

i-RNA

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7.46	/home/amine/workspace/iRNA/irna/iRNA_stat/Draw_data.py File - Reference	250
7.47	/home/amine/workspace/iRNA/irna/iRNA_stat/Ecdf.py File Reference . .	250
7.48	/home/amine/workspace/iRNA/irna/iRNA_stat/Execute.py File Reference	251
7.49	/home/amine/workspace/iRNA/irna/iRNA_stat/Exp_data.py File - Reference	251

7.50	/home/amine/workspace/iRNA/irna/iRNA_stat/iRNA_stat.py	File	-	
	Reference			251
7.51	/home/amine/workspace/iRNA/irna/iRNA_stat/NormScore.py	File	-	
	Reference			252
7.52	/home/amine/workspace/iRNA/irna/iRNA_stat/Pickling.py	File	Reference	252
7.53	/home/amine/workspace/iRNA/irna/iRNA_stat/pValue_selection.py	File		
	Reference			252
7.54	/home/amine/workspace/iRNA/irna/iRNA_stat/Rand_data.py	File	-	
	Reference			252
7.55	/home/amine/workspace/iRNA/irna/iRNA_stat/Regression.py	File	-	
	Reference			253
7.56	/home/amine/workspace/iRNA/irna/iRNA_stat/Soft.py	File	Reference	253
7.57	/home/amine/workspace/iRNA/irna/iRNA_stat/Threshold.py	File	-	
	Reference			253

Chapter 1

Namespace Index

1.1 Namespace List

Here is a list of all namespaces with brief descriptions:

irna	9
irna::David2tulip	9
irna::David2tulip::David	10
irna::David2tulip::David2tulip	10
irna::David2tulip::Davidconfig	10
irna::David2tulip::Edge	11
irna::David2tulip::Files	11
irna::David2tulip::Gene_list	11
irna::David2tulip::Graph	11
irna::David2tulip::Interact	11
irna::David2tulip::Multilist	12
irna::David2tulip::Mycarn_data	12
irna::David2tulip::Name	12
irna::David2tulip::Node	12
irna::David2tulip::Parser	12
irna::David2tulip::pValue	12
irna::David2tulip::Similarity	13
irna::David2tulip::Sqlite_manager	13
irna::iRNA_pred	13
irna::iRNA_pred::Comparison	13
irna::iRNA_pred::Fasta	13
irna::iRNA_pred::Files	14
irna::iRNA_pred::Interaction	14
irna::iRNA_pred::iRNA_pred	14
irna::iRNA_pred::Merger	15
irna::iRNA_pred::Mpi	15
irna::iRNA_pred::Parse	15
irna::iRNA_pred::RanRNA	16
irna::iRNA_pred::Sqlite_manager	16

irna::iRNA_pred::Stat	16
irna::iRNA_seq	16
irna::iRNA_seq::Files	17
irna::iRNA_seq::Genbank	17
irna::iRNA_seq::iRNA_seq	17
irna::iRNA_seq::Sequences	17
irna::iRNA_seq::sRNA	17
irna::iRNA_stat	18
irna::iRNA_stat::Analysis	18
irna::iRNA_stat::Communication	18
irna::iRNA_stat::Computer	18
irna::iRNA_stat::Draw_data	19
irna::iRNA_stat::Ecdf	20
irna::iRNA_stat::Execute	20
irna::iRNA_stat::Exp_data	20
irna::iRNA_stat::Files	20
irna::iRNA_stat::Interaction	20
irna::iRNA_stat::iRNA_stat	20
irna::iRNA_stat::Mpi	21
irna::iRNA_stat::NormScore	21
irna::iRNA_stat::Parser	22
irna::iRNA_stat::Pickling	22
irna::iRNA_stat::pValue	22
irna::iRNA_stat::pValue_selection	22
irna::iRNA_stat::Rand_data	22
irna::iRNA_stat::Regression	22
irna::iRNA_stat::Soft	23
irna::iRNA_stat::Sqlite_manager	23
irna::iRNA_stat::Threshold	23

Chapter 2

Class Index

2.1 Class Hierarchy

This inheritance list is sorted roughly, but not completely, alphabetically:

irna::iRNA_stat::Analysis::Analysis	25
irna::iRNA_stat::Draw_data::draw_data	43
irna::iRNA_stat::Interaction::Interaction	90
irna::iRNA_stat::Regression::Regression	169
irna::iRNA_stat::Communication::Communication	26
irna::iRNA_pred::Comparison::Comparaison	27
irna::iRNA_stat::Computer::Computer	34
irna::David2tulip::Davidconfig::Davidconfig	41
irna::iRNA_stat::Ecdf::Ecdf	52
irna::David2tulip::Edge::Edge	53
irna::David2tulip::Files::Files	65
irna::iRNA_pred::Files::Files	69
irna::iRNA_stat::Files::Files	72
irna::iRNA_seq::Files::Files	77
irna::iRNA_seq::Genbank::Genbank	80
irna::David2tulip::Gene_list::Gene_list	82
irna::David2tulip::Graph::Graph	84
irna::iRNA_pred::Interaction::Interaction	97
irna::iRNA_pred::Merger::Merger	103
irna::iRNA_stat::Mpi::Mpi	106
irna::iRNA_pred::Mpi::Mpi	112
irna::David2tulip::Node::Node	127
irna::iRNA_stat::NormScore::NormScore	130
irna::iRNA_pred::Parse::Parse	134
irna::iRNA_stat::Parser::Parser	147
irna::iRNA_stat::Execute::Execute	56
irna::iRNA_stat::Exp_data::Exp_data	58
irna::iRNA_stat::pValue_selection::pValue_selection	158
irna::iRNA_stat::Rand_data::Rand_data	163

irna::iRNA_stat::Soft::Soft	179
irna::iRNA_stat::Threshold::Threshold	234
irna::David2tulip::Parser::Parser	149
irna::David2tulip::David::David	38
irna::David2tulip::Interact::Interact	88
irna::David2tulip::Multilist::Multilist	118
irna::David2tulip::Mycarn_data::Mycarn_data	122
irna::David2tulip::Name::Name	125
irna::David2tulip::pValue::pValue	156
irna::David2tulip::Similarity::Similarity	177
irna::iRNA_stat::Pickling::Pickling	153
irna::iRNA_stat::pValue::pValue	154
irna::iRNA_pred::RanRNA::RanRNA	166
irna::iRNA_seq::Sequences::Sequences	172
irna::David2tulip::Sqlite_manager::Sqlite_manager	181
irna::iRNA_pred::Sqlite_manager::Sqlite_manager	197
irna::iRNA_stat::Sqlite_manager::Sqlite_manager	213
irna::iRNA_seq::sRNA::sRNA	229
irna::iRNA_pred::Stat::Stat	231
irna::iRNA_pred::Fasta::Fasta	61

Chapter 3

Class Index

3.1 Class List

Here are the classes, structs, unions and interfaces with brief descriptions:

irna::iRNA_stat::Analysis::Analysis	25
irna::iRNA_stat::Communication::Communication	
: Empty object used for mpi communication	26
irna::iRNA_pred::Comparison::Comparison	
: Create coupled files and the list of comparison	27
irna::iRNA_stat::Computer::Computer	34
irna::David2tulip::David::David	38
irna::David2tulip::Davidconfig::Davidconfig	41
irna::iRNA_stat::Draw_data::draw_data	43
irna::iRNA_stat::Ecdf::Ecdf	52
irna::David2tulip::Edge::Edge	
: Handle interaction	53
irna::iRNA_stat::Execute::Execute	56
irna::iRNA_stat::Exp_data::Exp_data	58
irna::iRNA_pred::Fasta::Fasta	
: Write fasta needed for the different software from a multifasta	61
irna::David2tulip::Files::Files	65
irna::iRNA_pred::Files::Files	
:	69
irna::iRNA_stat::Files::Files	72
irna::iRNA_seq::Files::Files	77
irna::iRNA_seq::Genbank::Genbank	80
irna::David2tulip::Gene_list::Gene_list	
: Handle DAVID enrichment data	82
irna::David2tulip::Graph::Graph	84
irna::David2tulip::Interact::Interact	88
irna::iRNA_stat::Interaction::Interaction	90
irna::iRNA_pred::Interaction::Interaction	
: Store information on interaction	97

irna::iRNA_pred::Merger::Merger	
Merge the xml files in a sqlite database	103
irna::iRNA_stat::Mpi::Mpi	
: Manage Mpi run	106
irna::iRNA_pred::Mpi::Mpi	
: Manage Mpi run	112
irna::David2tulip::Multilist::Multilist	118
irna::David2tulip::Mycarn_data::Mycarn_data	122
irna::David2tulip::Name::Name	125
irna::David2tulip::Node::Node	
: Handle RNA information	127
irna::iRNA_stat::NormScore::NormScore	130
irna::iRNA_pred::Parse::Parse	
: Parse data from the different software	134
irna::iRNA_stat::Parser::Parser	147
irna::David2tulip::Parser::Parser	149
irna::iRNA_stat::Pickling::Pickling	153
irna::iRNA_stat::pValue::pValue	154
irna::David2tulip::pValue::pValue	156
irna::iRNA_stat::pValue_selection::pValue_selection	158
irna::iRNA_stat::Rand_data::Rand_data	163
irna::iRNA_pred::RanRNA::RanRNA	166
irna::iRNA_stat::Regression::Regression	169
irna::iRNA_seq::Sequences::Sequences	172
irna::David2tulip::Similarity::Similarity	177
irna::iRNA_stat::Soft::Soft	179
irna::David2tulip::Sqlite_manager::Sqlite_manager	
: Handle database connection, disconnection and querying	181
irna::iRNA_pred::Sqlite_manager::Sqlite_manager	
: Handle database connection, disconnection and querying	197
irna::iRNA_stat::Sqlite_manager::Sqlite_manager	213
irna::iRNA_seq::sRNA::sRNA	229
irna::iRNA_pred::Stat::Stat	231
irna::iRNA_stat::Threshold::Threshold	234

Chapter 4

File Index

4.1 File List

Here is a list of all files with brief descriptions:

/home/amine/workspace/iRNA/irna/David2tulip/___init___py	237
/home/amine/workspace/iRNA/irna/David2tulip/David.py	238
/home/amine/workspace/iRNA/irna/David2tulip/David2tulip.py	238
/home/amine/workspace/iRNA/irna/David2tulip/Davidconfig.py	238
/home/amine/workspace/iRNA/irna/David2tulip/Edge.py	239
/home/amine/workspace/iRNA/irna/David2tulip/Files.py	239
/home/amine/workspace/iRNA/irna/David2tulip/Gene_list.py	240
/home/amine/workspace/iRNA/irna/David2tulip/Graph.py	240
/home/amine/workspace/iRNA/irna/David2tulip/Interact.py	241
/home/amine/workspace/iRNA/irna/David2tulip/Multilist.py	241
/home/amine/workspace/iRNA/irna/David2tulip/Mycarn_data.py	241
/home/amine/workspace/iRNA/irna/David2tulip/Name.py	242
/home/amine/workspace/iRNA/irna/David2tulip/Node.py	242
/home/amine/workspace/iRNA/irna/David2tulip/Parser.py	242
/home/amine/workspace/iRNA/irna/David2tulip/pValue.py	243
/home/amine/workspace/iRNA/irna/David2tulip/Similarity.py	243
/home/amine/workspace/iRNA/irna/David2tulip/Sqlite_manager.py	244
/home/amine/workspace/iRNA/irna/iRNA_pred/___init___py	237
/home/amine/workspace/iRNA/irna/iRNA_pred/Comparison.py	244
/home/amine/workspace/iRNA/irna/iRNA_pred/Fasta.py	245
/home/amine/workspace/iRNA/irna/iRNA_pred/Files.py	239
/home/amine/workspace/iRNA/irna/iRNA_pred/Interaction.py	245
/home/amine/workspace/iRNA/irna/iRNA_pred/iRNA_pred.py	246
/home/amine/workspace/iRNA/irna/iRNA_pred/Merger.py	246
/home/amine/workspace/iRNA/irna/iRNA_pred/Mpi.py	246
/home/amine/workspace/iRNA/irna/iRNA_pred/Parse.py	247
/home/amine/workspace/iRNA/irna/iRNA_pred/RanRNA.py	247
/home/amine/workspace/iRNA/irna/iRNA_pred/Sqlite_manager.py	244
/home/amine/workspace/iRNA/irna/iRNA_pred/Stat.py	248

/home/amine/workspace/iRNA/irna/iRNA_seq/__init__.py	237
/home/amine/workspace/iRNA/irna/iRNA_seq/Files.py	239
/home/amine/workspace/iRNA/irna/iRNA_seq/Genbank.py	248
/home/amine/workspace/iRNA/irna/iRNA_seq/iRNA_seq.py	248
/home/amine/workspace/iRNA/irna/iRNA_seq/Sequences.py	249
/home/amine/workspace/iRNA/irna/iRNA_seq/sRNA.py	249
/home/amine/workspace/iRNA/irna/iRNA_stat/__init__.py	237
/home/amine/workspace/iRNA/irna/iRNA_stat/Analysis.py	249
/home/amine/workspace/iRNA/irna/iRNA_stat/Communication.py	249
/home/amine/workspace/iRNA/irna/iRNA_stat/Computer.py	250
/home/amine/workspace/iRNA/irna/iRNA_stat/Draw_data.py	250
/home/amine/workspace/iRNA/irna/iRNA_stat/Ecdf.py	250
/home/amine/workspace/iRNA/irna/iRNA_stat/Execute.py	251
/home/amine/workspace/iRNA/irna/iRNA_stat/Exp_data.py	251
/home/amine/workspace/iRNA/irna/iRNA_stat/Files.py	240
/home/amine/workspace/iRNA/irna/iRNA_stat/Interaction.py	245
/home/amine/workspace/iRNA/irna/iRNA_stat/iRNA_stat.py	251
/home/amine/workspace/iRNA/irna/iRNA_stat/Mpi.py	247
/home/amine/workspace/iRNA/irna/iRNA_stat/NormScore.py	252
/home/amine/workspace/iRNA/irna/iRNA_stat/Parser.py	242
/home/amine/workspace/iRNA/irna/iRNA_stat/Pickling.py	252
/home/amine/workspace/iRNA/irna/iRNA_stat/pValue.py	243
/home/amine/workspace/iRNA/irna/iRNA_stat/pValue_selection.py	252
/home/amine/workspace/iRNA/irna/iRNA_stat/Rand_data.py	252
/home/amine/workspace/iRNA/irna/iRNA_stat/Regression.py	253
/home/amine/workspace/iRNA/irna/iRNA_stat/Soft.py	253
/home/amine/workspace/iRNA/irna/iRNA_stat/Sqlite_manager.py	244
/home/amine/workspace/iRNA/irna/iRNA_stat/Threshold.py	253

Chapter 5

Namespace Documentation

5.1 irna Namespace Reference

Namespaces

- namespace [David2tulip](#)
- namespace [iRNA_pred](#)
- namespace [iRNA_seq](#)
- namespace [iRNA_stat](#)

5.2 irna::David2tulip Namespace Reference

Namespaces

- namespace [David](#)
- namespace [David2tulip](#)
- namespace [Davidconfig](#)
- namespace [Edge](#)
- namespace [Files](#)
- namespace [Gene_list](#)
- namespace [Graph](#)
- namespace [Interact](#)
- namespace [Multilist](#)
- namespace [Mycarn_data](#)
- namespace [Name](#)
- namespace [Node](#)
- namespace [Parser](#)
- namespace [pValue](#)
- namespace [Similarity](#)
- namespace [Sqlite_manager](#)

5.3 irna::David2tulip::David Namespace Reference

Classes

- class [David](#)

5.4 irna::David2tulip::David2tulip Namespace Reference

Functions

- def [main](#)
Main program ###.

5.4.1 Function Documentation

5.4.1.1 def irna::David2tulip::David2tulip::main ()

Main program ###.

Determine les fichiers fournis en arguments def getArguments(): """ Determine the argument

Returns

```
: arguments """ #Parsing arguments parser = argparse.ArgumentParser(description='
Create nodes and edge csv for Tulip from multiple datasets.') parser.
add_argument('-m', '--multilist',help='Multilist file from Mycarn',required=True)
parser.set_defaults(pValue=None) parser.add_argument('-l', '--filter',help='
Filter multilist for only known metabolites and use it for analysis') parser.
add_argument('-s','--similarity',help='Set similarity of sRNA groups') parser.
add_argument('-p', '--pValue',help='pValue of selected files') parser.add_
argument('-r', '--results',help='Path to result repertory',required=True) parser.
add_argument('-d', '--david',help='Submit multilist to DAVID',action='store_
true') parser.add_argument('-i', '--interact',help='Path to interaction file')
parser.add_argument('-e', '--enrichment',help='Path to DAVID enrichment file')
parser.add_argument('-y','--mycarn',help='Path to Mycarn db file') parser.add_
argument('-f', '--fastmode',help='Use sqlitebck package to get faster sqlite
implementation',action='store_true') args = parser.parse_args()
```

#Verify usage usage(parser,args) return args

Main program function

Definition at line 114 of file David2tulip.py.

5.5 irna::David2tulip::Davidconfig Namespace Reference

Classes

- class [Davidconfig](#)

5.6 irna::David2tulip::Edge Namespace Reference

Classes

- class [Edge](#)
: *Handle interaction*

5.7 irna::David2tulip::Files Namespace Reference

Classes

- class [Files](#)

5.8 irna::David2tulip::Gene_list Namespace Reference

Classes

- class [Gene_list](#)
: *Handle DAVID enrichment data*

5.9 irna::David2tulip::Graph Namespace Reference

Classes

- class [Graph](#)

5.10 irna::David2tulip::Interact Namespace Reference

Classes

- class [Interact](#)

5.11 irna::David2tulip::Multilist Namespace Reference

Classes

- class [Multilist](#)

5.12 irna::David2tulip::Mycarn_data Namespace Reference

Classes

- class [Mycarn_data](#)

5.13 irna::David2tulip::Name Namespace Reference

Classes

- class [Name](#)

5.14 irna::David2tulip::Node Namespace Reference

Classes

- class [Node](#)
: *Handle RNA information*

5.15 irna::David2tulip::Parser Namespace Reference

Classes

- class [Parser](#)

5.16 irna::David2tulip::pValue Namespace Reference

Classes

- class [pValue](#)

5.17 irna::David2tulip::Similarity Namespace Reference

Classes

- class [Similarity](#)

5.18 irna::David2tulip::Sqlite_manager Namespace Reference

Classes

- class [Sqlite_manager](#)
: Handle database connection, disconnection and querying.

5.19 irna::iRNA_pred Namespace Reference

Namespaces

- namespace [Comparison](#)
- namespace [Fasta](#)
- namespace [Files](#)
- namespace [Interaction](#)
- namespace [iRNA_pred](#)
- namespace [Merger](#)
- namespace [Mpi](#)
- namespace [Parse](#)
- namespace [RanRNA](#)
- namespace [Sqlite_manager](#)
- namespace [Stat](#)

5.20 irna::iRNA_pred::Comparison Namespace Reference

Classes

- class [Comparison](#)
: Create coupled files and the list of comparison

5.21 irna::iRNA_pred::Fasta Namespace Reference

Classes

- class [Fasta](#)
: Write fasta needed for the different software from a multifasta

5.22 irna::iRNA_pred::Files Namespace Reference

Classes

- class [Files](#)

:

5.23 irna::iRNA_pred::Interaction Namespace Reference

Classes

- class [Interaction](#)

: Store information on interaction.

5.24 irna::iRNA_pred::iRNA_pred Namespace Reference

Functions

- def [WriteAllExecTime](#)

Write execution time.

- def [saveData](#)

Save data in a sqlite database.

- def [main](#)

: Main program

5.24.1 Function Documentation

5.24.1.1 def irna::iRNA_pred::iRNA_pred::main ()

: Main program

Author

: Amine Ghozlane

Definition at line 68 of file iRNA_pred.py.

References [saveData\(\)](#), and [WriteAllExecTime\(\)](#).

Referenced by [saveData\(\)](#).

5.24.1.2 `def irna::iRNA_pred::iRNA_pred::saveData (data_files, fastmode)`

Save data in a sqlite database.

Definition at line 40 of file `iRNA_pred.py`.

References `main()`.

Referenced by `main()`, and `WriteAllExecTime()`.

5.24.1.3 `def irna::iRNA_pred::iRNA_pred::WriteAllExecTime (result_out, start, end)`

Write execution time.

Parameters

<i>result_out,:</i>	Time result
<i>start,:</i>	Date of start
<i>end,:</i>	Date of end

Definition at line 25 of file `iRNA_pred.py`.

References `saveData()`.

Referenced by `main()`.

5.25 irna::iRNA_pred::Merger Namespace Reference

Classes

- class [Merger](#)
Merge the xml files in a sqlite database.

5.26 irna::iRNA_pred::Mpi Namespace Reference

Classes

- class [Mpi](#)
: Manage [Mpi](#) run

5.27 irna::iRNA_pred::Parse Namespace Reference

Classes

- class [Parse](#)
: [Parse](#) data from the different software.

5.28 irna::iRNA_pred::RanRNA Namespace Reference

Classes

- class [RanRNA](#)

Variables

- tuple [generator](#) = [RanRNA](#)(0.41728640,141,100,"/home/amine/workspace/-Mycarn_old/data/test/")

5.28.1 Variable Documentation

5.28.1.1 tuple irna::iRNA_pred::RanRNA::generator =
RanRNA(0.41728640,141,100,"/home/amine/workspace/Mycarn_old/data/test/")

Definition at line 113 of file RanRNA.py.

5.29 irna::iRNA_pred::Sqlite_manager Namespace Reference

Classes

- class [Sqlite_manager](#)
: Handle database connection, disconnection and querying.

5.30 irna::iRNA_pred::Stat Namespace Reference

Classes

- class [Stat](#)

5.31 irna::iRNA_seq Namespace Reference

Namespaces

- namespace [Files](#)
- namespace [Genbank](#)
- namespace [iRNA_seq](#)
- namespace [Sequences](#)
- namespace [sRNA](#)

5.32 irna::iRNA_seq::Files Namespace Reference

Classes

- class [Files](#)

5.33 irna::iRNA_seq::Genbank Namespace Reference

Classes

- class [Genbank](#)

5.34 irna::iRNA_seq::iRNA_seq Namespace Reference

Functions

- def [main](#)
Main program function.

5.34.1 Function Documentation

5.34.1.1 def irna::iRNA_seq::iRNA_seq::main ()

Main program function.

Definition at line 18 of file iRNA_seq.py.

5.35 irna::iRNA_seq::Sequences Namespace Reference

Classes

- class [Sequences](#)

5.36 irna::iRNA_seq::sRNA Namespace Reference

Classes

- class [sRNA](#)

5.37 irna::iRNA_stat Namespace Reference

Namespaces

- namespace [Analysis](#)
- namespace [Communication](#)
- namespace [Computer](#)
- namespace [Draw_data](#)
- namespace [Ecdf](#)
- namespace [Execute](#)
- namespace [Exp_data](#)
- namespace [Files](#)
- namespace [Interaction](#)
- namespace [iRNA_stat](#)
- namespace [Mpi](#)
- namespace [NormScore](#)
- namespace [Parser](#)
- namespace [Pickling](#)
- namespace [pValue](#)
- namespace [pValue_selection](#)
- namespace [Rand_data](#)
- namespace [Regression](#)
- namespace [Soft](#)
- namespace [Sqlite_manager](#)
- namespace [Threshold](#)

5.38 irna::iRNA_stat::Analysis Namespace Reference

Classes

- class [Analysis](#)

5.39 irna::iRNA_stat::Communication Namespace Reference

Classes

- class [Communication](#)
: Empty object used for mpi communication

5.40 irna::iRNA_stat::Computer Namespace Reference

Classes

- class [Computer](#)

5.41 irna::iRNA_stat::Draw_data Namespace Reference

Classes

- class [draw_data](#)

Variables

- tuple [graphics](#) = `importtr('graphics')`
- tuple [grdevices](#) = `importtr('grDevices')`
- tuple [base](#) = `importtr('base')`
- tuple [stats](#) = `importtr('stats')`
- tuple [pROC](#) = `importtr('pROC')`
- tuple [Cairo](#) = `importtr('Cairo')`

5.41.1 Variable Documentation

5.41.1.1 tuple `irna::iRNA_stat::Draw_data::base = importtr('base')`

Definition at line 17 of file `Draw_data.py`.

5.41.1.2 tuple `irna::iRNA_stat::Draw_data::Cairo = importtr('Cairo')`

Definition at line 20 of file `Draw_data.py`.

5.41.1.3 tuple `irna::iRNA_stat::Draw_data::graphics = importtr('graphics')`

Definition at line 15 of file `Draw_data.py`.

5.41.1.4 tuple `irna::iRNA_stat::Draw_data::grdevices = importtr('grDevices')`

Definition at line 16 of file `Draw_data.py`.

5.41.1.5 tuple `irna::iRNA_stat::Draw_data::pROC = importtr('pROC')`

Definition at line 19 of file `Draw_data.py`.

5.41.1.6 tuple `irna::iRNA_stat::Draw_data::stats = importtr('stats')`

Definition at line 18 of file `Draw_data.py`.

5.42 irna::iRNA_stat::Ecdf Namespace Reference

Classes

- class [Ecdf](#)

5.43 irna::iRNA_stat::Execute Namespace Reference

Classes

- class [Execute](#)

5.44 irna::iRNA_stat::Exp_data Namespace Reference

Classes

- class [Exp_data](#)

5.45 irna::iRNA_stat::Files Namespace Reference

Classes

- class [Files](#)

5.46 irna::iRNA_stat::Interaction Namespace Reference

Classes

- class [Interaction](#)

5.47 irna::iRNA_stat::iRNA_stat Namespace Reference

Functions

- def [usage](#)
Test correct usage of arguments.
- def [main](#)
Determine les fichiers fournis en arguments def getArgument(): "" Determine the argument.

5.47.1 Function Documentation

5.47.1.1 def irna::iRNA_stat::iRNA_stat::main ()

Determine les fichiers fournis en arguments def getArguments(): "" Determine the argument.

Returns

```
: arguments "" #Parsing arguments parser = argparse.ArgumentParser(description='-
Statistical analysis of RNA-RNA predict interaction.') parser.add_argument('-d', '--i-
RNA_db',help='Path to mycarn db',required=True) parser.add_argument('-i', '--soft-
_inf',help='Path to soft information file',required=True) parser.add_argument('-e',
'--exp_inf',help='Path to experimental data file') parser.add_argument('-n', '--rand-
_inf',help='Path to random data file') parser.add_argument('-a', '--random',help='-
Random analysis',action='store_true') parser.add_argument('-r', '--results',help='-
Path to result repertory',required=True) args = parser.parse_args()
```

#Verify usage usage(parser,args) return args

Main program function

Definition at line 66 of file iRNA_stat.py.

Referenced by usage().

5.47.1.2 def irna::iRNA_stat::iRNA_stat::usage (parser, args)

Test correct usage of arguments.

Parameters

<i>parser,</i>	Parser object
<i>args,</i>	Arguments

Definition at line 32 of file iRNA_stat.py.

References main().

5.48 irna::iRNA_stat::Mpi Namespace Reference

Classes

- class [Mpi](#)
: Manage [Mpi](#) run

5.49 irna::iRNA_stat::NormScore Namespace Reference

Classes

- class [NormScore](#)

5.50 irna::iRNA_stat::Parser Namespace Reference**Classes**

- class [Parser](#)

5.51 irna::iRNA_stat::Pickling Namespace Reference**Classes**

- class [Pickling](#)

5.52 irna::iRNA_stat::pValue Namespace Reference**Classes**

- class [pValue](#)

5.53 irna::iRNA_stat::pValue_selection Namespace Reference**Classes**

- class [pValue_selection](#)

5.54 irna::iRNA_stat::Rand_data Namespace Reference**Classes**

- class [Rand_data](#)

5.55 irna::iRNA_stat::Regression Namespace Reference**Classes**

- class [Regression](#)

5.56 irna::iRNA_stat::Soft Namespace Reference

Classes

- class [Soft](#)

5.57 irna::iRNA_stat::Sqlite_manager Namespace Reference

Classes

- class [Sqlite_manager](#)

5.58 irna::iRNA_stat::Threshold Namespace Reference

Classes

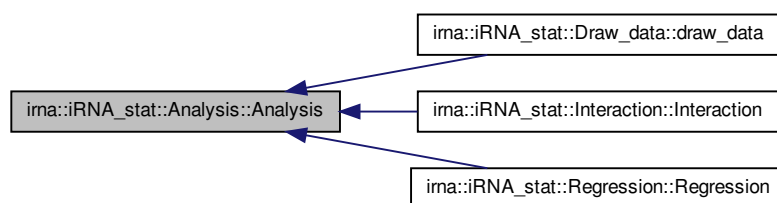
- class [Threshold](#)

Chapter 6

Class Documentation

6.1 `irna::iRNA_stat::Analysis::Analysis` Class Reference

Inheritance diagram for `irna::iRNA_stat::Analysis::Analysis`:



Public Member Functions

- `def __init__`
Instantiate [Analysis](#) object.
- `def commun_values`
Detect commune nan values.
- `def getRangePosit`
Get one column.

6.1.1 Detailed Description

Definition at line 9 of file `Analysis.py`.

6.1.2 Constructor & Destructor Documentation

6.1.2.1 `def irna::iRNA_stat::Analysis::Analysis::__init__(self)`

Instantiate [Analysis](#) object.

Definition at line 14 of file Analysis.py.

6.1.3 Member Function Documentation

6.1.3.1 `def irna::iRNA_stat::Analysis::Analysis::commun_values (self, cumneg_nanvalues, normscore_nanvalues)`

Detect commune nan values.

Definition at line 21 of file Analysis.py.

References [getRangePosit\(\)](#).

Referenced by [irna::iRNA_stat::Regression::Regression::linear_regression\(\)](#), and [irna::iRNA_stat::Draw_data::draw_data::plot_linear_regression\(\)](#).

6.1.3.2 `def irna::iRNA_stat::Analysis::Analysis::getRangePosit (self, array, col)`

Get one column.

Parameters

<i>array</i> ,:	Matrix array of data
<i>col</i> ,:	Selected column

Definition at line 33 of file Analysis.py.

Referenced by [commun_values\(\)](#), [irna::iRNA_stat::Interaction::Interaction::Interaction_data\(\)](#), and [irna::iRNA_stat::Draw_data::draw_data::write_interaction\(\)](#).

The documentation for this class was generated from the following file:

- [/home/amine/workspace/iRNA/irna/iRNA_stat/Analysis.py](#)

6.2 `irna::iRNA_stat::Communication::Communication` Class - Reference

: Empty object used for mpi communication

Public Member Functions

- `def __init__`

Empty object used to send messages.

6.2.1 Detailed Description

: Empty object used for mpi communication

Author

: Amine Ghozlane

Version

: 1.0

Definition at line 7 of file Communication.py.

6.2.2 Constructor & Destructor Documentation

6.2.2.1 `def irna::iRNA_stat::Communication::Communication::__init__(self)`

Empty object used to send messages.

Definition at line 12 of file Communication.py.

The documentation for this class was generated from the following file:

- `/home/amine/workspace/iRNA/irna/iRNA_stat/Communication.py`

6.3 irna::iRNA_pred::Comparison::Comparaison Class Reference

: Create coupled files and the list of comparison

Public Member Functions

- `def __init__`
The constructor.
- `def runCommand`
Run command.
- `def createCouple`
Create the couple.
- `def createRNAcofoldCouple`
Create the couple for RNAcofold.
- `def getCouple`
Get a couple in sRNA repertory.
- `def getRNAcofoldCouple`

Get a couple in sRNA repertory.

- def [getName](#)

Get the name of the fasta file.

- def [getCommand](#)

Build the command.

- def [getFastaFiles](#)

Get the list of data.

- def [getUnique](#)

Get unique data.

- def [getComparison](#)

Define the comparison.

- def [runComparison](#)

Run a comparison.

- def [manageCouple](#)

Manage the creation of couples.

- def [prepareComparison](#)

Control [Mpi](#) procedure.

Public Attributes

- [comp_list](#)
- [sRNA_out](#)
- [mRNA_out](#)
- [soft_path](#)
- [mf_mRNA](#)

6.3.1 Detailed Description

: Create coupled files and the list of comparison

Definition at line 15 of file Comparison.py.

6.3.2 Constructor & Destructor Documentation

6.3.2.1 `def irna::iRNA_pred::Comparison::Comparison::__init__(self, comp_list, sRNA_out, mRNA_out, soft_path, mf_mRNA)`

The constructor.

