

CellQuant Installation Instructions

Sarah Hawbaker

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Mac

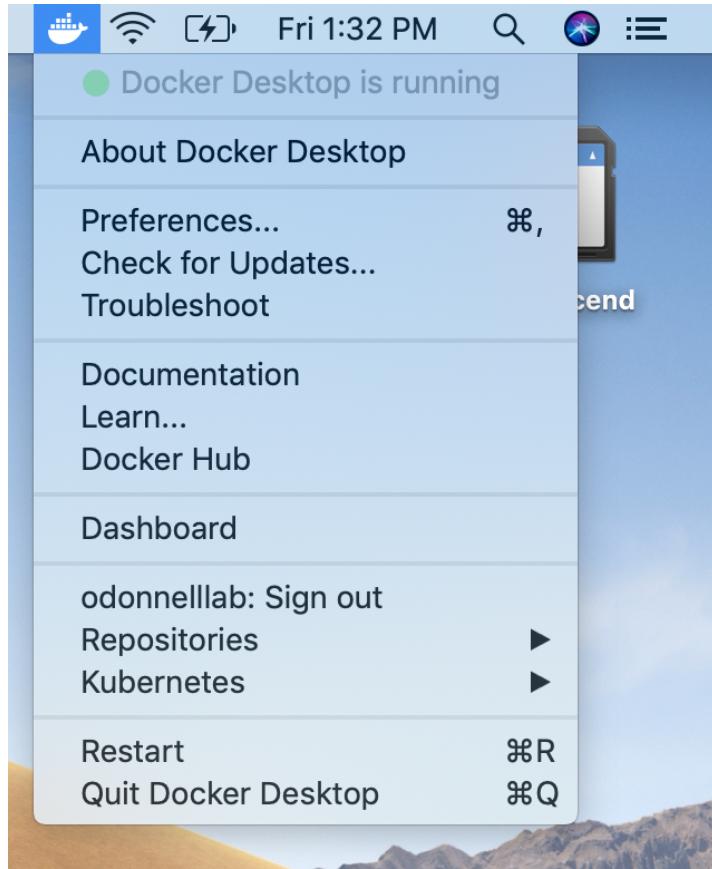
Docker

Install Docker

Docker is a platform used to “containerize” programs so that they run identically across platforms with no individual configuration required on the user computer. This means that you can run the program, which is written in R, without R installed on your computer. Docker Desktop is a program that makes Docker extremely easy to use. To run CellQuant on Mac you will need to download Docker Desktop. The download is free and available [here](#).

Run Docker

Once Docker Desktop is installed, it will be placed in the Applications folder. Open it. (Note: you do not need to set up an account with Docker but it may ask you do so.) When you open Docker a whale icon will appear in the upper-right hand corner of your screen. You should see a yellow dot with the message “Docker Desktop is starting” at the top of the drop-down menu. Wait until the dot changes to green with the message “Docker Desktop is running”. Whenever you want to run the program, Docker Desktop will need to be running.

