canu for DNA long reads assembly:

/home/nanxi/Genome\_anaysis/code/

**batch script in DNA\_long\_assembly\_canu.job**

#!/bin/bash -l#SBATCH -A uppmax2022-2-5#SBATCH -M snowy#SBATCH -p core#SBATCH -n 4#SBATCH -t 20:00:00#SBATCH -J Dna\_long\_assembly\_Canu\_11#SBATCH --mail-type=ALL#SBATCH --mail-user nanxing.liu.3019@student.uu.semodule load bioinfo-tools

module load canu

canu \

output

-p DNA\_pacbio\_assembly\_11 -d /home/nanxi/Genome\_anaysis/analyses/01\_DNA\_assembly \

genomeSize=24m \

useGrid=false \

-pacbio-raw /home/nanxi/Genome\_anaysis/data/raw\_data/4\_Tean\_Teh\_2017/pacbio\_data/SRR6037732\_scaffold\_11.fq.gz

input

echo 'end'

/home/nanxi/Genome\_anaysis/code/

**terminal:**

$ sbatch -M snowy DNA\_long\_assembly\_canu.job

$ squeue -M snowy -u nanxi  
$ jobinfo -M snowy -u nanxi

/home/nanxi/Genome\_anaysis/code/ will be the slurm-\*.out

less it to see if it sart to run or some error appear!

文本

描述已自动生成

see the slurm\_... it running

result: .fasta is the result we need to do BWA next step

电脑屏幕截图

描述已自动生成