

shinemas2R

An R package to visualize outputs from the data base Seed History and Network Management System (SHiNeMaS)

version 0.10

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Pierre Rivière^{1,2} Yannick de Oliveira³

¹ Réseau Semences Paysannes, 3 avenue de la gare, F-47190 Aiguillon, France

² INRA, UMR 0320, Génétique Quantitative et Evolution, DEAP team, Ferme du Moulin F-91190 Gif sur Yvette, France

³ INRA, UMR 0320, Génétique Quantitative et Evolution, ABI team, Ferme du Moulin F-91190 Gif sur Yvette, France

Contact: pierre@semencespaysannes.org

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Le Réseau Semences Paysannes (the French Farmers' Seeds Network (RSP)), created in 2003, brings together a great diversity of collectives and people who preserve farmers' seeds in fields, orchards, vineyards and gardens. They are involved in supporting the consolidation of local initiatives to maintain and renew cultivated biodiversity through Community Seeds Systems. Over 80 organizations have come together to promote and develop farmers' seeds, and to protect farmers' rights over their seeds.
www.semencespaysannes.org (in french).



The Diversity, Evolution and Adaptation of Populations (DEAP) team led by Isabelle Goldringer is part of INRA UMR 0320 Quantitative Genetic and Evolution. Its work is based on the analysis of the genetic and evolutionary mechanisms underlying evolution and adaptation of crop populations. DEAP develops strategies for on farm management of crop genetic diversity and for plant breeding (evolutionary and/or participatory) adapted to organic and low input agriculture. Assessing the benefits of in-field genetic diversity (variety mixtures, populations) and designing / breeding optimized mixtures adapted to local conditions are also key research objectives.

<http://moulin.inra.fr/index.php/en/team/deap>

The bioinformatics and informatics facility (ABI, Atelier Bioinformatique et Informatique) provides bioinformatics expertise and IT support. The staff includes 6 experts in system administration, software development or bio-analysis, and develops databases and softwares for proteomics, genetics and genomics. ABI offers hardware resources, scientific programming and consulting for DNA, RNA and protein sequence analysis up to genome-wide scale. ABI works in tight collaboration with the Bioinformatics facilities of University Paris-Sud and INRA, and contributes to the future French Bioinformatics Institute.

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Wheat trials on farm within our participatory plant breeding programme, summer 2012, Auvergne, France.
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1 Philosophy of shinemas2R

1.1 What is SHiNeMaS?

Started in 2009, DEAP and ABI teams from INRA Le Moulon developed a data base to store data in a reliable way during research programs dedicated to the study of dynamic management of crop diversity within experimental stations and farmer networks (Thomas, 2011).

From 2011 to 2013, this data base was migrated to Seed History and Network Management System (SHiNeMaS) and has evolved in a participatory plant breeding program involving INRA Le Moulon and the Réseau Semences Paysannes (RSP) on bread wheat (Rivière, 2014).

From 2014 to today, farmers organisations' facilitators informed on their specific needs for their data management, involving other species than bread wheat such as maize, tomatoes or trees. Specific developments were performed to fit the farmers organisations' needs.

SHiNeMaS stores information related to (Figure 1):

- network relations between seed-lots
- data linked to the seed-lots and to the relations between seed-lots

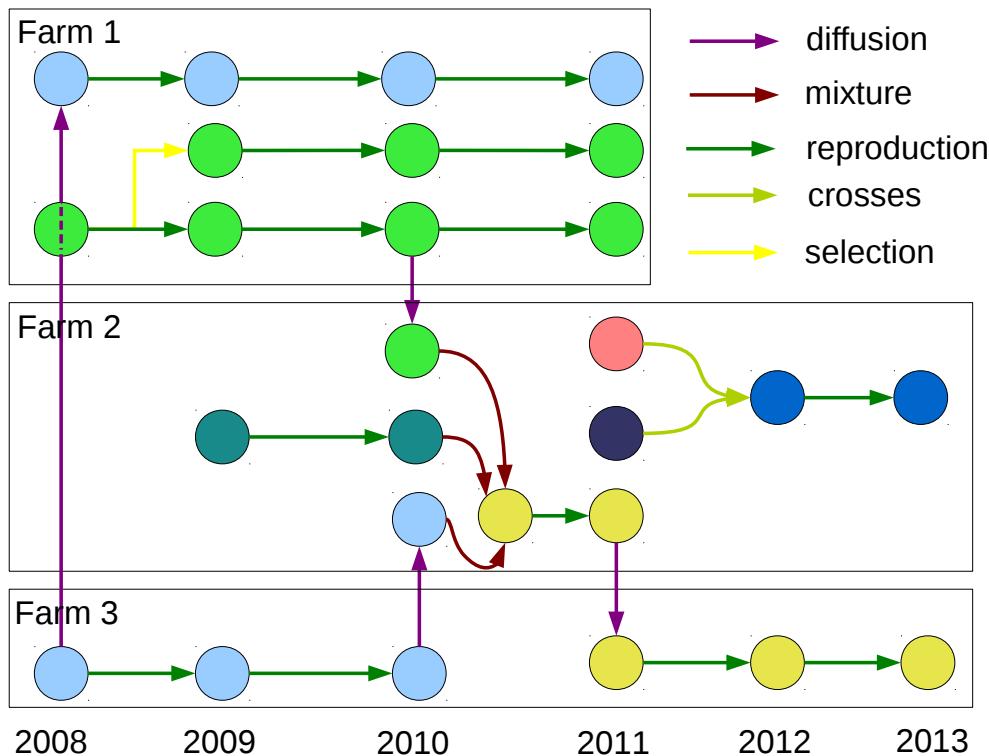


Figure 1: Seed-lots relations in SHiNeMaS. The seed-lots are represented by a circle. The color represents a germplasm (i.e. a variety). The arrows represent the relations between seed-lots (diffusion, mixture, reproduction, crosses and selection). Data are linked to the seed-lots and to the relations between seed-lots.

SHiNeMaS can be downloaded [here](#). More information on the history of SHiNeMaS and its uses with tutorials can be found on the [website](#) (De Oliveira et al., 2015).

shinemmas2R is an R package that analyses outputs from SHiNeMaS. It does descriptive analysis, formats data for existing R packages to perform statistical analysis as well as compiling results in pdf.

1.2 Function relations in shinemas2R

shinemmas2R is divided into three steps (Figure 2):

- Get the data from SHiNeMaS with `get.data`. It is possible to use data in the same format than `get.data` outputs. This can be done with `is.get.data.output`. This is useful when the user do not have SHiNeMaS but wish to use the other functions of the package.

You may encrypt the data with `encrypt.data` or translate it with `translate.data`. There are two types of data:

- network relations between seed-lots (section 3)
- data linked to the seed-lots and to the relations between seed-lots (section 4)

- From the data,

- Get descriptive outputs from the data: plots with `get.ggplot` or tables with `get.table`
- Get statistical outputs by formating the data with `format.data` in order to use an existing R package (the following package can be used: `PPBstats`).

- Get a pdf that compiles the outputs in a pdf document with `get.pdf` (section 6)

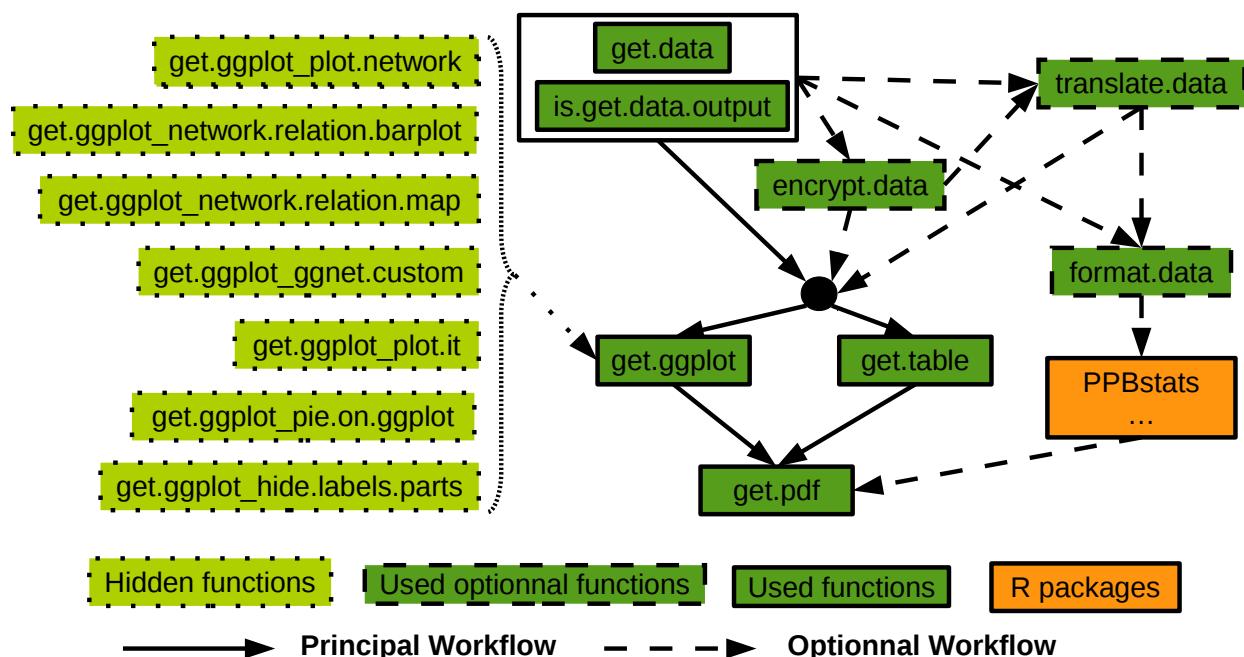


Figure 2: Relations between functions in `shinemasm2R`

`get.ggplot` is based on `ggplot2` package. It is therefore easy to customize a plot generated by `get.ggplot` by adding layers. More details can be found on the `ggplot2` documentation website: <http://ggplot2.org>.

1.3 Let's go!

To continue, load the package:

```
library(shinemasm2R)
```

For an easier visualization in the vignette, all warning messages are not represented (NAs introduced, rows deleted, etc.)

1.3.1 Test with SHiNeMaS installed

It may be useful to test the `get.data` function on SHiNeMaS directly. Two options:

- SHiNeMaS is installed on a server you can have access to. You need to ask the admin the following information: `db_user`, `db_host`, `db_name`, `db_password`. Add these information into `info_db`, which is needed in the next steps in `get.data`. For example:

```
info_db = list(  
    db_user = "pierre",  
    db_host = "127.0.0.1", # localhost  
    db_name = "shinemasm_dev",  
    db_password = "toto"  
)
```

- install a demo of SHiNeMaS on your computer. The procedure to do so is explained in appendix A.

As you will use `get.data`, you should set:

```
use.get.data = TRUE
```

1.3.2 Test without SHiNeMaS installed

In this vignette, you can test `shinemasm2R` without installing SHiNeMaS. You do not use the `get.data` function:

```
use.get.data = FALSE
```

And you can download the data-sets here : https://www.dropbox.com/sh/u1wrwttbn4mq5l4/AACXqZNtzI6TPUeZ-15eyHz_a?dl=0 and put it in the folder data.

The following code is specific to my computer.

```
system("mkdir data")  
system("cp -r /home/pierre/Documents/geek/R-stats/Rdev/R_package_shinemasm2R/shinemasm2R_data/*RData ./data")
```

and then `load()` it.

In this vignette, there are no examples with `is.get.data.output`. Refer to appendix D to know the format that must have the data to be used in the other functions of the package (i.e. `get.ggplot` and `get.table` followed by `get.pdf`).

2 Raw information on levels and variables

Several information are stored in SHiNeMaS. To get information on raw information, levels and variable, you must use the argument `query.type` in `get.data`. The following table summarize the different possibilities:

<code>query.type</code>	type of information present in SHiNeMaS
"species"	species
"variable"	variable
"person"	person
"year"	year
"project"	project
"seed.lot"	seed-lots
"selection.person"	persons that did intra-varietal mass selection
"reproduction.type"	reproduction type
"germplasm.type"	germplasm type
"germplasm"	germplasm

For example,

```
if(use.get.data){  
    person = get.data(  
        db_user = info_db$db_user, db_host = info_db$db_host, # db infos  
        db_name = info_db$db_name, db_password = info_db$db_password, # db infos  
        query.type = "person" # information on person present in SHiNeMaS  
    )  
} else {  
    load("data/person.RData")  
}  
  
person$data  
  
## [1] "JFB" "JSG" "MLN" "OLR"  
## attr(,"shinemasm2R.object")  
## [1] "person"
```

3 Network relations between seed-lots

3.1 Get the data set

To get the data, use the function `get.data` with `query.type = "network"`.

You can set filters to the query with the following argument :

- `filter.in` to choose nothing except `filter.in`
- `filter.out` to choose everything except `filter.out`

values of filters can be `germplasm`, `germplasm.type`, `year`, `person`, `project`, `seed-lots`, `relation` or `reproduction.type`.

It is important to choose if you apply the filter on the `father` or the `son` of a relation. This can be done with the argument `filter.on`. Possibles values are "`father`", "`son`" or "`father-son`". It is set by default to "`father-son`".

It is possible to get the `Mdist` square matrix with the number of reproductions that separate two seed-lots since their last common diffusion (argument `Mdist = TRUE`). Note that a value of 1 means a distance between

- a seed-lot that has been diffused to location A without beeing sown and harvested on location B and
- a seed-lot that has been diffused to location B and beeing sown and harvested on location B

This square matrix can be compared to a differentiation distance. It can be put in relation with genetic F_{st} for example (Nei, 1973)¹.

```
if(use.get.data){  
    data_network = get.data(  
        db_user = info_db$db_user, db_host = info_db$db_host, # db infos  
        db_name = info_db$db_name, db_password = info_db$db_password, # db infos  
        query.type = "network", # network query  
        filter.on = "father-son", # filter on father AND son  
        Mdist = TRUE  
    )  
}  
} else {  
    # 1. Query SHiNeMaS ...  
    # Mixtures from replication have been deleted and replaced by reproductions.  
    # 2. Create network matrix ...  
    # 3. Link information to vertex and edges ...  
    # 4. Get network information on seed-lots ...  
    # 5. Get Mdist square matrix ...  
  
    load("./data/data_network.RData")  
}
```

The function returns a list with:

- the netwok object

```
n = data_network$data$network  
n  
  
## Network attributes:  
##   vertices = 98  
##   directed = TRUE  
##   hyper = FALSE  
##   loops = FALSE  
##   multiple = FALSE
```

¹The R package `adegenet` can be used for that.

```

##  bipartite = FALSE
##  total edges= 102
##  missing edges= 0
##  non-missing edges= 102
##
##  Vertex attribute names:
##      germplasm germplasm.type person sex vertex.names year
##
##  Edge attribute names:
##      generation relation

```

Note you can convert this object to an `igraph` object. This may be useful if you like to use the `igraph` package. See <http://mbojan.github.io/intergraph/> for more information.

```

n_igraph = intergraph::asIgraph(n)
n_igraph

## IGRAPH D--- 98 102 --
## + attr: germplasm (v/c), germplasm.type (v/c), na (v/l),
## | person (v/c), sex (v/c), vertex.names (v/c), year (v/c),
## | generation (e/c), na (e/l), relation (e/c)
## + edges:
## [1] 7-> 1 1-> 2 7-> 2 2-> 3 1-> 4 5-> 7 6-> 7 12-> 8 1-> 9
## [10] 9->10 1->11 11->12 6->14 13->14 14->15 15->16 16->17 15->18
## [19] 18->19 25->20 20->21 20->22 22->23 13->25 24->25 20->26 30->27
## [28] 20->28 28->29 22->30 37->31 31->32 31->33 33->34 33->35 24->37
## [37] 36->37 31->38 35->39 31->40 40->41 46->42 42->43 13->45 44->45
## [46] 45->46 46->47 42->48 51->49 49->50 6->51 36->51 49->52 49->53
## + ... omitted several edges

```

- the network.query dataframe coming from the query

```

head(data_network$data$network.query)

##   son_species son_project          son son_germplasm
## 1 ble-tendre     DEMO C1#a_JFB_2013_0001            C1
## 2 ble-tendre     DEMO C1#a_JFB_2014_0001            C1
## 3 ble-tendre     DEMO C1#a_JSG_2014_0001            C1
## 4 ble-tendre     DEMO C1#c_JFB_2014_0001            C1
## 5 ble-tendre     DEMO C1_JFB_2011_0001            C1
## 6 ble-tendre     DEMO C1_JFB_2011_0001            C1
##   son_person son_year son_germplasm_type son_alt son_long  son_lat
## 1       JFB    2013             <NA>      NA 0.616363 44.20314
## 2       JFB    2014             <NA>      NA 0.616363 44.20314
## 3       JSG    2014             <NA>      NA 3.087025 45.77722
## 4       JFB    2014             <NA>      NA 0.616363 44.20314
## 5       JFB    2011             <NA>      NA 0.616363 44.20314
## 6       JFB    2011             <NA>      NA 0.616363 44.20314
##   son_total_generation_nb son_local_generation_nb
## 1                      1                         1
## 2                      1                         3
## 3                      2                         1
## 4                      1                         5
## 5                      2                         8
## 6                      5                         2

