Welcome to MinION meta-barcoding mobile laboratory!

Raw reads directory: /home/kumarm/MinION-data/MetONTIIME/fastq_pass
Basecalled reads directory: /home/kumarm/MinION-data/MetONTIIME/fastq_pass_analysis/basecalling
Preprocessing directory: /home/kumarm/MinION-data/MetONTIIME/fastq_pass_analysis/preprocessing
Analysis and results directory: /home/kumarm/MinION-data/MetONTIIME/fastq_pass_analysis/analysis
Flow-cell: FLO-MIN106
Kit: SQK-RAB204
Expected amplicon length [bp]: 1400
Barcodes used in this experiment: BC01, BC02, BC03, BC04, BC05, BC06, BC07, BC08, BC09, BC10, BC11, BC12
Basecalling is going to be performed by : Guppy Basecalling Software, (C) Oxford Nanopore Technologies, Limited. Version 3.1.5+781ed57
Basecalling model: fast
Demultiplexing is going to be performed by guppy_barcoder after basecalling
The second round of demultiplexing by Porechop is going to be be skipped
Taxonomic classifier: Blast

Basecalling started at Thu Jan 9 10:13:50 2020
ONT Guppy basecalling software version 3.1.5+781ed57
config file: /home/kumarm/MinION-data/ont-guppy/data/dna_r9.4.1_450bps_fast.cfg
model file: /home/kumarm/MinION-data/ont-guppy/data/template_r9.4.1_450bps_fast.jsn
input path: /home/kumarm/MinION-data/MetONTIIME/fastq_pass
save path: /home/kumarm/MinION-data/MetONTIIME/fastq_pass_analysis/basecalling
chunk size: 1000
chunks per runner: 20
records per file: 4000
num basecallers: 4
cpu mode: ON
threads per caller: 8

Found 0 fast5 files to process.
Init time: 396 ms

0%   10   20   30   40   50   60   70   80   90   100%
|----|----|----|----|----|----|----|----|----|----|
****
Caller time: 101 ms, Samples called: 0, samples/s: 0
Finishing up any open output files.
Basecalling completed successfully.
Basecalling finished at Thu Jan 9 10:13:50 2020

```
Demultiplexing started at Thu Jan  9 10:13:50 2020
ONT Guppy barcoding software version 3.1.5+781ed57
input path:       /home/kumarm/MinION-data/MetONTIIME/fastq_pass_analysis/basecalling
save path:        /home/kumarm/MinION-data/MetONTIIME/fastq_pass_analysis/preprocessing
arrangement files:  barcode_arrs_rab.cfg
min. score front:   60
min. score rear:    60


Found 0 fastq files.

0%   10   20   30   40   50   60   70   80   90   100%
|----|----|----|----|----|----|----|----|----|----|
Done in 0 ms.
Demultiplexing finished at Thu Jan  9 10:13:50 2020

Error in file(con, "r") : cannot open the connection
Calls: grep -> readLines -> file
In addition: Warning message:
In file(con, "r") : cannot open file 'NA': No such file or directory
Execution halted
```