modality analysis software release notes: August 2025

Contents

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modality analysis software v1.0.0b2 (beta)

We have issued the following bug fixes and feature improvements in the current beta release:

Updated HTML reports

Biological QC Sample Information table

- If a sample metadata file is provided, the Sample Information table will display all of the sample sheet metadata information, in addition to the mean CpG coverage statistic, that is calculated form the Zarr store(s).

DMR Summary table

- The DMR visualisation report generated by 'modality dmr plot' now contains a summary table, defining the Control and Test groups for the current analysis, and statistics for the number of regions, mean coverage, mean number of contexts, and number of DMRs passing analysis filters.

Sample aggregation and grouping

Rename the --group-name option for 'modality get' and 'biological-qc'

- The --group-name option has been renamed to --aggregate-by-group to inform the data handling when this option is invoked.
- Methylation counts are aggregated for all samples with the same group name, and is therefore most applicable to technical replicates or top-up sequencing.
- User documentation guidance has also been updated.
- The --group-name option is still recognised by both entry points.

Addition of group-by-colour function on Biological QC HTML report PCA plots.

- When providing a sample sheet metadata file with the 'biological-qc' command, all group and covariate header names will be available to select for colour-based grouping of individual sample datapoints on HTML PCA scatterplots.
- Data is inferred as categorical.

Defining regions

Reduced the lower window size limit for 'modality get'

- Window size of ≥100 bp are now supported.

Documentation updates

Core Workflow script

- Addition of Core Workflow script and user guide section.

Updated documentation in response to user feedback

- Clarifications and updates to support new features and fixes.

Added pre-prepared bed files for mouse mm10p6

- Download link to region bed files with revised contig names.

Issues and fixes

Biological QC

- Fixed an issue where the group name was not displayed in the Sample Information table.

DMR calling

- Fixed issue where strand merging did not work as expected in the DMR CLI.

DMR plot

- Fixed an issue where chart titles showed a timestamp.

Track plots

- Fixed an issue with spurious smoothing in trace track and mod-difference tracks.
- Fixed issue with merge-cpg-strands parameter not being propagated in the tracks plot.

beta testing

This beta version of modality is intended for early access evaluation. We welcome your feedback as we continue to improve modality. Please report any issues or suggestions via the support channels provided in the user documentation or by e-mail to support@biomodal.com