```

```

##   son_generation_confidence son_comments father_species
## 1                         1    blablabla    ble-tendre
## 2                         0    blablabla    ble-tendre
## 3                         1    blablabla    ble-tendre
## 4                         1    blablabla    ble-tendre
## 5                         1    blablabla    ble-tendre
## 6                         1    blablabla    ble-tendre
##   father_project          father father_germplasm
## 1      DEMO            C1_JFB_2012_0001           C1
## 2      DEMO            C1#a_JFB_2013_0001           C1
## 3      DEMO            C1#a_JFB_2014_0001           C1
## 4      DEMO            C1_JFB_2013_0001           C1
## 5      DEMO    Blé-du-Lot_JFB_2010_0001    Blé-du-Lot
## 6      DEMO  Rouge-du-Roc_JFB_2010_0001  Rouge-du-Roc
##   father_person father_year father_germplasm_type father_alt
## 1      JFB        2012             <NA>       NA
## 2      JFB        2013             <NA>       NA
## 3      JFB        2014             <NA>       NA
## 4      JFB        2013             <NA>       NA
## 5      JFB        2010             <NA>       NA
## 6      JFB        2010             <NA>       NA
##   father_long father_lat father_total_generation_nb
## 1  0.616363  44.20314                  5
## 2  0.616363  44.20314                  5
## 3  0.616363  44.20314                  2
## 4  0.616363  44.20314                  1
## 5  0.616363  44.20314                  8
## 6  0.616363  44.20314                  6
##   father_local_generation_nb father_generation_confidence
## 1                           6                      0
## 2                           7                      0
## 3                           8                      0
## 4                           4                      0
## 5                           4                      1
## 6                           5                      1
##   father_comments reproduction_id reproduction_method_name is_male
## 1    blablabla           467             <NA>       X
## 2    blablabla           484             <NA>       X
## 3    blablabla           <NA>            <NA>       X
## 4    blablabla           483             <NA>       X
## 5    blablabla           454            cross       M
## 6    blablabla           454            cross       F
##   block selection_id selection_person mixture_id diffusion_id
## 1     1         40            JFB        <NA>      <NA>
## 2     1        <NA>           <NA>        <NA>      <NA>
## 3  <NA>        <NA>           <NA>        <NA>     266
## 4     1         48            JFB        <NA>      <NA>
## 5     1        <NA>           <NA>        <NA>      <NA>
## 6     1        <NA>           <NA>        <NA>      <NA>
##   relation_year_start relation_year_end
## 1                 2012           2013
## 2                 2013           2014
## 3                <NA>           <NA>
## 4                 2013           2014
## 5                 2010           2011
## 6                 2010           2011

```

- the network.info matrix with information on relation in the network.

```
head(data_network$data$network.info)

##          sl alt      long      lat diffusion id.diff
## 1 C1#a_JFB_2013_0001 NA 0.616363 44.20314    <NA>    <NA>
## 2 C1#a_JFB_2014_0001 NA 0.616363 44.20314    <NA>    <NA>
## 3 C1#a_JSG_2014_0001 NA 3.087025 45.77722  receive     19
## 4 C1#c_JFB_2014_0001 NA 0.616363 44.20314    <NA>    <NA>
## 5 C1_JFB_2011_0001 NA 0.616363 44.20314    <NA>    <NA>
## 6 C1_JFB_2011_0001 NA 0.616363 44.20314    <NA>    <NA>
##   reproduction mixture selection cross.info germplasm person year
## 1       <NA>    <NA> selection    <NA>      C1    JFB 2013
## 2 harvest    <NA>    <NA>    <NA>      C1    JFB 2014
## 3       <NA>    <NA>    <NA>    <NA>      C1    JSG 2014
## 4       <NA>    <NA> selection    <NA>      C1    JFB 2014
## 5 harvest-sow <NA>    <NA>    <NA>      C1    JFB 2011
## 6 harvest-sow <NA>    <NA>    <NA>      C1    JFB 2011
```

- the Mdist square matrix

```
dim(data_network$data$Mdist)

## [1] 98 98
```

You may want to fill gaps into your network data set regarding diffusion events (if the information is stored in SHiNeMaS!). This may be usefull, regarding a network on one person, to know where seed-lots come from. To do so, use `fill.diffusion.gap = TRUE`.

```
if(use.get.data){
  data_network_OLR = get.data(
    db_user = info_db$db_user, db_host = info_db$db_host, # db infos
    db_name = info_db$db_name, db_password = info_db$db_password, # db infos
    query.type = "network", # network query
    person.in = "OLR", # person to keep
    filter.on = "father-son" # filter on father AND son
  )
} else {
  # 1. Query SHiNeMaS ...
  # Mixtures from replication have been deleted and replaced by reproductions.
  # 2. Create network matrix ...
  # 3. Link information to vertex and edges ...
  # 4. Get network information on seed-lots ...

  load("./data/data_network_OLR.RData")
}

if(use.get.data){
  data_network_OLR_fill_gap = get.data(
    db_user = info_db$db_user, db_host = info_db$db_host, # db infos
    db_name = info_db$db_name, db_password = info_db$db_password, # db infos
    query.type = "network", # network query
    person.in = "OLR", # person to keep
    filter.on = "father-son", # filter on father AND son
  )
}
```

```

        fill.diffusion.gap = TRUE
    )
} else {
    # 1. Query SHiNeMaS ...
    # Mixtures from replication have been deleted and replaced by reproductions.
    # 2. Create network matrix ...
    # 2.1. Fill diffusion gaps ...
    # 3. Link information to vertex and edges ...
    # 4. Get network information on seed-lots ...

    load("./data/data_network_OLR_fill_gap.RData")
}

```

Sometimes, seed-lots are replicated and then mixed. This can be seen as 'false' mixture compared to 'real' mixture where the germplasm father and son are different. In order to take this into account in the analysis of the network, it can be useful to delete the 'false' mixture and declare it as a reproduction. This can be done with the argument `mixrep_to_repro` which transform the mixtures of replications into reproductions, i.e. the network keeps only 'real' mixtures (i.e. different germplasm for father and son) and correct the information regarding what have been harvested and sown after as the mixture disappear. The value of `mixrep_to_repro` is `TRUE` by default.

3.2 Get the ggplots

Once, you have got the data, you can create plots with the function `get.ggplot`.

```

default_network_ggplot = get.ggplot(data_network)

## As ggplot.type is NULL, ggplot.type is set to network-network, network-reproduction-sown,
## network-reproduction-harvested, network-reproduction-positive-inter-selected, network-reproduction-po
## network-reproduction-negative-inter-selected, network-reproduction-crossed, network-diffusion-sent,
## network-diffusion-received, network-diffusion-relation, network-mixture-real, network-mixture-rep,
## network-mixture-all, network-positive-intra-selected
## As ggplot.display is NULL, ggplot.display is set to c("barplot", "map"). Note that for
## ggplot.type == "network-diffusion-relation", ggplot.display is set to "map"
## As x.axis and in.col are NULL, all the combinaisons of x.axis and in.col are done for barplot.

## [1] "A METTRE A JOUR QUAND ON AURA EVENT YEAR"
## [1] "A METTRE A JOUR QUAND ON AURA EVENT YEAR"

```

By default, all the possible plots or maps are done.

```

names(default_network_ggplot)

## [1] "network-network"
## [2] "network-reproduction-sown"
## [3] "network-reproduction-harvested"
## [4] "network-reproduction-positive-inter-selected"
## [5] "network-reproduction-negative-inter-selected"
## [6] "network-diffusion-sent"
## [7] "network-diffusion-received"
## [8] "network-diffusion-relation"
## [9] "network-mixture-real"
## [10] "network-mixture-rep"
## [11] "network-mixture-all"
## [12] "network-positive-intra-selected"
## [13] "network-reproduction-crossed"

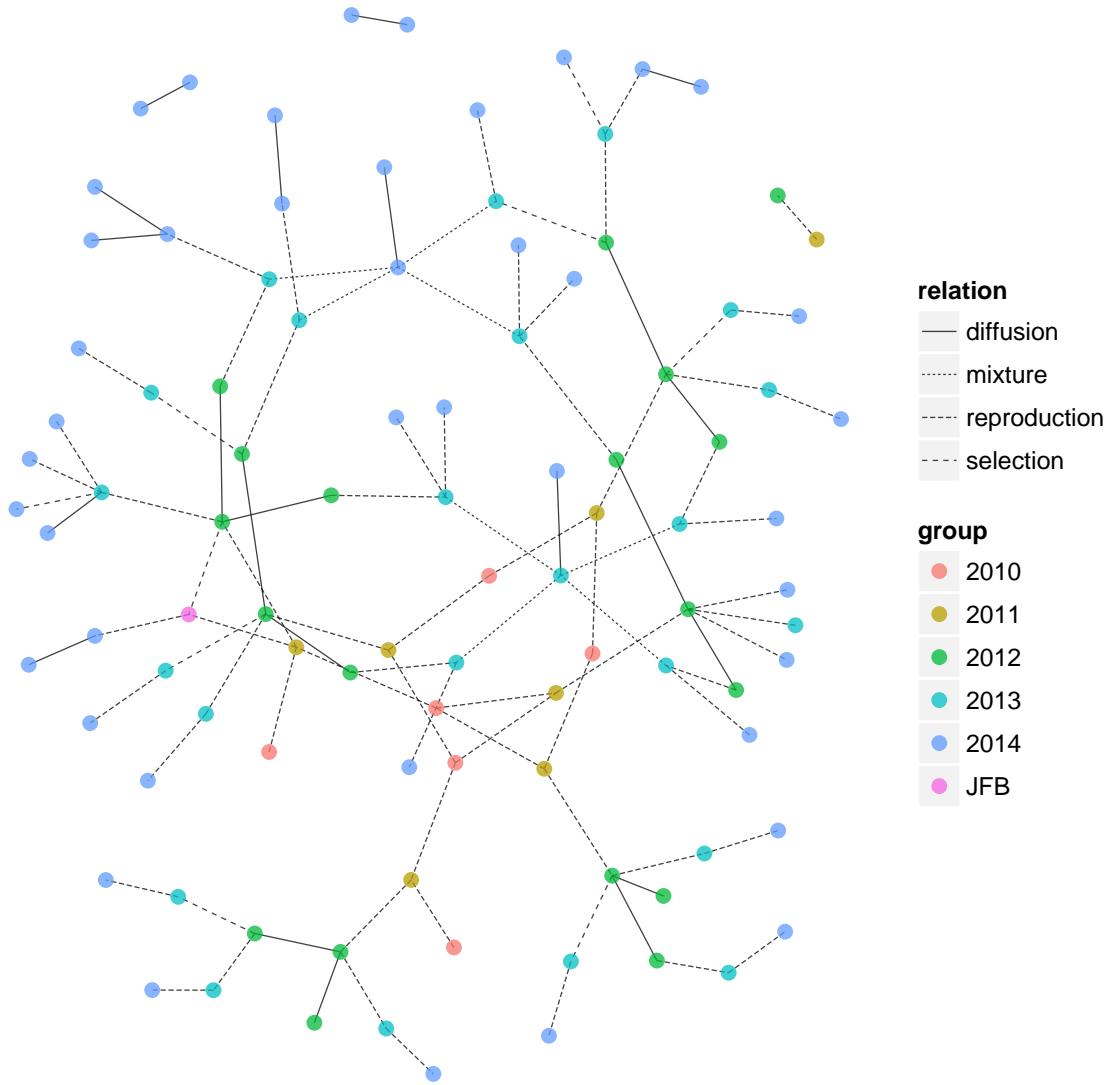
```

It is possible to get only one plot by choosing one of the above names with the argument `ggplot.type`. Each `ggplot.type` with default and custom arguments are explained in the following sub-sections.

3.2.1 ggplot.type = "network-network"

Default arguments By default, the following network is displayed:

```
p_net_C1 = default_network_ggplot$"network-network"
p_net_C1
```



Regarding the argument `fill.diffusion.gap` in the function `get.data`:

```
p_OLR = get.ggplot(
  data_network_OLR,
  ggplot.type = "network-network",
  vertex.color = "person"
)
p_OLR = p_OLR$`network-network`

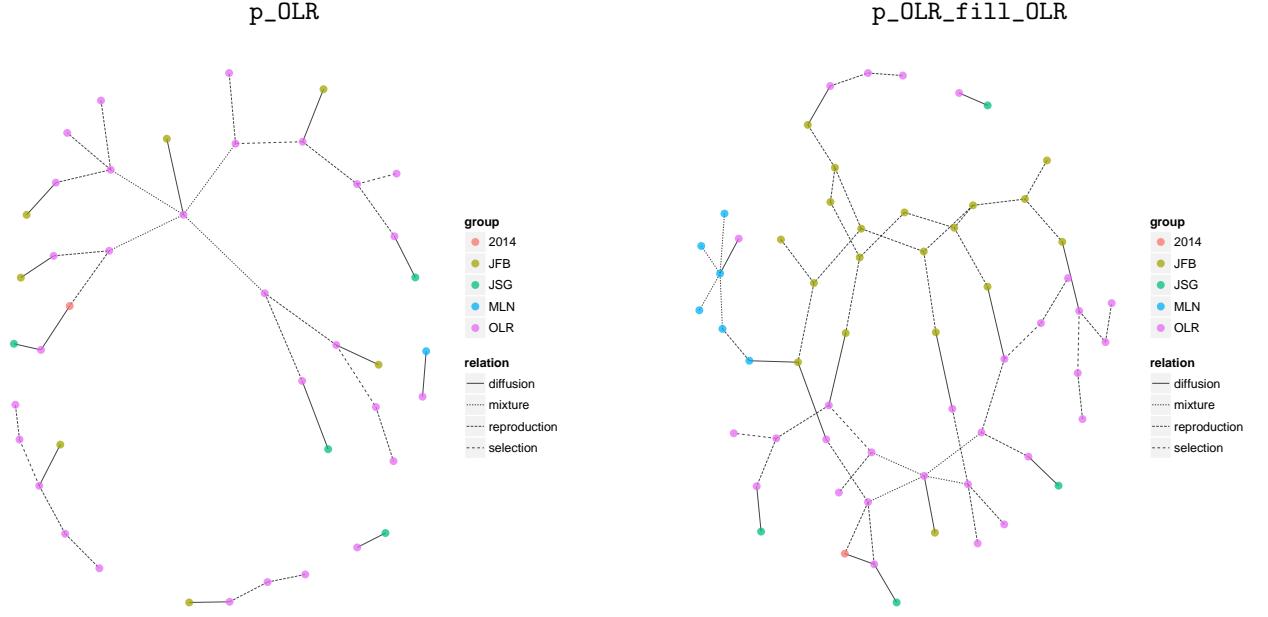
p_OLR_fill_gap = get.ggplot(
  data_network_OLR_fill_gap,
```

```

ggplot.type = "network-network",
vertex.color = "person"
)
p_OLR_fill_gap = p_OLR_fill_gap`network-network`

```

We can see that extra information are added to know from where the seed-lots come from.



Custom arguments It is possible to tune the following arguments (Table 1):

argument	default value	description
vertex.size	3	size of the vertex
vertex.color	"year"	color of the vertex. It can be chosen according to "person", "germplasm" or "year". If NULL, it is in black.
organise.sl	FALSE	organize seed-lots for an easier visualization
hide.labels.parts	"all"	parts of the label hidden: "germplasm", "person", "year", "person:germplasm", "year:germplasm", "person:year", "all". "all" means that no label is displayed. If NULL labels are displayed. Labels are based on seed-lots names under the form <code>germplasm_year_person_digit</code> . For easier visualisation, digit is never display unless you choose NULL.
labels.sex	TRUE	if TRUE, display the sex of the seed-lot if it has been used in a cross. Nothing is displayed if hide.labels.parts = "all".
labels.generation	TRUE	if TRUE, display generation for each reproduction.
labels.size	3	size of the labels

Table 1: Possible arguments to custom arguments regarding network.

