

deepARG

Korištenje

Dostupne verzije

Verzija	Modul
1.0.6	bioinfo/deepARG



Važno

Zbog nemogućnosti postavljanja limita na resurse i mogućeg smetanja/zauzimanja resursa drugima, potrebno je cijeli čvor zauzet sa *mpifull.

Primjer 1:

shor_read_pipeline.sge

```
#!/bin/bash
#$ -N deepARG-SRP
#$ -pe a16-mpifull 16
#$ -cwd

module load bioinfo/deepARG

deeparg short_reads_pipeline --forward_pe_file F.fq.gz --reverse_pe_file R.fq.gz --output_file reads -d
$DEEPARGDB --bowtie_16s_identity 100
```

Primjer 2:

predict.sge

```
#!/bin/bash
#$ -N deepARG-predict
#$ -pe a16-mpifull 16
#$ -cwd

module load bioinfo/deepARG

deeparg predict --model LS -i ORFs.fa -o pred -d $DEEPARGDB --type nucl --min-prob 0.8 --arg-alignment-identity
30 --arg-alignment-evaluate 1e-10 --arg-num-alignments-per-entry 1000
```

Instalacija:

conda instalacija

```
source /apps/miniforge/bin/activate
conda create -p /apps/virtenv/deepARG python=2.7.15
conda activate /apps/virtenv/deepARG
conda install -c bioconda diamond==0.9.24
pip install deeparg==1.0.2
conda install -c bioconda trimmomatic
conda install -c bioconda vsearch
conda install -c bioconda bedtools
conda install -c bioconda bowtie2
conda install -c bioconda samtools
#baze podataka su runo skinite sa https://bench.cs.vt.edu/ftp/data/deeparg/data/ u /apps/virtenv/deepARG
/deeparg_data
```