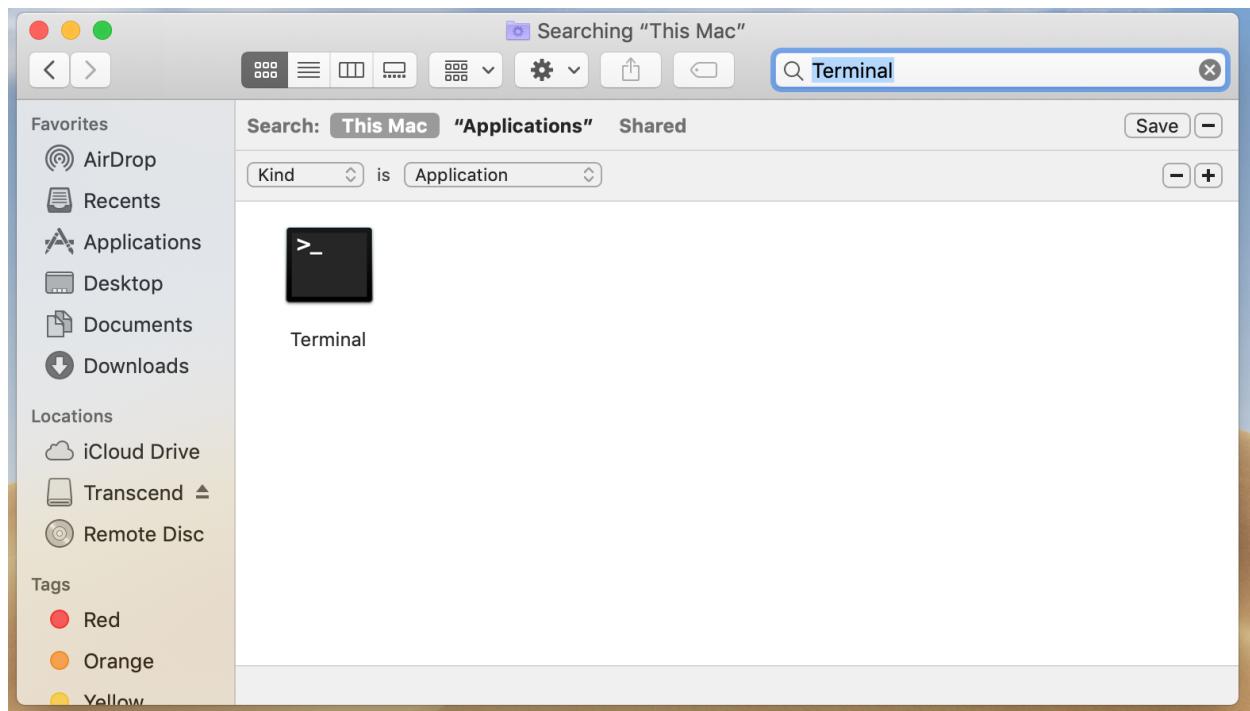


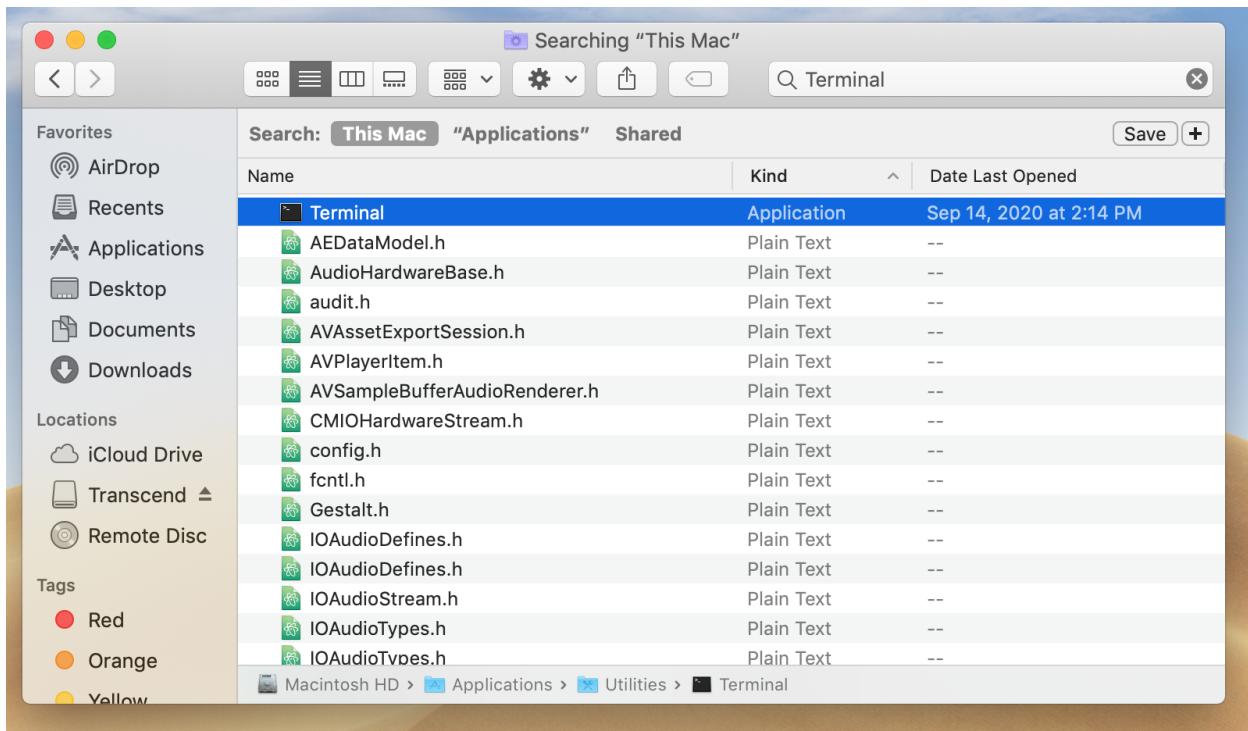
Installation

You will need to “pull” (install) the CellQuant source code from the odonnelllab account on DockerHub. **This only needs to be done once.** However, if a new version of the program is released you will need to pull the updated source code to download the latest version.

