

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**