

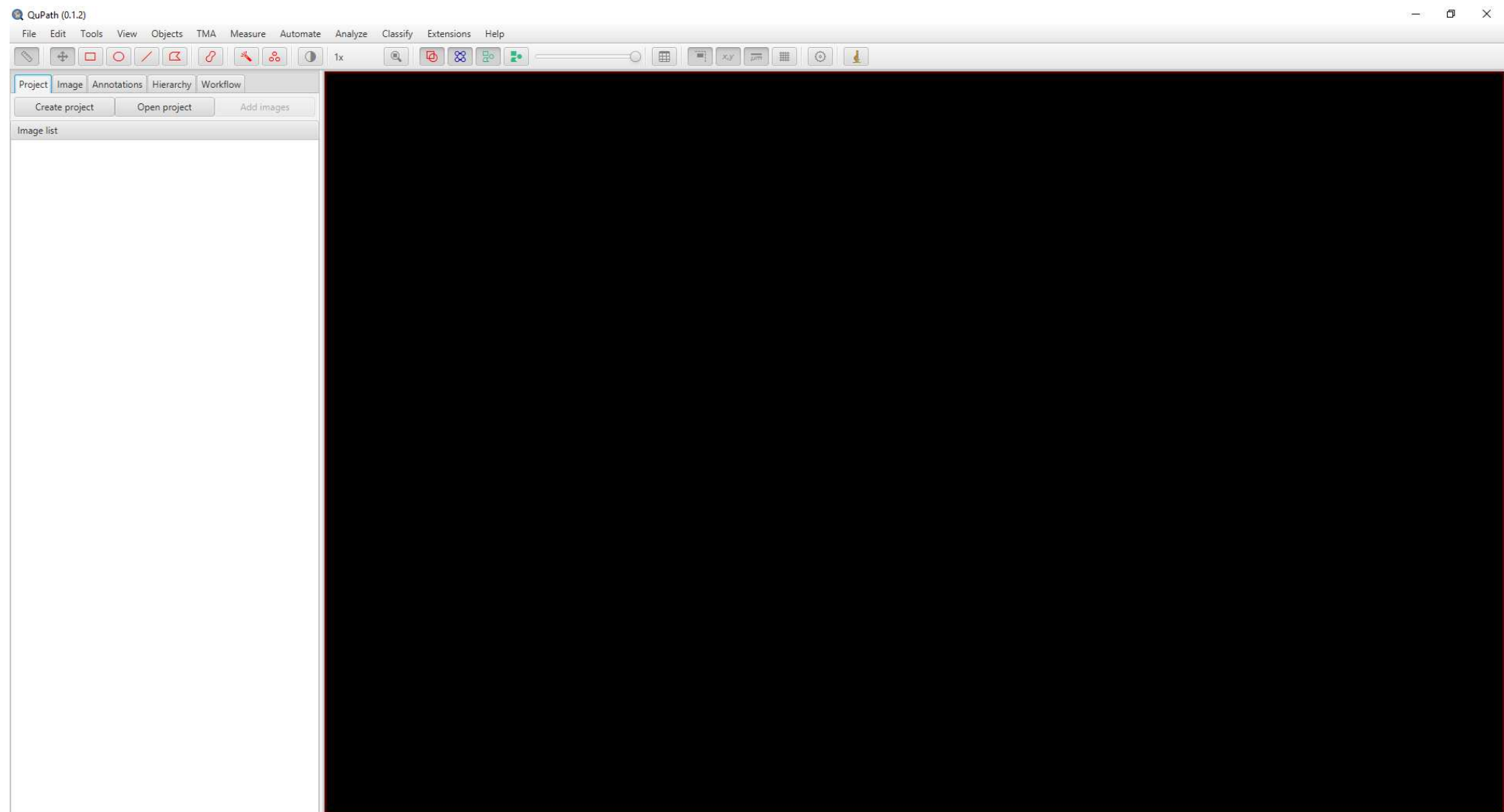
## Requirements :