Terminal

Downloading and running the program is done by two simple commands executed in Terminal, which is a command-line interface present on all Macs by default. You can find Terminal in your Applications folder, though it may not be visible. If that is the case, search for “Terminal” in Finder with the filter **Kind » is » Application**, as any file containing code could theoretically be run by Terminal and might show up in the search results. Alternatively, you can sort the results by “Kind” to achieve the same result.





Pulling the Source Code

Open Terminal and copy-paste the command

```
docker pull odonnelllab/cellquant
```

into the Terminal window and press enter. Your computer will then pull the source code and configuration from DockerHub. This may take a few minutes.

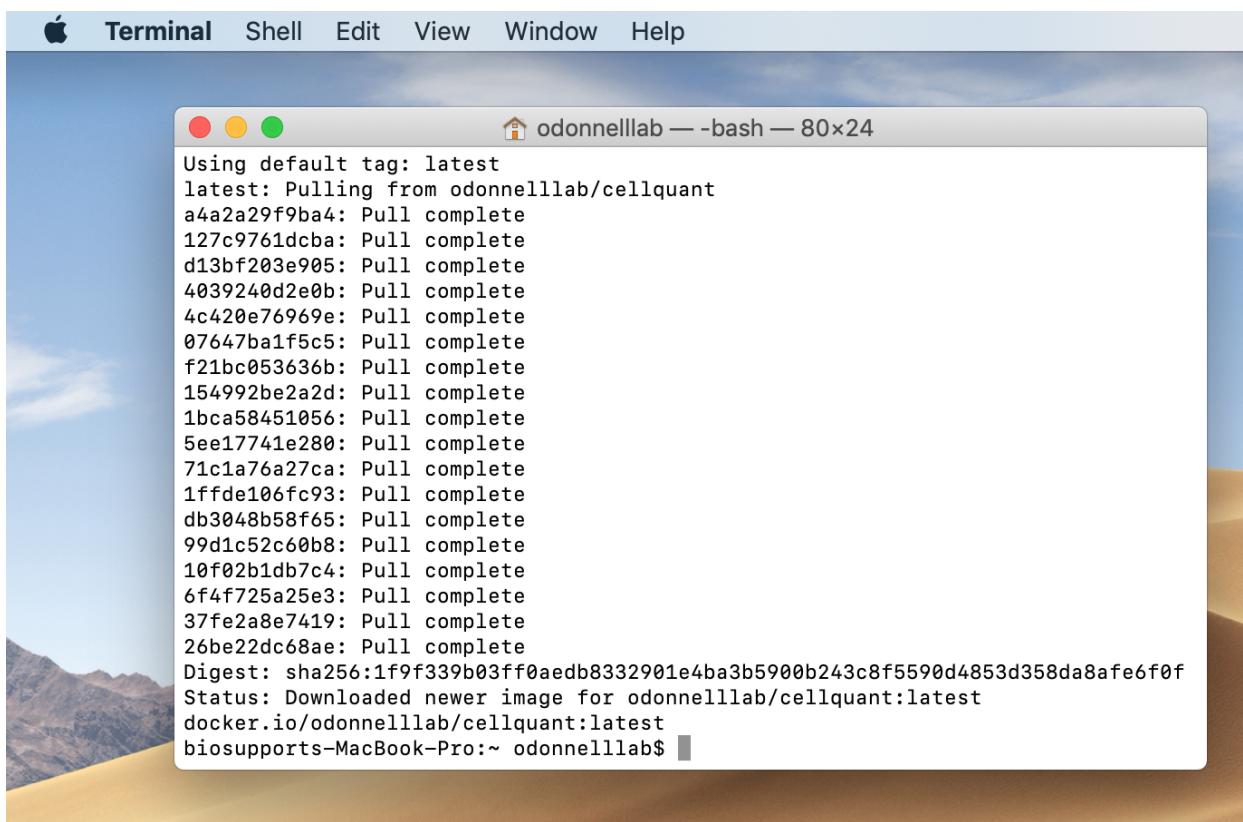


Terminal Shell Edit View Window Help



odonnelllab — bash — 80x24

```
Last login: Fri Sep 25 13:01:12 on ttys001  
biosupports-MacBook-Pro:~ odonnelllab$ docker pull odonnelllab/cellquant
```



A screenshot of a macOS Terminal window titled "odonnelllab — bash — 80x24". The window shows the output of a "docker pull" command for the "odonnelllab/cellquant" image. The output lists many image IDs followed by "Pull complete" messages, and concludes with the Digest and Status information.

