

TestWorkflow × A edgeR diff exp × T GSE59364_DC_all.csv × C ColumnGroupContainer × T TableC.csv ×

```
Analysis edgeR diff exp
{
  import table GSE59364_DC_all.csv
  subset rows GSE59364_DC_all.csv when true: $(gene) != "Total" -> filtered
  edgeR counts= filtered model: ~ 0 + LPS
    comparing LPS=YES - LPS=NO -> Results (normalize with tagwise dispersion )
  join ( filtered, Results ) by group ID -> MergedResults
  subset rows MergedResults when true: ($(FDR) < 0.01) & ($(logFC) > 2 | $(logFC) < -2) -> 1% FDR
  build heatmap with 1% FDR select data by one or more group LPS=YES, group LPS=NO -> plot [annotate with these groups: LPS
  scale values: scale by row
  cluster columns: false cluster rows: true
]
Multiplot -> PreviewHeatmap [ 1 cols x 1 rows ] Hide preview
plot
```

render plot as PDF named "heatmap.pdf" ... rendering

+ A edgeR diff exp T GSE59364_DC_all.csv C ColumnGroupContainer

MetaR Documentation Booklet

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Credits

We thank the developers of the Meta Programming System, who have developed MPS since the early 2000. MetaR would not have been possible without them.

MPS Project leaders, in chronological order: Sergey Dmitriev, Igor Alshannikov, Konstantin Solomatov and Alexander Shatalin. **Current team members:** Alexander Shatalin, Fedor Isakov, Mihail Muhin, Michael Vlassiev, Václav Pech, Simon Alperovich, Daniil Elovkov, Victor Matchenko, Artem Tikhomirov, Mihail Buryakov and Alexey Pyshkin. **Earlier members of the MPS team:** Evgeny Gryaznov, Timur Abishev, Julia Beliaeva, Cyril Konopko, Ilya Lintsbah, Gleb Leonov, Evgeny Kurbatsky, Sergey Sinchuk, Timur Zambalayev, Maxim Mazin, Vadim Gurov, Evgeny Geraschenko, Darja Chembrovskaya, Vyacheslav Lukianov and Alexander Anisimov. **And these external contributors:** Sascha Lisson, Thiago Tonelli Bartolomei and Alexander Eliseyev.

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1 — Introduction

Background

1.1

The MetaR software <http://MetaR.campagnelab.org> is an example of a new kind of interactive tool for data analysis. It was developed by the Campagne laboratory using the Meta Programming System (MPS) (see <http://www.jetbrains.com/mps> [Dmitriev:2004]). MPS is a mature Language Workbench that makes it relatively easy to create new languages and tools to help users of these languages [[campagne2014mps](#)].

Intended audience

1.2

This booklet is designed to teach how to use MetaR for data analysis. In the first chapters, we will assume that you have no prior scripting or programming experience, but will expect you to know how to use a computer.

Key Concepts

High-level data abstractions

MetaR is designed to make it easier to conduct data analysis. To achieve this goal, and in contrast to programming languages such as the R language, Julia or Python, that are often low-level and require good programming skills, MetaR offers high-level data abstractions and provides assistance in manipulating data. High-level abstractions used in MetaR analyses include the following concepts:

1. Tables, Columns, Column Groups and Group usages,
2. Analyses
3. Plot
4. Model

These high-level abstractions will be explained in the following chapters.

R program generation

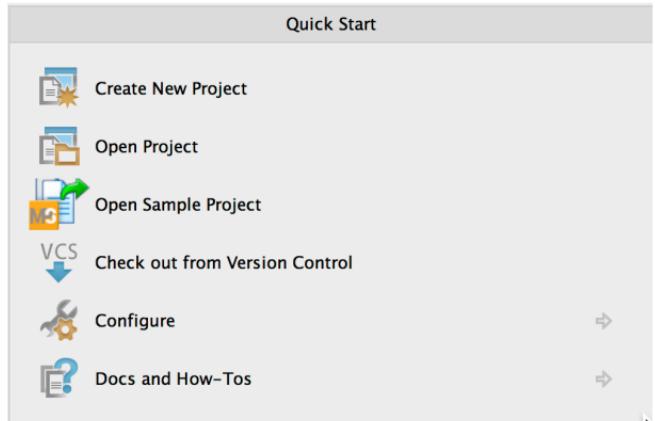
Analyses developed with MetaR are transformed into R programs when the user needs to execute them. MetaR is tightly integrated with MPS to make it seamless to run analyses without prior knowledge of the R language.

 Note that while most users can use MetaR without knowledge of the R language, all users will need to install the R language in order to execute MetaR analyses.

Composable language

MetaR is built as an MPS language. In contrast to languages built with compiler technology, MPS languages are composable. Briefly, language composition is the ability to compose, or combine, two or more languages. This ability is particularly useful to extend MetaR. It is possible to define micro-languages, made of one or two statement types, that when composed with MetaR make it possible to customize MetaR for specific application domains. The EdgeR language provides an example of composition, where an R/Bioconductor package called EdgeR has been integrated with MetaR and exposes a new kind of statement

Figure 1.1: The Quick Start menu. This menu is displayed when you first open MPS, or when you have no project currently open in MPS. The first item in the menu is used to create a new project.



to perform calls of differential expression. See Chapter 4 to learn more about language composition in MetaR.

Solutions and Models

1.4

Developing an analysis with MetaR is done by creating nodes of the MetaR concepts in MPS models. Models exist in MPS solutions. To learn how to create an MPS solution, read the preview of the MPS language workbench available at [http://campagnelab.org/publications/our-books/\[campagne2014mps\]](http://campagnelab.org/publications/our-books/[campagne2014mps]), or watch the beginning of the MetaR training video at <http://campagnelab.org/software/metar/video-tutorials/>. Figures 1.1-1.2 provide a brief walk-through of the steps you should follow to create a project and solution. After the project open, open the project tab(see [campagne2014mps]) and right-click on the solution name. Import the metaR devkit and create a model.

You can create as many models as you need to store your analyses. In the following chapter, we assume that you have created a solution and at least one model in this solution.

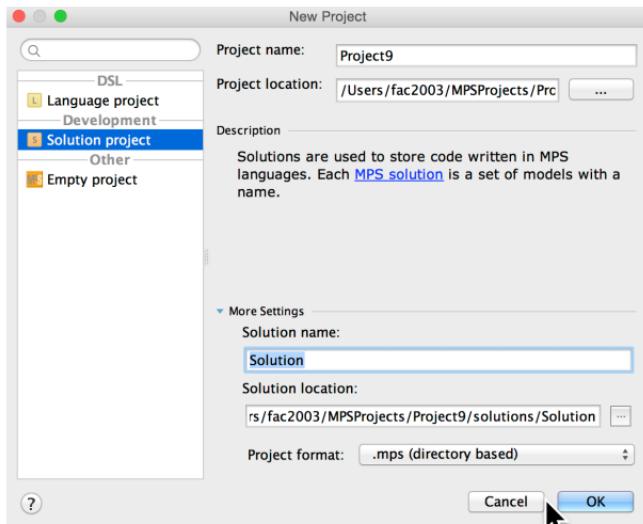


Figure 1.2: The New Project Dialog. Use this dialog to create a new Solution. Solutions are used to store models and express your solutions to specific analysis problems. Select the “Solution Project” project type on the left panel, name the project, and name the solution you wish to create.

Overview
Create a Table
Column Groups Container
Column Groups
Column Group Usage
Example Column Group Container
Column Groups from a Table
Table Viewer Tool

2 — Tables

Overview

2.1

Before you start an analysis, you will need to define Table nodes that represent the data files needed in the analysis. MetaR explicitly models files that contain tables of data. This is done so that you can easily refer to these tables, without having to remember where the original file is located on your computer.

In this Chapter, you will learn how to

1. define a MetaR table,
2. adjust the types of the columns of the data described in the file,
3. annotate a table with groups,
4. link groups in column group usage.

Create a Table

2.2

To create a Table, right-click on a model in the project tab and select `right-click` `> New > o.c.metar.tables > Table`. This will create an empty table, as shown in Figure 2.1. Tables have a name, a `pathToResolve` attribute and a list of

columns. The following paragraphs describe these attributes.

name

The table name is set automatically from the path when you use the file selection button. You can change the name to match your analysis needs and make it easier to remember what is in the table.

File Path (pathToResolve)

This attribute contains a path to the TSV file that you wish to analyze. The path may contain references to path variables that will be automatically resolved before MetaR attempts to load table information from the path. Path variable references can be written as `$a.b.c/data/file.tsv`. Such a reference will require you to define the `a.b.c` path variable name and associate it with a value on each machine where the table will be used. You can define path variables with the Preferences/Settings MPS menu (`MPS > Preferences > PathVariables` on Mac, `MPS > Settings > PathVariables` on PC).

