Filter W4M data by sample class

Purpose of the w4mclassfilter package

The purpose of the w4mclassfilter R package is to provide the computational back-end of a Galaxy tool for inclusion in Workflow4Metabolomics (W4M).

Galaxy tools are file-oriented; because of this, the w4mclassfilter::w4m_filter_by_sample_class method reads from and writes to files. General-purpose R packages usually use data structures in memory for their input and output, which may mean that this R package is not generally useful outside of the context of Galaxy.

The w4mclassfilter::w4m_filter_imputation function is the default imputation method used by w4m_filter_by_sample_class; if other methods are to be used in the Galaxy tool, they might best be incorporated into the w4mclassfilter R package, although they could be implemented in another R package to be used by the Galaxy tool.

How the w4m filter by sample class function is used

A Galaxy tool wrapper invokes w4m_filter_by_sample_class. For exploratory or debugging purposes, the package may be installed loaded into R and help may then be obtained with the following command:

?w4mclassfilter::w4m_filter_by_sample_class

W4M uses the XCMS and CAMERA packages to preprocess GC-MS or LC-MS data, producing three files (which are documented in detail on the Workflow4Metabolomics (W4M) web site). In summary:

- 1. sampleMetadata.tsv: a tab-separated file with metadata for the samples, one line per sample
- One column of this file indicates the *class* of the sample.
- It is the class that is used by this function to determine whether to include the sample in, or exclude the sample from, further analysis.
- 2. variableMetadata.tsv: a tab-separated file with metadata for the features detected, one line per feature
- A feature is a location in the two dimensional space defined by the GC-MS or LC-MS data set, which corresponds to a compound or a group of compounds.
- One dimension is the mass-to-charge ratio, m/z.
- The other dimension is the retention time, i.e., how long until the solvent gradient eluted the compound(s) from the column.
- 3. dataMatrix.tsv: a tab separated file with the MS intensities for each sample for each feature:
- There is one column per sample.
- There is one row per feature.
- If a feature is missing for a sample, the intensity value is NA.
- For numerical reasons, intenisities may be negative, but this has no meaning in the real world.

By default, the w4m_filter_by_sample_class function imputes negative and NA intensity values as zero using the w4m filter imputation function.

When w4m_filter_by_sample_class is invoked, an array of class names is supplied in the classes argument. If the include argument is true, then only samples whose class column in sampleMetadata.tsv will be included in the output; by contrast, if the include argument is false, then only samples whose class column in sampleMetadata.tsv will be excluded from the output.

Even if no rows or columns of the dataMatrix.tsv input have zero variance, there is the possibility that eliminating samples may result in some rows or columns having zero variance, adversely impacting downstream statistical analysis. Consequently, w4m_filter_by_sample_class eliminates these rows or columns and the corresponding rows from sampleMetadata.tsv and variableMetadata.tsv.

When w4m_filter_by_sample_class completes running, it writes out updated sampleMetadata.tsv, variableMetadata.tsv, and dataMatrix.tsv files. The paths to the output files must be different from the paths to the input files.

As of v0.98.3, w4m_filter_by_sample_class can interface not only with files but also with data structures; see release note below.

New in release v0.98.2 - support regular expressions

Beginning with v0.98.2, w4mclassfilter supports use of R regular expression patterns to select class-names.

The R base::grep1 function (at the core of this functionality) uses POSIX 1003.2 standard regular expressions, which allow precise pattern-matching and are exhaustively defined at: http://pubs.opengroup.org/onlinepubs/9699919799/basedefs/V1 chap09.html

However, only a few basic building blocks of regular expressions need to be mastered for most cases:

- ^ matches the beginning of a class-name
- \$ matches the end of a class-name
- . outside of square brackets matches a single character
- * matches character specified immediately before zero or more times
- square brackets specify a set of characters to be matched.

Within square brackets

- ^ as the first character specifies that the list of characters are those that should * not * be matched.
- - is used to specify ranges of characters

Caveat: The tool wrapper uses the comma (,) to split a list of sample-class names, so commas may not be used within regular expressions for this tool

First Example: Consider a field of class-names consisting of marq3, marq6, marq9, marq12, front3, front6, front9, front12

- The regular expression ^front [0-9] [0-9] *\$ will match the same sample-classes as front3, front6, front9, front12
- The regular expression ^[a-z][a-z]3\$ will match the same sample-classes as front3,marq3
- The regular expression [a-z][a-z]12 will match the same sample-classes as front12,marq12
- The regular expression ^[a-z] [a-z] [0-9] will match the same sample-classes as front3, front6, front9, marq3, marq6

Second Example: Consider these regular expression patterns as possible matches to a sample-class name 'AB0123':

- ^[A-Z][A-Z][0-9][0-9]*\$ MATCHES **^AB0123\$**
- ^[A-Z][A-Z]*[0-9][0-9]*\$ MATCHES **^AB0123\$**
- ^[A-Z][0-9]*- MATCHES **^A** B0123\$ (The first character is a letter, * can specify zero characters, and end of line did not need to be matched.)
- ^[A-Z][A-Z][0-9] MATCHES **^ABO** 123\$ (The first two characters are letters aind the third is a digit.)
- [A-Z][A-Z]*[0-9][0-9] NO MATCH (The name does not end with the pattern [A-Z][0-9][0-9]\$, i.e., it ends with four digits, not two.)
- ^[A-Z][0-9]*\$ NO MATCH (The pattern specifies that second character and all those that follow, if present, must be digits.)

New in release v0.98.3 - more flexible input and output

R package v0.98.3 - add support for env, list, data.frame, and matrix I/O * To support XCMS outside the context of Galaxy, w4m_filter_by_sample_class now supports input from and output to data structures as follows:

Inputs:

- 1. dataMatrix_in
- if a string, treat as a file path (i.e., same as in previous releases)
- else if an env or list, read dataMatrix_in\$dataMatrix
- else if a data.frame, use as.matrix(dataMatrix in)
- else if a matrix, use directly
- else error
- 2. sampleMetadata_in
- if a string, treat as a file path (i.e., same as in previous releases)
- else if an env or list, read sampleMetadata_in\$sampleMetadata
- else if a data.frame, use directly
- else error
- 3. variableMetadata_in
- if a string, treat as a file path (i.e., same as in previous releases)
- else if an env or list, read sampleMetadata_in\$sampleMetadata
- else if a data.frame, use directly
- else error

Outputs:

- 1. dataMatrix_out
- if a string, treat as a file path (i.e., same as in previous releases)
- else if an env or list, write dataMatrix_out\$dataMatrix
- else error
- 2. sampleMetadata_out
- if a string, treat as a file path (i.e., same as in previous releases)
- else if an env or list, write sampleMetadata_out\$sampleMetadata
- else error
- $3.\ {\tt variableMetadata_out}$
- if a string, treat as a file path (i.e., same as in previous releases)
- else if an env or list, write sampleMetadata_out\$sampleMetadata
- else error