

Supplementary Data S3:

FAIR Genomes MOLGENIS Docker

Command-line tool prerequisites

- Git client (see: <https://git-scm.com/downloads>)
- Docker client (see: <https://docs.docker.com/get-docker>)

Test if everything is installed correctly

`git --version` should return something like `git version 2.8.1`

`docker --version` should return something like `Docker version 20.10.5`

Clone MOLGENIS Docker and FAIR Genomes

```
git clone https://github.com/fairgenomes/fairgenomes-semantic-model.git
```

Bring MOLGENIS Docker online and load the fair genomes data

- Start MOLGENIS services in docker

```
cd fairgenomes-semantic-model/misc/molgenis/docker
docker-compose up -d
```

- Many files will be imported, to check the logs type:

```
docker-compose logs --follow commander
```

This process should look like

```
✓ Importing sys_md_Package.tsv
✓ Importing study_inclusioncriteria_attributes.tsv
✓ Importing personal_phenotypicsex_attributes.tsv
⋆ Importing personal_genotypicsex_attributes.tsv
```

All done!

- Start using FAIR Genomes by going to <http://localhost/>
- Anonymous users (i.e. not logged in) should already have edit/view rights
- To do and see absolutely everything, log in as admin, pw admin

Troubleshooting

To recreate everything, run `nuke.sh`

***Alternative:* How to manually install FAIR Genomes on a MOLGENIS Docker image**

Command-line tool prerequisites

- Git client (see: <https://git-scm.com/downloads>)
- Docker client (see: <https://docs.docker.com/get-docker>)
- Python3 (see: <https://www.python.org/downloads>)
- pip3 (use e.g. `sudo apt-get -y install python3-pip`)
- MOLGENIS Commander (use e.g. `pip3 install molgenis-commander`)

Test if everything is installed correctly

```
git --version should return something like git version 2.8.1
docker --version should return something like Docker version 20.10.5
python3 --version should return something like Python 3.7.2
pip3 --version should return something like pip 19.3.1
mcmd --version should return something like MOLGENIS Commander 1.10.3
```

Clone MOLGENIS Docker and FAIR Genomes

```
git clone https://github.com/molgenis/docker.git
git clone https://github.com/fairgenomes/fairgenomes-semantic-model.git
```

Bring MOLGENIS Docker online

- Start your Docker client
- Then compose the MOLGENIS Docker image

```
cd docker/molgenis/8.7
docker-compose up
```

Connect MOLGENIS Commander to MOLGENIS Docker

- Either follow step-by-step setup instructions by running `mcmd`, or
- Edit `~/mcmd/mcmd.yaml` file to include

```
selected: http://localhost/  
auth:  
- url: http://localhost/  
  username: admin  
  password: admin
```

- If all is well, ping the server using `mcmd ping` which should return something like

```
Host: http://localhost/  
Status: Online  
Version: 8.7.2  
User: admin
```

Setup FAIR Genomes in the MOLGENIS Docker

- Go back to the directory where `git clone` was executed
- Step into the FAIR Genomes `molgenis-emx` folder and run the setup script

```
cd fairgenomes-semantic-model/generated/molgenis-emx/  
sh setup.sh
```

- Many files will be imported. This process should look like

```
✓ Importing sys_md_Package.tsv  
✓ Importing study_inclusioncriteria_attributes.tsv  
✓ Importing personal_phenotypicsex_attributes.tsv  
⋆ Importing personal_genotypicsex_attributes.tsv
```

All done!

- Start using FAIR Genomes by going to <http://localhost/>
- Anonymous users (i.e. not logged in) should already have edit/view rights
- To do and see absolutely everything, log in as `admin`, pw `admin`

Troubleshooting

- If you want to override existing imports, open the `~/.mcmd/mcmd.yaml` file and change `import_action: add` into `import_action: add_update_existing`