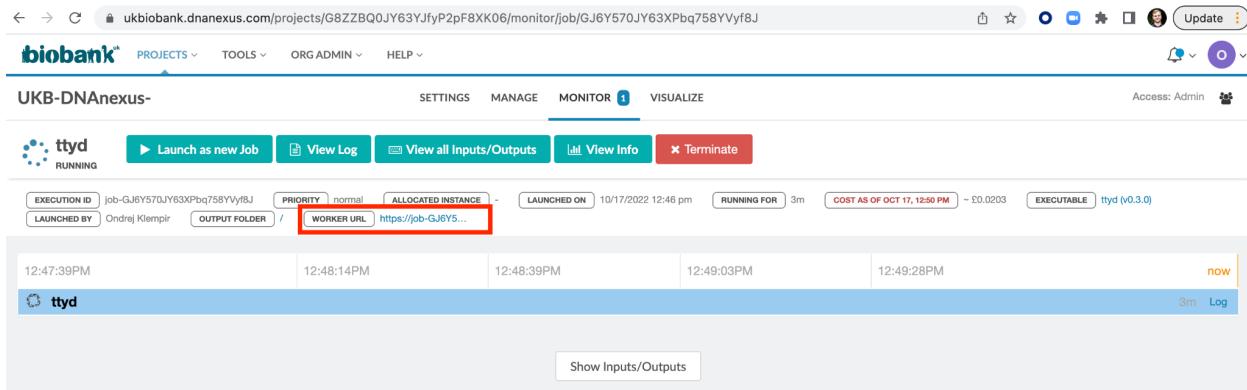


# Matlab on UKB RAP

For all experiments presented in this document, we will be using the tttyd app on UKB RAP. For better performance of the graphical interface, data visualization and deep learning algorithms, we recommend selecting a gpu based instance type, e.g. mem2\_ssd1\_gpu\_x16. You can activate a tttyd instance either via the graphical user interface from the Tools library or via CLI (see screenshot below).



*Screenshot of a running tttyd job, accessible from the Monitor tab. Cloud based CLI could be opened by clicking on the WORKER URL link.*

Tttd is a simple command-line tool for sharing a terminal over the Web. It can be used as a workstation inside of the DNAexus cloud platform that is accessible from your local Web browser via <https://job-xxxx.dnanexus.cloud> URL, where job-xxxx is the ID of the job that is running the app. A typical use case for this app is launching additional browser-accessible applications on ports 8080 and 8081 of a DNAexus worker. For more information about tttyd, see <https://ukbiobank.dnanexus.com/app/app-tttd>.

## How to run dockerized version of Matlab 2022b (Dec. 2022)

For the convenience of Matlab users and for easier deployment to cloud, Matlab developed a repository with dockerized Matlab versions. Since we are going to work with imaging data and deep learning on RAP, we would like to work with the latest one to get the best version in terms of preinstalled functionalities. In this doc, we aim to provide a set of guidelines to follow. For additional information not documented here (licensing etc.), please go visit: <https://hub.docker.com/r/mathworks/matlab-deep-learning>

Let's start with something super straightforward and simple. On the dnax tttyd worker, pull the desired docker image (16GB base image, so it can take a couple of minutes).

---

*docker pull mathworks/matlab-deep-learning:r2022b*

```

← → C job-gj6y570jy63xpbq758yyf8j.dnanexus.cloud
root@job-GJ6Y570JY63XPbq758YYf8J:~# docker pull mathworks/matlab-deep-learning:r2022b
r2022b: Pulling from mathworks/matlab-deep-learning
7blaab2e44d: Pull complete
799ceeb5a576: Pull complete
a4233c5ca44: Pull complete
15622dd0b036: Pull complete
04cd001d16e5: Pull complete
49b64a08783: Pull complete
5a721692e03: Pull complete
0d0183a1d2e9: Pull complete
a5fb38d8be30: Pull complete
a35a01352a78: Pull complete
cfef5f612cf1: Downloading [=====] 2.706GB/6.422GB
9a2ec418c2b7: Download complete
9c016bccd1e: Download complete
2d601242741b: Download complete

```

Once pulling is done, you can check which images are available:

REPOSITORY	TAG	IMAGE ID	CREATED	SIZE
mathworks/matlab-deep-learning	r2022b	0661d1152878	2 weeks ago	16.1GB

