tranSMART 16.1 Release Notes

17 June 2016

These release notes apply to the tranSMART release 16.1. This release was formerly referred to as v1.2.5 prior to the change in the Foundation's release nomenclature in Fall 2015. The new nomenclature is in the form *<year>.<half>*, so that for example the 16.1 release occurs in the first half of 2016. The change is designed to avoid overlap and conflicts with versioning of key external tranSMART projects such as eTRIKS.

The tranSMART 16.1 release is focused primarily on quality and stability, and contains relatively little new functionality. Changes have been made to the development, release governance, and support processes to ensure that this release is of high quality and that all functionality works as advertised, and on both Oracle and Postgres. These processes will now be implemented as standard operating procedures for all subsequent tranSMART Foundation releases.

We have also initiated an Administrator's Mailing List to provide more timely information and get feedback for administrators of tranSMART Platform deployments. See below for details.

What the 16.1 release contains

Streamlined installation procedure

The installation documentation and procedures have been overhauled to make it easier for a person with basic UNIX skills to perform a new install and to install data. A typical install on a relatively fast network should now take 3-4 hours. See the wiki page [Install the current official release](#) for details.

Database

There are minor database schema changes in 16.1 as compared to v1.2.4:
- New column to support "change password" utility menu option (required change to support 16.1 new code)
- New column in de_gpl_info platform annotation table (required to support 16.1 ETL procedures)
- Some new tables and views for GWAS functionality
- Updated stored procedures/functions for data loading
- Moving a data formatting table from tm_cz to searchapp to avoid granting privileges to access the control zone for biomart_user. Used only by GWAS data upload pages.
- Some increases to column widths required by one or more of the public datasets

If upgrading from v1.2.4 to 16.1, the necessary database upgrade scripts are contained in the release package. See the file `database_upgrade_readme.txt` in the release package for details on how to apply the upgrades. These scripts are not needed for a new installation.

tranSMART App

The following visible changes have been made to the transmartApp UI. Numbers in parentheses refer to JIRA reports.

- There is a new button at the bottom right of every page, labelled **Report a Problem**. Clicking this button presents a page where you can post a bug report to the tranSMART Foundation's JIRA bug-tracking system. You should include as much information as possible, including your version number, platform, database, steps leading up to the problem, etc., so that engineers can reproduce the problem. Screen shots can be included using the Attach File. Be sure to include your name and email address before clicking **Submit**.
- The *Utilities->Contact Us* menu item sends an email to support@transmartfoundation.org, rather than to v12-testathon@transmartfoundation.org.
- Users can now change their own passwords using *Utilities->Change My Password.*
- Various issues with the Loading and Editing of Browse-page panels (tranSMART JIRA issues 5, 6, 7, 8, 9, 10, 15, 22, 73) are fixed - many of these were related to the fact that SOLR was not running when the reporter encountered the problem; others were known problems that were fixed. SOLR must be running for Browse functionality to work.
- Various Minor GUI issues were fixed
    - General search filter panel was out of place (14, 18)
    - Selecting subsets: (21) when the only selection criteria are 'excludes' this led to a strange state; the issue has been fixed; the user must select at least one include criteria and the excludes are computed against the union of the includes.
    - A problem with sorting Roles in the Admin panel (23) - fixed
    - Extra trailing whitespace in export of High Dimensional data (24)- fixed
    - When subsets are selected and Grid View, Export, or Advance Workflow follows directly with an intervening view of Summary Statistics the data is not fetched correctly (82) - fixed
- GWAS search does not work if SOLR is not running; code was added to detect the condition and display an appropriate error message.
- A *Status of Support Connections* panel was added to the Admin page (at the bottom of the item tabs on the left of the page) to report health of SOLR, R, and GWAVA - (33)
- Across Trials: NOTE Across Trials is still an experimental feature and not fully functional, nor fully integrated – it can be disabled in the configuration file. tranSMART 17.1 will provide enhanced Across Trials functionality. That said:
    - The displays of counts in the category hierarchy works and summary statistics was fixed and works (55)

- - Data loading of across trials data ([71](#)) is still in a primitive state, but working when the input data is properly configured.
  - The Genome Browser (Dalliance) menu item has been removed because it is an experimental add-on and not fully-supported functionality. For instructions on how to add it to your installation on an unsupported basis, see the instructions here.

