Data Query Form
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2021-04-28-0915

Introduction

This document gives simple instructions for using the Data Query Form -- the Query Form is part of the MBatch Omic Browser combined GUI, which allows the user to sort and select datasets. This document will provide minimal, but some, descriptions of elements such as Platforms and data descriptions. It also includes instructions for accessing Standardized Data from the DAPIR (Data API for R) R package.

Links

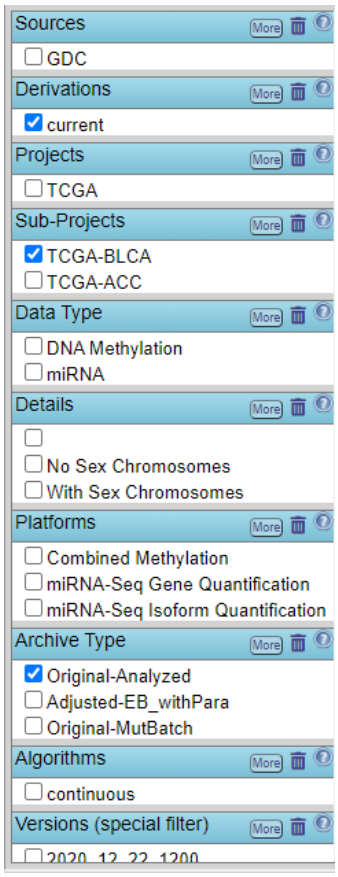
DAPIR on GitHub
https://github.com/MD-Anderson-Bioinformatics/DataAPI

BCB on GitHub (source code and additional documentation)
https://github.com/MD-Anderson-Bioinformatics/

BCB on Docker Hub (Docker images)
https://hub.docker.com/u/mdabcb

Categories and Category Options

The Data Query Form has several categories. Most categories work the same for selecting and filtering data---Versions is the one exception. For the regular categories, we emulate the GDC Portal search algorithm with selections within categories operating as OR and between categories as AND. Categories options are narrowed based on selections from other categories.



DSC P-Value

This is only available in the MBatch Omic Browser Query Form when DSC values are selected. DSC P-Values are not corrected for multiple testing. The DSC P-Value Category lists common p-value cut-offs.

Min DSC Value

This is only available in the MBatch Omic Browser Query Form when DSC values are selected. The Min DSC Value indicates the DSC of the results should be less than or equal to this value. Empty means accept any value.

Max DSC Value

This is only available in the MBatch Omic Browser Query Form when DSC values are selected. The Max DSC Value indicates the DSC of the results should be less than or equal to this value. Empty means accept any value.

Sources

The Source Category lists the source of the data, such as the GDC or PanCan Study Group.

Derivations

The Derivations Category lists the derivation of data within a Source, such as, for the GDC, "current" or "legacy" data.

Projects

The Projects Category lists the higher-level project, like TCGA or TARGET, for the dataset.

Sub-Projects

The Sub-Projects Category lists what is generally the disease (cancer type) being processed. Some Projects do not divide data by disease, hence the more generic name for this Category.

Data Type

The Data Type Category divides the datasets into general type of data. Some names have been converted to generic version for usability.

Details

The Details Category allows filtering on detailed options for datasets, in particular the Methylation data option to include (wXY) or exclude (noXY) sex chromosomes.

Platforms

The Platforms Category lists the available platforms. We have standardized names when possible, but note differences like the Legacy GDC data having "Illumina Human Methylation 27" and "Illumina Human Methylation 450" compared to the Current GDC data using "Methylation Combined". (The GDC converts all methylation files to a single platform.)

Archive Type

The Archive Type Category lists the variation of data in the dataset--for the GDC, this is "standardized". Other datasets may provide other Archive Type Categories.

Algorithms

The Algorithms Category divides the data into "continuous", amenable to most standard statistical processing, and "discrete", generally sparse matrices and not amenable to many statistical methods.

Versions (special filter)

The Versions Category are the timestamps for when the data was acquired by the Query Form. This Category works different from the rest. By default, the Query Form will show the newest version of each dataset. Selecting one or more Versions, limits the results to that particular version. Note that in Standardized Data, each Version may only contain a single dataset.

Files

The Files Category lists the available types of files found within each dataset archive. You can use this to look for data with batch information or mutation files.