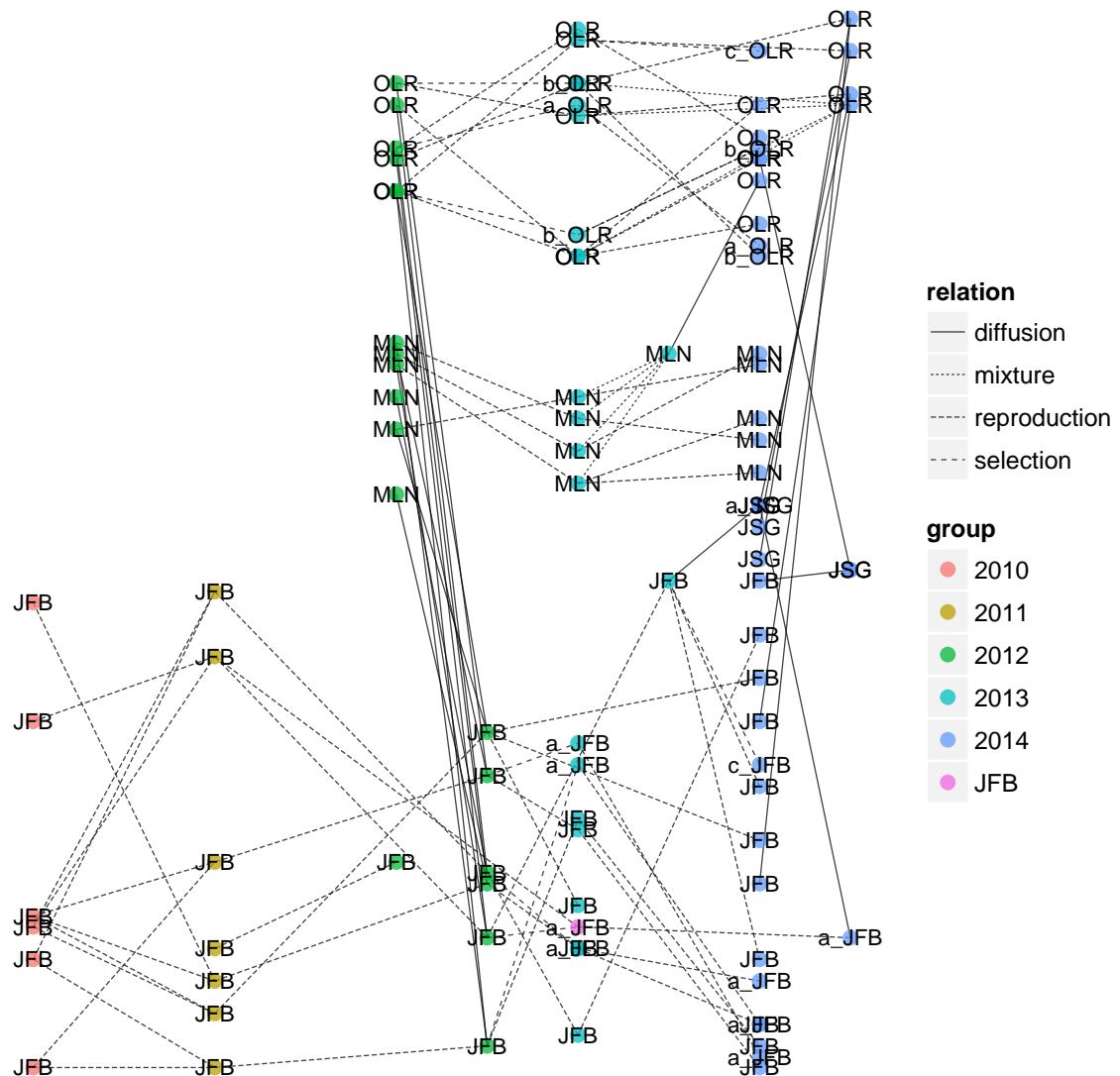
For example,

```

get.ggplot(
  data_network,
  ggplot.type = "network-network",
  organise.sl = TRUE,
  hide.labels.parts = "year:germplasm",
  vertex.color = "year"
)

## $`network-network`

```



3.2.2 ggplot.type = "network-reproduction-harvested"

ggplot.type = "network-reproduction-harvested" corresponds to seed-lots that have been harvested after a reproduction.

Two plots are possible regarding ggplot.display.

argument	default value	description
ggplot.display	NULL	"barplot" or "map". It can be a vector of several elements i.e. c("barplot", "map"). NULL by default: both are done.

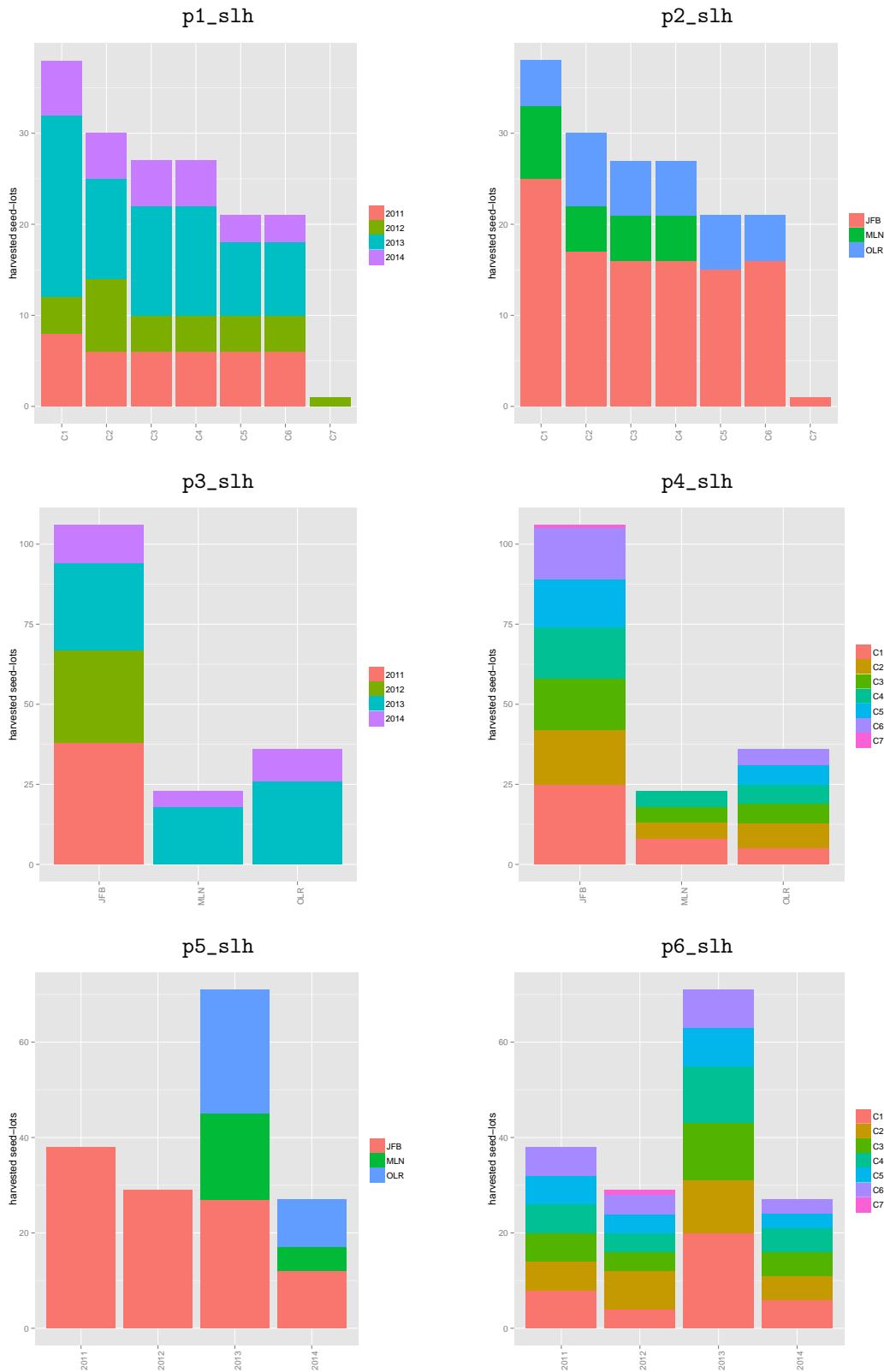
ggplot.display = barplot For ggplot.display = "barplot", you may chose what you want in the x axis (`x.axis` argument) and in color (`in.col` argument). The possible values for `x.axis` and `in.col` are: `germplasm`, `year`, `person`. By default all combinaisons of `x.axis` and `in.col` are done with default argument settings. The name of the plot is under the form `x.axis-in.col`.

- Default arguments

```
p_slh = default_network_ggplot$`network-reproduction-harvested`$barplot
p1_slh = p_slh$`germplasm-year`$`x.axis-1|in.col-1`
p2_slh = p_slh$`germplasm-person`$`x.axis-1|in.col-1`
p3_slh = p_slh$`person-year`$`x.axis-1|in.col-1`
p4_slh = p_slh$`person-germplasm`$`x.axis-1|in.col-1`
p5_slh = p_slh$`year-person`$`x.axis-1|in.col-1`
p6_slh = p_slh$`year-germplasm`$`x.axis-1|in.col-1`
```

with

plot	x.axis	in.col
p1_slh	"germplasm"	"year"
p2_slh	"germplasm"	"person"
p3_slh	"person"	"year"
p4_slh	"person"	"germplasm"
p5_slh	"year"	"person"
p6_slh	"year"	"germplasm"



- Custom arguments

It is possible to tune the following arguments:

argument	default value	description
x.axis	NULL	factor displayed on the x.axis of a plot: "germplasm", "year" or "person" referring to the attributes of a seed-lots. If NULL, all the combinaison are done for x.axis and in.col.
in.col	NULL	display in color of a plot: "germplasm", "year" or "person" referring to the attributes of a seed-lots. If NULL, in.col is not displayed.
nb_parameters_per_plot_x.axis	NULL	the number of parameters per plot on x.axis argument
nb_parameters_per_plot_in.col	NULL	the number of parameters per plot for in.col argument

Table 2: Possible arguments to custom arguments regarding barplot.

For example, for a given `x.axis` and a given `in.col`:

```
p_slh = get.ggplot(  
    data_network,  
    ggplot.type = "network-reproduction-harvested",  
    ggplot.display = "barplot",  
    x.axis = "person",  
    in.col = "year"  
)
```

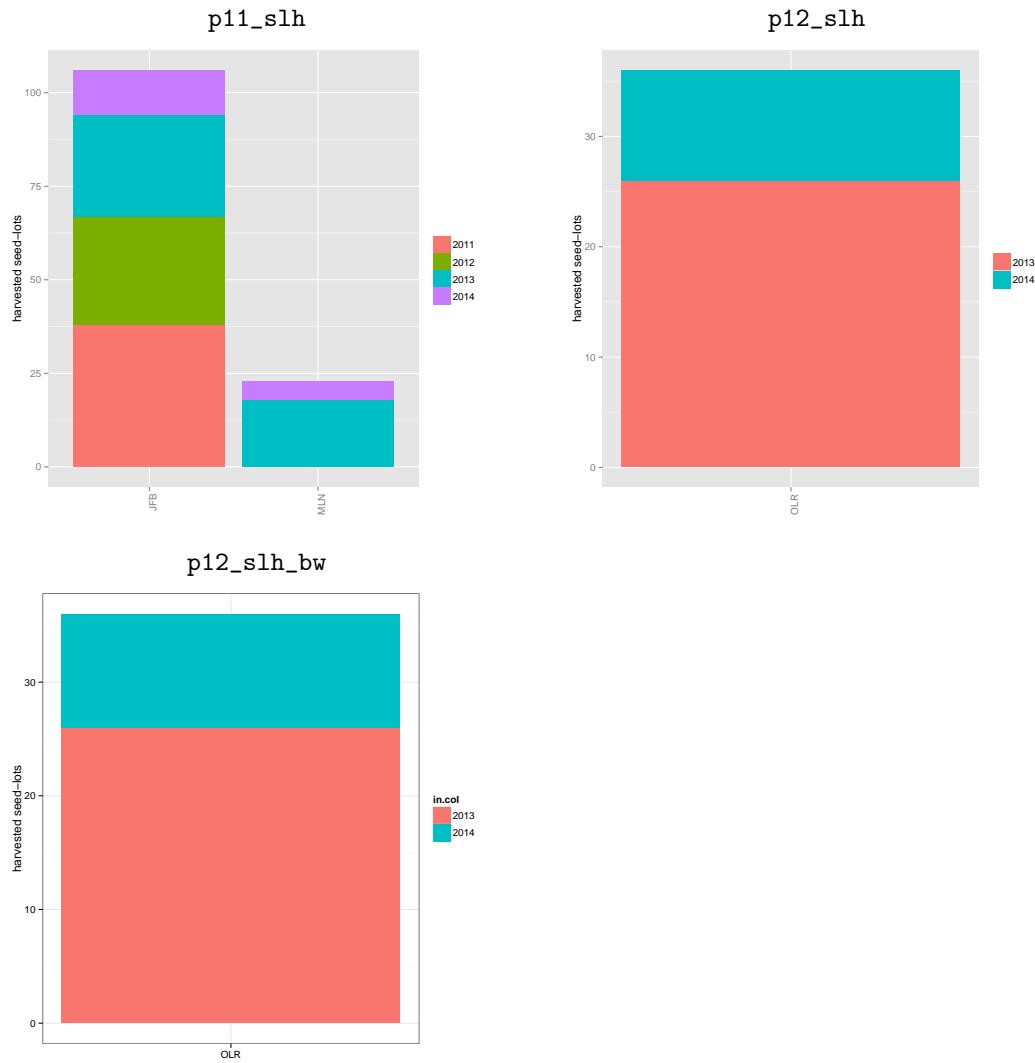
It can be useful to separate the plot in several plots regarding x.axis:

```
p1_slh = get.ggplot(  
    data_network,  
    ggplot.type = "network-reproduction-harvested",  
    ggplot.display = "barplot",  
    x.axis = "person",  
    in.col = "year",  
    nb_parameters_per_plot_x.axis = 2  
)
```

```
p11_slh = p1_slh$`network-reproduction-harvested`$barplot$`person-year`$`x.axis-1`in.col-1`  
p12_slh = p1_slh$`network-reproduction-harvested`$barplot$`person-year`$`x.axis-2`in.col-1`
```

Note that you can easily change settings of the plot as it is a `ggplot` object, for example

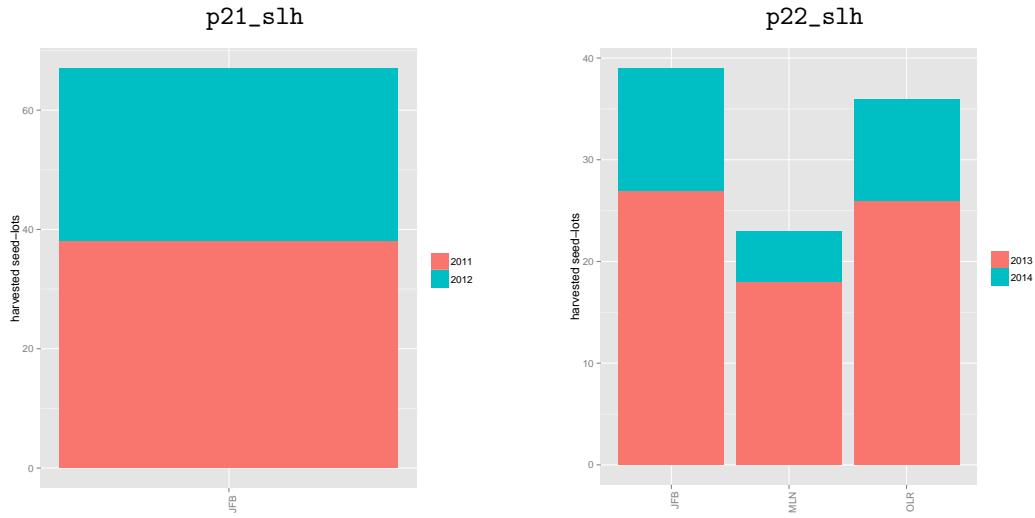
```
p12_slh_bw = p12_slh + theme_bw()
```



Or for `in.col`:

```
p2_slh = get.ggplot(
    data_network,
    ggplot.type = "network-reproduction-harvested",
    ggplot.display = "barplot",
    x.axis = "person",
    in.col = "year",
    nb_parameters_per_plot_in.col = 2
)

p21_slh = p2_slh$`network-reproduction-harvested`$barplot$`person-year`$`x.axis-1|in.col-1`  
p22_slh = p2_slh$`network-reproduction-harvested`$barplot$`person-year`$`x.axis-1|in.col-2`
```



Or for both, for each subset of `x.axis`, you have the set of `in.col`.

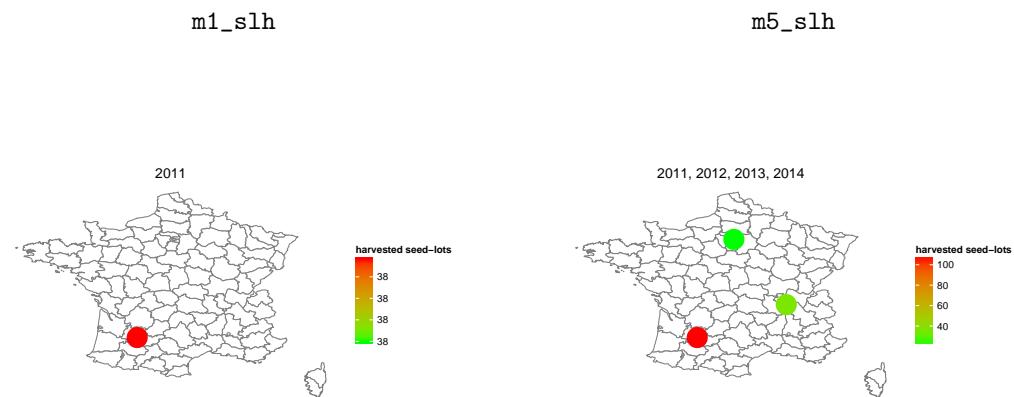
`ggplot.display = map` There are as many maps as years and a map with all the years mixed. The scale represent the number of seed-lots harvested.

