visAPPprot Windows Installation

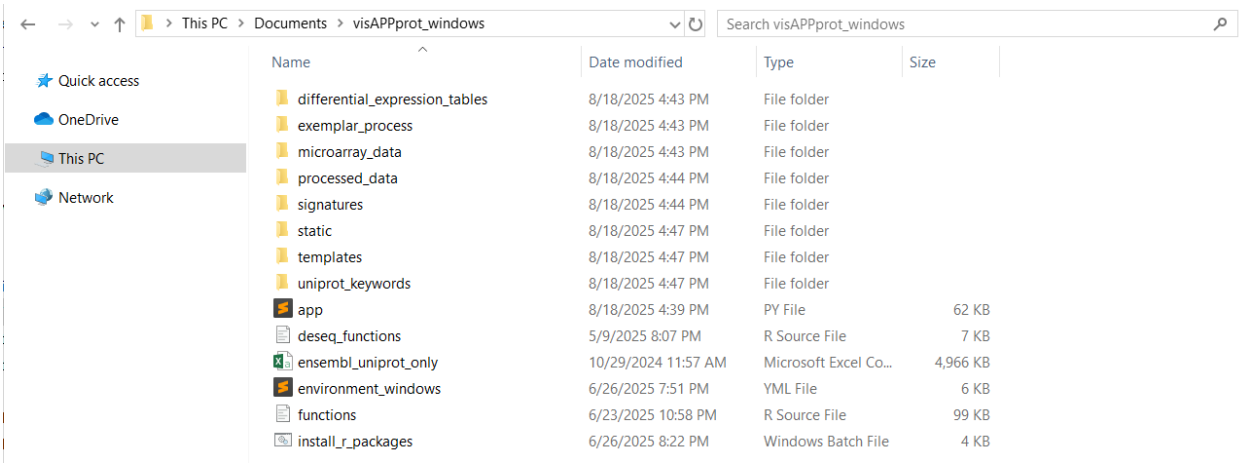
In the following pages we detail instructions for setting up our visualization application *visAPPprot*.

Installation should take approximately 1 hour to complete. The estimate for time required to complete each section is noted at the beginning of each section.

These are the following sections of this document:

1. Download Files

Go to your Documents folder and then into the *visAPPprot_windows* folder (about 33MB in size). The *visAPPprot_windows* folder should contain the following files and folders:
- differential_expression_tables/
- exemplar_process/
- microarray_data/
- processed_data/
- signatures/
- static/
- templates/
- uniprot_keywords/
- app.py
- deseq_functions.R
- ensembl_uniprot_only.csv
- environment_windows.yml
- functions.R
- install_r_packages.bat



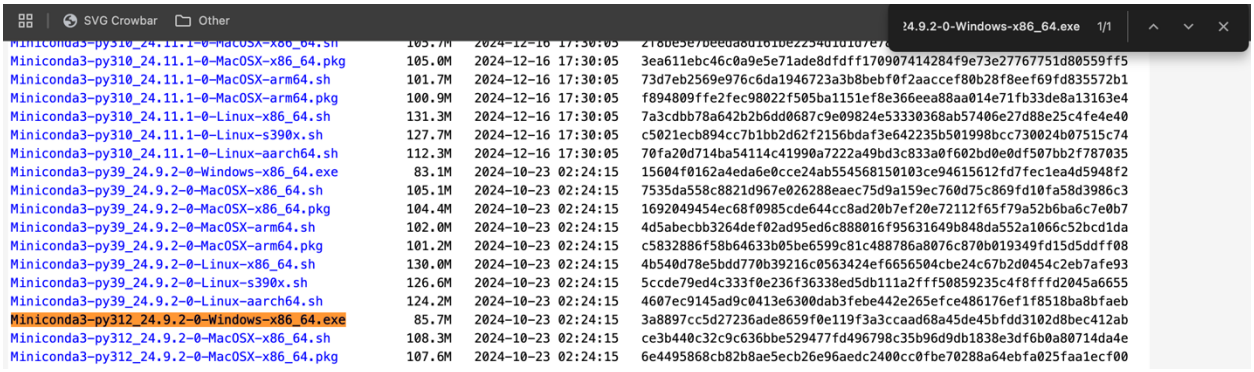
2. Install Miniconda Environment

(Time Estimate: 4 minutes)

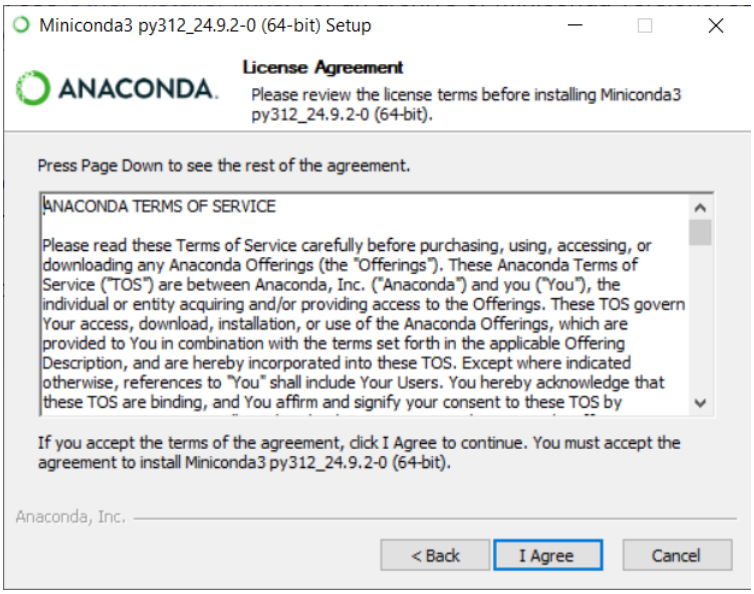
Install Miniconda: https://repo.anaconda.com/miniconda/

Download the Miniconda installer from the site above: in your browser on the page, search for "`Miniconda3-py312_24.9.2-0-Windows-x86_64.exe`". Once you find it, click to download.

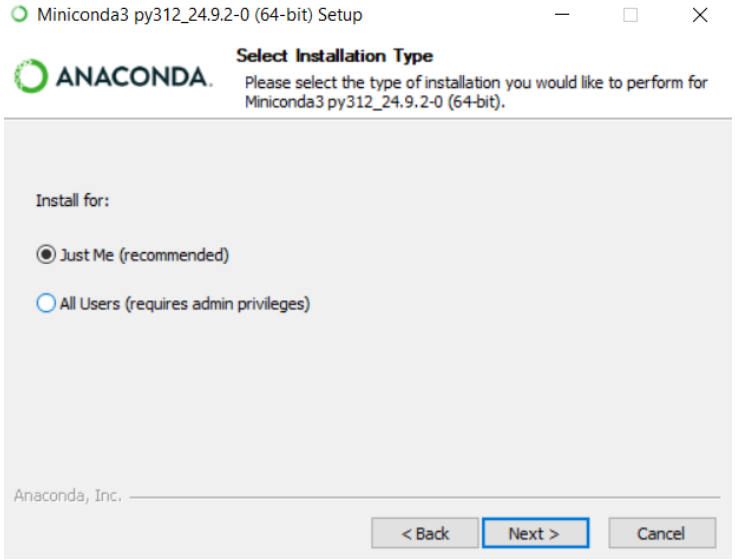
Go to your Downloads folder and double click on the Miniconda installer. When the first step of the setup pops up click "Next."