Definition at line 20 of file Comparison.py.

6.3.3 Member Function Documentation

6.3.3.1 `def irna::iRNA_pred::Comparison::Comparaison::createCouple (self, sRNA, mRNA)`

Create the couple.

Parameters

<i>sRNA</i> ,:	name of the sRNA file
<i>mRNA</i> ,:	name of the mRNA file

Definition at line 57 of file Comparison.py.

References `createRNAcofoldCouple()`, `mRNA_out`, and `sRNA_out`.

Referenced by `manageCouple()`, and `runCommand()`.

6.3.3.2 `def irna::iRNA_pred::Comparison::Comparaison::createRNAcofoldCouple (self, sRNA, mRNA)`

Create the couple for RNAcofold.

Parameters

<i>sRNA</i> ,:	name of the sRNA file
<i>mRNA</i> ,:	name of the mRNA file

Definition at line 82 of file Comparison.py.

References `getCouple()`, `mRNA_out`, and `sRNA_out`.

Referenced by `createCouple()`, and `manageCouple()`.

6.3.3.3 `def irna::iRNA_pred::Comparison::Comparaison::getCommand (self, build_command, sRNA, mRNA, RNAcofold_flag)`

Build the command.

Parameters

<i>build_ - command</i> ,:	Soft command
<i>sRNA</i> ,:	name of the sRNA file
<i>mRNA</i> ,:	name of the mRNA file
<i>RNAcofold_ - flag</i> ,:	Flag for RNAcofold special case

Returns

: [Comparison](#) command

Definition at line 158 of file Comparison.py.

References getCouple(), getFastaFiles(), getRNAcofoldCouple(), and getUnique().

Referenced by getComparison(), and getRNAcofoldCouple().

```
6.3.3.4 def irna::iRNA_pred::Comparison::Comparison::getComparison ( self, command,
                             RNAcofold_flag )
```

Define the comparison.

Parameters

<i>command</i> ,:	Soft command
<i>RNAcofold_flag</i> ,:	Flag for RNAcofold special case

Returns

: [Comparison](#) list and the number of comparison

Definition at line 206 of file Comparison.py.

References comp_list, getCommand(), getFastaFiles(), getUnique(), mRNA_out, run-Comparison(), and sRNA_out.

Referenced by getFastaFiles().

```
6.3.3.5 def irna::iRNA_pred::Comparison::Comparison::getCouple ( self, sRNA, mRNA )
```

Get a couple in sRNA repertory.

Parameters

<i>sRNA</i> ,:	name of the sRNA file
<i>mRNA</i> ,:	name of the mRNA file

Returns

: Return the file couple

Definition at line 109 of file Comparison.py.

References getRNAcofoldCouple(), and sRNA_out.

Referenced by createRNAcofoldCouple(), and getCommand().

6.3.3.6 def irna::iRNA_pred::Comparison::Comparaison::getFastaFiles (*self*, *repertory*)

Get the list of data.

Parameters

<i>repertory</i> ,:	Interest repertory
---------------------	--------------------

Returns

: Return the list of file of interest

Definition at line 183 of file Comparison.py.

References getComparison().

Referenced by getCommand(), getComparison(), and manageCouple().

6.3.3.7 def irna::iRNA_pred::Comparison::Comparaison::getName (*self*, *regex*, *fasta_file*)

Get the name of the fasta file.

Parameters

<i>regex</i> ,:	Regex used to detect the name
<i>fasta_file</i> ,:	A standard fasta file with her path

Returns

: The name of the fasta file

Definition at line 141 of file Comparison.py.

References mf_mRNA, mRNA_out, soft_path, and sRNA_out.

Referenced by getRNAcofoldCouple().

6.3.3.8 def irna::iRNA_pred::Comparison::Comparaison::getRNAcofoldCouple (*self*, *sRNA*, *mRNA*)

Get a couple in sRNA repertory.

Parameters

<i>sRNA</i> ,:	name of the sRNA file
<i>mRNA</i> ,:	name of the mRNA file

Returns

: Return the file couple

Definition at line 125 of file Comparison.py.

References `getCommand()`, and `getName()`.

Referenced by `getCommand()`, and `getCouple()`.

6.3.3.9 `def irna::iRNA_pred::Comparison::Comparaision::getUnique (self, data_list)`

Get unique data.

Parameters

<i>data_list</i> :	list of data
--------------------	--------------

Definition at line 192 of file Comparison.py.

References `comp_list`.

Referenced by `irna::iRNA_stat::pValue_selection::pValue_selection::compute_Davidmatrix()`, `getCommand()`, and `getComparison()`.

6.3.3.10 `def irna::iRNA_pred::Comparison::Comparaision::manageCouple (self)`

Manage the creation of couples.

Definition at line 308 of file Comparison.py.

References `comp_list`, `createCouple()`, `createRNAcofoldCouple()`, `getFastaFiles()`, `manageCouple()`, `mRNA_out`, `prepareComparison()`, and `sRNA_out`.

Referenced by `manageCouple()`, and `runComparison()`.

6.3.3.11 `def irna::iRNA_pred::Comparison::Comparaision::prepareComparison (self)`

Control [Mpi](#) procedure.

Definition at line 344 of file Comparison.py.

Referenced by `manageCouple()`.

6.3.3.12 `def irna::iRNA_pred::Comparison::Comparaision::runCommand (self, cmd)`

Run command.

Parameters

<i>cmd</i> :	Command to run
--------------	----------------

Definition at line 39 of file Comparison.py.

References createCouple(), and sRNA_out.

6.3.3.13 `def irna::iRNA_pred::Comparison::Comparaison::runComparison (self, cmd)`

Run a comparison.

Parameters

<i>cmd</i> ,:	Soft command
---------------	--------------

Returns

: Return soft result

Definition at line 288 of file Comparison.py.

References comp_list, manageCouple(), mRNA_out, and sRNA_out.

Referenced by getComparison().

6.3.4 Member Data Documentation

6.3.4.1 `irna::iRNA_pred::Comparison::Comparaison::comp_list`

Definition at line 20 of file Comparison.py.

Referenced by getComparison(), getUnique(), manageCouple(), and runComparison().

6.3.4.2 `irna::iRNA_pred::Comparison::Comparaison::mf_mRNA`

Definition at line 20 of file Comparison.py.

Referenced by getName().

6.3.4.3 `irna::iRNA_pred::Comparison::Comparaison::mRNA_out`

Definition at line 20 of file Comparison.py.

Referenced by createCouple(), createRNAcofoldCouple(), getComparison(), getName(), manageCouple(), and runComparison().

6.3.4.4 `irna::iRNA_pred::Comparison::Comparaison::soft_path`

Definition at line 20 of file Comparison.py.

Referenced by getName().

6.3.4.5 `irna::iRNA_pred::Comparison::Comparison::sRNA_out`

Definition at line 20 of file `Comparison.py`.

Referenced by `createCouple()`, `createRNAcofoldCouple()`, `getComparison()`, `getCouple()`, `getName()`, `manageCouple()`, `runCommand()`, and `runComparison()`.

The documentation for this class was generated from the following file:

- `/home/amine/workspace/iRNA/irna/iRNA_pred/Comparison.py`

6.4 `irna::iRNA_stat::Computer::Computer` Class Reference

Public Member Functions

- `def __init__`
Instantiate `Computer` object.

Public Attributes

- `ppv`
- `sensitivity`
- `classtype`
- `curve_param`
- `softid`
- `numsoft`
- `name`
- `cumneg`
- `type_sol`
- `score_type`
- `pValue_type`
- `nbinteract`
- `interactions`
- `sRNAid_tab`
- `unique_sRNAidinint`
- `norm_score`
- `pos`
- `pValue`
- `select`
- `interact`

6.4.1 Detailed Description

Definition at line 9 of file `Computer.py`.

6.4.2 Constructor & Destructor Documentation

6.4.2.1 `def irna::iRNA_stat::Computer::Computer::__init__(self, softid, name, numsoft, type_sol, score_type, dbmanage, args)`

Instantiate [Computer](#) object.

Parameters

<i>softid,:</i>	Id of the software
<i>name,:</i>	Name of the software
<i>numsoft,:</i>	Corresponding numsoft in soft_inf
<i>type_sol,:</i>	Type of solution
<i>score_type,:</i>	Type of score
<i>dbmanage,:</i>	Access to the database
<i>args,:</i>	Arguments

Definition at line 22 of file Computer.py.

6.4.3 Member Data Documentation

6.4.3.1 `irna::iRNA_stat::Computer::Computer::classtype`

Definition at line 22 of file Computer.py.

Referenced by `irna::iRNA_stat::Interaction::Interaction::compute_sensitivity()`.

6.4.3.2 `irna::iRNA_stat::Computer::Computer::cumneg`

Definition at line 22 of file Computer.py.

Referenced by `irna::iRNA_stat::Regression::Regression::ecdf_estimate()`, `irna::iRNA_stat::Regression::Regression::linear_regression()`, and `irna::iRNA_stat::Regression::Regression::run()`.

6.4.3.3 `irna::iRNA_stat::Computer::Computer::curve_param`

Definition at line 22 of file Computer.py.

Referenced by `irna::iRNA_stat::Regression::Regression::ecdf_estimate()`, `irna::iRNA_stat::Regression::Regression::linear_regression()`, and `irna::iRNA_stat::Regression::Regression::run()`.

6.4.3.4 `irna::iRNA_stat::Computer::Computer::interact`

Definition at line 22 of file Computer.py.

6.4.3.5 irna::iRNA_stat::Computer::Computer::interactions

Definition at line 22 of file Computer.py.

Referenced by irna::iRNA_stat::Interaction::Interaction::compute_sensitivity(), irna::iRNA_stat::NormScore::NormScore::normUniqueSolution(), irna::iRNA_stat::pValue::pValue::run(), and irna::iRNA_stat::NormScore::NormScore::run().

6.4.3.6 irna::iRNA_stat::Computer::Computer::name

Definition at line 22 of file Computer.py.

6.4.3.7 irna::iRNA_stat::Computer::Computer::nbinteract

Definition at line 22 of file Computer.py.

6.4.3.8 irna::iRNA_stat::Computer::Computer::norm_score

Definition at line 22 of file Computer.py.

Referenced by irna::iRNA_stat::Regression::Regression::ecdf_estimate(), irna::iRNA_stat::Regression::Regression::linear_regression(), irna::iRNA_stat::NormScore::NormScore::normSeveralContactScore(), irna::iRNA_stat::NormScore::NormScore::normSeveralEnergy(), irna::iRNA_stat::NormScore::NormScore::normSeveralScore(), irna::iRNA_stat::NormScore::NormScore::normUniqueSolution(), irna::iRNA_stat::pValue::pValue::run(), and irna::iRNA_stat::NormScore::NormScore::run().

6.4.3.9 irna::iRNA_stat::Computer::Computer::numsoft

Definition at line 22 of file Computer.py.

6.4.3.10 irna::iRNA_stat::Computer::Computer::pos

Definition at line 22 of file Computer.py.

Referenced by irna::iRNA_stat::NormScore::NormScore::defnormfunction(), irna::iRNA_stat::Interaction::Interaction::Interaction_data(), irna::iRNA_stat::NormScore::NormScore::normSeveralContactScore(), irna::iRNA_stat::NormScore::NormScore::normSeveralEnergy(), irna::iRNA_stat::NormScore::NormScore::normSeveralScore(), irna::iRNA_stat::NormScore::NormScore::normUniqueSolution(), and irna::iRNA_stat::NormScore::NormScore::run().

6.4.3.11 irna::iRNA_stat::Computer::Computer::ppv

Definition at line 22 of file Computer.py.

Referenced by irna::iRNA_stat::Interaction::Interaction::compute_sensitivity().

6.4.3.12 irna::iRNA_stat::Computer::Computer::pValue

Definition at line 22 of file Computer.py.

Referenced by irna::iRNA_stat::Files::Files::case(), irna::iRNA_stat::Files::Files::data_format(), and irna::iRNA_stat::Files::Files::getfiles().

6.4.3.13 irna::iRNA_stat::Computer::Computer::pValue_type

Definition at line 22 of file Computer.py.

Referenced by irna::iRNA_stat::Regression::Regression::ecdf_estimate().

6.4.3.14 irna::iRNA_stat::Computer::Computer::score_type

Definition at line 22 of file Computer.py.

Referenced by irna::iRNA_stat::NormScore::NormScore::run().

6.4.3.15 irna::iRNA_stat::Computer::Computer::select

Definition at line 22 of file Computer.py.

6.4.3.16 irna::iRNA_stat::Computer::Computer::sensitivity

Definition at line 22 of file Computer.py.

Referenced by irna::iRNA_stat::Interaction::Interaction::compute_sensitivity().

6.4.3.17 irna::iRNA_stat::Computer::Computer::softid

Definition at line 22 of file Computer.py.

6.4.3.18 irna::iRNA_stat::Computer::Computer::sRNAid_tab

Definition at line 22 of file Computer.py.

Referenced by irna::iRNA_stat::Regression::Regression::ecdf_estimate(), and irna::iRNA_stat::Regression::Regression::linear_regression().

6.4.3.19 irna::iRNA_stat::Computer::Computer::type_sol

Definition at line 22 of file Computer.py.

Referenced by irna::iRNA_stat::NormScore::NormScore::defnormfunction(), and irna::iRNA_stat::Interaction::Interaction::Interaction_data().

6.4.3.20 `irna::iRNA_stat::Computer::Computer::unique_sRNAid`

Definition at line 22 of file `Computer.py`.

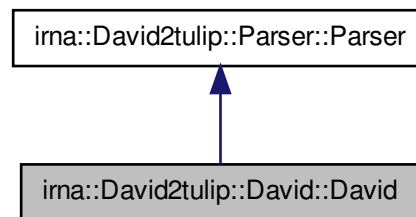
Referenced by `irna::iRNA_stat::Regression::Regression::ecdf_estimate()`, and `irna::iRNA_stat::Regression::Regression::linear_regression()`.

The documentation for this class was generated from the following file:

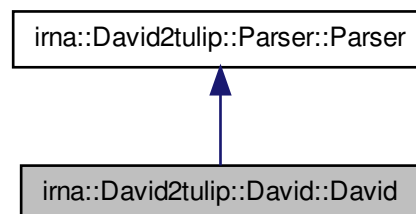
- `/home/amine/workspace/iRNA/irna/iRNA_stat/Computer.py`

6.5 `irna::David2tulip::David::David` Class Reference

Inheritance diagram for `irna::David2tulip::David::David`:



Collaboration diagram for `irna::David2tulip::David::David`:



Public Member Functions

- def `__init__`
Instantiate david object.
- def `davidConnection`
Connection to david.
- def `analysis`
Proceed to DAVID enrichment and store useful data.
- def `parseChart`
Parse DAVID chart data.
- def `writefile`
Pickle DAVID information.
- def `setdata`
Set data from DAVID into the graph.

Public Attributes

- `listType`
- `david_chart`

6.5.1 Detailed Description

Definition at line 14 of file David.py.

6.5.2 Constructor & Destructor Documentation

6.5.2.1 `def irna::David2tulip::David::David::__init__(self, david_file = None)`

Instantiate david object.

Parameters

<code>david_file,:</code>	Path to david file
---------------------------	--------------------

Definition at line 21 of file David.py.

6.5.3 Member Function Documentation

6.5.3.1 `def irna::David2tulip::David::David::analysis(self, graph)`

Proceed to DAVID enrichment and store useful data.

Parameters

<i>graph</i> ,:	Graph object
-----------------	------------------------------

Definition at line 44 of file David.py.

References `david_chart`, `irna::David2tulip::Parser::Parser::getsRNA()`, `irna::David2tulip::Parser::Parser::getTarget()`, `listType`, `parseChart()`, and `writefile()`.

Referenced by `davidConnection()`.

6.5.3.2 `def irna::David2tulip::David::David::davidConnection (self)`

Connection to david.

Definition at line 32 of file David.py.

References `analysis()`, and `davidConnection()`.

Referenced by `davidConnection()`.

6.5.3.3 `def irna::David2tulip::David::David::parseChart (self, david_chart, sRNA)`

Parse DAVID chart data.

Parameters

<i>david_ - chart</i> ,:	DAVID result
<i>sRNA</i> ,:	sRNA

Definition at line 68 of file David.py.

References `david_chart`, `irna::David2tulip::Parser::Parser::printObject()`, and `setdata()`.

Referenced by `analysis()`.

6.5.3.4 `def irna::David2tulip::David::David::setdata (self, node_objects, edge_objects)`

Set data from DAVID into the graph.

Parameters

<i>node_ - objects</i> ,:	List of node objects
<i>edge_ - objects</i> ,:	List of edge objects

Returns

: [Node](#) and edge objects

Definition at line 86 of file David.py.

Referenced by `parseChart()`.

6.5.3.5 def irna::David2tulip::David::David::writefile (*self*, *results*)

Pickle DAVID information.

Parameters

<i>results,</i>	Path to result file
-----------------	---------------------

Definition at line 76 of file David.py.

References `david_chart`, and `irna::David2tulip::Parser::Parser::getlinkededge()`.

Referenced by `analysis()`.

6.5.4 Member Data Documentation**6.5.4.1 irna::David2tulip::David::David::david_chart**

Definition at line 21 of file David.py.

Referenced by `analysis()`, `parseChart()`, and `writefile()`.

6.5.4.2 irna::David2tulip::David::David::listType

Definition at line 21 of file David.py.

Referenced by `analysis()`.

The documentation for this class was generated from the following file:

- `/home/amine/workspace/iRNA/irna/David2tulip/David.py`

6.6 irna::David2tulip::Davidconfig::Davidconfig Class Reference**Public Member Functions**

- def `__init__`
 Instantiate [Davidconfig](#) object.
- def `readconfig`
 Read david config.

- def [writeconfig](#)
Write david config.

Public Attributes

- [config](#)
- [davidconfig_file](#)

6.6.1 Detailed Description

Definition at line 9 of file Davidconfig.py.

6.6.2 Constructor & Destructor Documentation

6.6.2.1 def irna::David2tulip::Davidconfig::Davidconfig::__init__(*self*, *config*)

Instantiate [Davidconfig](#) object.

Parameters

<i>config</i> ,:	config path
------------------	-------------

Definition at line 16 of file Davidconfig.py.

6.6.3 Member Function Documentation

6.6.3.1 def irna::David2tulip::Davidconfig::Davidconfig::readconfig (*self*, *davidobject*)

Read david config.

Parameters

<i>davidobject</i> ,:	David pkl
-----------------------	---------------------------

Definition at line 26 of file Davidconfig.py.

References [davidconfig_file](#), and [writeconfig\(\)](#).

6.6.3.2 def irna::David2tulip::Davidconfig::Davidconfig::writeconfig (*self*)

Write david config.

Definition at line 43 of file Davidconfig.py.

References [davidconfig_file](#).

Referenced by [readconfig\(\)](#).

6.6.4 Member Data Documentation

6.6.4.1 irna::David2tulip::Davidconfig::Davidconfig::config

Definition at line 16 of file Davidconfig.py.

Referenced by irna::David2tulip::Files::Files::data_format(), and irna::David2tulip::Files::Files::getfiles().

6.6.4.2 irna::David2tulip::Davidconfig::Davidconfig::davidconfig_file

Definition at line 16 of file Davidconfig.py.

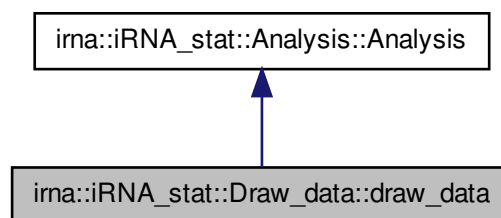
Referenced by readconfig(), and writeconfig().

The documentation for this class was generated from the following file:

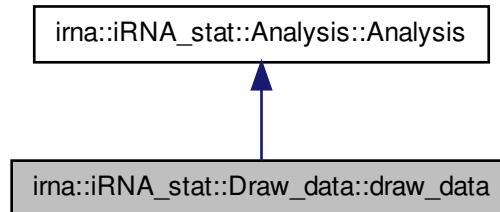
- [/home/amine/workspace/iRNA/irna/David2tulip/Davidconfig.py](#)

6.7 irna::iRNA_stat::Draw_data::draw_data Class Reference

Inheritance diagram for irna::iRNA_stat::Draw_data::draw_data:



Collaboration diagram for `irna::iRNA_stat::Draw_data::draw_data`:



Public Member Functions

- def `__init__`
Instantiate `draw_data` object.
- def `write_curve_param_data`
- def `plot_linear_regression`
Plot linear regression of random data.
- def `getnames`
name of softwares
- def `plot_roc_curves`
Plot roc curve.
- def `plot_roc_curves_statistics`
Statistical analysis of roc.
- def `write_pValue`
Print `pValue`.
- def `write_rocthresValue`
- def `write_rocAuc`
write AUC
- def `meanArray`
Mean array.
- def `getPredplotvect`
Get float vector from listobj.
- def `pred_plot`
Plot sensitivity and ppv mean.
- def `write_pred_plot`
Write mean sensitivity and ppv of each software.
- def `write_sens_ppv`
Write sensitivity and ppv.

- def [exec_plot](#)
Plot execution time.
- def [write_pValueSelect](#)
- def [write_frequency](#)
- def [write_similarity](#)
- def [frequency_plot](#)
- def [similarity_plot](#)
- def [write_pValueInteract](#)
- def [getBoolselect](#)
- def [write_interaction](#)
- def [write_general_data](#)
- def [plot](#)
Plot main function.

Public Attributes

- [result](#)

6.7.1 Detailed Description

Definition at line 22 of file Draw_data.py.

6.7.2 Constructor & Destructor Documentation

6.7.2.1 `def irna::iRNA_stat::Draw_data::draw_data::__init__(self, result)`

Instantiate [draw_data](#) object.

Definition at line 28 of file Draw_data.py.

6.7.3 Member Function Documentation

6.7.3.1 `def irna::iRNA_stat::Draw_data::draw_data::exec_plot(self, execution_time)`

Plot execution time.

Parameters

<i>execution_time</i> ,:	Execution time
--------------------------	----------------

Definition at line 362 of file Draw_data.py.

References [result](#), and [write_frequency\(\)](#).

Referenced by [plot\(\)](#), and [write_sens_ppv\(\)](#).

6.7.3.2 `def irna::iRNA_stat::Draw_data::draw_data::frequency_plot (self, listobj)`

Parameters

<i>listobj</i> :	List of Computer object
------------------	---

Definition at line 419 of file Draw_data.py.

References result.

Referenced by plot(), and write_frequency().

6.7.3.3 `def irna::iRNA_stat::Draw_data::draw_data::getBoolselect (self, obj, i)`

Definition at line 459 of file Draw_data.py.

References result, and write_general_data().

Referenced by similarity_plot(), and write_pValueInteract().

6.7.3.4 `def irna::iRNA_stat::Draw_data::draw_data::getnames (self, listobj)`

name of softwares

Parameters

<i>listobj</i> :	List of Computer object
------------------	---

Definition at line 151 of file Draw_data.py.

References plot_roc_curves(), and result.

Referenced by getPredplotvect(), plot_linear_regression(), and plot_roc_curves().

6.7.3.5 `def irna::iRNA_stat::Draw_data::draw_data::getPredplotvect (self, listobj)`

Get float vector from listobj.

Parameters

<i>listobj</i> :	List of Computer object
------------------	---

Definition at line 296 of file Draw_data.py.

References getnames(), result, and write_pred_plot().

Referenced by meanArray(), and write_rocAuc().

6.7.3.6 `def irna::iRNA_stat::Draw_data::draw_data::meanArray (self, array)`

Mean array.

Parameters

<i>array</i> ,:	Matrix array
-----------------	--------------

Definition at line 282 of file Draw_data.py.

References `getPredplotvect()`, `meanArray()`, and `pred_plot()`.

Referenced by `meanArray()`, `pred_plot()`, and `write_rocAuc()`.

```
6.7.3.7 def irna::iRNA_stat::Draw_data::draw_data::plot ( self, args, soft_inf, listobj,
               dbmanage, execution_time )
```

Plot main function.

Definition at line 504 of file Draw_data.py.

References `exec_plot()`, `frequency_plot()`, `pred_plot()`, `similarity_plot()`, `write_frequency()`, `write_pred_plot()`, `write_pValueSelect()`, `write_sens_ppv()`, and `write_similarity()`.

Referenced by `write_interaction()`.

```
6.7.3.8 def irna::iRNA_stat::Draw_data::draw_data::plot_linear_regression ( self, obj, soft_inf,
               numsoft, dbmanage )
```

Plot linear regression of random data.

Parameters

<i>obj</i> ,:	Computer object
<i>soft_inf</i> ,:	Software information
<i>numsoft</i> ,:	Number of the soft
<i>dbmanage</i> ,:	Access to the database

Definition at line 109 of file Draw_data.py.

References `irna::iRNA_stat::Analysis::Analysis::commun_values()`, `getnames()`, and `result`.

Referenced by `write_curve_param_data()`, and `write_interaction()`.

```
6.7.3.9 def irna::iRNA_stat::Draw_data::draw_data::plot_roc_curves ( self, listobj )
```

Plot roc curve.

Parameters

<i>listobj</i> ,:	List of Computer object
-------------------	---

Definition at line 162 of file Draw_data.py.

References `getnames()`, `plot_roc_curves_statistics()`, and `result`.

Referenced by `getnames()`, and `write_general_data()`.

6.7.3.10 `def irna::iRNA_stat::Draw_data::draw_data::plot_roc_curves_statistics (self, listobj)`

Statistical analysis of roc.

Parameters

<i>listobj</i> ,:	List of Computer object
-------------------	---

Definition at line 203 of file `Draw_data.py`.

References `result`, and `write_pValue()`.

Referenced by `plot_roc_curves()`, and `write_general_data()`.

6.7.3.11 `def irna::iRNA_stat::Draw_data::draw_data::pred_plot (self, listobj)`

Plot sensitivity and ppv mean.

Parameters

<i>listobj</i> ,:	List of Computer object
-------------------	---

Definition at line 307 of file `Draw_data.py`.

References `meanArray()`, `result`, and `write_sens_ppv()`.

Referenced by `meanArray()`, and `plot()`.

6.7.3.12 `def irna::iRNA_stat::Draw_data::draw_data::similarity_plot (self, listobj)`

Parameters

<i>listobj</i> ,:	List of Computer object
-------------------	---

Definition at line 430 of file `Draw_data.py`.

References `getBoolselect()`, and `write_interaction()`.

Referenced by `plot()`, and `write_similarity()`.

6.7.3.13 `def irna::iRNA_stat::Draw_data::draw_data::write_curve_param_data (self, listobj, dbmanage)`

Parameters

<i>listobj</i> ,:	List of Computer object
<i>dbmanage</i> ,:	Access to the database

Definition at line 37 of file Draw_data.py.

References `plot_linear_regression()`.

Referenced by `write_interaction()`.

6.7.3.14 `def irna::iRNA_stat::Draw_data::draw_data::write_frequency (self, listobj)`

Parameters

<i>listobj</i> ,:	List of Computer object
-------------------	---

Definition at line 387 of file Draw_data.py.

References `frequency_plot()`, and `result`.

Referenced by `exec_plot()`, and `plot()`.

6.7.3.15 `def irna::iRNA_stat::Draw_data::draw_data::write_general_data (self, listobj)`

Parameters

<i>listobj</i> ,:	List of Computer object
-------------------	---

Definition at line 488 of file Draw_data.py.

References `plot_roc_curves()`, `plot_roc_curves_statistics()`, `write_general_data()`, `write_interaction()`, `write_pValue()`, `write_pValueInteract()`, `write_rocAuc()`, and `write_rocthesValue()`.

Referenced by `getBoolselect()`, and `write_general_data()`.

6.7.3.16 `def irna::iRNA_stat::Draw_data::draw_data::write_interaction (self, listobj, dbmanage, selection)`

Definition at line 466 of file Draw_data.py.

References `irna::iRNA_stat::Analysis::Analysis::getRangePosit()`, `plot()`, `plot_linear_regression()`, and `write_curve_param_data()`.

Referenced by `similarity_plot()`, and `write_general_data()`.

6.7.3.17 `def irna::iRNA_stat::Draw_data::draw_data::write_pred_plot (self, listobj)`

Write mean sensitivity and ppv of each software.

Parameters

<i>listobj</i> ,:	List of Computer object
<i>dbmanage</i> ,:	Access to the database

Definition at line 325 of file Draw_data.py.

References result.

Referenced by `getPredplotvect()`, and `plot()`.

6.7.3.18 `def irna::iRNA_stat::Draw_data::draw_data::write_pValue (self, listobj, dbmanage)`

Print `pValue`.

Parameters

<i>listobj</i> ,:	List of Computer object
<i>dbmanage</i> ,:	Access to the database

Definition at line 225 of file `Draw_data.py`.

References result, and `write_rocthesValue()`.

Referenced by `plot_roc_curves_statistics()`, and `write_general_data()`.

6.7.3.19 `def irna::iRNA_stat::Draw_data::draw_data::write_pValueInteract (self, listobj, dbmanage)`

Parameters

<i>listobj</i> ,:	List of Computer object
<i>dbmanage</i> ,:	Access to the database

Definition at line 442 of file `Draw_data.py`.

References `getBoolselect()`, and result.

Referenced by `write_general_data()`, and `write_similarity()`.

6.7.3.20 `def irna::iRNA_stat::Draw_data::draw_data::write_pValueSelect (self, listobj)`

Parameters

<i>listobj</i> ,:	List of Computer object
-------------------	---

Definition at line 372 of file `Draw_data.py`.

References result, and `write_similarity()`.

Referenced by `plot()`, and `write_sens_ppv()`.

6.7.3.21 `def irna::iRNA_stat::Draw_data::draw_data::write_rocAuc (self, listobj, auc_result)`

write AUC

Parameters

<i>listobj</i> ,:	List of Computer object
<i>auc_result</i> ,:	AUC result

Definition at line 264 of file Draw_data.py.

References `getPredplotvect()`, and `meanArray()`.

Referenced by `write_general_data()`, and `write_rocthresValue()`.

```
6.7.3.22 def irna::iRNA_stat::Draw_data::draw_data::write_rocthresValue ( self, listobj,
                                coords_roc, dbmanage )
```

Parameters

<i>listobj</i> ,:	List of Computer object
<i>coords_roc</i> ,:	Roc coordinates
<i>dbmanage</i> ,:	Access to the database

Definition at line 245 of file Draw_data.py.

References `result`, and `write_rocAuc()`.

Referenced by `write_general_data()`, and `write_pValue()`.

```
6.7.3.23 def irna::iRNA_stat::Draw_data::draw_data::write_sens_ppv ( self, listobj, dbmanage )
```

Write sensitivity and ppv.

Parameters

<i>listobj</i> ,:	List of Computer object
<i>dbmanage</i> ,:	Access to the database

Definition at line 342 of file Draw_data.py.

References `exec_plot()`, `result`, and `write_pValueSelect()`.

Referenced by `plot()`, and `pred_plot()`.

```
6.7.3.24 def irna::iRNA_stat::Draw_data::draw_data::write_similarity ( self, listobj )
```

Parameters

<i>listobj</i> ,:	List of Computer object
-------------------	---

Definition at line 403 of file Draw_data.py.

References `result`, `similarity_plot()`, and `write_pValueInteract()`.

Referenced by `plot()`, and `write_pValueSelect()`.

6.7.4 Member Data Documentation

6.7.4.1 `irna::iRNA_stat::Draw_data::draw_data::result`

Definition at line 28 of file `Draw_data.py`.

Referenced by `exec_plot()`, `frequency_plot()`, `getBoolselect()`, `getnames()`, `getPredplotvect()`, `plot_linear_regression()`, `plot_roc_curves()`, `plot_roc_curves_statistics()`, `pred_plot()`, `write_frequency()`, `write_pred_plot()`, `write_pValue()`, `write_pValueInteract()`, `write_pValueSelect()`, `write_rocthresValue()`, `write_sens_ppv()`, and `write_similarity()`.

The documentation for this class was generated from the following file:

- [/home/amine/workspace/iRNA/irna/iRNA_stat/Draw_data.py](#)

6.8 `irna::iRNA_stat::Ecdf::Ecdf` Class Reference

Public Member Functions

- [def `__init__`](#)
- [def `__call__`](#)

Public Attributes

- [observations](#)

6.8.1 Detailed Description

Definition at line 12 of file `Ecdf.py`.

6.8.2 Constructor & Destructor Documentation

6.8.2.1 `def irna::iRNA_stat::Ecdf::Ecdf::__init__(self, observations)`

Definition at line 14 of file `Ecdf.py`.

