***Idotea baltica* Assembly Evaluation**

TransDecoder v2.0.1

**INSTALLING**

Change directory to USERAPPL and create new directory

cd $USERAPPL

mkdir transdecoder

Go to the new directory and download the installation package

cd transdecoder

wget https://github.com/TransDecoder/TransDecoder/archive/2.0.1.tar.gz

Unzip the package

tar -zxvf 2.0.1.tar.gz

Build it

cd TransDecoder-2.0.1

make

Tell the shell the location of the executable

export PATH=${PATH}:${USERAPPL}/transdecoder/TransDecoder-2.0.1

**NOTE!** This command must be run every time logging into Taito

**RUNNING**

TransDecoder.LongOrfs -t trinity\_25.fa

\*\*\* ~5min

TransDecoder.Predict -t trinity\_25.fa

\*\*\* ~20min

**RESULTS**

Peptide sequences in “.pep” file

Check how many sequences

grep -c “^>” trinity\_25.fa.transdecoder.pep

# 33,731 putative peptides

\*\*\*

**RERUN**

Run using filtered (“good”) reads

TransDecoder.LongOrfs -t trinity.K25.good.fa

\*\*\* ~3min

TransDecoder.Predict -t trinity.K25.good.fa

\*\*\* ~20min

Check how many sequences

# 21,439 putative peptides