Columns

Columns is an attribute that presents the list of columns identified in the TSV file. Each column has a name, a type, and may be annotated with a set of column groups (see Section 2.4 for details about column groups). MetaR supports the following column types, which map to the R data types:

1. **Numeric.** Any number. Technically, can be a floating number or an integer.
2. **String.** A string of characters.
3. **Boolean.** A type that can only have two values: `true` or `false`.
4. **Category.** A type that can take only a limited number of values (e.g., `{RED, GREEN, BLUE}` would be a category with these values, (RED, GREEN and BLUE in our example).

These types are automatically determined from the data in the table file. However, in case the automatic algorithm failed for a table, you can change the types

Figure 2.1: **New Table.** This figure presents a freshly created Table AST Root node. You can use the button located to the right, after the <no name> red label (…), to open a file selection dialog. Use this dialog to locate a TSV file to configure this table.

manually. To do this, put the cursor over the name of the type in the column section, and use auto-completion in the inspector to change to the desired type.

Figure 2.2 presents a MetaR table annotated with groups.

Column Groups Container

2.3

Column Groups Containers are used to define column groups and annotate these groups with group usages. To create a new Column Group Container, right-click on a model and select **New > o.c.tables.ColumnGroupContainer**. This will create the empty container shown in Figure 2.3. You need and should have only one container per model. The container will hold the groups and group usages that you need across the MetaR Tables defined in the model.

Column Groups

2.4

Column Groups can be defined by pressing ↵ either on top of the « ... » (immediately below **Define Groups:**), when the list of groups is empty, or with the cursor immediately before the name of an existing group. Each group has a name and an optional set of group usages. Figure 2.4 presents a new

Table GSE59364_DC_all.csv ...

File Path

\${org.campagnelab.metaR.home}/data/GSE59364_DC_all.csv

Columns

```
gene: string [ ID ]
mRNA len: numeric [ << ... >> ]
genomic span: numeric [ << ... >> ]
DC_normal: numeric [ << ... >> ]
DC_treated: numeric [ << ... >> ]
DC0904: numeric [ LPS=NO, counts ]
DC0907: numeric [ LPS=NO, counts ]
DCLPS0910: numeric [ LPS=NO, counts ]
DCLPS0913: numeric [ LPS=NO, counts ]
A_DC: numeric [ LPS=NO, counts ]
A_DC_LPS: numeric [ LPS=YES, counts ]
B_DC: numeric [ LPS=NO, counts ]
B_DC_LPS: numeric [ LPS=YES, counts ]
C_DC: numeric [ LPS=NO, counts ]
C_DC_LPS: numeric [ LPS=YES, counts ]
C2DC: numeric [ LPS=NO, counts ]
C2DCLPS: numeric [ LPS=YES, counts ]
C3DC: numeric [ LPS=NO, counts ]
C3DCLPS: numeric [ LPS=YES, counts ]
```

Figure 2.2: **Example Table.** The figure presents an example table annotated with groups.

Figure 2.3: Empty Column Group Container.

Use a column group container to define column groups and associated group usages. Place the cursor over the « ... » symbol and press  to add a new group or group usage. Name the group or usage immediately after creating it.

Define Usages:

<< ... >>

Define Groups:

<< ... >>

Figure 2.4: New Group.

`<no name> used for << ... >>`

You should name a new group immediately after creating it.

column group (group for short).

name

The name of the group is a string that should mean something in the context of your analysis. Some MetaR analysis statements require specific group names to be defined in a model container and referenced in an input table. Other groups will be created by you with meaningful names to help identify columns that have certain properties, so that you can refer to them collectively by the group name.

used for

Column groups can be annotated with a set of group usages. You can enter references to usages already defined in the column group container following the `used for` keyword shown in Figure 2.4. Press  on the « ... » to insert

the first group usage. Make sure the usage is defined (its name should be visible in the **Define Usages:** section of the container (see Section 2.5 to learn how to create a new Group Usage). You can bind a group usage reference to a Group usage by using auto-completion (**ctrl**+**Space** to locate the name, then pressing **Enter** to accept one completion choice), or by typing the name of the group usage directly (note that group usage names are case sensitive).

R Pressing **Enter** before <no name> will not have the desired effect if you have not yet named a group. Make sure you name groups immediately after you create them.

Column Group Usage

2.5

A Column Group Usage can be defined by pressing **Enter** either on top of the « ... » (immediately below **Define Usages:**), when the list of group usages is empty, or with the cursor immediately before the name of an existing group usage. When the list already contains one or more group usages, you can add more by placing the cursor over a group usage name and pressing **Enter**. Keep pressing **Enter** to add more empty group usages.

Example Column Group Container

2.6

Figure 2.5 presents an example of a configured Column Group Container. This container defines two groups LPS=yes and LPS=no, which can be used to annotate Table columns that contain data about gene expression of samples treated with LPS or not. The group usage LPS_Treatment is associated to both groups to indicate that they belong together and are two kinds of treatment.

Column Groups from a Table

2.7

An alternative way to automatically create Column Groups and attach them to Columns at the same time is to use a so-called annotation table. These

Figure 2.5: **Example Group Container.** This example presents a container with several groups and group usages.

Column Groups and Usages

Define Usages:

LPS_Treatment
ID
heatmap

Define Groups:

LPS=YES used for LPS_Treatment heatmap
LPS=NO used for LPS_Treatment heatmap
ID used for ID
counts used for heatmap

tables are normal Table nodes (created as specified 2.2) with a special structure and content. When created, MetaR is able to recognize them and allows the user to use these tables to annotate other tables.

The structure of an annotation table requires the following two columns:

- *SampleID*: values of this column are sample names
- *Groups*: values of this column are comma-separated lists of group names

When annotation tables are available in the current model, the user can

1. open the Table to annotate
2. use the "Use Column Groups From Table: <table name>" intention (💡) when the cursor is on top of the Table node

This way, Sample IDs are matched with the column names and the groups listed in the same row are attached to the corresponding Column. In addition, if the groups are not defined in the ColumnGroupContainer, they are created in the annotation process. The Column Group Container is also created if it does not exist.

To see how they work in practice, we will create the same groups shown in Figure 2.2 using an annotation table. To do that, we firstly need to create a CVS file with the content shown in Figure 2.6.

The next step is to load this table in a Table node (Figure 2.7).

Table

SampleID	Groups
gene	ID
DC0904	LPS=NO,counts
DC0907	LPS=NO,counts
DCLPS0910	LPS=NO,counts
DCLPS0913	LPS=NO,counts
A_DC	LPS=NO,counts
A_DC_LPS	LPS=YES,counts
B_DC	LPS=NO,counts
B_DC_LPS	LPS=YES,counts
C_DC	LPS=NO,counts
C_DC_LPS	LPS=YES,counts
C2DC	LPS=NO,counts
C2DCLPS	LPS=YES,counts
C3DC	LPS=NO,counts
C3DCLPS	LPS=YES,counts

Figure 2.6: Content of a Sample Annotation Table

Table AnnotationTableForGSE59364_DC_all.csv 
File Path \${org.campagnelab.metaR.home}/data/AnnotationTableForGSE59364_DC_all.csv
Columns
SampleID: *string*
Groups: *string*

Figure 2.7: **Table with Samples and Groups.** An annotation table loaded as Table node.

Finally, we invoke the "Use Column Groups From Table: AnnotationTableForGSE59364_DC_all.csv" intention as shown in Figure 2.8 to apply the group names from the table to our destination Table.

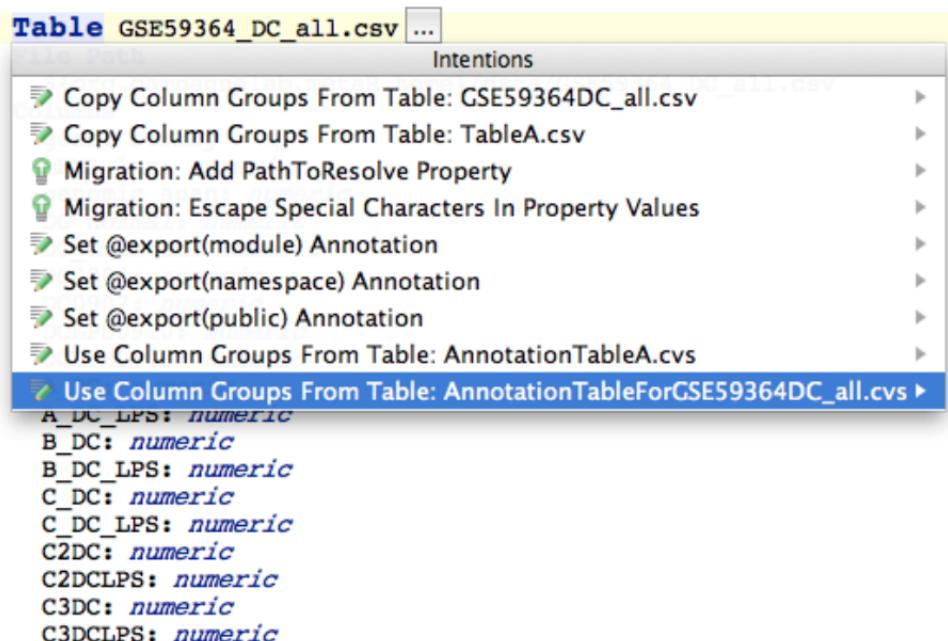


Figure 2.8: Intention to Annotate a Table using another Table

These steps will result in exactly the same annotated table shown in Figure 2.2.

