



FaNDOM

Opis

FaNDOM izvodi poravnanje Bionano Saphyr molekula optičke karte i kontiga s referencom, koristeći filtar temeljen na sjemenu. FaNDOM je implementiran u C++ i podržava multithreading.

Verzije

Verzija	Modul	Supek	Padobran
0.2	scientific/FaNDOM		

Službena dokumentacija

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

Primjeri

FaNDOM pokretanje

```
#!/bin/bash

#PBS -N FaNDOM-test
#PBS -q cpu
#PBS -l select=1:ncpus=12

cd $PBS_O_WORKDIR

module load scientific/FaNDOM/0.2

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

Primjer sa python skriptom

```
#!/bin/bash

#PBS -N FaNDOM-test
#PBS -q cpu
#PBS -l select=1:ncpus=12:mem=12GB

cd $PBS_O_WORKDIR

module load scientific/FaNDOM/0.2

FaNDOM.sh python3 $PYSCRIPTS/wrapper_contigs.py -f $PWD -t $NCPUS -r test_data/reference.cmap -q test_data/query.cmap -n res -o $PWD/test_data -c 19 -m 1
```

Popis python skripti:

```
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
```