

Script d'installation de tous les packages.

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Mise à jour de la machine virtuelle.

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

Installation de Dada2 et de Phyloseq avec BiocManager.

A partir des instructions <https://benjjneb.github.io/dada2/dada-installation.html>

Installation de BiocManager.

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

Installation de Dada2.

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

Installation de Phyloseq.

```
BiocManager::install("phyloseq", version = "3.11")
```

Installation de packages pour phyloseq.

Installation de phangorn.

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

Installation de DECIPHER.

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

Installation de gridExtra

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

Installation de packages pour des analyses complémentaires sur phyloseq.

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

```
install.packages(.cran_packages)  
devtools::install_github(.github_packages)  
BiocManager::install(.bioc_packages)
```