Table Viewer Tool

2.8

The content of a Table can be inspected with the Table Viewer Tool distributed with MetaR. The tool adds to the MPS interface the capabilities to load the

table's content and show it in a graphical context. Wherever a table name appears (in a Table node or in an Analysis script, see Chapter 3), the tool can be open to see the rows and columns of that table along with their values. Figure 2.9 shows how to activate the tool on a Table node. The first time is activated, the tool appears at the bottom of the MPS UI, as shown in Figure 2.10.

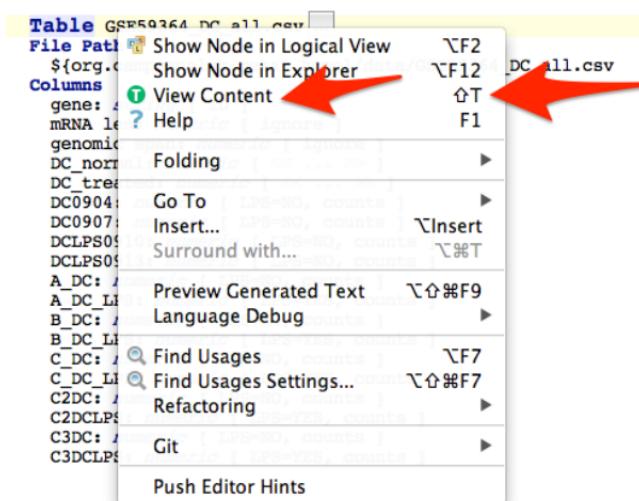


Figure 2.9: **How to activate the Table Viewer Tool.** The Table Viewer Tool can be activated by right-clicking on the Table and select **View Content** from the menu. An alternative way is to put the cursor on the Table node and press + .

The tool is immediately available for those tables directly loaded from the file system (e.g. Table nodes) and their references. Other tables are instead created by Analysis scripts. In this latter case, the tool is available after the first script execution (see Chapter 3). Moreover, if the structure or content of a table change, the script must be executed again in order to reflect such changes

Table node

Table Viewer Tool

```

Table GSE59364_DC_all.csv ...
File Path
${org.campagnelab.metaR.home}/data/GSE59364_DC_all.csv
Columns
  gene: string [ ID ]
  mRNA_len: numeric [ ignore ]
  genomic_span: numeric [ ignore ]
  DC_normal: numeric [ << ... >> ]
  DC_treated: numeric [ << ... >> ]
  DC0904: numeric [ LPS=NO, counts ]
  DC0907: numeric [ LPS=NO, counts ]
  DCLPS0910: numeric [ LPS=NO, counts ]
  DCLPS0913: numeric [ LPS=NO, counts ]
  A_DC: numeric [ LPS=NO, counts ]
  A_DC_LPS: numeric [ LPS=YES, counts ]
  B_DC: numeric [ LPS=NO, counts ]
  B_DC_LPS: numeric [ LPS=YES, counts ]
  C_DC: numeric [ LPS=NO, counts ]
  C_DC_LPS: numeric [ LPS=YES, counts ]

```

MetaTable Viewer

gene	mRNA_len	geno...	DC_n...	DC_tr...	DC09...	DCLP...	DCLP...	A_DC	A_DC...	B_DC	B_DC...	C_DC	C_DC...	C2DC	C2DC...	C3DC	C3DC...	
"Total"		3442	3565	1899	1542	1929	1635	1581	1835	1591	2957	2068	2665	2495	2679	3019	2302...	
"10a..."	361	472	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
"16G2"	1444	12549	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
"21A..."	2522	31972	119	137	83	36	76	61	93	83	9	68	275	355	302	303	414	312
"28A"	949	24007	0	0	0	0	0	13	0	0	0	29	58	61	106	56	37	
"2E4"	1787	9122	0	0	0	0	0	0	94	73	0	0	101	107	145	85	153	92
44050	2315	19035	0	0	0	0	0	0	14	0	0	0	0	0	0	0	0	0
"5-O..."	1020	1284	70	34	37	33	6	28	77	34	4	41	146	269	155	171	323	188
"5H9"	970	35347	268	51	163	105	19	32	367	200	0	250	1516	1406	1953	1857	1425	1399
"6M1..."	478	29431	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
"6a8b"	1551	8982	1881	1313	1303	578	529	784	663	1033	2186	1956	751	880	1847	1932	3307	1950
"7M1..."	69	907	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
"A-3..."	1570	1958	63	0	57	6	0	0	64	0	0	0	260	164	336	120	399	88
"A1"	1751	37974	0	0	0	0	0	0	132	25	0	0	17	8	0	0	30	0
"A12..."	1164	2772	873	1210	477	396	631	579	299	565	411	948	7634	14397	10090	17750	12150	14826
"A1Bc"	1772	6693	256	46	113	143	46	0	183	57	192	149	134	174	254	186	450	278
"A1Cf"	2386	79110	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
"A2B..."	4791	1694...	0	0	0	0	0	0	22	0	0	0	0	0	0	0	0	0

4: Run 9: Changes 3: Usages Console Version Control 0: Messages T: MetaTable Viewer

Figure 2.10: The Table Viewer Tool in the MPS UI.

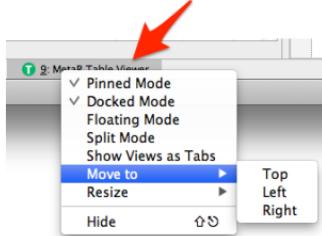


Figure 2.11: Visualization Options for Table Viewer Tool. Different visualization options are available for the Table Viewer Tool. By right clicking on the tool name in the Tool Buttons bar (if not visible, select **View > Tool Buttons** from the MPS menu), a user can explore them and choose the one that best fits a project needs. In our experience, the floating mode or the Docked/Pinned mode with the panel on the right are very effective.

gene	mRNA len	genomic span	DC_normal	DC...	DC...	DC...	DC...	A_DC	A...	B_DC	B...	C...	C...	C...	...
"Total"			3442174	15...	189...	15...	19...	16...	15...	18...	15...	29...	2...	2...	...
"10a.87289 (loc..."	361	472	0	0	0	0	0	0	0	0	0	0	0	0	0
"16G2"	1444	12549	0	0	0	0	0	0	0	0	0	0	0	0	0
"214K23.2"	2522	31972	119	137	83	36	76	61	93	83	9	68	275	355	302
"ZB4"	949	24007	0	0	0	0	0	0	13	0	0	0	29	58	61
"ZE4"	1787	9122	0	0	0	0	0	0	94	73	0	0	101	107	145
44050	2315	19035	0	0	0	0	0	0	14	0	0	0	0	0	0
"5'-OPase"	1020	1284	70	34	37	33	6	28	77	34	4	41	146	269	155
"5H9"	970	35347	268	51	163	105	19	32	367	200	0	250	1...	1...	1...
"6M1-18"	478	29431	0	0	0	0	0	0	0	0	0	0	0	0	0

Figure 2.12: The Table Viewer Tool. The tool displays the content of the selected table. At the top, we can see the name of the table and the number of records loaded. Columns can be resized and rows scrolled for a full visualization of their values.

in the tool.

The MetaR Analysis Root Node

Styles

Working with Tables

Subset Rows

Join Tables

Plotting Data

3 — Analyses

The MetaR Analysis Root Node

3.1

MetaR analyses are represented with an Analysis AST Root node. An analysis often imports one or more tables, performs data transformations and writes a table or generates some plots. You can create as many Analysis root nodes as needed in a model. You create an analysis by right-clicking on a model and selecting `New > o.c.metar.tables > Analysis`. Analysis can exist as direct child of a model, and for this reason is called a root node. Figure 3.1 presents a new Analysis root node.

name

Each analysis has a name. You should name the analysis after creating it. The name you enter will be shown in the Project Tab after the  icon.

statements

An analysis contains a list of statements. You can enter new statements by typing between the curly brackets `{ }`.

```
Analysis <no name>
{
    << ... >>
}
```

Figure 3.1: New MetaR Analysis Root Node. This figure presents a freshly created MetaR analysis root node. You can press  over the « ... » to add Statement nodes to the analysis. Use auto-completion to discover which types of statements are available.

