

# Introduction to Single-cell RNA-seq Analysis

## Setup Tutorial

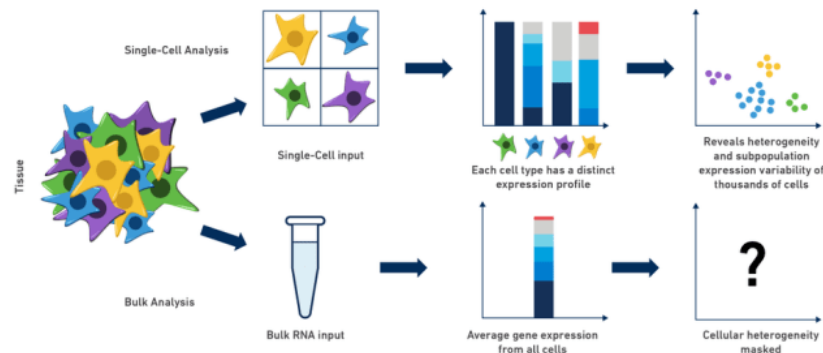
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# Latest Version of R, RStudio, and Rtools

Download R-4.5-1 from <https://www.r-project.org/>

Download Rstudio from <https://posit.co/download/rstudio-desktop/>

Open your Rstudio and create a new project called "single-cell-workshop".

In the Rstudio console, use function ``install.packages()`` to install the following software:

- Seurat, ggplot2, cowplot, dplyr, Matrix, viridis, gprofiler2, hdf5r, ggExtra, devtools

For example, ``install.packages("Seurat")``

Install Rtools-4.5 if you are a Windows user: <https://cran.r-project.org/bin/windows/Rtools/>

- You might need to run the installer as a system administrator



# Bioconductor

Run the following to install the development version of Bioconductor:

```
``
```

```
if (!require("BiocManager", quietly = TRUE))  
  install.packages("BiocManager")  
BiocManager::install(version = "devel")
```

```
``
```

Then, use the function `BiocManager::install()` to install the following packages:

- SingleR
- cellIdex
- EnhancedVolcano
- DESeq2

For example, `BiocManager::install("SingleR")`.



# Install presto from source

There is a package that is only available on GitHub, and we need to install it using devtools.

In your R console, run ``devtools::install_github("immunogenomics/presto")``



# Data

Please download the data from: [https://genomedata.org/cri-workshop/counts\\_gex/](https://genomedata.org/cri-workshop/counts_gex/)

We need the six ".h5" files. You can download the zip file, and it contains all the six h5 files.

Save it under your project folder "single-cell-workshop".



# Thank you

## Contact us

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