

OSIRIS Release Notes Version 2.10.2

Improvements in OSIRIS Version 2.10.2

Version 2.10 includes substantial improvements over previous versions and multiple bug fixes. Version 2.10.2 incorporates bug fixes to version 2.10 and a couple of improvements.

Version 2.10

New Features

Sample Deletion

A new feature allows users to delete selected samples from an analysis without the need to reanalyze the batch and redo the review and editing of all the other profiles. This can be useful in situations where an incorrect sample was included in the analysis, or a batch needs to be split for reporting purposes, such as discovery requests for a criminal trial or clinical testing review, where sample confidentiality may be an issue.

Analysis Archives

A new feature allows the creation of an OSIRIS archive file, with an '.orz' extension. This archive file contains the OSIRIS analysis files from a batch. Users can also optionally include the .fsa/.hid files that were used to generate the analysis. If samples have been deleted from an analysis, the files specific to the analysis are not included in the archive. OSIRIS also can extract the files and data in an archive into a new folder.

These archives have multiple uses:

- Discovery requests can be easily fulfilled without including confidential information from other cases.
- Sharing data. Archives make sharing an analysis simple.
- Data archiving. An archive that includes the .fsa/.hid files is about half the size of an uncompressed folder containing the analysis and .fsa/.hid files.
- Troubleshooting analysis. An archive can be sent to us which includes the files and all the parameters necessary to troubleshoot an issue.

Improved ladder analysis

Made the algorithm for identifying internal marker ILS peaks in ladders more efficient and more robust. This reduces the number of ladders that fail to analyze, particularly in RAPID DNA data. This is a lab setting that users can optionally disable.

Improved spike analysis

Identification and analysis of spikes was improved with the addition of a new curve type to better model spike peaks that consist of a single data point.

Kit improvements

PowerPlex S5 kit was improved to make ladder analysis robust.

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New Features

Optional peak sensitivity setting

Improved optional peak-detection sensitivity settings have been added that also improve the performance of the pull-up algorithm.

Peak sensitivity in previous versions has been determined by the “Ignore noise analysis in peak detection when above detection threshold” and “Percentage of Standard Noise Threshold for Peak Identification” settings, requiring users to adjust the detection threshold in some cases to increase the sensitivity at very low RFU Analysis Thresholds. Those settings have been renamed for clarity. (See the User’s Guide.) The optional new sensitivity settings separate the function of the detection limit from peak -detection sensitivity.

Improved small (bp) artifacts filter

The “Ignore artifacts smaller than” parameter has been improved. Previously, if users mistakenly set this to ignore the smallest ladder allele, the analysis would fail. This function has been improved to automatically adjust to allow inclusion of the smallest ladder allele.

Version Number display

The OSIRIS version number used for an analysis is now displayed in the Analysis Parameters window. This allows users to determine which version of the software was used for a particular analysis.

New Kits

Added the Promega GenePrint 24 kit definition.

Bug Fixes

Version 2.10

1. Fixed several minor bugs that are unlikely to occur and that would not affect allele calls.
2. Fixed a rarely occurring bug that would cause a sample to be analyzed as a positive control if the file or sample name contained the default positive control name such as 2800M, resulting in positive control allele mismatch artifacts.
3. Fixed a bug dating to version 2.9 that in certain circumstances could result in a tall peak (with a poor “fit”) in a locus not being called if the “Enable Residual Displacement Allele Validation Test” was selected. This bug largely affected RAPID DNA platform data. The likelihood of this bug occurring in non-RAPID DNA platform data is extremely low.

4. Fixed a bug dating to version 2.9 which under rare circumstances where there are two very closely spaced peaks (a “noisy” peak) that have the same allele call, and one of the two side peaks was below the fraction filter threshold, when the fractional filter was selected, the peak might not be called.
5. Fixed a bug that could happen when a primary peak causing a pull-up in an adjacent channel also had pull-up signal (partial pull-up) from a third channel. Under the extremely rare circumstances that this might occur, it could affect analysis of the pull-up pattern, resulting in missing pull-up artifacts.
6. Fixed a bug where in rare circumstances a very narrow peak in one channel that comigrated with a very wide peak in another channel could be interpreted as a pull-up and not be called. The likelihood of this bug occurring is extremely low.
7. Fixed a bug which would have prevented off-ladder allele calls on partial pull-up peaks (Version 2.9 or later) or on pull-up peaks (prior to Version 2.9) regardless of whether the “Do Not Call OL Allele If Pull-up” Lab Setting was selected. In extremely rare circumstances, this might result in not calling a valid microvariant allele.
8. Fixed a bug that prevented the “Do Not Call OL Alleles If Excessive Number of OL’s” lab setting from working when selected, resulting in additional editing required by the analyst.
9. Fixed a bug that caused the date format in the Mac version to be inconsistent with the format in the Windows versions.

Version 2.10.1

1. Fixed a bug that prevented entry of custom positive control data in the Lab Settings Assignments tab.
2. Fixed a bug that prevented the correct Directory folder from opening upon data export.

Version 2.10.2

1. Fixed several minor User interface bugs that did not affect analysis.
2. Fixed a bug in the optional enhanced shoulder calling algorithm introduced in version 2.9 that prevented it from working in rare circumstances.
3. Fixed a bug that in some circumstances for some kits could prevent poorly separated alleles 1 nt apart from getting allele calls, rather being flagged as an artifact. This prevented analysis of the ladders in certain kits (e.g., PowerPlex ESI 17), resulting in failed analysis runs.