

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