biomodal

modality XPLR analysis software release notes: November 2025

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modality XPLR analysis software v1.0.0

We have issued the following features, fixes and improvements for General Release:

New features

Authentication

- Upon first use of modality XPLR v1.0.0, users will need to authenticate by entering their existing biomodal credentials (as used for duet Software).
- Users who are not yet registered with biomodal can self-register to access modality XPLR via the links shown in the user documentation or the terminal prompt upon first use.
- Authentication is required once per machine. Contact support@biomodal.com if you have difficulty authenticating modality XPLR.

New HTML report for Feature Extraction (modality `get` commands)

- The previous `--plot` option has been deprecated. The HTML report with violin and Pearson correlation matrix plots will automatically be generated for `mean` and `regional-frac` operations.
- Plots for all requested modification types are included in the same HTML report.

Regional correlation dendrogram heatmaps

- Feature Extraction supports plotting a dendrogram heatmap for regional modification fractions with `modality get`.
- The heatmap supports up to 200 regions, and can be included by using the `--heatmap` flag.
- Sample and region clustering is performed according to the correlation of the extracted statistic.

CpG-informed segmentation

- A new entry-point that generates an optionally annotated bedfile of genomic regions segmented by user-defined parameters, according to the distribution of CpG contexts.
- Users can select the maximum region size, minimum number of contexts, and maximum distance between CpG contexts before a new segment is defined.
- Regions can then be annotated using user-supplied GFF3, CpG island annotation (BED), or custom BED4+ files, with a minimum overlap setting.
- The resulting region definitions can be used in downstream modality XPLR analyses.

Fixes and improvements

CpG strand merging behaviour

- Support for merging strands prior to analysis was previously only available to dmr call, but has now been extended to all entry-points (export, biological-qc, get).
- The default behaviour is to merge strands. To disable strand merging use the --disable-strand-merging flag.
- The previous --merge-cpg-strands <TRUE/FALSE> option in dmr call has been deprecated.
- Merging strands will affect the number of reported contexts and mean CpG coverage (e.g in the Biological QC report). A section has been added to the documentation to describe this.
- The INI file that is created by dmr call and used to generate tracks plots, contains the --disable-strand-merging status that was set during DMR calling (default: FALSE). This setting is used to draw the methylation trace plot, directly from the Zarr store data.

Unify sample aggregation across entry-points

- The behaviour of the --aggregate-by-group option has been unified across entry-points. This feature is most relevant for merging sample technical replicates under a common ID.
- When used, result files and plots will appear reduced, as sample data is grouped according to the metadata column specified.
- A new option, --order-by-group has been introduced to display the group label information in visualisations, but does not aggregate any samples and will not reduce the result file output by group. This improves the visualisation of sample groups and is recommended for regular use.

Filter regions by number of contexts

- An additional option for dmr call and get operations.
- Use --num-contexts <integer> to filter the input regions by a minimum number of contexts.

Support multiple Annotation types in DMR Report visualisations

- To support the analysis of prepare-regions bedfiles that contain multiple annotation types, the DMR Report (volcano and p-value histogram) shows Annotations by colour and includes a legend.
- Click on an Annotation name in the legend to toggle the series on or off in the HTML plot.

Improved support for Zarr store merging

- Resolves an issue when merging Zarr stores where one was created with a primary assembly and the other with a primary assembly plus misplaced contigs.
- Handles merging non-critical, mismatches in metadata between Zarr stores.
- Zarr stores are still required to use the same reference genome, assay (duet evoC or duet +modC), and contexts (CpG, CHG, CHH) to allow merging.

Handle DMR calling edge case 1 sample in one or both condition groups

- Added robust sample size validation to the DMR workflow: Statistical tests now run only when each group has sufficient samples. If requirements aren't met, the workflow outputs conservative results (all p-values = 1, test statistics = 0) while still computing effect sizes.
- A warning is displayed in the HTML report when this case is detected.
- Ensures that the DMR Report volcano plot still includes DMRs but with the loss of the y-axis dimension.

Fixed TypeError caused by numeric metadata in sample sheets

- Numeric metadata is supported for columns in the sample sheet and is aligned across all entry-points.

Coverage filter introduced for export commands

- `export` commands support context coverage filtering using the `--min-coverage` flag.

Modification type included in DMR report file

- DMR Report filenames include modification types, modC, mC and hmC for easy identification.