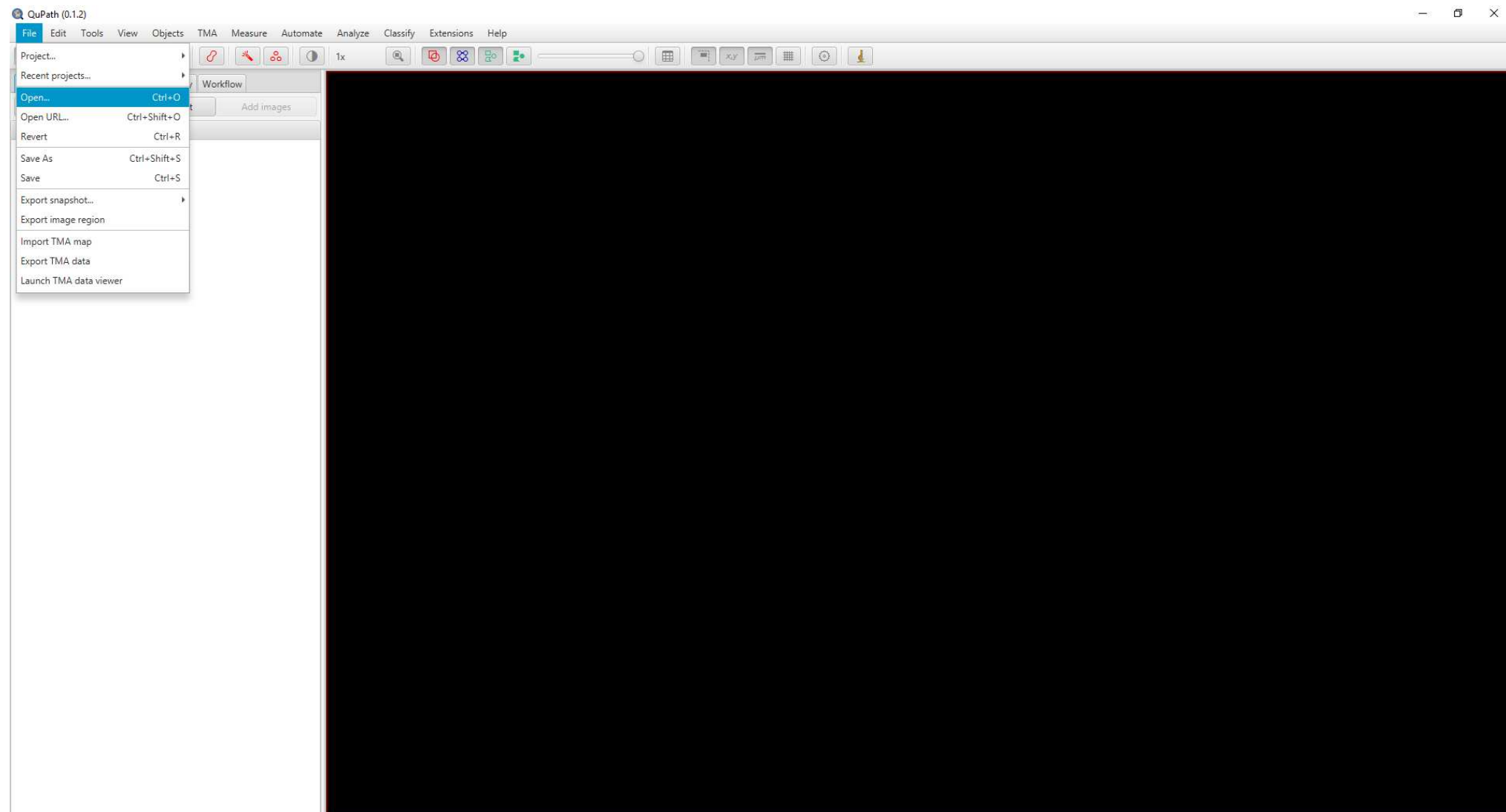
**<https://qupath.github.io>**

You need to install Qupath from the following website. The scripts used should be run with v0.1.2 or 0.1.3. Running scripts with other versions (i.e 0.2.0) haven't been tested.

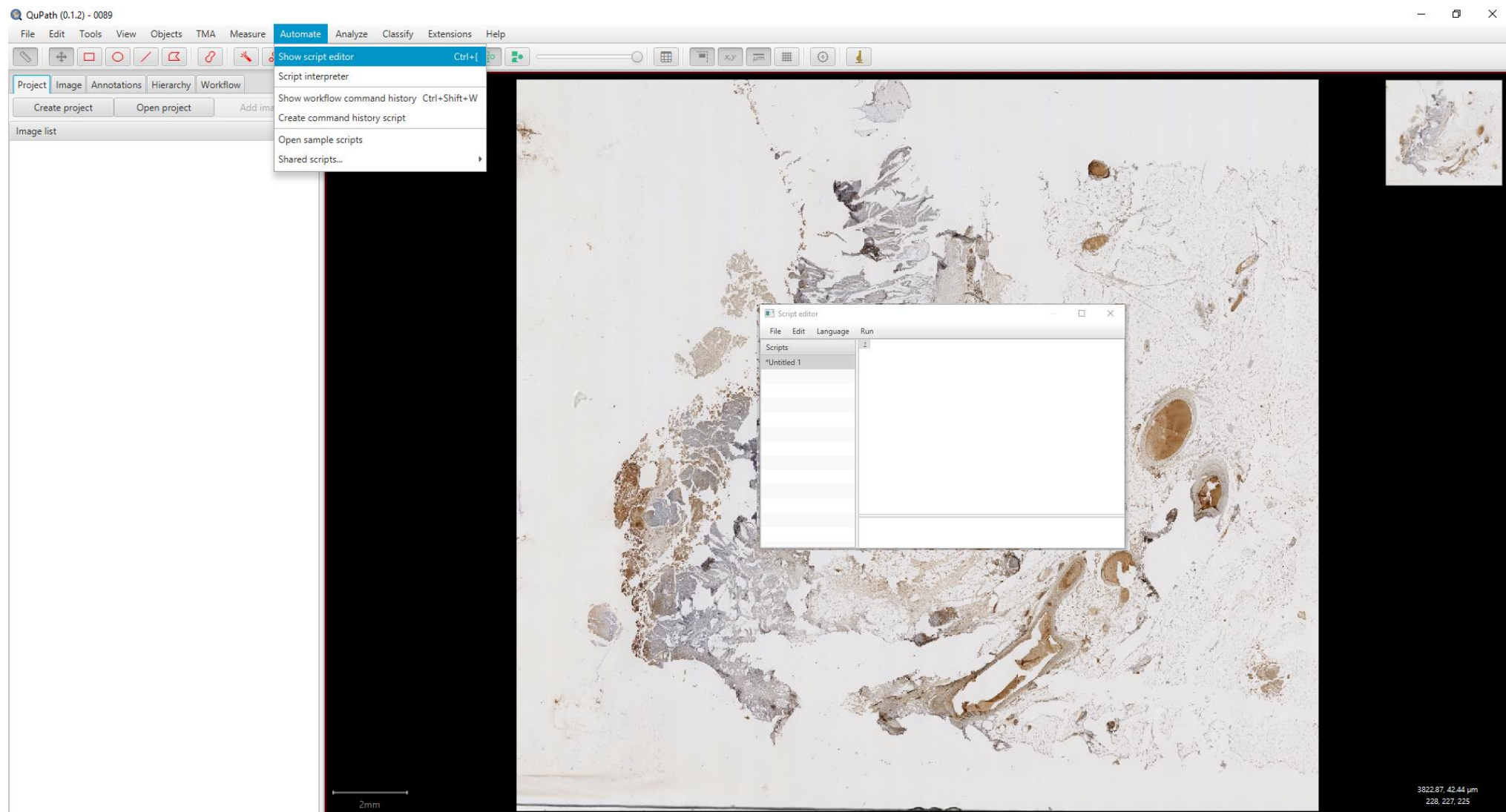
# Window that shows up when you start QuPath



