

Chromosome Analysis Suite (ChAS) 2.1, 3.0 and 3.1. New Features and Release Notes

(For research use only. Not for use in diagnostic procedures.)

New Features/Improvements

ChAS 3.1 (compared to ChAS 3.0):

1. Edit Application Configuration now saves up to 3 unique hostnames.
2. Whole Genome View now persists graph settings based on array type.
3. Enables querying of ChAS DB for samples as well as segments.
4. Enables deletion of samples in ChAS DB
5. Segment Intersections View has 2 new columns (Publisher and Published)
6. User can choose to manually or automatically interact with ChAS DB.
7. Use in Report function is now available for PDF, DOCX, and text.
8. OncoScan CNV arrays are now supported in the analysis workflow.
9. Manual Recentering for OncoScan arrays
10. Enhancements to the Backup/Restore feature.
11. For somatic mutation processing of OncoScan FFPE arrays, MutScore is computed differently as of ChAS 3.1 and in the release after OncoScan Console 1.2. The new algorithm also corrects for sample-specific effects, and thereby reduces false positive calls, which were sample specific. As part of this change, a new somatic mutation threshold file is available for use.
12. Starting with Chas 3.1, the positive control sample in the OncoScan kit needs to be run with the new Control Analysis workflow.

CDL 3.1 includes the following new features/improvements:

1. CDL enables you to upload CHP files analyzed from any version of ChAS as long as the chp files were generated using analysis files from genome build Hg19. You may upload up to 500 files of varying array types into the ChAS database at a time.
2. CDL supports the following array types:
 - a. Genomewide SNP 6
 - b. CytoScan 750K
 - c. CytoScan HD
 - d. CytoScan Optima
 - e. OncoScan FFPE Assay
 - f. OncoScan_CNV
 - g. Cytogenetics 2.7M

ChAS 3.0 (compared to ChAS 2.1)

1. Addition of a database for storing and querying segment data for enhanced analysis. The database can be used locally by a single user or installed on a server/common workstation for multi-person use.
2. Histogram track displays contents of the database in the Detail View. In addition
3. A new Matching Segments view shows the current segments overlap of segments from the database.
4. Duo/Trio Mendelian Error check analysis for viewing sample relatedness and identifying chromosomes with higher Mendelian errors rates.
5. OncoScan CEL to OSCHP file analysis.
6. Copy Number Expression Overlap Report allows users to view their expression data analyzed in TAC 3.0 with copy number data in the same table and graphical view.
7. Sample Level annotation has been added to CHP files.
8. Automatic Dynamic Ranges can now be assigned to the Y axis of the Detail View graph.
9. Enhanced flexible in Reporting including: exporting in MS Word .docx format, paragraph style for the Segment Table, automatic report filename generation, and quick export button for all graphs and tables.
10. Normal Diploid Normalization Workflow for CytoScan arrays.
11. Addition of an Inheritance column for segment annotation.
12. New NetAffx Genomic Annotation File NA33.1 containing updated content from DGV, OMIM, and RefSeq. The genomic locations are from Hg19 and are the same as in NA32.3 and NA33.

ChAS 2.1 (compared to ChAS 2.0):

1. Whole Genome View.
2. OncoScan OSCHP file visualization including somatic mutation calls.
3. Auto-Dots graph type enables the transition from points to big dots graph type based on user-defined region.
4. New Analysis and Visualization Library files (NA33) for CytoScan arrays. Allows for simultaneous viewing of OncoScan and Cytoscan files.
5. Automatic Autosome Percentage LOH calculation based on user defined LOH filter setting.
6. New Column in Segment Table (Full Location) containing genomic coordinate in 1 column for ease of use in external websites.
7. Updates to the Analysis Workflow including export of probe level data for the entire sample.

8. New library file folder location outside any hidden folders.
9. Y axis coordinates no longer have fixed boundaries.
10. Median log₂ data values calculated for each CN Segment in both the Segments table and mouse over.
11. Disabled mosaic segment calls for the Y chromosome.

Changes/Updates

ChAS 3.1 (compared to ChAS 3.0):