- Default arguments

```
m_slh = default_network_ggplot$`network-reproduction-harvested`$map
names(m_slh)

## [1] "map-[2011]"           "map-[2012]"
## [3] "map-[2013]"           "map-[2014]"
## [5] "map-[2011, 2012, 2013, 2014]"

m1_slh = m_slh$`map-[2011]` 
m5_slh = m_slh$`map-[2011, 2012, 2013, 2014]`
```



- Custom arguments

It is possible to tune the following arguments (Table 3):

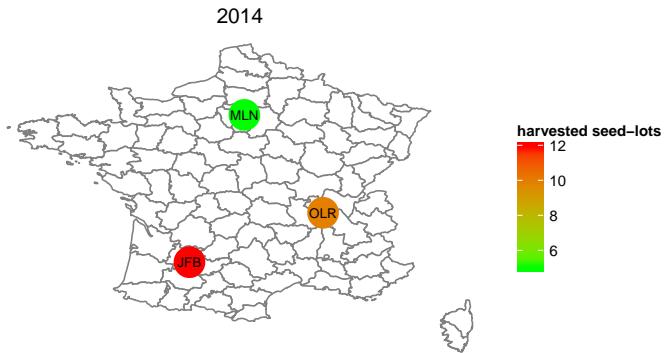
argument	default value	description
hide.labels.parts	NULL	can be NULL or "all" as only person can be display. NULL by default
labels.size	3	size of the labels
location.map	"france"	location of the map see ?map for more details
pie.size	.5	size of the pie when using pies

Table 3: Possible arguments to custom arguments regarding maps.

For example,

```
p_slh = get.ggplot(
  data_network,
  ggplot.type = "network-reproduction-harvested",
  ggplot.display = "map",
  hide.labels.parts = NULL
)

p_slh$`network-reproduction-harvested`$map$`map-[2014]`
```



3.2.3 ggplot.type = "network-diffusion-relation"

ggplot.type = "network-diffusion-relation" corresponds to diffusion of seed-lots on a map. Note that ggplot.display is useless here.

There are as many maps as years and a map with all the years mixed. The size of the arrows is proportional to the number of diffusions (nb_diffusions).

- Default arguments

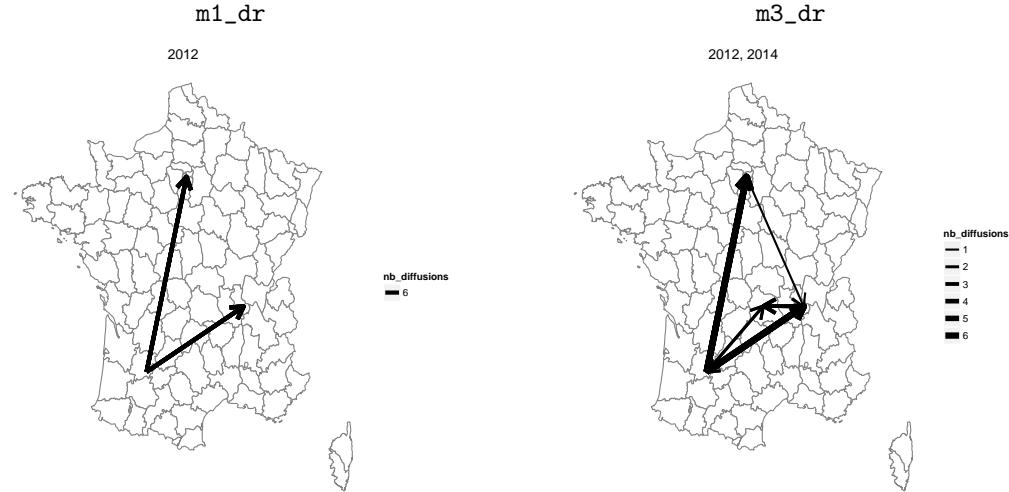
```

m_dr = default_network_ggplot$`network-diffusion-relation`$map
names(m_dr)

## [1] "map-[2012]"      "map-[2014]"      "map-[2012, 2014]"

m1_dr = m_dr$`map-[2012]` 
m3_dr = m_dr$`map-[2012, 2014]` 

```



- Custom arguments

Arguments can be customized related to maps. See Table 3.

3.2.4 ggplot.type = "network-reproduction-crossed"

Information on the crosses, their parents (mother and father) and grandparents (grandmother and grandfather). It may be useful to know information on grandparents, especially location, if the cross have been done on another location.

Note that in this example, it represents all the cross where Rouge-du-Roc is involved as "father" or "son" in relation. This is because in `get.data`, the following arguments were set: `germplasm.in = Rouge-du-Roc` and `filter.on = "father-son"`.

- Default arguments

```

cb = default_network_ggplot$`network-reproduction-crossed`$barplot
names(cb)

## [1] "cross"       "father"       "grandfather"  "mother"
## [5] "grandmother"

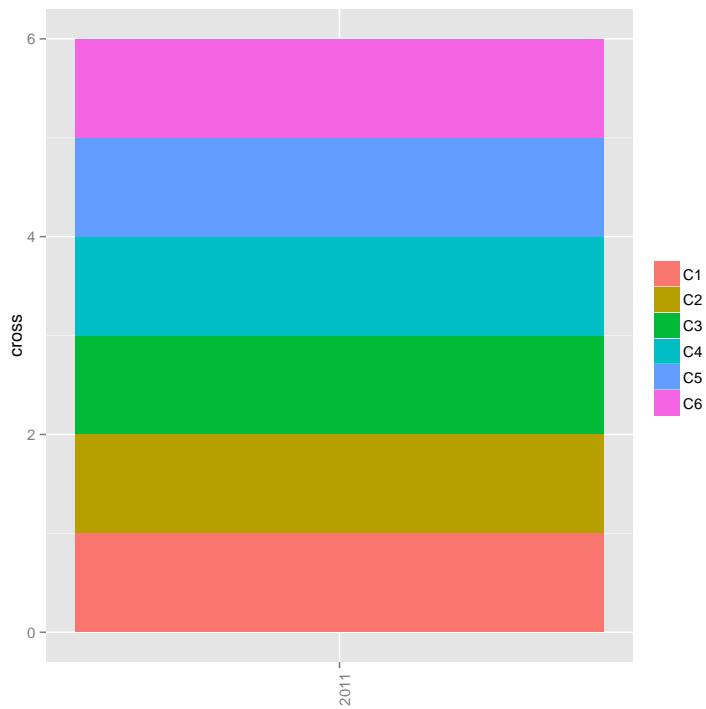
cm = default_network_ggplot$`network-reproduction-crossed`$map
names(cm)

## [1] "cross"       "father"       "grandfather"  "mother"
## [5] "grandmother"

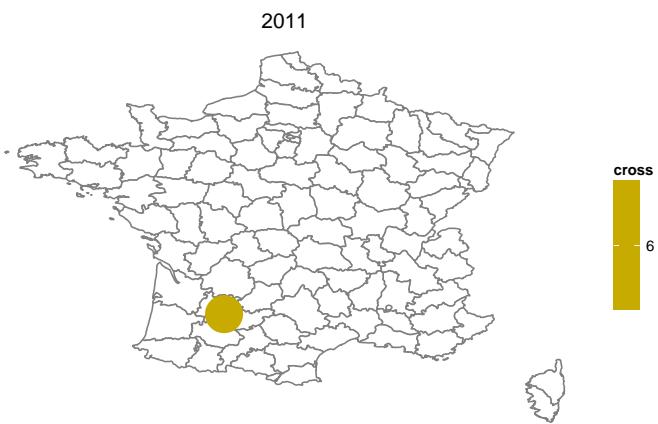
```

For example:

```
cb$cross$barplot$`year-germplasm`$`x.axis-1|in.col-1`
```



```
cm$cross$map$`map-[2011]`
```



- Custom arguments

Arguments can be customized related to barplots (Table 2) or maps (Table 3).

3.2.5 Others ggplot.type

For the other `ggplot.type`, as it is exactly the same type of plots than for `ggplot.type = "network-reproduction-harvest"` no example is displayed in this vignette.

The following table describe the different `ggplot.type`:

<code>ggplot.type</code>	description
"network-reproduction-sown"	seed-lots that have been sown.
"network-reproduction-positive-inter-selected"	seed-lots that have been harvested after a reproduction and have been sown the next season. It corresponds to positive inter selection.
"network-reproduction-negative-inter-selected"	seed-lots that have been harvested after a reproduction and have NOT been sown the next season. It corresponds to negative inter selection.
"network-diffusion-sent"	seed-lots that have been sent to another location.
"network-diffusion-received"	seed-lots that have been received in a given location.
"network-mixture-real"	seed-lots that have been 'really' mixed into a mixture.
"network-mixture-rep"	seed-lots coming from replication that have been mixed into a mixture. Note that it is <code>NULL</code> when the argument <code>mixrep_to_repro</code> in <code>get.data</code> is <code>TRUE</code> (default argument).
"network-mixture-all"	seed-lots that have been mixed into a mixture (i.e. "network-mixture-real" + "network-mixture-rep").
"network-positive-intra-selected"	seed-lots where intra germplasm selection have been done. It corresponds to mass selection.

3.3 Get the tables

It is possible to get the table from the data used for the plot. For example,

```
p = default_network_ggplot`network-reproduction-crossed`$barplot$cross$barplot
p = p$`year-germplasm`$`x.axis-1|in.col-1`
tab_p = get.table(p)
tab_p

##   mean germplasm year
## 1     1       C1 2011
## 2     1       C2 2011
## 3     1       C3 2011
## 4     1       C4 2011
## 5     1       C5 2011
## 6     1       C6 2011
```

4 Data linked to the seed-lots and to the relations between seed-lots

4.1 Get the data set

Three types of queries are possible:

- `query.type = "data-classic"` to study classic variables for each seed-lot or relation between seed-lots (subsection 4.1.1)
- `query.type = "data-S"` to study selection differential (subsection 4.1.2)
- `query.type = "data-SR"` to study response to selection (subsection 4.1.2)

You can set filters to the query with the following argument :

- `filter.in` to choose nothing except `filter.in`
- `filter.out` to choose everything except `filter.out`

values of filters can be `germplasm`, `germplasm.type`, `year`, `person`, `project`, `seed-lots`, `relation`, `reproduction.type` or `variable`.

It is important to choose if you apply the filter on the `father` or the `son` of a relation. This can be done with the argument `filter.on`. Possible values are "`father`", "`son`" or "`father-son`".

You can either query information on relation between seed-lots or on seed-lots. This is set with the argument `data.type`. Possibles values are

- "`relation`" for data linked to relation between seed lots and
- "`seed-lots`" for data linked to seed lots

The function returns a list with

- a data frame with the data set
- a list with data set with individuals that are correlated for a set of variables
- the description of methods used for each variable with its description and units

Note that for data linked to seed-lots, all the data are correlated as there is one measure for a given seed-lot. Therefore the element of the list for correlated data is always NULL. For data linked to relations, as it can be linked to individual within a seed-lot, data may be correlated (data taken on the same individual) or not.

A data set with only correlated variables for each individual is useful when doing multivariate analysis such as PCA.

The names of the variables in the output of the function are under the form `variable_name--methods`.

In the following examples, three variables are studied:

```
vec_variables = c("hauteur", "pmg", "poids_episodes")
```

4.1.1 `query.type = "data-classic"`

```
if(use.get.data){  
    data_classic = get.data(  
        db_user = info_db$db_user, db_host = info_db$db_host, # db infos  
        db_name = info_db$db_name, db_password = info_db$db_password, # db infos  
        query.type = "data-classic", # data-classic query  
        person.in = "JFB", # person to keep  
        filter.on = "father-son", # filters on father AND son
```

```

        data.type = "relation", # data linked to relation between seed-lots
        variable = vec_variables, # the variables to display
        project.in = "DEMO" # the project
    )
}

} else {
    # 1. Query SHiNeMaS ...
    # 2. Set up data set ...
    # ===== / 100%
}

load("./data/data_classic.RData")
}

names(data_classic$data)

## [1] "data"
## [2] "data.with.correlated.variables"
## [3] "methods"

colnames(data_classic$data$data)

## [1] "son_species"                      "son_project"
## [3] "son"                             "son_ind"
## [5] "son_year"                        "son_germplasm"
## [7] "son_germplasm_type"              "son_person"
## [9] "son_alt"                         "son_long"
## [11] "son_lat"                         "son_total_generation_nb"
## [13] "son_local_generation_nb"         "son_generation_confidence"
## [15] "son_comments"                    "father_species"
## [17] "father_project"                 "father"
## [19] "father_year"                    "father_germplasm"
## [21] "father_germplasm_type"          "father_person"
## [23] "father_alt"                     "father_long"
## [25] "father_lat"                     "father_total_generation_nb"
## [27] "father_local_generation_nb"     "father_generation_confidence"
## [29] "father_comments"                "reproduction_id"
## [31] "reproduction_method_name"       "selection_id"
## [33] "selection_person"               "mixture_id"
## [35] "diffusion_id"                  "relation_year_start"
## [37] "relation_year_end"              "X"
## [39] "Y"                             "block"
## [41] "hauteur---hauteur_tige"        "hauteur---hauteur_tige$date"
## [43] "pmg---pmg"                     "pmg---pmg-2"
## [45] "pmg---pmg-2$date"              "pmg---pmg$date"
## [47] "poids_epis---poids_epis"       "poids_epis---poids_epis$date"

head(data_classic$data$methods)

##   method_name variable_name method_description unit
## 1 hauteur_tige      hauteur
## 2   poids_epis      poids_epis
## 3         pmg          pmg
## 4         pmg-2         pmg
##   variable---methods
## 1 hauteur---hauteur_tige
## 2   poids_epis---poids_epis
## 3           pmg---pmg
## 4           pmg---pmg-2

```

The data with correlated variables :

```
names(data_classic$data$data.with.correlated.variables)
## [1] "A_2013" "B_2013" "A_2014" "B_2014"
```

The methods related to each variable :

```
data_classic$data$methods

##   method_name variable_name method_description unit
## 1 hauteur_tige      hauteur
## 2 poids_epis       poids_epis
## 3          pmg        pmg
## 4          pmg-2       pmg
##      variable---methods
## 1 hauteur---hauteur_tige
## 2 poids_epis---poids_epis
## 3           pmg---pmg
## 4           pmg---pmg-2
```

4.1.2 Selection differential (query.type = "data-S"), response to selection (query.type = "data-SR") and heritability

For a given trait, selection differential corresponds to the difference between mean of the selected spikes and mean of the bulk (i.e. spikes that have not been selected). Response to selection corresponds to the difference between mean of spikes coming from the selected spikes and the spikes coming from the bulk (Figure 3).

Selection differential (S) and response to selection (R) are linked with the realized heritability (h_r^2):

$$R = h_r^2 \times S$$

See appendix B for more details on the theory behind this.

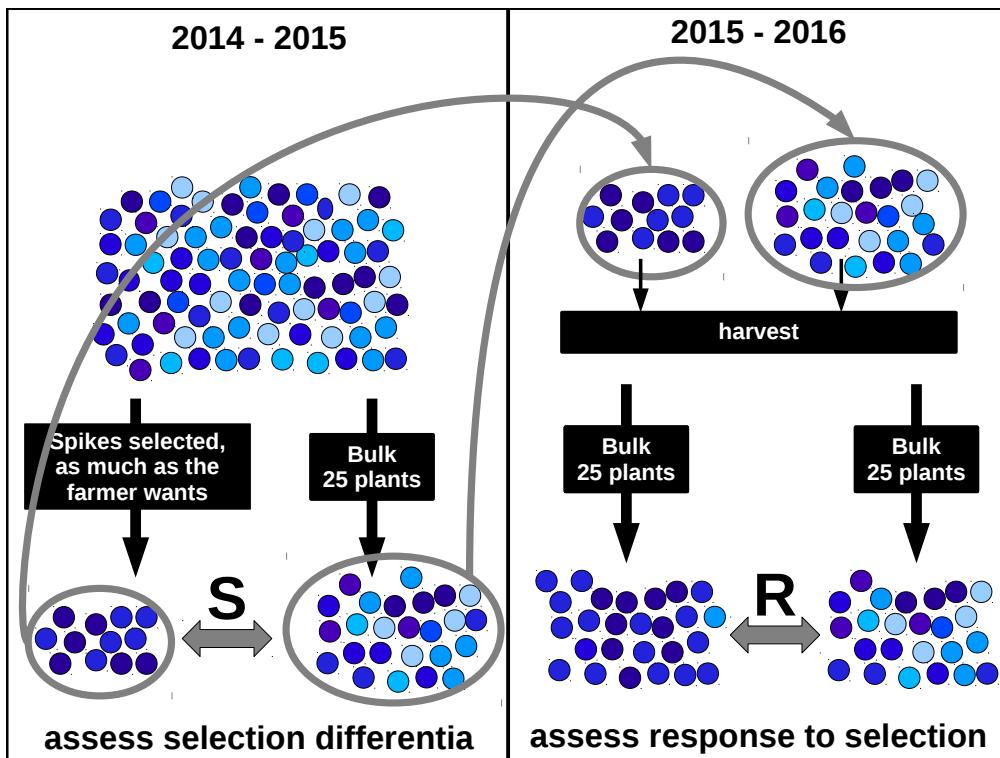


Figure 3: Selection differential (S) in 2014-2015 and response to selection (R) in 2015-2016. Circles and arrows in gray represent the seed-lots that have been sown in 2015 after harvest in 2015.