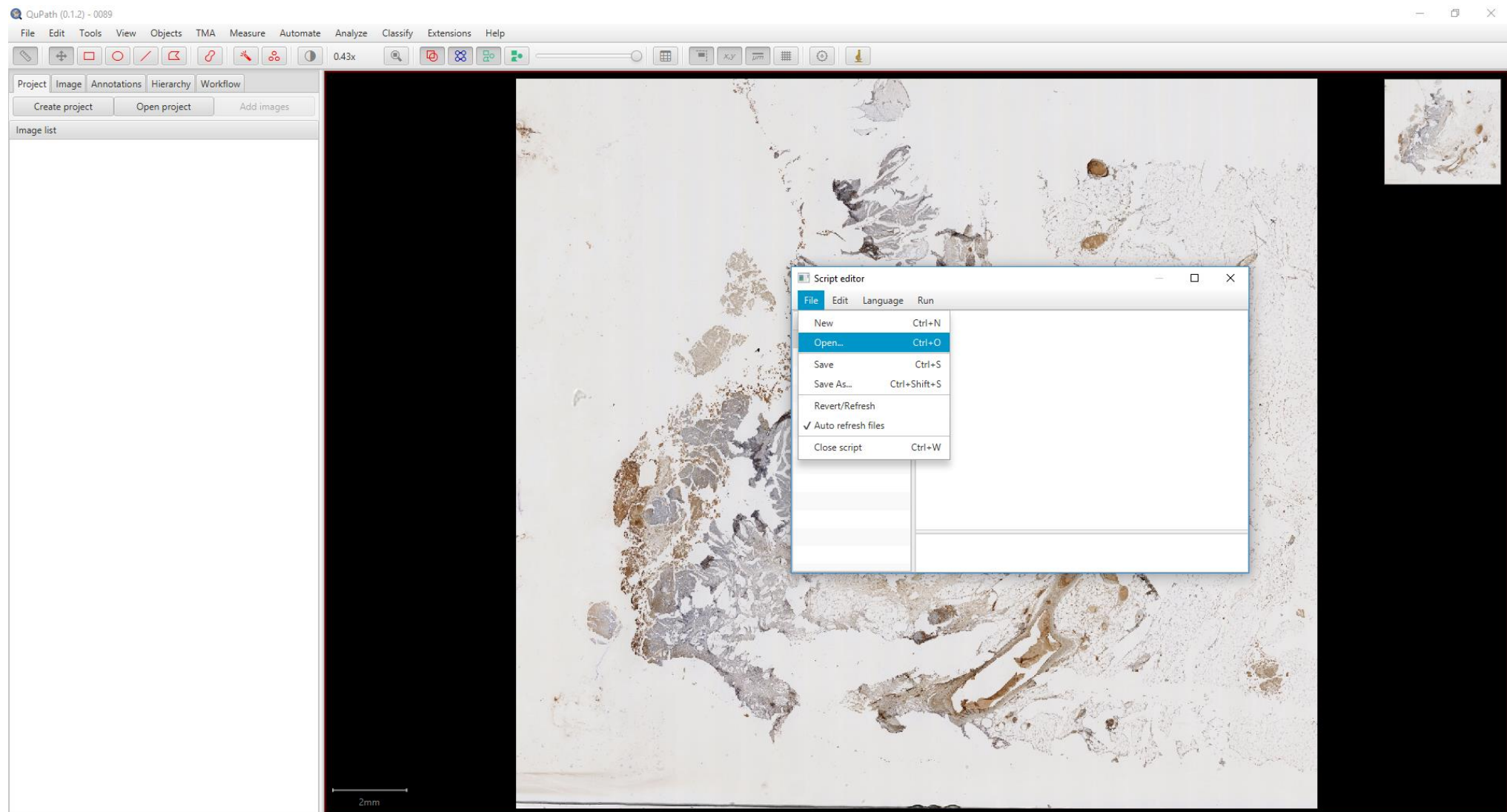
**With File>Open ; select the slide you want to analyse**