1. ChAS 3.1 supports NetAffx version NA33 files for generation of CYCHP and OSCHP files for CytoScan and OncoScan arrays. There is no support for NA 32.3.
2. For Somatic Mutations to be displayed for OSCHP files, NA33 copy number annotation files and NA33.1 somatic mutations annotation files need to be downloaded.
3. ChAS 3.1 will install both ChAS 3.1 and CDL 3.1 applications.
4. ChAS 3.1 will upgrade from ChAS 2.0 and higher.
5. If a version of ChAS 1.x or earlier is installed, ChAS 3.1 does not support upgrading from these versions. Use the "Add/Remove Program" feature of the Windows operating system to completely uninstall the current version of ChAS and then re-run the ChAS 3.1 installer.
6. For all upgrades from ChAS 2.0 and higher, the ChAS 3.1 installer will automatically archive all previous ChAS analysis files into an archive folder in the ChAS library folder under C:\Affymetrix\ChAS\Library\Archived_ChAS_Lib_Files
7. After the installation/upgrade you need to download the latest library files from NetAffx from within ChAS for NA33 annotation files, or copy the contents of the Analysis Files folder file from the zip package available on the website.
8. The Allele Peaks calculation is now called Allele Difference for Cytoscan arrays.
9. ChAS 3.0/ChAS 3.1 uses a higher precision calculation algorithm that might result in small numerical differences when compared to previous versions of ChAS. The changes in results are smaller than those seen in technical replicates run through the same version of ChAS. For further details, please contact support@affymetrix.com
10. ChAS 3.1 has an additional algorithm enhancement for CytoScan arrays that helps reduce the number of small false positive segments.
11. The menu item Reports has been changed to Exports. The functionality remains the same

ChAS Database Loader (CDL) 3.1 (compared to CDL previous version):

1. CDL 3.1 supports the publishing of segments/annotations from the following array types: GenomeWideSNP 6.0, CytoScan Optima, CytoScan 750K, CytoScan HD, OncoScan FFPE Assay, OncoScan_CNV, and Cytogenetics 2.7M.
2. CDL 3.1 supports publishing of chp files analyzed using Hg19 library files only. Chp files analyzed using Hg18 library files (NetAffx version NA30 or lower) will not be published and should be reanalyzed using Hg19 library files.
3. File Level annotations (Sample Type, Phenotype, Interpretation, and Sample ID) can be appended to the chp file using a text tab delimited file.
4. Annotations (i.e. Call, Interpretation) and Parameter Settings (i.e. smoothing and joining) in the chpcar file will supersede those in the text file
5. The CDL application is now included as part of the ChAS 3.1 installer.

ChAS 3.0 (Compared to ChAS 2.1):

1. ChAS 3.0 supports NetAffx version NA33 files for generation of CYCHP and OSCHP files for CytoScan and OncoScan arrays. There is no support for NA 32.3.
2. For Somatic Mutations to be displayed for OSCHP files, NA33 copy number annotation files and NA33.1 somatic mutations annotation files need to be downloaded.
3. ChAS 3.0 will upgrade from ChAS 2.0 and higher.
4. If a version of ChAS 1.x or earlier is installed, ChAS 3.0 does not support upgrading from these versions. Use the "Add/Remove Program" feature of the Windows operating system to completely uninstall the current version of ChAS and then re-run the ChAS 3.0 installer.
5. For all upgrades from ChAS 2.0 and higher, the ChAS 3.0 installer will automatically archive all previous ChAS analysis files into an archive folder in the ChAS library folder under C:\Affymetrix\ChAS\Library\Archived_ChAS_Lib_Files
6. After the installation/upgrade you must download the latest library files from NetAffx within ChAS for NA33 annotation files, or copy the contents of the Analysis Files folder file from the zip package.
7. The Allele Peaks calculation is now called Allele Difference for Cytoscan arrays.
8. ChAS 3.0 uses a higher precision calculation algorithm that might result in small numerical differences when compared to previous versions of ChAS. The changes in results are smaller than those seen in technical replicates run through the same version of ChAS. For further details, please contact support@affymetrix.com

ChAS 2.1 (compared to ChAS 2.0):

1. ChAS 2.1 supports NetAffx version NA32.3 files for generation of CYCHP files for CytoScan arrays.
2. ChAS 2.1 supports NetAffx version NA33 to simultaneously view OncoScan and CytoScan array data.

3. For Somatic Mutations to be displayed for OSCHP files, NA33 annotation files need to be downloaded.
4. ChAS 2.1 will upgrade from ChAS 1.2.1 and higher.
5. If a version of ChAS 1.2 or earlier is installed, ChAS 2.1 does not support upgrading from these versions. Use the "Add/Remove Program" feature of the Windows operating system to completely uninstall the current version of ChAS and then re-run the ChAS 2.1 installer.
6. For all upgrades from ChAS 1.2.1 or above, the ChAS 2.1 installer will automatically copy appropriate Library files from the x:\Documents and Settings\All Users\Application Data\Affymetrix\ChAS\Library folder to the x:\Affymetrix\ChAS\Library folder. Library files to be copied are:
 - Array-specific files will be copied/updated to the new locationUser Profile and User Preference files will be copied from x:\...\Chromosome Analysis Suite\Users folder to the x:\...\ChAS\Users folder.
7. After the installation/upgrade you may download the latest library files from NetAffx from within ChAS for NA33 annotation files, or copy the contents of the Analysis Files folder file from the zip package.