

# FaNDOM

## Dostupne verzije i moduli

Verzija	Modul
0.2	bioinfo/FaNDOM/0.2

## Korištenje

- Primjer : <https://github.com/jluebeck/FaNDOM>

```
#!/bin/bash

#$ -N fndm
#$ -cwd
#$ -pe *mpisingle 10

module load bioinfo/FaNDOM/0.2

FaNDOM -t=$NSLOTS -r=test_data/reference.cmap -q=test_data/query.cmap -sname=test_data/res -outfmt=xmap
```

- Korištenje python skripti

```
#!/bin/bash

#$ -N fndm-py
#$ -cwd
#$ -pe *mpisingle 2

module load bioinfo/FaNDOM/0.2

python $PYSCRIPTS/wrapper_contigs.py -f $PWD -t $NSLOTS -r test_data/reference.cmap -q test_data/query.cmap -n res -o $PWD/test_data -c 19 -m 1
```

Popis python skripti:

```
$ls -l $PYSCRIPTS
assemble_reads.py
cluster_indels.py
filter_assembled_contig_alignment.py
filter_contigs.py
filter_individual.py
indel_detection_contigs.py
indel_detection_individual.py
new_cnv.py
post_process.py
preprocess.py
Preprocess_reference.py
remove_part.py
split.py
SV_detection_contigs.py
SV_detection_individual.py
translate.py
wrapper_contigs.py
wrapper_individual.py
```