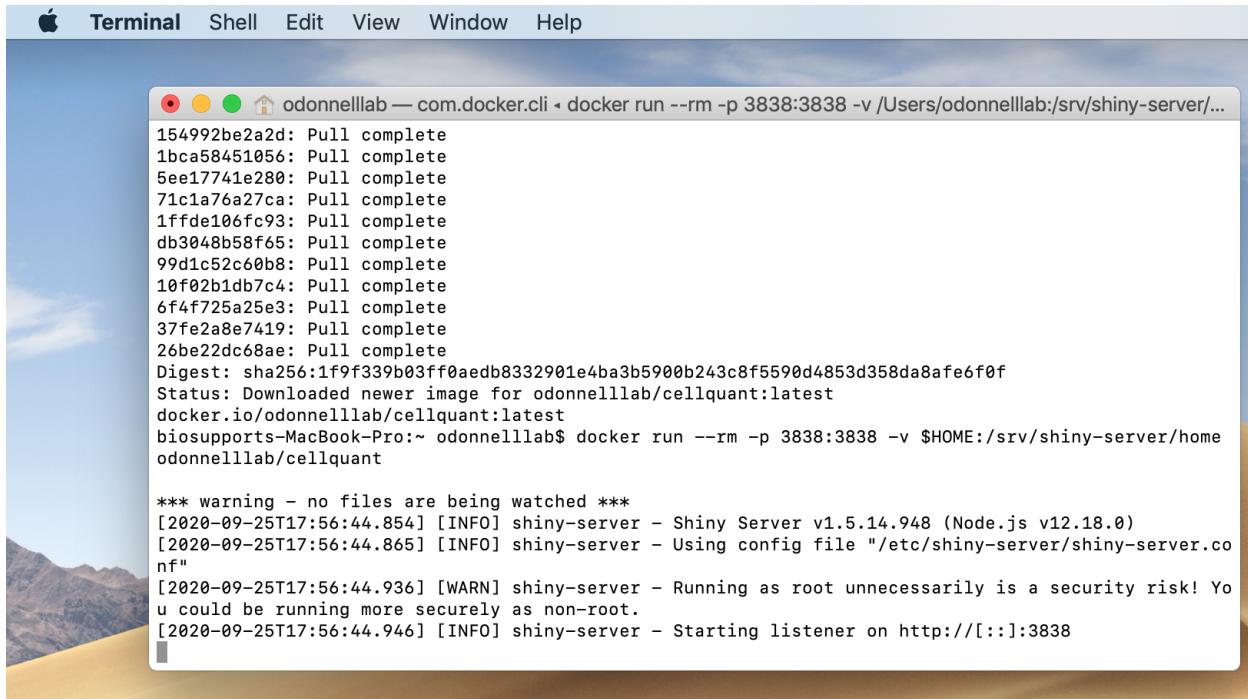
```
Using default tag: latest
latest: Pulling from odonnelllab/cellquant
a4a2a29f9ba4: Pull complete
127c9761dcba: Pull complete
d13bf203e905: Pull complete
4039240d2e0b: Pull complete
4c420e76969e: Pull complete
07647ba1f5c5: Pull complete
f21bc053636b: Pull complete
154992be2a2d: Pull complete
1bca58451056: Pull complete
5ee17741e280: Pull complete
71c1a76a27ca: Pull complete
1ffde106fc93: Pull complete
db3048b58f65: Pull complete
99d1c52c60b8: Pull complete
10f02b1db7c4: Pull complete
6f4f725a25e3: Pull complete
37fe2a8e7419: Pull complete
26be22dc68ae: Pull complete
Digest: sha256:1f9f339b03ff0aedb8332901e4ba3b5900b243c8f5590d4853d358da8afe6f0f
Status: Downloaded newer image for odonnelllab/cellquant:latest
docker.io/odonnelllab/cellquant:latest
biosupports-MacBook-Pro:~ odonnelllab$
```

Running

Once CellQuant is pulled from DockerHub, any time you want to run the program simply open Terminal and copy-paste this command:

```
docker run --rm -p 3838:3838 -v $HOME:/srv/shiny-server/home odonnelllab/cellquant
```

into the Terminal window and press Enter. This will create a local server on your computer and run the program on port 3838.