6.8.3 Member Function Documentation

6.8.3.1 `def irna::iRNA_stat::Ecdf::Ecdf::__call__(self, x)`

Definition at line 18 of file `Ecdf.py`.

References `observations`.

6.8.4 Member Data Documentation

6.8.4.1 irna::iRNA_stat::Ecdf::Ecdf::observations

Definition at line 14 of file Ecdf.py.

Referenced by `__call__()`.

The documentation for this class was generated from the following file:

- `/home/amine/workspace/iRNA/irna/irna_stat/Ecdf.py`

6.9 irna::David2tulip::Edge::Edge Class Reference

: Handle interaction

Public Member Functions

- `def __init__`
Instantiate [Edge](#) object.
- `def println`
Print edge value.
- `def __cmp__`
General method to compare edge based on the name of nodes.

Public Attributes

- `node1`
- `node2`
- `pValue`
- `similarity`
- `category`
- `categoryName`
- `termName`
- `sRNA_deb`
- `sRNA_end`
- `mRNA_deb`
- `mRNA_end`
- `dbrec`

6.9.1 Detailed Description

: Handle interaction

Author

: Amine Ghozlane

Version

: 1.0

Definition at line 7 of file Edge.py.

6.9.2 Constructor & Destructor Documentation

6.9.2.1 `def irna::David2tulip::Edge::Edge::__init__(self, node1, node2)`

Instanciate [Edge](#) object.

Parameters

<i>node1</i> ,:	sRNA node
<i>node2</i> ,:	mRNA node

Definition at line 15 of file Edge.py.

6.9.3 Member Function Documentation

6.9.3.1 `def irna::David2tulip::Edge::Edge::__cmp__(self, other)`

General method to compare edge based on the name of nodes.

Parameters

<i>other</i> ,:	Compared value
-----------------	----------------

Definition at line 43 of file Edge.py.

Referenced by `println()`.

6.9.3.2 `def irna::David2tulip::Edge::Edge::println (self)`

Print edge value.

Returns

: String converted values

Definition at line 33 of file Edge.py.

References `__cmp__()`, `node1`, and `node2`.

6.9.4 Member Data Documentation

6.9.4.1 irna::David2tulip::Edge::Edge::category

Definition at line 15 of file Edge.py.

6.9.4.2 irna::David2tulip::Edge::Edge::categoryName

Definition at line 15 of file Edge.py.

6.9.4.3 irna::David2tulip::Edge::Edge::dbrec

Definition at line 33 of file Edge.py.

6.9.4.4 irna::David2tulip::Edge::Edge::mRNA_deb

Definition at line 15 of file Edge.py.

6.9.4.5 irna::David2tulip::Edge::Edge::mRNA_end

Definition at line 15 of file Edge.py.

6.9.4.6 irna::David2tulip::Edge::Edge::node1

Definition at line 15 of file Edge.py.

Referenced by println().

6.9.4.7 irna::David2tulip::Edge::Edge::node2

Definition at line 15 of file Edge.py.

Referenced by println().

6.9.4.8 irna::David2tulip::Edge::Edge::pValue

Definition at line 15 of file Edge.py.

Referenced by irna::iRNA_stat::Files::Files::case(), irna::David2tulip::Files::Files::data_format(), irna::iRNA_stat::Files::Files::data_format(), irna::iRNA_stat::Files::Files::getfiles(), and irna::David2tulip::Files::Files::getfiles().

6.9.4.9 `irna::David2tulip::Edge::Edge::similarity`

Definition at line 15 of file `Edge.py`.

Referenced by `irna::David2tulip::Files::Files::data_format()`, and `irna::David2tulip::Files::Files::getfiles()`.

6.9.4.10 `irna::David2tulip::Edge::Edge::sRNA_deb`

Definition at line 15 of file `Edge.py`.

6.9.4.11 `irna::David2tulip::Edge::Edge::sRNA_end`

Definition at line 15 of file `Edge.py`.

6.9.4.12 `irna::David2tulip::Edge::Edge::termName`

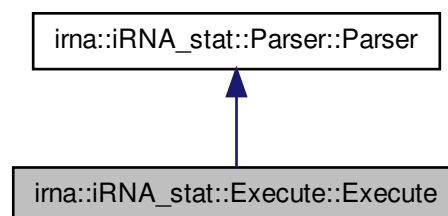
Definition at line 15 of file `Edge.py`.

The documentation for this class was generated from the following file:

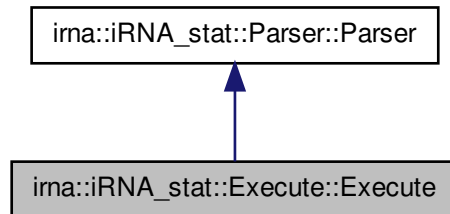
- `/home/amine/workspace/iRNA/irna/David2tulip/Edge.py`

6.10 `irna::iRNA_stat::Execute::Execute` Class Reference

Inheritance diagram for `irna::iRNA_stat::Execute::Execute`:



Collaboration diagram for ima::iRNA_stat::Execute::Execute:



Public Member Functions

- def `__init__`
Instantiate `Execute` object.
- def `getExecinf`
Parse execution information file.

Public Attributes

- `soft`
- `duration`

6.10.1 Detailed Description

Definition at line 11 of file `Execute.py`.

6.10.2 Constructor & Destructor Documentation

6.10.2.1 `def ima::iRNA_stat::Execute::Execute::__init__(self, exec_file)`

Instantiate `Execute` object.

Definition at line 18 of file `Execute.py`.

References `getExecinf()`.

6.10.3 Member Function Documentation

6.10.3.1 `def irna::iRNA_stat::Execute::Execute::getExecinf (self, exec_file)`

Parse exection information file.

Parameters

<code>exec_file,:</code>	Execution file
--------------------------	----------------

Definition at line 27 of file Execute.py.

Referenced by `__init__()`.

6.10.4 Member Data Documentation

6.10.4.1 `irna::iRNA_stat::Execute::Execute::duration`

Definition at line 27 of file Execute.py.

6.10.4.2 `irna::iRNA_stat::Execute::Execute::soft`

Definition at line 27 of file Execute.py.

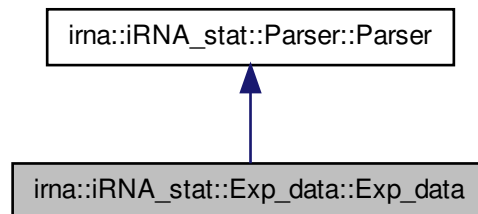
Referenced by `irna::iRNA_stat::Threshold::Threshold::getSoftnum()`.

The documentation for this class was generated from the following file:

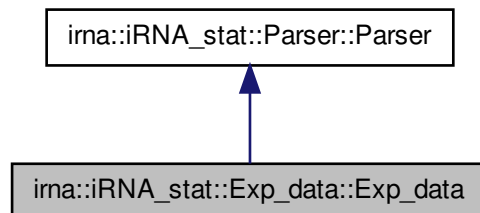
- `/home/amine/workspace/iRNA/irna/iRNA_stat/Execute.py`

6.11 `irna::iRNA_stat::Exp_data::Exp_data` Class Reference

Inheritance diagram for `irna::iRNA_stat::Exp_data::Exp_data`:



Collaboration diagram for irna::iRNA_stat::Exp_data::Exp_data:



Public Member Functions

- def [__init__](#)
Instantiate [Exp_data](#) object.
- def [getExpinf](#)
Parse experiment file.
- def [getExpPair](#)
Get the experimental experience for one sRNA-mRNA interaction.

Public Attributes

- [combined](#)
- [sRNA](#)
- [mRNA](#)
- [sRNA_deb](#)
- [sRNA_fin](#)
- [mRNA_deb](#)
- [mRNA_fin](#)
- [lenexp_data](#)

6.11.1 Detailed Description

Definition at line 10 of file `Exp_data.py`.

6.11.2 Constructor & Destructor Documentation

6.11.2.1 `def irna::iRNA_stat::Exp_data::Exp_data::__init__(self, exp_file)`

Instantiate [Exp_data](#) object.

Definition at line 17 of file `Exp_data.py`.

References `getExpinf()`.

6.11.3 Member Function Documentation

6.11.3.1 `def irna::iRNA_stat::Exp_data::Exp_data::getExpinf (self, exp_file)`

Parse experiment file.

Parameters

<i>exp_file</i> ,:	Experiment file
--------------------	-----------------

Definition at line 26 of file `Exp_data.py`.

Referenced by `__init__()`.

6.11.3.2 `def irna::iRNA_stat::Exp_data::Exp_data::getExpPair (self, sRNA, mRNA)`

Get the experimental experience for one sRNA-mRNA interaction.

Parameters

<i>sRNA</i> ,:	name of sRNA
<i>mRNA</i> ,:	name of mRNA

Definition at line 56 of file `Exp_data.py`.

6.11.4 Member Data Documentation

6.11.4.1 `irna::iRNA_stat::Exp_data::Exp_data::combined`

Definition at line 26 of file `Exp_data.py`.

Referenced by `irna::iRNA_stat::Rand_data::Rand_data::getAllSofts()`.

6.11.4.2 `irna::iRNA_stat::Exp_data::Exp_data::lenexp_data`

Definition at line 26 of file `Exp_data.py`.

6.11.4.3 irna::iRNA_stat::Exp_data::Exp_data::mRNA

Definition at line 26 of file Exp_data.py.

6.11.4.4 irna::iRNA_stat::Exp_data::Exp_data::mRNA_deb

Definition at line 26 of file Exp_data.py.

6.11.4.5 irna::iRNA_stat::Exp_data::Exp_data::mRNA_fin

Definition at line 26 of file Exp_data.py.

6.11.4.6 irna::iRNA_stat::Exp_data::Exp_data::sRNA

Definition at line 26 of file Exp_data.py.

6.11.4.7 irna::iRNA_stat::Exp_data::Exp_data::sRNA_deb

Definition at line 26 of file Exp_data.py.

6.11.4.8 irna::iRNA_stat::Exp_data::Exp_data::sRNA_fin

Definition at line 26 of file Exp_data.py.

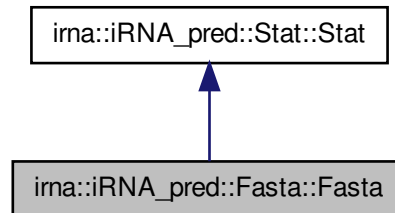
The documentation for this class was generated from the following file:

- [/home/amine/workspace/iRNA/irna/iRNA_stat/Exp_data.py](#)

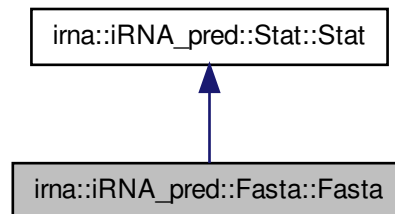
6.12 irna::iRNA_pred::Fasta::Fasta Class Reference

: Write fasta needed for the different software from a multifasta

Inheritance diagram for `irna::iRNA_pred::Fasta::Fasta`:



Collaboration diagram for `irna::iRNA_pred::Fasta::Fasta`:



Public Member Functions

- def [__init__](#)
Build fasta object.
- def [WriteFasta](#)
Write the fasta.
- def [EmptyRep](#)
Empty the folder of fasta files.
- def [ExtractFasta](#)

Public Attributes

- [cacheFasta](#)

- [fastafile](#)

Static Public Attributes

- tuple [regex](#) = re.compile(">(\S+)\s*\S*")
- tuple [regex_seq](#) = re.compile("[ATGCatgc]+\s*")
- tuple [multifasta](#) = open(mf, "r")
- [cacheData](#) = False
- tuple [a](#) = regex.match(i)
- tuple [seqname](#) = a.group(1)

6.12.1 Detailed Description

: Write fasta needed for the different software from a multifasta

Definition at line 15 of file Fasta.py.

6.12.2 Constructor & Destructor Documentation

6.12.2.1 `def irna::iRNA_pred::Fasta::Fasta::__init__(self)`

Build fasta object.

Reimplemented from [irna::iRNA_pred::Stat::Stat](#).

Definition at line 21 of file Fasta.py.

6.12.3 Member Function Documentation

6.12.3.1 `def irna::iRNA_pred::Fasta::Fasta::EmptyRep(self, fasta_out)`

Empty the folder of fasta files.

Parameters

<i>fasta_out</i> ,:	Fasta repertory
---------------------	---------------------------------

Definition at line 49 of file Fasta.py.

References [ExtractFasta\(\)](#).

Referenced by [ExtractFasta\(\)](#), and [WriteFasta\(\)](#).

6.12.3.2 `def irna::iRNA_pred::Fasta::Fasta::ExtractFasta(self, mf, fasta_out)`

Definition at line 64 of file Fasta.py.

References [EmptyRep\(\)](#), [irna::iRNA_pred::RanRNA::RanRNA::GC](#), [irna::iRNA_pred::](#)

RanRNA::RanRNA::NbSeq, and irna::iRNA_pred::Stat::Stat::openSeqInf().

Referenced by EmptyRep().

6.12.3.3 `def irna::iRNA_pred::Fasta::Fasta::WriteFasta (self)`

Write the fasta.

Definition at line 33 of file Fasta.py.

References cacheFasta, EmptyRep(), and fastafile.

Referenced by irna::iRNA_pred::RanRNA::RanRNA::WriteFasta().

6.12.4 Member Data Documentation

6.12.4.1 `tuple irna::iRNA_pred::Fasta::Fasta::a = regex.match(i) [static]`

Definition at line 89 of file Fasta.py.

6.12.4.2 `irna::iRNA_pred::Fasta::Fasta::cacheData = False [static]`

Definition at line 87 of file Fasta.py.

6.12.4.3 `irna::iRNA_pred::Fasta::Fasta::cacheFasta`

Definition at line 21 of file Fasta.py.

Referenced by WriteFasta().

6.12.4.4 `irna::iRNA_pred::Fasta::Fasta::fastafile`

Definition at line 21 of file Fasta.py.

Referenced by WriteFasta(), and irna::iRNA_pred::RanRNA::RanRNA::WriteFasta().

6.12.4.5 `tuple irna::iRNA_pred::Fasta::Fasta::multifasta = open(mf, "r") [static]`

Definition at line 85 of file Fasta.py.

6.12.4.6 `tuple irna::iRNA_pred::Fasta::Fasta::regex = re.compile(">(\S+)\s*\S*") [static]`

Extract multifasta to fasta.

@param mf: Multifasta file

@param fasta_out: Fasta repertory

Definition at line 81 of file Fasta.py.

```
6.12.4.7 tuple irna::iRNA_pred::Fasta::Fasta::regex_seq =  
    re.compile("^[ATGCatgc]+\S*") [static]
```

Definition at line 82 of file Fasta.py.

```
6.12.4.8 tuple irna::iRNA_pred::Fasta::Fasta::seqname = a.group(1) [static]
```

Definition at line 91 of file Fasta.py.

The documentation for this class was generated from the following file:

- /home/amine/workspace/iRNA/irna/iRNA_pred/Fasta.py

6.13 irna::David2tulip::Files::Files Class Reference

Public Member Functions

- def [__init__](#)
Instantiate [Files](#) object.
- def [usage](#)
Give information to use Mycarn.
- def [case](#)
Test if necessary document are available.
- def [data_format](#)
Check if information are correct.
- def [getfiles](#)
Determine the files provided as arguments.

Public Attributes

- [multilist](#)
- [filter](#)
- [similarity](#)
- [pValue](#)
- [results](#)
- [david](#)
- [interact](#)
- [enrichment](#)
- [fastmode](#)
- [iRNA_db](#)
- [config](#)
- [name](#)

6.13.1 Detailed Description

Definition at line 10 of file Files.py.

6.13.2 Constructor & Destructor Documentation

6.13.2.1 `def irna::David2tulip::Files::Files::__init__(self)`

Instantiate [Files](#) object.

Definition at line 16 of file Files.py.

6.13.3 Member Function Documentation

6.13.3.1 `def irna::David2tulip::Files::Files::case (self)`

Test if necessary document are available.

Parameters

<i>operation,:</i>	list of options called
<i>fasta,:</i>	list fasta related information
<i>predict,:</i>	list comparison related information

Definition at line 66 of file Files.py.

References [data_format\(\)](#), [results](#), and [usage\(\)](#).

Referenced by [irna::iRNA_seq::Files::Files::getfiles\(\)](#), [irna::iRNA_stat::Files::Files::getfiles\(\)](#), [getfiles\(\)](#), [irna::iRNA_pred::Files::Files::getfiles\(\)](#), and [usage\(\)](#).

6.13.3.2 `def irna::David2tulip::Files::Files::data_format (self)`

Check if information are correct.

Definition at line 77 of file Files.py.

References [irna::David2tulip::Davidconfig::Davidconfig::config](#), [config](#), [david](#), [enrichment](#), [filter](#), [getfiles\(\)](#), [interact](#), [iRNA_db](#), [multilist](#), [name](#), [irna::David2tulip::Edge::Edge::pValue](#), [pValue](#), [results](#), [irna::David2tulip::Edge::Edge::similarity](#), [similarity](#), and [usage\(\)](#).

Referenced by [case\(\)](#), [irna::iRNA_seq::Files::Files::getfiles\(\)](#), [irna::iRNA_stat::Files::Files::getfiles\(\)](#), [getfiles\(\)](#), and [irna::iRNA_pred::Files::Files::getfiles\(\)](#).

6.13.3.3 `def irna::David2tulip::Files::Files::getfiles (self)`

Determine the files provided as arguments.

Returns

: Chosen options

Definition at line 131 of file Files.py.

References `case()`, `irna::David2tulip::Davidconfig::Davidconfig::config`, `config`, `data_format()`, `david`, `enrichment`, `fastmode`, `filter`, `interact`, `iRNA_db`, `multilist`, `name`, `irna::David2tulip::Edge::Edge::pValue`, `pValue`, `results`, `irna::David2tulip::Edge::Edge::similarity`, `similarity`, and `usage()`.

Referenced by `data_format()`.

6.13.3.4 def irna::David2tulip::Files::Files::usage (self, info)

Give information to use Mycarn.

Parameters

<i>info</i> :	Error texte
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Returns

: Use of Mycarn

Definition at line 37 of file Files.py.

References `case()`, `multilist`, and `usage()`.

Referenced by `irna::iRNA_seq::Files::Files::case()`, `case()`, `irna::iRNA_stat::Files::Files::case()`, `irna::iRNA_pred::Files::Files::case()`, `irna::iRNA_seq::Files::Files::data_format()`, `data_format()`, `irna::iRNA_stat::Files::Files::data_format()`, `irna::iRNA_pred::Files::Files::data_format()`, `irna::iRNA_seq::Files::Files::getfiles()`, `irna::iRNA_stat::Files::Files::getfiles()`, `getfiles()`, `irna::iRNA_pred::Files::Files::getfiles()`, `irna::iRNA_seq::Files::Files::usage()`, `irna::iRNA_pred::Files::Files::usage()`, `usage()`, and `irna::iRNA_stat::Files::Files::usage()`.

6.13.4 Member Data Documentation**6.13.4.1 irna::David2tulip::Files::Files::config**

Definition at line 16 of file Files.py.

Referenced by `data_format()`, and `getfiles()`.

6.13.4.2 irna::David2tulip::Files::Files::david

Definition at line 16 of file Files.py.

Referenced by `data_format()`, and `getfiles()`.

6.13.4.3 `irna::David2tulip::Files::Files::enrichment`

Definition at line 16 of file `Files.py`.

Referenced by `data_format()`, and `getfiles()`.

6.13.4.4 `irna::David2tulip::Files::Files::fastmode`

Definition at line 16 of file `Files.py`.

Referenced by `irna::iRNA_stat::Sqlite_manager::Sqlite_manager::disconnectDB()`, `irna::iRNA_pred::Sqlite_manager::Sqlite_manager::disconnectDB()`, `irna::David2tulip::Sqlite_manager::Sqlite_manager::disconnectDB()`, `irna::iRNA_stat::Files::Files::getfiles()`, `getfiles()`, and `irna::iRNA_pred::Files::Files::getfiles()`.

6.13.4.5 `irna::David2tulip::Files::Files::filter`

Definition at line 16 of file `Files.py`.

Referenced by `data_format()`, and `getfiles()`.

6.13.4.6 `irna::David2tulip::Files::Files::interact`

Definition at line 16 of file `Files.py`.

Referenced by `data_format()`, and `getfiles()`.

6.13.4.7 `irna::David2tulip::Files::Files::iRNA_db`

Definition at line 16 of file `Files.py`.

Referenced by `irna::iRNA_stat::Files::Files::case()`, `data_format()`, `irna::iRNA_stat::Files::Files::getfiles()`, `getfiles()`, and `irna::iRNA_stat::Files::Files::usage()`.

6.13.4.8 `irna::David2tulip::Files::Files::multilist`

Definition at line 16 of file `Files.py`.

Referenced by `data_format()`, `getfiles()`, and `usage()`.

6.13.4.9 `irna::David2tulip::Files::Files::name`

Definition at line 16 of file `Files.py`.

Referenced by `data_format()`, `getfiles()`, `irna::iRNA_pred::Mpi::Mpi::Mpi_getmyrank()`, `irna::David2tulip::Node::Node::printgroupdata()`, and `irna::David2tulip::Node::Node::println()`.

6.13.4.10 irna::David2tulip::Files::Files::pValue

Definition at line 16 of file Files.py.

Referenced by irna::iRNA_stat::Files::Files::case(), data_format(), irna::iRNA_stat::Files::Files::data_format(), irna::iRNA_stat::Files::Files::getfiles(), and getfiles().

6.13.4.11 irna::David2tulip::Files::Files::results

Definition at line 16 of file Files.py.

Referenced by irna::iRNA_seq::Files::Files::case(), case(), irna::iRNA_stat::Files::Files::case(), irna::iRNA_seq::Files::Files::data_format(), data_format(), irna::iRNA_stat::Files::Files::data_format(), irna::iRNA_seq::Files::Files::getfiles(), irna::iRNA_stat::Files::Files::getfiles(), and getfiles().

6.13.4.12 irna::David2tulip::Files::Files::similarity

Definition at line 16 of file Files.py.

Referenced by data_format(), and getfiles().

The documentation for this class was generated from the following file:

- /home/amine/workspace/iRNA/irna/David2tulip/[Files.py](#)

6.14 irna::iRNA_pred::Files::Files Class Reference

:

Public Member Functions

- def [__init__](#)
Instantiate [Files](#) object.
- def [usage](#)
Give information to use Mycarn.
- def [case](#)
Test if necessary document are available.
- def [data_format](#)
Check if information are correct.
- def [getfiles](#)
Determine the files provided as arguments.

Public Attributes

- [myrank](#)
- [operation](#)
- [fasta](#)
- [predict](#)
- [random](#)
- [fastmode](#)

6.14.1 Detailed Description

:

Definition at line 13 of file Files.py.

6.14.2 Constructor & Destructor Documentation

6.14.2.1 `def irna::iRNA_pred::Files::Files::__init__ (self, myrank)`

Instantiate [Files](#) object.

Definition at line 19 of file Files.py.

6.14.3 Member Function Documentation

6.14.3.1 `def irna::iRNA_pred::Files::Files::case (self)`

Test if necessary document are available.

Parameters

<i>operation</i> ,:	list of options called
<i>fasta</i> ,:	list fasta related information
<i>predict</i> ,:	list comparison related information

Definition at line 78 of file Files.py.

References [data_format\(\)](#), [fasta](#), [operation](#), [predict](#), [random](#), [usage\(\)](#), and [irna::David2tulip::Files::Files::usage\(\)](#).

Referenced by [irna::iRNA_seq::Files::Files::getfiles\(\)](#), [irna::iRNA_stat::Files::Files::getfiles\(\)](#), [getfiles\(\)](#), and [usage\(\)](#).

6.14.3.2 `def irna::iRNA_pred::Files::Files::data_format (self)`

Check if information are correct.

Definition at line 130 of file Files.py.

References `fasta`, `getfiles()`, `operation`, `predict`, `random`, `usage()`, and `irna::David2tulip::Files::Files::usage()`.

Referenced by `case()`, `irna::iRNA_seq::Files::Files::getfiles()`, `irna::iRNA_stat::Files::Files::getfiles()`, and `getfiles()`.

6.14.3.3 `def irna::iRNA_pred::Files::Files::getfiles (self)`

Determine the files provided as arguments.

Returns

: Chosen options

Definition at line 166 of file `Files.py`.

References `irna::David2tulip::Files::Files::case()`, `case()`, `irna::David2tulip::Files::Files::data_format()`, `data_format()`, `fasta`, `irna::David2tulip::Files::Files::fastmode`, `fastmode`, `irna::David2tulip::Sqlite_manager::Sqlite_manager::fastmode`, `myrank`, `operation`, `predict`, `random`, `usage()`, and `irna::David2tulip::Files::Files::usage()`.

Referenced by `data_format()`.

6.14.3.4 `def irna::iRNA_pred::Files::Files::usage (self, info)`

Give information to use Mycarn.

Parameters

<i>info</i> ,	Error texte
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Returns

: Use of Mycarn

Definition at line 36 of file `Files.py`.

References `case()`, `operation`, `usage()`, and `irna::David2tulip::Files::Files::usage()`.

Referenced by `irna::iRNA_seq::Files::Files::case()`, `irna::iRNA_stat::Files::Files::case()`, `case()`, `irna::iRNA_seq::Files::Files::data_format()`, `irna::iRNA_stat::Files::Files::data_format()`, `data_format()`, `irna::iRNA_seq::Files::Files::getfiles()`, `irna::iRNA_stat::Files::Files::getfiles()`, `getfiles()`, `irna::iRNA_seq::Files::Files::usage()`, `usage()`, and `irna::iRNA_stat::Files::Files::usage()`.

6.14.4 Member Data Documentation

6.14.4.1 `irna::iRNA_pred::Files::Files::fasta`

Definition at line 19 of file `Files.py`.

Referenced by `case()`, `data_format()`, and `getfiles()`.

6.14.4.2 `irna::iRNA_pred::Files::Files::fastmode`

Definition at line 19 of file `Files.py`.

Referenced by `irna::iRNA_stat::Sqlite_manager::Sqlite_manager::disconnectDB()`, `irna::iRNA_pred::Sqlite_manager::Sqlite_manager::disconnectDB()`, `irna::iRNA_stat::Files::Files::getfiles()`, and `getfiles()`.

6.14.4.3 `irna::iRNA_pred::Files::Files::myrank`

Definition at line 19 of file `Files.py`.

Referenced by `getfiles()`, `irna::iRNA_pred::Mpi::Mpi::Mpi_end_processus()`, `irna::iRNA_pred::Mpi::Mpi::Mpi_getnprocs()`, and `irna::iRNA_pred::Mpi::Mpi::Mpi_slave()`.

6.14.4.4 `irna::iRNA_pred::Files::Files::operation`

Definition at line 19 of file `Files.py`.

Referenced by `case()`, `data_format()`, `getfiles()`, and `usage()`.

6.14.4.5 `irna::iRNA_pred::Files::Files::predict`

Definition at line 19 of file `Files.py`.

Referenced by `case()`, `data_format()`, and `getfiles()`.

6.14.4.6 `irna::iRNA_pred::Files::Files::random`

Definition at line 19 of file `Files.py`.

Referenced by `irna::iRNA_stat::Files::Files::case()`, `case()`, `data_format()`, `irna::iRNA_stat::Files::Files::getfiles()`, and `getfiles()`.

The documentation for this class was generated from the following file:

- `/home/amine/workspace/iRNA/irna/iRNA_pred/Files.py`

6.15 `irna::iRNA_stat::Files::Files` Class Reference

Public Member Functions

- `def __init__`
Instantiate `Files` object.
- `def usage`

Give information to use [iRNA_stat](#).

- def [case](#)
Test if necessary document are available.
- def [data_format](#)
Check if information are correct.
- def [getfiles](#)
Determine the files provided as arguments.

Public Attributes

- [iRNA_db](#)
- [soft_inf](#)
- [rand_inf](#)
- [exp_inf](#)
- [random](#)
- [save](#)
- [results](#)
- [exec_inf](#)
- [thres_inf](#)
- [myrank](#)
- [overwrite](#)
- [fastmode](#)
- [pValue](#)

6.15.1 Detailed Description

Definition at line 10 of file Files.py.

6.15.2 Constructor & Destructor Documentation

6.15.2.1 def irna::iRNA_stat::Files::Files::__init__(self, myrank)

Instantiate [Files](#) object.

Definition at line 16 of file Files.py.

6.15.3 Member Function Documentation

6.15.3.1 def irna::iRNA_stat::Files::Files::case (self)

Test if necessary document are available.

Parameters

<i>operation,:</i>	list of options called
<i>fasta,:</i>	list fasta related information
<i>predict,:</i>	list comparison related information

Definition at line 70 of file Files.py.

References `data_format()`, `irna::David2tulip::Files::Files::iRNA_db`, `iRNA_db`, `irna::David2tulip::Edge::Edge::pValue`, `pValue`, `irna::David2tulip::Files::Files::pValue`, `irna::iRNA_stat::Computer::Computer::pValue`, `random`, `irna::iRNA_pred::Files::Files::random`, `results`, `irna::David2tulip::Files::Files::results`, `irna::iRNA_seq::Files::Files::results`, `soft_inf`, `irna::iRNA_seq::Files::Files::usage()`, `irna::iRNA_pred::Files::Files::usage()`, `irna::David2tulip::Files::Files::usage()`, and `usage()`.

Referenced by `getfiles()`, and `usage()`.

6.15.3.2 `def irna::iRNA_stat::Files::Files::data_format (self)`

Check if information are correct.

Definition at line 85 of file Files.py.

References `exec_inf`, `exp_inf`, `getfiles()`, `irna::David2tulip::Edge::Edge::pValue`, `pValue`, `irna::David2tulip::Files::Files::pValue`, `irna::iRNA_stat::Computer::Computer::pValue`, `rand_inf`, `irna::iRNA_seq::Files::Files::results`, `irna::David2tulip::Files::Files::results`, `results`, `save`, `soft_inf`, `thres_inf`, `irna::iRNA_seq::Files::Files::usage()`, `irna::iRNA_pred::Files::Files::usage()`, `irna::David2tulip::Files::Files::usage()`, and `usage()`.

Referenced by `case()`, and `getfiles()`.

6.15.3.3 `def irna::iRNA_stat::Files::Files::getfiles (self)`

Determine the files provided as arguments.

Returns

: Chosen options

Definition at line 121 of file Files.py.

References `irna::iRNA_seq::Files::Files::case()`, `irna::David2tulip::Files::Files::case()`, `case()`, `irna::iRNA_pred::Files::Files::case()`, `irna::iRNA_seq::Files::Files::data_format()`, `irna::David2tulip::Files::Files::data_format()`, `data_format()`, `irna::iRNA_pred::Files::Files::data_format()`, `exec_inf`, `exp_inf`, `irna::David2tulip::Files::Files::fastmode`, `fastmode`, `irna::iRNA_pred::Files::Files::fastmode`, `irna::David2tulip::Sqlite_manager::Sqlite_manager::fastmode`, `irna::iRNA_pred::Sqlite_manager::Sqlite_manager::fastmode`, `irna::David2tulip::Files::Files::iRNA_db`, `iRNA_db`, `overwrite`, `irna::David2tulip::Edge::Edge::pValue`, `pValue`, `irna::David2tulip::Files::Files::pValue`, `irna::iRNA_stat::Computer::Computer::pValue`, `rand_inf`, `random`, `irna::iRNA_pred::Files::Files::random`, `irna::David2tulip::Files::Files::results`, `irna::iRNA_seq::Files::Files::results`, `results`, `save`, `soft_inf`, `thres_inf`, `irna::iRNA_seq::Files::Files::usage()`, `irna::iRNA_pred::Files::Files::usage()`, `irna::David2tulip::Files::Files::usage()`, and `usage()`.

Referenced by `data_format()`.

6.15.3.4 def irna::iRNA_stat::Files::Files::usage (*self*, *info*)

Give information to use [iRNA_stat](#).

Parameters

<i>info</i> ,	Error texte
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Returns

: Use of Mycarn

Definition at line 38 of file Files.py.

References [case\(\)](#), [irna::David2tulip::Files::Files::iRNA_db](#), [iRNA_db](#), [irna::iRNA_seq::Files::Files::usage\(\)](#), [irna::iRNA_pred::Files::Files::usage\(\)](#), [irna::David2tulip::Files::Files::usage\(\)](#), and [usage\(\)](#).

Referenced by [case\(\)](#), [data_format\(\)](#), [getfiles\(\)](#), and [usage\(\)](#).