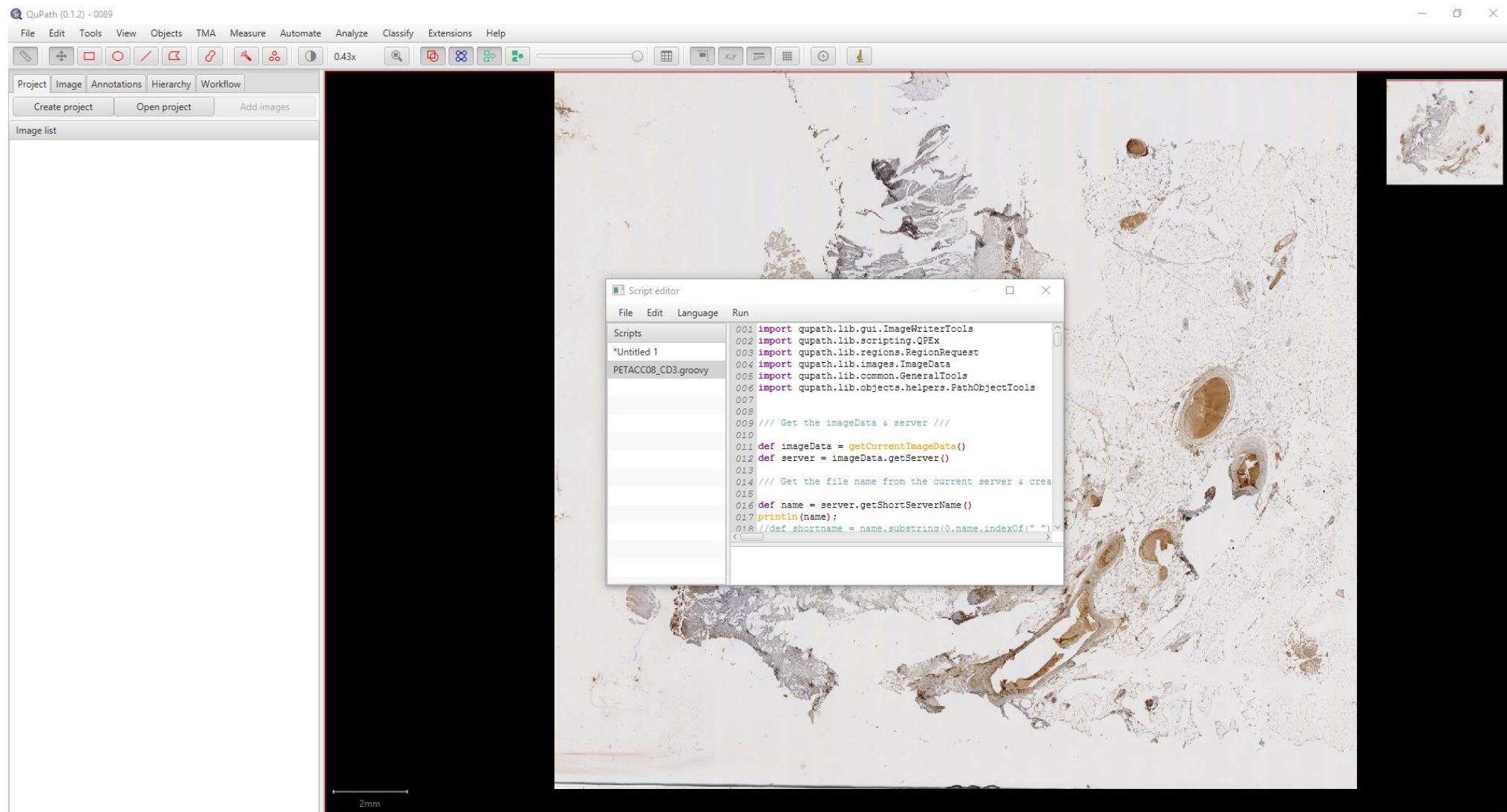
Once the slide opened, use **Automate>Show script editor**, the window inset will open



In the script editor window, **Select File>Open** and browse to select **PETACC08\_CD3.groovy**



The script is now opened in the window, **CHANGE ALL** the paths where the script will generate files. You can easily find them all along the script with the words `‘/insert/your/path/’`