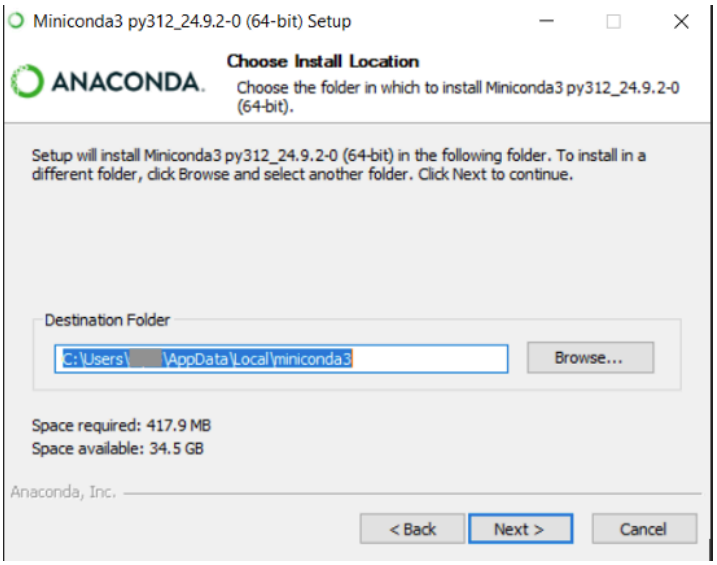
On the next step of the setup click "I agree."



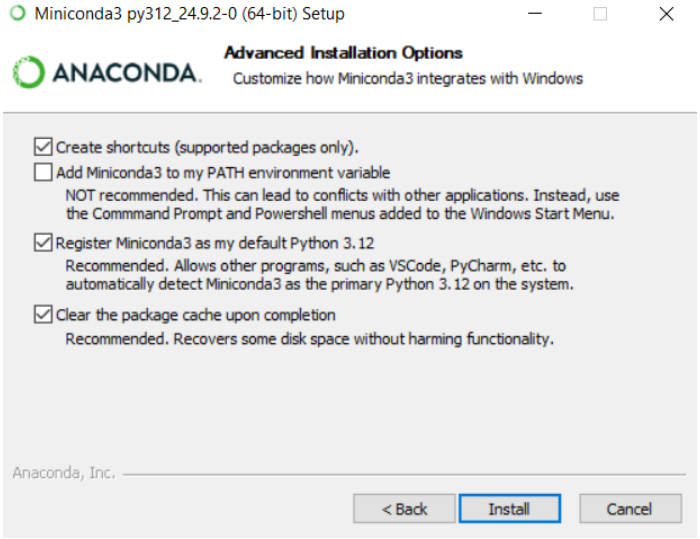
Then leave the selection as “Just Me (recommended)” and click “Next.”



Leave the “Destination Folder” path as is and **copy this path to a word document as we will need it later.** Click “Next.”



Check “Create start menu shortcuts,” “Register Miniconda3 as my default Python 3.12” and “Clear the package cache upon completion.” Click “Install.”

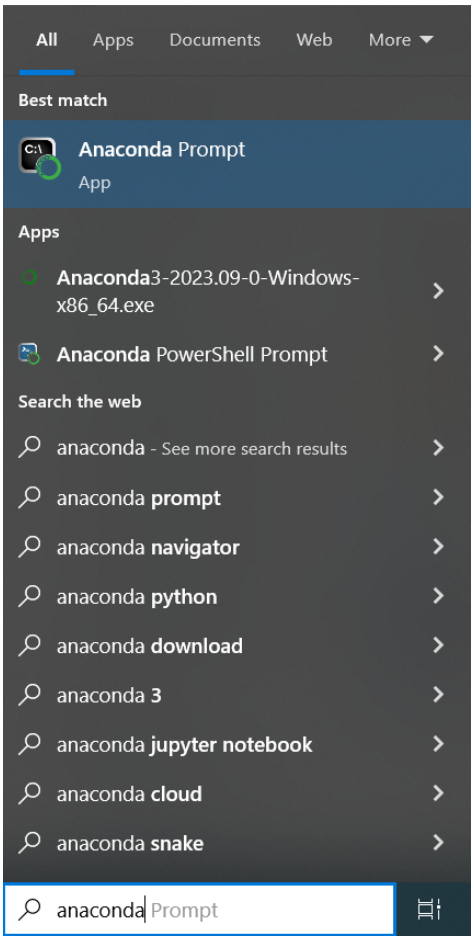


When the installation is complete, click “Next” and on the following page uncheck all the options and click “Finish”.

3. Install Conda Environment

(Time Estimate: 7 minutes)

In the Windows search bar on the bottom left of the screen search for “anaconda” and click on “Anaconda Prompt”.



When your command prompt opens you should see "(base)" indicating this is the raw, base conda environment.

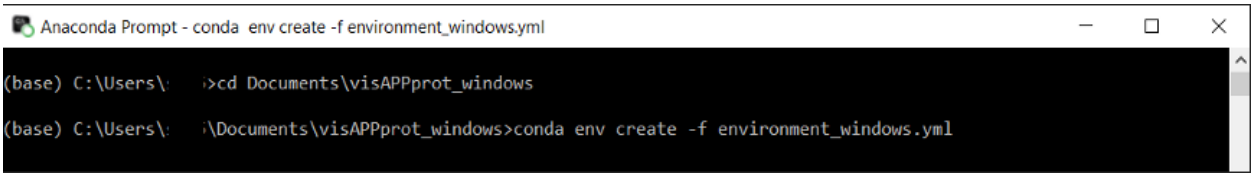
In the command prompt copy the following line and paste into the command prompt (hit Ctrl+V to paste). Then hit Enter.

cd Documents\visAPPprot_windows

Copy and paste the following line into the command prompt as well, and hit enter after pasting.

conda env create -f environment_windows.yml

This creates the conda environment and should take around 10 minutes.



Once the conda environment is created, you should see the suggestion to "conda activate omics_env". As suggested, type (or preferably copy and paste the following line)

conda activate omics_env

and then hit Enter to activate the environment. Keep your Anaconda command prompt open.

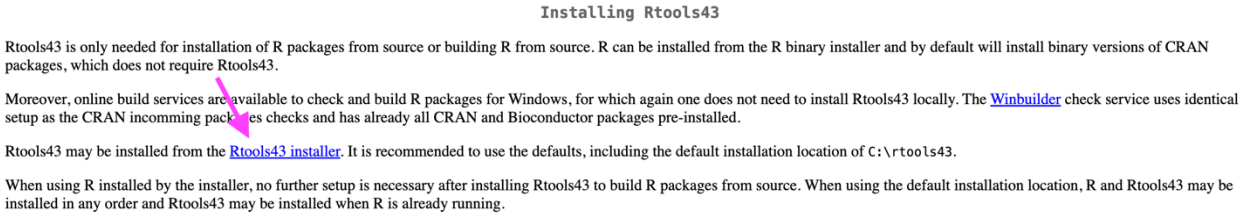
4. Install Rtools

(Time Estimate: 4 minutes)

We will need Rtools to compile some of our R package dependencies. Follow this link and download the Rtools43 installer: https://cran.r-project.org/bin/windows/Rtools/rtools43/rtools.html

Once the installer is downloaded, execute the installer. It will prompt you for the location to install Rtools.