6.15.4 Member Data Documentation

6.15.4.1 irna::iRNA_stat::Files::Files::exec_inf

Definition at line 16 of file Files.py.

Referenced by [data_format\(\)](#), and [getfiles\(\)](#).

6.15.4.2 irna::iRNA_stat::Files::Files::exp_inf

Definition at line 16 of file Files.py.

Referenced by [data_format\(\)](#), [getfiles\(\)](#), and [irna::iRNA_stat::Interaction::Interaction::Interaction_data\(\)](#).

6.15.4.3 irna::iRNA_stat::Files::Files::fastmode

Definition at line 16 of file Files.py.

Referenced by [irna::iRNA_stat::Sqlite_manager::Sqlite_manager::disconnectDB\(\)](#), and [getfiles\(\)](#).

6.15.4.4 irna::iRNA_stat::Files::Files::iRNA_db

Definition at line 16 of file Files.py.

Referenced by [case\(\)](#), [getfiles\(\)](#), and [usage\(\)](#).

6.15.4.5 `irna::iRNA_stat::Files::Files::myrank`

Definition at line 16 of file Files.py.

6.15.4.6 `irna::iRNA_stat::Files::Files::overwrite`

Definition at line 16 of file Files.py.

Referenced by `getfiles()`.

6.15.4.7 `irna::iRNA_stat::Files::Files::pValue`

Definition at line 16 of file Files.py.

Referenced by `case()`, `data_format()`, and `getfiles()`.

6.15.4.8 `irna::iRNA_stat::Files::Files::rand_inf`

Definition at line 16 of file Files.py.

Referenced by `data_format()`, `getfiles()`, and `irna::iRNA_stat::pValue::pValue::run()`.

6.15.4.9 `irna::iRNA_stat::Files::Files::random`

Definition at line 16 of file Files.py.

Referenced by `case()`, and `getfiles()`.

6.15.4.10 `irna::iRNA_stat::Files::Files::results`

Definition at line 16 of file Files.py.

Referenced by `case()`, `data_format()`, and `getfiles()`.

6.15.4.11 `irna::iRNA_stat::Files::Files::save`

Definition at line 16 of file Files.py.

Referenced by `data_format()`, and `getfiles()`.

6.15.4.12 `irna::iRNA_stat::Files::Files::soft_inf`

Definition at line 16 of file Files.py.

Referenced by `case()`, `data_format()`, and `getfiles()`.

6.15.4.13 irna::iRNA_stat::Files::Files::thres_inf

Definition at line 16 of file Files.py.

Referenced by data_format(), and getfiles().

The documentation for this class was generated from the following file:

- /home/amine/workspace/iRNA/irna/iRNA_stat/Files.py

6.16 irna::iRNA_seq::Files::Files Class Reference

Public Member Functions

- def [__init__](#)
Instantiate [Files](#) object.
- def [usage](#)
Give information to use [iRNA_seq](#).
- def [case](#)
Test if necessary document are available.
- def [data_format](#)
Check if information are correct.
- def [getfiles](#)
Determine the files provided as arguments.

Public Attributes

- [genbank](#)
- [results](#)
- [sRNA_file](#)
- [begin](#)
- [end](#)
- [nucleo](#)
- [complete](#)

6.16.1 Detailed Description

Definition at line 10 of file Files.py.

6.16.2 Constructor & Destructor Documentation

6.16.2.1 def irna::iRNA_seq::Files::Files::__init__ (*self*)

Instantiate [Files](#) object.

Definition at line 16 of file Files.py.

6.16.3 Member Function Documentation

6.16.3.1 `def irna::iRNA_seq::Files::Files::case (self)`

Test if necessary document are available.

Parameters

<i>operation</i> ,:	list of options called
<i>fasta</i> ,:	list fasta related information
<i>predict</i> ,:	list comparison related information

Definition at line 55 of file Files.py.

References `begin`, `data_format()`, `end`, `results`, `irna::David2tulip::Files::Files::results`, `usage()`, `irna::iRNA_pred::Files::Files::usage()`, and `irna::David2tulip::Files::Files::usage()`.

Referenced by `getfiles()`, `irna::iRNA_stat::Files::Files::getfiles()`, and `usage()`.

6.16.3.2 `def irna::iRNA_seq::Files::Files::data_format (self)`

Check if information are correct.

Definition at line 68 of file Files.py.

References `genbank`, `getfiles()`, `results`, `irna::David2tulip::Files::Files::results`, `sRNA_file`, `usage()`, `irna::iRNA_pred::Files::Files::usage()`, and `irna::David2tulip::Files::Files::usage()`.

Referenced by `case()`, `getfiles()`, and `irna::iRNA_stat::Files::Files::getfiles()`.

6.16.3.3 `def irna::iRNA_seq::Files::Files::getfiles (self)`

Determine the files provided as arguments.

Returns

: Chosen options

Definition at line 91 of file Files.py.

References `begin`, `case()`, `irna::David2tulip::Files::Files::case()`, `irna::iRNA_pred::Files::Files::case()`, `complete`, `data_format()`, `irna::David2tulip::Files::Files::data_format()`, `irna::iRNA_pred::Files::Files::data_format()`, `end`, `genbank`, `irna::David2tulip::Files::Files::results`, `results`, `sRNA_file`, `usage()`, `irna::iRNA_pred::Files::Files::usage()`, and `irna::David2tulip::Files::Files::usage()`.

Referenced by `data_format()`.

6.16.3.4 def irna::iRNA_seq::Files::Files::usage (self, info)

Give information to use [iRNA_seq](#).

Parameters

<i>info,</i>	Error texte
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Returns

: Use of Mycarn

Definition at line 32 of file Files.py.

References [case\(\)](#), [genbank](#), [usage\(\)](#), [irna::iRNA_pred::Files::Files::usage\(\)](#), and [irna::David2tulip::Files::Files::usage\(\)](#).

Referenced by [case\(\)](#), [irna::iRNA_stat::Files::Files::case\(\)](#), [data_format\(\)](#), [irna::iRNA_stat::Files::Files::data_format\(\)](#), [getfiles\(\)](#), [irna::iRNA_stat::Files::Files::getfiles\(\)](#), [usage\(\)](#), and [irna::iRNA_stat::Files::Files::usage\(\)](#).

6.16.4 Member Data Documentation

6.16.4.1 irna::iRNA_seq::Files::Files::begin

Definition at line 16 of file Files.py.

Referenced by [case\(\)](#), and [getfiles\(\)](#).

6.16.4.2 irna::iRNA_seq::Files::Files::complete

Definition at line 16 of file Files.py.

Referenced by [getfiles\(\)](#).

6.16.4.3 irna::iRNA_seq::Files::Files::end

Definition at line 16 of file Files.py.

Referenced by [case\(\)](#), and [getfiles\(\)](#).

6.16.4.4 irna::iRNA_seq::Files::Files::genbank

Definition at line 16 of file Files.py.

Referenced by [data_format\(\)](#), [getfiles\(\)](#), and [usage\(\)](#).

6.16.4.5 irna::iRNA_seq::Files::Files::nucleo

Definition at line 16 of file Files.py.

6.16.4.6 `irna::iRNA_seq::Files::Files::results`

Definition at line 16 of file `Files.py`.

Referenced by `case()`, `irna::iRNA_stat::Files::Files::case()`, `data_format()`, `irna::iRNA_stat::Files::Files::data_format()`, `getfiles()`, and `irna::iRNA_stat::Files::Files::getfiles()`.

6.16.4.7 `irna::iRNA_seq::Files::Files::sRNA_file`

Definition at line 16 of file `Files.py`.

Referenced by `data_format()`, and `getfiles()`.

The documentation for this class was generated from the following file:

- `/home/amine/workspace/iRNA/irna/iRNA_seq/Files.py`

6.17 `irna::iRNA_seq::Genbank::Genbank` Class Reference

Public Member Functions

- `def __init__`
Instantiate `Genbank` object.
- `def readGenbank`
Read `Genbank` file and save into a set of readlines.
- `def getGenes`
Get genes data.
- `def getDNA`
Read DNA sequence and transform into string.
- `def getOrganism`
Get organism name.
- `def setdata`
Add genbank information.

Public Attributes

- `genbankString`

6.17.1 Detailed Description

Definition at line 9 of file `Genbank.py`.

6.17.2 Constructor & Destructor Documentation

6.17.2.1 `def irna::iRNA_seq::Genbank::Genbank::_init_ (self, genbank_file)`

Instantiate [Genbank](#) object.

Definition at line 15 of file Genbank.py.

6.17.3 Member Function Documentation

6.17.3.1 `def irna::iRNA_seq::Genbank::Genbank::getDNA (self)`

Read DNA sequence and transform into string.

Parameters

<i>nom_fichier</i> ,:	File
<i>ADN</i> ,:	DNA string

Definition at line 82 of file Genbank.py.

References [genbankString](#), and [getOrganism\(\)](#).

Referenced by [getGenes\(\)](#), and [getOrganism\(\)](#).

6.17.3.2 `def irna::iRNA_seq::Genbank::Genbank::getGenes (self)`

Get genes data.

Returns

: List of dictionnary with all genes data

Definition at line 40 of file Genbank.py.

References [genbankString](#), and [getDNA\(\)](#).

Referenced by [getOrganism\(\)](#), and [readGenbank\(\)](#).

6.17.3.3 `def irna::iRNA_seq::Genbank::Genbank::getOrganism (self)`

Get organism name.

Definition at line 100 of file Genbank.py.

References [genbankString](#), [getDNA\(\)](#), [getGenes\(\)](#), and [setdata\(\)](#).

Referenced by [getDNA\(\)](#), and [setdata\(\)](#).

6.17.3.4 `def irna::iRNA_seq::Genbank::Genbank::readGenbank (self, genbank_file)`

Read [Genbank](#) file and save into a set of readlines.

Parameters

<i>genbank_ - file,:</i>	Path to Genbank file
------------------------------	--------------------------------------

Returns

: List contening [Genbank](#) text

Definition at line 25 of file Genbank.py.

References `getGenes()`.

6.17.3.5 `def irna::iRNA_seq::Genbank::Genbank::setdata (self, organism, list_genes, DNA)`

Add genbank information.

Parameters

<i>organism,:</i>	
<i>list_genes,:</i>	
<i>DNA,:</i>	

Returns

:

Definition at line 115 of file Genbank.py.

References `getOrganism()`.

Referenced by `getOrganism()`.

6.17.4 Member Data Documentation

6.17.4.1 `irna::iRNA_seq::Genbank::Genbank::genbankString`

Definition at line 15 of file Genbank.py.

Referenced by `getDNA()`, `getGenes()`, and `getOrganism()`.

The documentation for this class was generated from the following file:

- `/home/amine/workspace/iRNA/irna/iRNA_seq/Genbank.py`

6.18 `irna::David2tulip::Gene_list::Gene_list` Class Reference

: Handle DAVID enrichment data

Public Member Functions

- `def __init__`
Instantiate [Gene_list](#) object.

Public Attributes

- [sRNA](#)
- [categoryName](#)
- [genelds](#)
- [termName](#)

6.18.1 Detailed Description

: Handle DAVID enrichment data

Author

: Amine Ghozlane

Version

: 1.0

Definition at line 7 of file `Gene_list.py`.

6.18.2 Constructor & Destructor Documentation

6.18.2.1 `def irna::David2tulip::Gene_list::Gene_list::__init__(self, sudsobject, sRNA)`

Instantiate [Gene_list](#) object.

Parameters

<i>sudsobject</i> ,:	suds object
<i>sRNA</i> ,:	Name of the sRNA

Definition at line 15 of file `Gene_list.py`.

6.18.3 Member Data Documentation

6.18.3.1 `irna::David2tulip::Gene_list::Gene_list::categoryName`

Definition at line 15 of file `Gene_list.py`.

6.18.3.2 `irna::David2tulip::Gene_list::Gene_list::genelds`

Definition at line 15 of file `Gene_list.py`.

6.18.3.3 `irna::David2tulip::Gene_list::Gene_list::sRNA`

Definition at line 15 of file `Gene_list.py`.

6.18.3.4 `irna::David2tulip::Gene_list::Gene_list::termName`

Definition at line 15 of file `Gene_list.py`.

The documentation for this class was generated from the following file:

- `/home/amine/workspace/iRNA/irna/David2tulip/Gene_list.py`

6.19 `irna::David2tulip::Graph::Graph` Class Reference

Public Member Functions

- `def __init__`
Instanciate graph object.
- `def parse`
Parse and information to node and edge objects.
- `def printnodes`
Write nodes csv.
- `def getCategories`
Get active categories.
- `def getNumCategory`
Get the position of on element in a list.
- `def verif`
Verif value for sRNA_100.
- `def filterTermName`
Detect the method to use for filtering.
- `def printedges`
Write edges csv.
- `def writefile`
Write node and edge csv.

Public Attributes

- [node_objects](#)
- [edge_objects](#)
- [fcategoryid](#)
- [gocategoryid](#)
- [fregex](#)
- [goregex](#)

6.19.1 Detailed Description

Definition at line 12 of file Graph.py.

6.19.2 Constructor & Destructor Documentation

6.19.2.1 `def irna::David2tulip::Graph::Graph::__init__(self)`

Instantiate graph object.

Definition at line 18 of file Graph.py.

6.19.3 Member Function Documentation

6.19.3.1 `def irna::David2tulip::Graph::Graph::filterTermName (self, category, term)`

Detect the method to use for filtering.

Definition at line 89 of file Graph.py.

References `getCategories()`, and `printededges()`.

Referenced by `printededges()`, and `verif()`.

6.19.3.2 `def irna::David2tulip::Graph::Graph::getCategories (self)`

Get active categories.

Returns

: Unique categories

Definition at line 58 of file Graph.py.

References `getNumCategory()`, and `verif()`.

Referenced by `filterTermName()`, and `printnodes()`.

6.19.3.3 `def irna::David2tulip::Graph::Graph::getNumCategory (self, element, liste)`

Get the position of on element in a list.

Parameters

<i>element</i> ,:	an element of the list
<i>liste</i> ,:	a list

Definition at line 71 of file Graph.py.

References `edge_objects`.

Referenced by `getCategories()`.

6.19.3.4 `def irna::David2tulip::Graph::Graph::parse (self, obj)`

Parse and information to node and edge objects.

Parameters

<i>obj</i> ,:	Parser-linked object
---------------	----------------------

Definition at line 31 of file Graph.py.

References `printnodes()`.

6.19.3.5 `def irna::David2tulip::Graph::Graph::printedges (self, results)`

Write edges csv.

Parameters

<i>results</i> ,:	Path to result repertory
-------------------	--------------------------

Definition at line 108 of file Graph.py.

References `edge_objects`, `filterTermName()`, `printedges()`, `printnodes()`, and `writefile()`.

Referenced by `filterTermName()`, and `printedges()`.

6.19.3.6 `def irna::David2tulip::Graph::Graph::printnodes (self, results)`

Write nodes csv.

Parameters

<i>results</i> ,:	Path to result repertory
-------------------	--------------------------

Definition at line 39 of file Graph.py.

References `edge_objects`, `getCategories()`, and `node_objects`.

Referenced by `parse()`, and `printedges()`.

6.19.3.7 def irna::David2tulip::Graph::Graph::verif (*self*)

Verif value for sRNA_100.

Definition at line 78 of file `Graph.py`.

References `fcategoryid`, `filterTermName()`, and `gocategoryid`.

Referenced by `getCategories()`.

6.19.3.8 def irna::David2tulip::Graph::Graph::writefile (*self*, *results*)

Write node and edge csv.

Parameters

<i>results</i> ,	Path to result repertory
------------------	--------------------------

Definition at line 171 of file `Graph.py`.

Referenced by `printedges()`.

6.19.4 Member Data Documentation

6.19.4.1 irna::David2tulip::Graph::Graph::edge_objects

Definition at line 18 of file `Graph.py`.

Referenced by `getNumCategory()`, `printedges()`, and `printnodes()`.

6.19.4.2 irna::David2tulip::Graph::Graph::fcategoryid

Definition at line 18 of file `Graph.py`.

Referenced by `verif()`.

6.19.4.3 irna::David2tulip::Graph::Graph::fregex

Definition at line 18 of file `Graph.py`.

6.19.4.4 irna::David2tulip::Graph::Graph::gocategoryid

Definition at line 18 of file `Graph.py`.

Referenced by `verif()`.

6.19.4.5 `irna::David2tulip::Graph::Graph::goregex`

Definition at line 18 of file Graph.py.

6.19.4.6 `irna::David2tulip::Graph::Graph::node_objects`

Definition at line 18 of file Graph.py.

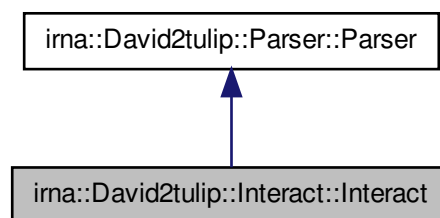
Referenced by `printnodes()`.

The documentation for this class was generated from the following file:

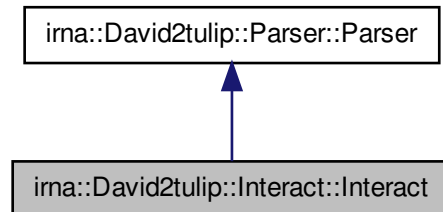
- `/home/amine/workspace/iRNA/irna/David2tulip/Graph.py`

6.20 `irna::David2tulip::Interact::Interact` Class Reference

Inheritance diagram for `irna::David2tulip::Interact::Interact`:



Collaboration diagram for irna::David2tulip::Interact::Interact:



Public Member Functions

- `def __init__`
Instantiate similarity parser object.
- `def setdata`
Add sRNA - sRNA edges based on their similarity.

Public Attributes

- `interact_file`

6.20.1 Detailed Description

Definition at line 10 of file `Interact.py`.

6.20.2 Constructor & Destructor Documentation

6.20.2.1 `def irna::David2tulip::Interact::Interact::__init__(self, interact_file)`

Instantiate similarity parser object.

Parameters

<code>interact_file,</code>	interact file
-----------------------------	---------------

Definition at line 17 of file `Interact.py`.

6.20.3 Member Function Documentation

6.20.3.1 `def irna::David2tulip::Interact::Interact::setdata (self, node_objects, edge_objects)`

Add sRNA - sRNA edges based on their similarity.

Parameters

<i>node_objects</i> ,:	list of node objects
<i>edge_objects</i> ,:	list of edge objects

Definition at line 27 of file `Interact.py`.

References `irna::David2tulip::Parser::Parser::getlinkededge()`, and `interact_file`.

6.20.4 Member Data Documentation

6.20.4.1 `irna::David2tulip::Interact::Interact::interact_file`

Definition at line 17 of file `Interact.py`.

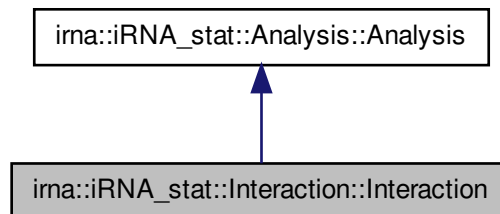
Referenced by `setdata()`.

The documentation for this class was generated from the following file:

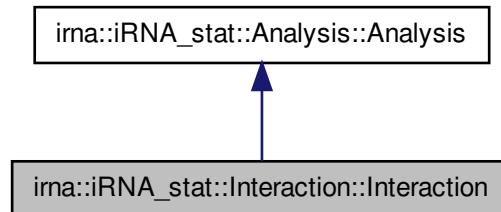
- `/home/amine/workspace/iRNA/irna/David2tulip/Interact.py`

6.21 `irna::iRNA_stat::Interaction::Interaction` Class Reference

Inheritance diagram for `irna::iRNA_stat::Interaction::Interaction`:



Collaboration diagram for irna::iRNA_stat::Interaction::Interaction:



Public Member Functions

- def `__init__`
Instantiate [Interaction](#) object.
- def `defintefunction`
Determine the function to apply depending of the type of solution.
- def `intebestsol`
Case best solution.
- def `inteseveralcontact`
Case several contacts score - several contacts energy.
- def `inteonesol`
Case : one solution.
- def `getInteraction`
Compute interaction position.
- def `ncbp`
Compute the number of correctly predicted base pairings.
- def `compute_ppv`
Compute PPV.
- def `compute_sensitivity`
Compute sensitivity.
- def `compute_sens_ppv`
Compute sensitivity and ppv of the interaction.
- def `Interaction_data`
Get interaction position data.
- def `run`
Compute interaction precision and sensitivity.

Public Attributes

- [intfuncmap](#)
- [interactions](#)
- [type_sol](#)
- [pos](#)
- [exp_inf](#)
- [dbmanage](#)
- [ppv](#)
- [sensitivity](#)
- [classtype](#)

6.21.1 Detailed Description

Definition at line 11 of file Interaction.py.

6.21.2 Constructor & Destructor Documentation

6.21.2.1 `def irna::iRNA_stat::Interaction::Interaction::__init__(self, data, dbmanage, exp_inf)`

Instantiate [Interaction](#) object.

Parameters

<i>data,:</i>	Communication object
<i>dbmanage,:</i>	Access to the database
<i>exp_inf,:</i>	Exp_inf object

Definition at line 20 of file Interaction.py.

6.21.3 Member Function Documentation

6.21.3.1 `def irna::iRNA_stat::Interaction::Interaction::compute_ppv (self, Pinteract, Rinteract)`

Compute PPV.

Parameters

<i>Pinteract,:</i>	Predicted interaction position
<i>Rinteract,:</i>	Real interaction position

Returns

: PPV of one interation

Definition at line 143 of file Interaction.py.

References `compute_sens_ppv()`, and `ncbp()`.

Referenced by `getInteraction()`.

6.21.3.2 `def irna::iRNA_stat::Interaction::Interaction::compute_sens_ppv (self)`

Compute sensitivity and ppv of the interaction.

Definition at line 168 of file `Interaction.py`.

Referenced by `compute_ppv()`, and `Interaction_data()`.

6.21.3.3 `def irna::iRNA_stat::Interaction::Interaction::compute_sensitivity (self, Pinteract, Rinteract)`

Compute sensitivity.

Parameters

<i>Pinteract</i> ,:	Predicted interaction position
<i>Rinteract</i> ,:	Real interaction position

Returns

: sensitivity of one interaction

Definition at line 157 of file `Interaction.py`.

References `irna::iRNA_stat::Computer::Computer::classtype`, `classtype`, `defintefunction()`, `interactions`, `irna::iRNA_stat::Computer::Computer::interactions`, `irna::iRNA_stat::Computer::Computer::ppv`, `ppv`, `irna::iRNA_stat::Computer::Computer::sensitivity`, and `sensitivity`.

Referenced by `ncbp()`.

6.21.3.4 `def irna::iRNA_stat::Interaction::Interaction::defintefunction (self)`

Determine the function to apply depending of the type of solution.

Definition at line 34 of file `Interaction.py`.

References `intebestsol()`, and `intefuncmap`.

Referenced by `compute_sensitivity()`.

6.21.3.5 `def irna::iRNA_stat::Interaction::Interaction::getInteraction (self, posit, sRNA_deb, sRNA_end, mRNA_deb, mRNA_end, predict, intefuncpoint)`

Compute interaction position.

Parameters

<i>posit</i> ,:	Position in the list
<i>sRNA_deb</i> ,:	sRNA begin list
<i>sRNA_end</i> ,:	sRNA end list
<i>mRNA_deb</i> ,:	sRNA begin list
<i>mRNA_ - end</i> ,:	mRNA end list
<i>predict</i> ,:	Flag Predict position
<i>intefuncpoint</i> ,:	Function pointer to analysis function

Returns

: Position selected and normalised

Definition at line 112 of file Interaction.py.

References compute_ppv(), and ncbp().

Referenced by irna::iRNA_stat::Mpi::Mpi::getpValue(), inteonesol(), and Interaction_data().

```
6.21.3.6 def irna::iRNA_stat::Interaction::Interaction::intebestsol ( self, posit, sRNA_deb,
sRNA_end, mRNA_deb, mRNA_end )
```

Case best solution.

Parameters

<i>posit</i> ,:	Position in the list
<i>sRNA_deb</i> ,:	sRNA begin list
<i>sRNA_end</i> ,:	sRNA end list
<i>mRNA_deb</i> ,:	sRNA begin list
<i>mRNA_ - end</i> ,:	mRNA end list

Returns

: Position selected and normalised

Definition at line 49 of file Interaction.py.

References inteseveralcontact().

Referenced by defintefunction().


```
6.21.3.7 def irna::iRNA_stat::Interaction::Interaction::inteesol ( self, posit, sRNA_deb,
sRNA_end, mRNA_deb, mRNA_end )
```

Case : one solution.

Parameters

<i>posit</i> ,:	Position in the list
<i>sRNA_deb</i> ,:	sRNA begin list
<i>sRNA_end</i> ,:	sRNA end list
<i>mRNA_deb</i> ,:	sRNA begin list
<i>mRNA_end</i> ,:	mRNA end list

Returns

: Position selected and normalised

Definition at line 92 of file Interaction.py.

References getInteraction().

Referenced by inteseveralcontact().

```
6.21.3.8 def irna::iRNA_stat::Interaction::Interaction::Interaction_data ( self )
```

Get interaction position data.

Definition at line 205 of file Interaction.py.

References compute_sens_ppv(), irna::iRNA_stat::Files::Files::exp_inf, exp_inf, getInteraction(), irna::iRNA_stat::Analysis::Analysis::getRangePosit(), Interaction_data(), pos, irna::iRNA_stat::Computer::Computer::pos, run(), type_sol, and irna::iRNA_stat::Computer::Computer::type_sol.

Referenced by Interaction_data().

```
6.21.3.9 def irna::iRNA_stat::Interaction::Interaction::inteseveralcontact ( self, posit,
sRNA_deb, sRNA_end, mRNA_deb, mRNA_end )
```

Case several contacts score - several contacts energy.

Parameters

<i>posit</i> ,:	Position in the list
<i>sRNA_deb</i> ,:	sRNA begin list
<i>sRNA_end</i> ,:	sRNA end list
<i>mRNA_deb</i> ,:	sRNA begin list
<i>mRNA_end</i> ,:	mRNA end list

Returns

: Position selected and normalised

Definition at line 67 of file Interaction.py.

References inteonesol().

Referenced by intebestsol().

6.21.3.10 `def irna::iRNA_stat::Interaction::Interaction::ncbp (self, pRNA, rRNA)`

Compute the number of correctly predicted base pairings.

Definition at line 130 of file Interaction.py.

References compute_sensitivity(), and ncbp().

Referenced by compute_ppv(), getInteraction(), and ncbp().

6.21.3.11 `def irna::iRNA_stat::Interaction::Interaction::run (self)`

Compute interaction precision and sensitivity.

Definition at line 238 of file Interaction.py.

Referenced by Interaction_data().

6.21.4 Member Data Documentation

6.21.4.1 `irna::iRNA_stat::Interaction::Interaction::classtype`

Definition at line 168 of file Interaction.py.

Referenced by compute_sensitivity().

6.21.4.2 `irna::iRNA_stat::Interaction::Interaction::dbmanage`

Definition at line 20 of file Interaction.py.

6.21.4.3 `irna::iRNA_stat::Interaction::Interaction::exp_inf`

Definition at line 20 of file Interaction.py.

Referenced by Interaction_data().

6.21.4.4 `irna::iRNA_stat::Interaction::Interaction::intefuncmap`

Definition at line 20 of file Interaction.py.

Referenced by defintefunction().

6.21.4.5 irna::iRNA_stat::Interaction::Interaction::interactions

Definition at line 20 of file Interaction.py.

Referenced by compute_sensitivity(), irna::iRNA_stat::NormScore::NormScore::normUniqueSolution(), irna::iRNA_stat::pValue::pValue::run(), and irna::iRNA_stat::NormScore::NormScore::run().

6.21.4.6 irna::iRNA_stat::Interaction::Interaction::pos

Definition at line 20 of file Interaction.py.

Referenced by irna::iRNA_stat::NormScore::NormScore::defnormfunction(), - Interaction_data(), irna::iRNA_stat::NormScore::NormScore::normSeveralContactScore(), irna::iRNA_stat::NormScore::NormScore::normSeveralEnergy(), irna::iRNA_stat::NormScore::NormScore::normSeveralScore(), irna::iRNA_stat::NormScore::NormScore::normUniqueSolution(), and irna::iRNA_stat::NormScore::NormScore::run().

6.21.4.7 irna::iRNA_stat::Interaction::Interaction::ppv

Definition at line 168 of file Interaction.py.

Referenced by compute_sensitivity().

6.21.4.8 irna::iRNA_stat::Interaction::Interaction::sensitivity

Definition at line 168 of file Interaction.py.

Referenced by compute_sensitivity().

6.21.4.9 irna::iRNA_stat::Interaction::Interaction::type_sol

Definition at line 20 of file Interaction.py.

Referenced by irna::iRNA_stat::NormScore::NormScore::defnormfunction(), and - Interaction_data().

The documentation for this class was generated from the following file:

- /home/amine/workspace/iRNA/irna/iRNA_stat/[Interaction.py](#)

6.22 irna::iRNA_pred::Interaction::Interaction Class Reference

: Store information on interaction.

Public Member Functions

- def [__init__](#)
Init [Interaction](#) object.
- def [setSoft](#)
Set software node.
- def [getlastmRNA](#)
Get mRNA attribute.
- def [getlastsRNA](#)
Get sRNA attribute.
- def [addListOfComparison](#)
Add a list of comparison node.
- def [addComparison](#)
Add a comparison node.
- def [getLastchildnode](#)
- def [setScoreList](#)
Set ListOfComparison score.
- def [getResult](#)
- def [println](#)
Print object data.
- def [setMatrix](#)
Manage matrix load and format.
- def [formatMatrix](#)
Format into integer the matrix.
- def [loadMatrix](#)
Load the matrix of score.
- def [getPosition](#)
Get the position on matrix.
- def [scoreSequence](#)
Score two sequences.

Public Attributes

- [root](#)
- [schema_root](#)

Static Public Attributes

- [matrix](#) = None

6.22.1 Detailed Description

: Store information on interaction.

Definition at line 14 of file Interaction.py.

6.22.2 Constructor & Destructor Documentation

6.22.2.1 `def irna::iRNA_pred::Interaction::Interaction::__init__(self)`

Init [Interaction](#) object.

Definition at line 21 of file Interaction.py.

6.22.3 Member Function Documentation

6.22.3.1 `def irna::iRNA_pred::Interaction::Interaction::addComparison (self, data)`

Add a comparison node.

Parameters

<i>data</i> ,:	Comparison result
----------------	-----------------------------------

Definition at line 65 of file Interaction.py.

References [getLastchildnode\(\)](#), [schema_root](#), and [setScoreList\(\)](#).

Referenced by [getlastsRNA\(\)](#).

6.22.3.2 `def irna::iRNA_pred::Interaction::Interaction::addListOfComparison (self, mRNA,
sRNA)`

Add a list of comparison node.

Parameters

<i>mRNA</i> ,:	mRNA id
<i>sRNA</i> ,:	sRNA id

Definition at line 57 of file Interaction.py.

References [getLastchildnode\(\)](#).

Referenced by [getlastmRNA\(\)](#).

6.22.3.3 `def irna::iRNA_pred::Interaction::Interaction::formatMatrix (self, mat)`

Format into integer the matrix.

Parameters

<i>mat</i> ,:	Matrix data in string format
---------------	------------------------------

Returns

: Matrix in integer format

Definition at line 118 of file Interaction.py.

Referenced by `println()`.

6.22.3.4 `def irna::iRNA_pred::Interaction::Interaction::getLastchildnode (self)`

Returns

: The last child from root

Definition at line 73 of file Interaction.py.

References `getResult()`, and `root`.

Referenced by `addComparison()`, `addListOfComparison()`, `getlastmRNA()`, and `setSoft()`.

6.22.3.5 `def irna::iRNA_pred::Interaction::Interaction::getlastmRNA (self)`

Get mRNA attribute.

Returns

: Value of mRNA attribute

Definition at line 38 of file Interaction.py.

References `addListOfComparison()`, `getLastchildnode()`, and `schema_root`.

6.22.3.6 `def irna::iRNA_pred::Interaction::Interaction::getlastsRNA (self)`

Get sRNA attribute.

Returns

: Value of sRNA attribute

Definition at line 47 of file Interaction.py.

References `addComparison()`.

Referenced by `setSoft()`.

6.22.3.7 `def irna::iRNA_pred::Interaction::Interaction::getPosition (self, letter)`

Get the position on matrix.

Parameters

<i>letter,:</i>	One letter in the sequence
-----------------	----------------------------

Returns

: The position on matrix

Definition at line 158 of file Interaction.py.