File Formats

There are five files provided within datasets.

matrix_data.tsv

The Standardized Data "Data Matrix" format is a tab delimited file. The first line of the file begins with a tab and contains sample identifiers. For Standardized Data, the sample identifiers are bar codes. Each subsequent row begins with a Feature Identifier and is followed by numeric data. Feature Identifiers are specific to the platform but can be values such as Hugo Gene ids, probe ids, or microRNA identifiers.

This extract from the Data Matrix format shows four sample ids and five feature ids. Note that the first blank cell indicates the starting tab for the sample identifiers line. The features (left-most column) can be any set of unique strings. For proper processing, the rows and columns should be sorted.

	TCGA-OR-A5J2-01A-21-A39K-20	TCGA-OR-A5J3-01A-21-A39K-20	TCGA-OR-A
14-3-3_beta-R-V	0.211404	-0.14778	0.220188
14-3-3_epsilon-M-C	-0.03151	-0.12861	-0.0762
14-3-3_zeta-R-V	-0.01203	0.032791	-0.34541
4E-BP1-R-V	0.589134	0.365167	0.297887

batches.tsv

The Standardized Data Batch File format is also a tab delimited file. The first line of the file contains the sample id column id and batch type identifiers, none of which should contain spaces. The first entry should be the "Sample" column, which contains sample ids. Some non-batch types may include type and patient entries for cross-reference purposes.

Sample	Type	BatchId	PlateId	ShipDate	TSS
TCGA-OR-A5J2-01A-21-A39K-20	1	304	A39K	5/7/2014	OR - University of Michigan
TCGA-OR-A5J3-01A-21-A39K-20	1	304	A39K	5/7/2014	OR - University of Michigan
TCGA-OR-A5J6-01A-41-A39K-20	1	304	A39K	5/7/2014	OR - University of Michigan
TCGA-OR-A5J7-01A-21-A39K-20	1	304	A39K	5/7/2014	OR - University of Michigan

clinical.tsv

Clinical TSV files follow the same format as batches.tsv with different column headers rather than batch information.

index.json

This is a simple JSON file describing each Category option that defines this dataset:

{

"source": "GDC",

"variant": "current",

"project": "TCGA",

"subProject": "TCGA-CHOL",

"category": "Copy Number Segment",

"platform": "DNAcopy",

"data": "standardized",

"algorithm": "discrete",

"details": "",

"version": "2020_01_31_0845"

}

mutations.tsv

The mutations.tsv file is a tab delimited file based on the Mutation MAF files with column headers standardized. Headers should be self-evident to users familiar with mutation datasets.

URLs and R Package Utilities

Copy Query String for R Package

Clicking the "Copy Query String for R Package" button copies a string to the clipboard based on the data query selected in the GUI. For example, this string gives current TCGA-ACC data from the 2020_01_31_0845 data run.

{\"mFiles\":[\"batches.tsv\"],\"mSources\":[],\"mVariants\":[\"current\"],\"mProjects\":[],\"mSubprojects\":[\"T
ACC\"],\"mCategories\":[],\"mPlatforms\":[],\"mData\":[],\"mAlgorithms\":[],\"mDetails\":[],\"mVersions\":[\"2

This string is used in the DAPIR R Package function checkDownloadedDataStatus to create and update a local copy of Standardized Data.

Copy Bookmark-able URL

Clicking the "Copy Bookmark-able URL" button copies a string to the clipboard based on the data query selected in the GUI. The string is a URL that links to the selected query defined in the GUI.

DAPIR R Package

The DataAPI project page (https://github.com/MD-Anderson-Bioinformatics/DataAPI) on GitHub gives instructions for installing the DAPIR R package.

And example of downloading data using the Query String is given below.

```
# TCGA-ACC data -- pasted the "Copy Query String for R Package" button into queryOne <- paste("")

queryOne <- paste("{\"mFiles\":[\"batches.tsv\"],\"mSources\":[],\"mVariants\":[\"current\"],",

"\"mProjects\":[],\"mSubprojects\":[\"TCGA-ACC\"],\"mCategories\":[],",

"\"mPlatforms\":[],\"mData\":[],\"mAlgorithms\":[],\"mDetails\":[],",

"\"mVersions\":[]}", sep="")

# temp directory

datasetDir <- file.path(tempdir(), "DAPIR")

print(datasetDir)

dir.create(datasetDir, showWarnings=FALSE, recursive=TRUE)
```

```
# get data status
results <- checkDownloadedDataStatus(queryOne, datasetDir)
print(results)
# Download initial datasets
newDatasets <- results$NEW
downloadData(newDatasets, datasetDir)
```