

User Guide

A. nWGS Paths

1. Data directory: **`/data/routine_nWGS`**
2. Pipeline directory: **`/data/routine_nWGS_pipeline/nWGS_pipeline`**
3. Merged BAM files: **`/data/routine_nWGS/routine_bams`**
4. Epi2me and Clair3/ClairS-TO outputs: **`/data/routine_epi2me`**
5. Analysis output: **`/data/routine_nWGS/routine_analysis`**
6. Final results: **`/data/routine_nWGS/routine_results`**

B. Input Preparation

Update the file **`sample_ids_bam.txt`** located at **`/data/routine_nWGS`** based on the sample ID, flowcell ID, and the content of **`sample_ids.txt`**.

C. Run from Sequencing

To start monitoring sequencing data:

- **`smart_sample_monitor.sh -d /data/WGS_Dummy`**

D. Start the Pipeline After Sequencing Is Finished

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

E. Start Epi2me and Analysis

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

F. Start Only Epi2me or Analysis

- **Epi2me:**

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

- **Analysis (R Markdown mode):**

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