To enter a specific statement, you can type the alias of the statement (for instance `import table`). When you have typed a complete alias, the node will be inserted in place of the alias. Note that there is no actual indication that the text you are typing matches a valid alias. You need to finish typing the full alias before the node is substituted for the alias. The text you type will remain red until the substitution occurs even if the text is matching a valid alias. See Figure 3.3.

The following sections describe the kinds of statements offered by the MetaR `org.campagnelab.MetaR.tables` language. The simplest way to learn which statements are supported by the release of MetaR that you are using is to use auto-completion. Figure 3.2 provides a snapshot of the auto-completion menu when looking for statements to insert in the Analysis statement list.

Styles

3.2

MetaR comes with a styles language that allows to customize the graphical aspects of plots and files generated by statements. A Style is represented by a root node in the model with a given name.

N	boxplot	Plot a box plot
N	build heatmap	Plot a heatmap
N	define	define something
N	fit x by y	fit a linear model and show an annotated plot of the fit
N	histogram	Plot a histogram
N	import table	Import a table in this analysis
N	join	Join/combine two or more tables
N	multiplot	A Plot to arrange other plots
N	predict	Predict with a model and put values in a new column
N	render	Render plot to output format
N	set key	define one column as key of a table
N	subset of rows	Calculates the subset of rows for a table

Figure 3.2: **Auto-completion Dialog for Statements.** This dialog is obtained by placing the cursor where a Statement is valid, and pressing **ctrl**+**space**.

```
Analysis Typing aliases tutorial
{
    import
    import table <no table>
}
```

Figure 3.3: **Typing Statement Aliases.** The user has typed “import” on the third line. This text is a prefix of the import table statement, but is shown in red because the alias is not yet complete. The fourth line shows the import statement which is substituted to the text when the user has just finished typing “import table”, the complete alias of the statement. Note that pressing **enter** immediately after import will create the node if the prefix “import” matches a single type of node in the languages imported in this model.

To create a Style, right-click on a model in the project tab and select right-click ➤ New ➤ o.campagnelab.styles ➤ Style. This will create an empty Style, as shown in Figure 3.4.

```
Style <no name> extends <no extends> {  
    << ... >>  
}
```

Figure 3.4: **New Style.** A newly created Style AST Root node.

Style nodes are identified by a  icon. A Style is essentially a container for *style items*. Items are well-defined settings that are applied by MetaR during the rendering of a graphical object. Figure 3.5 shows a snapshot of the auto-completion menu when looking for items to add to a style. All possible style items are shown because this style is not yet bound to a specific statement.

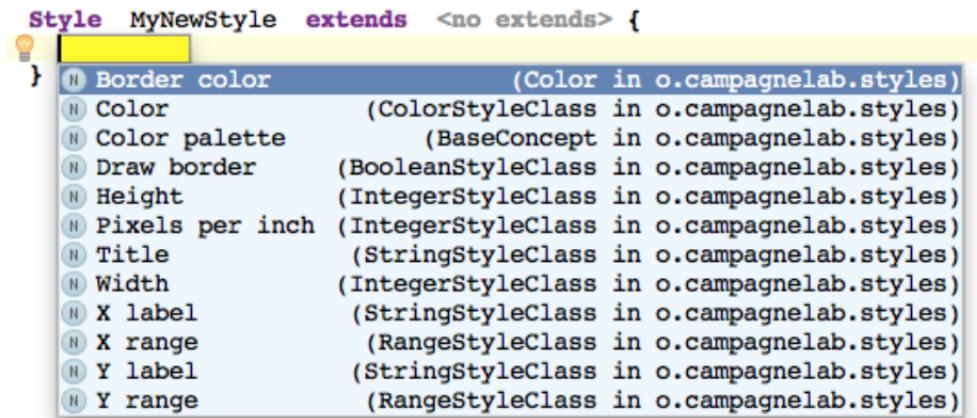


Figure 3.5: **Adding Style Items to a Style.** A Style is a container for Style Items. By using auto-completion **ctrl** + **space**, style items can be added to the node.

Styles can extend other styles, which provides an ability to modularize appearance. This is useful if you need to build collections of plots, and most plots have a subset of style attributes, but the title of each plot or the X or Y variable changes. You would define the common style attributes in a style, and extend this style each time you need to specialize the style.

Binding Styles to Statements

3.2.1

In order to use a Style, you have to bind a statement to it. There are different approaches you can follow to create this binding and the choice depends on your needs and flexibility.

The simplest way to create a style and bind it to a statement is to use the intention "Create New Style" available on compatible statements as shown in Figure 3.6. This intention will create a new style and bind it to the statement. This has the advantage that the style items are immediately restricted to only the items compatible with the statement.



Figure 3.6: **Create New Style Intention on Statements.** The user has pressed **option** + **⇨** on a statement that can be bound to a style. By selecting the **Create New Style** intention, a new default style is created in the model and bound to the statement.

Once bound to a statement (or more than one), the list of items that can be added to the Style is restricted to the ones compatible with the statement(s). For instance, if the style shown in Figure 3.5 is bound to a statement that uses only a Color Palette and some kind of border drawing, the auto-completion menu will appear as shown in Figure 3.7.

However, styles can be created independently from statements and bound

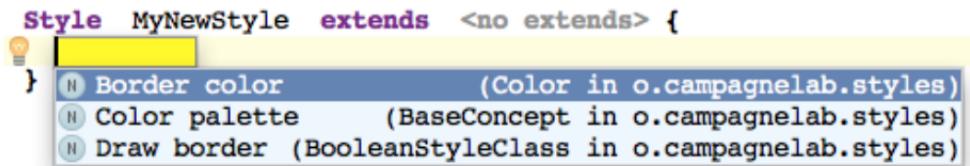


Figure 3.7: **Style with Restricted Items.** A subset of Style Items is displayed in the auto-completion menu when the Style is bound to a statement.

at a later time. In this case, the list of styles visible to a statement in the auto-completion menu is limited to the compatible styles available (see Figure 3.8). A style is defined compatible with a statement if its items or a subset of them are used by the statement.



Figure 3.8: **Styles visible from a Statement.** A statement can be bound only to Styles that define items compatible with the statement.

A library of Styles could be created and reused across multiple Statements, Analyses or even Models. The capability to extends other Styles promotes reuse, reduces redundancies and allows to keep the number of Styles in a model at a minimum.

Working with Tables

3.3

Import Table

3.3.1

The `import table` statement makes it possible to import a table, defined in the model, into the analysis. The columns of the imported table will become visible to the statements that follow the import. You can create an import table

Figure 3.9: New Write `write <no table> to "<no path>" ...`
Statement. Use this statement to write the content of a table to a file.

statement by typing the alias `import table` on an empty line of Analysis. Once you have bound the reference to a table, the import statement will look like this: `import table SomeData`. The name in green is the name of the table the statement imports. See Section 2.2 to learn how to create a Table Root node.

table

The table attribute is a reference to an AST root node. You can set this reference by typing the name of the table you wish to import, or by using auto-completion `ctrl + space` to locate the table AST root node.

Write Table

3.3.2

MetaR analyses can create new tables. You can write the data in these tables to a file using the `write` statement (see Figure 3.9 for a new write statement). The `write` statement has two attributes: `table` and `filename`.

table

This reference should be set to the table that you want to write to a file.

output

The output should be set to a filename where you want the data contained in the table to be written. Notice that `output` has a button to let you select the output filename.

```
subset rows <no table> filter how? -> subset
```

Figure 3.10: New Subset Rows Statement.
Use this statement to filter the rows of a table.

Identify a Set of Columns

3.3.3

Several types of statements require the user to select one or more columns of a table. MetaR provides several ways to select a set of columns.

- You can use the `columns` node to identify a set of columns.
- You can use the `group` node to name a single group, and identify all columns annotated with this group.
- You can use the `groups` node to name a set of groups, and identify all columns annotated with any of these groups.

Each strategy identifies a set of columns, which may contain one or more columns.

Subset Rows

3.4

You can use this statement (alias `subset rows`) to filter a table and produce a new table with a subset of the rows of the input table. Figure 3.10 shows a new `subset rows` statement.

table

The input table reference must be set to a table. The table must be either imported or produced by another statement.

filter

The filter determines which rows are kept. Use auto-completion to select one of the alternatives:

1. `when true`: will keep a row when the boolean expression following `when true`: evaluates to `true`.

2. with `IDS` will keep a row when the value of the column marked with group ID exists in the list provided as an argument. See the `define` statement to create a list of IDs.

subset

The output table is called `subset` by default. Feel free to rename this table to better match the data in it.

Example

3.4.1

Figure 3.11 presents examples of subset row statements.

```
{  
  import table GSE59364_DC_all.csv  
  define Set of IDs GeneList {  
    MAPK PSEN1  
  }  
  subset rows GSE59364_DC_all.csv with IDs keep rows matching any ID in GeneList -> for geneslist  
  subset rows GSE59364_DC_all.csv when true: ${genomic span} > 20000 -> genomic span>2000  
}
```

Figure 3.11: **Subset Rows Examples.** This figure illustrates the two alternatives available for filtering rows: by expression (with `when true:`, or with a set of ID values).

