

# HTSeq

Verzija	Modul
2.0.2	bioinfo/HTSeq/2.0.2

## Korištenje:

```
#!/bin/bash
#$ -N HTSeq-py
#$ -cwd
#$ -pe *mpisingle 2

module load bioinfo/HTSeq/2.0.2

python HTSeq-example.py
```

### HTSeq-example.py

```
import HTSeq
import numpy
import itertools

fastq_file = HTSeq.FastqReader( "yeast_RNASeq_excerpt_sequence.txt", "solexa" )

for read in itertools.islice( fastq_file, 10 ):
    print(read)

read.name
read.seq

qualsum = numpy.zeros(len(read), int)

nreads = 0
for read in fastq_file:
    qualsum += read.qual
    nreads += 1

r =qualsum / float(nreads)

numpy.savetxt('qualsum.out', r, newline=" ", fmt="%f")
```

Primjer je rađen po uzoru: [https://htseq.readthedocs.io/en/release\\_0.11.1/tour.html](https://htseq.readthedocs.io/en/release_0.11.1/tour.html)

## Instalacija:

### Conda instalacija

```
source /apps/miniforge3/bin/activate
conda create -p /apps/virtenv/HTSeq2.0.2
conda activate /apps/virtenv/HTSeq2.0.2
conda install -c bioconda htseq
```