🎉 We are now ready to run Matlab on UKB RAP! 🎉

The command is:

`docker run --gpus all -it -p 8080:8888 --shm-size=40gb mathworks/matlab-deep-learning:r2022b -browser`

```

root@job-GJ6Y570JY63XPbq758YYf8J:~# docker run --gpus all -it -p 8080:8888 --shm-size=40gb mathworks/matlab-deep-learning:r2022b -browser
Welcome to the MATLAB Deep Learning Container

This container includes commercial software products of The MathWorks,
Inc. ("MathWorks Programs") and related materials. MathWorks Programs are
licensed under the MathWorks Software License Agreement, available in the
MATLAB installation in this container. Related materials in this
container are licensed under separate licenses which can be found in
their respective folders.

Use the -help flag to learn more about the usage of this container:
  docker run mathworks/matlab-deep-learning:r2022b -help

```

“**--gpus all**” specifies that we want to use all GPU hardware available on the worker

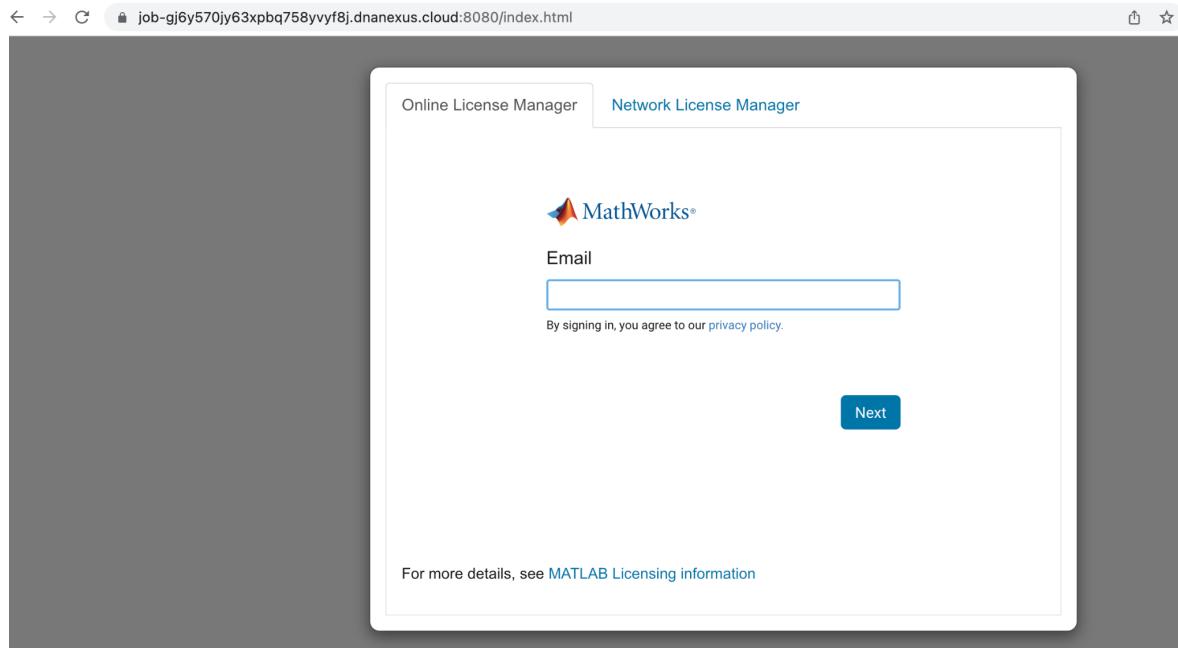
“**-p 8080:8888**” performs the magic for running Matlab in the web browser

