

GNU nano 2.0.9File: name_of_my_file.shModified

```
#!/bin/bash

#BSUB -L /bin/bash
#BSUB -J Extraction_MinION
#BSUB -q priority
#BSUB -o Extraction_MinIon.out
#BSUB -e Extraction_MinIon.err

## prepare directory

# define working directory for user
work_dir=/scratch/beegfs/weekly/$USER
# create working directory for MinION extraction
mkdir -p $work_dir/lambda_MinION/fast5/
# create links to the raw sequencing files
ln -s /scratch/beegfs/monthly/SIB_long_read_workshop/MinION_lambda_reads/*.fast5 $work_dir/lambda_MinION/fast5/

## load poretools for read extraction
module add UHTS/Analysis/poretools/0.5.1

### extract reads

# convert all fast5 reads to fastq
poretools fastq --type 2D $work_dir/lambda_MinION/fast5/*.fast5 > $work_dir/lambda_MinION/MinION_Lambda2D.fastq

# get some stats on the raw data using poretools
poretools stats $work_dir/lambda_MinION/fast5/*.fast5 > $work_dir/lambda_MinION/MinION_Lambda_all_stats.txt
```

Mandatory two lines for vital-it jobs submission

#BSUB -J name_of_my_job (defined by the user)

#BSUB -q which queue I would like to use

#BSUB -o name_of_my_standard_output_file.out

#BSUB -e name_of_my_standard_error_file.err

Each script should include this fixed part

Commented lines starting with '#' describing the following command line

Each script should include this flexible part depending on the exercise you are working on

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