

**Introduction to Bioinformatics**  
**10<sup>th</sup> practice**  
**Metagenomics - mothur**

Today you are going to practice how to analyze illumina pair-end, 16S rDNA sequencing data with the Mothur program.

**The required software is only a console as described in the document [pract10\\_connect\\_to\\_cloud\\_windows.pdf](#).**

**Mothur:**

The first step is creating a local copy of the data (mothur requires a folder, where it can modifies the file contents)

```
mkdir 10gyak
cp /gfs/data/metagenomics/mothur/* ~/10gyak/
cd 10gyak
#listing the content:
ls -lah
#starting mothur
mothur
```

Go to the webpage: [https://www.mothur.org/wiki/MiSeq\\_SOP](https://www.mothur.org/wiki/MiSeq_SOP) and the "Getting started" paragraph.

Start the tutorial! :)