metabarcoding with dada2: environment installation

update VM configuration

```
sudo apt-get update -y
sudo apt-get install -y libbz2-dev
sudo apt-get install -y liblzma-dev
```

```
## sudo: unable to resolve host bbffce91a3f0: Name or service not known
## Hit:1 http://archive.ubuntu.com/ubuntu focal InRelease
## Hit:2 http://archive.ubuntu.com/ubuntu focal-updates InRelease
## Hit:3 http://security.ubuntu.com/ubuntu focal-security InRelease
## Hit:4 http://archive.ubuntu.com/ubuntu focal-backports InRelease
## Reading package lists...
## sudo: unable to resolve host bbffce91a3f0: Name or service not known
## Reading package lists...
## Building dependency tree...
## Reading state information...
## libbz2-dev is already the newest version (1.0.8-2).
## 0 upgraded, 0 newly installed, 0 to remove and 39 not upgraded.
## sudo: unable to resolve host bbffce91a3f0: Name or service not known
## Reading package lists...
## Building dependency tree...
## Reading state information...
## liblzma-dev is already the newest version (5.2.4-1ubuntu1).
## 0 upgraded, 0 newly installed, 0 to remove and 39 not upgraded.
```

#package install Following instruction on https://benjjneb.github.io/dada2/dada-installation.html

```r
if (!requireNamespace("BiocManager", quietly = TRUE))
  install.packages("BiocManager")
BiocManager::install(version = '3.11')
```

```
## Bioconductor version 3.11 (BiocManager 1.30.10), R 4.0.3 (2020-10-10)
```

```
## Installation path not writeable, unable to update packages: codetools,
##   KernSmooth, nlme
```

```r
BiocManager::install("dada2", version = "3.11")
```

```
## Bioconductor version 3.11 (BiocManager 1.30.10), R 4.0.3 (2020-10-10)
```

```
## Installing package(s) 'dada2'
```

```
## Installation path not writeable, unable to update packages: codetools,
##   KernSmooth, nlme
```

```r
BiocManager::install("phangorn")
```

```
## Bioconductor version 3.11 (BiocManager 1.30.10), R 4.0.3 (2020-10-10)
```

```
## Installing package(s) 'phangorn'
```

```
## Installation path not writeable, unable to update packages: codetools,
##   KernSmooth, nlme
```

```r
BiocManager::install("DECIPHER")
```

```
## Bioconductor version 3.11 (BiocManager 1.30.10), R 4.0.3 (2020-10-10)
```

```
## Installing package(s) 'DECIPHER'
```

```
## Installation path not writeable, unable to update packages: codetools,
##   KernSmooth, nlme
```

```r
BiocManager::install("DESseq2")
```

```
## Bioconductor version 3.11 (BiocManager 1.30.10), R 4.0.3 (2020-10-10)
```

```
## Installing package(s) 'DESseq2'
```

```
## Warning: package 'DESseq2' is not available for this version of R
##
## A version of this package for your version of R might be available elsewhere,
## see the ideas at
## https://cran.r-project.org/doc/manuals/r-patched/R-admin.html#Installing-packages
```

```
## Installation path not writeable, unable to update packages: codetools,
##   KernSmooth, nlme
```

```r
install.packages("gridExtra")
```

```
## Installing package into '/usr/local/lib/R/site-library'
## (as 'lib' is unspecified)
```

```r
install.packages('tinytex')
```

```
## Installing package into '/usr/local/lib/R/site-library'
## (as 'lib' is unspecified)
```

```r
tinytex::install_tinytex()
```

```
## tlmgr option sys_bin ~/bin
```

```r
.cran_packages <- c( "shiny","miniUI", "caret", "pls", "e1071", "ggplot2", "randomForest", "dplyr", "gg
                     "reshape2", "PMA", "structSSI", "ade4",
                     "ggnetwork", "intergraph", "scales")
.github_packages <- c("jfukuyama/phyloseqGraphTest")
.bioc_packages <- c("genefilter", "impute")
```

```r
install.packages(.cran_packages)
```

```
## Installing packages into '/usr/local/lib/R/site-library'
## (as 'lib' is unspecified)
```

```
## Warning: package 'structSSI' is not available for this version of R
##
## A version of this package for your version of R might be available elsewhere,
## see the ideas at
## https://cran.r-project.org/doc/manuals/r-patched/R-admin.html#Installing-packages
```

```r
devtools::install_github(.github_packages)
```

```
## Skipping install of 'phyloseqGraphTest' from a github remote, the SHA1 (3fb6c274) has not changed sir
##    Use 'force = TRUE' to force installation
```

```r
BiocManager::install(.bioc_packages)
```

```
## Bioconductor version 3.11 (BiocManager 1.30.10), R 4.0.3 (2020-10-10)
```

```
## Installing package(s) 'genefilter', 'impute'
```

```
## Installation path not writeable, unable to update packages: codetools,
##    KernSmooth, nlme
```

```
wget https://cran.r-project.org/src/contrib/Archive/structSSI/structSSI_1.1.1.tar.gz
```

```
## --2020-11-24 21:24:30--  https://cran.r-project.org/src/contrib/Archive/structSSI/structSSI_1.1.1.tar
## Resolving cran.r-project.org (cran.r-project.org)... 137.208.57.37
## Connecting to cran.r-project.org (cran.r-project.org)|137.208.57.37|:443... connected.
## HTTP request sent, awaiting response... 200 OK
## Length: 25591 (25K) [application/x-gzip]
## Saving to: 'structSSI_1.1.1.tar.gz.3'
##
##      OK .......... .......... ....                          100% 1.13M=0.02s
##
## 2020-11-24 21:24:30 (1.13 MB/s) - 'structSSI_1.1.1.tar.gz.3' saved [25591/25591]
```

```r
library(devtools)
```

```
## Loading required package: usethis
```

```r
install_local("./structSSI_1.1.1.tar.gz")
```

```
## Skipping 1 packages not available: multtest
```

```
##      checking for file '/tmp/Rtmprf75ag/remotes60c359f1279b/structSSI/DESCRIPTION' ...  v  checking
## -  preparing 'structSSI':
##      checking DESCRIPTION meta-information ...  v  checking DESCRIPTION meta-information
## -  checking for LF line-endings in source and make files and shell scripts
## -  checking for empty or unneeded directories
## -  looking to see if a 'data/datalist' file should be added
## -  building 'structSSI_1.1.1.tar.gz'
##
##
```

```
## Installing package into '/usr/local/lib/R/site-library'
## (as 'lib' is unspecified)
```