`query.type = "data-S"` The data frame returned has a column "expe" which corresponds to an id of one selection differential.

```

if(use.get.data){
  data_S = get.data(
    db_user = info_db$db_user, db_host = info_db$db_host,
    db_name = info_db$db_name, db_password = info_db$db_password,
    query.type = "data-S",
    person.in = "JFB",
    filter.on = "father-son",
    data.type = "relation",
    variable = vec_variables,
    project.in = "DEMO"
  )
} else {
  # 1. Query SHiNeMaS ...
  # 2. Set up data set ...
  # /=====| 100%
}

load("./data/data_S.RData")
}

colnames(data_S$data$data)

## [1] "son"                      "expe"
## [3] "sl_statut"                 "expe_name"
## [5] "expe_name_2"                "son_species"
## [7] "son_project"               "son_ind"

```

```

## [9] "son_year"                      "son_germplasm"
## [11] "son_germplasm_type"            "son_person"
## [13] "son_alt"                       "son_long"
## [15] "son_lat"                        "son_total_generation_nb"
## [17] "son_local_generation_nb"        "son_generation_confidence"
## [19] "son_comments"                  "father_species"
## [21] "father_project"                "father"
## [23] "father_year"                  "father_germplasm"
## [25] "father_germplasm_type"         "father_person"
## [27] "father_alt"                   "father_long"
## [29] "father_lat"                   "father_total_generation_nb"
## [31] "father_local_generation_nb"    "father_generation_confidence"
## [33] "father_comments"              "reproduction_id"
## [35] "reproduction_method_name"      "selection_id"
## [37] "selection_person"             "mixture_id"
## [39] "diffusion_id"                 "relation_year_start"
## [41] "relation_year_end"            "X"
## [43] "Y"                            "block"
## [45] "hauteur---hauteur_tige"       "hauteur---hauteur_tige$date"
## [47] "pmg---pmg"                    "pmg---pmg-2"
## [49] "pmg---pmg-2$date"            "pmg---pmg$date"
## [51] "poids_epis---poids_epis"     "poids_epis---poids_epis$date"

```

`query.type = "data-SR"` The data frame returned has a column "`expe`" which corresponds to an id of one selection differential and the corresponding response to selection

The query takes into account when selection have been done in a seed lot, that this seed lot have been merged and then have been sown. It is the case when selection have been carried out in a replication that have been merge afterwards. Even if this case should not arise, it might happen.

```

if(use.get.data){
  data_SR = get.data(
    db_user = info_db$db_user, db_host = info_db$db_host,
    db_name = info_db$db_name, db_password = info_db$db_password,
    query.type = "data-SR",
    person.in = "JFB",
    filter.on = "father-son",
    data.type = "relation",
    variable = vec_variables,
    project.in = "DEMO"
  )
} else {
  # 1. Query SHiNeMaS ...
  # 2. Set up data set ...
  # ====== / 100%
}

load("./data/data_SR.RData")
}

colnames(data_SR$data$data)

## [1] "son"                      "expe"
## [3] "sl_statut"                "expe_name"
## [5] "expe_name_2"               "son_species"
## [7] "son_project"               "son_ind"
## [9] "son_year"                  "son_germplasm"

```

```

## [11] "son_germplasm_type"           "son_person"
## [13] "son_alt"                     "son_long"
## [15] "son_lat"                     "son_total_generation_nb"
## [17] "son_local_generation_nb"      "son_generation_confidence"
## [19] "son_comments"                 "father_species"
## [21] "father_project"              "father"
## [23] "father_year"                 "father_germplasm"
## [25] "father_germplasm_type"       "father_person"
## [27] "father_alt"                  "father_long"
## [29] "father_lat"                  "father_total_generation_nb"
## [31] "father_local_generation_nb"   "father_generation_confidence"
## [33] "father_comments"              "reproduction_id"
## [35] "reproduction_method_name"     "selection_id"
## [37] "selection_person"             "mixture_id"
## [39] "diffusion_id"                "relation_year_start"
## [41] "relation_year_end"            "X"
## [43] "Y"                            "block"
## [45] "hauteur---hauteur_tige"       "hauteur---hauteur_tige$date"
## [47] "pmg---pmg"                   "pmg---pmg-2"
## [49] "pmg---pmg-2$date"            "pmg---pmg$date"
## [51] "poids_epis---poids_epis"      "poids_epis---poids_epis$date"

```

4.2 Get the ggplots

To get the plots, use the function `get.ggplot`.

First of all ,you need to choose

- on which data set you get the ggplots. This can be done on `correlated_group` having the following argument:
 - `NULL`, the default argument (`shinemas2R::get.data()$data$data`)
 - the name of a given `correlation_group` (`shinemas2R::get.data()$data$data.with.correlated.variables`)
- if you want to merge germplasm name and selection name with the argument `merge_g_and_s` which is `TRUE` by default

The names of the variables are under the form `variable_name--methods`:

```

plot_vec_variables = c(
  "hauteur---hauteur_tige",
  "pmg---pmg",
  "poids_epis---poids_epis"
)

```

4.2.1 ggplots for data-classic

- barplot, boxplot, interaction, radar and biplot
 - Default arguments

```

default_data_classic_ggplot = get.ggplot(
  data_classic,
  vec_variables = plot_vec_variables
)

```

```

## As ggplot.type is NULL, ggplot.Type is set to data-barplot, data-boxplot, data-interaction
## data-radar, data-biplot
## As x.axis and in.col are NULL, all the combinaisons of x.axis and in.col are done
## for data-barplot, data-boxplot and data-interaction.
## As in.col is NULL, each in.col are done for data-radar and data-biplot.
## [1] "A Virer quand les données seront propres dans get.data"
## [1] "A Virer quand les données seront propres dans get.data"
## [1] "A Virer quand les données seront propres dans get.data"
## For data-biplot, hide.labels.parts has been set to NULL instead of "all".

```

By default, the following plots are done:

```

names(default_data_classic_ggplot)

## [1] "data-barplot"      "data-boxplot"       "data-interaction"
## [4] "data-radar"        "data-biplot"

```

which correpond to `ggplot.type` arguments:

<code>ggplot.type</code>	description
"data-barplot"	barplot, there is one barplot per variable
"data-boxplot"	boxplot, there is one boxplot per variable
"data-interaction"	interaction, there is one interation plot per variable
"data-radar"	radar, there is one radar per set of variables (i.e. the whole <code>vec_variables</code>). It is the mean that is represented.
"data-biplot"	biplot, there is one biplot per pairs of variables. Note that no plots are possible for between raw data linked to individuals and raw data linked to relation.

For `ggplot.type = data-barplot, data-boxplot and data-interaction`, you may chose what you want in the x axis (`x.axis` argument) and in color (`in.col` argument). The possible values for `x.axis` and `in.col` are: `germplasm, year, person`. By default all combinaisons of `x.axis` and `in.col` are done with default argument settings. The name of the plot is under the form `x.axis-in.col`.

```

names(default_data_classic_ggplot$`data-barplot`)

## [1] "germplasm-year"    "germplasm-person"   "person-year"
## [4] "person-germplasm" "year-person"       "year-germplasm"

```

Knowing a combinaison of `x.axis` and `in.col`, choose the variable you want to get. For example:

- * For barplot:

```

p_cal_ph_bar_all = default_data_classic_ggplot$`data-barplot`$`germplasm-year`
p_cal_ph_bar = p_cal_ph_bar_all$`hauteur---hauteur_tige`$`x.axis-1|in.col-1` 

```

- * For boxplot:

```

p_cal_ph_box_all = default_data_classic_ggplot$`data-boxplot`$`germplasm-year`
p_cal_ph_box = p_cal_ph_box_all$`hauteur---hauteur_tige`$`x.axis-1|in.col-1` 

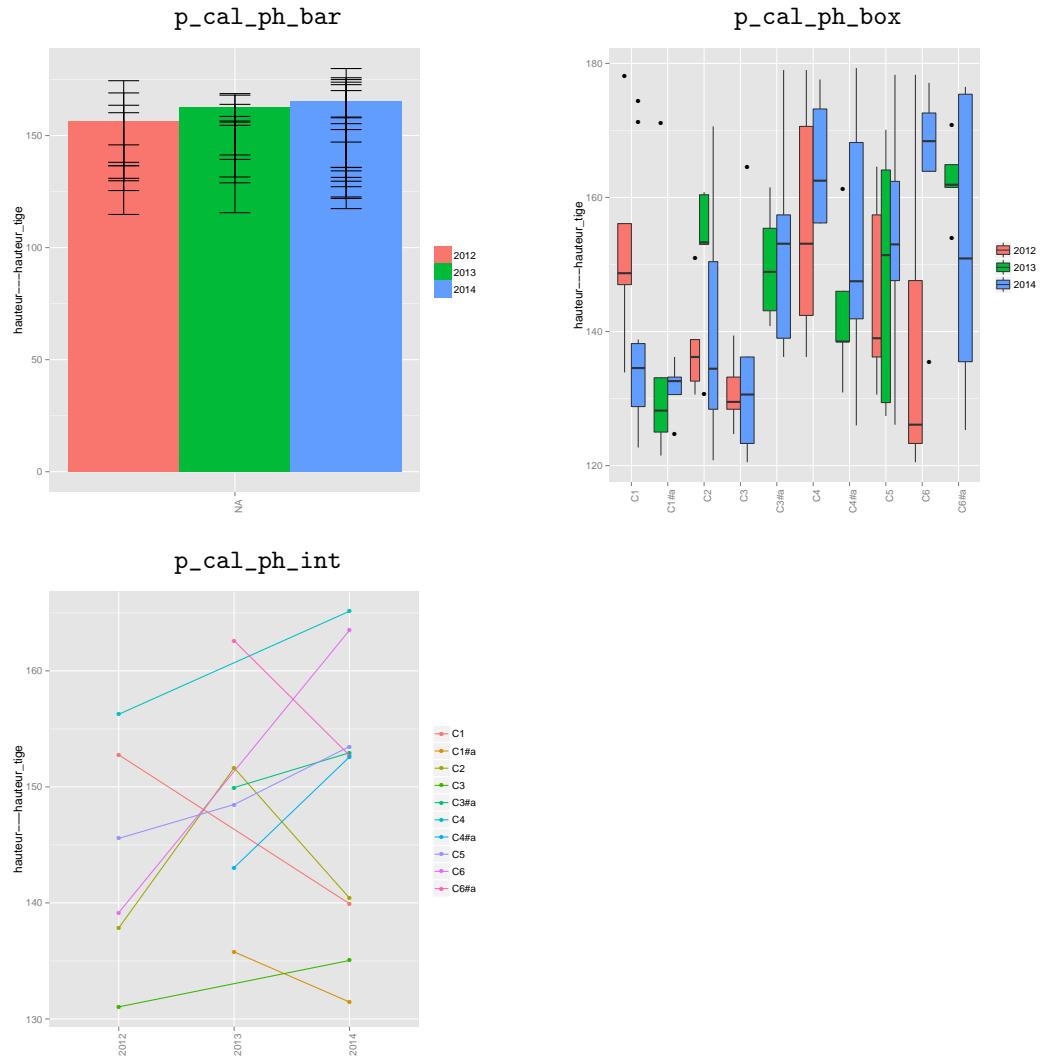
```

- * For interaction plot:

```

p_cal_ph_int_all = default_data_classic_ggplot$`data-interaction`$`year-germplasm` 
p_cal_ph_int = p_cal_ph_int_all$`hauteur---hauteur_tige`$`x.axis-1|in.col-1` 

```



For `ggplot.type = "data-radar, data-biplot"`, you may choose what you want in color (`in.col` argument). The possible values for `in.col` are: `germplasm`, `year` and `person`.

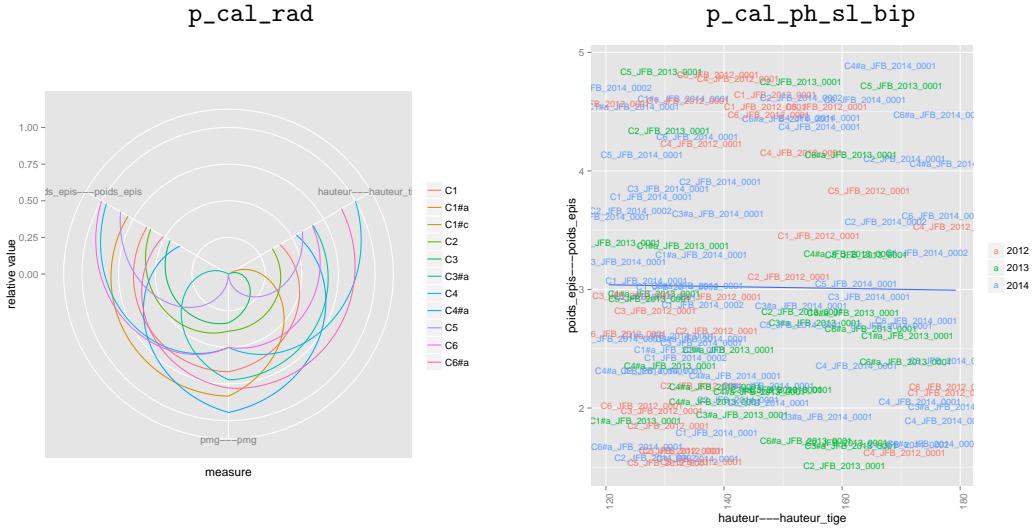
```
names(default_data_classic_ggplot$`data-radar`)
## [1] "NA-year"        "NA-person"       "NA-germplasm"
```

For example,

```
p_cal_rad_all = default_data_classic_ggplot$`data-radar`
p_cal_rad = p_cal_rad_all$`NA-germplasm`$`x.axis-1|in.col-1`
```

For biplot, you must choose the pair of variables you wish, for example,

```
p_cal_ph_sl_bip_all = default_data_classic_ggplot$`data-biplot`
p_cal_ph_sl_bip = p_cal_ph_sl_bip_all$`NA-year`
p_cal_ph_sl_bip = p_cal_ph_sl_bip$`hauteur--hauteur_tige - poids_epis---poids_epis` 
p_cal_ph_sl_bip = p_cal_ph_sl_bip$`x.axis-1|in.col-1`
```



– Custom arguments

According to `ggplot.type`, arguments can be customized:

argument	default value	description	data-barplot	data-boxplot	data-interaction	data-radar	data-biplot
ggplot.on	"son"	"father" or "son" depending on which seed-lot you want to plot..	X	X	X	X	X
x.axis	NULL	factor displayed on the x.axis of a plot: "germplasm", "year" or "person" referring to the attributes of a seed-lots. If NULL, all the combination are done for x.axis and in.col.	X	X	X		
in.col	NULL	display in color of a plot: "germplasm", "year" or "person" referring to the attributes of a seed-lots. If NULL, in.col is not displayed. Note it is compulsory for data-biplot and data-radar as in these cases x.axis is not used.	X	X	X	X	X
nb_parameters_per_plot_x.axis	NULL	the number of parameters per plot on x.axis argument	X	X	X		
nb_parameters_per_plot_in.col	NULL	the number of parameters per plot for in.col argument	X	X	X	X	X
hide.labels.parts	"all"	parts of the label hidden: "germplasm", "person", "year", "person:germplasm", "year:germplasm", "person:year", "all". "all" means that no label is displayed. If NULL labels are displayed. Labels are based on seed-lots names under the form germplasm_year_person_digit. For "data-biplot", the default value is NULL. For easier visualisation, digit is never displayed unless you choose NULL.					X

Table 4: Possible arguments regarding ggplot.type. A cross (X) means that for a given ggplot.type, a given argument can be used.

- pies on network

- Default arguments

It is possible to add pies on seed-lots represented on a network. The pie represent the distribution of a given variable for a given seed-lot.

In the following example, as we're working with encrypted data, get.ggplot reverse the transcription to query SHiNeMaS and encrypt again.

Note that this example is done on a little data set. Indeed, the pies are drawn with a polygon which needs lots of points that take memory.

```
if(use.get.data){
  data_classic_bis = get.data(
    db_user = info_db$db_user, db_host = info_db$db_host, # db infos
    db_name = info_db$db_name, db_password = info_db$db_password, # db infos
    query.type = "data-classic", # data-classic query
```

```

    person.in = "OLR", # person to keep
    filter.on = "father-son", # filters on father AND son
    data.type = "relation", # data linked to relation between seed-lots
    variable = "poids_epis", # the variables to display
    project.in = "DEMO" # the project
  )

  pn = get.ggplot(
    data_classic_bis,
    ggplot.type = "data-pie.on.network",
    vec_variables = "poids_epis---poids_epis",
    pie.size = .25,
    hide.labels.parts = "person"
  )

} else {
  # 1. Query SHiNeMaS ...
  # 2. Set up data set ...
  # ===== / 100%
  load("./data/data_classic_bis.RData")

  # 1. Query SHiNeMaS ...
  # 2. Create network matrix ...
  # 3. Link information to vertex and edges ...
  load("./data/pn.RData")
}

```

As we're working on one person, we set `hide.labels.parts = "person"`.

