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/2.1.1`.
- In job specific commands, type
  `Trinity --seqType fq \ --left data/wt_SRR1582649_1.fastq,data/wt_SRR1582651_1.fastq,data/wt_SRR1582650_1.fastq,data/GSNO_SRR1582648_1.fas`
- 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_workshop` directory as `trinity.job`.

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

Soon your transcriptome assembly will be finished!