## SETUP of Galaxy

For genome assembly we start with using Galaxy through a docker instance

<https://github.com/bgruening/docker-galaxy-stable>

**Building the docker file**

docker build -t ibiosystems/galaxy .

**Pusing to remote:**

docker login

docker push ibiosystems/galaxy

**Using a local folder to store your sessions in**

docker run -d -p 8080:80 -p 8022:21 -p 8800:8800 --privileged=true -e "GALAXY\_CONFIG\_ADMIN\_USERS=jasper.koehorst@wur.nl" -e "GALAXY\_CONFIG\_BRAND='iBioSystems'" -v ~/iBioSystems/galaxy\_ibiosystems:/export/ ibiosystems/galaxy

**Configurations**

**Admin:** -e "GALAXY\_CONFIG\_ADMIN\_USERS=jasper.koehorst@wur.nl" \

**Brand:** -e "GALAXY\_CONFIG\_BRAND='iBioSystems'"

**Docker inside docker:** --privileged=true

## Personalize your Galaxy

The Galaxy welcome screen can be changed by providing a welcome.html page in /home/user/galaxy\_storage/. All files starting with welcome will be copied during startup and served as introduction page. If you want to include images or other media, name them welcome\_\* and link them relative to your welcome.html (example).

## Modules to install using the toolshed approach..

By modifying the my\_tool\_list.yml specific modules that could be useful are implemented.

**SPADes FASTQC RNAmmer tRNA Prodigal CRT**

If

Prodigal generates a proper protein fasta file this perhaps can be loaded into KEGG?

## SETUP of docker management web interface

The following command will run the user interface for docker on port 9000 of a server (e.g. ssb2.wurnet.nl:9000)

**docker run -d -p 9000:9000 --privileged -v /var/run/docker.sock:/var/run/docker.sock uifd/ui-for-docker**