

Portable Proteomics Pipeline (P3)

Use Case: FTP

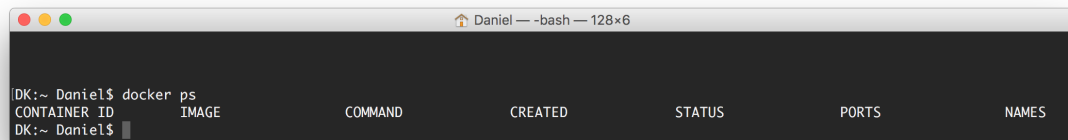
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This is a use case/manual for a P3 pipeline with files retrieved from Pride database.

1. Make sure Docker engine is installed and running.

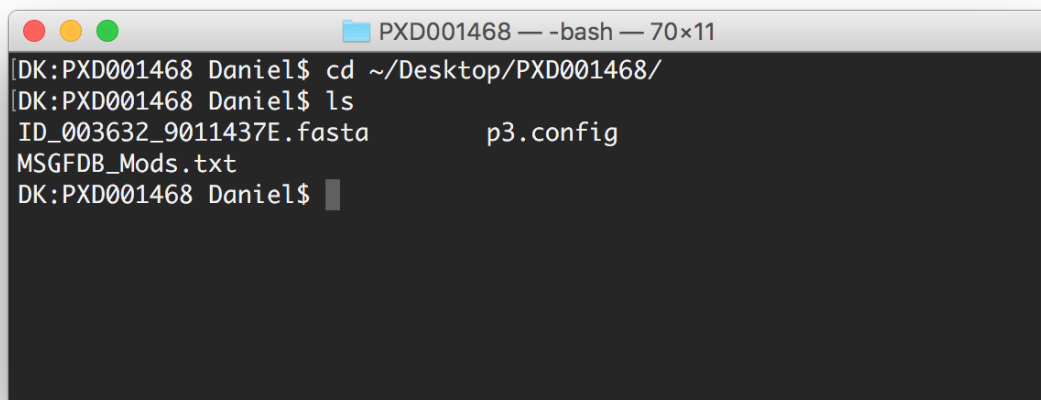
```
docker ps
```



```
DK:~ Daniel$ docker ps
CONTAINER ID    IMAGE    COMMAND    CREATED    STATUS    PORTS    NAMES
DK:~ Daniel$
```

2. Download a sample p3.config and MSGFDB_Mods.txt file and put it to a directory. e.g. ~/Desktop/PXD001468

```
cd ~/Desktop/PXD001468
```



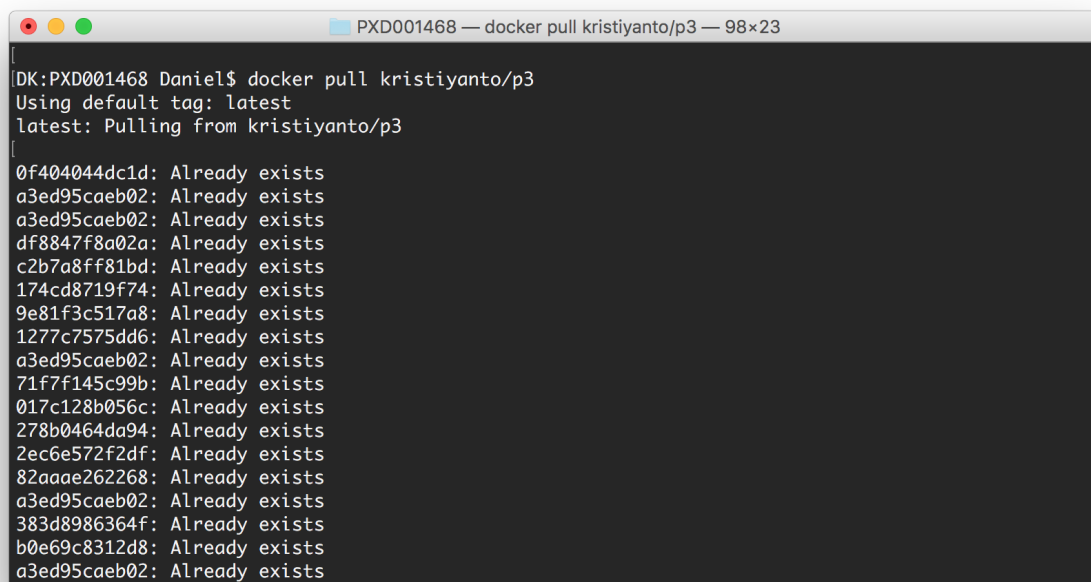
```
DK:PX001468 Daniel$ cd ~/Desktop/PXD001468/
DK:PX001468 Daniel$ ls
ID_003632_9011437E.fasta    p3.config
MSGFDB_Mods.txt
DK:PX001468 Daniel$
```