“**--shm-size=40gb**” how much memory we want to use

Then, copy the ttyd URL into a new browser window, and add :8080 at the end

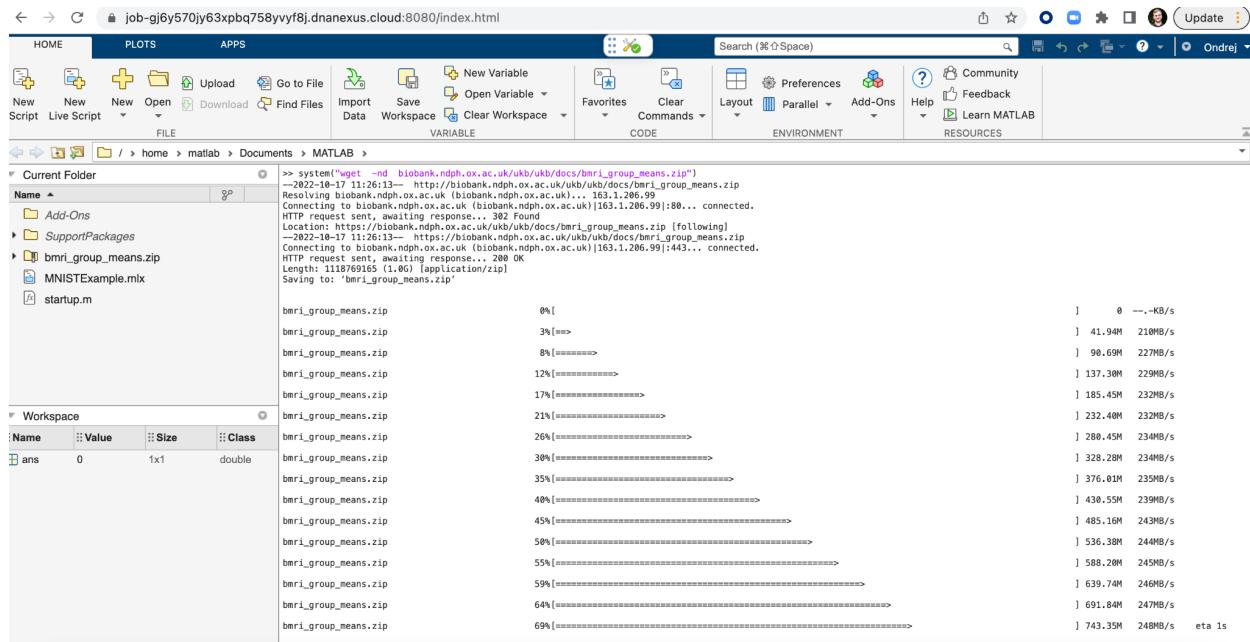
<https://job-XXXX.dnanexus.cloud:8080>

This should open a Matlab session on RAP. You will now need to login into Matlab using your academic or personal license.



Once this is loaded, that's it! Now, we can use UKB data in Matlab -e.g. we can use `system` command to download an example UKB image file format from UKB Showcase:

```
system("wget -nd biobank.ndph.ox.ac.uk/ukb/ukb/docs/bmri_group_means.zip")
```



*Tip / Note: Matlab is a great tool for working with directory structure and file unzipping (great features for UKB RAP data). Try that!*

Command `gpuDevice` can help you to identify and select which GPU device you want to use.

UKB data can also be accessed as a mounted “/mnt/project” directory. This will then appear in the Matlab workspace. See the example command below (-v does the job):

```
docker run -v "/mnt/project/Bulk/Brain MRI/":/home/dnax/ -it -p 8080:8888 --shm-size=40gb  
mathworks/matlab-deep-learning:r2022b -browser
```

