

Installation Guide

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Installation Guide

To go through this workshop, you will need to install a set of packages. Note that no installation is required for all sections that occur before we work with a count matrix (we will run those tools through the Galaxy browser tool).

Please make sure you are using R 4.0.0 or above for this session,

If you encounter any issues with the installation, please take a screenshot of the full error message and contact me at adrien.osakwe@mail.mcgill.ca!

Looking forward to the workshop!

Standard Packages

```
# General Packages
if (!require('tidyverse')){
  install.packages('tidyverse')
}
```

DESeq2 Packages

```
#Packages for DESeq2 Section
if (!require('BiocManager')){
  install.packages('BiocManager')
}

BiocManager::install('DESeq2')
BiocManager::install('fgsea')
BiocManager::install('org.Hs.eg.db')
```

```
BiocManager::install('apeglm')
```

Single Cell Packages

```
#Packages for Single Cell Analysis
BiocManager::install('DropletUtils')
BiocManager::install('scater')
BiocManager::install('scraper')
BiocManager::install('SingleR')
```

Test Loading Packages

```
library(tidyverse)
library(DESeq2)
library(fgsea)
library(org.Hs.eg.db)
library(DropletUtils)
library(scater)
library(scran)
library(SingleR)
library(apeglm)
```