

Salmon

Verzija	Modul
0.14.1	bioinfo/Salmon/0.14
1.9.0	bioinfo/Salmon/1.9.0
1.10.0	bioinfo/Salmon/1.10.0

Korištenje

Primjer je preuzet s : ftp://ftp.ensemblgenomes.org/pub/plants/release-28/fasta/arabidopsis_thaliana/cdna/Arabidopsis_thaliana.TAIR10.28.cdna.all.fa.gz -o athal.fa.gz

Indeksiranje

```
#!/bin/bash
#$ -N Salmon-index_test
#$ -cwd
#$ -pe *mpisingle 12

module load bioinfo/Salmon/1.9.0

salmon index -t athal.fa.gz -i athal_index --threads $NSLOTS
```



Napomena

Alociranje 8-12 threadova za Salmon postiže najviše brzine za izračune. Odabir threadova više od 12 će rezultirati da ti threadovi budu zauzeti i neiskorišteni.

Instalacija

- Korišten je prevodioc gcc/9 za verziju 1.9.0

Instalacija

```
#v1.0.9

wget https://github.com/COMBINE-lab/salmon/archive/refs/tags/v1.9.0.tar.gz
tar -xvf v1.9.0.tar.gz
cd salmon-1.9.0
mkdir build
module load gcc/9
cmake3 CMakeLists.txt -DCMAKE_INSTALL_PREFIX=/home/mhrzenja/Salmon/salmon-1.9.0/build -DBOOST_ROOT=/apps/boost/1.80/ -DNO_IPO=TRUE
make
make install

#v1.10.0
mamba creatamba create -p /apps/bioinfo/salmon/1.10.0 python=3.8 salmon=1.10.0 -c bioconda
```