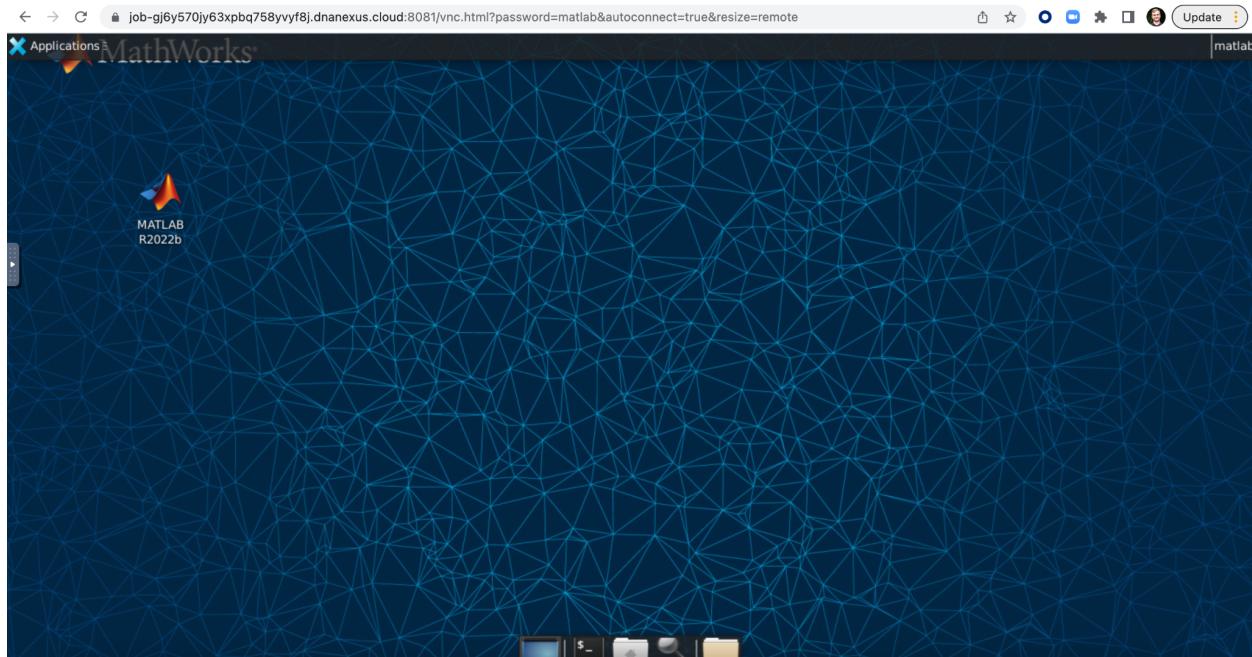
As an alternative to this “browser” view, we can utilize another port and open a second Matlab session via VNC. VNC stands for Virtual Network Computing (VNC) and it is a graphical desktop-sharing system (remote desktop). In my experience, this might have better performance for some 3D visualizations and actually provides us with a “desktop” machine with a GUI, so it might also be great for other applications, e.g. combining with GUI FSL or SPM. This is also an easy way to install additional tools and toolboxes, see the next chapter for more details.

First run:

```
docker run --gpus all -it -p 8081:6080 --shm-size=40gb mathworks/matlab-deep-learning:r2022b -vnc
```

Then open:

<https://XXXX.dnanexus.cloud:8081/>



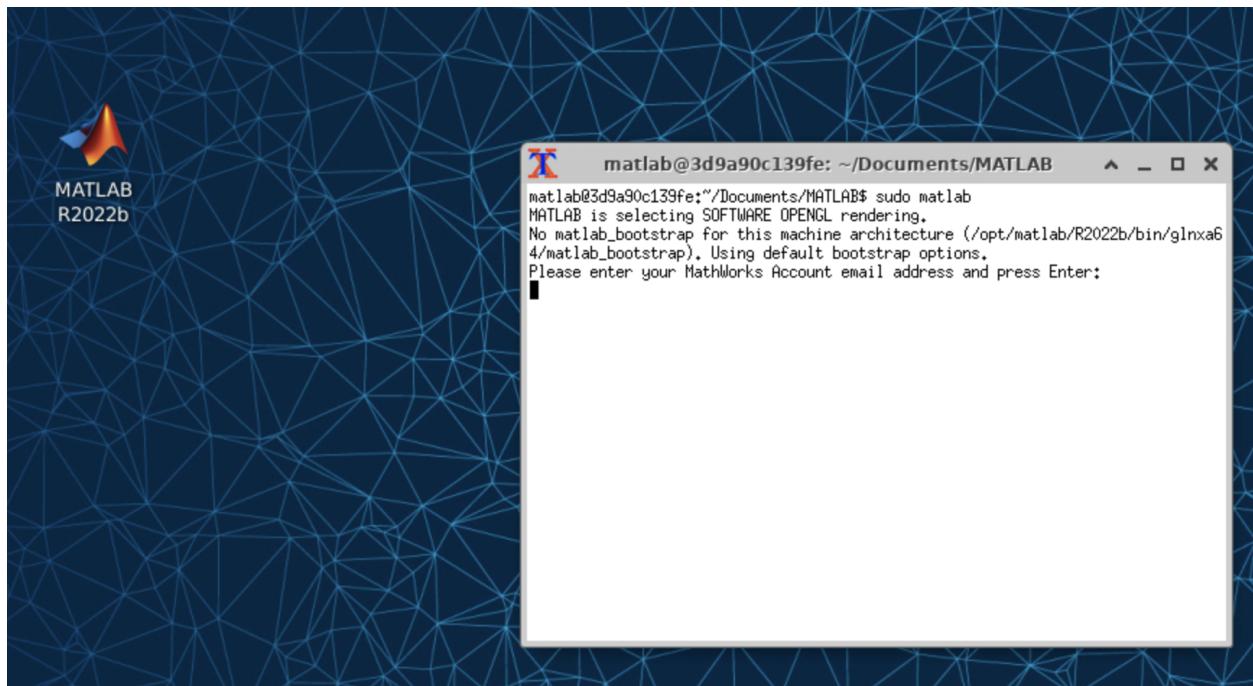
*Screenshot of a VNC session, providing a remote desktop.*

