Creating MAGE-TAB files using mtcreator

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1 Abstract

This package contains a program that supports users in creating files to comply the MIAME-standart compliant format MAGE-TAB. The format enables the user to upload his high dimensional and related metadata to the public database Array Express. The upload is required before you publish the data or results that has been generated using the data.

2 Introduction

This vignette was created to give an introduction to the usage of the package mtcreator. It gives you exact information what has to be done to and how to achieve the aim successfully. In chapter 5 an example workflow with a publicly available dataset that can be received from bioconductor is shown.

3 Initial state

Before you run the program you should have finished your calculations and preprocessing steps. The program supports just the final step of converting your data into the required format, so you can upload it manually into the public database.

4 Usage of the program

4.1 Outputfolder

At first the program asks you to name the path to an existing outputfolder, where the programs output is placed.

4.2 Raw data

In the second step the program asks you to name the path to the raw data. If you prefer to add it into the outputfolder manually at a later point of time you can do that as well. It is even possible not to provide your rawdata, but it is strongly recommended.

4.3 Processed data

The circumstances for the processed data are similar to the raw data ones, but it is also strongly recommended to provide the processed data to each rawdata file.

4.4 IDF file

In this step the IDF file is created. It contains mainly metadata like the experimenters name among others. The program gathers all information from the output of the `experimentData()` command and converts it into the MAGE-TAB format. The output of this step is written into the IDF file. As usually not all information is contain in the data it is strongly recommended to complete the file manually.

4.5 SRDF file

In this step the SRDF file is created. It contains information about the relationships of the files, that means how the belong together and how they should be interpreted.

5 Example

In this section an example usage of the package is shown. First you have to load the expressionset that we use for demonstration purposes:

```
> source("http://bioconductor.org/biocLite.R")
> biocLite("affydata")
> library(affydata)
> data(Dilution)
```

Then you start the programm with:

```
> mtcreator(rawbool = FALSE, expressionset = Dilution, output_path = "./output3")

No rawdata was given -> has to be added manually.
 Please check the output files in ./output3 for mistakes and missing values!
```

The following parameters can be configurated:

Parameter	Description
interact	Logical. Use interactive mode or command line call.
rawbool	Logical. Use rawdata or not.
rawlocation	The location of the raw data.
expressionset	The name of the expressionset in your workspace.
output _path	Path from current location to the folder where the programt's output will be placed.

6 The interactive mode

Usually the step of converting data into the MAGE-TAB format is not done very often. Thus this package provides an interactive mode that asks for every detail particularly and gives a short explaination to the parameter, so the user does not need to work in into this package. As interactive mode is almost self-explaining, this vignette provides just the initial call:

```
mtcreator(interact=TRUE, expressionset = Dilution)
```

7 What mtcreator does not do

It is mandatory that you check the output of this package manually. It is strongly recommended, that you complete the files by adding missing value and give as much information as possible. This package is not able to create missing values. Data that is not given are not generated by this package. It just helps you to create the correct files and fills in given information. The package contains an predefined file (inst/idf.txt) that should give you an idea of how the idf file should look like. For further information please check the overview of the MAGE-TAB format.