Decide on the path to use for your Rtools installation and copy this path to a Word Document. We will use this path later. Click "Next".



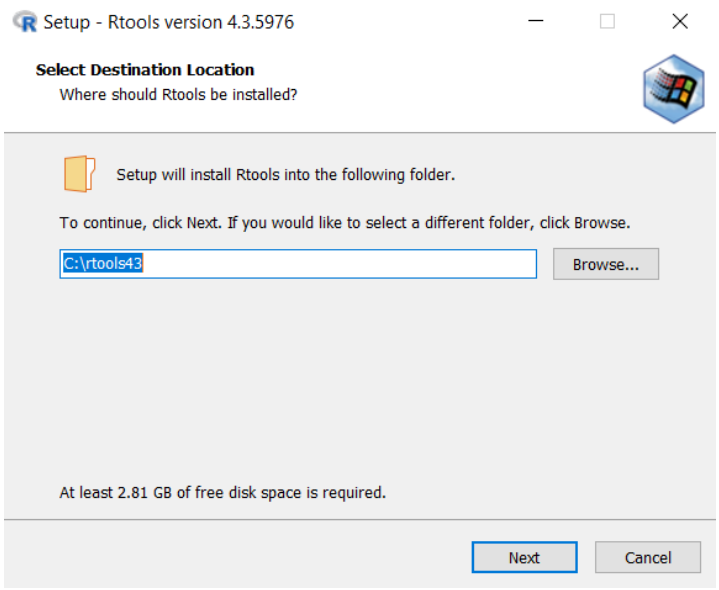
Installing Rtools43

Rtools43 is only needed for installation of R packages from source or building R from source. R can be installed from the R binary installer and by default will install binary versions of CRAN packages, which does not require Rtools43.

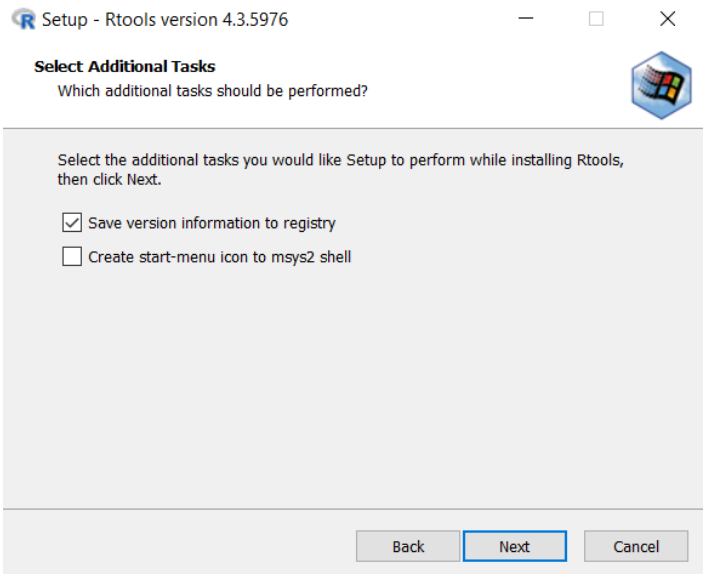
Moreover, online build services are available to check and build R packages for Windows, for which again one does not need to install Rtools43 locally. The Winbuilder check service uses identical setup as the CRAN incomming package checks and has already all CRAN and Bioconductor packages pre-installed.

Rtools43 may be installed from the Rtools43 installer. It is recommended to use the defaults, including the default installation location of `C:\rtools43`.

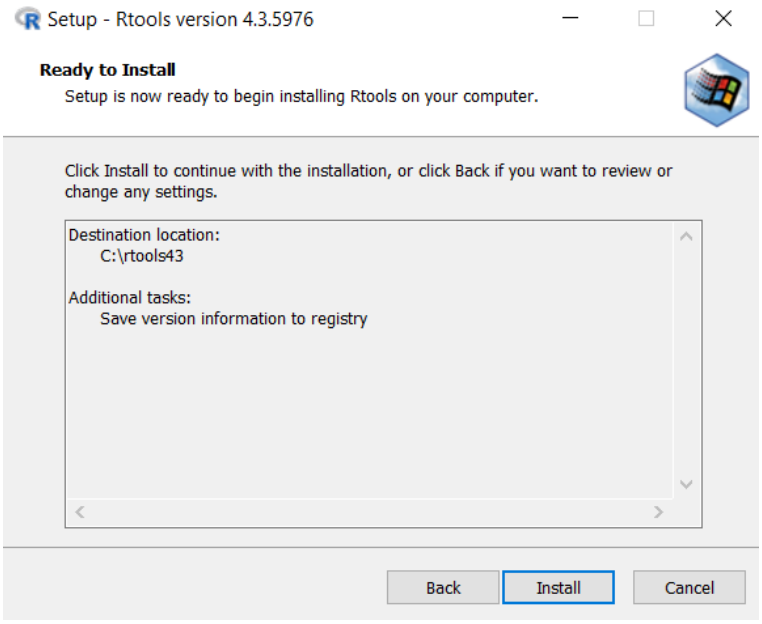
When using R installed by the installer, no further setup is necessary after installing Rtools43 to build R packages from source. When using the default installation location, R and Rtools43 may be installed in any order and Rtools43 may be installed when R is already running.



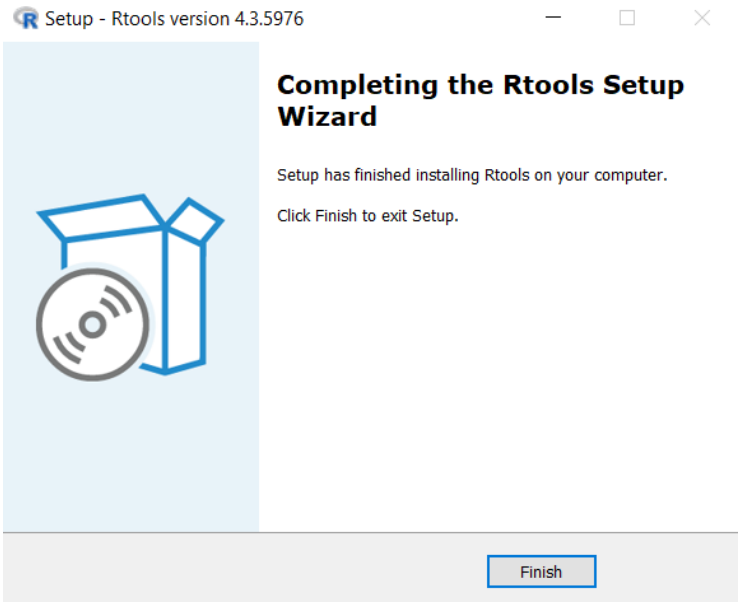
Check the box for "Save version information to registry." The other box is optional for you to check. Then click "Next".