The result is divided into two plots: the empty network and the network with the pies.

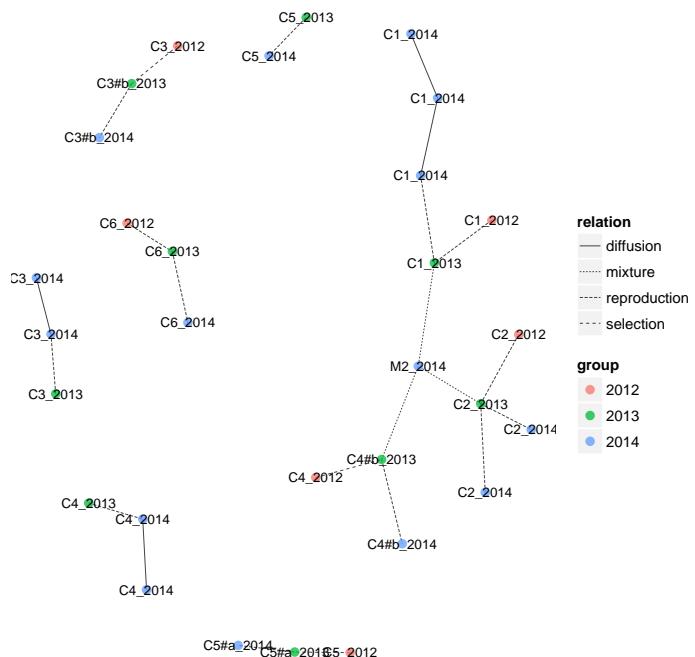
```

names(pn$data-pie.on.network)
## [1] "poids_epis---poids_epis"

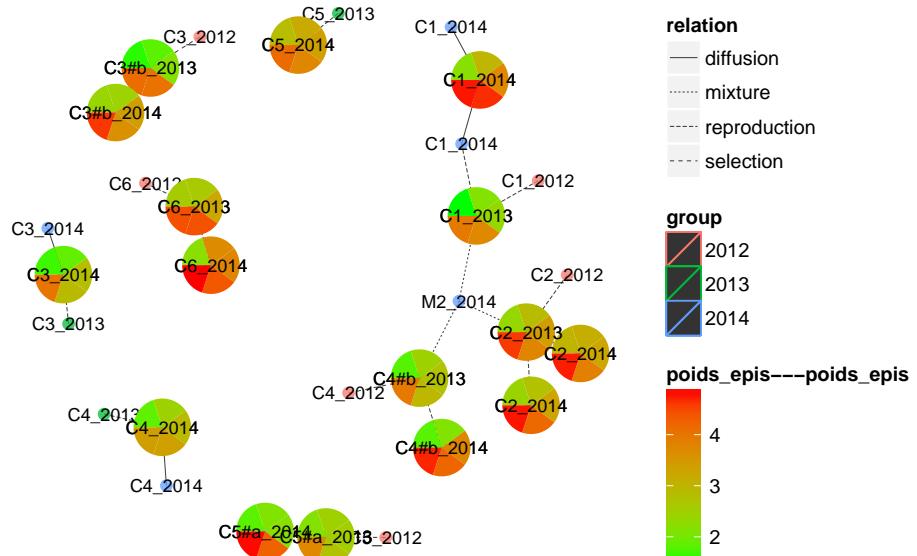
p1 = pn$data-pie.on.network`$`poids_epis---poids_epis`$network
p2 = pn$data-pie.on.network`$`poids_epis---poids_epis`$pie.on.network

```

p1



p2



- Custom arguments
Arguments can be customized related to network plots (Table 1).
- pies on map

- Default arguments
`get.data` is called to get the coordinates data.

```

if(use.get.data){
  data_classic_ter = get.data(
    db_user = info_db$db_user, db_host = info_db$db_host, # db infos
    db_name = info_db$db_name, db_password = info_db$db_password, # db infos
    query.type = "data-classic", # data-classic query
    germplasm.in = "C1", # germplasm to keep
    person.in = c("OLR", "MLN", "JFB"), # person to keep
    filter.on = "father-son", # filters on father AND son
    data.type = "relation", # data linked to relation between seed-lots
    variable = "poids_epis", # the variables to display
    project.in = "DEMO" # the project
  )

  pm = get.ggplot(
    data_classic_ter,
    ggplot.type = "data-pie.on.map",
    vec_variables = "poids_epis---poids_epis"
  )
} else {
  load("./data/data_classic_ter.RData")
  load("./data/pm.RData")
}

names(pm$data-pie.on.map)
## [1] "poids_epis---poids_epis"

```

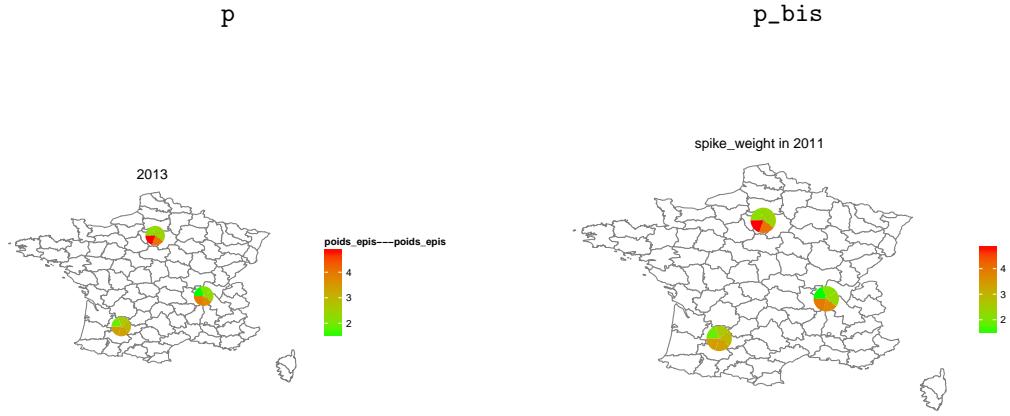
You can get the default ggplot (`p`) or customized it (`p_bis`):

```

p = pm$data-pie.on.map`$`poids_epis---poids_epis`$`map-[2013]`

p_bis = p +
  ggtitle("spike_weight in 2011") + # change the title
  theme(legend.title=element_blank()) # delete the name of the legend

```



- Custom arguments

Arguments can be customized related to map plots (Table 3).

For `data-pie.on.map`, it is also possible to choose `x.axis` in order to get a map for each `year` or each `germplasm`.

In the example, as `data_classic` is done on one germplasm (C1), `x.axis = year` has been chosen (default argument).

4.2.2 ggplots for data-S

```
default_data_S_ggplot = get.ggplot(
    data_S,
    vec_variables = plot_vec_variables,
    nb_parameters_per_plot_x.axis = 5
)

## As ggplot.type is NULL, ggplot.Type is set to data-barplot, data-boxplot, data-interaction,
## data-radar, data-biplot
## As ggplot.type is NULL and data come from "data-S" or "data-SR", ggplot.type is set to "data-barplot",
## "data-boxplot", "data-interaction".
## With "data-S" and "data-SR", in.col and x.axis are set automatically.

## [1] "A Virer quand les données seront propres dans get.data"
## [1] "A Virer quand les données seront propres dans get.data"
## [1] "A Virer quand les données seront propres dans get.data"
```

By default, the following plots are done with `x.axis` and `in.col` (you can not change it). Note that NA are put when there are no data for `bouquet` AND `vrac` (i.e. nothing is displayed).

```
names(default_data_S_ggplot)

## [1] "data-barplot"      "data-boxplot"      "data-interaction"
```

which correspond to `ggplot.type` arguments as explained in the previous section.

- For barplot:

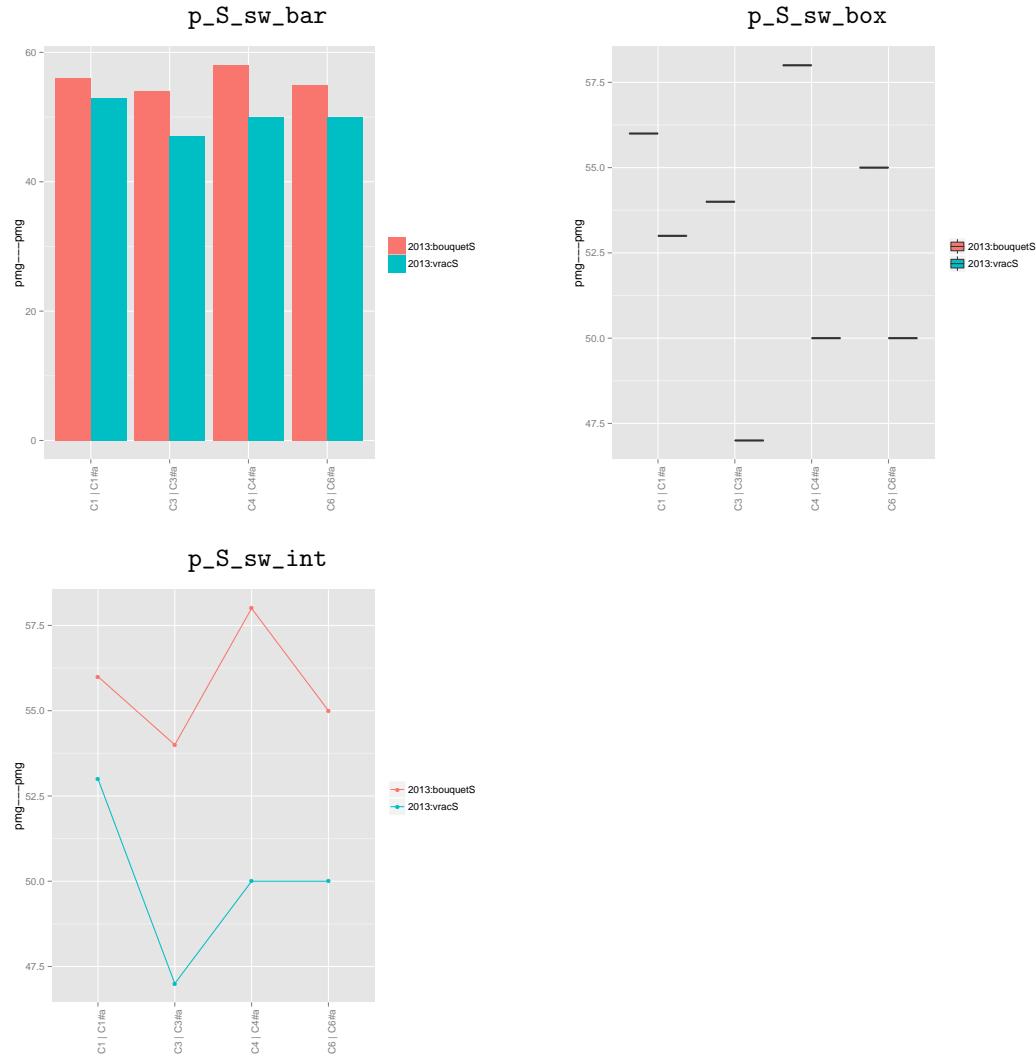
```
p_S_sw_bar_all = default_data_S_ggplot$data-barplot`  
p_S_sw_bar = p_S_sw_bar_all$`pmg---pmg`$`x.axis-1|in.col-1`
```

- For boxplot:

```
p_S_sw_box_all = default_data_S_ggplot$data-boxplot`  
p_S_sw_box = p_S_sw_box_all$`pmg---pmg`$`x.axis-1|in.col-1`
```

- For interaction plot:

```
p_S_sw_int_all = default_data_S_ggplot$data-interaction`  
p_S_sw_int = p_S_sw_int_all$`pmg---pmg`$`x.axis-1|in.col-1`
```



It is possible to customize the plots as presented in Table 4.

4.2.3 ggplots for data-SR

```
default_data_SR_ggplot = get.ggplot(  
  data_SR,  
  vec_variables = plot_vec_variables,  
  nb_parameters_per_plot_x.axis = 5  
)
```

```

## As ggplot.type is NULL, ggplot.Type is set to data-barplot, data-boxplot, data-interaction,
data-radar, data-biplot
## As ggplot.type is NULL and data come from "data-S" or "data-SR", ggplot.type is set to "data-barplot",
"data-boxplot", "data-interaction".
## With "data-S" and "data-SR", in.col and x.axis are set automatically.

## [1] "A Virer quand les données seront propres dans get.data"
## [1] "A Virer quand les données seront propres dans get.data"
## [1] "A Virer quand les données seront propres dans get.data"

```

By default, the following plots are done with `x.axis` and `in.col` (you can not change it). Note that NA are put when there are no data for `bouquet` AND `vrac` (i.e. nothing is displayed).

```

names(default_data_SR_ggplot)

## [1] "data-barplot"      "data-boxplot"      "data-interaction"

```

which correpond to `ggplot.type` arguments as explained in the previsou section.

- For barplot:

```

p_SR_sw_bar_all = default_data_SR_ggplot$data-barplot
p_SR_sw_bar = p_SR_sw_bar_all$poids_episodes---poids_episodes$x.axis-1|in.col-1

```

- For boxplot:

```

p_SR_sw_box_all = default_data_SR_ggplot$data-boxplot
p_SR_sw_box = p_SR_sw_box_all$poids_episodes---poids_episodes$x.axis-1|in.col-1

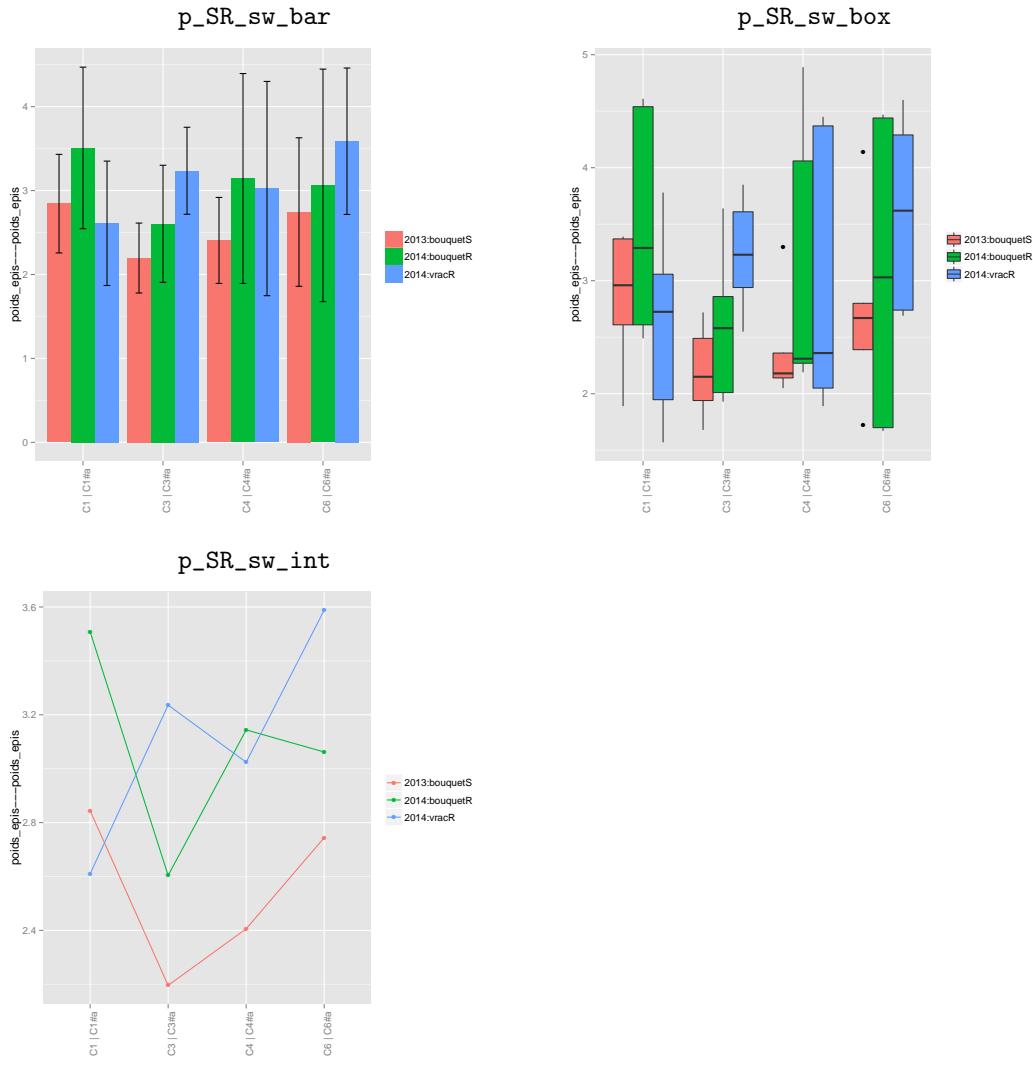
```

- For interaction plot:

```

p_SR_sw_int_all = default_data_SR_ggplot$data-interaction
p_SR_sw_int = p_SR_sw_int_all$poids_episodes---poids_episodes$x.axis-1|in.col-1

```



It is possible to customize the plots as presented in Table 4.