A screenshot of a Mac OS X Terminal window. The title bar says "Terminal". The window shows the command "odonnelllab — com.docker.cli < docker run --rm -p 3838:3838 -v /Users/odonnelllab:/srv/shiny-server/..." followed by the output of a Docker pull and run command. The output includes a list of image IDs being pulled, their completion status, the final image digest, the status message, and the command used to run the container. It also shows several warning messages from the Shiny Server application about running as root and starting the listener on port 3838.

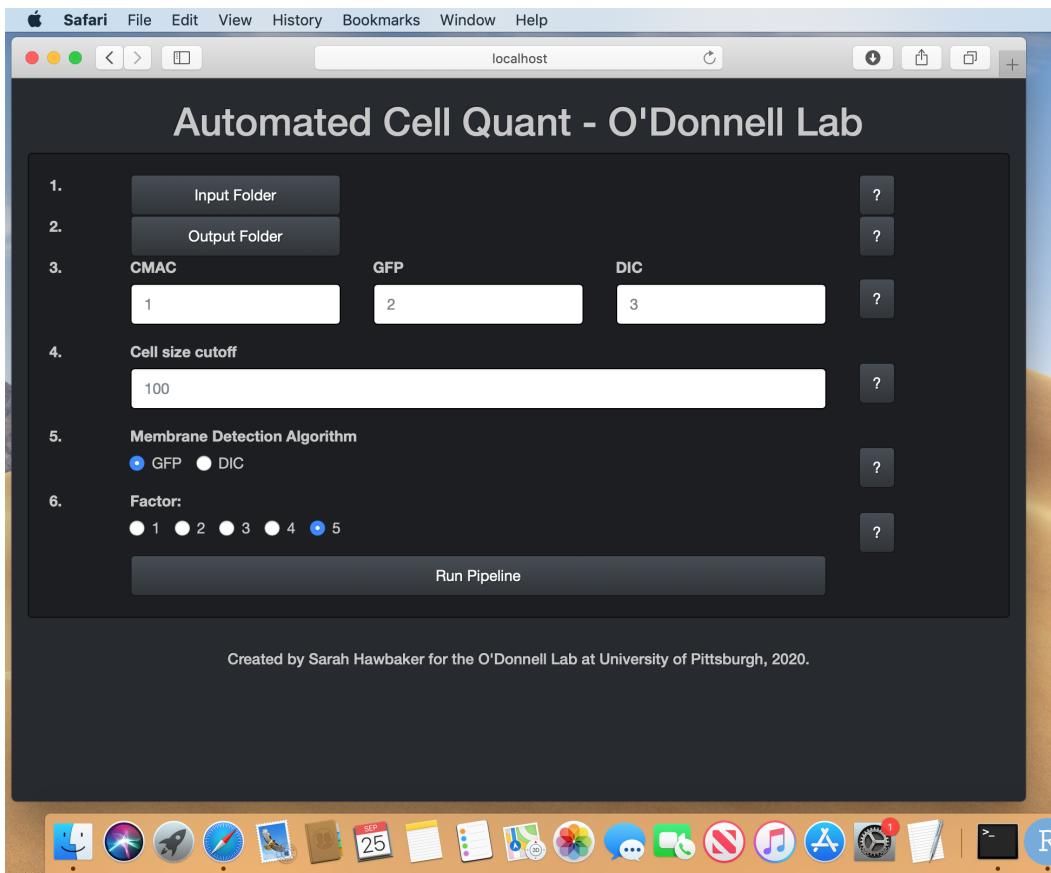
```
154992be2a2d: Pull complete
1bca58451056: Pull complete
5ee17741e280: Pull complete
71c1a76a27ca: Pull complete
1ffde106fc93: Pull complete
db3048b58f65: Pull complete
99d1c52c60b8: Pull complete
10f02b1db7c4: Pull complete
6f4f725a25e3: Pull complete
37fe2a8e7419: Pull complete
26be22dc68ae: Pull complete
Digest: sha256:1ff339b03ff0aedb8332901e4ba3b5900b243c8f5590d4853d358da8afe6f0f
Status: Downloaded newer image for odonnelllab/cellquant:latest
docker.io/odonnelllab/cellquant:latest
biosupports-MacBook-Pro:~ odonnelllab$ docker run --rm -p 3838:3838 -v $HOME:/srv/shiny-server/home
odonnelllab/cellquant

*** warning - no files are being watched ***
[2020-09-25T17:56:44.854] [INFO] shiny-server - Shiny Server v1.5.14.948 (Node.js v12.18.0)
[2020-09-25T17:56:44.865] [INFO] shiny-server - Using config file "/etc/shiny-server/shiny-server.conf"
[2020-09-25T17:56:44.936] [WARN] shiny-server - Running as root unnecessarily is a security risk! You could be running more securely as non-root.
[2020-09-25T17:56:44.946] [INFO] shiny-server - Starting listener on http://[::]:3838
```