Verify the path for Rtools installation and click “Install”.



Once the installation is complete you will see the end page. Click “Finish” to exit the installation.

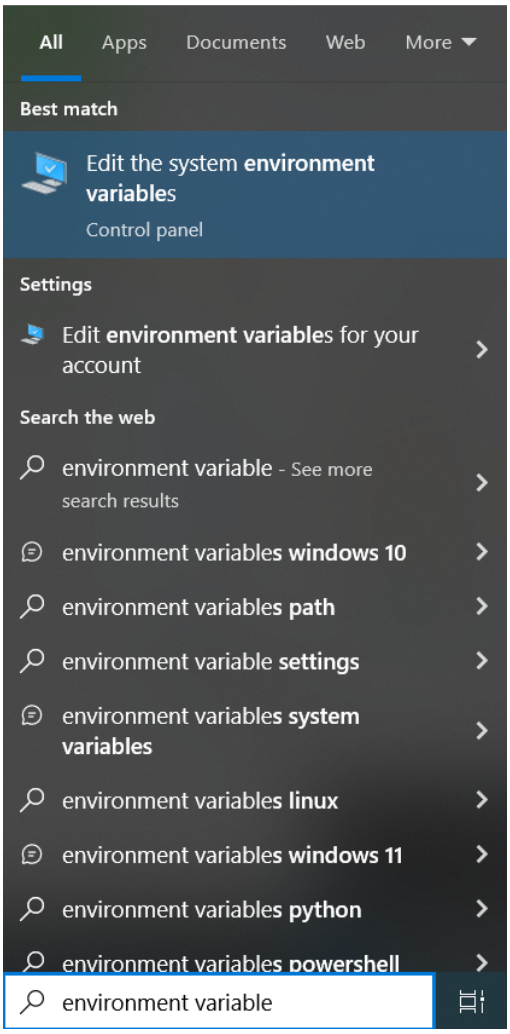


5. Add R_HOME and Rtools Environment Variable

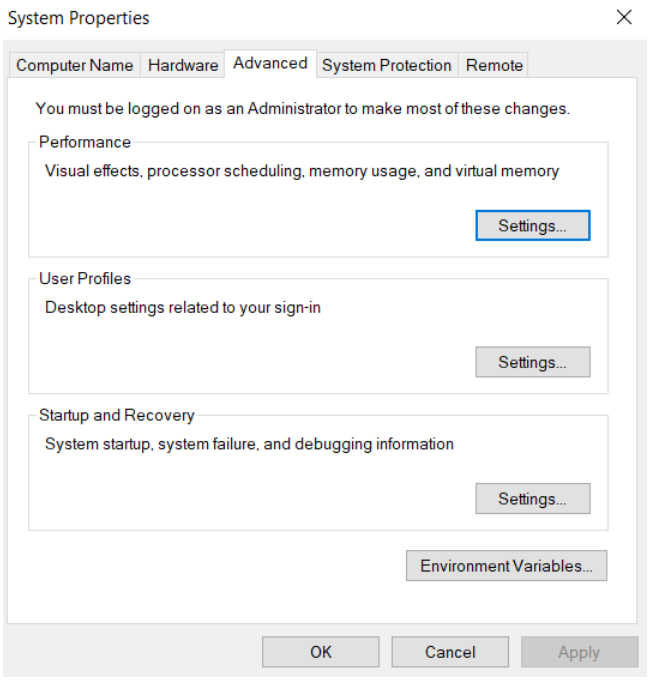
(Time Estimate: 2 minutes)

Before we install the R packages, let's first set the R_HOME environment variable for R to run in our conda environment.

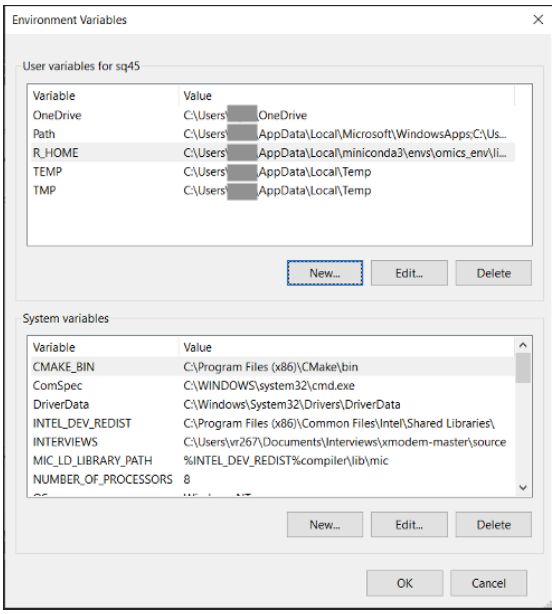
In the Windows search bar in the bottom left of the screen, search for "environment variable." Click on "Edit the system environment variables (Control panel)". You may see a warning pop up indicating that you need admin privileges to access and change these settings. If you see such a pop-up, please contact your admin to acquire the appropriate privileges and return to this step.



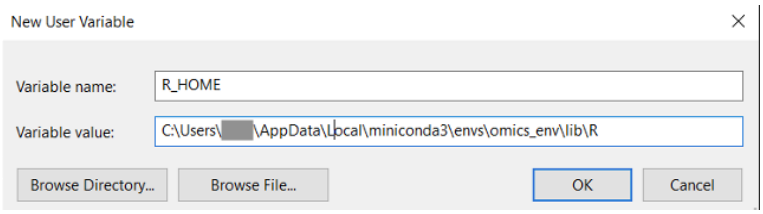
Then click “Environment Variables”.



Click “New” to create a new environment variable.

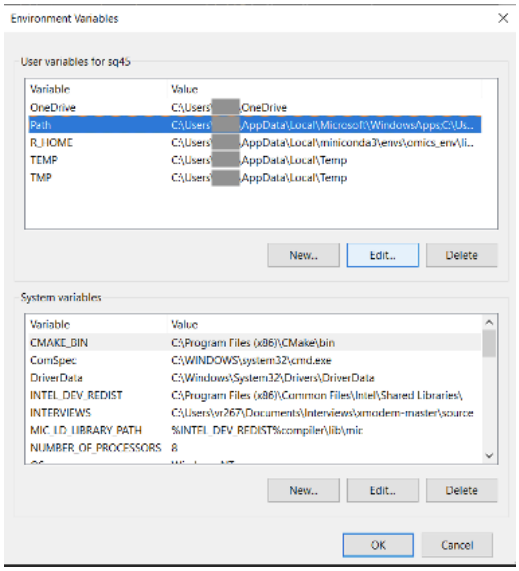


Name the new variable “R_HOME” and set the value to the path you saved on a word document while installing Miniconda (see Install Miniconda step) and append \envs\omics_env\lib\R to the path you saved on your word document. The whole path should look something like below. Click “OK” when you’re finished.

