modality XPLR analysis software release notes: May 2026

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modality XPLR analysis software v1.1.0

We are pleased to announce the latest release of modality XPLR, version 1.1.0.

The key feature of this release is modality XPLR Viewer which is available in beta form. The Viewer acts as a (locally running) graphical user interface (GUI) to enable users to easily explore and filter analyses output from modality XPLR CLI, as well as allowing generation of additional visualisations.

The core workflow has been updated (to 2.0) to fully support the Viewer, and several processes have been optimised to improve performance/lower memory usage.

New features

modality XPLR data Viewer (beta):

Intelligent result file discovery and filtering

- Users can easily find, categorise and filter analyses carried out by modality XPLR. On launching the Viewer these are detected within a folder and presented by analysis type e.g., DMR, biological QC. The intelligent discovery also detects metadata used when the analysis was carried out which is then highlighted in the report tile and can be used to filter the data e.g. by minimum coverage, common sample sheet etc.

Enhancements to Biological QC and Extract reports

- Samples can be interactively ordered based on metadata values on the Extract & Biological QC Viewer report pages, as a dynamic alternative to using the --order-by-group CLI option. Re-ordered sheets can be exported as CSV files.
- Outliers can be easily spotted in PCA by interactively colouring by metadata value, similar to existing HTML reports.

Enhancements to DMR

- Manhattan plots are now generated, showing where significant methylation differences are located across the epigenome.
- It's now easy to compare multiple DMR volcano plots, for example across stages of disease progression, on the same page.
- Significance thresholds and axis can be interactively changed, making it easy to highlight regions of interest.
- Data tables combine DMR regions from selected plots, and can be filtered by significance and occurrence in one or all DMR results included in the analysis.
- Genes lists or locations can be supplied to highlight genes/regions of interest on DMR plots.
- Points of interest on plots can be selected to discover location information and to launch the tracks view to explore them in more detail.
- High quality images can be exported for publication.
- Ability to toggle overdispersion on/off if modality dmr call overdispersion setting is set to both.
- Toggle between p- and q-value in volcano plot y-axes.

Tracks plot enhancements

- Tracks plots now use embedded IGV to view methylation trace, methylation difference, DMR bar (with tooltip to visualise significance) and gene annotation tracks. This allows users to clearly

see location-specific changes in 5hmC or 5mC between conditions and locate nearby genes, as well as producing quality images for publication.
- Tracks plots can be generated in the Viewer directly from a DMR report, either from the volcano or Manhattan plots, or from the DMR table.
- Changes (such as region, track order, colours etc.) can be made interactively, no need for editing .ini files.
- Track plots automatically fetches gene annotations when used with human or mouse genomes (hg38, hg19, mm39, mm10) when connected to the internet.

Association heatmaps

- Users can easily generate association heatmaps though the Viewer GUI without running additional CLI commands.
- Users can subset and export Extract regional-frac or DMR mod-difference results to key regions, or choose to upload custom-curated region lists (TSV/BED) for use in association heatmaps.
- Drop-down menus allow easy metadata-aware grouping and labelling from sample sheet metadata to surface biological and technical attributes for clearer pattern recognition in the heatmaps.
- Flexible clustering & normalisation controls, including optional hierarchical dendrograms and per-sample/group or per-region scaling allow correlations to be more easily seen.
- 5mC and 5hmC association heatmaps can be displayed on the same plot or split into two plots.
- Publication is easy with high-quality PNG export (300 DPI) with all labels, colour bars, and dendrograms preserved.

Full metadata/provenance for analysis and easy command copying

- The full provenance of the analysis and the command used to generate it is available on each report page, allowing easy copy/paste to re-run analyses on the CLI.

