

# tranSMART 19.0 Full Feature List

## A. Login

By default, login uses usernames and encrypted passwords stored in the database.

Usernames have associated roles.

Administration by default is defined for user 'admin'

User guest can be defined to login automatically with basic access to unrestricted studies.

## B. Browse Tab

The Browse Tab is the usual first page (landing page) displayed.

This page holds metadata about known studies, organised under "Programs".

Studies can have associated Assays, Analyses, Folders and Files.

Studies are linked by STUDY\_ID to studies loaded in the Analyze tab.

### Search Box

Various searches are available in the text box. The pull-down list defines the search category, listed in alphabetical order. The categories are defined in the searchapp.search\_keywords table use dto generate the list in the UI automatically.

Category	Description
All	All fields
FreeText	Text fields e.g. Description
Country	Country in a Browse Study definition
Disease	Disease are in a Browse Study definition
File_type	File type stored in a Browse folder
Gene	Gene of interest in a Browse Assay
Metabolite	Metabolite of interest in a Browse Assay
Mirna	MicroRNA of interest in a Browse Assay
Organism	Organism defined for a Browse Study
Protein	Protein of interest in a Browse Assay

### Active Filters Box

Searched by controlled vocabularies of Browse Tab attributes offering a choice of all defined values.

Filter	Description
Program Therapeutic Domain	
Study Phase	
Study Objective	
Study Design	
Study Biomarker Type	
Study Access Type	
Assay Type of Biomarkers	
Assay Measurement Type	
Assay Technology	
Assay Vendor	

Assay Platform Name	
Analysis Measurement Type	
Analysis Technology	
Analysis Vendor	
Analysis Platform Name	
File Type	

## Program Explorer

The nodes should be expandable and closable.

If loaded, Private Studies may be restricted to Admin users. The usual example is the Cell-Line Use Case from the TraIT project.

## C. Analyze Tab

The Analyze tab is the main working area in tranSMART.

### Search Box

### Active Filters Box

### Navigate Terms

## Comparison

Builds queries in one or two subsets to explore a cohort or to compare two cohorts.

Any node from the Navigate Terms tree can be dragged to either subset.

A query must have at least one "Include" criterion to identify the study of interest.

### Categorical nodes

A single string leaf node (e.g. Demographics: Female) will select those individuals with the term defined

Additional strings can be dragged to the same subquery to select any of the values as matching.

A folder node will include all individuals with that node defined

### Numeric nodes

Numeric nodes will offer a choice of value ranges or all nodes with a value defined.

### High-dimensional nodes

High-dimensional nodes will offer all nodes with a value defined or allow a search for a single gene and a range of expression values.

## Summary Statistics

A default set of i2b2 values is displayed: Age, Sex/Gender, Race.

Any other nodes used in the query definition will also be displayed.

Further nodes can be dragged into the summary statistics panel, including high-dimensional nodes.

## Grid View

A default set of i2b2 values is displayed: Age, Sex/Gender, Race plus patient ID, sample ID, subset

Additional nodes can be dragged from the Navigate Terms tree.

Column headings are kept unique. If two columns have the same last-level value in their paths further levels are added until the displayed column name is unique.

## Advanced Workflows

### aCGH Survival Analysis

**Box Plot with ANOVA**  
**Correlation Analysis**  
**Frequency Plot for aCGH**  
**Group Test for aCGH**  
**heatmap**  
**Hierarchical Clustering**  
**IC50**  
**K-Means Clustering**  
**Line Graph**  
**Logistic Regression**  
**Marker Selection**  
**PCA**  
**Scatter Plot with Linear Regression**  
**Survival Analysis**  
**Table with Fisher Test**  
**Waterfall**  
**GWAS Plink**  
**SmartR**  
**Boxplot Workflow**  
**Correlation Workflow**  
**Heatmap Workflow**  
**IpaConnector Workflow**  
**Linegraph Workflow**  
**PatientMapper Workflow**  
**VolcanoPlot Workflow**  
**Data Export**  
**Export Jobs**  
**Analysis Jobs**  
**Workspace**  
**Sample Details**  
**Galaxy Export**  
**Metacore Enrichment Analysis**  
**Genome Browser**  
**Image Viewer**  
**D. Sample Explorer**

E. Gene Signature/Lists

F. GWAS

G. Upload data

H. Admin

**H.1 Access Log**

**H.2 Groups**

**H.3 Users**

**H.4 Access Control**

**H.5 Study**

**H.6 Secure Object Paths**

**H.7 Roles**

**H.8 Requestmap Setup**

**H.9 Package and Configuration**

**H.9.1 Configuration Detail**

**H.9.2 Build Information**

**H.9.3 Status of Support Connections**

**XNAT Importer**

I. Utilities Menu

Help

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user Profile

Change My Password

Log Out