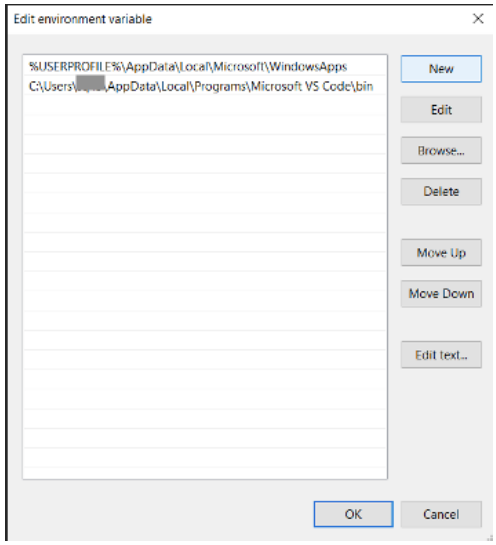


Now you should see your new R_HOME variable show up under your user variables.

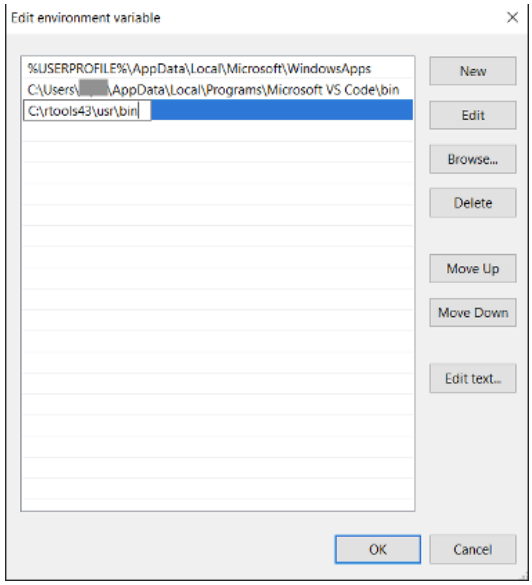
We then need to set up the Rtools environment variables for installing R packages. To do this, click on the "PATH" variable to highlight it and then click "Edit. . . " to change the PATH variable.



Click "New" to append to the PATH variable.

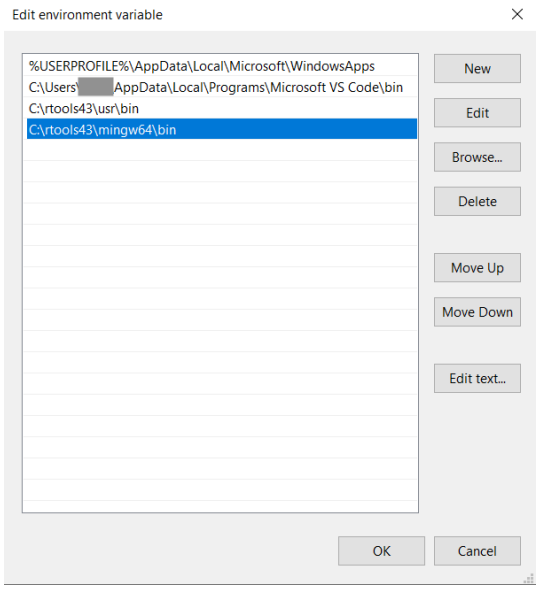


Copy the Rtools location we saved to a Word Document earlier during the Rtools installation and add "\usr\bin" to the end of it. If you have any forward slashes (/) in your location replace them with back slashes (\). For example, in this case the Rtools installation location was "C:\rtools43" so now our complete path is "C:\rtools43\usr\bin".

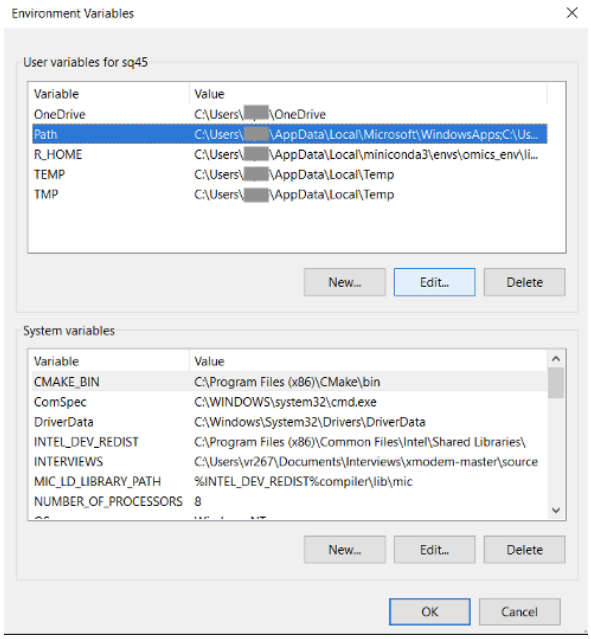


Click "New" to append again to the PATH variable.

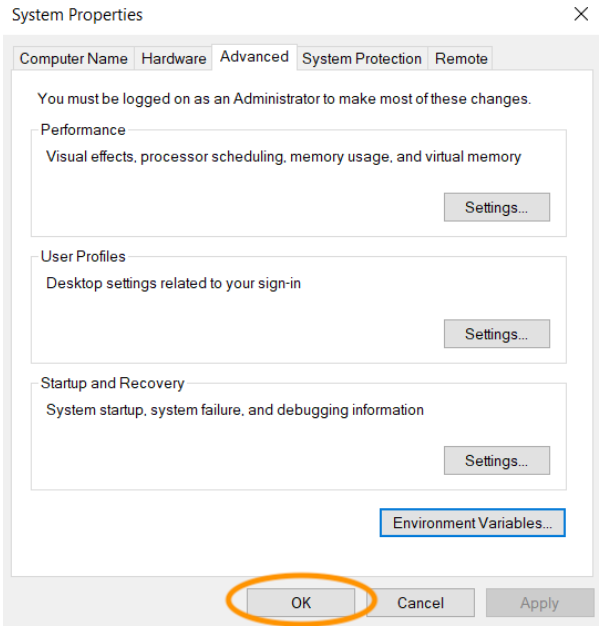
Copy the Rtools location we saved to a Word Document earlier during the Rtools installation, but this time add "\mingw64\bin" to the end. In this example, the rtools path is "C:\rtools43" so adding on "\mingw64\bin" results in "C:\rtools43\mingw64\bin". Now we are finished editing the PATH variable – click "OK".



We are finished setting up our environment variables. Click "OK".



Click “OK” to close out of System Properties.



6. Activate Conda Environment

(Time Estimate: 35 minutes)

After adding our new environment variable telling our system where to find and execute R and rtools, we need to restart our conda environment to incorporate these changes. To do so, close your current Anaconda command prompt window (click the X at the top right of the command prompt). Then go to the Windows search bar at the bottom left of your computer and search for “anaconda ” and open up “Anaconda Prompt”. This should be familiar, we went through these steps above.

Once your command prompt window is up, copy and paste the following line into the command prompt (hit Ctrl+V to paste). Then hit Enter.

cd Documents\visAPPprot_windows

Next copy and paste the following line into the command prompt and hit the Enter key.

conda activate omics_env

These steps should also be familiar, as we went through them above as well.