References getPosition(), and matrix.

Referenced by getPosition(), and loadMatrix().

6.22.3.8 def irna::iRNA_pred::Interaction::Interaction::getResult (*self*)

Returns

: The tree in text format

Definition at line 88 of file Interaction.py.

References loadMatrix(), and setMatrix().

Referenced by getLastchildnode().

6.22.3.9 def irna::iRNA_pred::Interaction::Interaction::loadMatrix (*self*, *matrix*)

Load the matrix of score.

Parameters

<i>matrix,:</i>	Matrix file
-----------------	-------------

Returns

: Matrix of score

Definition at line 133 of file Interaction.py.

References getPosition(), matrix, and scoreSequence().

Referenced by getResult(), and setMatrix().

6.22.3.10 def irna::iRNA_pred::Interaction::Interaction::println (*self*)

Print object data.

Definition at line 96 of file Interaction.py.

References formatMatrix(), and matrix.

Referenced by setScoreList().

6.22.3.11 `def irna::iRNA_pred::Interaction::Interaction::scoreSequence (self, seqs)`

Score two sequences.

Parameters

<i>seqs</i> ,:	Table of two sequences
----------------	------------------------

Returns

: The score of the alignment

Definition at line 175 of file Interaction.py.

Referenced by loadMatrix().

6.22.3.12 `def irna::iRNA_pred::Interaction::Interaction::setMatrix (self, matrix)`

Manage matrix load and format.

Parameters

<i>matrix</i> ,:	Matrix file
------------------	-------------

Definition at line 105 of file Interaction.py.

References loadMatrix().

Referenced by getResult().

6.22.3.13 `def irna::iRNA_pred::Interaction::Interaction::setScoreList (self, score)`

Set ListOfComparison score.

Parameters

<i>score</i> ,:	Score the whole comparison
-----------------	----------------------------

Definition at line 81 of file Interaction.py.

References println(), and schema_root.

Referenced by addComparison().

6.22.3.14 `def irna::iRNA_pred::Interaction::Interaction::setSoft (self, soft_name, ref)`

Set software node.

Parameters

<i>soft_name,:</i>	Software name
<i>ref,:</i>	Software num

Definition at line 30 of file Interaction.py.

References getLastchildnode(), getlastsRNA(), and schema_root.

6.22.4 Member Data Documentation

6.22.4.1 irna::iRNA_pred::Interaction::Interaction::matrix = None [static]

Definition at line 15 of file Interaction.py.

Referenced by getPosition(), loadMatrix(), and println().

6.22.4.2 irna::iRNA_pred::Interaction::Interaction::root

Definition at line 21 of file Interaction.py.

Referenced by getLastchildnode().

6.22.4.3 irna::iRNA_pred::Interaction::Interaction::schema_root

Definition at line 30 of file Interaction.py.

Referenced by addComparison(), getlastmRNA(), setScoreList(), and setSoft().

The documentation for this class was generated from the following file:

- /home/amine/workspace/iRNA/irna/iRNA_pred/[Interaction.py](#)

6.23 irna::iRNA_pred::Merger::Merger Class Reference

Merge the xml files in a sqlite database.

Public Member Functions

- def [__init__](#)
Initiate the constructor.
- def [buildTree](#)
Read the xml tree and copy the data into the sqlite database.
- def [getData](#)
Parse xml tree.
- def [setRNA](#)

Parse RNA_inf file.

- def [merge](#)

Merge mycamn xml files into a sqlite database.

Public Attributes

- [repln](#)
- [files](#)
- [softprevious](#)

Static Public Attributes

- tuple [result_data](#) = etree.Element("result")

6.23.1 Detailed Description

Merge the xml files in a sqlite database.

Definition at line 14 of file Merger.py.

6.23.2 Constructor & Destructor Documentation

6.23.2.1 `def irna::iRNA_pred::Merger::Merger::__init__(self, repln)`

Initiate the constructor.

Parameters

<i>repln</i> ,:	Result repertory
-----------------	------------------

Definition at line 23 of file Merger.py.

6.23.3 Member Function Documentation

6.23.3.1 `def irna::iRNA_pred::Merger::Merger::buildTree (self, tree, dbmanage)`

Read the xml tree and copy the data into the sqlite database.

Parameters

<i>tree</i> ,:	xml tree parsed
<i>dbmanage</i> ,:	Database manager

Definition at line 38 of file Merger.py.

References [getData\(\)](#), and [softprevious](#).

Referenced by merge().

6.23.3.2 `def irna::iRNA_pred::Merger::Merger::getData (self, file)`

[Parse](#) xml tree.

Parameters

<i>file</i> ,:	Result part in Xml format
----------------	---------------------------

Returns

: resulting tree

Definition at line 71 of file Merger.py.

References setRNA().

Referenced by buildTree(), irna::iRNA_stat::Rand_data::Rand_data::getAllSofts(), and merge().

6.23.3.3 `def irna::iRNA_pred::Merger::Merger::merge (self, dbmanage)`

Merge mycarn xml files into a sqlite database.

Parameters

<i>dbmanage</i> ,:	Database manager
--------------------	------------------

Definition at line 101 of file Merger.py.

References buildTree(), getData(), and repln.

Referenced by setRNA().

6.23.3.4 `def irna::iRNA_pred::Merger::Merger::setRNA (self, dbmanage, RNA_inf, type)`

[Parse](#) RNA_inf file.

Parameters

<i>RNA_inf</i> ,:	Path to RNA_inf file
<i>dbmanage</i> ,:	Access to the database
<i>type</i> ,:	Type of RNA

Definition at line 87 of file Merger.py.

References files, and merge().

Referenced by getData().

6.23.4 Member Data Documentation

6.23.4.1 `irna::iRNA_pred::Merger::Merger::files`

Definition at line 23 of file `Merger.py`.

Referenced by `setRNA()`.

6.23.4.2 `irna::iRNA_pred::Merger::Merger::repln`

Definition at line 23 of file `Merger.py`.

Referenced by `merge()`.

6.23.4.3 `tuple irna::iRNA_pred::Merger::Merger::result_data = etree.Element("result")` `[static]`

Definition at line 16 of file `Merger.py`.

6.23.4.4 `irna::iRNA_pred::Merger::Merger::softprevious`

Definition at line 23 of file `Merger.py`.

Referenced by `buildTree()`.

The documentation for this class was generated from the following file:

- `/home/amine/workspace/iRNA/irna/iRNA_pred/Merger.py`

6.24 `irna::iRNA_stat::Mpi::Mpi` Class Reference

: Manage `Mpi` run

Public Member Functions

- `def __init__`
The Constructor.
- `def waiting`
Test de reduction de consommation de ressource.
- `def instanciate_analysis`
Instanciate object of analysis.
- `def worker`
Worker process.
- `def working_step`
Defines what each worker will compute.

- def [getCorrespondingSoft](#)
Get corresponding soft between soft_param and current database.
- def [getSendCom](#)
Create communication object.
- def [Mpi_end_processus](#)
End of all process.
- def [Mpi_finalize](#)
Fin.
- def [getNormScore](#)
Get results of score normalisation.
- def [getInteraction](#)
Get results of the interaction analysis.
- def [getInteraction_data](#)
Get results of the interaction analysis.
- def [getpValue](#)
*Get results of *pValue* analysis.*
- def [getRegression](#)
Get results of linear regression.
- def [getAnalysis](#)
Get the analysis function to apply.
- def [run](#)
Manage comunication and data sending.

Public Attributes

- [comm](#)
- [nprocs](#)
- [myrank](#)
- [name](#)
- [setdata](#)

6.24.1 Detailed Description

: Manage [Mpi](#) run

Definition at line 20 of file Mpi.py.

6.24.2 Constructor & Destructor Documentation

6.24.2.1 def irna::iRNA_stat::Mpi::Mpi::__init__(self)

The Constructor.

Note

comm: Broadcast communicator
nprocs: Number of thread
myrank: Rank of the thread

Definition at line 28 of file `Mpi.py`.

6.24.3 Member Function Documentation**6.24.3.1** `def irna::iRNA_stat::Mpi::Mpi::getAnalysis (self, type_analysis)`

Get the analysis function to apply.

Definition at line 225 of file `Mpi.py`.

Referenced by `getInteraction_data()`.

6.24.3.2 `def irna::iRNA_stat::Mpi::Mpi::getCorrespondingSoft (self, computer, dbmanage, rand_inf)`

Get corresponding soft between `soft_param` and current database.

Definition at line 117 of file `Mpi.py`.

References `getSendCom()`.

Referenced by `getSendCom()`, and `working_step()`.

6.24.3.3 `def irna::iRNA_stat::Mpi::Mpi::getInteraction (self, computer, tab, source, result)`

Get results of the interaction analysis.

Definition at line 194 of file `Mpi.py`.

References `getRegression()`.

Referenced by `getpValue()`, and `Mpi_finalize()`.

6.24.3.4 `def irna::iRNA_stat::Mpi::Mpi::getInteraction_data (self, computer, tab, source, result)`

Get results of the interaction analysis.

Definition at line 203 of file `Mpi.py`.

References `getAnalysis()`, `getNormScore()`, and `setdata`.

Referenced by `getNormScore()`, and `getpValue()`.

6.24.3.5 `def irna::iRNA_stat::Mpi::Mpi::getNormScore (self, computer, tab, source, result)`

Get results of score normalisation.

Definition at line 186 of file Mpi.py.

References `getInteraction_data()`, and `getpValue()`.

Referenced by `getInteraction_data()`, and `Mpi_end_processus()`.

6.24.3.6 `def irna::iRNA_stat::Mpi::Mpi::getpValue (self, computer, tab, source, result)`

Get results of [pValue](#) analysis.

Definition at line 210 of file Mpi.py.

References `irna::iRNA_stat::Interaction::Interaction::getInteraction()`, `getInteraction()`, `getInteraction_data()`, `getpValue()`, `getRegression()`, `run()`, and `setdata`.

Referenced by `getNormScore()`, and `getpValue()`.

6.24.3.7 `def irna::iRNA_stat::Mpi::Mpi::getRegression (self, computer, tab, source, result)`

Get results of linear regression.

Definition at line 217 of file Mpi.py.

References `working_step()`.

Referenced by `getInteraction()`, and `getpValue()`.

6.24.3.8 `def irna::iRNA_stat::Mpi::Mpi::getSendCom (self, computer, type_analysis, tab, dbmanage, rand_inf)`

Create communication object.

Definition at line 138 of file Mpi.py.

References `getCorrespondingSoft()`, `Mpi_end_processus()`, `Mpi_finalize()`, `irna::iRNA_pred::Mpi::Mpi::nprocs`, and `nprocs`.

Referenced by `getCorrespondingSoft()`.

6.24.3.9 `def irna::iRNA_stat::Mpi::Mpi::instanciate_analysis (self, data_obj, dbmanage, exp_inf, rand_inf)`

Instantiate object of analysis.

Parameters

<i>data_obj,:</i>	Communication object
<i>dbmanage,:</i>	Access to the database
<i>exp_inf,:</i>	Experimental data
<i>rand_inf,:</i>	Random data

Definition at line 50 of file `Mpi.py`.

References `waiting()`, and `worker()`.

Referenced by `waiting()`, and `worker()`.

6.24.3.10 `def irna::iRNA_stat::Mpi::Mpi::Mpi_end_processus (self)`

End of all process.

Definition at line 168 of file `Mpi.py`.

References `getNormScore()`.

Referenced by `getSendCom()`.

6.24.3.11 `def irna::iRNA_stat::Mpi::Mpi::Mpi_finalize (self)`

Fin.

Definition at line 176 of file `Mpi.py`.

References `getInteraction()`.

Referenced by `getSendCom()`, and `worker()`.

6.24.3.12 `def irna::iRNA_stat::Mpi::Mpi::run (self, computer, type_analysis, dbmanage = None, rand_inf = None)`

Manage communication and data sending.

Parameters

<code>computer,:</code>	Computer object
<code>type_ - analysis,:</code>	Type of analysis

Definition at line 239 of file `Mpi.py`.

Referenced by `getpValue()`.

6.24.3.13 `def irna::iRNA_stat::Mpi::Mpi::waiting (self)`

Test de reduction de consommation de ressource.

Definition at line 38 of file `Mpi.py`.

References `instanciate_analysis()`.

Referenced by `instanciate_analysis()`.

6.24.3.14 `def irna::iRNA_stat::Mpi::Mpi::worker (self, dbmanage, exp_inf, rand_inf)`

Worker process.

Parameters

<i>dbmanage</i> ,:	Access to the database
<i>exp_inf</i> ,:	Experimental data
<i>rand_inf</i> ,:	Random data

Definition at line 65 of file Mpi.py.

References `instanciate_analysis()`, `Mpi_finalize()`, `irna::iRNA_pred::Mpi::Mpi::Mpi_finalize()`, `irna::iRNA_pred::Mpi::Mpi::nprocs`, `nprocs`, and `working_step()`.

Referenced by `instanciate_analysis()`.

6.24.3.15 `def irna::iRNA_stat::Mpi::Mpi::working_step (self, nbinteract)`

Defines what each worker will compute.

Parameters

<i>nbinteract</i> ,:	Number of operation to do
----------------------	---------------------------

Definition at line 88 of file Mpi.py.

References `getCorrespondingSoft()`.

Referenced by `getRegression()`, and `worker()`.

6.24.4 Member Data Documentation

6.24.4.1 `irna::iRNA_stat::Mpi::Mpi::comm`

Definition at line 28 of file Mpi.py.

6.24.4.2 `irna::iRNA_stat::Mpi::Mpi::myrank`

Definition at line 28 of file Mpi.py.

6.24.4.3 `irna::iRNA_stat::Mpi::Mpi::name`

Definition at line 28 of file Mpi.py.

6.24.4.4 `irna::iRNA_stat::Mpi::Mpi::nprocs`

Definition at line 28 of file Mpi.py.

Referenced by `getSendCom()`, and `worker()`.

6.24.4.5 `irna::iRNA_stat::Mpi::Mpi::setdata`

Definition at line 225 of file `Mpi.py`.

Referenced by `getInteraction_data()`, and `getpValue()`.

The documentation for this class was generated from the following file:

- `/home/amine/workspace/iRNA/irna/iRNA_stat/Mpi.py`

6.25 `irna::iRNA_pred::Mpi::Mpi` Class Reference

: Manage `Mpi` run

Public Member Functions

- `def __init__`
The Constructor.
- `def Mpi_getComm`
- `def Mpi_getnprocs`
- `def Mpi_getmyrank`
- `def Mpi_getname`
- `def Mpi_write_exectime`
Write exectime of command.
- `def Mpi_master`
Master process.
- `def Mpi_sup_process`
Termine les processus supplementaire.
- `def Mpi_getSoft`
Test if that soft has already been used.
- `def Mpi_write_data`
Write xml result file.
- `def Mpi_slave`
Slave process.
- `def Mpi_exit_processus`
End of all process.
- `def Mpi_end_processus`
End of all process.
- `def Mpi_finalize`
Fin.
- `def Mpi_run`
Control Mpi procedure.

Public Attributes

- [comm](#)
- [nprocs](#)
- [myrank](#)
- [name](#)

6.25.1 Detailed Description

: Manage [Mpi](#) run

Definition at line 20 of file Mpi.py.

6.25.2 Constructor & Destructor Documentation

6.25.2.1 `def irna::iRNA_pred::Mpi::Mpi::__init__(self)`

The Constructor.

Note

comm: Broadcast communicator
nprocs: Number of thread
myrank: Rank of the thread

Definition at line 28 of file Mpi.py.

6.25.3 Member Function Documentation

6.25.3.1 `def irna::iRNA_pred::Mpi::Mpi::Mpi_end_processus (self)`

End of all process.

Definition at line 350 of file Mpi.py.

References [Mpi_master\(\)](#), [Mpi_slave\(\)](#), [irna::iRNA_pred::Files::Files::myrank](#), and [myrank](#).

Referenced by [Mpi_master\(\)](#), and [Mpi_slave\(\)](#).

6.25.3.2 `def irna::iRNA_pred::Mpi::Mpi::Mpi_exit_processus (self)`

End of all process.

Definition at line 337 of file Mpi.py.

References [Mpi_finalize\(\)](#), and [Mpi_run\(\)](#).

Referenced by [Mpi_master\(\)](#), and [Mpi_slave\(\)](#).

6.25.3.3 `def irna::iRNA_pred::Mpi::Mpi::Mpi_finalize (self)`

Fin.

Definition at line 358 of file Mpi.py.

References `Mpi_finalize()`.

Referenced by `Mpi_exit_processus()`, `Mpi_finalize()`, and `irna::iRNA_stat::Mpi::Mpi::worker()`.

6.25.3.4 `def irna::iRNA_pred::Mpi::Mpi::Mpi_getComm (self)`

Returns

: Communicator

Definition at line 38 of file Mpi.py.

References `Mpi_getmyrank()`, and `nprocs`.

6.25.3.5 `def irna::iRNA_pred::Mpi::Mpi::Mpi_getmyrank (self)`

Returns

: The rank value

Definition at line 52 of file Mpi.py.

References `Mpi_write_exectime()`, `irna::David2tulip::Node::Node::name`, `irna::David2tulip::Files::Files::name`, and `name`.

Referenced by `Mpi_getComm()`.

6.25.3.6 `def irna::iRNA_pred::Mpi::Mpi::Mpi_getname (self)`

Returns

: The name

Definition at line 59 of file Mpi.py.

Referenced by `Mpi_getnprocs()`.

6.25.3.7 `def irna::iRNA_pred::Mpi::Mpi::Mpi_getnprocs (self)`

Returns

: The number of processor

Definition at line 45 of file Mpi.py.

References `Mpi_getname()`, `irna::iRNA_pred::Files::Files::myrank`, and `myrank`.

6.25.3.8 def irna::iRNA_pred::Mpi::Mpi::Mpi_getSoft (*self*, *soft_list*, *soft_name*)

Test if that soft has already been used.

Parameters

<i>soft_list</i> ,:	List of soft already used
<i>soft_name</i> ,:	Soft name

Returns

: soft file name

Definition at line 235 of file Mpi.py.

References `Mpi_write_data()`.

Referenced by `Mpi_sup_process()`, and `Mpi_write_exectime()`.

6.25.3.9 def irna::iRNA_pred::Mpi::Mpi::Mpi_master (*self*, *soft_list*, *comp_list*, *result_out*, *matrix*, *compair*)

Master process.

Parameters

<i>soft_list</i> ,:	List of soft
<i>comp_list</i> ,:	List of comparison
<i>result_out</i> ,:	Result repertory
<i>matrix</i> ,:	Matrix file
<i>compair</i> ,:	Comparison object

Definition at line 102 of file Mpi.py.

References `Mpi_end_processus()`, `Mpi_exit_processus()`, `Mpi_sup_process()`, `Mpi_write_exectime()`, and `nprocs`.

Referenced by `Mpi_end_processus()`, and `Mpi_write_exectime()`.

6.25.3.10 def irna::iRNA_pred::Mpi::Mpi::Mpi_run (*self*, *predict*, *compair*)

Control [Mpi](#) procedure.

Parameters

<i>predict</i> ,:	List of data for comparison
<i>compair</i> ,:	Comparison object

Definition at line 370 of file Mpi.py.

Referenced by `Mpi_exit_processus()`.

6.25.3.11 `def irna::iRNA_pred::Mpi::Mpi::Mpi_slave (self, result_out, buffer_size, compair)`

Slave process.

Parameters

<i>compair</i> ,:	Comparison object
-------------------	-----------------------------------

Definition at line 272 of file Mpi.py.

References `Mpi_end_processus()`, `Mpi_exit_processus()`, `Mpi_write_data()`, `irna::iRNA_pred::Files::Files::myrank`, `myrank`, and `nprocs`.

Referenced by `Mpi_end_processus()`, and `Mpi_write_data()`.

6.25.3.12 `def irna::iRNA_pred::Mpi::Mpi::Mpi_sup_process (self, status, j, max_comparison)`

Termine les processus supplementaire.

Parameters

<i>status</i> ,:	
<i>j</i> ,:	
<i>max_files</i> ,:	

Definition at line 198 of file Mpi.py.

References `Mpi_getSoft()`.

Referenced by `Mpi_master()`.

6.25.3.13 `def irna::iRNA_pred::Mpi::Mpi::Mpi_write_data (self, result_data, result_out, soft_name, ref, thread, part)`

Write xml result file.

Parameters

<i>result_data</i> ,:	Interact object
<i>result_out</i> ,:	Result repertory
<i>soft_name</i> ,:	Software name
<i>ref</i> ,:	Number of the ref
<i>part</i> ,:	Number of the part

Definition at line 255 of file Mpi.py.

References `Mpi_slave()`.

Referenced by `Mpi_getSoft()`, and `Mpi_slave()`.

6.25.3.14 `def irna::iRNA_pred::Mpi::Mpi::Mpi_write_exectime (self, exec_time, result_out)`

Write exectime of command.

Parameters

<i>exec_time,:</i>	Tab of execution time for each command
<i>result_out,:</i>	Result repertory

Definition at line 68 of file Mpi.py.

References `Mpi_getSoft()`, and `Mpi_master()`.

Referenced by `Mpi_getmyrank()`, and `Mpi_master()`.

6.25.4 Member Data Documentation

6.25.4.1 `irna::iRNA_pred::Mpi::Mpi::comm`

Definition at line 28 of file Mpi.py.

6.25.4.2 `irna::iRNA_pred::Mpi::Mpi::myrank`

Definition at line 28 of file Mpi.py.

Referenced by `Mpi_end_processus()`, `Mpi_getnprocs()`, and `Mpi_slave()`.

6.25.4.3 `irna::iRNA_pred::Mpi::Mpi::name`

Definition at line 28 of file Mpi.py.

Referenced by `Mpi_getmyrank()`.

6.25.4.4 `irna::iRNA_pred::Mpi::Mpi::nprocs`

Definition at line 28 of file Mpi.py.

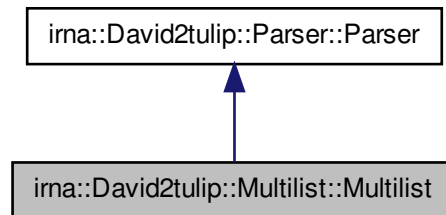
Referenced by `irna::iRNA_stat::Mpi::Mpi::getSendCom()`, `Mpi_getComm()`, `Mpi_master()`, `Mpi_slave()`, and `irna::iRNA_stat::Mpi::Mpi::worker()`.

The documentation for this class was generated from the following file:

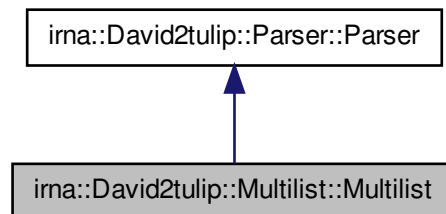
- /home/amine/workspace/iRNA/irna/iRNA_pred/Mpi.py

6.26 irna::David2tulip::Multilist::Multilist Class Reference

Inheritance diagram for irna::David2tulip::Multilist::Multilist:



Collaboration diagram for irna::David2tulip::Multilist::Multilist:



Public Member Functions

- def [__init__](#)
Instanciate multilist object.
- def [getnodelists](#)
Read nodes.
- def [getPosTable](#)
- def [createedges](#)
Create edges.
- def [setdata](#)

- Build the graph.*
- def [getFilter](#)
Parse gene known.
- def [writefilterlist](#)
Write the filtered multilist.
- def [GOfilter](#)
Filter mRNA based on GO-known gene.

Public Attributes

- [multilist_file](#)
- [filtered](#)

6.26.1 Detailed Description

Definition at line 12 of file Multilist.py.

6.26.2 Constructor & Destructor Documentation

6.26.2.1 `def irna::David2tulip::Multilist::Multilist::__init__(self, multilist_file)`

Instantiate multilist object.

Parameters

<i>multilist_file</i> :	Multilist file
-------------------------	--------------------------------

Definition at line 19 of file Multilist.py.

6.26.3 Member Function Documentation

6.26.3.1 `def irna::David2tulip::Multilist::Multilist::createedges (self, header_nodes, tail_nodes)`

Create edges.

Parameters

<i>header_nodes</i> :	list of header nodes
<i>tail_nodes</i> :	list of tail nodes

Returns

: list of edges

Definition at line 100 of file Multilist.py.

References `irna::David2tulip::Parser::Parser::createnodes()`, `irna::David2tulip::Parser::Parser::getlinknode()`, `getnodelists()`, `getPosTable()`, `multilist_file`, and `setdata()`.

Referenced by `getPosTable()`, and `setdata()`.

6.26.3.2 `def irna::David2tulip::Multilist::Multilist::getFilter (self, filter_file)`

Parse gene known.

Parameters

<i>filter_file</i> ,:	GO file
-----------------------	---------

Returns

: List of mRNA known from the GO

Definition at line 155 of file Multilist.py.

References `filtered`, `multilist_file`, and `writefilterlist()`.

Referenced by `setdata()`, and `writefilterlist()`.

6.26.3.3 `def irna::David2tulip::Multilist::Multilist::getnodelists (self)`

Read nodes.

Definition at line 66 of file Multilist.py.

References `getPosTable()`, and `multilist_file`.

Referenced by `createedges()`.

6.26.3.4 `def irna::David2tulip::Multilist::Multilist::getPosTable (self, header_nodes, header)`

Parameters

<i>header_nod</i> ,:	
----------------------	--

Definition at line 85 of file Multilist.py.

References `createedges()`, and `multilist_file`.

Referenced by `createedges()`, and `getnodelists()`.

6.26.3.5 `def irna::David2tulip::Multilist::Multilist::GOfilter (self, filter_file, results)`

Filter mRNA based on GO-known gene.

Parameters

<i>filter_file,:</i>	GO file
<i>results,:</i>	Path to result repertory

Definition at line 198 of file Multilist.py.

Referenced by writefilterlist().

6.26.3.6 `def irna::David2tulip::Multilist::Multilist::setdata (self, node_objects, edge_objects)`

Build the graph.

Parameters

<i>node_ - objects,:</i>	list of node objects
<i>edge_ - objects,:</i>	list of edge objects

Returns

: List of node and edge objects

Definition at line 136 of file Multilist.py.

References createedges(), and getFilter().

Referenced by createedges().

6.26.3.7 `def irna::David2tulip::Multilist::Multilist::writefilterlist (self, go_list, results)`

Write the filtered multilist.

Parameters

<i>go_list,:</i>	List of mRNA known
<i>results,:</i>	Path to result repertory

Definition at line 175 of file Multilist.py.

References filtered, getFilter(), GOfilter(), multilist_file, and writefilterlist().

Referenced by getFilter(), and writefilterlist().

6.26.4 Member Data Documentation

6.26.4.1 `irna::David2tulip::Multilist::Multilist::filtered`

Definition at line 175 of file `Multilist.py`.

Referenced by `getFilter()`, and `writefilterlist()`.

6.26.4.2 `irna::David2tulip::Multilist::Multilist::multilist_file`

Definition at line 19 of file `Multilist.py`.

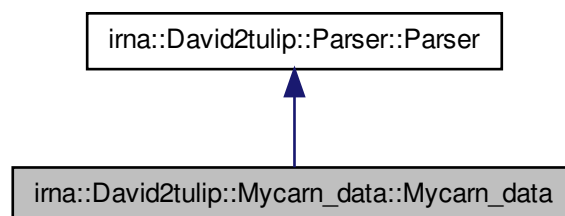
Referenced by `createedges()`, `getFilter()`, `getnodelists()`, `getPosTable()`, and `writefilterlist()`.

The documentation for this class was generated from the following file:

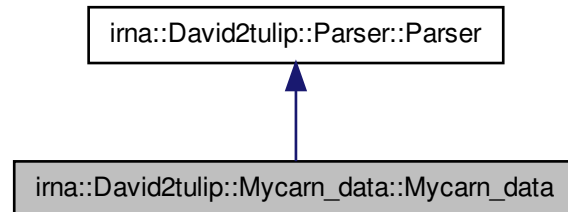
- `/home/amine/workspace/iRNA/irna/David2tulip/Multilist.py`

6.27 `irna::David2tulip::Mycarn_data::Mycarn_data` Class Reference

Inheritance diagram for `irna::David2tulip::Mycarn_data::Mycarn_data`:



Collaboration diagram for irna::David2tulip::Mycarn_data::Mycarn_data:



Public Member Functions

- def `__init__`
Instantiate *pValue* object.
- def `setRNAlength`
Set RNA length.
- def `setdata`
Add Length information to nodes.

Public Attributes

- `dbmanage`

6.27.1 Detailed Description

Definition at line 13 of file `Mycarn_data.py`.

6.27.2 Constructor & Destructor Documentation

6.27.2.1 def `irna::David2tulip::Mycarn_data::Mycarn_data::__init__(self, mycarn_db, fastmode)`

Instantiate *pValue* object.

Parameters

<i>pValue_file</i> ,:	<i>pValue</i> file
-----------------------	--------------------

Definition at line 20 of file Mycarn_data.py.

6.27.3 Member Function Documentation

6.27.3.1 `def irna::David2tulip::Mycarn_data::Mycarn_data::setdata (self, node_objects, edge_objects)`

Add Length information to nodes.

Parameters

<i>node_objects</i> ,:	List of node objects
<i>edge_objects</i> ,:	List of edge objects

Definition at line 43 of file Mycarn_data.py.

References setRNAlength().

Referenced by setRNAlength().

6.27.3.2 `def irna::David2tulip::Mycarn_data::Mycarn_data::setRNAlength (self, type_RNA, node_objects)`

Set RNA length.

Parameters

<i>type_RNA</i> ,:	Type of RNA
<i>node_objects</i> ,:	List of node object

Definition at line 31 of file Mycarn_data.py.

References setdata().

Referenced by setdata().

6.27.4 Member Data Documentation

6.27.4.1 `irna::David2tulip::Mycarn_data::Mycarn_data::dbmanage`

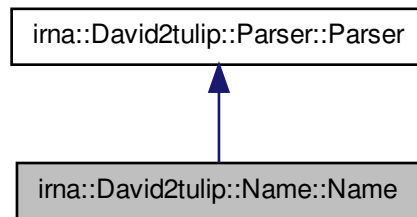
Definition at line 20 of file Mycarn_data.py.

The documentation for this class was generated from the following file:

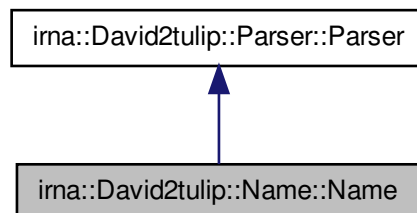
- /home/amine/workspace/iRNA/irna/David2tulip/Mycarn_data.py

6.28 irna::David2tulip::Name::Name Class Reference

Inheritance diagram for irna::David2tulip::Name::Name:



Collaboration diagram for irna::David2tulip::Name::Name:



Public Member Functions

- def [__init__](#)
Instantiate name parser object.
- def [setdata](#)
Add sRNA - sRNA edges based on their similarity.

Public Attributes

- [name_file](#)

6.28.1 Detailed Description

Definition at line 11 of file Name.py.

6.28.2 Constructor & Destructor Documentation

6.28.2.1 `def irna::David2tulip::Name::Name::__init__(self, name_file)`

Instantiate name parser object.

Parameters

<i>name_file</i> ,:	Name file
---------------------	---------------------------

Definition at line 18 of file Name.py.

6.28.3 Member Function Documentation

6.28.3.1 `def irna::David2tulip::Name::Name::setdata (self, node_objects, edge_objects)`

Add sRNA - sRNA edges based on their similarity.

Parameters

<i>node_objects</i> ,:	list of node objects
<i>edge_objects</i> ,:	list of edge objects

Definition at line 28 of file Name.py.

References `irna::David2tulip::Parser::Parser::getlinknode()`, and `name_file`.

6.28.4 Member Data Documentation

6.28.4.1 `irna::David2tulip::Name::Name::name_file`

Definition at line 18 of file Name.py.

Referenced by `setdata()`.

The documentation for this class was generated from the following file:

- `/home/amine/workspace/iRNA/irna/David2tulip/Name.py`

6.29 irna::David2tulip::Node::Node Class Reference

: Handle RNA information

Public Member Functions

- def `__init__`
Instantiate [Node](#) object.
- def `addgroupelement`
Add a group element.
- def `setuniquegroup`
Set unique element in the group.
- def `printgroupdata`
Print group data.
- def `println`
Print object values.
- def `__cmp__`
General method to compare node based on the name.

Public Attributes

- `name`
- `code`
- `gender`
- `num`
- `group`
- `length`

6.29.1 Detailed Description

: Handle RNA information

Author

: Amine Ghozlane

Version

: 1.0

Definition at line 7 of file Node.py.