Then in the script editor window, just **select Run>Run**, and the slide should be processed, please be aware that it could take a important time

```

Script editor
File Edit Language Run
Scripts
*Untitled 1
*PETACC08_CD3.groovy
Run
Run selected
Run for project
Run for project (without save)
Kill running script
Include default bindings
Send output to log
Log script start time
Auto clear console
ImageWriterTools
ImageRequest
ImageData
ImageTools
ImageTools.PathObjectTools
Data()
()
current server & create folder///
Name ()
017 println(name);
018 //def shortname = name.substring(0,name.indexOf(" "));
019 def shortname=name
020 print shortname
021 def Path1 = '/insert/your/path/'+shortname;
022 File dir=new File(Path1);
023 dir.mkdir();
024
025 /// Slide preprocess ///
026
027 setImageType('BRIGHTFIELD_H_DAB');
028 setColorDeconvolutionStains('{"Name": "CD3-PETIAC", "Stain 1": "Hematoxylin", "Values 1": "0.73662 0.59869 0.31457", "Stain 2": "DAB", "Values 2": "0.27578 0.54782 0.78983", "Background": " 229 228 227 "}');
029 print("Deconvolution done!");
030
031
032 /// Make full image as Annotation ///
033 createSelectAllObject(true);
034
035
036 ///Image export///
037
038 double requestedPixelSize = 10
039 def BZ = QPEX.getSelectedROI()
040 double downsample = requestedPixelSize / server.getAveragedPixelSizeMicrons()
041 def request = RegionRequest.createInstance(imageData.getServerPath(), downsample, BZ)
042 def fileImage = new File(Path1, shortname+'.jpg')
043 def imgBZ =ImageWriterTools.writeImageRegion(server, request,fileImage.getAbsolutePath())
044
045 print 'GZ exported as JPEG!'
046
047 ///Export GZ X&Y///
048
049 selectAnnotations();
050
051 // Define how many decimal places to use in output
052 int nDecimalPlaces = 3
053
054 // Create an output file & get a PrintWriter in a Groovy way
055 def fileXY = new File(Path1, shortname+'_GZ_XY.txt')
056 def i=1;
057 def j=1;
058 def XName=""
059 fileXY.withPrintWriter { writer ->
060 writer.println("Point"+'\t'+XName+'\t'+Y)
061 // Loop through all detections
062 for (Detection in QPEX.annotationObjects()) {

