



NimbleScan v2.5 Software

Release Notes

October 2008

NimbleScan v2.5 Software introduces a number of new features and benefits designed to enhance the user experience when performing data analysis using Roche NimbleGen microarrays. Refer to NimbleScan v2.5 Software User's Guide for more detailed information.

New Functionality

User Interface Enhancements: A number of user interface enhancements and changes have been implemented in this release.

- A new keyboard shortcut (F12) for **Save As...** under the **File** menu is now available for saving edited images quickly.
- New keyboard shortcuts Ctrl + 1, Ctrl + 3, Ctrl + 7, and Ctrl + 9 are available for moving respectively to the lower left, lower right, upper left, and upper right corners to efficiently manage the manual gridding process.
- A new checkbox in the Open an Alignment dialog box provides the ability to *Hide gridded TIFs* and display only a filtered list of images that have not been gridded when selected or to show all TIFFs when not selected. The same panel within the dialog box also displays information about the selected TIFF, such as its size and whether it is aligned.
- The new Experimental Metric Report feature under the main **Analysis** menu replaces the former functionality of the Experimental Quality Analysis submenu under Expression analysis.
- NimbleScan v2.5 will automatically analyze how much memory is available on the user's computer and adjust heap space allocation accordingly.

Application-specific Feature Enhancements: New analysis parameters and features are now available for the CGH, ChIP-chip, and Methylation analyses.

- CGH:
 - The spatial correction algorithm previously provided as a plug-in for NimbleScan v2.4 is now fully integrated into NimbleScan v2.5.
 - segMNT analysis now includes two new parameters, *Number of candidate breakpoints* and *Number of permutations*, which were previously hard-coded in the algorithm settings, and a modified default value (set to 0.1) for *Min segment difference*.
- ChIP-chip and Methylation:
 - The spatial correction algorithm setting has been added to both the ChIP and Methylation Compute Ratio Files analyses.
 - Unique file names can now be generated automatically for export files that are compatible with Microsoft Excel.

Experimental Metrics Report: Provides a set of metrics that can be used to evaluate the quality of the signals and thereby establish guidelines for determining the quality of the data. Details about each metric and usage guidelines are described in the "Guide to Interpreting the Experimental Metrics Report" and the User's Guide provided with NimbleScan v2.5 software.

Significant Revisions:

- In addition to using .pair files as input files for analysis, NimbleScan v2.5 software now supports aligned TIFF or unit TIFF files as input files for image analysis.
- A new click-wrap license agreement is presented to the user during installation of NimbleScan v2.5 that the user can opt to accept or reject.
- The NimbleScan v2.5 software installer offers options to install the software either as the fully licensed version (requires purchase of software with a valid license key from Roche NimbleGen, Inc.) or as a free, 30-day trial version.
- The 30-day trial version can be upgraded to a fully licensed version without reinstallation by typing the purchased license key when the trial version is launched or during installation.
- The LOESS¹ algorithm for spatial correction is now supported on the Macintosh operating system.

Known Bug Fixes

- A display refresh problem related to image cropping, which led to improper saving of images after cropping, has been corrected.
- A display refresh problem related to transformation has been corrected.
- The installer or application launch issue on 64-bit version of Macintosh operating system has been corrected to support analysis of 2.1M arrays.

Known Issues

- While NimbleScan v2.5 software is supported on multiple operating systems, Roche NimbleGen strongly recommends that all analysis be carried out on 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.
- Roche NimbleGen strongly recommends using underscore characters as delimiters in file names instead of periods. Using a period in a file name (other than as a prefix to a file type extension) may lead to TIFF images not being parsed correctly or not paired correctly for 2-color analysis by NimbleScan v2.5 software.

¹ Source code from Software for Locally-Weighted Regression (© 1989, 1992 by AT&T) has been incorporated into this product. The authors of this software are Cleveland, Grosse, and Shyu. This software is being provided “as is,” without any express or implied warranty. In particular, neither the authors nor AT&T make any representation or warranty of any kind concerning the merchantability of this software or its fitness for any particular purpose.



HIGH - DEFINITION GENOMICSSM



© 2008 Roche NimbleGen, Inc. All Rights Reserved.
10/08

Roche NimbleGen, Inc.
504 S. Rosa Road
Madison, WI 53719 USA

For life science research use only. Not for use in diagnostic procedures.
NIMBLEGEN is a trademark of Roche. Other brands or product names are trademarks of their respective holders.