

Running cas\_pipeline on personal computer or server

1) load the container in your computer

```
docker load < CAS_PIPELINE
```

2.) start the docker container

```
docker start <image id>
```

3.) Create a directory containing one directory for metagenomes and another with hmm profiles

Mount this directory to work directory in docker

Additionally also mount the /home/cas\_pipeline/all\_final\_output folder to another folder in server. This is where all our output will be stored.

#this line is just for mounting volumes to an already existing container

```
docker run -it -v all_inputs_path:/home/all_inputs -v
```

```
all_outputs_path:/home/cas_pipeline/all_final_output /bin/bash
```

Now execute this docker.

```
#####
```

```
docker exec -it <image ID> /bin/bash #
```

```
#####
```

! delete all cas profiles from /home/cas\_pipeline/standard\_hmm\_profiles or just copy them to a separate folder within the container

4) create soft links from work\_directory/ metagenomes to /home/cas\_pipeline/all\_initial\_input

And soft links from work\_directory/ hmm profiles to /home/cas\_pipeline/all\_standard\_hmms

```
ln -s /home/all_inputs/metagenomes/* /home/cas_pipeline/all_initial_input
```

```
ls -s /home/all_inputs/hmms/* /home/cas_pipeline/standard_hmm_profiles
```

5.) Execute metagen\_pipeline.sh

```
bash metagen_pipeline.sh
```