# biomodal software release notes March 2025

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# duet pipeline v1.4.2

We have issued the following bug fix and feature improvement in the current release:

### Read pair resolution

- **Minor change to the prelude docker container**
    - A minor change to the prelude docker container (pinned the numpy version) was introduced to fix a potential bug that might arise on some platforms or environments.
    - Previously, NumPy versions could vary across environments, sometimes causing inconsistencies, especially in converted Singularity containers.
    - Now, the NumPy version is explicitly pinned in the Prelude module, ensuring a more stable and predictable behaviour across all setups.

### Methylation quantification

**Updated methylation quantification module (epiquant) for improved HPC environment support:**

- **Fix to address relative path issues**
    - Previously, some users encountered errors during epigenetic quantification when running the pipeline on some HPC environments. This occurred because the epiquant module attempted to create a zarr store using a relative path, rather than an absolute path.
    - The pipeline has now been updated to use an absolute path when creating a zarr store. This fix benefits users on certain HPC setups only, please contact your bioinformatics FAS for further clarifications.

- **Fix to address file latency issues**
    - Previously, some users encountered errors in the epiquant module caused by file latency when running the pipeline on some HPC environments.
    - This has been addressed by introducing a retry strategy with exponential backoff, allowing the pipeline to successfully complete even on HPC environments that experience file latency.
    - This fix benefits users on certain HPC setups only, please contact your bioinformatics FAS for further clarifications. .

**Improved zarr store output directory structure for downstream 5mC or 5hmC DMR analysis**

- **Muti-context zarr store outputs now separated by context**
    - The pipeline includes an option to generate multi-sample zarr stores containing methylation quantification information for the CHG and CHH contexts, in addition to the default CG context.
    - Previously, when generating multi-sample Zarr stores, all contexts (CG, CHG, CHH) were output to a single directory (`sample_outputs/zarr_store/`). This caused issues during downstream DMR analysis, as DMR calling can only be performed on zarr stores

containing methylation information for a single context only. Users had to manually separate context-specific zarr stores into different directories to avoid errors.
    - The pipeline now automatically outputs each context into its own subdirectory (e.g., `sample_outputs/zarr_store/CG/`, `CHG/`, `CHH/`), eliminating the risk of users performing DMR calling on zarr stores of different context.

### Variant Calling

- **Updated somatic variant calling syntax for improved compatibility**
    - The pipeline includes an option to perform somatic variant calling, which is performed using Mutect2 followed by GATK recommended filtering using FilterMutectCalls.
    - Previously, the legacy syntax in the mutect2.nf Nextflow module was incompatible with some later combinations of Nextflow and Java versions.
    - The syntax has now been updated to ensure compatibility with these newer versions.

- **Improved documentation, output file locations, and output files names for joint variant calling.**
    - The pipeline includes an option to perform joint variant calling.
    - Previously, the documentation, output file locations, and filenames for joint variant calling were less consistent with other pipeline outputs.
    - This has now been improved with clearer documentation in the Data Interpretation Guide and updated output file locations and naming conventions, aligning them with the other output files generated by the pipeline.

### Targeted sequencing

- **Bug fix to improve support for custom target panels in targeted sequencing mode**
    - The pipeline features by default a targeted (hybrid capture) mode for use with target panels.
    - Previously, the pipeline could fail if a custom panel did not include at least one target on every autosome. This affected users running the pipeline with certain custom panel designs.
    - This has now been fixed to handle custom targeted panels where some feature no targets, allowing the analysis to complete successfully without errors.