

## User Guide

### A. To run from sequencing:

```
bash smart_sample_monitor.sh -d /data/WGS_Dummy -s /data/routine_nWGS/sample_ids_bam.txt
```

- The sequencing folder **/data/WGS\_Dummy**
- The *sample\_ids\_bam.txt* need to be updated base on the sample id and flowcell ID and *sample\_ids.txt*

### B. Start the run after the sequencing is finished

```
bash run_pipeline_singularity.sh --run_mode_order --log-dir /data/trash -w /data/trash
```

### C. Start epi2me and analysis

```
bash run_pipeline_singularity.sh --run_mode_epianalyse --log-dir /data/trash -w /data/trash
```

### D. Start only epi2me/ analysis

```
bash run_pipeline_singularity.sh --run_mode_epi2me all --log-dir /data/trash -w /data/trash  
bash run_pipeline_singularity.sh --run_mode_analysis rmd --log-dir /data/trash -w /data/trash
```

The working directory is **/data/routine\_nWGS** which contains the following folder (**routine\_analysis**, **routine\_bams**, **routine\_epi2me**, **routine\_results**) and files (sample\_ids\_bam.txt, sample\_ids.txt)

The pipeline is installed in **/data/routine\_nWGS\_pipeline/nWGS\_pipeline**