4.3 Get the tables

From the data, to get the tables, use the function `get.table`.

First of all ,you need to choose

- on which data set you get the ggplots. This can be done with `correlated_group` having the following argument:
 - `NULL`, the default argument (`shinemas2R::get.data()$data$data`)
 - the name of a given `correlation_group` (`shinemas2R::get.data()$data$data.with.correlated.variables`)
- if you want to merge germplasm name and selection name with the argument `merge_g_and_s` which is `TRUE` by default

Five types of tables can be displayed according to `table.type` argument :

<code>table.type</code>	description
"raw"	display raw data. Useful with text for example
"mean"	displayed for each variable columns with mean
"mean.sd"	displayed for each variable columns with mean and standard deviation
"mean.sd.cv"	displayed for each variable columns with mean, standard deviation and coefficient of variation
"summary"	display "Min.", "1st Qu.", "Median", "3rd Qu.", "Max." of the data

The table always display information with seed-lots on the left side. For information on relations, you must choose if the seed-lots displayed in the table are the son or the father with the argument `table.on`. For information on seed-lots, there is no problem.

Then you should set `vec_variables` with the variables displayed in the table.

4.3.1 tables for data-classic

- Default arguments

```
tab_class = get.table(
  data_classic,
  table.type = "raw",
  vec_variables = plot_vec_variables
)
```

the function returns a list with two elements:

```
names(tab_class)

## [1] "duplicated_infos"      "not_duplicated_infos"
```

– `"duplicated_infos"`: lists of two elements with seed-lots involved and variable values

```
tab_class$duplicated_infos$`set-1`  
## NULL
```

It is `NULL` as there is no duplicated information here.

An example with duplicated information:

```
if(use.get.data){
  data_classic_4 = get.data(
    db_user = info_db$db_user, db_host = info_db$db_host, # db infos
    db_name = info_db$db_name, db_password = info_db$db_password, # db infos
    query.type = "data-classic", # data-classic query
    person.in = "JFB", # person to keep
    filter.on = "father-son", # filters on father AND son
    data.type = "relation", # data linked to relation between seed-lots
    variable = "densite_semis", # the variables to display
    project.in = "DEMO" # the project
  )

} else {
  load("./data/data_classic_4.RData")
}

tab_class_4 = get.table(
  data_classic_4,
  table.type = "raw",
  vec_variables = "densite_semis---densite_semis"
)
```

The information is divided in two:

```
names(tab_class_4$duplicated_infos$`set-1`)

## [1] "duplicated_infos_seed-lots" "duplicated_infos_variables"
```

The seed-lots that are concerned. By default `col_to_display = c("person", "germplasm", "year", "block", "X", "Y")`, therefore, the information is under the form : person-germplasm-year-block-

```
tab_class_4$duplicated_infos`set-1`$duplicated_infos_seed-lots`  
##  
## 1 JFB-C1-2014-1-A-2, JFB-C1-2014-1-A-1, JFB-C1-2014-2-C-1, JFB-C2-2014-1-A-3, JFB-C2-2014-2-C-2
```

And the data linked to these seed lots:

```
tab_class_4$duplicated_infos`set-1`$duplicated_infos_variables`  
##   densite_semis---densite_semis densite_semis---densite_semis$date  
## 1                      200                  2013-11-01
```

– `"not_duplicated_infos"`: a list with the table of non duplicated information

```
dim(tab_class$not_duplicated_infos`set-1`)  
## [1] 138 14
```

Note that the threshold up to which the information are duplicated or not is tuned with the argument `nb_duplicated_rows` (see Custom arguments).

Instead of raw information, some statistics may be useful, for example,

```
tab_class = get.table(  
  data_classic,  
  table.type = "mean.sd.cv",  
  vec_variables = plot_vec_variables  
)  
names(tab_class$not_duplicated_infos)  
  
## [1] "set-1"  
  
colnames(tab_class$not_duplicated_infos`set-1`)  
  
## [1] "person"  
## [2] "germplasm"  
## [3] "year"  
## [4] "block"  
## [5] "X"  
## [6] "Y"  
## [7] "hauteur---hauteur_tige mean"  
## [8] "hauteur---hauteur_tige sd"  
## [9] "hauteur---hauteur_tige cv"  
## [10] "hauteur---hauteur_tige$date mean"  
## [11] "hauteur---hauteur_tige$date sd"  
## [12] "hauteur---hauteur_tige$date cv"  
## [13] "pmg---pmg mean"  
## [14] "pmg---pmg sd"  
## [15] "pmg---pmg cv"  
## [16] "pmg---pmg-2 mean"  
## [17] "pmg---pmg-2 sd"  
## [18] "pmg---pmg-2 cv"  
## [19] "pmg---pmg-2$date mean"  
## [20] "pmg---pmg-2$date sd"  
## [21] "pmg---pmg-2$date cv"
```

```

## [22] "pmg---pmg$date mean"
## [23] "pmg---pmg$date sd"
## [24] "pmg---pmg$date cv"
## [25] "poids_episodes---poids_episodes mean"
## [26] "poids_episodes---poids_episodes sd"
## [27] "poids_episodes---poids_episodes cv"
## [28] "poids_episodes---poids_episodes$date mean"
## [29] "poids_episodes---poids_episodes$date sd"
## [30] "poids_episodes---poids_episodes$date cv"

dim(tab_class$not_duplicated_infos`set-1`)

## [1] 24 30

```

- Custom arguments

The following arguments can be customized:

argument	default value	description
<code>nb_row</code>	<code>NULL</code>	the number of rows in the table
<code>nb_col</code>	<code>NULL</code>	the number of columns for variables in the table. <code>col_to_display</code> remains fixed.
<code>nb_duplicated_rows</code>	<code>NULL</code>	minimum number of duplicated rows for each variable of a table up to which the information is put in only one row.
<code>col_to_display</code>	<code>c("person", "germplasm", "year", "block", "X", "Y")</code>	columns to display in the table. It can be a vector with "person", "year", "germplasm", "block", "X" and "Y". If <code>NULL</code> , none of these columns is displayed. The variables follow these columns. For "data-S" and "data-SR" type, the column "expe" and "sl_statut" are added by default.
<code>invert_row_col</code>	<code>FALSE</code>	if <code>TRUE</code> , invert row and col in the table. This is possible only for <code>col_to_display = NULL</code> .

Table 5: Possible arguments to customize `get.table`.

For example,

```

tab_class = get.table(
  data_classic,
  table.type = "mean.sd.cv",
  vec_variables = plot_vec_variables,
  nb_row = 10
)
names(tab_class$not_duplicated_infos)

## [1] "set-1" "set-2" "set-3"

```

The information is split into several tables with at least 10 rows.

```

dim(tab_class$not_duplicated_infos`set-1`)

## [1] 10 30

```

4.3.2 tables for data-S and data-SR

Tables are the same than for `classic-data`, there is just the column "expe" and "sl_statut" added by default.

For example,

```
tab_S_msc = get.table(
  data_S,
  table.type = "mean.sd.cv",
  vec_variables = plot_vec_variables,
  nb_col = 3 # Otherwise, the table is too large
)

colnames(tab_S_msc$not_duplicated_infos$`set-1`)

## [1] "person"                  "germplasm"
## [3] "year"                    "block"
## [5] "X"                      "Y"
## [7] "expe"                    "sl_statut"
## [9] "hauteur---hauteur_tige mean" "hauteur---hauteur_tige sd"
## [11] "hauteur---hauteur_tige cv"
```

It is possible to customize the tables as presented in Table 5.

4.4 Format the data for existing R packages

It is often useful to go beyond descriptive analysis and apply statistical tests to your data. To do so, you need to use existing R packages to perform such analysis.

You need to format your data in order to use these packages. This is done with `format.data` which format your data for the following packages: `PPBstats`.

For example, if you want to use the `PPBstats` package:

```
data_for_PPBstats = format.data(
  data_classic,
  format = "PPBstats"
)

head(data_for_PPBstats)

##   year location germplasm block X Y hauteur---hauteur_tige
## 1 2013     JFB      C1    1 A 1           171.1
## 5 2013     JFB      C1    1 A 1           128.2
## 9 2013     JFB      C1    1 A 1           121.5
## 13 2013    JFB      C1    1 A 1           125.0
## 17 2013    JFB      C1    1 A 1           133.1
## 21 2013    JFB      C1    1 A 1          <NA>
##   hauteur---hauteur_tige$date pmg---pmg pmg---pmg-2
## 1                   2013-07-04 <NA>       <NA>
## 5                   2013-07-04 <NA>       <NA>
## 9                   2013-07-04 <NA>       <NA>
## 13                  2013-07-04 <NA>       <NA>
## 17                  2013-07-04 <NA>       <NA>
## 21                   <NA>        56 <NA>
##   pmg---pmg-2$date pmg---pmg$date poids_epis---poids_epis
## 1                   <NA>        <NA>       2.61
## 5                   <NA>        <NA>       2.96
## 9                   <NA>        <NA>       3.39
```

```
## 13          <NA>          <NA>          1.89
## 17          <NA>          <NA>          3.37
## 21          <NA> 2013-07-15          <NA>
##   poids_epis---poids_epis$date
## 1            2013-07-23
## 5            2013-07-23
## 9            2013-07-23
## 13           2013-07-23
## 17           2013-07-23
## 21           <NA>
```

5 Other information in SHiNeMaS

For the following `query.type`, you can set filters to the query with the following argument :

- `filter.in` to choose nothing except `filter.in`
- `filter.out` to choose everything except `filter.out`

Values of filter depends on the `query.type`.

5.1 `query.type = "cross"`

values of filters can be `germplasm`, `germplasm.type`, `year`, `person` or `project`.

5.2 `query.type = "method"`

values of filters can be `variable`.

5.3 `query.type = "person-info"`

values of filters can be `person`.

5.4 `query.type = "grandfather"`

values of filters can be `germplasm`, `germplasm.type`, `year`, `person`, `project`, `seed-lots` or `reproduction.type`.

6 pdf compilation with L^AT_EX

`get.pdf` aggregates texts and outputs from `get.ggplot` and `get.table`. This is particularly useful in participatory research to give feedback to stakeholders such as farmers.

`get.pdf` creates a `.tex` file that is compiled into a `.pdf` file. You need to install L^AT_EX and the following packages : `longtable`, `lscaping`, `graphicx`, `pdffpages`, `float`, `hyperref` and `fancyhdr`. To download LaTeX, go to latex-project.org/ftp.html.

6.1 Philosophy of `get.pdf`

The idea of `get.pdf` is to create a list (`LaTeX_body` argument) with several elements that can be:

- "titlepage" : a list containing the following elements :
 - "title" : the title of the document. Nothing by default.
 - "authors" : the authors of the document. Nothing by default.
 - "email" : the corresponding email. Nothing by default.
 - "date" : the date of the document. Nothing by default.
- "tableofcontents" : if TRUE, a table of content is displayed.
- "chapter" : name of a chapter
- "section" : name of a section
- "subsection" : name of a subsection
- "subsubsection" : name of a subsubsection
- "text" : text to add
- "includepdf" : path of a `.pdf` to include
- "input" : path of a `.tex` to insert
- "table" : a list containing the following elements :
 - "content" : output from `get.table`
 - "caption" : caption of the table
 - "landscape" : If TRUE, the table is in landscape. FALSE by default.
 - "display.rownames" : If TRUE, display the row names of the table. FALSE by default.
- "figure" : a list containing the following elements :
 - "content" : output from `get.ggplot`
 - "caption" : caption of the figure
 - "layout" : the layout of the plots. It is a matrix under the form `layout = matrix(c(1:4), ncol = 2, nrow = 2)`. It is `layout = matrix(1, ncol = 1, nrow= 1)` by default.
 - "width" : width of the figure in textwidth unit. 1 means as width as the text. It is 1 by default.
 - "landscape" : If TRUE, the figure is in landscape. FALSE by default.

The elements of this list will be in the same order in the final pdf.

You do not have to know L^AT_EX. `get.pdf` uses it for you. Nevertheless, if you use L^AT_EX you'll be able to customize the `.pdf` document by creating the tex structure of the document (`LaTeX_head` argument). It is also possible to add specific tex files (`input` element of `LaTeX_body` argument). If you use L^AT_EX macro, do not forget to use the escape mode (Table 6),

macro	description
\textbf{blod}	blod
\textit{italique}	<i>italique</i>
\underline{underline}	<u>underline</u>
\texttt{type writer}	type writer

Table 6: Basic maros in L^AT_EX to use in get.pdf with escape mode.

Tutorials on L^AT_EX can be found here: en.wikibooks.org/wiki/LaTeX. See appendix C for some examples.

6.2 Examples

6.2.1 First Information

First, set the directory where you want the pdf to be stored:

```
dir = "/home/pierre/"
```

Then, choose a name for your pdf (as well as a folder that contain all the raw information to create the pdf)

```
form.name = "my_first_pdf"
```

6.2.2 L^AT_EX body

Then, create the list with the different elements. The names of plots and tables are coming from sections 3 and 4.

```
OUT = NULL

#####
# 1. Title page
#####
out = list(
  "titlepage" = list(
    "title" = "Example of \texttt{shinemas2R::get.pdf}",
    "authors" = "P. Riviere",
    "date" = "\today",
    "email" = "pierre@semencespaysannes.org")
); OUT = c(OUT, out)

#####
# 2. Table of contents
#####
out = list("tableofcontents" = TRUE); OUT = c(OUT, out)

#####
# 3. Network relations between seed-lots
#####
out = list(
  "chapter" = "Network relations between seed-lots"
); OUT = c(OUT, out)
```

```

out = list(
    "section" = "Network for Rouge du Roc"
); OUT = c(OUT, out)

out = list(
    "text" = "The following figure display the network for Rouge du Roc"
); OUT = c(OUT, out)

out = list(
    "figure" = list(
        "caption" = "Network for C1",
        "content" = p_net_C1,
        "width" = 1)
); OUT = c(OUT, out)

out = list(
    "section" = "Seed-lots harvested for Rouge du Roc after a reproduction"
); OUT = c(OUT, out)

out = list(
    "figure" = list(
        "caption" = "Seed-lots harvested for each person by year for Rouge du Roc",
        "content" = p3_slh,
        "width" = 1)
); OUT = c(OUT, out)

out = list(
    "figure" = list(
        "caption" = "Repartition of seed-lots harvested
since the beginning of the project.",
        "content" = m5_slh,
        "width" = 1)
); OUT = c(OUT, out)

#####
# 4. Data linked to the relations between seed-lots
#####

out = list(
    "chapter" = "Data linked to the relations between seed-lots"
); OUT = c(OUT, out)

out = list(
    "section" = "Data related to sowing practices"
); OUT = c(OUT, out)

out = list(
    "table" = list(
        "caption" = "Sowing practices for seed-lots at RAB",
        "content" = tab_class_4,
        "landscape" = FALSE
    )
); OUT = c(OUT, out)

```

```

out = list(
  "section" = "Data on selection differentia"
); OUT = c(OUT, out)

out = list(
  "figure" = list(
    "caption" = paste("Selection differentia for spike weight on RAB farm."),
    "content" = p_S_sw_bar,
    "width" = 1)
); OUT = c(OUT, out)

# Here, all the plots in the list are displayed:
# Set "layout" argument is useful as there are more than one plot
out = list(
  "figure" = list(
    "caption" = paste("Selection differentia for spike weight on RAB farm."),
    "content" = p_S_sw_box_all,
    "layout" = matrix(c(1,2), ncol = 1),
    "width" = 1)
); OUT = c(OUT, out)

out = list(
  "table" = list(
    "caption" = "Mean, standard deviation and coefficient of variation
for differentia to selection",
    "content" = tab_S_msc,
    "landscape" = TRUE
  )
); OUT = c(OUT, out)

out = list(
  "section" = "Data on response to selection"
); OUT = c(OUT, out)

out = list(
  "figure" = list(
    "caption" = paste("Selection differentia for spike weight on RAB farm."),
    "content" = p_SR_sw_bar,
    "width" = .5)
); OUT = c(OUT, out)

```

6.2.3 Compile the pdf

It is possible to custom the color of the rows of tables with `color1` (color of the head of the table) or `color2` (color of the row, the color of the rows is an alternation of white and `color2`). `compile.tex = TRUE` compiles the pdf.

```

get.pdf(
  dir = dir,
  form.name = form.name,
  LaTeX_head = NULL,
  LaTeX_body = OUT,
  compile.tex = TRUE
)

```

```
## 1. Get LaTeX head ...
## 2. Get LaTeX body ...
## 3. Compilation of .tex ...
## /home/pierre/my_first_pdf.pdf has been compiled.
```

7 Common use rules

The use of a tool such as a data base rises questions in collaborative research. The Réseau Semences Paysannes is a network that brings together a great diversity of collectives. Some collectives are known as Community Seed Houses (CSH) (Réseau Semences Paysannes, 2014).