```

## Requirements :



<https://www.rstudio.com/>



<https://cran.r-project.org/>

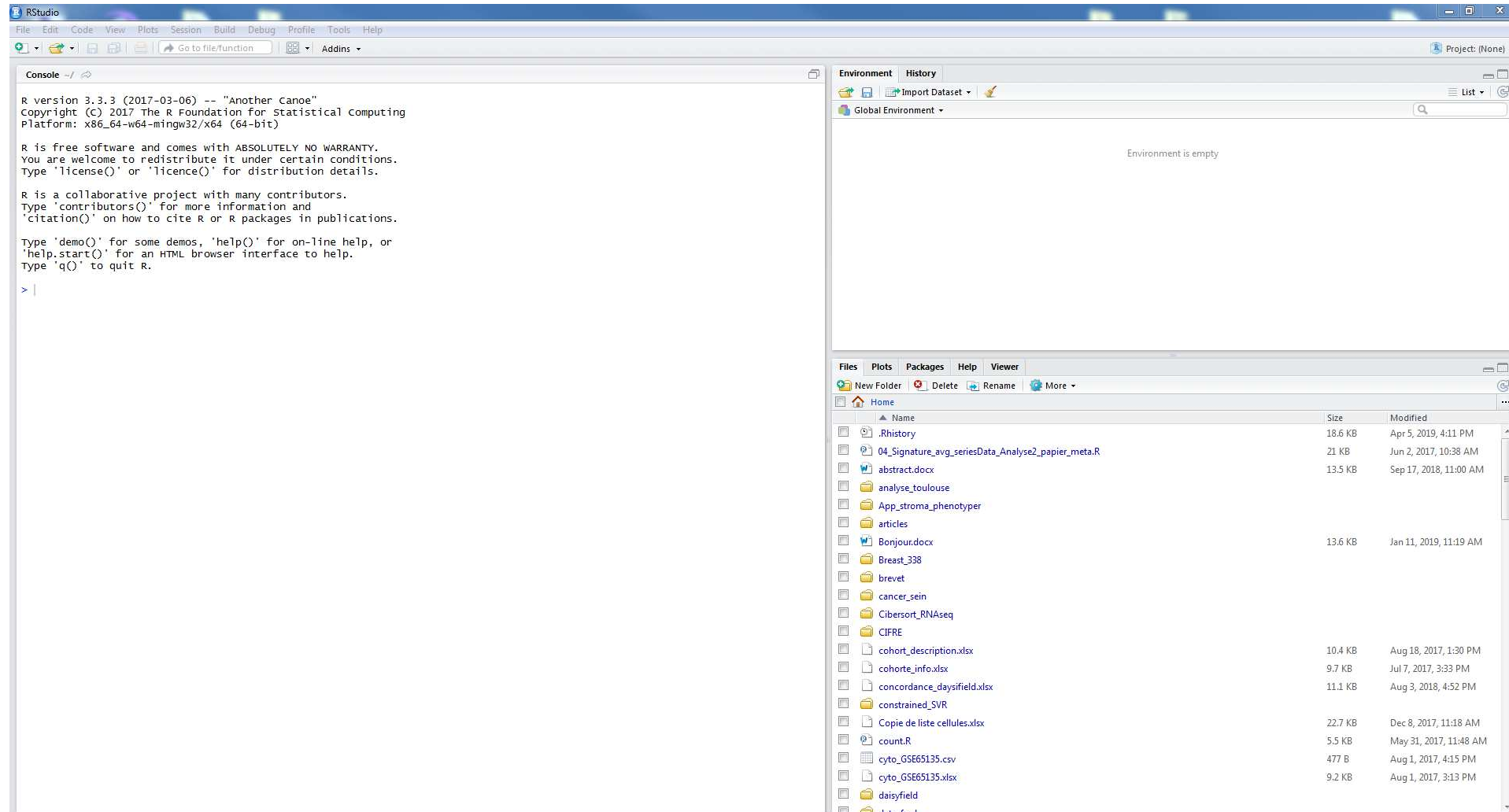


<https://github.com/Klopfe/PETTAC8>

## Instructions

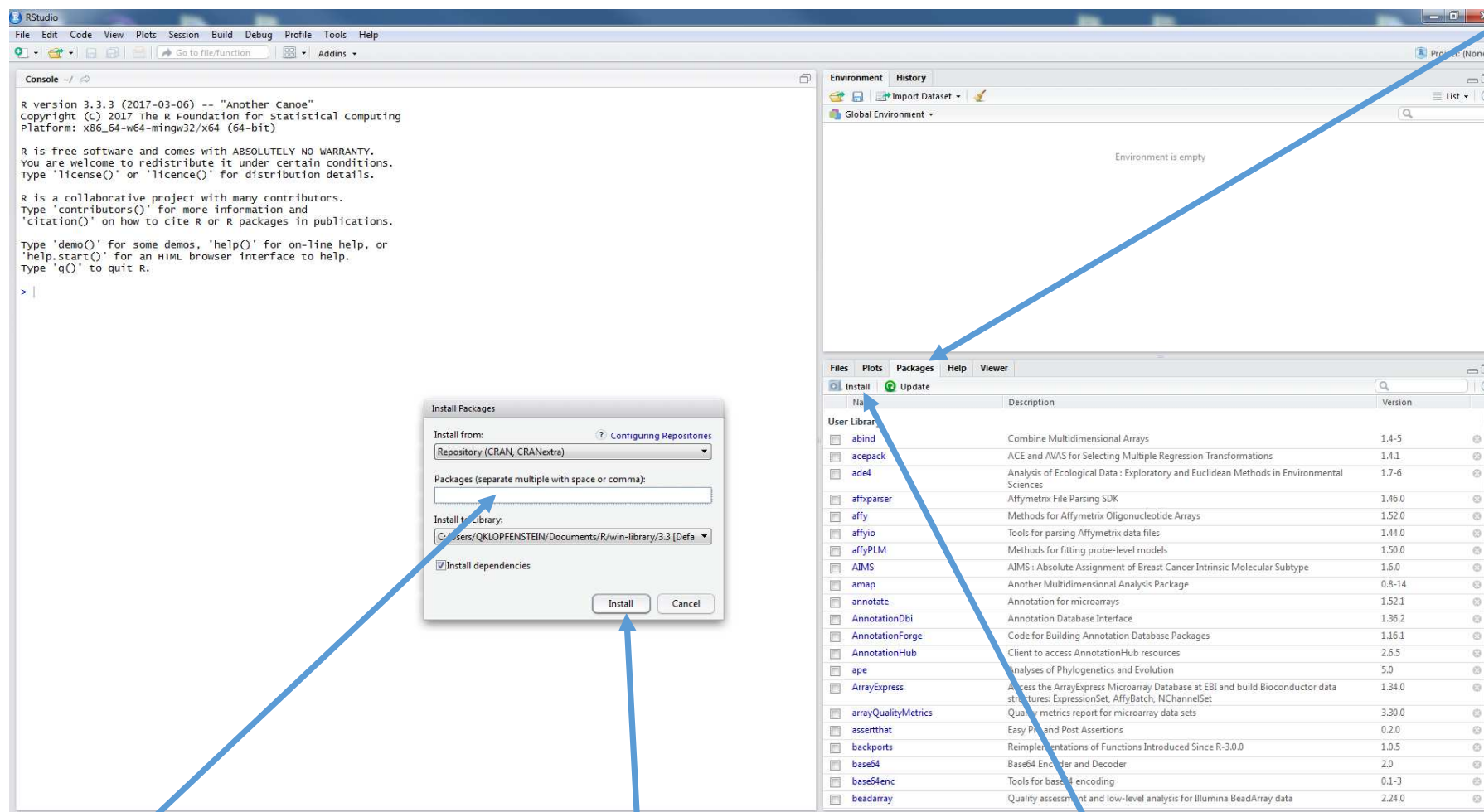
1. Install Rstudio from the following website depending on the OS you are using
2. Install the current version of R on your computer from CRAN website choosing the R version related to your OS again
3. Download from the `dgmunes_package` directory