Ignore the warnings shown above if they appear. Open your browser of choice and type

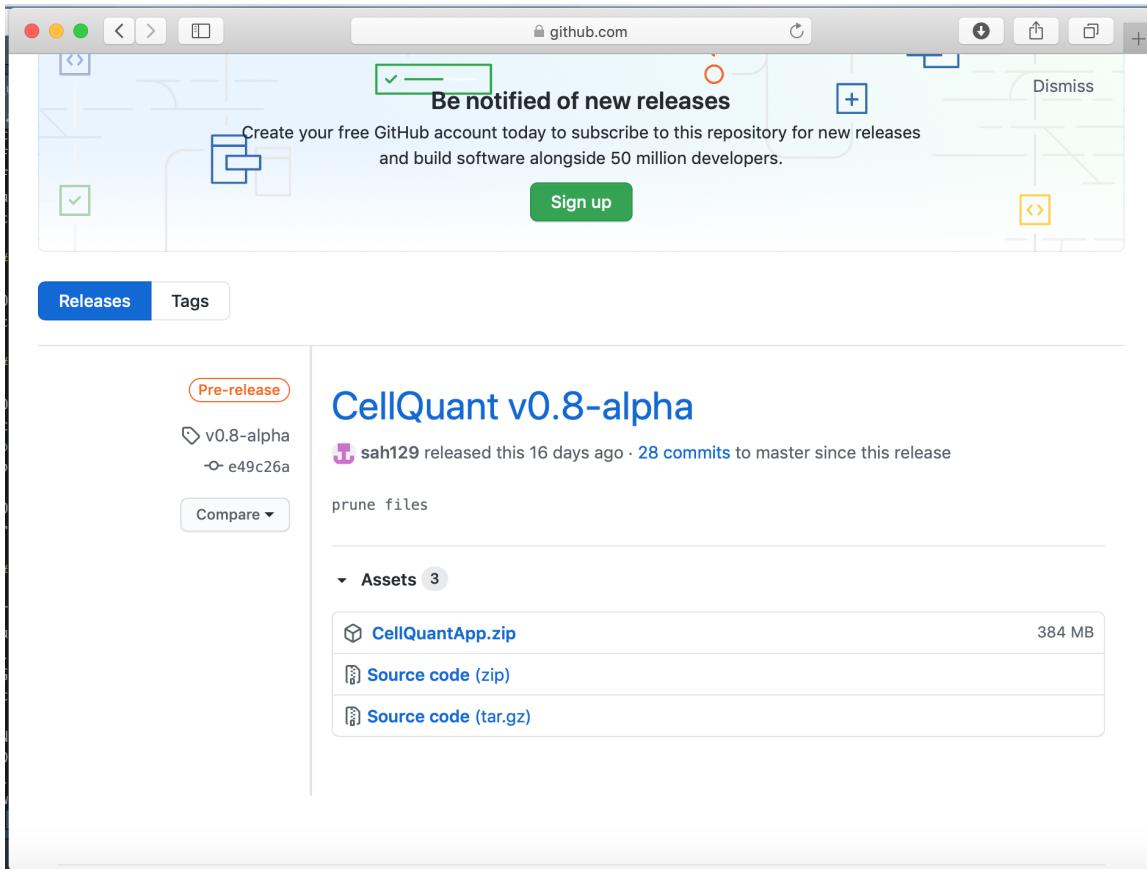
<localhost:3838>

in the address bar. The program will be running in your browser window.



Windows

The instructions above will work for Windows computers as well. However, Docker Desktop is not available for all versions of Windows. If Docker Desktop is not compatible with your version of Windows, there is a zip file of the program available on my GitHub [here](#). Go to the latest release available. The **CellQuantApp.zip** file will be in the “assets” drop-down menu.



Click the link to download.

Note: The zip file is large as it contains a local version of R. I strongly recommend using Docker Desktop over the zip file download as the configuration is standardized and independent of the individual computer. The zip file download may cause issues depending on the individual computer that will not be present when using Docker.

Additional Info

A video tutorial discussing the different settings of the pipeline is available here. Always check the [CellQuant GitHub page](#) for the latest information.