Install R Packages

In your Miniconda command prompt copy and paste the following line

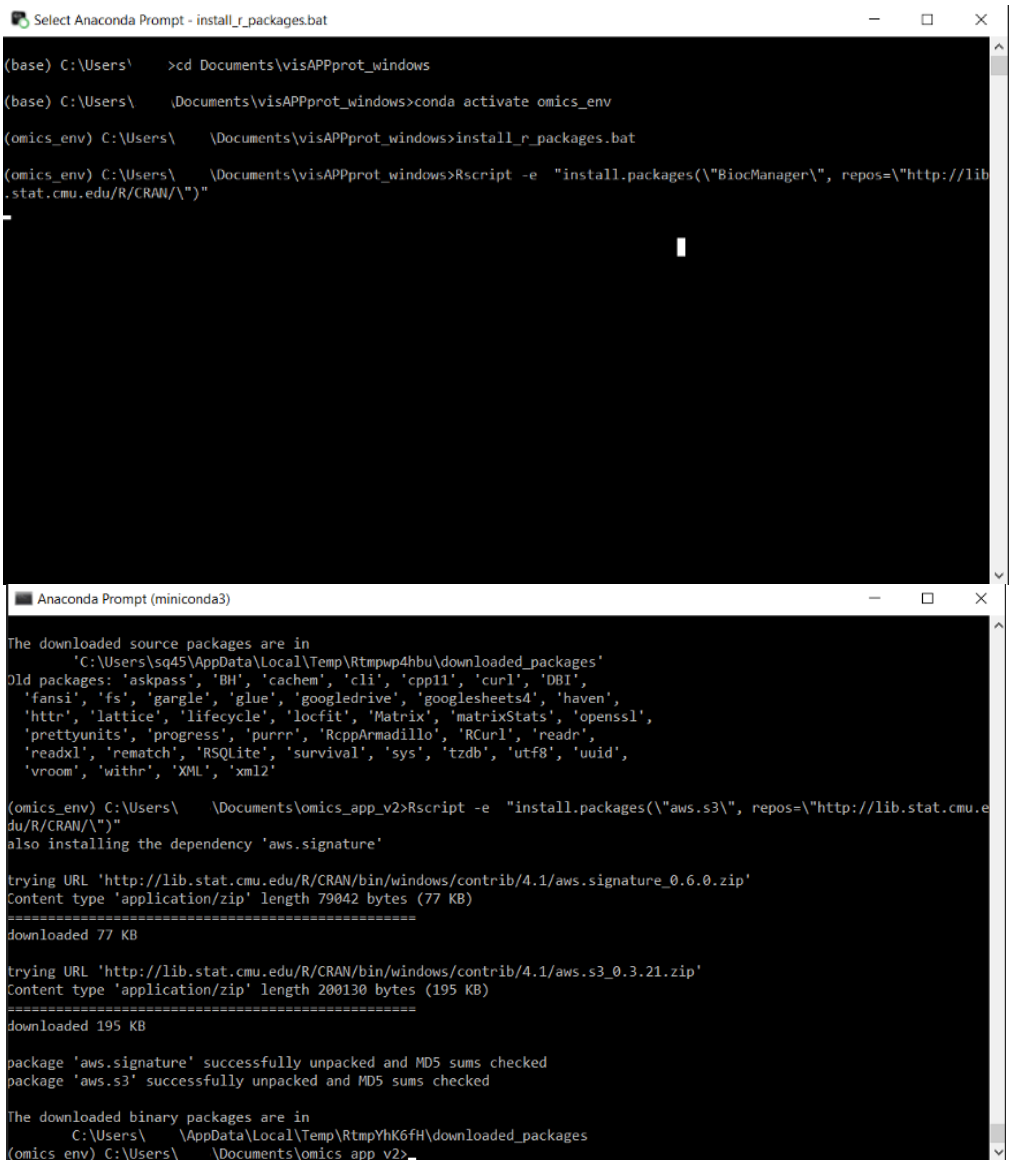
install_r_packages.bat

followed by the Enter key to install all the R packages necessary for this application. This could take up to 1 hour.

Once you see

package 'aws.s3' successfully unpacked

all the R packages have been installed. Keep your Anaconda command prompt open, even after installation!



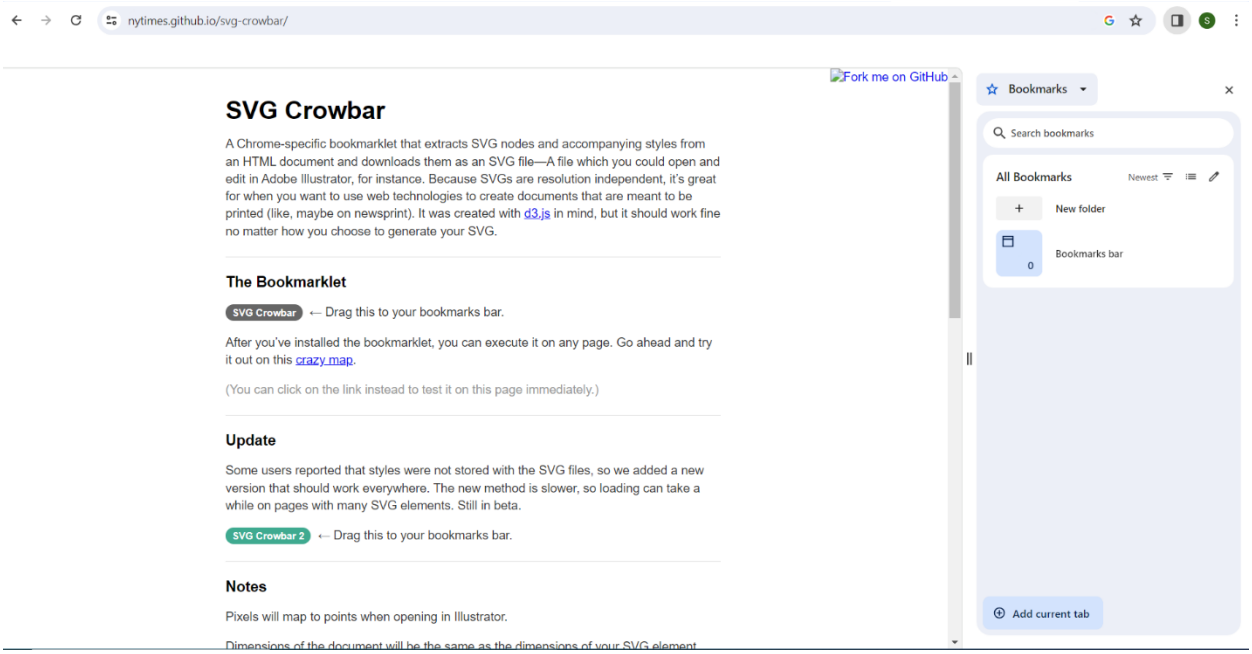
7. Install SVG-Crowbar

(Time Estimate: 1 minute)

Open this link in your Chrome browser: https://nytimes.github.io/svg-crowbar/

On the right of the address bar, find the rectangular "Bookmarks" icon (most likely placed right next to your user icon). Click on the "Bookmarks" icon and a bookmarks panel should open up on the right side of your screen. If you do not see your "Bookmarks" icon, you can find this panel by clicking the vertical 3 dots symbol to the far right of the address bar, then "Bookmarks and Lists" and finally "Show all Bookmarks".