Within RSP, biodiversity is seen as a common. Therefore, common use rules are needed to manage this common, especially on data management.

Common use rules related to data management within CSHs can be seen at two levels :

1. Internal organization rules of the group and their relations with juridic, social, agronomic and economic environments:

- Up to which level dematerialize the information ?
- Which data to store ?
- Which access to data ?

2. Biopiracy risks:

- Which data to store ?
- Which access to data ?
- Link of CSHs with research : which protections of CSHs'work, ressources and knowledge ?

More information on this topic can be found in Réseau Semences Paysannes (2015).

To cite shinemas2R

To cite this package and or this vignette:

```
citation("shinemas2R")

##
## To cite package 'shinemas2R' in publications use:
##
##  Pierre Riviere (2016). shinemas2R: An R package to
##  visualize outputs from the data base Seed History and
##  Network Management System (SHiNeMaS). R package version
##  0.9.2. http://github.com/priviere/shinemas2R
##
## A BibTeX entry for LaTeX users is
##
## @Manual{,
##   title = {shinemas2R: An R package to visualize outputs from the data base Seed History and Net-
##             work Management System (SHiNeMaS)},
##   author = {Pierre Riviere},
##   year = {2016},
##   note = {R package version 0.9.2},
##   url = {http://github.com/priviere/shinemas2R},
## }
```

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References

- Y. De Oliveira, L. Burlot, M. Lefebvre, D. Madi, P. Rivière, and M. Thomas. SHiNeMaS : a database dedicated to seed lots genealogy, phenotyping and cultural practices. Poster at Jobim, Clermont-Ferrand, 2015.
- M. Nei. Analysis of gene diversity in subdivided populations. *Proceedings of the National Academy of Sciences*, 70:3321–3323, 1973.
- Réseau Semences Paysannes. *Les maisons des semences paysannes : Regards sur la gestion collective de la biodiversité cultivée en France*. Réseau Semences Paysannes, 2014.
- Réseau Semences Paysannes. *Éléments de réflexion sur la gestion des données dans les Maisons des Semences Paysannes*. Réseau Semences Paysannes, 2015.
- P. Rivière. *Méthodologie de la sélection décentralisée et participative: un exemple sur le blé tendre*. PhD thesis, Université Paris Sud, 2014.
- M. Thomas. *Gestion dynamique à la ferme de l'agrobiodiversité : relation entre la structure des populations de blé tendre et les pratiques humaines*. PhD thesis, Université Paris Diderot, 2011.

A Install SHiNeMaS on localhost

A.1 Install PostgreSQL and SHiNeMaS

With Linux, first install postgresql and create your account and password.

```
pierre@RSP:~$ sudo apt-get install postgresql
pierre@RSP:~$ sudo -i -u postgres
postgres@RSP:~$ psql
postgres=# ALTER USER postgres with password 'postgres';
postgres=# create user pierre;
postgres=# ALTER ROLE pierre WITH CREATEDB;
postgres=# ALTER USER pierre SUPERUSER;
postgres=# alter user pierre with encrypted password 'pierre';
```

Then, create the empty data base shinemas_tuto:

```
postgres=# create database shinemas_tuto owner pierre;
postgres=# GRANT ALL PRIVILEGES ON DATABASE shinemas_tuto TO pierre;
```

To exit `postgres#`, press `ctrl + D`.

Once you've done this, download `shinemas_tuto.sql`. You can find it in the package:

```
system.file("extdata", "shinemas_tuto.sql", package = "shinemas2R")
## [1] "/home/pierre/Documents/geek/R-stats/Rdev/R_package_shinemas2R/shinemas2R/inst/extdata/shinema
```

Put it in your `/home/pierre`, and install it on postgresql.

Note that `shinemas_tuto.sql` must be accessible in writing and reading.

```
pierre@RSP:~$ psql -h localhost -d shinemas_tuto -U pierre -f /home/pierre/shinemas_tuto.sql
```

You can look at the data base you have:

```
sudo -i -u postgres
postgres@RSP:~$ psql -l
```

You can delete the database with

```
sudo -i -u postgres
postgres@RSP:~$ dropdb shinemas_tuto
```

More information on postgresql can be found here: <http://help.ubuntu.com/community/PostgreSQL>

A.2 Set up the information to connect to SHiNeMaS with get.data

```
info_db = list(
  db_user = "pierre",
  db_host = "127.0.0.1", # localhost
  db_name = "shinemas_tuto",
  db_password = "pierre"
)
```

`db_info` is used in `get.data` function.

B Theory regarding selection differential, response to selection and heritability

to do !!!

C get.pdf examples

C.1 LaTeX_head examples

to do !

C.2 .tex examples for input

to do !

D Examples of `is.get.data.output`

In this appendix, you can find empty data-set that will fit in `is.get.data.output`.

D.1 `shinemas2R.object == "network"`

```
network = NULL

network.query = data.frame(
  son_species = factor(c("a", "b", "c")),
  son_project = factor(c("a", "b", "c")),
  son = factor(c("a", "b", "c")),
  son_germplasm = factor(c("a", "b", "c")),
  son_person = factor(c("a", "b", "c")),
  son_year = factor(c("a", "b", "c")),
  son_germplasm_type = factor(c("a", "b", "c")),
  son_alt = as.numeric(c(0, 0, 0)),
  son_long = as.numeric(c(0, 0, 0)),
  son_lat = as.numeric(c(0, 0, 0)),
  son_total_generation_nb = as.numeric(c(0, 0, 0)),
  son_local_generation_nb = as.numeric(c(0, 0, 0)),
  son_generation_confidence = c("a", "b", "c"),
  son_comments = c("a", "b", "c"),

  father_species = factor(c("a", "b", "c")),
  father_project = factor(c("a", "b", "c")),
  father = factor(c("a", "b", "c")),
  father_germplasm = factor(c("a", "b", "c")),
  father_person = factor(c("a", "b", "c")),
  father_year = factor(c("a", "b", "c")),
  father_germplasm_type = factor(c("a", "b", "c")),
  father_alt = as.numeric(c(0, 0, 0)),
  father_long = as.numeric(c(0, 0, 0)),
  father_lat = as.numeric(c(0, 0, 0)),
  father_total_generation_nb = as.numeric(c(0, 0, 0)),
  father_local_generation_nb = as.numeric(c(0, 0, 0)),
  father_generation_confidence = c("a", "b", "c"),
  father_comments = c("a", "b", "c"),

  reproduction_id = c("a", "b", "c"),
  reproduction_method_name = factor(c("a", "b", "c")),
  is_male = factor(c("a", "b", "c")),
  block = factor(c("a", "b", "c")),

  selection_id = c("a", "b", "c"),
  selection_person = factor(c("a", "b", "c")),
  mixture_id = c("a", "b", "c"),
  diffusion_id = c("a", "b", "c"),
  relation_year_start = factor(c("a", "b", "c")),
  relation_year_end = factor(c("a", "b", "c"))
)

network.query$son_generation_confidence = as.character(network.query$son_generation_confidence)
network.query$son_comments = as.character(network.query$son_comments)
network.query$father_generation_confidence = as.character(network.query$father_generation_confidence)
network.query$father_comments = as.character(network.query$father_comments)
```

```

network.query$reproduction_id = as.character(network.query$reproduction_id)
network.query$selection_id = as.character(network.query$selection_id)
network.query$mixture_id = as.character(network.query$mixture_id)
network.query$diffusion_id = as.character(network.query$diffusion_id)

network.info = data.frame(
  sl = factor(c("a", "b", "c")),
  alt = as.numeric(c(0, 0, 0)),
  long = as.numeric(c(0, 0, 0)),
  lat = as.numeric(c(0, 0, 0)),
  diffusion = factor(c("give", "receive", "give-receive")),
  id.diff = factor(c(1, 2, 3)),
  reproduction = factor(c("sow", "harvest", "harvest-sow")),
  mixture = factor(c("mixture", NA, NA)),
  selection = factor(c("selection", NA, NA)),
  cross.info = factor(c("a", "b", "c")),
  germplasm = factor(c("a", "b", "c")),
  person = factor(c("a", "b", "c")),
  year = factor(c("a", "b", "c"))
)
Mdist = NULL

n = list("network" = network, "network.query" = network.query, "network.info" = network.info, "Mdist" = Mdist)
n = is.get.data.output(n)

## The data has been sucessfully updated with shinemas2R.object = "network".

```

D.2 shinemas2R.object == "data..."

In all data, you need a methods format:

```

methods = data.frame(
  method_name = c("a", "b"),
  variable_name = c("a", "b"),
  method_description = c("a", "b"),
  unit = c("a", "b"),
  varmeth = c("a", "b")
)

methods$method_name = as.character(methods$method_name)
methods$variable_name = as.character(methods$variable_name)
methods$method_description = as.character(methods$method_description)
methods$unit = as.character(methods$unit)
methods$varmeth = as.character(methods$varmeth)

colnames(methods) [5] = "variable--methods"

```

D.2.1 shinemas2R.object == "data-classic-seed-lots"

```

data = data.frame(
  species = factor(c("a", "b", "c")),
  project = factor(c("a", "b", "c")),

```

```

sl = factor(c("a", "b", "c")),
germplasm = factor(c("a", "b", "c")),
germplasm_type = factor(c("a", "b", "c")),
person = factor(c("a", "b", "c")),
year = factor(c("a", "b", "c")),
lat = as.numeric(c(0, 0, 0)),
long = as.numeric(c(0, 0, 0)),
alt = as.numeric(c(0, 0, 0)),
total_generation_nb = as.numeric(c(0, 0, 0)),
local_generation_nb = as.numeric(c(0, 0, 0)),
generation_confidence = as.numeric(c(0, 0, 0)),
sl_comments = factor(c("a", "b", "c"))
)

data.with.correlated.variables = list(data, data)

out = list("data" = data, "data.with.correlated.variables" = data.with.correlated.variables, "methods"
out = is.get.data.output(out, shinemas2R.object = "data-classic-seed-lots")

## The data has been sucessfully updated with shinemas2R.object = "data-classic-seed-lots".

```

D.2.2 shinemas2R.object == "data-classic-relation"

```

data = data.frame(
  son_species = factor(c("a", "b", "c")),
  son_project = factor(c("a", "b", "c")),
  son = factor(c("a", "b", "c")),
  son_ind = factor(c("a", "b", "c")),
  son_year = factor(c("a", "b", "c")),
  son_germplasm = factor(c("a", "b", "c")),
  son_germplasm_type = factor(c("a", "b", "c")),
  son_person = factor(c("a", "b", "c")),
  son_alt = as.numeric(c(0, 0, 0)),
  son_long = as.numeric(c(0, 0, 0)),
  son_lat = as.numeric(c(0, 0, 0)),
  son_total_generation_nb = as.numeric(c(0, 0, 0)),
  son_local_generation_nb = as.numeric(c(0, 0, 0)),
  son_generation_confidence = as.numeric(c(0, 0, 0)),
  son_comments = factor(c("a", "b", "c")),

  father_species = factor(c("a", "b", "c")),
  father_project = factor(c("a", "b", "c")),
  father = factor(c("a", "b", "c")),
  father_year = factor(c("a", "b", "c")),
  father_germplasm = factor(c("a", "b", "c")),
  father_germplasm_type = factor(c("a", "b", "c")),
  father_person = factor(c("a", "b", "c")),
  father_alt = as.numeric(c(0, 0, 0)),
  father_long = as.numeric(c(0, 0, 0)),
  father_lat = as.numeric(c(0, 0, 0)),
  father_total_generation_nb = as.numeric(c(0, 0, 0)),
  father_local_generation_nb = as.numeric(c(0, 0, 0)),
  father_generation_confidence = as.numeric(c(0, 0, 0)),
  father_comments = factor(c("a", "b", "c")),

```

```

reproduction_id = factor(c("a", "b", "c")),
reproduction_method_name = factor(c("a", "b", "c")),
selection_id = factor(c("a", "b", "c")),
selection_person = factor(c("a", "b", "c")),
mixture_id = factor(c("a", "b", "c")),
diffusion_id = factor(c("a", "b", "c")),
relation_year = factor(c("a", "b", "c")),
X = factor(c("a", "b", "c")),
Y = factor(c("a", "b", "c")),
block = factor(c("a", "b", "c"))
)

data.with.correlated.variables = list(data, data)

out = list("data" = data, "data.with.correlated.variables" = data.with.correlated.variables, "methods"
out = is.get.data.output(out, shinemas2R.object = "data-classic-relation")

## The data has been sucessfully updated with shinemas2R.object = "data-classic-relation".

```

D.2.3 shinemas2R.object == "data-S-seed-lots" & shinemas2R.object == "data-SR-seed-lots"

```

data = data.frame(
  expe = factor(c("a", "b", "c")),
  sl_statut = factor(c("a", "b", "c")),
  expe_name = factor(c("a", "b", "c")),
  expe_name_2 = factor(c("a", "b", "c")),
  species = factor(c("a", "b", "c")),
  project = factor(c("a", "b", "c")),
  sl = factor(c("a", "b", "c")),
  germplasm = factor(c("a", "b", "c")),
  germplasm_type = factor(c("a", "b", "c")),
  person = factor(c("a", "b", "c")),
  year = factor(c("a", "b", "c")),
  lat = as.numeric(c(0, 0, 0)),
  long = as.numeric(c(0, 0, 0)),
  alt = as.numeric(c(0, 0, 0)),
  total_generation_nb = as.numeric(c(0, 0, 0)),
  local_generation_nb = as.numeric(c(0, 0, 0)),
  generation_confidence = as.numeric(c(0, 0, 0)),
  sl_comments = factor(c("a", "b", "c"))
)

data.with.correlated.variables = list(data, data)

out = list("data" = data, "data.with.correlated.variables" = data.with.correlated.variables, "methods"
out_S = is.get.data.output(out, shinemas2R.object = "data-S-seed-lots")

## The data has been sucessfully updated with shinemas2R.object = "data-S-seed-lots".

out_SR = is.get.data.output(out, shinemas2R.object = "data-SR-seed-lots")

## The data has been sucessfully updated with shinemas2R.object = "data-SR-seed-lots".

```

D.2.4 shinemas2R.object == "data-S-relation" & shinemas2R.object == "data-SR-relation"

```

data = data.frame(
  expe = factor(c("a", "b", "c")),
  sl_statut = factor(c("a", "b", "c")),
  expe_name = factor(c("a", "b", "c")),
  expe_name_2 = factor(c("a", "b", "c")),

  son_species = factor(c("a", "b", "c")),
  son_project = factor(c("a", "b", "c")),
  son = factor(c("a", "b", "c")),
  son_ind = factor(c("a", "b", "c")),
  son_year = factor(c("a", "b", "c")),
  son_germplasm = factor(c("a", "b", "c")),
  son_germplasm_type = factor(c("a", "b", "c")),
  son_person = factor(c("a", "b", "c")),
  son_alt = as.numeric(c(0, 0, 0)),
  son_long = as.numeric(c(0, 0, 0)),
  son_lat = as.numeric(c(0, 0, 0)),
  son_total_generation_nb = as.numeric(c(0, 0, 0)),
  son_local_generation_nb = as.numeric(c(0, 0, 0)),
  son_generation_confidence = as.numeric(c(0, 0, 0)),
  son_comments = factor(c("a", "b", "c")),

  father_species = factor(c("a", "b", "c")),
  father_project = factor(c("a", "b", "c")),
  father = factor(c("a", "b", "c")),
  father_year = factor(c("a", "b", "c")),
  father_germplasm = factor(c("a", "b", "c")),
  father_germplasm_type = factor(c("a", "b", "c")),
  father_person = factor(c("a", "b", "c")),
  father_alt = as.numeric(c(0, 0, 0)),
  father_long = as.numeric(c(0, 0, 0)),
  father_lat = as.numeric(c(0, 0, 0)),
  father_total_generation_nb = as.numeric(c(0, 0, 0)),
  father_local_generation_nb = as.numeric(c(0, 0, 0)),
  father_generation_confidence = as.numeric(c(0, 0, 0)),
  father_comments = factor(c("a", "b", "c")),

  reproduction_id = factor(c("a", "b", "c")),
  reproduction_method_name = factor(c("a", "b", "c")),
  selection_id = factor(c("a", "b", "c")),
  selection_person = factor(c("a", "b", "c")),
  mixture_id = factor(c("a", "b", "c")),
  diffusion_id = factor(c("a", "b", "c")),
  relation_year = factor(c("a", "b", "c")),
  X = factor(c("a", "b", "c")),
  Y = factor(c("a", "b", "c")),
  block = factor(c("a", "b", "c"))
)

data.with.correlated.variables = list(data, data)

out = list("data" = data, "data.with.correlated.variables" = data.with.correlated.variables, "methods"
out_S = is.get.data.output(out, shinemas2R.object = "data-S-relation")

## The data has been sucessfully updated with shinemas2R.object = "data-S-relation".
out_SR = is.get.data.output(out, shinemas2R.object = "data-SR-relation")

```

```
## The data has been sucessfully updated with shinemas2R.object = "data-SR-relation".
```