Importing complete Phyloseq objects.

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Jun 5, 2019

Contents

This code commentary is included in the R code itself and can be rendered at any stage using
`rmarkdown::render ("/Users/paul/Documents/AAD_combined/Github/090_get_full_ps_obj.R")`.
(The path may have to be adjusted.) Please check the session info at the end of the document for further
notes on the coding environment.

Prepare Environment

Empty Buffer

```
rm(list=ls())
```

Load Packages

```
library("ape")          # read tree file
library("Biostrings")   # read fasta file
library("phyloseq")     # filtering and utilities for such objects
library("data.table")   # fast and convenient handling of large tables
library("tidyverse")    # useful, but mainly loading for `dplyr`
library("data.table")
```

Construct 16S Object

Set Paths

```
bim_fpath = "/Users/paul/Documents/AAD_combined/Zenodo/Qiime/085_16S_merged_qiime_artefacts/features-ta
# tre_fpath = ""
seq_fpath = "/Users/paul/Documents/AAD_combined/Zenodo/Qiime/085_16S_merged_qiime_artefacts/dna-sequenc
```

Import

```
phsq <- import_biom (bim_fpath)

## Warning in strsplit(conditionMessage(e), "\n"): input string 1 is invalid
## in this locale
# tre <- ape::read.tree(tre_fpath)
fas <- Biostrings::readDNAStringSet(seq_fpath)
```

Construct Object and Export

```
bak_phsq <- merge_phyloseq(phsq, tre, fas)
save(bak_phsq, file = "/Users/paul/Documents/AAD_combined/Zenodo/R/16S_physeq_obj.Rdata")
```

Construct 18S Object

Set Paths

```
bim_fpath = "/Users/paul/Documents/AAD_combined/Zenodo/Qiime/085_18S_merged_qiime_artefacts/features-ta
# tre_fpath = ""
seq_fpath = "/Users/paul/Documents/AAD_combined/Zenodo/Qiime/085_18S_merged_qiime_artefacts/dna-sequenc
```

Import

```
phsq <- import_biom (bim_fpath)

## Warning in strsplit(conditionMessage(e), "\n"): input string 1 is invalid
## in this locale
# tre <- ape::read.tree(tre_fpath)
fas <- Biostrings::readDNAStringSet(seq_fpath)
```

Construct Object and Export

```
euk_phsq <- merge_phyloseq(phsq, tre, fas)
save(euk_phsq, file = "/Users/paul/Documents/AAD_combined/Zenodo/R/18S_physeq_obj.Rdata")
```

Session info

The code and output in this document were tested and generated in the following computing environment:

```
## R version 3.5.3 (2019-03-11)
## Platform: x86_64-apple-darwin15.6.0 (64-bit)
## Running under: macOS High Sierra 10.13.6
##
## Matrix products: default
## BLAS: /Library/Frameworks/R.framework/Versions/3.5/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/3.5/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
```

```
##
## attached base packages:
## [1] stats4    parallel  stats     graphics  grDevices utils     datasets
## [8] methods   base
##
## other attached packages:
##  [1] forcats_0.4.0     stringr_1.4.0     dplyr_0.8.1
##  [4] purrr_0.3.2       readr_1.3.1       tidyr_0.8.3
##  [7] tibble_2.1.1      ggplot2_3.1.1     tidyverse_1.2.1
## [10] data.table_1.12.2 phyloseq_1.26.1   Biostrings_2.50.2
## [13] XVector_0.22.0    IRanges_2.16.0    S4Vectors_0.20.1
## [16] BiocGenerics_0.28.0 ape_5.3
##
## loaded via a namespace (and not attached):
##  [1] Biobase_2.42.0   httr_1.4.0        jsonlite_1.6
##  [4] splines_3.5.3    foreach_1.4.4     modelr_0.1.4
##  [7] assertthat_0.2.1 highr_0.8         cellranger_1.1.0
## [10] yaml_2.2.0       pillar_1.4.0      backports_1.1.4
## [13] lattice_0.20-38  glue_1.3.1        digest_0.6.19
## [16] rvest_0.3.4      colorspace_1.4-1  htmltools_0.3.6
## [19] Matrix_1.2-17    plyr_1.8.4        pkgconfig_2.0.2
## [22] broom_0.5.2      haven_2.1.0       zlibbioc_1.28.0
## [25] scales_1.0.0     mgcv_1.8-28       generics_0.0.2
## [28] withr_2.1.2      lazyeval_0.2.2    cli_1.1.0
## [31] survival_2.44-1.1 magrittr_1.5     crayon_1.3.4
## [34] readxl_1.3.1     evaluate_0.13     nlme_3.1-140
## [37] MASS_7.3-51.4    xml2_1.2.0        vegan_2.5-5
## [40] tools_3.5.3      hms_0.4.2         Rhdf5lib_1.4.3
## [43] munsell_0.5.0    cluster_2.0.9     ade4_1.7-13
## [46] compiler_3.5.3   rlang_0.3.4       rhdf5_2.26.2
## [49] grid_3.5.3       iterators_1.0.10  biomformat_1.10.1
## [52] rstudioapi_0.10  igraph_1.2.4.1    rmarkdown_1.12
## [55] gtable_0.3.0     codetools_0.2-16  multtest_2.38.0
## [58] reshape2_1.4.3   R6_2.4.0          lubridate_1.7.4
## [61] knitr_1.23       permute_0.9-5     stringi_1.4.3
## [64] Rcpp_1.0.1       tidyselect_0.2.5  xfun_0.7
```