

# Running rnaQUAST + BUSCO step by step

## Installation of rnaQUAST

- Create an anaconda environment for rnaQUAST and install it in the new environment.

```
conda create --name "quastbusco"
conda activate quastbusco

#install rnaQUAST
conda install -c bioconda rnaquast
```

- If you forgot the commands for this, remember that you can always google the conda cheat sheet.\*/

- Next, test your installation by running:

```
#this will create an output-folder in your current directory:
rnaQUAST.py --test
```

## Running BUSCO

rnaQUAST is a tool for evaluating RNA-Seq assemblies using reference genome and gene database. In our case, we don't have a reference genome so we use a [BUSCO](#) set. The datasets of BUSCO contain only those genes which are shared between all members of a certain taxonomic group.

- Thinking of that, try to answer the following questions:
  1. Which BUSCO dataset contains more genes, the one of the eukaryotes or the one of the plants?
  2. Which BUSCO dataset should you choose for your rnaQUAST analysis? Try to have in mind what rnaQUAST is doing exactly and why we are using BUSCO in the first place.
- Document your choice and your reasoning. Discuss with your colleagues if you're not sure.
- Identify the appropriate BUSCO data set from the list that you obtain with

```
busco --list
```

- Download the chosen data set with the following command:

```
busco --download <NAME_OF_DATASET>
```

## Running rnaQUAST

- Try to extract all the parameters you need from the [rnaQUAST github page](#) and run rnaQUAST

- Run this command in your rnaQUAST conda environment:

```
rnaQUAST.py --transcripts </path/to/>Trinity.fasta --busco  
</path/to/buscoset_odb12> -o </home/practixeXX/path/to/output>
```

## Interpretation of the rnaQUAST output

- Have a look at the test output and try to interpret it with the [rnaQUAST github page](#). Document what you learned about the usage of rnaQUAST.
- After the rnaQUAST + BUSCO run has finished, interpret and document the results. As always, try to
  1. State your expectations
  2. Summarize the results
  3. Discuss

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