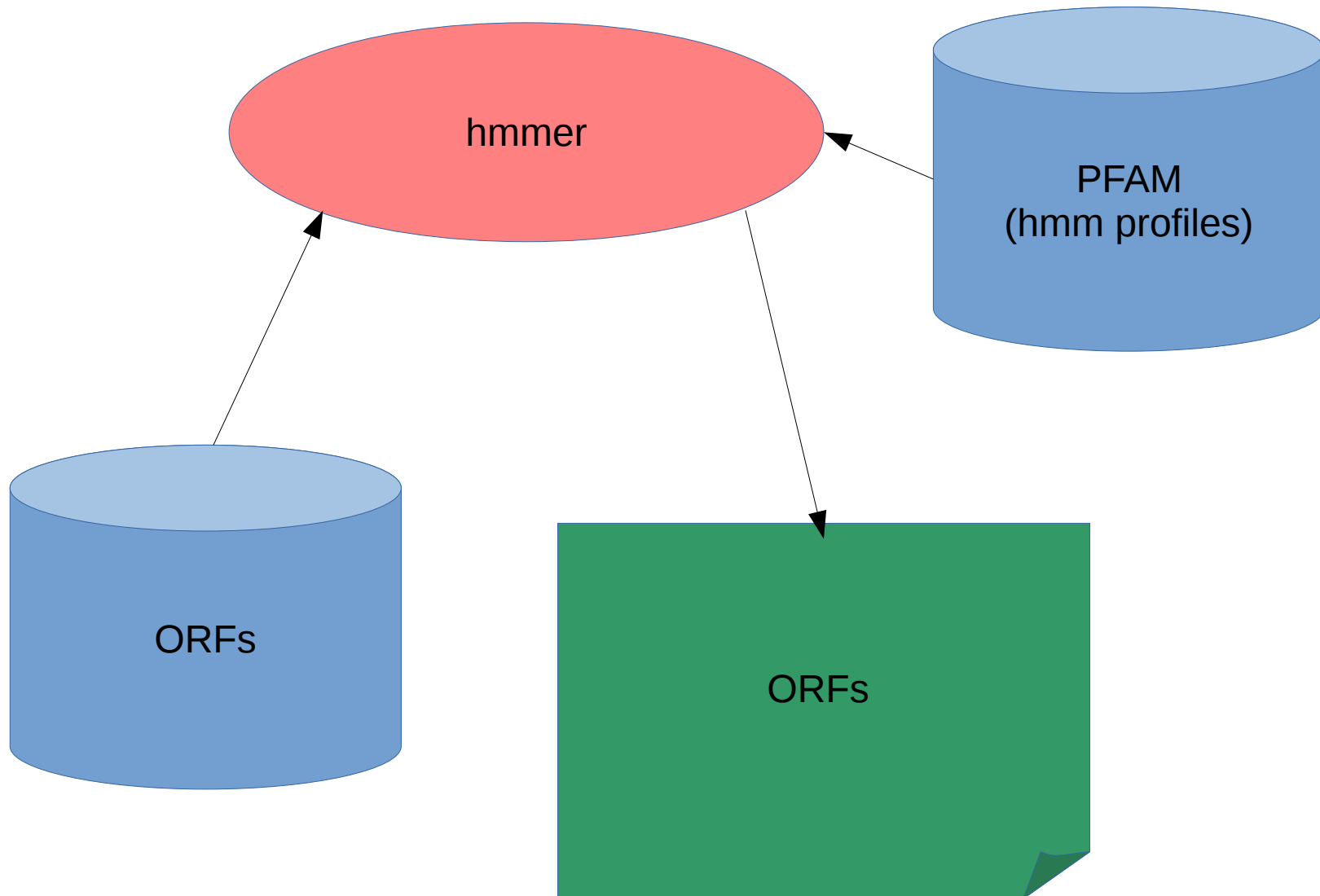


Task 6:
PFAM annotation for
ORFs

Task 6: Summary



Task 6: hmmer Installation

installing hidden Markov Model searcher.

cd ~/Programs

download the the binary version of hmmer## remove temporary files

wget http://eddylab.org/software/hmmer3/3.1b2/hmmer-3.1b2-linux-intel-x86_64.tar.gz

To extract data from the archive

tar -xvf hmmer-3.1b2-linux-intel-x86_64.tar.gz

##make all commands executable

chmod +x hmmer-3.1b2-linux-intel-x86_64/binaries/*

~/Programs/hmmer-3.1b2-linux-intel-x86_64/binaries/hmmscan -h

Task 6: Download PFAM

Download the pfam from the ftp server

ftp://ftp.ebi.ac.uk/pub/databases/Pfam/releases/ choose the most recent one.

for now we are using Pfam31

mkdir ~/Databases/PFAM

cd ~/Databases/PFAM

download pfam hmm database

wget ftp://ftp.ebi.ac.uk/pub/databases/Pfam/releases/Pfam31.0/Pfam-A.hmm.gz

Task 6: Compile PFAM

```
## get
```

```
time gzip -d Pfam-A.hmm.gz
```

```
## compile database
```

```
time ~/Programs/hmmer-3.1b2-linux-intel-  
x86_64/binaries/hmmpress Pfam-A.hmm
```

Task 6: PFAM annotation of metagenomic ORFs

```
mkdir ~/Data/PFAM
```

```
cd ~/Data/PFAM
```

```
## identify pfam domains of the orfs
```

```
## needed protein sequences of the orfs
```

```
time ~/Programs/hmmer-3.1b2-linux-intel-  
x86_64/binaries/hmmscan --cpu 1 --notextw --noali --tblout  
PFAM.result ~/Databases/PFAM/Pfam-A.hmm  
../orfs.protein.fa
```

```
cat PFAM.result
```