

caArray 2.4.0.2 Release Note

Release Notes =====

Product: caArray
Version: 2.4.0.2
Date: February 2011

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Introduction -----

caArray is an open-source, web and programmatically accessible array data management system. caArray guides the annotation and exchange of array data using a federated model of local installations whose results are shareable across the cancer Biomedical Informatics Grid (caBIG). caArray furthers translational cancer research through acquisition, dissemination and aggregation of semantically interoperable array data to support subsequent analysis by tools and services on and off the Grid. As array technology advances and matures, caArray will extend its logical library of assay management.

- <https://array.nci.nih.gov/>

Release History -----

- caArray v2.4.0.2 – February 2011
- caArray v2.4.0.1 – January 2011
- caArray v2.4.0 – September 2010
- caArray v2.3.1 – February 2010
- caArray v2.3.0.1 – November 2009
- caArray v2.2.1 – May 2009
- caArray v2.2.0 – January 2009
- caArray v2.1.1 – October 2008
- caArray v2.1.0 – August 2008
- caArray v2.0.2 – May 2008
- caArray v2.0.1 – April 2008
- caArray v2.0.0 – February 2008

Anticipated Releases -----

- caArray v2.5.0 – Q2 2011 (new features)

Features and Defects Addressed in this Release -----

This release represents a feature release of the caArray 2 software.
Highlights of caArray 2.4.0 are:

- Parsers for several new data types:
- Agilent raw TXT for aCGH, expression and miRNA assays.
- Agilent GEML/xml array designs
- Nimblegen pair Report TXT (raw and normalized)
- Nimblegen NDF array designs
- Illumina Sample Probe Profile TXT
- Illumina genotyping processed data matrix TXT
- Illumina BGX/TXT array designs
- Affymetrix CEL and CHP in AGCC/Calvin formats in addition to the old GCOS formats
- Affymetrix CNCHP copy number data (CN4 and CN5)
- Copy Number data in a prescribed MAGE-TAB Data Matrix format.
For details about the parsing of these files, please refer to the chapter "Importing Data Files" in the caArray User's Guide.
- If there are array design files or data files already in the system that are "imported not parsed", and if there are new parsers available that allow those file types to now be parsed, the system provides the ability to reimport these files.

- If you have copy number data that is not in the caArray-prescribed Copy Number MAGE-TAB Data Matrix format, we provide a conversion utility. The conversion utility is found inside the cn2magnetab.jar file, and is invoked from the command line. Please see the README_copy_number_conversion.txt for more details on its operation.
- For experiments created from 2.4.0 onwards, the experiment public identifier will be composed of the string "EXP-" followed by a number. Already-existing experiment public identifiers will not be changed.

We gratefully acknowledge our collaborators at Yale and UPMC for their contribution of the Nimblegen parsers to the release.

The 2.4.0.2 release addresses the following issues with the 2.4.0 release:

- Fixes out-of-memory errors with the parsers.
- Fixes null pointer exception in the upgrade installer.
- Adds probe name validation to the data file parsers.
- Adds a security patch to Struts 2.1.x.
- Correctly validates Genepix GAL array designs with non-integer block header information.
- Fixes an error which causes copy number data to not parse.
- Addresses issues recently found with 2.4.0 installers.

Known Issues/Defects

See the GForge tracker for existing open defects, community requests, resolutions and feature requests. The following issues are highlighted.

<https://tracker.nci.nih.gov/browse/ARRAY>

- The total import job size (defined as sum of uncompressed file sizes) must be less than 3GB.
- A collaborator cannot see files in the "Uploaded" state even with read-write permissions to the experiment.
- If you are still using the Legacy API and your query results in >10,000 results, your transaction may time out. The workaround is to modify your query into multiple queries that return smaller result sets.
- The installer does not support configuring SSL support in JBoss.
- After installing a local copy of caArray, you must go to http://<IP_address_or_host_name>:<port>/caarray in order to test your installation. Even if you are running the browser on the same machine as your caArray installation, you cannot go to <http://localhost:<port>/caarray>.
- Image files referenced in a MAGE-TAB SDRF cannot be validated or imported.
- Multiple MAGE-TAB imports can result in duplicate persons in the database.
- Experiments with multiple array designs may cause copy number data to be Imported (not parsed). For more information, please go to <https://tracker.nci.nih.gov/browse/ARRAY-1811>.
- Data import can fail if experiment is associated with multiple array designs. For more information, please go to <https://tracker.nci.nih.gov/browse/ARRAY-1837>.
- In IE browser only, pane overflows "Download Selected Experiment Files" leaf in Download Data tab so buttons are obscured. For more information, please go to <https://tracker.nci.nih.gov/browse/ARRAY-1626>.
- GUI installer suddenly quits when illegal characters present in password fields.

Bug Reports, Feature Requests, And Support

Send email to ncicb@pop.nci.nih.gov to request technical support. To report a bug or request a new feature, please visit the Molecular Analysis Tools Knowledge Center resources at:

https://cabig-kc.nci.nih.gov/Molecular/KC/index.php/Main_Page

Existing requests and resolution may be viewed at the caArray issue tracker URL:

<https://tracker.nci.nih.gov/browse/ARRAY>

Documentation And Files

Please note: new wiki based technical guide and the installation guide can be found at following locations:

[caArray 2.4.0 Installation Guide](#)
[caArray 2.4.0 Technical Guide](#)
[caArray 2.4.0 API Guide](#) (unchanged for this release)

Links to all other documentation and files can be found at:

<https://cabig.nci.nih.gov/tools/caArray>

NCI CBIIT Web Pages

- The NCI Center for Bioinformatics, <http://ncicb.nci.nih.gov/>
- NCI CBIIT Application Support, <http://ncicb.nci.nih.gov/NCICB/support>
- NCI CBIIT Download Center, <http://ncicb.nci.nih.gov/download/>

Getting Started with the caArray API

To get started with the caArray Service API v1.0, please download the client libraries (caarray-client-external-v1_0.zip). Example client code for the Java API is available in java_api_client_examples_v1_0.zip. Example client code for the Grid API is available in grid_api_client_examples_v1_0.zip. Both the example packages contain a README.txt that will get you started.

Please note that applications with no authentication requirement can use the Java API or the Grid API. But applications needing authenticated access must use the Java API. We will add authentication support to the Grid API in a future release.

If, for some reason, you do not wish to use the new Service API yet, you can continue to use the legacy API, but you must upgrade to the latest version. To do this, please download the client libraries (caarray-client-legacy.zip).

FEEDBACK

Please post feedback on the Molecular Analysis Tools Knowledge Center forum: https://cabig-kc.nci.nih.gov/Molecular/KC/index.php/Main_Page