

NimbleScan v2.6 Software

Release Notes

March 2010

NimbleScan v2.6 Software introduces several new features and benefits designed to enhance the user experience when analyzing data that was obtained using NimbleGen microarrays. Refer to *NimbleScan Software User's Guide v2.6* for more detailed information.

New Functionality

- Parameters for segMNT analysis have been refined to improve CGH analysis. New segMNT analysis parameters have been implemented to provide end users with finer control over CGH analysis.
- For CGH analysis, a new option enables analysis without segmentation so that the output files can be used in 3rd party segmentation software.
- The Experimental Metrics report includes new metrics for arrays processed using the NimbleGen Labeling and Hybridization Control (LHC) Kit to be released in the near future.



Additional documentation describing the use of the LHC reagents as well as interpretation of the results will be provided with the release of the kit. Checking the *LHC* checkbox in the software without LHCs being present on the arrays results in “n/a” or zeroes being reported in an LHC column.

- Application-specific data analysis now generates a settings file that records the various analysis parameters used for that particular analysis session. The settings file is placed in the same output directory as the analysis results and can be viewed using a text editor. In addition to analysis parameters, the settings file also records the names of the various input files that were used. For example, the session for a CGH segMNT analysis will create a file called “segMNT_settings.txt” in the output directory. The information in the settings file can be used either for troubleshooting purposes or reanalysis.
- Significant performance enhancements to the image analysis component have been implemented for gridding and alignment of 2 μ m images generated from the NimbleGen MS 200 Microarray Scanner.
- NimbleScan v2.6 Software is fully supported on Microsoft Windows 7 (32-bit and 64-bit) operating system as well as Macintosh OS 10.6 (Snow Leopard).
- NimbleScan v2.6 Software fully supports NimbleGen CGX-6 arrays to be released in the near future.
- Bug fixes to some of the critical issues found in previous releases have been included in this release as described below.

Known Bug Fixes

- A bug related to a missing semi-colon in ratio_peaks.gff files generated by ChIP-chip analysis has been fixed.
- A failure to overwrite image files to TIFF while doing repeated extractions of subarrays from a multiplex array has been fixed.
- A performance problem when writing reports on some Microsoft Windows network drives has been fixed.
- An issue resulting in an empty column being generated while running the MapPeaks analysis for DNA methylation experiments has been fixed.
- The Reorient functionality for image analysis now provides user-controlled flip and rotate capabilities to provide support for all array formats. Nearly square features on arrays were not properly reoriented by the functionality previously.
- A bug resulting in missing gene description information from Expression analysis results has been fixed.

Known Issues

- While NimbleScan v2.6 Software is supported on multiple operating systems, Roche NimbleGen strongly recommends that all analyses be performed using one operating system. Analysis of data generated across operating systems is not supported and could lead to either data corruption or data files not being recognized by the software because of differences in file naming conventions and other issues.
- NimbleScan v2.6 Software is no longer supported on Microsoft Windows 2000 or Macintosh OS 10.4 operating systems.
- The uniformity score is no longer supported or displayed after gridding in the lower left corner of the image window.
- The alignment score is no longer supported or provided in the header of these reports: Feature report, Probe report, Pair report, Macro Feature report, and X, Y and Signal report.



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