## Install additional toolbox(es)

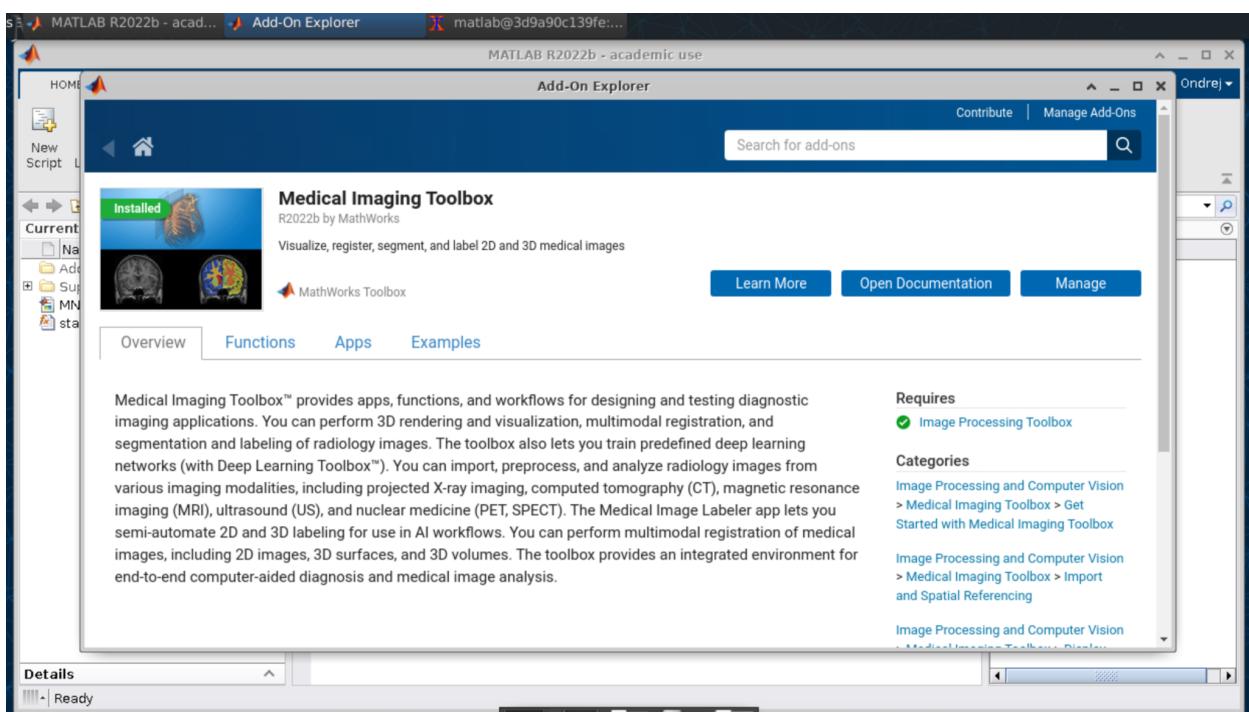
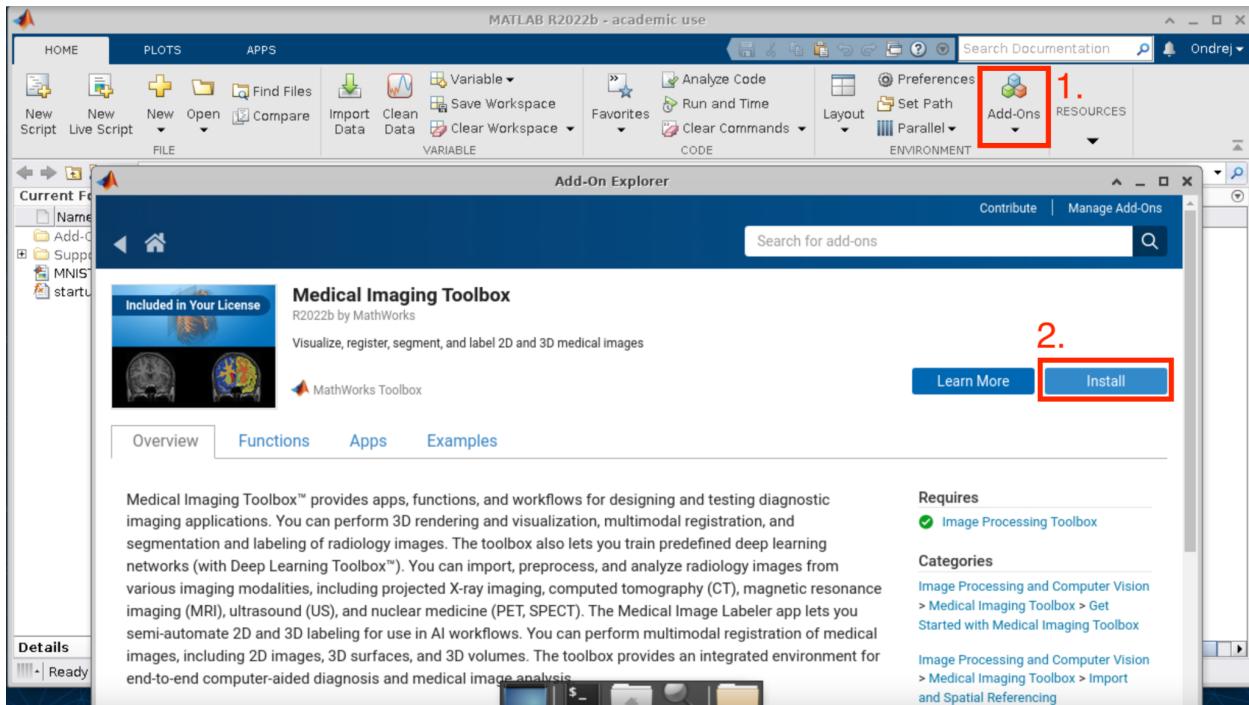
For our UKB RAP experiments, our main interest is to install the newly added product called [Medical Imaging Toolbox](#). We investigated several options on how to add it to the already existing dockerized Matlab 2022b and avoid customizing Dockerfile, rebuilding etc. The following way appears to be easy and effective on RAP.