ETL

The following changes have been made to ETL functionality:
- Various problems with test data were fixed in the data loading scripts.
- The [ICE](#) (Integrated Curation Environment) functionality has been fixed to work properly with Postgres as well as Oracle.
- [Transmart-batch](#) has been updated to work with almost all data types and multiple sets of the same datatype per study.

Known issues and bugs deferred to 16.2

Several issues that were raised in the course of 16.1 release have been deferred to the 16.2 release, due in the second half of 2016. In particular:
- LDAP ([13](#)) not fixed, or tested; we need a champion – someone who needs the fixes, can test them, and can contribute any needed changes.
- GWAS functionality issues ([19](#), [46](#), [76](#), [93](#), [101](#))
  - Data related issues - we do not have a means of loading a definitive test set (nor is it clear that one exists) - a single specific dataset is available (Magic) this is still an open issue
  - The *Upload GWAS* menu item (formerly *Upload Data*) does not work at this time, so this option has been removed, to be fixed in 16.2
- Grid View column headings ([57](#)) were not changed to include full path names (an experimental version with more inclusive column names proved to be unworkable). Since the mouse-over pop-up shows the entire path and can be used to disambiguate column headings this was assumed to be sufficient; in addition to this, the columns in exported data are labeled with the full path.
- The *Analysis Jobs* page does not work for all types of advanced workflows ([62](#), [91](#)). It does work with particular advanced workflows (aCGH and RNA-Seq) but the page is disabled by default. There is a configuration parameter (ui.tabs.datasetExplorer.analysisJobs.show) to enable it.
- Large datasets cause export function to crash ([TRANSREL-66](#)). This bug occurs on data sets that have a large tree size (not because of a large number of subjects). A fix has been contributed by Pfizer but could not be integrated in time for this release. The fix will be included as part of the JIRA backlog for 16.2.
- Advanced Workflow: MetaCore Enrichment Analysis fails ([TRANSREL-63](#)).
- qPCR miRNA: no Heatmap generated by adding a mirID ([TRANSREL-79](#)).
- Error when running a workflow using 2 gene expression platforms in a study ([TRANSREL-103](#))

- Search not working on browse tab ([TRANSREL-106](#))
- Advanced Workflow 'IC50' is unresponsive ([TRANSREL-67](#))

Administrators Mailing List

We have created a mailing list for administrators of tranSMART deployments. We will use this list to communicate directly with administrators to provide updates, important information on current and upcoming releases of the platform and to solicit suggestions for future versions.

Please use the link below to add yourself to the mailing list:
[ADMIN LIST SIGN UP](#)

We similarly have a list for developers:
[DEVELOPERS LIST SIGN UP](#)

To make suggestions, ask questions or offer comments, you can also use this link:
[SUGGESTIONS/QUESTIONS/COMMENTS](#)

Appendix A - Installing the Genome Browser

Background. The Genome Browser was included in the previous release as an experimental development effort that is offered on an "as is basis". It is a contribution to the tranSMART Foundation open source from theHyve. By default, the Genome Browse is excluded from this release. However, by setting the code configuration and recompiling the transmartApp, the Genome Browse can be added to a custom configuration of transmartApp. Herein, instructions for making those changes.

To add it the Genome Browser in, you have to build the tranSMART web application, transmartApp, from the source code with slightly modified `BuildConfig.groovy`. In that configuration file, you uncomment two code blocks demarcated with `// -- Genome Browser plugin --` line. Or add the corresponding lines if your version for some reasons does not have them commented out. See [line 52](#) and [line 154](#) of the release version of the code for BuildConfig.groovy.

1. At line 52, your `BuildConfig.groovy` has to have The Hyve's maven repository included:
   `` `mavenRepo "https://repo.thehyve.nl/content/repositories/public/"` ``
2. At line 154, the Genome Browser consists actually from the two plugins. They have to be included into plugins section of your `BuildConfig.groovy` file:
   ```
   runtime ':dalliance-plugin:unknown'
   runtime ':transmart-mydas:unknown''
   ```

NOTE: Replace '*unknown*' (the version) with the version of choice. At the moment of writing this document `0.2-SNAPSHOT` is the last version of the Dalliance plugin and `0.1-SNAPSHOT` is the last version of the MyDAS plugin.

Once these updates are done, recompile to the war file, **transmar.war**, which you can use to replace the one that you originally installed. Or (alternatively) compile and run, with grails, in development mode.