Drag the "SVG Crowbar" icon with the grey background to your "Bookmarks Bar" section of the bookmarks panel.



If your bookmarks bar is already showing below your address bar, you should see the SVG Crowbar bookmark now appear in the bookmarks bar below your address bar. Otherwise, open the bookmarks row by pressing Ctrl+Shift+B.

8. Run visAPPprot

(Time Estimate: 1 minute)

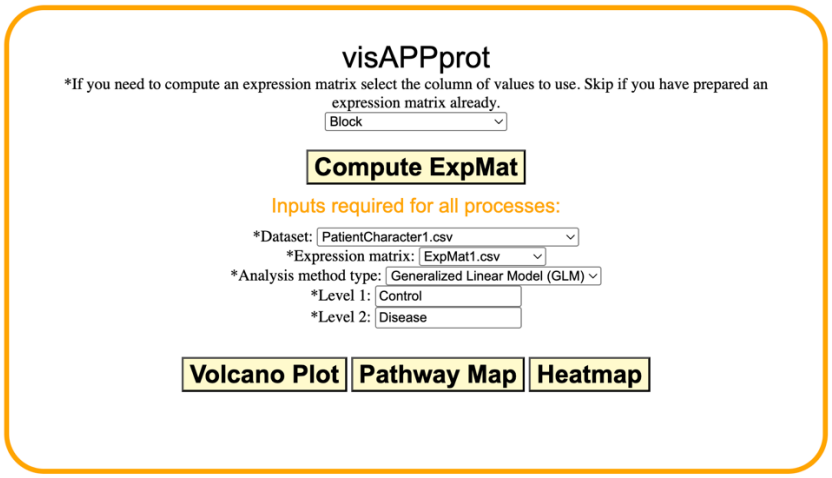
In your Anaconda command prompt, make sure you are still in the ~/Documents/visAPPprot_windows directory. Copy and paste the following line and then hit the Enter key:

python app.py

It may take up to 2 minutes to start up. Once you see the following on your command prompt, the application is ready:

```
R[write to console]: The following objects are masked from 'package:rjson':

    fromJSON, toJSON


R[write to console]: The following object is masked from 'package:purrr':

    flatten


R[write to console]:
Attaching package: 'limma'


R[write to console]: The following object is masked from 'package:DESeq2':

    plotMA


R[write to console]: The following object is masked from 'package:BiocGenerics':

    plotMA


 * Debugger is active!
 * Debugger PIN: 114-008-706
 * Running on http://localhost:8888/ (Press CTRL+C to quit)
```

Now you can open up a new window in Chrome. **Make sure you are in normal browsing mode and *not* Incognito! Keep your command prompt open as you use the application.** Navigate to the address *localhost:8888* and you should see the following page:

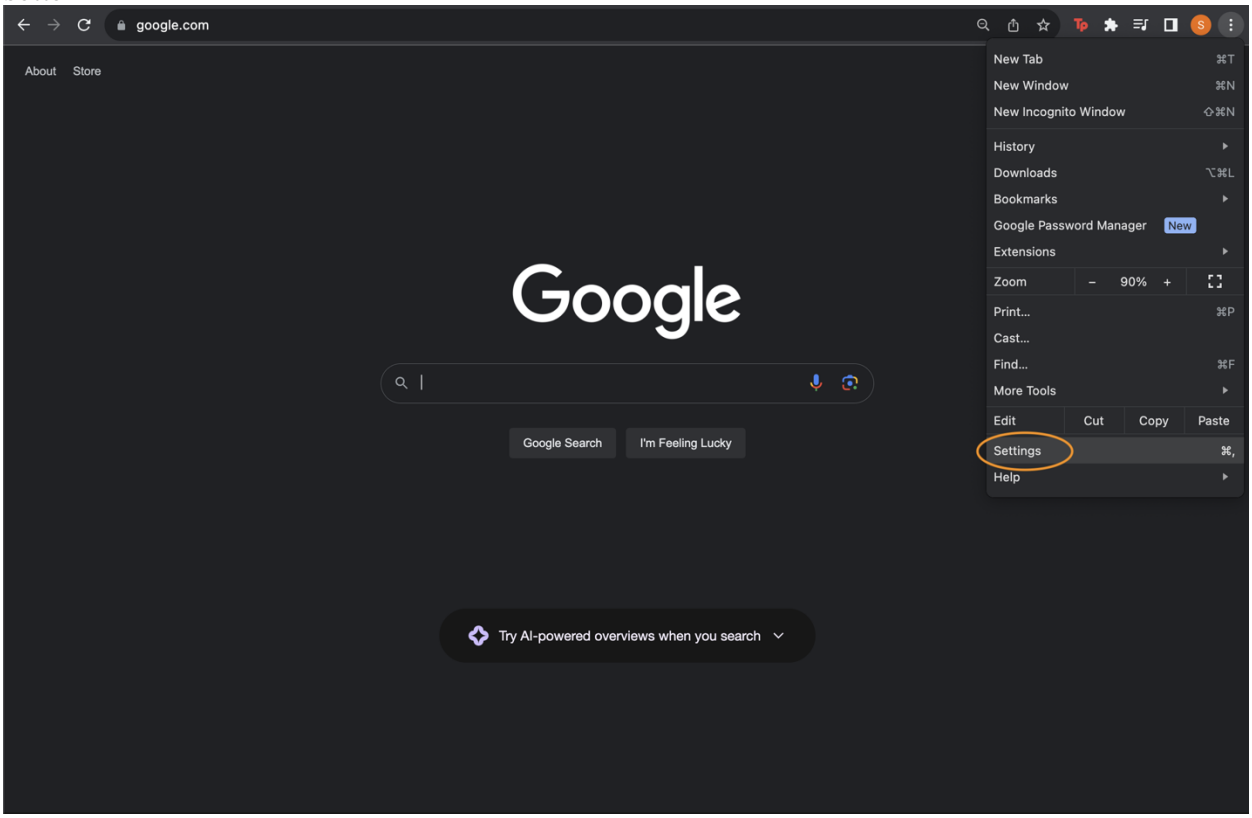


9. Set Up Chrome Downloads

(Time Estimate: 1 minute)

