eggNOG mapper

Verzija	Modul
2.1.9	bioinfo/eggNOG-mapper/2.1.9

Korištenje

Primjer

```
#!/bin/bash
#$ -N eggNOG-test
#$ -cwd
#$ -pe *mpisingle 16

module load bioinfo/eggNOG-mapper/2.1.9

emapper.py -i proteins.fasta -o test --cpu $NSLOTS
```

Dostupne baze:

- taxa
- diamond
- novel families diamond
- Pfam
- MMseqs2
- HMMER

Baze su pod varijablom **`EGGNOG_DATA_DIR`**

Instalacija

```
mamba create -p /apps/virtenv/eggNOG-mapper/2.1.9/ python=3.8
mamba activate /apps/virtenv/eggNOG-mapper/2.1.9
mamba install -c bioconda eggnog-mapper
mkdir /apps/virtenv/eggNOG-mapper/2.1.9/db
export EGGNOG_DATA_DIR=/apps/virtenv/eggNOG-mapper/2.1.9/db
download_eggnog_data.py -F -P -M -H
```