6.29.2 Constructor & Destructor Documentation

6.29.2.1 `def irna::David2tulip::Node::Node::__init__(self, name, gender, num)`

Instantiate [Node](#) object.

Parameters

<i>name</i> ,:	Name of the node
<i>gender</i> ,:	Gender of the node
<i>num</i> ,:	Num of the node

Definition at line 16 of file Node.py.

6.29.3 Member Function Documentation

6.29.3.1 `def irna::David2tulip::Node::Node::__cmp__(self, other)`

General method to compare node based on the name.

Parameters

<i>other</i> ,:	Compared value
-----------------	----------------

Definition at line 63 of file Node.py.

Referenced by `printgroupdata()`.

6.29.3.2 `def irna::David2tulip::Node::Node::addgroupelement (self, numgroup)`

Add a group element.

Parameters

<i>numgroup</i> ,:	Number of a group
--------------------	-------------------

Definition at line 31 of file Node.py.

References `group`, `printgroupdata()`, and `setuniquegroup()`.

6.29.3.3 `def irna::David2tulip::Node::Node::printgroupdata (self)`

Print group data.

Definition at line 45 of file Node.py.

References `__cmp__()`, `code`, `gender`, `length`, `irna::David2tulip::Files::Files::name`, `name`, `num`, `printgroupdata()`, and `println()`.

Referenced by `addgroupelement()`, and `printgroupdata()`.

6.29.3.4 `def irna::David2tulip::Node::Node::println (self)`

Print object values.

Definition at line 55 of file Node.py.

References `irna::David2tulip::Files::Files::name`, and `name`.

Referenced by `printgroupdata()`.

6.29.3.5 `def irna::David2tulip::Node::Node::setuniquegroup (self)`

Set unique element in the group.

Definition at line 38 of file Node.py.

References `group`, and `setuniquegroup()`.

Referenced by `addgroupelement()`, and `setuniquegroup()`.

6.29.4 Member Data Documentation**6.29.4.1** `irna::David2tulip::Node::Node::code`

Definition at line 16 of file Node.py.

Referenced by `printgroupdata()`.

6.29.4.2 `irna::David2tulip::Node::Node::gender`

Definition at line 16 of file Node.py.

Referenced by `printgroupdata()`.

6.29.4.3 `irna::David2tulip::Node::Node::group`

Definition at line 16 of file Node.py.

Referenced by `addgroupelement()`, and `setuniquegroup()`.

6.29.4.4 `irna::David2tulip::Node::Node::length`

Definition at line 16 of file Node.py.

Referenced by `printgroupdata()`.

6.29.4.5 `irna::David2tulip::Node::Node::name`

Definition at line 16 of file Node.py.

Referenced by `irna::iRNA_pred::Mpi::Mpi::Mpi_getmyrank()`, `printgroupdata()`, and `println()`.

6.29.4.6 `irna::David2tulip::Node::Node::num`

Definition at line 16 of file `Node.py`.

Referenced by `printgroupdata()`.

The documentation for this class was generated from the following file:

- `/home/amine/workspace/iRNA/irna/David2tulip/Node.py`

6.30 `irna::iRNA_stat::NormScore::NormScore` Class Reference

Public Member Functions

- `def __init__`
Instantiate `NormScore` object.
- `def defnormfunction`
Determine the function to apply depending on the type of software.
- `def normSeveralScore`
Compute normalised score in several score context.
- `def normSeveralEnergy`
Compute normalised energy in several energy context.
- `def normSeveralContactScore`
Compute normalised energy in several energy context.
- `def normUniqueSolution`
Compute normalised score/energy in several contact context.
- `def run`
Compute normalized score.

Public Attributes

- `normfuncmap`
- `interactions`
- `type_sol`
- `score_type`
- `dbmanage`
- `norm_score`
- `pos`

6.30.1 Detailed Description

Definition at line 11 of file `NormScore.py`.

6.30.2 Constructor & Destructor Documentation

6.30.2.1 `def irna::iRNA_stat::NormScore::NormScore::__init__(self, data, dbmanage)`

Instantiate [NormScore](#) object.

Parameters

<i>data</i> ,:	Communication object
<i>dbmanage</i> ,:	Access to the database

Definition at line 19 of file NormScore.py.

6.30.3 Member Function Documentation

6.30.3.1 `def irna::iRNA_stat::NormScore::NormScore::defnormfunction (self)`

Determine the function to apply depending on the type of software.

Definition at line 30 of file NormScore.py.

References [normfuncmap](#), [normSeveralScore\(\)](#), [irna::iRNA_stat::Interaction::Interaction::pos](#), [irna::iRNA_stat::Computer::Computer::pos](#), [pos](#), [type_sol](#), [irna::iRNA_stat::Interaction::Interaction::type_sol](#), and [irna::iRNA_stat::Computer::Computer::type_sol](#).

Referenced by [run\(\)](#).

6.30.3.2 `def irna::iRNA_stat::NormScore::NormScore::normSeveralContactScore (self, score, loglen, score_type, i)`

Compute normalised energy in several energy context.

Parameters

<i>score</i> ,:	Score
<i>loglen</i> ,:	Log length value
<i>score_type</i> ,:	Type of score
<i>i</i> ,:	Position in the tab

Definition at line 75 of file NormScore.py.

References [irna::iRNA_stat::Computer::Computer::norm_score](#), [norm_score](#), [irna::iRNA_stat::Interaction::Interaction::pos](#), [irna::iRNA_stat::Computer::Computer::pos](#), [pos](#), and [run\(\)](#).

Referenced by [normSeveralEnergy\(\)](#).

6.30.3.3 `def irna::iRNA_stat::NormScore::NormScore::normSeveralEnergy (self, score, loglen, score_type, i)`

Compute normalised energy in several energy context.

Parameters

<i>score</i> ,:	Score
<i>loglen</i> ,:	Log length value
<i>score_type</i> ,:	Type of score
<i>i</i> ,:	Position in the tab

Definition at line 58 of file NormScore.py.

References `irna::iRNA_stat::Computer::Computer::norm_score`, `norm_score`, `normSeveralContactScore()`, `normUniqueSolution()`, `irna::iRNA_stat::Interaction::Interaction::pos`, `irna::iRNA_stat::Computer::Computer::pos`, and `pos`.

Referenced by `normSeveralScore()`.

6.30.3.4 `def irna::iRNA_stat::NormScore::NormScore::normSeveralScore (self, score, loglen, score_type, i)`

Compute normalised score in several score context.

Parameters

<i>score</i> ,:	Score
<i>loglen</i> ,:	Log length value
<i>score_type</i> ,:	Type of score
<i>i</i> ,:	Position in the tab

Definition at line 44 of file NormScore.py.

References `irna::iRNA_stat::Computer::Computer::norm_score`, `norm_score`, `normSeveralEnergy()`, `irna::iRNA_stat::Interaction::Interaction::pos`, `irna::iRNA_stat::Computer::Computer::pos`, and `pos`.

Referenced by `defnormfunction()`.

6.30.3.5 `def irna::iRNA_stat::NormScore::NormScore::normUniqueSolution (self, score, loglen, score_type, i)`

Compute normalised score/energy in several contact context.

Parameters

<i>score</i> ,:	Score
<i>loglen</i> ,:	Log length value
<i>score_type</i> ,:	Type of score
<i>i</i> ,:	Position in the tab

Definition at line 88 of file NormScore.py.

References `interactions`, `irna::iRNA_stat::Interaction::Interaction::interactions`, `irna::iRNA_stat::Computer::Computer::interactions`, `irna::iRNA_stat::Computer::Computer::norm_score`, `norm_score`, `irna::iRNA_stat::Interaction::Interaction::pos`, `irna::iRNA_stat::Computer::Computer::pos`, and `pos`.

Referenced by `normSeveralEnergy()`.

6.30.3.6 def irna::iRNA_stat::NormScore::NormScore::run (self)

Compute normalized score.

Definition at line 97 of file NormScore.py.

References `defnormfunction()`, `interactions`, `irna::iRNA_stat::Interaction::Interaction::interactions`, `irna::iRNA_stat::Computer::Computer::interactions`, `irna::iRNA_stat::Computer::Computer::norm_score`, `norm_score`, `irna::iRNA_stat::Interaction::Interaction::pos`, `irna::iRNA_stat::Computer::Computer::pos`, `pos`, `score_type`, and `irna::iRNA_stat::Computer::Computer::score_type`.

Referenced by `normSeveralContactScore()`.

6.30.4 Member Data Documentation

6.30.4.1 irna::iRNA_stat::NormScore::NormScore::dbmanage

Definition at line 19 of file NormScore.py.

6.30.4.2 irna::iRNA_stat::NormScore::NormScore::interactions

Definition at line 19 of file NormScore.py.

Referenced by `normUniqueSolution()`, `irna::iRNA_stat::pValue::pValue::run()`, and `run()`.

6.30.4.3 irna::iRNA_stat::NormScore::NormScore::norm_score

Definition at line 97 of file NormScore.py.

Referenced by `irna::iRNA_stat::Regression::Regression::ecdf_estimate()`, `irna::iRNA_stat::Regression::Regression::linear_regression()`, `normSeveralContactScore()`, `normSeveralEnergy()`, `normSeveralScore()`, `normUniqueSolution()`, `irna::iRNA_stat::pValue::pValue::run()`, and `run()`.

6.30.4.4 irna::iRNA_stat::NormScore::NormScore::normfuncmap

Definition at line 19 of file NormScore.py.

Referenced by `defnormfunction()`.

6.30.4.5 `irna::iRNA_stat::NormScore::NormScore::pos`

Definition at line 97 of file NormScore.py.

Referenced by `defnormfunction()`, `normSeveralContactScore()`, `normSeveralEnergy()`, `normSeveralScore()`, `normUniqueSolution()`, and `run()`.

6.30.4.6 `irna::iRNA_stat::NormScore::NormScore::score_type`

Definition at line 19 of file NormScore.py.

Referenced by `run()`.

6.30.4.7 `irna::iRNA_stat::NormScore::NormScore::type_sol`

Definition at line 19 of file NormScore.py.

Referenced by `defnormfunction()`.

The documentation for this class was generated from the following file:

- `/home/amine/workspace/iRNA/irna/iRNA_stat/NormScore.py`

6.31 `irna::iRNA_pred::Parse::Parse` Class Reference

: [Parse](#) data from the different software.

Public Member Functions

- def [parseGoogle](#)
Parse Google result.
- def [parseIntaRNA](#)
Parse IntaRNA result.
- def [parseRNAup](#)
Parse RNAup result.
- def [parseRNAplex](#)
Parse RNAplex and RNAduplex result.
- def [parseRNAduplex](#)
Parse RNAplex and RNAduplex result.
- def [getposition_RNAfold0](#)
Get the position of interaction for RNAfold.
- def [getposition_RNAfold1](#)
Get the position of interaction for RNAfold.
- def [reverseElongate](#)
Get a double reverse for a tab of tab.

- def [forwardTable](#)
Reverse a table.
- def [parseRNAcofold](#)
Parse RNAcofold result.
- def [getResultSequence_RNAhybrid](#)
Get contact sequence.
- def [parseRNAhybrid](#)
Parse RNAhybrid result.
- def [getPositions_rip](#)
Get the positions for rip problem output.
- def [elongatePositions_rip](#)
Elongate the contact position.
- def [getSequences_53](#)
Get the sequence in contact in 5'3' sense.
- def [getSequences_local_reversed](#)
Get the sequence in contact in 5'3' sense.
- def [consensus](#)
Find the contact position between sRNA and mRNA.
- def [reverseSequence](#)
Reverse a sequence.
- def [reverseTablemax](#)
Reverse a table.
- def [reverseMinTable](#)
Reverse a table into 5'3'.
- def [parseRactip](#)
Parse Ractip result.
- def [readCompfile](#)
Read the comp_list file.
- def [comparaison](#)
Determine if comparison is needed.
- def [parseBlastall](#)
Parse Blastall result.
- def [parseBistaRNA](#)
Parse BistaRNA result.
- def [parseYass](#)
Parse Yass output.
- def [parseSsearch](#)
Parse ssearch output.
- def [parsePairfold](#)
Parse Pairfold result.
- def [runParsing](#)
Run the parsing.

6.31.1 Detailed Description

: [Parse](#) data from the different software.

Definition at line 14 of file Parse.py.

6.31.2 Member Function Documentation

6.31.2.1 `def irna::iRNA_pred::Parse::Parse::comparaison (self, mRNA, sRNA, comp_data)`

Determine if comparison is needed.

Parameters

<i>mRNA</i> ,:	mRNA name
<i>sRNA</i> ,:	sRNA name
<i>comp_data</i> ,:	Comparison data

Returns

: True if comparison is expected, False otherwise

Definition at line 705 of file Parse.py.

References `comparaison()`.

Referenced by `comparaison()`, `parseRactip()`, and `parseYass()`.

6.31.2.2 `def irna::iRNA_pred::Parse::Parse::consensus (self, resultsRNA, resultmRNA, tab_sRNA, tab_mRNA, debutsRNA, debutmRNA, i, j)`

Find the contact position between sRNA and mRNA.

Parameters

<i>resultsRNA</i> ,:	New table of contact for sRNA
<i>resultmRNA</i> ,:	New table of contact for mRNA
<i>tab_sRNA</i> ,:	Old table of contact for sRNA
<i>tab_mRNA</i> ,:	Old table of contact for mRNA
<i>debutsRNA</i> ,:	sRNA begin
<i>debutmRNA</i> ,:	mRNA begin
<i>i</i> ,:	Position in the old table of sRNA
<i>j</i> ,:	Position in the old table of mRNA

Definition at line 511 of file Parse.py.

References `consensus()`, `reverseMinTable()`, `reverseSequence()`, and `reverseTablemax()`.

Referenced by consensus(), getSequences_53(), parseBistaRNA(), parseRactip(), parseRNAcofold(), parseRNAhybrid(), and parseSsearch().

6.31.2.3 def irna::iRNA_pred::Parse::Parse::elongatePositions_rip (*self*, *tab*)

Elongate the contact position.

Parameters

<i>tab</i> ,:	Table of contact position
---------------	---------------------------

Returns

: Table elongate

Definition at line 452 of file Parse.py.

References getSequences_53(), and getSequences_local_reversed().

Referenced by parseBistaRNA(), parseRactip(), parseRNAcofold(), parseRNAhybrid(), and parseSsearch().

6.31.2.4 def irna::iRNA_pred::Parse::Parse::forwardTable (*self*, *tab_RNA*)

Reverse a table.

Parameters

<i>tab_RNA</i> ,:	Table of RNA
-------------------	--------------

Returns

: Reversed table

Definition at line 269 of file Parse.py.

Referenced by getposition_RNAcofold1(), parseRNAcofold(), and parseSsearch().

6.31.2.5 def irna::iRNA_pred::Parse::Parse::getposition_RNAcofold0 (*self*, *result*)

Get the position of interaction for RNAcofold.

Parameters

<i>result</i> ,:	sRNA result
------------------	-------------

Returns

: tabmRNA, tabsRNA

Definition at line 219 of file Parse.py.

References `getPosition_RNAfold1()`.

Referenced by `parseRNAfold()`, `parseRNA duplex()`, and `parseSsearch()`.

6.31.2.6 `def irna::iRNA_pred::Parse::Parse::getPosition_RNAfold1 (self, result)`

Get the position of interaction for RNAfold.

Parameters

<i>result</i> ,:	mRNA result
------------------	-------------

Returns

: tabmRNA, tabsRNA

Definition at line 235 of file Parse.py.

References `forwardTable()`, and `reverseElongate()`.

Referenced by `getPosition_RNAfold0()`, `parseRNAfold()`, and `parseSsearch()`.

6.31.2.7 `def irna::iRNA_pred::Parse::Parse::getPositions_rip (self, RNA_r, seq)`

Get the positions for rip problem output.

Parameters

<i>RNA_r</i> ,:	RNA result output
-----------------	-------------------

Returns

: Position of contact for RNA

Definition at line 438 of file Parse.py.

Referenced by `parseBistaRNA()`, `parseRactip()`, and `parseRNAhybrid()`.

6.31.2.8 `def irna::iRNA_pred::Parse::Parse::getResultSequence_RNAhybrid (self, out_RNA, in_RNA, RNA_begin, length_RNA, int_char)`

Get contact sequence.

Parameters

<i>out_RNA</i> ,:	Non contact nucleotid
<i>in_RNA</i> ,:	Contact nucleotid
<i>RNA_begin</i> ,:	Begining position of the RNA
<i>length_RNA</i> ,:	Length of the RNA sequence
<i>int_char</i> ,:	Interaction character

Definition at line 339 of file Parse.py.

References `parseRNAhybrid()`.

Referenced by `parseRNAcofold()`, and `parseRNAhybrid()`.

6.31.2.9 def irna::iRNA_pred::Parse::Parse::getSequences_53 (*self*, *RNA*, *tab_RNA*)

Get the sequence in contact in 5'3' sense.

Parameters

<i>RNA</i> ,:	RNA sequence
<i>tab_RNA</i> ,:	Position of contact for RNA

Returns

: RNA tab of contact sequences

Definition at line 477 of file Parse.py.

References `consensus()`, and `reverseSequence()`.

Referenced by `elongatePositions_rip()`, `parseBistaRNA()`, and `parseRactip()`.

6.31.2.10 def irna::iRNA_pred::Parse::Parse::getSequences_local_reversed (*self*, *RNA*)

Get the sequence in contact in 5'3' sense.

Parameters

<i>RNA</i> ,:	RNA sequence
---------------	--------------

Returns

: RNA tab of contact sequences

Definition at line 491 of file Parse.py.

Referenced by `elongatePositions_rip()`.

6.31.2.11 `def irna::iRNA_pred::Parse::Parse::parseBistaRNA (self, data, matrix, root)`

[Parse](#) BistaRNA result.

Parameters

<i>data,:</i>	Soft result
<i>matrix,:</i>	score matrix
<i>root,:</i>	xml root node

Definition at line 766 of file Parse.py.

References `consensus()`, `elongatePositions_rip()`, `getPositions_rip()`, `getSequences_53()`, `parseSsearch()`, and `parseYass()`.

Referenced by `parseBlastall()`, and `runParsing()`.

6.31.2.12 `def irna::iRNA_pred::Parse::Parse::parseBlastall (self, data, matrix, root, complist_file)`

[Parse](#) Blastall result.

Parameters

<i>data,:</i>	Soft result
<i>matrix,:</i>	score matrix
<i>root,:</i>	xml root node
<i>complist_file,:</i>	Comparison list file

Definition at line 721 of file Parse.py.

References `parseBistaRNA()`.

Referenced by `readCompfile()`, and `runParsing()`.

6.31.2.13 `def irna::iRNA_pred::Parse::Parse::parseGuugle (self, data, matrix, root)`

[Parse](#) Guugle result.

Parameters

<i>data,:</i>	result
<i>matrix,:</i>	score matrix
<i>root,:</i>	xml root node

Definition at line 22 of file Parse.py.

References `parseIntaRNA()`.

Referenced by `parsePairfold()`.

6.31.2.14 `def irna::iRNA_pred::Parse::Parse::parseIntaRNA (self, data, matrix, root)`

[Parse](#) IntaRNA result.

Parameters

<i>data</i> ,:	Soft result
<i>matrix</i> ,:	score matrix
<i>root</i> ,:	xml root node

Definition at line 109 of file Parse.py.

References `parseRNAup()`.

Referenced by `parseGuugle()`, and `parsePairfold()`.

6.31.2.15 `def irna::iRNA_pred::Parse::Parse::parsePairfold (self, data, matrix, root)`

[Parse](#) Pairfold result.

Parameters

<i>data</i> ,:	Soft result
<i>matrix</i> ,:	score matrix
<i>root</i> ,:	xml root node

Definition at line 892 of file Parse.py.

References `parseGuugle()`, `parseIntaRNA()`, `parseRNAcofold()`, `parseRNAduplex()`, `parseRNAplex()`, `parseRNAup()`, `reverseTablemax()`, and `runParsing()`.

Referenced by `parseSsearch()`, and `runParsing()`.

6.31.2.16 `def irna::iRNA_pred::Parse::Parse::parseRactip (self, data, matrix, root)`

[Parse](#) Ractip result.

Parameters

<i>data</i> ,:	Soft result
<i>matrix</i> ,:	score matrix
<i>root</i> ,:	xml root node

Definition at line 619 of file Parse.py.

References `comparaison()`, `consensus()`, `elongatePositions_rip()`, `getPositions_rip()`, `getSequences_53()`, `readCompfile()`, `reverseSequence()`, and `reverseTablemax()`.

Referenced by `reverseSequence()`, and `runParsing()`.

6.31.2.17 `def irna::iRNA_pred::Parse::Parse::parseRNAcofold (self, data, matrix, root)`

[Parse](#) RNAcofold result.

Parameters

<i>data</i> ,:	Soft result
<i>matrix</i> ,:	score matrix
<i>root</i> ,:	xml root node

Definition at line 283 of file Parse.py.

References `consensus()`, `elongatePositions_rip()`, `forwardTable()`, `getPosition_RNAcofold0()`, `getPosition_RNAcofold1()`, `getResultSequence_RNAhybrid()`, `reverseElongate()`, and `reverseTablemax()`.

Referenced by `parsePairfold()`, and `reverseElongate()`.

6.31.2.18 `def irna::iRNA_pred::Parse::Parse::parseRNAduplex (self, data, matrix, root)`

[Parse](#) RNAplex and RNAduplex result.

Parameters

<i>data</i> ,:	Soft result
<i>matrix</i> ,:	score matrix
<i>root</i> ,:	xml root node

Definition at line 200 of file Parse.py.

References `getPosition_RNAcofold0()`.

Referenced by `parsePairfold()`, and `parseRNAplex()`.

6.31.2.19 `def irna::iRNA_pred::Parse::Parse::parseRNAhybrid (self, data, matrix, root)`

[Parse](#) RNAhybrid result.

Parameters

<i>data</i> ,:	Soft result
<i>matrix</i> ,:	score matrix
<i>root</i> ,:	xml root node

Definition at line 365 of file Parse.py.

References `consensus()`, `elongatePositions_rip()`, `getPosition_rip()`, `getResultSequence_RNAhybrid()`, and `reverseTablemax()`.

Referenced by `getResultSequence_RNAhybrid()`, and `runParsing()`.

6.31.2.20 `def irna::iRNA_pred::Parse::Parse::parseRNAplex (self, data, matrix, root)`

[Parse](#) RNAplex and RNAduplex result.

Parameters

<i>data,:</i>	Soft result
<i>matrix,:</i>	score matrix
<i>root,:</i>	xml root node

Definition at line 180 of file Parse.py.

References `parseRNAduplex()`.

Referenced by `parsePairfold()`, and `parseRNAup()`.

6.31.2.21 `def irna::iRNA_pred::Parse::Parse::parseRNAup (self, data, matrix, root)`

[Parse](#) RNAup result.

Parameters

<i>data,:</i>	Soft result
<i>matrix,:</i>	score matrix
<i>root,:</i>	xml root node

Definition at line 152 of file Parse.py.

References `parseRNAplex()`.

Referenced by `parseIntaRNA()`, and `parsePairfold()`.

6.31.2.22 `def irna::iRNA_pred::Parse::Parse::parseSsearch (self, data, sRNA, matrix, root, complist_file)`

[Parse](#) ssearch output.

Parameters

<i>data,:</i>	Soft result
<i>sRNA,:</i>	sRNA name
<i>matrix,:</i>	score matrix
<i>root,:</i>	xml root node
<i>complist_file,:</i>	Comparison list file

Definition at line 851 of file Parse.py.

References `consensus()`, `elongatePositions_rip()`, `forwardTable()`, `getposition_RNAcofold0()`, `getposition_RNAcofold1()`, `parsePairfold()`, and `reverseElongate()`.

Referenced by `parseBistaRNA()`, and `runParsing()`.

```
6.31.2.23 def irna::iRNA_pred::Parse::Parse::parseYass ( self, data, matrix, root,
               complist_file )
```

[Parse](#) Yass output.

Parameters

<i>data</i> ,:	Soft result
<i>matrix</i> ,:	score matrix
<i>root</i> ,:	xml root node
<i>complist_file</i> ,:	Comparison list file

Definition at line 826 of file `Parse.py`.

References `comparaison()`, and `readCompfile()`.

Referenced by `parseBistaRNA()`, and `runParsing()`.

```
6.31.2.24 def irna::iRNA_pred::Parse::Parse::readCompfile ( self, complist_file )
```

Read the `comp_list` file.

Parameters

<i>complist_file</i> ,:	Comparison list file
-------------------------	--------------------------------------

Returns

: [Comparison](#) data

Definition at line 678 of file `Parse.py`.

References `parseBlastall()`, and `readCompfile()`.

Referenced by `parseRactip()`, `parseYass()`, and `readCompfile()`.

```
6.31.2.25 def irna::iRNA_pred::Parse::Parse::reverseElongate ( self, tab )
```

Get a double reverse for a tab of `tab`.

Parameters

<i>tab</i> ,:	Table of table
---------------	----------------

Returns

: Reversed table of table

Definition at line 255 of file Parse.py.

References parseRNAcofold().

Referenced by getposition_RNAcofold1(), parseRNAcofold(), and parseSsearch().

6.31.2.26 `def irna::iRNA_pred::Parse::Parse::reverseMinTable (self, tab_RNA)`

Reverse a table into 5'3'.

Parameters

<i>tab_RNA</i> ,:	Table of RNA
-------------------	--------------

Returns

: Reversed table

Definition at line 605 of file Parse.py.

Referenced by consensus().

6.31.2.27 `def irna::iRNA_pred::Parse::Parse::reverseSequence (self, seq)`

Reverse a sequence.

Parameters

<i>seq</i> ,:	Sequence of text
---------------	------------------

Returns

: Reversed sequence

Definition at line 582 of file Parse.py.

References parseRactip().

Referenced by consensus(), getSequences_53(), and parseRactip().

6.31.2.28 `def irna::iRNA_pred::Parse::Parse::reverseTablemax (self, tab_RNA, maxValue)`

Reverse a table.

Parameters

<i>tab_RNA</i> ,:	Table of RNA
-------------------	--------------

Returns

: Reversed table

Definition at line 593 of file Parse.py.

Referenced by consensus(), parsePairfold(), parseRactip(), parseRNAcofold(), and parseRNAhybrid().

```
6.31.2.29 def irna::iRNA_pred::Parse::Parse::runParsing ( self, soft_name, matrix,
               complist_file, sRNA, mRNA, data, root )
```

Run the parsing.

Parameters

<i>cmd,:</i>	Soft command
<i>complist_ - file,:</i>	Comparison list file
<i>data,:</i>	Soft result

Definition at line 935 of file Parse.py.

References parseBistaRNA(), parseBlastall(), parsePairfold(), parseRactip(), parseRNAhybrid(), parseSsearch(), and parseYass().

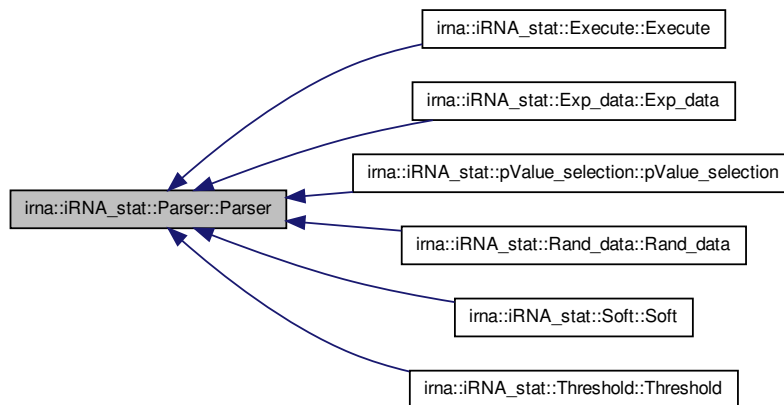
Referenced by parsePairfold().

The documentation for this class was generated from the following file:

- /home/amine/workspace/iRNA/irna/iRNA_pred/[Parse.py](#)

6.32 ima::iRNA_stat::Parser::Parser Class Reference

Inheritance diagram for ima::iRNA_stat::Parser::Parser:



Public Member Functions

- def [__init__](#)
Instantiate [Parser](#) object.
- def [sortdict](#)
Sort the dictionary.
- def [getData](#)
Search name in input list.
- def [getUnique](#)
Get unique data.

6.32.1 Detailed Description

Definition at line 10 of file Parser.py.

6.32.2 Constructor & Destructor Documentation

6.32.2.1 def ima::iRNA_stat::Parser::Parser::__init__(self)

Instantiate [Parser](#) object.

Definition at line 16 of file Parser.py.

6.32.3 Member Function Documentation

6.32.3.1 `def irna::iRNA_stat::Parser::Parser::getData (self, input_list, name)`

Search name in input list.

Parameters

<i>input_list,:</i>	List
<i>name,:</i>	Search criteria

Definition at line 34 of file Parser.py.

References `getUnique()`.

Referenced by `irna::iRNA_stat::Rand_data::Rand_data::getAllSofts()`, and `sortdict()`.

6.32.3.2 `def irna::iRNA_stat::Parser::Parser::getUnique (self, data_list)`

Get unique data.

Parameters

<i>data_list,:</i>	list of data
--------------------	--------------

Definition at line 46 of file Parser.py.

Referenced by `irna::iRNA_stat::pValue_selection::pValue_selection::compute_Davidmatrix()`, and `getData()`.

6.32.3.3 `def irna::iRNA_stat::Parser::Parser::sortdict (self, dictionnary, criteria)`

Sort the dictionnary.

Parameters

<i>dictionnary,:</i>	Dictionnary list
<i>criteria,:</i>	Sort criteria

Definition at line 25 of file Parser.py.

References `getData()`.

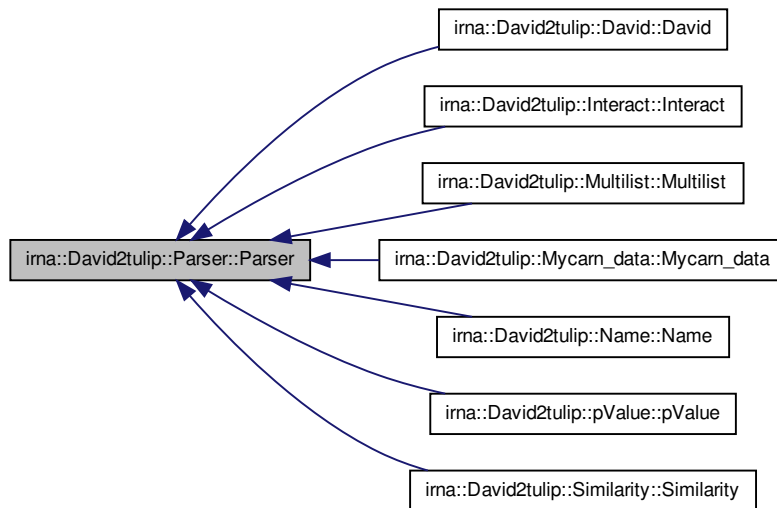
Referenced by `irna::iRNA_stat::pValue_selection::pValue_selection::compute_Davidmatrix()`, and `irna::iRNA_stat::pValue_selection::pValue_selection::compute_similarity()`.

The documentation for this class was generated from the following file:

- `/home/amine/workspace/iRNA/irna/iRNA_stat/Parser.py`

6.33 ima::David2tulip::Parser::Parser Class Reference

Inheritance diagram for ima::David2tulip::Parser::Parser:



Public Member Functions

- def `__init__`
 Instantiate *Parser* object.
- def `createnodes`
 Create the list of nodes.
- def `addelements`
 Add an element in list of objects.
- def `getlinknode`
 Get a node based on its name.
- def `getlinkedge`
- def `getsRNA`
 Get list of sRNA.
- def `getTarget`
 Get targets of one sRNA if category.
- def `loadObject`
 Load object.
- def `printObject`
 Write object.

6.33.1 Detailed Description

Definition at line 11 of file Parser.py.

6.33.2 Constructor & Destructor Documentation

6.33.2.1 `def irna::David2tulip::Parser::Parser::__init__(self)`

Instantiate [Parser](#) object.

Definition at line 17 of file Parser.py.

6.33.3 Member Function Documentation

6.33.3.1 `def irna::David2tulip::Parser::Parser::addelements (self, list_objects, element)`

Add an element in list of objects.

Parameters

<i>list_objects,:</i>	list of objects
<i>element,:</i>	object

Definition at line 44 of file Parser.py.

References [getlinknode\(\)](#).