Boolean Expressions

3.4.2

One form of the `subset rows` statement accepts a boolean expression to determine which rows to keep. Boolean expression have one of two values: `true` or `false`, and can be constructed by comparing values with an operator. The following operators are supported by MetaR:

- `$(column)` The value operator evaluates to the value of the column in the row currently considered.
- `expr1 == expr2` true when `expr1` evaluates to the same value as `expr2`.
- `expr1 != expr2` true when `expr1` does not evaluate to the same value as `expr2`.

```
join ( <no table> ) by <no name> -> <no name>
```

Figure 3.12: **New Join Statement.** Use this statement to join two or more tables into one.

- `expr1 | expr2` true when `expr1` is true or `expr2` is true (boolean or, either one of `expr1` or `expr2` needs to be true for the result to be true).
- `expr1 & expr2` true when `expr1` is true and `expr2` is true (boolean and, both `expr1` and `expr2` must be true for the result to be true).
- `expr1 < expr2` true when `expr1` evaluates to a value less than `expr2`.
- `expr1 > expr2` true when `expr1` evaluates to a value greater than `expr2`.
- `expr1 <= expr2` true when `expr1` evaluates to a value less or equal than `expr2`.
- `expr1 >= expr2` true when `expr1` evaluates to a value greater or equal than `expr2`.

 **R** MetaR infers the type of the expressions that you enter and will report type errors if the value of some values are not compatible with the test that you perform.

Join Tables

3.5

When you perform data analysis, you often need to combine data from different tables into one. This operation is called table joining. MetaR provides a powerful `join` statement that helps join an arbitrary number of tables. The alias of the statement is `join`. Figure 3.12 presents a newly created `join` statement. `Join` has three attributes: `input tables`, `by` and `output table`.

input tables

Use this attribute to enter references to tables you need to join. You can press  with the cursor inside the parentheses to create references to additional

input tables (either imported or created in the analysis up to that point).

by

Use the by attribute to specify how to join the input tables. Joining tables requires knowing which rows of the input tables go together. This is done by identifying a set of columns whose values must match across rows of the input tables that go together. See Section 3.3.3 to learn how to select groups of columns in MetaR. You can select one of the following joining strategies as value of the by attribute:

- **by columns:** The same column name must be defined in all the input tables.
- **by group:** If each table has exactly one column annotated with this group, the names of the columns do not need to be the same. Otherwise, if more than one columns is in the group, their names must match across all the tables.
- **by groups:** Similar to group, but with any (≥ 1) number of groups. Press  to insert new group references.

The group by columns are used to calculate a list of values. When rows of the input tables have the same group by values, they are joined in a single row, and the result put in the destination table.

-  The join statement will create new columns if the input tables have columns with the same name. In this case the shared columns are renamed “colname.TableName”. Place the cursor on result and look at the column preview in the inspector to see which column names are generated by a given join statement.

result

The output table is called Results by default. Feel free to rename this table to match the content of the destination table. Open the  to see which columns will result from the join. Notice that the column groups are transferred to the columns of the output table.

How Join works

The output table produced by the `join` statement can be very different, depending on the strategy selected to join the input tables and their structure. The statement takes also care to produce unique columns from columns common to all the input tables but not used in the joining strategy. To explain how `join` works we will apply two different strategies to the input tables (named A and B) presented in Figure 3.13 and check the structure and content of the output table.

Table A			Table B			
Gene	Column1[ID]	Column2	Gene	Column2	Column3	Column4[ID]
Ge1	Val1	34	Ge4	1	78	Val1
Ge2	Val2	452	Ge2	3	13	Val3
Ge3	Val3	113	Ge1	4	44	Val4

Figure 3.13: Sample Input Tables for Join Statement.

Do note that the two tables have columns in common (Gene and Column2) and that each table has a column annotated with a group named ID (Column1 in table A, Column4 in table B).

join by column

As first strategy, we join A and B by the column Gene. The results table generated by `join` is shown in Figure 3.14.

Table Results (by Column Gene)						
Gene	Column1	Column2.A	Column2.B	Column3	Column4	
Ge1	Val1	34	4	44	Val4	
Ge2	Val2	452	3	13	Val3	

Figure 3.14: Results Table for Join using by Column Strategy.

If we analyze the structure of the table, we note that:

- there is only one Gene column (the one used for joining)
- Column2, that was present in both the input tables, was split in two columns named Column2.A and Column2.B
- the rest of the columns are the same coming from their respective input tables

Looking at the table's content, we note that:

- rows from input tables with a matching value in the Gene column were merged into a single row.
- all the other columns keep their original value from the source table with respect to the Gene column's value

join by group

Our second strategy is to join A and B by group ID. As shown in Figure 3.13, there are two columns, one in each input table, annotated with such a group and they have different names. The `join` statement is able to work even in this case by matching the values of these two columns. The results table generated by Join is shown in Figure 3.15. Again, let's go over the structure of the table:

- Gene, that was present in both the input tables but this time not used as joining column, was split in two columns named Gene.A and Gene.B
- Column2, that was present in both the input table, was again split in two columns named Column2.A and Column2.B
- the rest of the columns are the same coming from their respective input tables

Table Results (by Group ID)						
Column1	Gene.A	Gene.B	Column2.A	Column2.B	Column3	Column4
Val1	Ge1	Ge4	34	1	78	Val1
Val3	Ge3	Ge2	113	3	13	Val3

Figure 3.15: **Results Table for Join using by Group Strategy.**

```
{  
  import table GSE59364_DC_all.csv  
  import table another Table  
  join ( GSE59364_DC_all.csv , another Table ) by group ID -> Results  
}
```

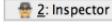
Figure 3.16: Example of Join Statement.

Looking at the table's content, we note that:

- rows from input tables with a matching value in Column1 from A and Column4 from B were merged into a single row
- all the other columns keep their original value from the source table with respect to their matching column's value

Example Join

3.5.2

Figure 3.16 presents an example of join statement. The statement joins two tables and creates the Result table. If you open the  2: Inspector, you will see a preview of the columns for the result table (shown in Figure 3.17).

Plotting Data

3.6

MetaR provides simple plotting capabilities¹. The following types of plots are currently supported:

- boxplot alias `boxplot`
- histogram alias `histogram`
- scatterplot: alias `fit`
- heatmap, alias `heatmap`
- multiplot alias `multiplot`, makes it possible to organize other plots in a matrix of n columns by n rows.

Each type of plot statement will create a plot, identified with the  icon when you are trying to auto-complete a reference to a plot. Plot names are also colored with the same dark blue as the icon.

¹These capabilities are simple, but can be extended very easily by adding new statements to draw other types of visualization. This is a key advantage of using Language Workbench technology.

```

path= /Users/fac2003/R_RESULTS/table_Results_0.tsv name: Results table.name Results groups= LPS=NO,counts,LPS=YES,ID
Columns (38) :
C3DC.GSE59364_DC_all.csv : numeric [ LPS=NO, counts ]
C3DC.another Table : numeric [ LPS=NO, counts ]
C2DC.another Table : numeric [ LPS=NO, counts ]
DC0904.another Table : numeric [ LPS=NO, counts ]
mRNA.len.another Table : numeric [ << ... >> ]
B_DC.GSE59364_DC_all.csv : numeric [ LPS=NO, counts ]
mRNA.len.GSE59364_DC_all.csv : numeric [ << ... >> ]
B_DC.another Table : numeric [ LPS=NO, counts ]
A_DC.GSE59364_DC_all.csv : numeric [ LPS=NO, counts ]
DCLPS0913.GSE59364_DC_all.csv : numeric [ LPS=NO, counts ]
DC0904.GSE59364_DC_all.csv : numeric [ LPS=NO, counts ]
C2DC.GSE59364_DC_all.csv : numeric [ LPS=NO, counts ]
C_DC.LPS.GSE59364_DC_all.csv : numeric [ LPS=YES, counts ]
DCLPS0910.another Table : numeric [ LPS=NO, counts ]
B_DC.LPS.another Table : numeric [ LPS=YES, counts ]
DC_treated.another Table : numeric [ << ... >> ]
A_DC.LPS.another Table : numeric [ LPS=YES, counts ]
gene.GSE59364_DC_all.csv : string [ ID ]
DC_normal.another Table : numeric [ << ... >> ]
C3DCLPS.GSE59364_DC_all.csv : numeric [ LPS=YES, counts ]
C_DC.LPS.another Table : numeric [ LPS=YES, counts ]
B_DC.LPS.GSE59364_DC_all.csv : numeric [ LPS=YES, counts ]
C2DCLPS.GSE59364_DC_all.csv : numeric [ LPS=YES, counts ]
DCLPS0910.GSE59364_DC_all.csv : numeric [ LPS=NO, counts ]
A_DC.LPS.GSE59364_DC_all.csv : numeric [ LPS=YES, counts ]
DC_normal.GSE59364_DC_all.csv : numeric [ << ... >> ]
C3DCLPS.another Table : numeric [ LPS=YES, counts ]
C_DC.another Table : numeric [ LPS=NO, counts ]
genomic.span.GSE59364_DC_all.csv : numeric [ << ... >> ]
C_DC.GSE59364_DC_all.csv : numeric [ LPS=NO, counts ]
C2DCLPS.another Table : numeric [ LPS=YES, counts ]
genomic.span.another Table : numeric [ << ... >> ]
A_DC.another Table : numeric [ LPS=NO, counts ]
DC_treated.GSE59364_DC_all.csv : numeric [ << ... >> ]
gene.another Table : string [ ID ]
DCLPS0913.another Table : numeric [ LPS=NO, counts ]
DC0907.another Table : numeric [ LPS=NO, counts ]
DC0907.GSE59364_DC_all.csv : numeric [ LPS=NO, counts ]

```

Figure 3.17: Column Preview for Result Table. Notice that all these columns were shared across the input tables because their name follows the pattern “`colName.tableName`”.

boxplot with `<no cols>` -> `<no name>` no style Figure 3.18: New Boxplot Statement.

