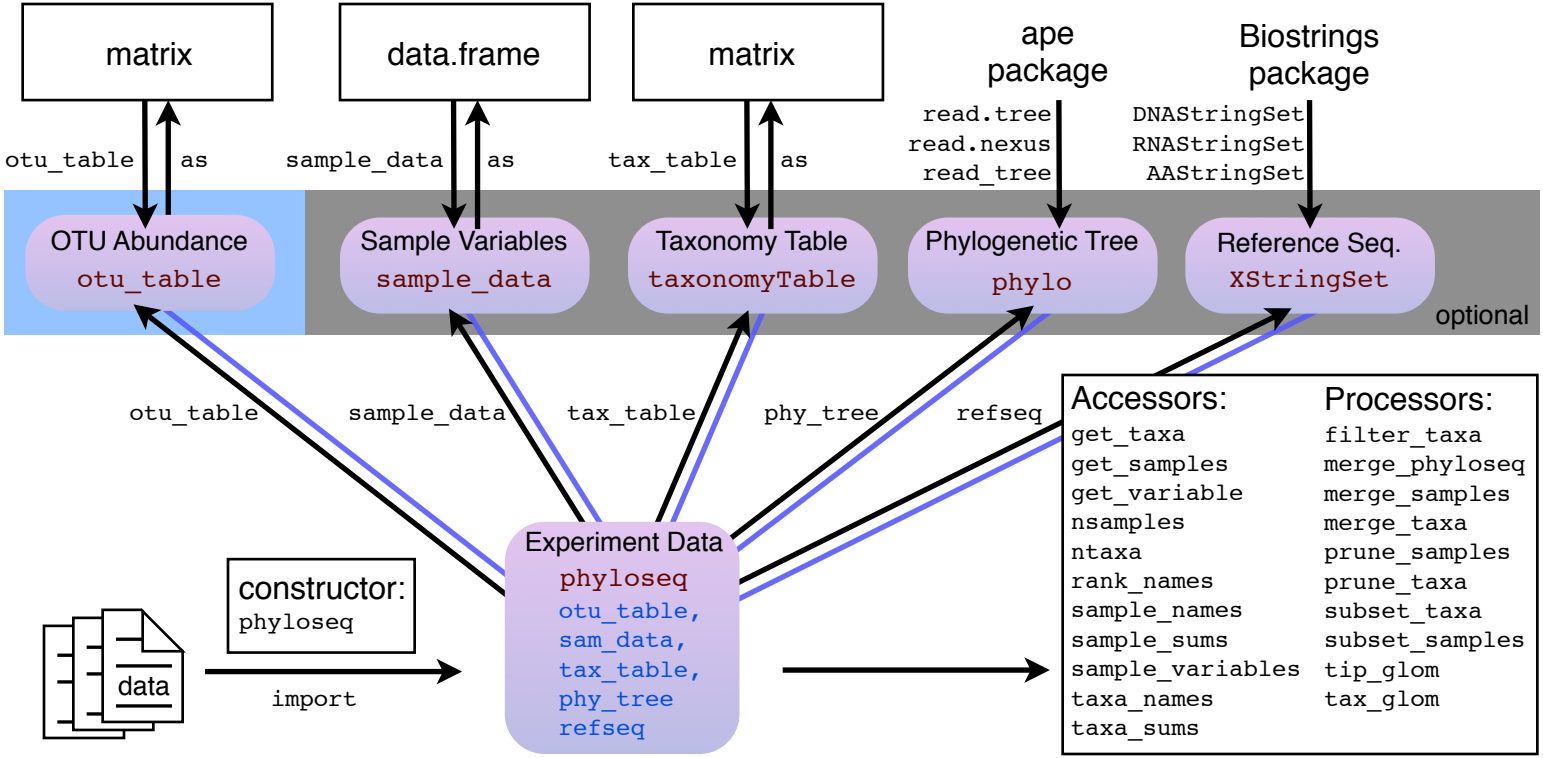
matrix
data.frame
matrix
ape package
Biostrings package
otu_table
as
sample_data
as
tax_table
as
read.tree
read.nexus
read_tree
DNAStringSet
RNAStringSet
AAStringSet
OTU Abundance
otu_table
Sample Variables
sample_data
Taxonomy Table
taxonomyTable
Phylogenetic Tree
phylo
Reference Seq.
XStringSet
optional
otu_table
sample_data
tax_table
phy_tree
refseq
Accessors:
get_taxa
get_samples
get_variable
nsamples
ntaxa
rank_names
sample_names
sample_sums
sample_variables
taxa_names
taxa_sums
Processors:
filter_taxa
merge_phyloseq
merge_samples
merge_taxa
prune_samples
prune_taxa
subset_taxa
subset_samples
tip_glom
tax_glom
constructor:
phyloseq
data
import
Experiment Data
phyloseq
otu_table,
sam_data,
tax_table,
phy_tree
refseq