in this case, p3.config must have the following fields:

```
REPO = FTP
FTP_1 = (e.g: ftp://ftp.pride.ebi.ac.uk/pride/data/archive/2015/06/PXD001468)
RUN_MSGF = (e.g: YES)
METHOD = (e.g: SPECTRUM_COUNT)
```

If other PrideID is desired, change the PRIDEID option in the p3.config. Ensure that the corresponding PrideID have the required files (*.fasta, *.mzml, etc.).

3. Download / update P3 from Dockerhub, and run the image.



```
PXD001468 — docker pull kristiyanto/p3 — 98x23
DK:PXD001468 Daniel$ docker pull kristiyanto/p3
Using default tag: latest
latest: Pulling from kristiyanto/p3
0f404044dc1d: Already exists
a3ed95caeb02: Already exists
a3ed95caeb02: Already exists
df8847f8a02a: Already exists
c2b7a8ff81bd: Already exists
174cd8719f74: Already exists
9e81f3c517a8: Already exists
1277c7575dd6: Already exists
a3ed95caeb02: Already exists
71f7f145c99b: Already exists
017c128b056c: Already exists
278b0464da94: Already exists
2ec6e572f2df: Already exists
82aaae262268: Already exists
a3ed95caeb02: Already exists
383d8986364f: Already exists
b0e69c8312d8: Already exists
a3ed95caeb02: Already exists
```

```
eval $(docker-machine env default)
docker pull kristiyanto/p3
docker run --rm -v ~/Desktop/PXD001468:/root/data kristiyanto/p3
```

On Windows:

```
docker run --rm -v /c/Users/daniel/Desktop/PXD001468:/root/data kristiyanto/p3
```



```
PXD001468 — docker run --rm -v ~/Desktop/PXD001468:/root/data kristiyanto/p3 — 117x14
DK:PXD001468 Daniel$ docker run --rm -v ~/Desktop/PXD001468:/root/data kristiyanto/p3
Starting at: 2016-06-24 21:24:10.982541
Reading from ftp://ftp.pride.ebi.ac.uk/pride/data/archive/2015/06/PXD001468 and ftp://ftp.pride.ebi.ac.uk/pride/data/
archive/2015/06/PXD001468.
Downloading from ftp://ftp.pride.ebi.ac.uk/pride/data/archive/2015/06/PXD001468
Downloading...
Downloading...
b1906_293T_proteinID_01A_QE3_122212.mzXML
```

if necessary, another image can be run simultaneously (in a different terminal windows).

```
docker run --rm -v ~/Desktop/PXD001468:/root/data kristiyanto/p3
```

4. Once processes completed, the directory will be populated with:

- Mass Spectrometry files downloaded from Pride repository (*.mzid, *.mzml)
- MSGF+ output files (*.mzid, *.canon, *.revCat.cnlcp, *.revCat.csarr, *.revCat.cseq)
- Output table (*.txt)
- Output file as R objects (*.rda)

If the process stop returning error: * Make sure all the required files are in the folder. E.g: In the case fasta file is not provided in the FTP/Pride repository and must be provided manually. * Remove all *.tmp files before re-run the containers.