Then start Rstudio and you should be able to do a window that looks like the one above

The **first time** you use our code you need to install all of these packages following the instructions below :



1. Click on Packages

3. Type name of package

4. Click on install

2. Click on install

### Install required package

sp  
rgeos  
GISTools  
survival

Viridis  
dplyr  
tidyr  
stringr

rgbif  
gridExtra  
rasterVis  
randomForest  
DynNom

Open **dgmunes.R** file with Rstudio and the script shown below should appear

Add path to the files created by QuPath  
(Important : for Windows users you need to add a double \ between each directory. Here is an example : C:\\Users\\name\\slide

```

1 # Code for obtaining dGMunes score
2
3 #Here put path to the files given by QuPath from the NDPI image file
4
5
6 pathToSlide="PUT HERE THE PATH TO THE FILES CREATED BY QUPATH"
7
8
9
10 # Here you have to give the information about the histopathology grading :
11 # "well"
12 # "moderately"
13 # "poorly"
14 # "undifferentiated"
15
16 #If you do not know you can leave the default value UNKNOWN
17 grade="UNKNOWN"
18
19
20
21
22 #First step is to read the files from the directory of the slide
23 source("daisyfield_function_v5.R")
24 setwd(pathToSlide)
25
26 if (grade=="well")
27 {
28   training=read.table("../data/meta_well.txt",header=FALSE,sep="\t")
29   var_selected=read.table("../data/var_selected_well.txt",sep="\t")
30 }else if (grade=="moderately"){
31   training=read.table("../data/meta_moderately.txt",header=FALSE,sep="\t")
32   var_selected=read.table("../data/var_selected_moderately.txt",sep="\t")
33 }else if (grade=="poorly"){
34   training=read.table("../data/meta_poorly.txt",header=FALSE,sep="\t")
35   var_selected=read.table("../data/var_selected_poorly.txt",sep="\t")
36 }else if (grade=="undifferentiated"){
37   training=read.table("../data/meta_undifferentiated.txt",header=FALSE,sep="\t")
38   var_selected=read.table("../data/var_selected_undifferentiated.txt",sep="\t")
39 }else{
40

```

Console output:

```

17:15 (Top Level) >
Copyright (C) 2017 The R Foundation for Statistical Computing
Platform: x86_64-w64-mingw32/x64 (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

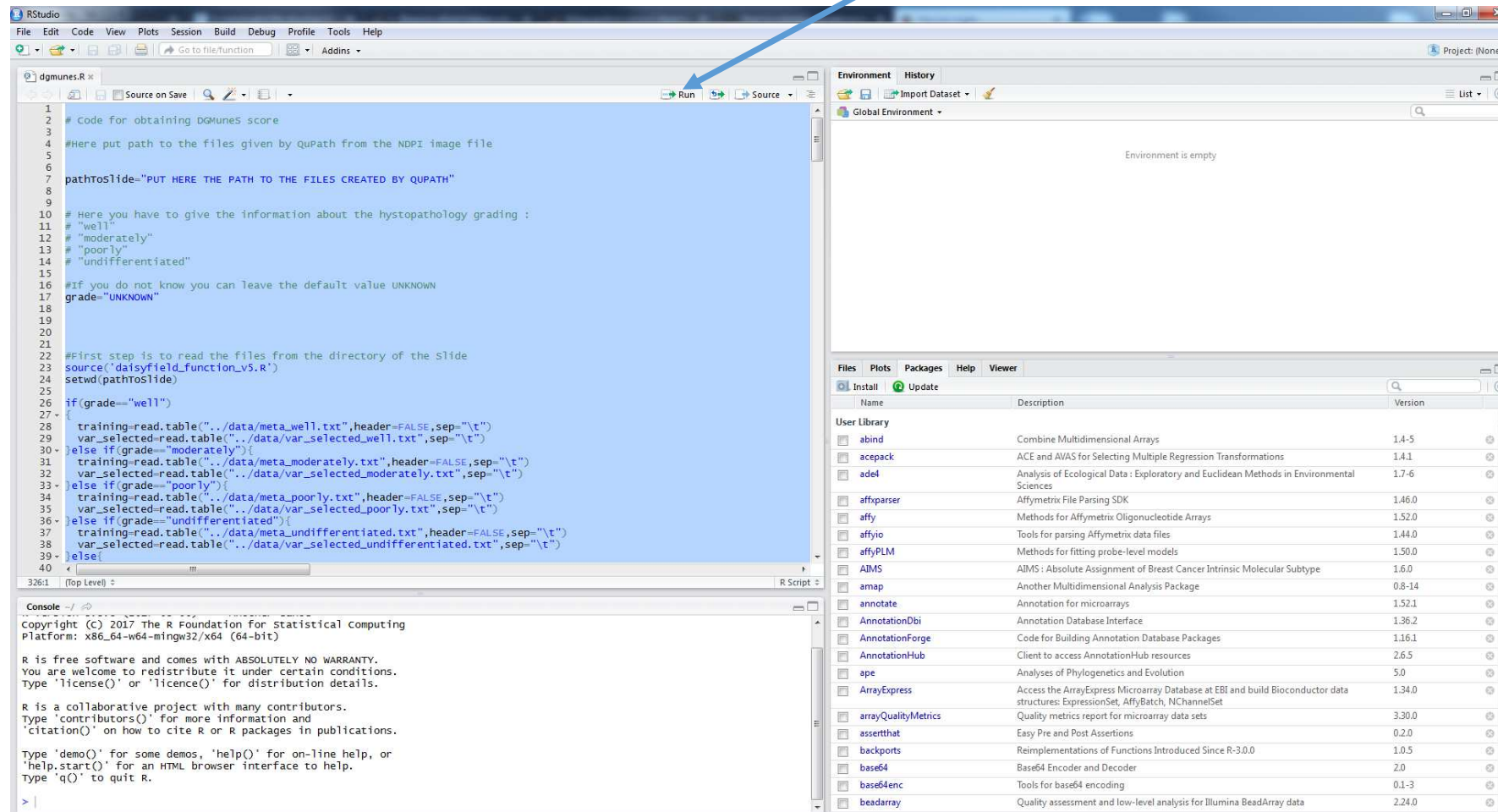
>