When running Matlab using VNC (this is an important step because VNC mode can run commands as a superuser - the “browser” option does not have this capability), just open the Terminal and run Matlab with *sudo*:

```
sudo matlab
```



After you login, you will be given a Matlab session with full access to the Add-Ons button.



You can now directly work with the Medical Imaging Toolbox.

For reusing the base Matlab plus Medical Imaging Toolbox in your future sessions we would recommend saving a modified dockerized image to a dnx project. Since we are not running

docker with “–rm option” you can now open a new ttyd window or exit the VNC container and do the following (replace the hardcoded values from the demo with your values and ids):

1. Check already running containers using `docker ps -a`

CONTAINER ID	IMAGE	COMMAND	CREATED	STATUS	PORTS	NAMES
3d9a90c139fe	mathworks/matlab-deep-learning:r2022b	"/bin/run.sh -vnc"	21 minutes ago	Up 21 minutes	5901/tcp, 8888/tcp, 0.0.0.0:8081->6080/tcp	romantic
cd231fa93583	mathworks/matlab-deep-learning:r2022b	"/bin/run.sh -browser"	47 minutes ago	Exited (130) 33 minutes ago		dazzling

2. Take container ID of the vnc session and use docker commit to create a new container

```
docker commit 3d9a90c139fe mathworks/matlab-deep-learning:r2022b-medical
```

3. Check whether the new matlab with medical imaging exists using `docker images`
4. `docker save mathworks/matlab-deep-learning:r2022b-medical | gzip > matlab_medical_image.tar.gz`
5. `matlab_medical_image.tar.gz`

For more information about how to commit a new docker image, please see our previous webinar [Using Docker for Reproducible Research on the Research Analysis Platform](#).