Generated plots can be customized and refined by binding each statement to a style (see 3.2). A reference to a style is back-colored with the same turquoise color as the  icon.

boxplot

3.6.1

Figure 3.18 presents a new boxplot statement.

columns

Indicate one or more columns to plot. The values of the columns will be plotted as individual boxplots in the same graph. Press  to define more than one column. Use auto-completion to locate individual columns from the imported tables, or the tables created by prior statements.

plot

The attribute after `->` is a plot. Enter a name for the boxplot here. Plot names are colored blue to make them easier to recognize.

style

If a style is bound to the box plot (see section 3.2), the statement will use a **ColorPalette** item from the style to draw the plot. A Color Palette is an AST Root Node identified with the  icon.

MetaR comes with several pre-defined palettes and colors ready for use. Figure shows the auto-completion menu for a Color Palette item listing the default palettes available.

You can create a new palette by right-clicking on a model and selecting `New > o.campagnelab.styles > Color Palette`. Colors can be added to a palette and their order will matter in the rendering of the plot. Figure 3.20

```
Style BoxplotStyle extends <no extends> {
    Color palette : ColorPalettes
        Diverging-BrBG      ColorPalette (o.c.m.a.styles.colors)
        Diverging-RdYlBu    ColorPalette (o.c.m.a.styles.colors)
        Qualitative-Dark2   ColorPalette (o.c.m.a.styles.colors)
        Qualitative-Paired  ColorPalette (o.c.m.a.styles.colors)
        Sequential-BuGn    ColorPalette (o.c.m.a.styles.colors)
        Sequential-BuPu    ColorPalette (o.c.m.a.styles.colors)
        Sequential-GnBu    ColorPalette (o.c.m.a.styles.colors)
        Sequential-Greys   ColorPalette (o.c.m.a.styles.colors)
        Sequential-PuBuGn  ColorPalette (o.c.m.a.styles.colors)
        Sequential-PuRd    ColorPalette (o.c.m.a.styles.colors)
        Sequential-YlOrRd  ColorPalette (o.c.m.a.styles.colors)
```

Figure 3.19: Auto-completion menu with default Color Palettes.

shows a Color Palette with some color items and the auto-completion menu listing some of the default colors available.

There are two classes of colors you can use in a palette:

- **Named Colors.** New named Colors can be created by right-clicking on a model and selecting `New > o.campagnelab.styles > Color`. A color is identified by the  icon and its name must be valid in the R language.
- **#RRGGBB Colors.** These colors can be created directly inside the Color Palette by selecting the `#RRGGBB` option in the auto-completion menu for a Color value. The color will be constructed from the combination of the Red, Green and Blue specified in the code.

histogram

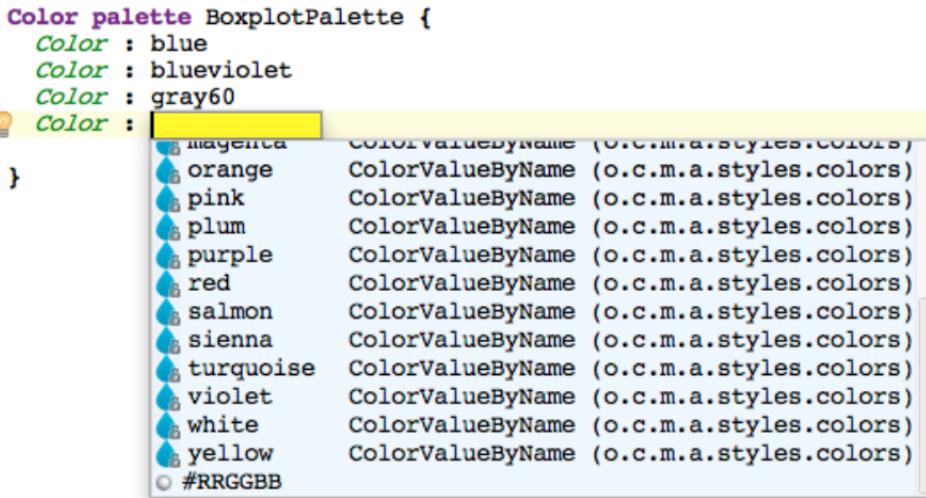
3.6.2

Use this statement to plot a histogram of the values of one column.

column

Indicate one column to plot a histogram for. Use auto-completion to locate the column from the imported tables, or the tables created by prior statements.

```
Color palette BoxplotPalette {  
    Color : blue  
    Color : blueviolet  
    Color : gray60  
    Color : magenta  
    Color : orange  
    Color : pink  
    Color : plum  
    Color : purple  
    Color : red  
    Color : salmon  
    Color : sienna  
    Color : turquoise  
    Color : violet  
    Color : white  
    Color : yellow  
    Color : #RRGGBB  
}
```



The screenshot shows an IDE interface with a code editor. A dropdown menu is open over the word 'Color'. The menu contains several color names: magenta, orange, pink, plum, purple, red, salmon, sienna, turquoise, violet, white, and yellow. Below these, there is an option labeled '#RRGGBB'. To the left of the menu, there is a small lightbulb icon with a question mark, indicating a tooltip or help feature.

Figure 3.20: **Auto-completion menu showing some default Colors and the `##RRGGBB` option.** The auto-completion menu lists the visible Colors and `#RRGGBB` option. By selecting this latter, you can create a custom color based on the Red Green Blue color components (RGB).

plot

The attribute after -> is a plot. Enter a name for the histogram here. Plot names are colored blue to make them easier to recognize.

style

The statement uses a **ColorPalette** item (see 3.6.1) from the associated style (see section 3.2) to draw the plot.

fit x by y

3.6.3

Use this statement (alias **fit**) to plot a scatter plot of x (one column) vs y (another column). A fit is performed, and the R² adjusted, and P-value corresponding to the linear regression is shown on the plot. Figure 3.21 presents a new **fit** statement.

```
fit <no_col> by <no_col> with table <no_table> -> <no_name> no style
```

Figure 3.21: New Fit X by Y.

x, y

Indicate which columns should be plotted. Use auto-completion to locate the x and y columns from the imported tables, or the tables created by prior statements.

plot

The attribute after -> is a plot. Enter a name for the scatterplot here. Plot names are colored blue to make them easier to recognize.

style

The fit statement uses the following items from the associated style (see section 3.2) to customize the scatterplot:

- **Title**. The main title on top of the plot.
- **X label**. A title for the x axis.

