De novo transcriptome assembly with Trinity

Trinity *de novo* assembly

Now we will start the Trinity run.

First open the QSubGen web application.

- Choose medium time limit and reserve 6GB of memory.
- Select 'multi-thread' and choose 10 CPUs.
- In the modules field, type `trinity` and the select the module `bioinformatics/trinity/2.6.6`.
- In job specific commands, type:

```
Trinity --seqType fq
--left data/RNA_Eye_1_val_1.fastq \
--right data/RNA_Eye_2_val_2.fastq \
--max_memory 60G --CPU $NSLOTS --full_cleanup
```

- Choose a descriptive job name then click on

- `Check if OK`

- If it passes, either save it and upload it to Hydra, or copy the text and paste it directly into your favority text editor.

Now save your text file into your `/pool/genomics/<username>/RNAseq_SMSC` directory as `trinity.job`.

Now submit your job with the command: `qsub trinity.job`

Soon your transcriptome assembly will be finished!

```
Results of all tutorials can be found here:
/data/genomics/workshops/smsc/RNA_Seq/SMSC_results.tar.gz
```