Copying the code from this document might lead to errors because Office messes up the quotes. If you copy quotes: remove them in RStudio and write them again!

R installation

The summer school will use R 4.6.0 !

If you are running an older version of R:

- remove the old R version and install R 4.6.0 (https://cloud.r-project.org/)

- on **Windows**: make sure you have Rtools 4.5 installed (https://cran.r-project.org/bin/windows/Rtools/rtools45/rtools.html)

Installing from CRAN

Make sure you have the following CRAN packages installed:

- anndata

- BiocManager

- doParallel

- dplyr

- ggplot2

- ggrepel

- kableExtra

- knitr

- pak

- remotes

- rmarkdown

- yaml

- renv

- sf

- tibble

Installing from Bioconductor

The summer school will use R 4.6 and Bioconductor 3.23

Check your Bioconductor version:

BiocManager::version()

To install Bioconductor 3.23:

- Run RStudio as administrator and run the following code:

BiocManager::install(version = "3.23")

If you see **Update a/s/n** type **a** and hit enter.

The installation might give warnings that source is unavailable for some packages but you can ignore this.

Install the following packages from Bioconductor:

(still running RStudio as administrator)

BiocManager::install(c("MSnbase", "BiocParallel", "SummarizedExperiment"))

BiocManager::install("scater")

BiocManager::install("ExploreModelMatrix")

pak::pkg_install("bioc::msqrob2")

pak::pkg_install("bioc::ComplexHeatmap")

Installing from Github

- Create a folder called sbivar in the spatial folder you created for the Python installations

- Open powershell (Windows) or terminal (Mac)

- Use cd to go to the sbivar folder and run the following code:

uv venv --python 3.11

uv pip install anndata numpy pandas scipy zarr h5py

- Close and reopen RStudio

- In RStudio: force R to use Python from the environment **(you need to adjust the path!)**

Sys.setenv(RETICULATE_PYTHON = "C:/Users/janic/spatial/sbivar/.venv/Scripts/python.exe")

Sys.setenv(RETICULATE_AUTOCONFIGURE="0")

- Load the reticulate package (to use Python in R):

library(reticulate)

- Check if R is using your environment:

py_config()

The python, pythonhome, virtualenv and numpy path should refer to your environment

- Check if anndata was installed:

py_list_packages()

anndata should be in the list

- Check if anndata can be used:

import("anndata")

should say Module(anndata)

- Install the sbivar package:

remotes::install_github("sthawinke/sbivar", build_vignettes=TRUE, dependencies=TRUE)

This takes a very long time on Windows.

- Check: load the sbivar package:

library(sbivar)

- Close RStudio

- **WINDOWS only**: install OpenBLAS by following the instructions in the README on: https://github.com/david-cortes/R-openblas-in-windows

Start following the instructions from the section "**Instructions in detail"** and stop following the instructions when you reach section "**Controlling number of threads".**

The version of OpenBLAS that I downloaded and that will work on most recent Windows laptops is: **OpenBLAS-0.3.33-x64.zip**.

Creating an R environment

Just like in Python you can set up virtual environments for R, using the renv package. These environments contain a specific version of the packages that you need to do a specific type of analysis. In this way each analysis gets its own collection of packages making it reproducible on any machine.

For the spatial omics summer school, we use such an environment.
To set up the environment you need to:

- create a folder called metabolomics in the spatial folder

- reopen RStudio

- use the metabolomics folder you have created as your Working Directory in RStudio

- make sure you have the renv package from CRAN installed

- create a project in RStudio. This is a folder that R treats as a single entity.

File in the top menu
New Project
Existing Directory: choose the metabolomics folder
Create Project

- close RStudio

- double click the **metabolomics.Rproj** file in the metabolomics folder

- run the following command in the console:

renv::init(bare=TRUE,bioconductor="3.23")

If he asks Do you want to proceed: type y and hit enter.

It creates all the files and folders that are necessary for the R environment (an environment is just a folder on your computer). One of the files is a .lock file that contains an overview of the installed packages and their versions.

The bare=TRUE argument ensures that you create a bare (empty) environment with no packages installed.

The bioconductor argument specifies the version of Bioconductor to use in the environment. This is why you should have installed the latest version of Bioconductor.

Run the following code:

renv::install("bioc::Cardinal")

renv::install("tibble","dplyr","ggplot2","yaml","rmarkdown")

If he asks Do you want to proceed: type y and hit enter.

This will install the required packages in the environment.

Run the following code in the console:

renv::snapshot()

If he asks How would you like to proceed? type 1 and hit enter.

This will write the details of the installed packages into the lock file.

Check: load the Cardinal package:

library(Cardinal)

Close the project (you need to do this or he will start up the project the next time you open RStudio):

In the top menu: **File -> Close Project**

Notify janick.mathys@vib.be if you encounter errors during these installations.