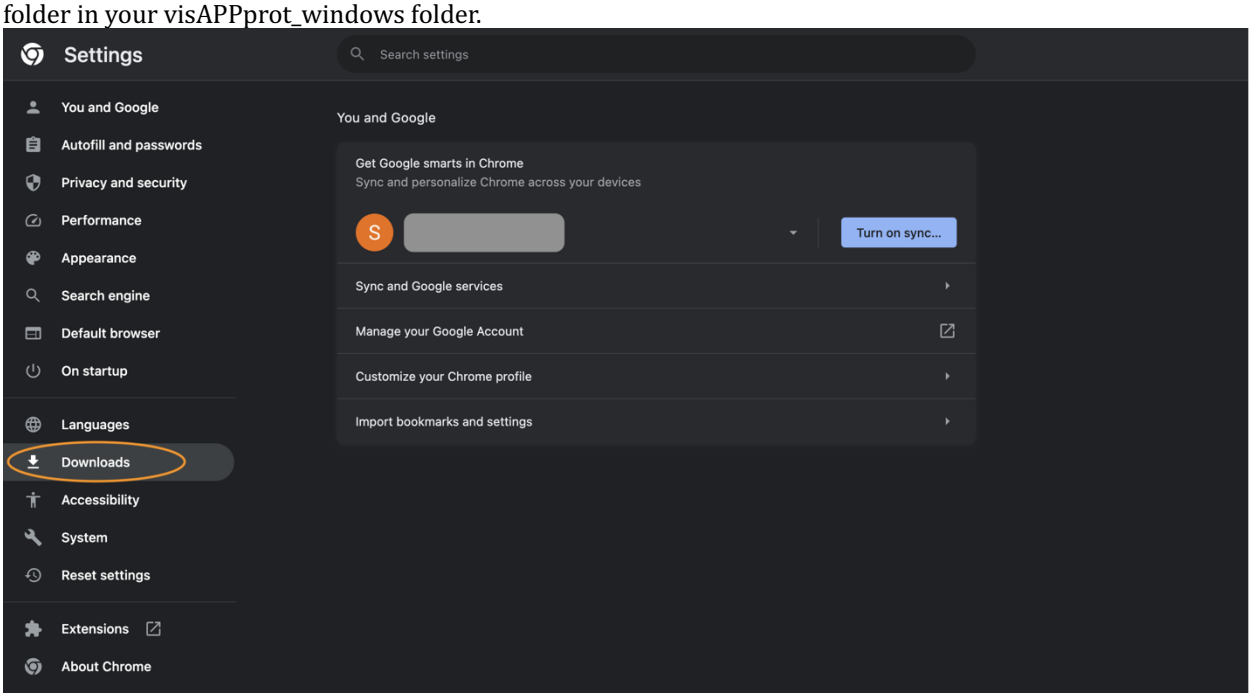
Change your Chrome downloads directory to the *download_imgs* folder that corresponds to the name of the dataset you are analyzing. For example, in our User Manual we demonstrate usage of the system with Toy Dataset 1, which involves PatientCharacter1.csv and ExpMat1.csv. This means we want to set up our downloads directory for PatientCharacter1, there we set it to *static/download_imgs_PatientCharacter1/* folder in your visAPPprot_windows folder. Here are the steps.

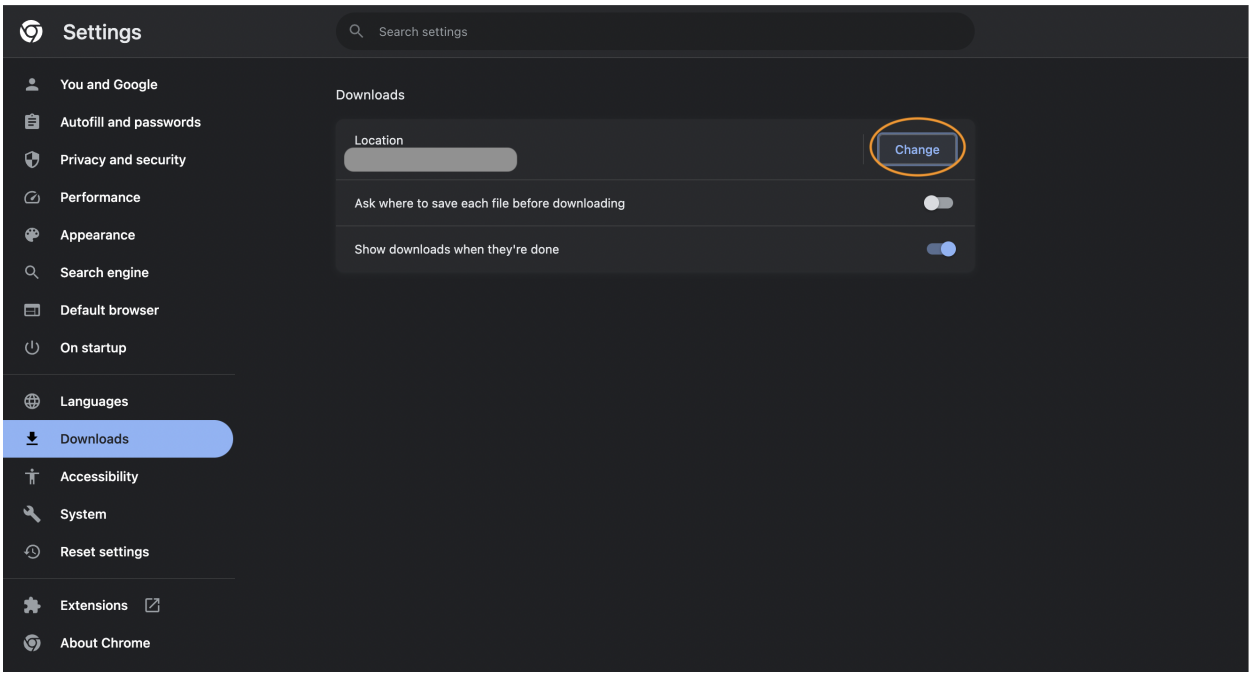
In Chrome, click on the vertical 3 dots symbol to the far right of the address bar. Then click *Settings* near the bottom.

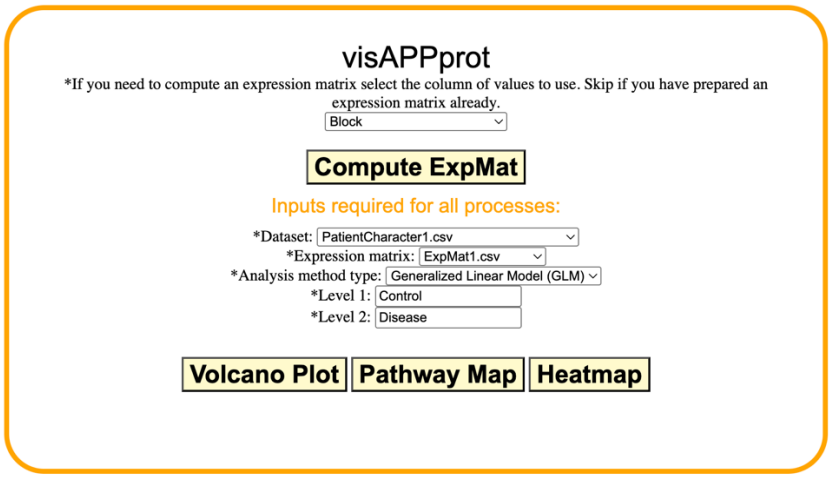


Click *Downloads* in the left side menu.

Click *Change* next to *Location* and set the Downloads directory to the *static/download_img_PatientCharacter1/* folder in your visAPPprot_windows folder.







You are now ready to move onto the User Manual!