- **Y label**. A title for the y axis.
- **X range**. Range of values for the x axis.
- **Y range**. Range of values for the y axis.
- **Width**. Width in pixels of the output image with the plot.
- **Height**. Height in pixels of the output image with the plot.

heatmap

3.6.4

Use this statement (`heatmap`) to construct a heatmap. Figure 3.22 presents a new `heatmap` statement.

```
heatmap with <no table> select data by<no dataSelection>-> <no name> no style [
```

Figure 3.22: **New Build Heatmap**. Notice the intention “Add Annotations” attached to the statement. You can use this intention to further customize the heatmap.

table

Specify the table that contains the data that will be used to draw the heatmap. Note that the table must meet certain conditions. An error message will be displayed if these conditions are not met:

- Some columns of the table must be annotated with at least one group whose usage is “heatmap”. Such columns are used to provide data values for the heatmap. If you don’t have a heatmap usage, just create one and add it to the groups you would like to include on the heatmap.
- The columns of the table must be annotated with groups and group usages to make it possible for you to use these group usages to construct a legend.

select data by

Use this attribute to customize the set of columns to plot on the heatmap. See Section 3.3.3 to learn how to select a set of columns.

plot

The `<no name>` attribute listed after `->` makes it possible to name the plot that will hold the heatmap. Use any name you like. This name will be used to refer to the heatmap plot, for instance if you wish to assemble panels of different heatmaps into one figure.

style

The statement uses the following items from the associated style (see section 3.2) to customize the heatmap:

- **Color palette.** The colors to use in the heat map (see 3.6.1).
- **Draw border.** A boolean value to enable or disable borders in the heatmap. A value of `true` will draw a border. A value of `false` will not. By default, borders are enabled.
- **Border color.** The color to use for the border (see section 3.6.1 to check out how to create/refer to colors). If not set, the default color is `grey60`.

annotations

You can use the “Attach Annotations” intention (💡) when the cursor is on top of `heatmap` to customize heatmap annotations. Figure 3.23 shows a heatmap statement with annotations.

```
heatmap with GSE59364_DC_all.csv select data by columns: A_DC B_DC -> heatmap HeatmapStyle [  
  annotate with these groups:<< ... >>  
  scale values:<no scaling>  
  cluster columns:false cluster rows:false  
]
```

Figure 3.23: **Build Heatmap With Annotations.** Annotations are shown after you have triggered the “Add Annotations” intention.

annotate with these groups. You can use this attribute to select usage names that should be listed in the heatmap legend. Listing a group usage will

annotate each column of data with the group that is associated to the usage.

scale values. You can choose to scale values by column or by row. Scaling will make differences easier to see by using colors more effectively.

cluster columns: You can choose to cluster by colors or by rows by changing the boolean values accordingly.

Example

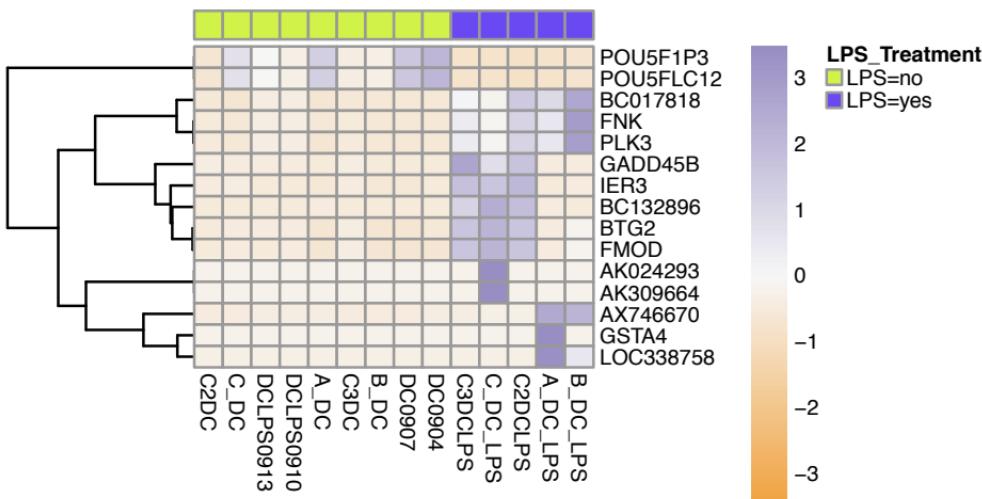


Figure 3.24: **Example of Heatmap Plot.** This heatmap has been customized with annotations. The LPS_Treatment group usage is shown in the legend, with two groups: LPS=yes and LPS=no. The values plotted have been scaled by rows, and the rows clustered. Data are from <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE59364>.

Figure 3.24 presents a heatmap constructed with the build heatmap statement,

using annotations and row clustering.

multiplot

3.6.5

This statement (alias `multiplot`) makes it possible to assemble a plot as a matrix of $m \times n$ plots. This is convenient if you would like to create a figure from panels of individual plots. In addition, `multiplot` provides a preview of the multi-panel plot that you can turn on and off at the click of a button. Figure 3.25 presents a new `Multiplot`.

```
multiplot -> <no name> [ <no numColumns> cols x <no numRows> rows ] Preview  
<<emptyTable>>
```

Figure 3.25: **New Multiplot Statement.** Click on the Preview/Hide Preview button to toggle the plot preview.

plot

The plot name is shown immediately after `->` (initially `<no name>`). Name the `multiplot` to be able to refer to it from other statements (such as `render` to make a PDF from it).

m cols x *n* rows

Define the number of columns and rows that you wish the `multiplot` to have. The product of m and n determines how many plot references must be filled in to construct the `multiplot`.

Preview/Hide Preview

These buttons will make it possible to preview/ hide the preview for the `multiplot`. Note that a preview is only available after you have run the analysis. If you don't see the image being refreshed after running the script, remember to hide the preview and show it again to refresh.

plot references

After you set the number of columns and rows, you need to link $m \times n$ references to plots that you have already constructed. Do this in table attribute (shown as «emptyTable» initially).

Multiplot Example

Figure 3.26 presents an example of multiplot.

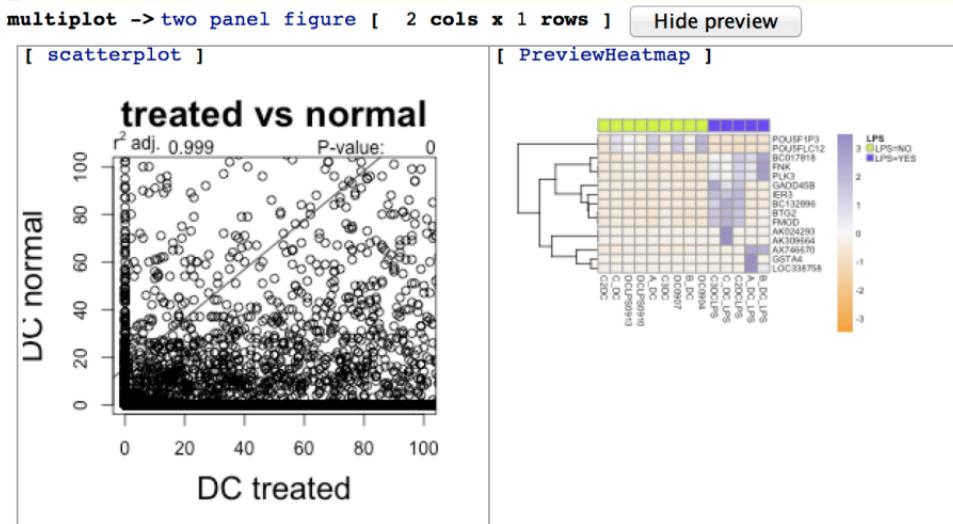


Figure 3.26: **Example of Multiplot.** This example shows a multiplot composed of two columns and one row. In the preview, a fit x by y plot is shown on the left, and a heatmap on the right.

render

3.6.6

This statement (alias `render`) makes it possible to save a plot or a multiplot in a local file according to a selected output format and style. Figure 3.27 presents

a new Render.

```
render <no plot> as <no alias> named "<no path>" ... no style
```

Figure 3.27: New Render Statement.

plot

The `<no plot>` attribute listed after the alias allows you to select the plot or multiplot to render.

rendering format

The rendering format is the format in which the plot will be stored on the file system. The current version of MetaR allows to use only PDF as format.

path

The `<no path>` attribute has to be set to a filename where you want the rendering is stored. Its extension must be compatible with the selected format (e.g. ".pdf" for PDF). If only a filename is specified

style

4 — EdgeR

Understanding Language Composition

4.1

The EdgeR language (`org.campagnelab.metaR.edgeR`) has been developed as a illustration of language composition with MetaR. When you import the `org.campagnelab.metaR` devkit into MPS, you are able to create analyses and the statements described in the previous Chapter. If you tried to enter the `edgeR` alias, the error shown in Figure 4.1 would appear. The reason is that by default, MetaR does not provide an EdgeR statement.

If you now also import the `org.campagnelab.metaR.edgeR` language (use  +  and import the `edgeR` language), you will be able to use the `edgeR` statement. A new EdgeR statement is shown in Figure 4.2. Adding

Figure 4.1: Error When Typing the EdgeR Alias.
The EdgeR statement is not yet defined.



the EdgeR language to MetaR contributes a new kind of Analysis statement, which becomes available through auto-completion. From a user point of view, importing languages is all that is required to extend MetaR with new language constructs. This new statement can be configured by the user and will generate R code together with the other statements. This happens seamlessly and requires no other configuration than declaring that the model uses another language.

```
edgeR counts= <no table> model: ~ 0  
comparing [REDACTED] -> <no name> (normalize with common dispersion estimations )
```

Figure 4.2: **New EdgeR Statement.** A new EdgeR statement created after you have added the `org.campagnelab.metaR.edgeR` language to the model's MPS Used Languages.