Referenced by [createnodes\(\)](#), and [irna::David2tulip::Similarity::Similarity::setdata\(\)](#).

6.33.3.2 `def irna::David2tulip::Parser::Parser::createnodes (self, list_element, gender, number)`

Create the list of nodes.

Parameters

<i>list - element,:</i>	
<i>gender,:</i>	Gender of the list

Returns

: list of nodes

Definition at line 27 of file Parser.py.

References [addelements\(\)](#).

Referenced by [irna::David2tulip::Multilist::Multilist::createedges\(\)](#).


```
6.33.3.3 def irna::David2tulip::Parser::Parser::getlinkededge ( self, edge_objects, sRNA, mRNA )
```

Parameters

<i>edge_objects,:</i>	List of edge objects
<i>sRNA,:</i>	sRNA
<i>mRNA,:</i>	mRNA

Definition at line 68 of file Parser.py.

References getsRNA(), and getTarget().

Referenced by getlinknode(), irna::David2tulip::Interact::Interact::setdata(), irna::David2tulip::pValue::pValue::setdata(), and irna::David2tulip::David::David::writefile().

```
6.33.3.4 def irna::David2tulip::Parser::Parser::getlinknode ( self, node_objects, name )
```

Get a node based on its name.

Parameters

<i>node_objects,:</i>	List of node objects
<i>name,:</i>	Name of searched object

Returns

: node

Definition at line 55 of file Parser.py.

References getlinkededge().

Referenced by addelements(), irna::David2tulip::Multilist::Multilist::createedges(), irna::David2tulip::Similarity::Similarity::setdata(), and irna::David2tulip::Name::Name::setdata().

```
6.33.3.5 def irna::David2tulip::Parser::Parser::getsRNA ( self, node_objects )
```

Get list of sRNA.

Parameters

<i>node_objects,:</i>	List of node objects
-----------------------	----------------------

Returns

: List of sRNA

Definition at line 82 of file Parser.py.

References loadObject().

Referenced by irna::David2tulip::David::David::analysis(), and getlinkededge().

6.33.3.6 `def irna::David2tulip::Parser::Parser::getTarget (self, sRNA, edge_objects)`

Get targets of one sRNA if category.

Parameters

<i>sRNA</i> ,:	sRNA name
<i>edge_</i> - <i>objects</i> ,:	List of edge objects

Definition at line 91 of file Parser.py.

Referenced by irna::David2tulip::David::David::analysis(), and getlinkededge().

6.33.3.7 `def irna::David2tulip::Parser::Parser::loadObject (self, pickledump)`

Load object.

Parameters

<i>pickledump</i> ,:	Filename
----------------------	----------

Returns

: Object loaded

Definition at line 100 of file Parser.py.

References printObject().

Referenced by getsRNA().

6.33.3.8 `def irna::David2tulip::Parser::Parser::printObject (self, obj, pickledump)`

Write object.

Parameters

<i>obj</i> ,:	Object to dump
<i>pickledump</i> ,:	Filename

Definition at line 117 of file Parser.py.

Referenced by loadObject(), and irna::David2tulip::David::David::parseChart().

The documentation for this class was generated from the following file:

- [/home/amine/workspace/iRNA/irna/David2tulip/Parser.py](#)

6.34 irna::iRNA_stat::Pickling::Pickling Class Reference

Public Member Functions

- def [__init__](#)
Instantiate [Pickling](#) object.
- def [loadobj](#)
Load the pickling object of the software result.
- def [saveobj](#)
Pickle the object.

Public Attributes

- [path](#)

6.34.1 Detailed Description

Definition at line 10 of file Pickling.py.

6.34.2 Constructor & Destructor Documentation

6.34.2.1 def irna::iRNA_stat::Pickling::Pickling::__init__(self, path)

Instantiate [Pickling](#) object.

Parameters

<i>path,</i>	Path of pickling object
--------------	-------------------------

Definition at line 17 of file Pickling.py.

6.34.3 Member Function Documentation

6.34.3.1 def irna::iRNA_stat::Pickling::Pickling::loadobj(self, name, num)

Load the pickling object of the software result.

Parameters

<i>name</i> ,:	Name of the software
<i>num</i> ,:	Software id

Definition at line 26 of file Pickling.py.

References path, and saveobj().

6.34.3.2 `def irna::iRNA_stat::Pickling::Pickling::saveobj (self, obj, name, num)`

Pickle the object.

Parameters

<i>obj</i> ,:	Computed object
<i>name</i> ,:	Name of the software
<i>num</i> ,:	Software id

Definition at line 46 of file Pickling.py.

Referenced by loadobj().

6.34.4 Member Data Documentation

6.34.4.1 `irna::iRNA_stat::Pickling::Pickling::path`

Definition at line 17 of file Pickling.py.

Referenced by loadobj().

The documentation for this class was generated from the following file:

- [/home/amine/workspace/iRNA/irna/iRNA_stat/Pickling.py](#)

6.35 `irna::iRNA_stat::pValue::pValue` Class Reference

Public Member Functions

- `def __init__`
Instantiate *pValue* object.
- `def run`
Compute *pValue*.

Public Attributes

- [dbmanage](#)

- [rand_inf](#)
- [softname](#)
- [norm_score](#)
- [interactions](#)

6.35.1 Detailed Description

Definition at line 10 of file pValue.py.

6.35.2 Constructor & Destructor Documentation

6.35.2.1 `def irna::iRNA_stat::pValue::pValue::__init__(self, data, dbmanage, rand_inf)`

Instantiate [pValue](#) object.

Parameters

<i>data</i> ,:	Data object
<i>dbmanage</i> ,:	Access to the database
<i>rand_inf</i> ,:	Rand_data object

Definition at line 19 of file pValue.py.

6.35.3 Member Function Documentation

6.35.3.1 `def irna::iRNA_stat::pValue::pValue::run (self)`

Compute [pValue](#).

Definition at line 30 of file pValue.py.

References [irna::iRNA_stat::NormScore::NormScore::interactions](#), [interactions](#), [irna::iRNA_stat::Interaction::Interaction::interactions](#), [irna::iRNA_stat::Computer::Computer::interactions](#), [norm_score](#), [irna::iRNA_stat::Computer::Computer::norm_score](#), [irna::iRNA_stat::NormScore::NormScore::norm_score](#), [irna::iRNA_stat::Files::Files::rand_inf](#), [rand_inf](#), and [softname](#).

6.35.4 Member Data Documentation

6.35.4.1 `irna::iRNA_stat::pValue::pValue::dbmanage`

Definition at line 19 of file pValue.py.

6.35.4.2 `irna::iRNA_stat::pValue::pValue::interactions`

Definition at line 19 of file pValue.py.

Referenced by `run()`.

6.35.4.3 `irna::iRNA_stat::pValue::pValue::norm_score`

Definition at line 19 of file `pValue.py`.

Referenced by `irna::iRNA_stat::Regression::Regression::ecdf_estimate()`, `irna::iRNA_stat::Regression::Regression::linear_regression()`, and `run()`.

6.35.4.4 `irna::iRNA_stat::pValue::pValue::rand_inf`

Definition at line 19 of file `pValue.py`.

Referenced by `run()`.

6.35.4.5 `irna::iRNA_stat::pValue::pValue::softname`

Definition at line 19 of file `pValue.py`.

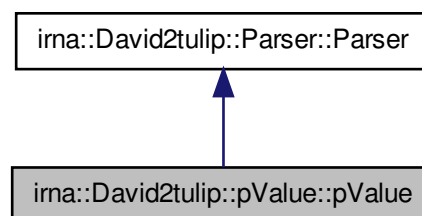
Referenced by `run()`.

The documentation for this class was generated from the following file:

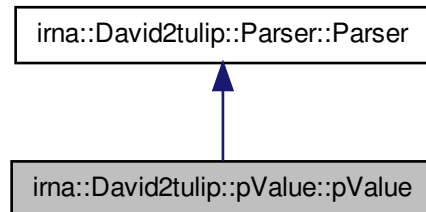
- [/home/amine/workspace/iRNA/irna/iRNA_stat/pValue.py](#)

6.36 `irna::David2tulip::pValue::pValue` Class Reference

Inheritance diagram for `irna::David2tulip::pValue::pValue`:



Collaboration diagram for irna::David2tulip::pValue::pValue:



Public Member Functions

- def `__init__`
Instantiate `pValue` object.
- def `setdata`
Add `pValue` information to edges.

Public Attributes

- `pValue_file`

6.36.1 Detailed Description

Definition at line 11 of file `pValue.py`.

6.36.2 Constructor & Destructor Documentation

6.36.2.1 def `irna::David2tulip::pValue::pValue::__init__ (self, pValue_file)`

Instantiate `pValue` object.

Parameters

<code>pValue_file,</code>	<code>pValue</code> file
---------------------------	--------------------------

Definition at line 18 of file `pValue.py`.

6.36.3 Member Function Documentation

6.36.3.1 `def irna::David2tulip::pValue::pValue::setdata (self, node_objects, edge_objects)`

Add `pValue` information to edges.

Parameters

<code>node_ - objects,:</code>	List of node objects
<code>edge_ - objects,:</code>	List of edge objects

Definition at line 28 of file `pValue.py`.

References `irna::David2tulip::Parser::Parser::getlinkededge()`, and `pValue_file`.

6.36.4 Member Data Documentation

6.36.4.1 `irna::David2tulip::pValue::pValue::pValue_file`

Definition at line 18 of file `pValue.py`.

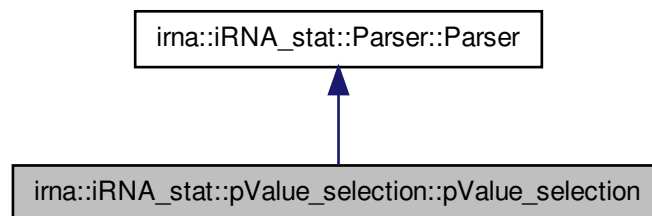
Referenced by `setdata()`.

The documentation for this class was generated from the following file:

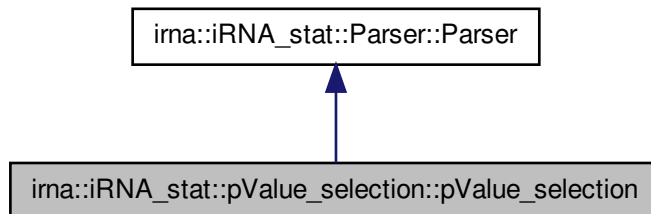
- `/home/amine/workspace/iRNA/irna/David2tulip/pValue.py`

6.37 `irna::iRNA_stat::pValue_selection::pValue_selection` Class - Reference

Inheritance diagram for `irna::iRNA_stat::pValue_selection::pValue_selection`:



Collaboration diagram for irna::iRNA_stat::pValue_selection::pValue_selection:



Public Member Functions

- def `__init__`
Instantiate `pValue_selection` object.
- def `getnumsRNA`
Get an sRNA in the list.
- def `compute_Davidmatrix`
Compute multilist target.
- def `compute_frequency`
Compute frequency of mRNA.
- def `getCommune`
Count Commune elements between lists.
- def `compute_similarity`
Compute similarity between target list of each sRNA.
- def `run`
Select targets depending on score and compute frequency and similarity between target groups.

Public Attributes

- `pValue_thres`

6.37.1 Detailed Description

Definition at line 10 of file `pValue_selection.py`.

6.37.2 Constructor & Destructor Documentation

6.37.2.1 `def irna::iRNA_stat::pValue_selection::pValue_selection::__init__(self, pValue_thres)`

Instantiate [pValue_selection](#) object.

Parameters

<i>pValue_thres</i> ,:	pValue_thres object
------------------------	---------------------

Definition at line 17 of file pValue_selection.py.

6.37.3 Member Function Documentation

6.37.3.1 `def irna::iRNA_stat::pValue_selection::pValue_selection::compute_Davidmatrix (self, computer, dbmanage, name, softid)`

Compute multilist target.

Parameters

<i>computer</i> ,:	Computer object
<i>dbmanage</i> ,:	Access to the database
<i>name</i> ,:	Software name
<i>softid</i> ,:	Software id

Definition at line 41 of file pValue_selection.py.

References [compute_frequency\(\)](#), [getnumsRNA\(\)](#), [irna::iRNA_stat::Parser::Parser::getUnique\(\)](#), [irna::iRNA_pred::Comparison::Comparison::getUnique\(\)](#), and [irna::iRNA_stat::Parser::Parser::sortdict\(\)](#).

Referenced by [compute_similarity\(\)](#), and [getnumsRNA\(\)](#).

6.37.3.2 `def irna::iRNA_stat::pValue_selection::pValue_selection::compute_frequency (self, computer, tabmRNA, unique_tabmRNA)`

Compute frequency of mRNA.

Parameters

<i>computer</i> ,:	Computer object
<i>tabmRNA</i> ,:	Redondant list of mRNA
<i>unique_tabmRNA</i> ,:	Unique mRNA

Definition at line 83 of file pValue_selection.py.

References [getCommune\(\)](#).

6.37 irna::iRNA_stat::pValue_selection::pValue_selection Class Reference 161

Referenced by compute_Davidmatrix(), and compute_similarity().

```
6.37.3.3 def irna::iRNA_stat::pValue_selection::pValue_selection::compute_similarity ( self,
                                             computer, matrix_sRNA )
```

Compute similarity between target list of each sRNA.

Parameters

<i>computer</i> ,:	Computer object
<i>matrix_sRNA</i> - <i>A</i> ,:	List of sRNA targets

Definition at line 107 of file pValue_selection.py.

References compute_Davidmatrix(), compute_frequency(), compute_similarity(), run(), and irna::iRNA_stat::Parser::Parser::sortdict().

Referenced by compute_similarity(), and getCommune().

```
6.37.3.4 def irna::iRNA_stat::pValue_selection::pValue_selection::getCommune ( self, list1,
                                                                              list2 )
```

Count Commune elements between lists.

Parameters

<i>list1</i> ,:	First list
<i>list2</i> ,:	Second list

Returns

: Count the number of elements

Definition at line 95 of file pValue_selection.py.

References compute_similarity(), and getCommune().

Referenced by compute_frequency(), and getCommune().

```
6.37.3.5 def irna::iRNA_stat::pValue_selection::pValue_selection::getnumsRNA ( self, allsRNA,
                                                                              sRNA )
```

Get an sRNA in the list.

Parameters

<i>allsRNA</i> ,:	List of sRNAs
<i>sRNA</i> ,:	An sRNA

Definition at line 26 of file pValue_selection.py.

References compute_Davidmatrix(), and pValue_thres.

Referenced by compute_Davidmatrix().

```
6.37.3.6 def irna::iRNA_stat::pValue_selection::pValue_selection::run ( self, computer,  
                                dbmanage, name, softid )
```

Select targets depending on score and compute frequency and similarity between target groups.

Parameters

<i>computer,:</i>	Computer object
<i>dbmanage,:</i>	Access to the database
<i>name,:</i>	Software name
<i>softid,:</i>	Software id

Definition at line 128 of file pValue_selection.py.

Referenced by compute_similarity().

6.37.4 Member Data Documentation

6.37.4.1 irna::iRNA_stat::pValue_selection::pValue_selection::pValue_thres

Definition at line 17 of file pValue_selection.py.

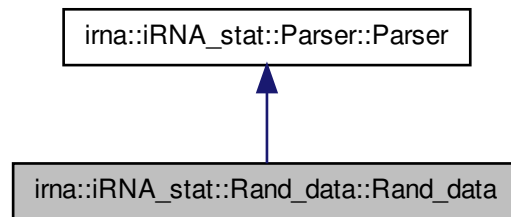
Referenced by getnumsRNA().

The documentation for this class was generated from the following file:

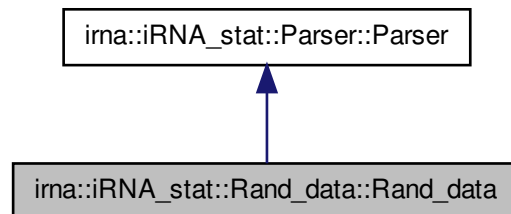
- /home/amine/workspace/iRNA/irna/iRNA_stat/[pValue_selection.py](#)

6.38 irna::iRNA_stat::Rand_data::Rand_data Class Reference

Inheritance diagram for irna::iRNA_stat::Rand_data::Rand_data:



Collaboration diagram for irna::iRNA_stat::Rand_data::Rand_data:



Public Member Functions

- def `__init__`
Instantiate rand_data object.
- def `getRandinf`
Load soft parameters.
- def `getallSofts`
Get soft corresponding to one name.
- def `getRandRna`
Get analysis of one sRNA by one soft.

Public Attributes

- [combined](#)
- [soft](#)
- [sRNA](#)
- [intercept](#)
- [slope](#)
- [unique_soft](#)

6.38.1 Detailed Description

Definition at line 10 of file Rand_data.py.

6.38.2 Constructor & Destructor Documentation

6.38.2.1 `def irna::iRNA_stat::Rand_data::Rand_data::__init__(self, rand_file)`

Instantiate rand_data object.

Definition at line 16 of file Rand_data.py.

References [getRandinf\(\)](#).

6.38.3 Member Function Documentation

6.38.3.1 `def irna::iRNA_stat::Rand_data::Rand_data::getallSofts (self, soft)`

Get soft corresponding to one name.

Parameters

<i>soft</i> ,:	Soft name
----------------	---------------------------

Definition at line 52 of file Rand_data.py.

References [combined](#), [irna::iRNA_stat::Exp_data::Exp_data::combined](#), [irna::iRNA_stat::Parser::Parser::getData\(\)](#), [irna::iRNA_pred::Merger::Merger::getData\(\)](#), and [getRandRna\(\)](#).

6.38.3.2 `def irna::iRNA_stat::Rand_data::Rand_data::getRandinf (self, rand_file)`

Load soft parameters.

Parameters

<i>rand_file</i> ,:	Random file
---------------------	-------------

Definition at line 25 of file Rand_data.py.

Referenced by `__init__()`.

6.38.3.3 `def irna::iRNA_stat::Rand_data::Rand_data::getRandRna (self, soft, sRNA)`

Get analysis of one sRNA by one soft.

Parameters

<i>soft</i> ,:	software name
<i>sRNA</i> ,:	sRNA name

Definition at line 66 of file `Rand_data.py`.

Referenced by `getAllSofts()`.

6.38.4 Member Data Documentation

6.38.4.1 `irna::iRNA_stat::Rand_data::Rand_data::combined`

Definition at line 25 of file `Rand_data.py`.

Referenced by `getAllSofts()`.

6.38.4.2 `irna::iRNA_stat::Rand_data::Rand_data::intercept`

Definition at line 25 of file `Rand_data.py`.

6.38.4.3 `irna::iRNA_stat::Rand_data::Rand_data::slope`

Definition at line 25 of file `Rand_data.py`.

6.38.4.4 `irna::iRNA_stat::Rand_data::Rand_data::soft`

Definition at line 25 of file `Rand_data.py`.

Referenced by `irna::iRNA_stat::Threshold::Threshold::getSoftnum()`.

6.38.4.5 `irna::iRNA_stat::Rand_data::Rand_data::sRNA`

Definition at line 25 of file `Rand_data.py`.

6.38.4.6 `irna::iRNA_stat::Rand_data::Rand_data::unique_soft`

Definition at line 25 of file `Rand_data.py`.

The documentation for this class was generated from the following file:

- /home/amine/workspace/iRNA/irna/iRNA_stat/[Rand_data.py](#)

6.39 irna::iRNA_pred::RanRNA::RanRNA Class Reference

Public Member Functions

- def [__init__](#)
- def [GetValues](#)
Get double random values.
- def [GetIntValues](#)
Get integer random values.
- def [SetLetters](#)
Set the nucleotide.
- def [GenerateSeq](#)
Generate a random sequence.
- def [WriteFasta](#)
Write the fasta.
- def [GenerateFile](#)
Generate a multifasta with random sequences.

Public Attributes

- [GC](#)
- [SeqLength](#)
- [NbSeq](#)
- [OutRep](#)

6.39.1 Detailed Description

Definition at line 12 of file RanRNA.py.

6.39.2 Constructor & Destructor Documentation

- 6.39.2.1 `def irna::iRNA_pred::RanRNA::RanRNA::__init__(self, GC, SeqLength, NbSeq, OutRep)`

Parameters

<i>GC</i> ,:	GC percentage
<i>SeqLength</i> ,:	Length of sequences
<i>NbSeq</i> ,:	Number of sequences
<i>OutRep</i> ,:	Output repertory

Definition at line 22 of file RanRNA.py.

6.39.3 Member Function Documentation

6.39.3.1 def irna::iRNA_pred::RanRNA::RanRNA::GenerateFile (*self*)

Generate a multifasta with random sequences.

Definition at line 103 of file RanRNA.py.

Referenced by WriteFasta().

6.39.3.2 def irna::iRNA_pred::RanRNA::RanRNA::GenerateSeq (*self*, *seqlength*)

Generate a random sequence.

Returns

: a random sequence

Definition at line 64 of file RanRNA.py.

References GC, OutRep, SetLetters(), and WriteFasta().

Referenced by SetLetters(), and WriteFasta().

6.39.3.3 def irna::iRNA_pred::RanRNA::RanRNA::GetIntValues (*self*, *val*, *nbseq*)

Get integer random values.

Returns

: Table of integer random values

Definition at line 42 of file RanRNA.py.

Referenced by GetValues(), and WriteFasta().

6.39.3.4 def irna::iRNA_pred::RanRNA::RanRNA::GetValues (*self*, *seqlength*)

Get double random values.

Returns

: Table of double random Values

Definition at line 33 of file RanRNA.py.

References GetIntValues(), and SetLetters().

Referenced by SetLetters().

6.39.3.5 `def irna::iRNA_pred::RanRNA::RanRNA::SetLetters (self, L1, L2)`

Set the nucleotide.

Parameters

<i>L1</i> ,:	Nucleotide 1
<i>L2</i> ,:	Nucleotide 1

Returns

: Nucleotide

Definition at line 52 of file RanRNA.py.

References `GenerateSeq()`, and `GetValues()`.

Referenced by `GenerateSeq()`, and `GetValues()`.

6.39.3.6 `def irna::iRNA_pred::RanRNA::RanRNA::WriteFasta (self, fastafile, seq)`

Write the fasta.

Parameters

<i>fastafile</i> ,:	Name of the fasta file
<i>seq</i> ,:	Generated sequence

Definition at line 84 of file RanRNA.py.

References `irna::iRNA_pred::Fasta::Fasta::fastafile`, `GenerateFile()`, `GenerateSeq()`, `-GetIntValues()`, `NbSeq`, `SeqLength`, `irna::iRNA_pred::Fasta::Fasta::WriteFasta()`, and `-WriteFasta()`.

Referenced by `GenerateSeq()`, and `WriteFasta()`.

6.39.4 Member Data Documentation

6.39.4.1 `irna::iRNA_pred::RanRNA::RanRNA::GC`

Definition at line 22 of file RanRNA.py.

Referenced by `irna::iRNA_pred::Fasta::Fasta::ExtractFasta()`, and `GenerateSeq()`.

6.39.4.2 `irna::iRNA_pred::RanRNA::RanRNA::NbSeq`

Definition at line 22 of file RanRNA.py.

Referenced by `irna::iRNA_pred::Fasta::Fasta::ExtractFasta()`, `irna::iRNA_pred::Stat::Stat::GetGC()`, and `WriteFasta()`.

6.39.4.3 irna::iRNA_pred::RanRNA::RanRNA::OutRep

Definition at line 22 of file RanRNA.py.

Referenced by GenerateSeq().

6.39.4.4 irna::iRNA_pred::RanRNA::RanRNA::SeqLength

Definition at line 22 of file RanRNA.py.

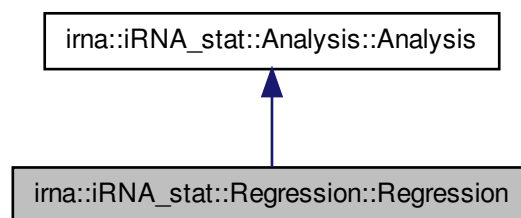
Referenced by WriteFasta().

The documentation for this class was generated from the following file:

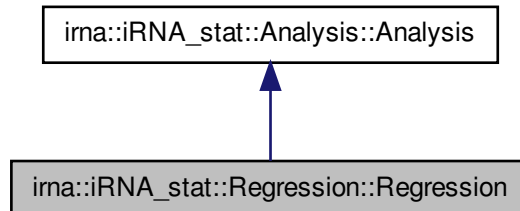
- /home/amine/workspace/iRNA/irna/iRNA_pred/[RanRNA.py](#)

6.40 irna::iRNA_stat::Regression::Regression Class Reference

Inheritance diagram for irna::iRNA_stat::Regression::Regression:



Collaboration diagram for `irna::iRNA_stat::Regression::Regression`:



Public Member Functions

- `def __init__`
Instantiate [Regression](#) object.
- `def ecdf_estimate`
Compute empirical cumulated distribution.
- `def linear_regression`
Compute linear regression for each sRNA.
- `def run`

Public Attributes

- `unique_sRNAid`
- `norm_score`
- `sRNAid_tab`
- `pValue_type`
- `cumneg`
- `curve_param`

6.40.1 Detailed Description

Definition at line 13 of file `Regression.py`.

6.40.2 Constructor & Destructor Documentation

6.40.2.1 `def irna::iRNA_stat::Regression::Regression::__init__(self, data)`

Instantiate [Regression](#) object.

Parameters

<i>data,</i>	Communication object
--------------	----------------------

Definition at line 20 of file Regression.py.

6.40.3 Member Function Documentation

6.40.3.1 def irna::iRNA_stat::Regression::Regression::ecdf_estimate (self)

Compute empirical cumulated distribution.

Definition at line 31 of file Regression.py.

References irna::iRNA_stat::Computer::Computer::cumneg, cumneg, irna::iRNA_stat::Computer::Computer::curve_param, curve_param, linear_regression(), irna::iRNA_stat::pValue::pValue::norm_score, norm_score, irna::iRNA_stat::Computer::Computer::norm_score, irna::iRNA_stat::NormScore::NormScore::norm_score, p-Value_type, irna::iRNA_stat::Computer::Computer::pValue_type, sRNAid_tab, irna::iRNA_stat::Computer::Computer::sRNAid_tab, unique_sRNAidinint, and irna::iRNA_stat::Computer::Computer::unique_sRNAidinint.

Referenced by linear_regression().

6.40.3.2 def irna::iRNA_stat::Regression::Regression::linear_regression (self)

Compute linear regression for each sRNA.

Definition at line 55 of file Regression.py.

References irna::iRNA_stat::Analysis::Analysis::commun_values(), irna::iRNA_stat::Computer::Computer::cumneg, cumneg, irna::iRNA_stat::Computer::Computer::curve_param, curve_param, ecdf_estimate(), irna::iRNA_stat::pValue::pValue::norm_score, norm_score, irna::iRNA_stat::Computer::Computer::norm_score, irna::iRNA_stat::NormScore::NormScore::norm_score, run(), sRNAid_tab, irna::iRNA_stat::Computer::Computer::sRNAid_tab, unique_sRNAidinint, and irna::iRNA_stat::Computer::Computer::unique_sRNAidinint.

Referenced by ecdf_estimate(), and run().

6.40.3.3 def irna::iRNA_stat::Regression::Regression::run (self)

Definition at line 80 of file Regression.py.

References irna::iRNA_stat::Computer::Computer::cumneg, cumneg, irna::iRNA_stat::Computer::Computer::curve_param, curve_param, and linear_regression().

Referenced by linear_regression().

6.40.4 Member Data Documentation

6.40.4.1 `irna::iRNA_stat::Regression::Regression::cumneg`

Definition at line 31 of file `Regression.py`.

Referenced by `ecdf_estimate()`, `linear_regression()`, and `run()`.

6.40.4.2 `irna::iRNA_stat::Regression::Regression::curve_param`

Definition at line 55 of file `Regression.py`.

Referenced by `ecdf_estimate()`, `linear_regression()`, and `run()`.

6.40.4.3 `irna::iRNA_stat::Regression::Regression::norm_score`

Definition at line 20 of file `Regression.py`.

Referenced by `ecdf_estimate()`, and `linear_regression()`.

6.40.4.4 `irna::iRNA_stat::Regression::Regression::pValue_type`

Definition at line 20 of file `Regression.py`.

Referenced by `ecdf_estimate()`.

6.40.4.5 `irna::iRNA_stat::Regression::Regression::sRNAid_tab`

Definition at line 20 of file `Regression.py`.

Referenced by `ecdf_estimate()`, and `linear_regression()`.

6.40.4.6 `irna::iRNA_stat::Regression::Regression::unique_sRNAidinint`

Definition at line 20 of file `Regression.py`.

Referenced by `ecdf_estimate()`, and `linear_regression()`.

The documentation for this class was generated from the following file:

- `/home/amine/workspace/iRNA/irna/iRNA_stat/Regression.py`

6.41 `irna::iRNA_seq::Sequences::Sequences` Class Reference

Public Member Functions

- `def __init__`
Instantiate Sequence object.
- `def parse`

- Get parsed data.*

 - def [invers_compl](#)

Inverse and complemente gene sequence.
- def [fractionalGene](#)

Get Gene between indicated set of position.
- def [completeGene](#)

Get the complete Gene.
- def [setGeneFunction](#)

Define the getGene function to use.
- def [setdefaultmRNAlen](#)

Compute default mRNA length.
- def [writemRNA](#)

Write mRNA multifasta file.
- def [writesRNA](#)

Write sRNA multifasta file.
- def [writeCorresponding](#)

Write corresponding geneID to genename for mRNA.

Public Attributes

- [organism](#)
- [list_genes](#)
- [DNA](#)

6.41.1 Detailed Description

Definition at line 9 of file Sequences.py.

6.41.2 Constructor & Destructor Documentation

6.41.2.1 `def irna::iRNA_seq::Sequences::Sequences::__init__(self)`

Instantiate Sequence object.

Definition at line 15 of file Sequences.py.

6.41.3 Member Function Documentation

6.41.3.1 `def irna::iRNA_seq::Sequences::Sequences::completeGene(self, genedict, begin = None, end = None)`

Get the complete Gene.

Parameters

<i>genedict</i> ,:	list of Gene dictionary
--------------------	-------------------------

Returns

: Complete gene sequence

Definition at line 63 of file Sequences.py.

References completeGene(), fractionalGene(), and setdefaultmRNAlen().

Referenced by completeGene(), invers_compl(), and writemRNA().

```
6.41.3.2 def irna::iRNA_seq::Sequences::Sequences::fractionalGene ( self, genedict, begin,
end )
```

Get Gene between indicated set of position.

Parameters

<i>genedict</i> ,:	list of Gene dictionary
--------------------	-------------------------

Returns

: Fractionnal gene sequence

Definition at line 54 of file Sequences.py.

References DNA, and setGeneFunction().

Referenced by completeGene(), and invers_compl().

```
6.41.3.3 def irna::iRNA_seq::Sequences::Sequences::invers_compl ( self, gene )
```

Inverse and complemente gene sequence.

Parameters

<i>gene</i> ,:	Gene sequence
----------------	---------------

Definition at line 33 of file Sequences.py.

References completeGene(), DNA, and fractionalGene().

Referenced by parse(), and writemRNA().

```
6.41.3.4 def irna::iRNA_seq::Sequences::Sequences::parse ( self, obj )
```

Get parsed data.

Parameters

<i>obj,:</i>	Data object
--------------	-------------

Definition at line 25 of file Sequences.py.

References `invers_compl()`.

6.41.3.5 `def irna::iRNA_seq::Sequences::Sequences::setDefaultmRNAlen (self, begin, end, complete)`

Compute default mRNA length.

Parameters

<i>begin,:</i>	sRNA begin
<i>end,:</i>	sRNA end
<i>complete,:</i>	Complete flag

Returns

: RNA length

Definition at line 84 of file Sequences.py.

References `list_genes`, `organism`, `setDefaultmRNAlen()`, `setGeneFunction()`, and `writemRNA()`.

Referenced by `completeGene()`, and `setDefaultmRNAlen()`.

6.41.3.6 `def irna::iRNA_seq::Sequences::Sequences::setGeneFunction (self, complete)`

Define the `getGene` function to use.

Parameters

<i>complete,:</i>	Complete flag
-------------------	---------------

Returns

: Function pointer

Definition at line 72 of file Sequences.py.

Referenced by `fractionalGene()`, and `setDefaultmRNAlen()`.

6.41.3.7 `def irna::iRNA_seq::Sequences::Sequences::writeCorresponding (self, results)`

Write corresponding `geneID` to `genename` for mRNA.

