***Idotea baltica* Assembly Annotation**

PANNZER (2015-12-04)

**RUNNING**

Load biokit

module load biokit

Run

pannzer-run -i trinity.K25.transdecoder.pep.fasta -query\_taxon 82763 -o pannzer\_dir

Taxonomy ID: 82763

scientific name: Idotea baltica

Total amount of sequences to be annotated: 33731

The job is split into 592 pieces

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Submitting jobs to batch job system of Taito with Pannzer settings listed below:

Query taxon (-query\_taxon): 82763

Treshold for the bitscore (-bitscore): 50

If sequence length is shorter than this,

it will not be handled (-sequence\_length): 20

Sequence identity percent has to exceed this

(-identity\_percent): 50

Alignment has to cover this portion from target sequence

(-target\_coverage): 0.6

Alignment has to cover this portion from query sequence

(-query\_coverage): 0.6

Description is counted as informative when it's information density

score exceeds this (-informative): 30

If this set 0, then parser goes trought the whole Blast/SANS list,

otherwise stops when the amount of informative sequences are exceed

(-informative\_hits): 100

Maximun TF-IDF distance between two description to be clustered

together (-cluster): 0.3

\*\*\* ~6hrs

Quit to run in the background

ctrl + c

Check the status of the job

pannzer-run -jobid

# shows the jobid

pannzer-run -jobid #####

**RESULTS**

pannzer\_dir.DE

\*\*\* ~20min