The edgeR Statement

4.2

The edgeR statement performs tests of differential expression using read counts contained in a table of data. The statement has the following attributes.

counts table

The table must contain columns annotated with the “counts” group. Bind this table reference to a table that contains non-normalized read counts.

model

You can use the model attribute to enter a linear model. EdgeR will use this model to model the mean and variance of the data. You can enter a linear model by typing `+` followed by the name of a group usage attached to the counts table. Repeat to add multiple factors to the model.



EdgeR will use an exact test when the model has one factor, but will use a Generalized Linear Model (GLM) when the model has more than one factor. This is handled transparently.

comparing

The comparing attribute makes it possible to define the statistics that should be tested for difference with zero. After you have defined a model with several factors (corresponding to group usage), the factor levels (corresponding to group names) will be offered for auto-completion. The factor level name stands for the average of the columns annotated with the group. See Figure 4.3 for an example.

normalize with

EdgeR supports three types of normalization methods, which estimate variance/dispersion in different ways:

- common dispersion
- trended dispersion
- tagwise dispersion

Place the cursor on the keyword following normalize with and use auto-completion to switch from one type of normalization method to another. The EdgeR Bioconductor documentation <http://www.bioconductor.org/packages/release/bioc/html/edgeR.html> for details about these approaches.

Example

4.3

Figure 4.3 presents an example where the edgeR statement is configured with a model (one factor: LPS) to call differences between columns labeled with the groups LPS=YES and LPS=NO.

```
edgeR counts= filtered model: ~ 0 + LPS
  comparing LPS=YES - LPS=NO -> Results (normalize with tagwise dispersion )
```

Figure 4.3: EdgeR Example.

5 — MPS Key Map

Windows or Linux	MacOS	Action
<code>⌘ + 0-9</code>	<code>⌘ + 0-9</code>	Open corresponding tool window
<code>ctrl + S</code>	<code>⌘ + S</code>	Save all
<code>ctrl + ⌘ + F11</code>	<code>N</code> or <code>A</code>	Toggle full screen mode
<code>ctrl + ⌄ + F12</code>	<code>N</code> or <code>A</code>	Toggle maximizing editor
<code>ctrl + BackQuote</code>	<code>ctrl + BackQuote</code>	Quick switch current scheme
<code>ctrl + ⌘ + S</code>	<code>⌘ + Comma</code>	Open Settings dialog
<code>ctrl + ⌘ + C</code>	<code>⌘ + ⌘ + C</code>	Model Checker

Table 5.1: General

Windows or Linux	MacOS	Action
		Find usages
		Highlight cell dependencies
		Highlight instances
		Highlight usages
		Find text
F3		Find next
		Find previous

Table 5.2: Usage and Text Search

Windows or Linux	MacOS	Action
		Import model
		Import language
		Import model by root name

Table 5.3: Import

Windows or Linux	MacOS	Action
<code>ctrl + []</code> <code>ctrl + ⌄ + click</code>	<code>ctrl + []</code> <code>⌘ + ⌄ + click</code>	Code completion Show descriptions of error or warning at caret
<code>⌄ + ↵</code> <code>ctrl + ⌄ + T</code> <code>ctrl + X</code> or <code>ctrl + ⌄ + ⌄ + X</code>	<code>⌄ + ↵</code> <code>⌘ + ⌄ + T</code> <code>⌘ + X</code>	Show intention actions Surround with...
<code>ctrl + C</code> <code>ctrl + Insert</code>	<code>⌘ + C</code>	Cut current line or selected block to buffer
<code>ctrl + V</code> <code>⌄ + Insert</code> <code>ctrl + D</code>	<code>⌘ + V</code> <code>⌘ + D</code>	Copy current line or selected block to buffer Paste from buffer Up current line or selected block
<code>⌄ + F5</code> <code>ctrl + ⌄ + ↑ or ↓</code>	<code>⌄ + F5</code> <code>⌘ + ⌄ + ↑ or ↓</code>	Clone root Expand or Shrink block selection region
<code>ctrl + ⌄ + ↑ + ↑ or ↓</code> <code>⌄ + Arrows</code>	<code>⌘ + ⌄ + ↑ + ↑ or ↓</code> <code>⌄ + Arrows</code>	Move statements Up or Down Extend the selected region to siblings
<code>ctrl + W</code>	<code>⌘ + W</code>	Select successively increasing code blocks
<code>ctrl + ⌄ + W</code>	<code>⌘ + ⌄ + W</code>	Decrease current selection to previous state

Windows or Linux	MacOS	Action
ctrl + Y	⌘ + Y	Delete line
ctrl + Z	⌘ + Z	Undo
ctrl + ⌂ + Z	⌘ + ⌂ + Z	Redo
⌞ + F12	⌞ + F12	Show note in AST explorer
F5	F5	Refresh
ctrl + MINUS	⌘ + MINUS	Collapse
ctrl + ⌂ + MINUS	⌘ + ⌂ + MINUS	Collapse all
ctrl + PLUS	⌘ + PLUS	Expand
ctrl + ⌂ + PLUS	⌘ + ⌂ + PLUS	Expand all
ctrl + ⌂ + 0-9	⌘ + ⌂ + 0-9	Set bookmark
ctrl + 0-9	ctrl + 0-9	Go to bookmark
Tab	Tab	Move to the next cell
⌂ + Tab	⌂ + Tab	Move to the previous cell
Insert	ctrl + N	Create Root Node (in the Project View)

Table 5.5: Editing (Part 2/2)

Windows or Linux	MacOS	Action
or 	 or	Go to root node
 	 	Go to declaration Go to file Go to node by id Go to action by name Go to model Go to solution Go to concept declaration Go to concept editor declaration
		Go to next or previous editor tab
		Go to editor (from tool window)
		Hide active or last active window
		Restore default window layout
 F12	 F12	Hide all tool windows Jump to the last tool window

Table 5.6: Navigation (Part 1/2)

Windows or Linux	MacOS	Action
<code>ctrl + E</code> <code>ctrl + ⌘ + Left</code> or <code>Right</code> <code>⌘ + F1</code>	<code>⌘ + E</code> <code>⌘ + ⌘ + Left</code> or <code>Right</code> <code>⌘ + F1</code>	Recent nodes popup Navigate back or forward Select current node in any view
<code>ctrl + H</code> <code>F4 or ⌘</code> <code>ctrl + F4</code> <code>⌘ + 2</code> <code>ctrl + F10</code> <code>ctrl + ⌘ +)</code> <code>ctrl + ⌘ + (</code> <code>ctrl + ⌘ + Right</code> <code>ctrl + ⌘ + Left</code> <code>ctrl + ⌘ + ⌘ + R</code> <code>ctrl + ⌘ + T</code> <code>ctrl + H</code> <code>ctrl + I</code>	<code>⌘ + H</code> <code>F4 or ⌘</code> <code>⌘ + F4</code> <code>⌘ + 2</code> <code>⌘ + F10</code> <code>⌘ + ⌘ + ⌘ +)</code> <code>⌘ + ⌘ + ⌘ + (</code> <code>ctrl + ⌘ + Right</code> <code>ctrl + ⌘ + Left</code> <code>⌘ + ⌘ + ⌘ + ⌘ + R</code> <code>⌘ + ⌘ + T</code> <code>ctrl + H</code> <code>⌘ + I</code>	Concept or Class hierarchy Edit source or View source Close active editor tab Go to inspector Show structure Go to next project window Go to previous project window Go to next aspect tab Go to previous aspect tab Go to type-system rules Show type Show in hierarchy view Inspect node

Table 5.7: Navigation (Part 2/2)

Windows or Linux	MacOS	Action
		Generate current module Generate current model
		Run
		Run context configuration
		Select and run a configuration
		Debug context configuration
		Select and debug a configuration
		Preview generated text
		Show type-system trace

Table 5.8: Generation

Windows or Linux	MacOS	Action
		Override methods
		Implement methods
		Comment or uncomment with block comment
		Show nodes
		Show parameters
		Show node information
		Create new ...
		Go to overriding methods or Go to inherited classifiers
		Go to overridden method

Table 5.9: BaseLanguage and Editing

Windows or Linux	MacOS	Action
 	 	Commit project to VCS
 	 	Update project from VCS
 		VCS operations popup
 	 	Add to VCS
 	 	Browse history
 		Show differences

Table 5.10: Version Control System and Local History

Windows or Linux	MacOS	Action
		Move
 	 	Rename
		Safe Delete
 	 	Inline
 	 	Extract Method
 	 	Introduce Variable
 	 	Introduce constant
 	 	Introduce field
 	 	Extract parameter
 	 	Extract method
 	 	Inline

Table 5.11: Refactoring

Windows or Linux	MacOS	Action
F8	F8	Step over
F7	F7	Step into
↑ + F8	↑ + F8	Step out
F9	F9	Resume
⌘ + F8	⌘ + F8	Evaluate expression
ctrl + F8	⌘ + F8	Toggle breakpoints
ctrl + ↑ + F8	⌘ + ↑ + F8	View breakpoints

Table 5.12: Debugger