Authentication and telemetry

- modality XPLR requires users to authenticate with a biomodal login for each machine where modality is installed. The username (email) and timestamp of each login attempt is shared with biomodal.
- modality XPLR v1.1.0 introduces opt-in telemetry sharing with biomodal, to help us improve our products and services. Upon initial login, you will be prompted to confirm your opt-in or opt-out status. You can change your opt-in or opt-out status at any time. Telemetry sharing captures the authenticated username (email), modality version, timestamp and modality top-level command that was executed. Telemetry does not include sample data or details of user-supplied file names or file paths within modality commands.
- modality XPLR features in beta status are subject to telemetry logging with an active internet connection. The modality XPLR Viewer feature is in beta status for v1.1.0 and telemetry is enabled. If this is a concern, we recommend not using the Viewer until it is out of beta status – in the meantime data can still be visualised using the existing HTML reports that are generated by the modality XPLR CLI.

Other fixes and improvements

Automatic modification type detection

- The modality dmr call and modality get functions will automatically detect if the dataset is 6-base (duet evoC) or 5-base (duet modC) and choose the appropriate --methylation-contexts or --fields options for you.

Biological QC supports modC in 6-base datasets

- Users can specify to run a modC Biological QC analysis from a 6-base dataset, e.g. to compare duet evoC results with a 5-base dataset by combining the 5mC and 5hmC readout to a single modC call.

New options for region preparation

- Introduced the --annotate intron option to the modality prepare-regions CLI command, to annotate intragenic intron regions i.e. introns within genes.
- Introduced a new --include-all-transcripts option to the modality prepare-regions CLI command. By default, prepare-regions only uses canonical transcripts for annotation. This can be overridden by passing the --include-all-transcripts flag.

Improved DMR calling

- DMR workflow memory utilisation has been improved.
- Updated the --overdispersion option to explicitly control true, false, or both. When set to both, DMR results with_od and without_od are generated in the same modality dmr call analysis, and indicated in the result file name. This saves significant time in producing DMR results with and without overdispersion correction.
- Added differentiation between dmr call and dmr plot commands in provenance metadata to improve user experience with the Viewer.

Simplified context counting

- The modality get count command no longer requires the --fields argument, since context counts are the same regardless of which field you choose.

Fixed output file placement for DMR plot results

- Fixed an issue where dmr plot result files were divided between two new directories if the output folder name contained the string “DMR_”. All result files (BED, JSON, HTML) now appear in a single DMR_* directory.

Added versioning to pre-prepared bedfiles

- Pre-prepared bedfiles for region exploration now include version (*.v1.1.0.zip). Previous versions are renamed to v1.0.0.zip.
- Fixed duplicate and overlapping entries in pre-prepared CpG shore and shelf annotation files that could occur when CpG islands were close together.

Improved warnings and error handling

- modality XPLR now shows a warning when setting a minimum coverage threshold that is higher than the dataset contains.
- The biological-qc tool validates the zarr structure and reports clear errors if it detects inconsistent methylation data (e.g., 5mC present without 5hmC in 6-base datasets).
- Addressed a silent failure when providing a path to missing DMR result or annotation files in the modality tracks command.

- Improved error handling when working with single versus multiple Zarr files.
- When running modality dmr call or modality get with strand merging enabled (default) in CHH or CHG methylation contexts, a warning is shown and analysis proceeds without strand merging.
- Covariate processing now logs a per-variable breakdown showing which covariates are continuous and which are categorical, along with the reference category and dummy column names added to the model.

Changes to Core Workflow

- Core Workflow is updated to v2.0, and optimised for result visualisation in Viewer.
- DMR calling overdispersion setting is set to both, by default, but can be modified in the config.txt.
- Supplied regions files for genes and promoters use the versioned file names, v1.1.0.bed.gz
- Toggle option in the config.txt to include modC as a --field or --methylation-contexts in Biological QC, Extract and DMR calling.
- Removed generation of DMR HTML reports with modality dmr plot, as these visualisations are now readily available through modality viewer.

Other fixes

- Resolved issue with modality tracks not able to accept full chromosome to --region flag.
- Resolved silent error when no annotation or DMR file passed to modality tracks.
- Resolved issue with reproducibility of violin plots in Viewer and Jinja2 HTML report caused by lack of random seed when downsampling. Downsampled size has been increased to better capture tail of distribution.
- The modality dmr call --covariates shortcut has been changed form -v to –va to avoid flag collision with verbosity settings. -v is no longer supported as an option in modality dmr call.