Routine User Guide

The working **conda** environment is:
conda activate p24env

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