modality analysis software release notes: September 2025

Contents

modality analysis software v1.0.0b3 (beta)

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

Functional Changes

General

- CLI now uses `--min-coverage` instead of `--filter-context-depth` for consistency. Backwards compatibility for `--filter-context-depth` is retained.
- In `modality dmr call`, the `--methylation-contexts` can now be specified as `mc`, `hmc` or `modc` for consistency with `modality get`. Backwards compatibility for `num_mc`, `num_hmc` and `num_modc` is retained.
- The underlying python API method, `subset_bycoverage`, has been unified to default to `method=mean` for both Feature Extraction (`modality get`) and DMR calling (`modality dmr call`) CLI workflows. When using the CLI `--min-coverage` option, the filter is applied to the mean context (e.g CpG) depth across all samples prior to any aggregation step. If the mean context depth is below the `--min-coverage` value, that context is omitted for all samples in downstream steps for the current command.

Biological QC (Pearson Correlation & PCA)

- Updated method to improve memory efficiency and scalability to support a higher number of samples.

Track plot smoothing

- The LOWESS-based smoothing method has been replaced with a Gaussian kernel-based approach. This improves performance and consistency across genomic regions, especially in sparse or noisy datasets.

Fixes and improvements

Core Workflow v1.2

- Fixed an issue in the bash script for validating the metadata `GROUP_COLUMN` name if it is the last column in the file.
- Added Overdispersion `<True/False>` as a settings option in the Interactive Configuration Generator userform and `config.txt` file to turn this flag on or off for all `modality dmr call` analyses. Previously, overdispersion correction was applied to DMR analyses with the `gencode.v44.human.genes.annotation.bed.gz` region file only.
- Increased the verbosity level (`-v`) for each command.

Output file naming

- Standardise the prefix folder and result file names when running `modality get` and `modality dmr`. e.g Extract_*, DMR_*, DMR_Report_*.

Resolve warnings

- Ensure no divide warning is triggered when running methods that compute fractions.

Reading Zarrs from remote locations

- Fixed an issue in validating Zarr paths if they are stored in a remote location e.g. cloud storage.

Documentation updates

--help text updates

- CLI `modality --help` banner and logo updated for terminal compatibility.
- The `modality dmr call --help` now explicitly states `modc` as the default.
- The `--help` output now provides a clearer explanation of how `--condition-array-name` (used in DMR analysis) and `--aggregate-by-group` share similar underlying functionality. This helps users better understand how to handle top-up sequencing and aggregation scenarios.

Updated documentation in response to user feedback

- Clarifications and updates to support new features and fixes.
- Updates to FAQs.

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