```

Add the histopathology grade if you know it otherwise leave the defaults value. **Be careful ! case** is important here and the possible values are : well, moderately, undifferentiated, poorly

1. Then click anywhere in the code and press :  
ctrl + a

2. Click on run



The screenshot displays the RStudio interface. The main editor window shows an R script named `dgmunes.R` with the following code:

```
1  
2 # Code for obtaining DGMunes score  
3  
4 #Here put path to the files given by qupath from the NDPi image file  
5  
6 pathToSlide="PUT HERE THE PATH TO THE FILES CREATED BY QUPATH"  
7  
8  
9  
10 # Here you have to give the information about the histopathology grading :  
11 # "well"  
12 # "moderately"  
13 # "poorly"  
14 # "undifferentiated"  
15  
16 #If you do not know you can leave the default value UNKNOWN  
17 grade="UNKNOWN"  
18  
19  
20  
21  
22 #First step is to read the files from the directory of the slide  
23 source('daisyfield_function_v5.R')  
24 setwd(pathToSlide)  
25  
26 if(grade=="well")  
27 {  
28   training=read.table("../data/meta_well.txt",header=FALSE,sep="\t")  
29   var_selected=read.table("../data/var_selected_well.txt",sep="\t")  
30 } else if(grade=="moderately"){  
31   training=read.table("../data/meta_moderately.txt",header=FALSE,sep="\t")  
32   var_selected=read.table("../data/var_selected_moderately.txt",sep="\t")  
33 } else if(grade=="poorly"){  
34   training=read.table("../data/meta_poorly.txt",header=FALSE,sep="\t")  
35   var_selected=read.table("../data/var_selected_poorly.txt",sep="\t")  
36 } else if(grade=="undifferentiated"){  
37   training=read.table("../data/meta_undifferentiated.txt",header=FALSE,sep="\t")  
38   var_selected=read.table("../data/var_selected_undifferentiated.txt",sep="\t")  
39 } else{  
40
```

The Environment pane on the right shows the Global Environment, which is currently empty. The Packages pane at the bottom right lists installed and available packages, including the User Library and various bioinformatics packages like `abind`, `acepack`, `ade4`, `affxparser`, `affy`, `affyio`, `affyPLM`, `AIMS`, `amap`, `annotate`, `AnnotationDbi`, `AnnotationForge`, `AnnotationHub`, `ape`, `ArrayExpress`, `arrayQualityMetrics`, `assertthat`, `backports`, `base64`, `base64enc`, and `beadarray`.

The Console pane at the bottom shows the R startup message:

```
326:1 | (Top Level) >  
Copyright (C) 2017 The R Foundation for Statistical Computing  
Platform: x86_64-w64-mingw32/x64 (64-bit)  
  
R is free software and comes with ABSOLUTELY NO WARRANTY.  
You are welcome to redistribute it under certain conditions.  
Type 'license()' or 'licence()' for distribution details.  
  
R is a collaborative project with many contributors.  
Type 'contributors()' for more information and  
'citation()' on how to cite R or R packages in publications.  
  
Type 'demo()' for some demos, 'help()' for on-line help, or  
'help.start()' for an HTML browser interface to help.  
Type 'q()' to quit R.  
|
```

If everything goes fine, you will have in the console the **DGMuneS Score** for your patient available after some computation time

A dynamic nomogram will show up and you will be able to **add clinical information** about the patient and **write the DGMuneS score** given by the script