Definition at line 162 of file Sequences.py.

Referenced by `writesRNA()`.

6.41.3.8 `def irna::iRNA_seq::Sequences::Sequences::writemRNA (self, begin, end, results, complete)`

Write mRNA multifasta file.

Parameters

<i>begin</i> ,:	sRNA begin
<i>end</i> ,:	sRNA end
<i>results</i> ,:	Path to result repertory
<i>complete</i> ,:	Complete flag

Definition at line 101 of file `Sequences.py`.

References `completeGene()`, `invers_compl()`, `organism`, and `writesRNA()`.

Referenced by `setdefaultmRNAlen()`.

6.41.3.9 `def irna::iRNA_seq::Sequences::Sequences::writesRNA (self, results, srna_data)`

Write sRNA multifasta file.

Parameters

<i>results</i> ,:	Path to result repertory
<i>srna_data</i> ,:	sRNA list

Definition at line 133 of file `Sequences.py`.

References `list_genes`, `organism`, and `writeCorresponding()`.

Referenced by `writemRNA()`.

6.41.4 Member Data Documentation

6.41.4.1 `irna::iRNA_seq::Sequences::Sequences::DNA`

Definition at line 15 of file `Sequences.py`.

Referenced by `fractionalGene()`, and `invers_compl()`.

6.41.4.2 `irna::iRNA_seq::Sequences::Sequences::list_genes`

Definition at line 15 of file `Sequences.py`.

Referenced by `setdefaultmRNAlen()`, and `writesRNA()`.

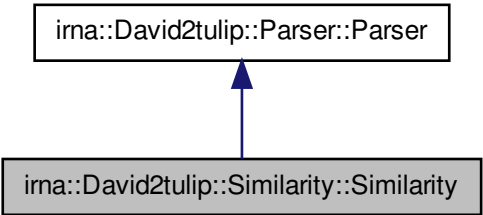
6.41.4.3 irna::iRNA_seq::Sequences::Sequences::organism

Definition at line 15 of file Sequences.py.
Referenced by setdefaultmRNAlen(), writemRNA(), and writesRNA().
The documentation for this class was generated from the following file:

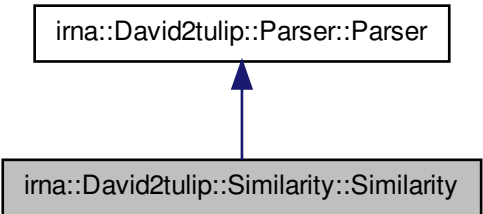
- /home/amine/workspace/iRNA/irna/iRNA_seq/[Sequences.py](#)

6.42 irna::David2tulip::Similarity::Similarity Class Reference

Inheritance diagram for irna::David2tulip::Similarity::Similarity:



Collaboration diagram for irna::David2tulip::Similarity::Similarity:



Public Member Functions

- def [__init__](#)
Instantiate similarity parser object.
- def [setdata](#)
Add sRNA - sRNA edges based on their similarity.

Public Attributes

- [similarity_file](#)

6.42.1 Detailed Description

Definition at line 11 of file Similarity.py.

6.42.2 Constructor & Destructor Documentation

6.42.2.1 def irna::David2tulip::Similarity::Similarity::__init__(*self*, *similarity_file*)

Instantiate similarity parser object.

Parameters

<i>similarity_file</i> ,:	Similarity file
---------------------------	---------------------------------

Definition at line 18 of file Similarity.py.

6.42.3 Member Function Documentation

6.42.3.1 def irna::David2tulip::Similarity::Similarity::setdata (*self*, *node_objects*, *edge_objects*)

Add sRNA - sRNA edges based on their similarity.

Parameters

<i>node_objects</i> ,:	list of node objects
<i>edge_objects</i> ,:	list of edge objects

Definition at line 28 of file Similarity.py.

References [irna::David2tulip::Parser::Parser::addelements\(\)](#), [irna::David2tulip::Parser::Parser::getlinknode\(\)](#), and [similarity_file](#).

6.42.4 Member Data Documentation

6.42.4.1 irna::David2tulip::Similarity::Similarity::similarity_file

Definition at line 18 of file Similarity.py.

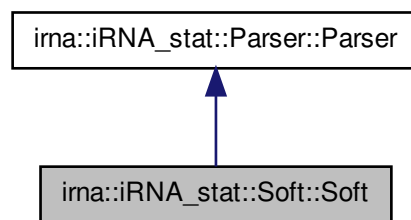
Referenced by setdata().

The documentation for this class was generated from the following file:

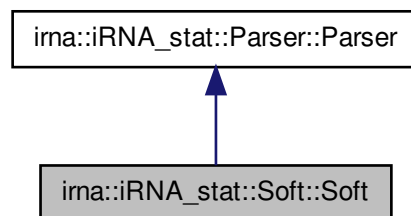
- [/home/amine/workspace/iRNA/irna/David2tulip/Similarity.py](#)

6.43 irna::iRNA_stat::Soft::Soft Class Reference

Inheritance diagram for irna::iRNA_stat::Soft::Soft:



Collaboration diagram for irna::iRNA_stat::Soft::Soft:



Public Member Functions

- def `__init__`
Instantiate soft object.
- def `getSoftinf`
- def `getSoftnum`
- def `__cmp__`
General method to compare node based on the name.

Public Attributes

- `id`
- `type_sol`
- `score_type`

6.43.1 Detailed Description

Definition at line 10 of file Soft.py.

6.43.2 Constructor & Destructor Documentation

6.43.2.1 `def irna::iRNA_stat::Soft::Soft::__init__(self, soft_file)`

Instantiate soft object.

Definition at line 17 of file Soft.py.

References `getSoftinf()`.

6.43.3 Member Function Documentation

6.43.3.1 `def irna::iRNA_stat::Soft::Soft::__cmp__(self, other)`

General method to compare node based on the name.

Parameters

<i>other,:</i>	Compared value
----------------	----------------

Definition at line 57 of file Soft.py.

Referenced by `getSoftnum()`.

6.43.3.2 `def irna::iRNA_stat::Soft::Soft::getSoftinf (self, soft_file)`

6.44 irna::David2tulip::Sqlite_manager::Sqlite_manager Class Reference 181

Parameters

<i>soft_file</i> ,:	
---------------------	--

Definition at line 25 of file Soft.py.

Referenced by `__init__()`.

6.43.3.3 def irna::iRNA_stat::Soft::Soft::getSoftnum (*self*, *name*)

Parameters

<i>name</i> ,:	
----------------	--

Definition at line 45 of file Soft.py.

References `__cmp__()`, and `id`.

6.43.4 Member Data Documentation

6.43.4.1 irna::iRNA_stat::Soft::Soft::id

Definition at line 25 of file Soft.py.

Referenced by `getSoftnum()`.

6.43.4.2 irna::iRNA_stat::Soft::Soft::score_type

Definition at line 25 of file Soft.py.

6.43.4.3 irna::iRNA_stat::Soft::Soft::type_sol

Definition at line 25 of file Soft.py.

The documentation for this class was generated from the following file:

- `/home/amine/workspace/iRNA/irna/iRNA_stat/Soft.py`

6.44 irna::David2tulip::Sqlite_manager::Sqlite_manager Class - Reference

: Handle database connection, disconnection and querying.

Public Member Functions

- def `__init__`

- Instantiate [Sqlite_manager](#) object.*

 - def [createSQLdb](#)

Create the database.
 - def [connectDB](#)

Connect to the database.
 - def [disconnectDB](#)

Disconnect the database.
 - def [disconnectDB2](#)

Disconnect the database and copy on to the disk.
 - def [setSoft](#)

Insert soft name.
 - def [setRNA](#)

Insert RNA.
 - def [setInteract](#)

Insert interaction.
 - def [commitRetry](#)

Retry the commit operation.
 - def [setContact](#)

Insert contacts.
 - def [getSoft](#)

Get if software exist by its id.
 - def [getSoftname](#)

Get if software exist by its id.
 - def [getidSoftsbyname](#)

Get id of softwares corresponding to one name.
 - def [getAllRNAlength](#)

Get all RNA length.
 - def [getAllRNA](#)

Get all RNA name from one type.
 - def [getRNA](#)

Get an RNA by its name and type.
 - def [getsRNAlenbyIntid](#)

Get an sRNA length from an interaction.
 - def [getAllsRNAlenbyIntid](#)

Get an sRNA length from an interaction.
 - def [getsRNAidbyIntid](#)

Get an sRNAid from an interaction.
 - def [getAllsRNAidbyIntid](#)

Get an sRNAid from an interaction.
 - def [getmRNAlenbyIntid](#)

Get an mRNA from an interaction.
 - def [getAllmRNAlenbyIntid](#)

Get an mRNA from an interaction.

- def [getNbInteract](#)
Count the number of interaction for one software.
- def [getInteract](#)
Get interactions of one software.
- def [getScore](#)
Get the score of an interaction.
- def [getAllScore](#)
Get the score for several interactions.
- def [getAllSoft](#)
Get all the software.
- def [getsRNAbyIntid](#)
Get the name of an sRNA from interaction key.
- def [getmRNAbyIntid](#)
Get the name of an mRNA from interaction key.
- def [listit](#)
Convert fetchall result into list of list.
- def [listscore](#)
Unlist score.
- def [getPositionbyIntid](#)
Get position for one interaction.
- def [getallsRNA](#)
Get all sRNA.
- def [getallsRNAname](#)
Get an sRNA name and unlist.
- def [getIntbysRNAid](#)
Get the interactid for an sRNA.
- def [IndexInteractidOnContact](#)
Create index on interactid for contact.
- def [IndexSrnaidOnInteract](#)
Create index on srnaid for interact.
- def [IndexMrnaidOnInteract](#)
Create index on mrnaid for interact.
- def [createIndexes](#)
Create index for most use connection.

Public Attributes

- [db_path](#)
- [db_file](#)
- [fastmode](#)
- [conn2](#)
- [conn](#)
- [cur](#)

6.44.1 Detailed Description

: Handle database connection, disconnection and querying.

Definition at line 16 of file `Sqlite_manager.py`.

6.44.2 Constructor & Destructor Documentation

6.44.2.1 `def irna::David2tulip::Sqlite_manager::Sqlite_manager::__init__(self, result, db_file, fastmode)`

Instantiate [Sqlite_manager](#) object.

Parameters

<i>result</i> ,:	Path where to write the database
<i>db_file</i> ,:	SQLite db file
<i>fastmode</i> ,:	fastmode flag

Definition at line 25 of file `Sqlite_manager.py`.

6.44.3 Member Function Documentation

6.44.3.1 `def irna::David2tulip::Sqlite_manager::Sqlite_manager::commitRetry (self)`

Retry the commit operation.

Returns

: State of the commit

Definition at line 154 of file `Sqlite_manager.py`.

Referenced by `irna::iRNA_stat::Sqlite_manager::Sqlite_manager::setContact()`, `setContact()`, `irna::iRNA_pred::Sqlite_manager::Sqlite_manager::setContact()`, `irna::iRNA_stat::Sqlite_manager::Sqlite_manager::setInteract()`, `setInteract()`, `irna::iRNA_A_stat::Sqlite_manager::Sqlite_manager::setRNA()`, `setRNA()`, `irna::iRNA_pred::Sqlite_manager::Sqlite_manager::setRNA()`, `irna::iRNA_stat::Sqlite_manager::Sqlite_manager::setSoft()`, `irna::iRNA_pred::Sqlite_manager::Sqlite_manager::setSoft()`, and `setSoft()`.

6.44.3.2 `def irna::David2tulip::Sqlite_manager::Sqlite_manager::connectDB (self)`

Connect to the database.

Definition at line 48 of file `Sqlite_manager.py`.

Referenced by `createSQLdb()`.

6.44.3.3 def irna::David2tulip::Sqlite_manager::Sqlite_manager::createIndexes (*self*)

Create index for most use connection.

Definition at line 531 of file Sqlite_manager.py.

Referenced by getallsRNAname().

6.44.3.4 def irna::David2tulip::Sqlite_manager::Sqlite_manager::createSQLdb (*self*)

Create the database.

Definition at line 34 of file Sqlite_manager.py.

References conn2, connectDB(), db_file, and db_path.

6.44.3.5 def irna::David2tulip::Sqlite_manager::Sqlite_manager::disconnectDB (*self*)

Disconnect the database.

Definition at line 63 of file Sqlite_manager.py.

References conn, conn2, disconnectDB2(), irna::David2tulip::Files::Files::fastmode, and fastmode.

6.44.3.6 def irna::David2tulip::Sqlite_manager::Sqlite_manager::disconnectDB2 (*self*)

Disconnect the database and copy on to the disk.

Definition at line 74 of file Sqlite_manager.py.

References cur, and setSoft().

Referenced by disconnectDB().

6.44.3.7 def irna::David2tulip::Sqlite_manager::Sqlite_manager::getAllmRNAlenbyIntid (*self*, *table_interactid*)

Get an mRNA from an interaction.

Parameters

<i>table_interactid</i> :	table of interaction id
---------------------------	-------------------------

Returns

: List of mRNA length

Definition at line 341 of file Sqlite_manager.py.

References getScore().

Referenced by `getAIsRNAidbyIntid()`.

6.44.3.8 `def irna::David2tulip::Sqlite_manager::Sqlite_manager::getallRNA (self, type_RNA)`

Get all RNA name from one type.

Parameters

<i>type_RNA</i> ,:	Type of RNA
--------------------	-------------

Returns

: list of RNA

Definition at line 240 of file `Sqlite_manager.py`.

References `getsRNAlenbyIntid()`.

Referenced by `getidSoftsbyname()`.

6.44.3.9 `def irna::David2tulip::Sqlite_manager::Sqlite_manager::getallRNAlength (self, type_RNA)`

Get all RNA length.

Parameters

<i>type_RNA</i> ,:	Type of RNA
--------------------	-------------

Returns

: list of RNA with their length

Definition at line 228 of file `Sqlite_manager.py`.

References `getRNA()`.

Referenced by `getSoftname()`.

6.44.3.10 `def irna::David2tulip::Sqlite_manager::Sqlite_manager::getAllScore (self, table_interactid)`

Get the score for several interactions.

Parameters

<i>table_ - interactid</i> ,:	list of interaction key
-------------------------------	-------------------------

Returns

: List of score

Definition at line 395 of file Sqlite_manager.py.

References getmRNAbyIntid(), and listit().

Referenced by getNbInteract().

6.44.3.11 def irna::David2tulip::Sqlite_manager::Sqlite_manager::getAllSoft (*self*)

Get all the software.

Returns

: List of software

Definition at line 409 of file Sqlite_manager.py.

References listit(), and listscore().

Referenced by getInteract().

6.44.3.12 def irna::David2tulip::Sqlite_manager::Sqlite_manager::getallsRNA (*self*)

Get all sRNA.

Returns

: List of rnaid

Definition at line 474 of file Sqlite_manager.py.

References IndexMrnaidOnInteract().

Referenced by getmRNAbyIntid().

6.44.3.13 def irna::David2tulip::Sqlite_manager::Sqlite_manager::getAllsRNAidbyIntid (*self*,
table_interactid)

Get an sRNAid from an interaction.

Parameters

<i>interactid,</i> :	Interaction id
----------------------	----------------

Returns

: List of sRNAid

Definition at line 310 of file Sqlite_manager.py.

References `getAllmRNAlenbyIntid()`, and `getmRNAbyIntid()`.

Referenced by `getAllsRNAlenbyIntid()`.

6.44.3.14 `def irna::David2tulip::Sqlite_manager::Sqlite_manager::getAllsRNAlenbyIntid (self, table.interactid)`

Get an sRNA length from an interaction.

Parameters

<i>table_ - interactid,:</i>	table of interaction id
------------------------------	-------------------------

Returns

: list of sRNA length

Definition at line 280 of file `Sqlite_manager.py`.

References `getAllsRNAidbyIntid()`.

Referenced by `getRNA()`.

6.44.3.15 `def irna::David2tulip::Sqlite_manager::Sqlite_manager::getallsRNAname (self)`

Get an sRNA name and unlist.

Returns

: List of rnaid

Definition at line 485 of file `Sqlite_manager.py`.

References `createIndexes()`, `IndexInteractidOnContact()`, `IndexMrnaidOnInteract()`, and `IndexSrnaidOnInteract()`.

Referenced by `listit()`.

6.44.3.16 `def irna::David2tulip::Sqlite_manager::Sqlite_manager::getidSoftsbyname (self, name)`

Get id of softwares corresponding to one name.

Parameters

<i>name,:</i>	name of a software
---------------	--------------------

6.44 irna::David2tulip::Sqlite_manager::Sqlite_manager Class Reference 189

Returns

: list of softid

Definition at line 216 of file Sqlite_manager.py.

References `getallRNA()`.

Referenced by `getSoft()`.

```
6.44.3.17 def irna::David2tulip::Sqlite_manager::Sqlite_manager::getIntbysRNAid ( self, srnaid )
```

Get the interactid for an sRNA.

Parameters

<i>srnaid</i> ,:	rna key
------------------	---------

Returns

: List of interactid

Definition at line 497 of file Sqlite_manager.py.

Referenced by `listscore()`.

```
6.44.3.18 def irna::David2tulip::Sqlite_manager::Sqlite_manager::getInteract ( self, softid )
```

Get interactions of one software.

Parameters

<i>softid</i> ,:	soft key
------------------	----------

Returns

: List of interactid

Definition at line 371 of file Sqlite_manager.py.

References `getAllSoft()`, and `listscore()`.

Referenced by `getmRNAlenbyIntid()`.

```
6.44.3.19 def irna::David2tulip::Sqlite_manager::Sqlite_manager::getmRNAbyIntid ( self, interactid )
```

Get the name of an mRNA from interaction key.

Parameters

<i>interactid,:</i>	interaction key
---------------------	-----------------

Returns

: name of the mRNA

Definition at line 433 of file Sqlite_manager.py.

References getallsRNA().

Referenced by getAllScore(), irna::iRNA_stat::Sqlite_manager::Sqlite_manager::get-AllsRNAidbyIntid(), irna::iRNA_pred::Sqlite_manager::Sqlite_manager::getAllsRNAidbyIntid(), and getAllsRNAidbyIntid().

```
6.44.3.20 def irna::David2tulip::Sqlite_manager::Sqlite_manager::getmRNAlenbyIntid ( self,
interactid )
```

Get an mRNA from an interaction.

Parameters

<i>interactid,:</i>	Interaction id
---------------------	----------------

Returns

: mRNA length

Definition at line 327 of file Sqlite_manager.py.

References getInteract(), and getNbInteract().

Referenced by getsRNAidbyIntid().

```
6.44.3.21 def irna::David2tulip::Sqlite_manager::Sqlite_manager::getNbInteract ( self, softid )
```

Count the number of interaction for one software.

Parameters

<i>softid,:</i>	soft key
-----------------	----------

Returns

: Number of interaction

Definition at line 358 of file Sqlite_manager.py.

References getAllScore(), and listscore().

Referenced by getmRNAlenbyIntid().

6.44 irna::David2tulip::Sqlite_manager::Sqlite_manager Class Reference 191

6.44.3.22 `def irna::David2tulip::Sqlite_manager::Sqlite_manager::getPositionbyIntid (self,
interactid)`

Get position for one interaction.

Parameters

<i>interactid</i> ,:	interact key
----------------------	--------------

Returns

: List of position

Definition at line 463 of file Sqlite_manager.py.

References IndexInteractidOnContact(), and IndexSrnaidOnInteract().

Referenced by getsRNAbyIntid().

6.44.3.23 `def irna::David2tulip::Sqlite_manager::Sqlite_manager::getRNA (self, name,
type_RNA)`

Get an RNA by its name and type.

Parameters

<i>name</i> ,:	RNA name
<i>type</i> ,:	RNA type

Returns

: A rnaid

Definition at line 254 of file Sqlite_manager.py.

References getAllsRNAlenbyIntid().

Referenced by getAllRNAlength().

6.44.3.24 `def irna::David2tulip::Sqlite_manager::Sqlite_manager::getScore (self, interactid)`

Get the score of an interaction.

Parameters

<i>interactid</i> ,:	interaction key
----------------------	-----------------

Returns

: List of score

Definition at line 383 of file Sqlite_manager.py.

References getsRNAbyIntid().

Referenced by getAllmRNAlenbyIntid().

6.44.3.25 `def irna::David2tulip::Sqlite_manager::Sqlite_manager::getSoft (self, softid)`

Get if software exist by its id.

Parameters

<i>softid</i> ,:	Soft key
------------------	----------

Returns

: A softid

Definition at line 192 of file Sqlite_manager.py.

References getidSoftsbyname().

Referenced by setContact().

6.44.3.26 `def irna::David2tulip::Sqlite_manager::Sqlite_manager::getSoftname (self, softid)`

Get if software exist by its id.

Parameters

<i>softid</i> ,:	Soft key
------------------	----------

Returns

: A software name

Definition at line 204 of file Sqlite_manager.py.

References getAllRNAlength(), and listscore().

Referenced by setContact().

6.44.3.27 `def irna::David2tulip::Sqlite_manager::Sqlite_manager::getsRNAbyIntid (self, interactid)`

Get the name of an sRNA from interaction key.

6.44 irna::David2tulip::Sqlite_manager::Sqlite_manager Class Reference 193

Parameters

<i>interactid</i> ,:	interaction key
----------------------	-----------------

Returns

: name of the sRNA

Definition at line 421 of file Sqlite_manager.py.

References getPositionsbyIntid().

Referenced by getScore(), irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getsRNAAlenbyIntid(), irna::iRNA_pred::Sqlite_manager::Sqlite_manager::getsRNAAlenbyIntid(), and getsRNAAlenbyIntid().

```
6.44.3.28 def irna::David2tulip::Sqlite_manager::Sqlite_manager::getsRNAidbyIntid ( self,
      interactid )
```

Get an sRNAid from an interaction.

Parameters

<i>interactid</i> ,:	Interaction id
----------------------	----------------

Definition at line 296 of file Sqlite_manager.py.

References getmRNAAlenbyIntid().

Referenced by getsRNAAlenbyIntid().

```
6.44.3.29 def irna::David2tulip::Sqlite_manager::Sqlite_manager::getsRNAlenbyIntid ( self,
      interactid )
```

Get an sRNA length from an interaction.

Parameters

<i>interactid</i> ,:	Interaction id
----------------------	----------------

Returns

: sRNA length

Definition at line 266 of file Sqlite_manager.py.

References getsRNAbyIntid(), and getsRNAidbyIntid().

Referenced by getallIRNA().

6.44.3.30 `def irna::David2tulip::Sqlite_manager::Sqlite_manager::IndexInteractidOnContact (self)`

Create index on interactid for contact.

Definition at line 507 of file Sqlite_manager.py.

Referenced by `irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getallsRNAname()`, `getallsRNAname()`, `irna::iRNA_pred::Sqlite_manager::Sqlite_manager::getallsRNAname()`, and `getPositionsbYIntid()`.

6.44.3.31 `def irna::David2tulip::Sqlite_manager::Sqlite_manager::IndexMrnaidOnInteract (self)`

Create index on mrnaid for interact.

Definition at line 523 of file Sqlite_manager.py.

Referenced by `getallsRNA()`, `irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getallsRNAname()`, `irna::iRNA_pred::Sqlite_manager::Sqlite_manager::getallsRNAname()`, and `getallsRNAname()`.

6.44.3.32 `def irna::David2tulip::Sqlite_manager::Sqlite_manager::IndexSrnaidOnInteract (self)`

Create index on srnaid for interact.

Definition at line 515 of file Sqlite_manager.py.

Referenced by `irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getallsRNAname()`, `getallsRNAname()`, `irna::iRNA_pred::Sqlite_manager::Sqlite_manager::getallsRNAname()`, and `getPositionsbYIntid()`.

6.44.3.33 `def irna::David2tulip::Sqlite_manager::Sqlite_manager::listit (self, t)`

Convert fetchall result into list of list.

Returns

: List of list

Definition at line 444 of file Sqlite_manager.py.

References `getallsRNAname()`.

Referenced by `getAllScore()`, `irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getAllSoft()`, `irna::iRNA_pred::Sqlite_manager::Sqlite_manager::getAllSoft()`, and `getAllSoft()`.

6.44.3.34 `def irna::David2tulip::Sqlite_manager::Sqlite_manager::listscore (self, score)`

Unlist score.

Returns

: List of score

Definition at line 452 of file Sqlite_manager.py.

References `getIntbysRNAid()`, and `listscore()`.

Referenced by `getAllSoft()`, `irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getInteract()`, `getInteract()`, `irna::iRNA_pred::Sqlite_manager::Sqlite_manager::getInteract()`, `irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getNbInteract()`, `getNbInteract()`, `irna::iRNA_pred::Sqlite_manager::Sqlite_manager::getNbInteract()`, `irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getSoftname()`, `getSoftname()`, `irna::iRNA_pred::Sqlite_manager::Sqlite_manager::getSoftname()`, `irna::iRNA_stat::Sqlite_manager::Sqlite_manager::listscore()`, `listscore()`, and `irna::iRNA_pred::Sqlite_manager::Sqlite_manager::listscore()`.

6.44.3.35 `def irna::David2tulip::Sqlite_manager::Sqlite_manager::setContact (self, interactid, tab)`

Insert contacts.

Parameters

<i>interactid,:</i>	Interaction key
<i>tab,:</i>	Table of contact

Definition at line 169 of file Sqlite_manager.py.

References `commitRetry()`, `getSoft()`, and `getSoftname()`.

Referenced by `setInteract()`.

6.44.3.36 `def irna::David2tulip::Sqlite_manager::Sqlite_manager::setInteract (self, sRNAid, mRNAid, softid)`

Insert interaction.

Parameters

<i>sRNAid,:</i>	sRNA key
<i>mRNAid,:</i>	mRNA key
<i>softid,:</i>	soft key

Returns

: Last insert id

Definition at line 137 of file Sqlite_manager.py.

References `commitRetry()`, and `setContact()`.

Referenced by `setRNA()`.

6.44.3.37 `def irna::David2tulip::Sqlite_manager::Sqlite_manager::setRNA (self, RNAtab)`

Insert RNA.

Parameters

<i>RNAtab,:</i>	Table of RNA
-----------------	--------------

Definition at line 107 of file Sqlite_manager.py.

References `commitRetry()`, `cur`, and `setInteract()`.

Referenced by `setSoft()`.

6.44.3.38 `def irna::David2tulip::Sqlite_manager::Sqlite_manager::setSoft (self, name)`

Insert soft name.

Parameters

<i>name,:</i>	Soft name
---------------	-----------

Returns

: Last insert id

Definition at line 90 of file Sqlite_manager.py.

References `commitRetry()`, and `setRNA()`.

Referenced by `disconnectDB2()`.

6.44.4 Member Data Documentation

6.44.4.1 `irna::David2tulip::Sqlite_manager::Sqlite_manager::conn`

Definition at line 48 of file Sqlite_manager.py.

Referenced by `irna::iRNA_stat::Sqlite_manager::Sqlite_manager::disconnectDB()`, `disconnectDB()`, and `irna::iRNA_pred::Sqlite_manager::Sqlite_manager::disconnectDB()`.

6.44.4.2 `irna::David2tulip::Sqlite_manager::Sqlite_manager::conn2`

Definition at line 48 of file Sqlite_manager.py.

Referenced by `irna::iRNA_stat::Sqlite_manager::Sqlite_manager::createSQLdb()`, `createSQLdb()`, `irna::iRNA_pred::Sqlite_manager::Sqlite_manager::createSQLdb()`, `irna::iRNA_stat::Sqlite_manager::Sqlite_manager::disconnectDB()`, `disconnectDB()`, and `irna::iRNA_pred::Sqlite_manager::Sqlite_manager::disconnectDB()`.

6.44.4.3 irna::David2tulip::Sqlite_manager::Sqlite_manager::cur

Definition at line 48 of file Sqlite_manager.py.

Referenced by irna::iRNA_stat::Sqlite_manager::Sqlite_manager::disconnectDB2(), disconnectDB2(), irna::iRNA_pred::Sqlite_manager::Sqlite_manager::disconnectDB2(), irna::iRNA_stat::Sqlite_manager::Sqlite_manager::setRNA(), setRNA(), and irna::iRNA_pred::Sqlite_manager::Sqlite_manager::setRNA().

6.44.4.4 irna::David2tulip::Sqlite_manager::Sqlite_manager::db_file

Definition at line 25 of file Sqlite_manager.py.

Referenced by irna::iRNA_stat::Sqlite_manager::Sqlite_manager::createSQLdb(), createSQLdb(), and irna::iRNA_pred::Sqlite_manager::Sqlite_manager::createSQLdb().

6.44.4.5 irna::David2tulip::Sqlite_manager::Sqlite_manager::db_path

Definition at line 25 of file Sqlite_manager.py.

Referenced by irna::iRNA_stat::Sqlite_manager::Sqlite_manager::createSQLdb(), createSQLdb(), and irna::iRNA_pred::Sqlite_manager::Sqlite_manager::createSQLdb().

6.44.4.6 irna::David2tulip::Sqlite_manager::Sqlite_manager::fastmode

Definition at line 25 of file Sqlite_manager.py.

Referenced by irna::iRNA_stat::Sqlite_manager::Sqlite_manager::disconnectDB(), irna::iRNA_pred::Sqlite_manager::Sqlite_manager::disconnectDB(), disconnectDB(), irna::iRNA_stat::Files::Files::getfiles(), and irna::iRNA_pred::Files::Files::getfiles().

The documentation for this class was generated from the following file:

- /home/amine/workspace/iRNA/irna/David2tulip/[Sqlite_manager.py](#)

6.45 irna::iRNA_pred::Sqlite_manager::Sqlite_manager Class - Reference

: Handle database connection, disconnection and querying.

Public Member Functions

- def [__init__](#)
Instantiate [Sqlite_manager](#) object.

- def [createSQLdb](#)
Create the database.
- def [connectDB](#)
Connect to the database.
- def [disconnectDB](#)
Disconnect the database.
- def [disconnectDB2](#)
Disconnect the database and copy on to the disk.
- def [setSoft](#)
Insert soft name.
- def [setRNA](#)
Insert RNA.
- def [setInteract](#)
Insert interaction.
- def [commitRetry](#)
Retry the commit operation.
- def [setContact](#)
Insert contacts.
- def [getSoft](#)
Get if software exist by its id.
- def [getSoftname](#)
Get if software exist by its id.
- def [getidSoftsbyname](#)
Get id of softwares corresponding to one name.
- def [getallRNAlength](#)
Get all RNA length.
- def [getallRNA](#)
Get all RNA name from one type.
- def [getRNA](#)
Get an RNA by its name and type.
- def [getsRNAlenbyIntid](#)
Get an sRNA length from an interaction.
- def [getAllsRNAlenbyIntid](#)
Get an sRNA length from an interaction.
- def [getsRNAidbyIntid](#)
Get an sRNAid from an interaction.
- def [getAllsRNAidbyIntid](#)
Get an sRNAid from an interaction.
- def [getmRNAlenbyIntid](#)
Get an mRNA from an interaction.
- def [getAllmRNAlenbyIntid](#)
Get an mRNA from an interaction.
- def [getNbInteract](#)

- Count the number of interaction for one software.*
- def [getInteract](#)
Get interactions of one software.
- def [getScore](#)
Get the score of an interaction.
- def [getAllScore](#)
Get the score for several interactions.
- def [getAllSoft](#)
Get all the software.
- def [getsRNAbyIntid](#)
Get the name of an sRNA from interaction key.
- def [getmRNAbyIntid](#)
Get the name of an mRNA from interaction key.
- def [listit](#)
Convert fetchall result into list of list.
- def [listscore](#)
Unlist score.
- def [getPositionbyIntid](#)
Get position for one interaction.
- def [getallsRNA](#)
Get all sRNA.
- def [getallsRNAname](#)
Get an sRNA name and unlist.
- def [getIntbysRNAid](#)
Get the interactid for an sRNA.
- def [IndexInteractidOnContact](#)
Create index on interactid for contact.
- def [IndexSrnaidOnInteract](#)
Create index on srnaid for interact.
- def [IndexMrnaidOnInteract](#)
Create index on mrnaid for interact.
- def [createIndexes](#)
Create index for most use connection.

Public Attributes

- [db_path](#)
- [db_file](#)
- [fastmode](#)
- [conn2](#)
- [conn](#)
- [cur](#)

6.45.1 Detailed Description

: Handle database connection, disconnection and querying.

Definition at line 16 of file `Sqlite_manager.py`.

6.45.2 Constructor & Destructor Documentation

6.45.2.1 `def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::__init__(self, result, db_file, fastmode)`

Instantiate [Sqlite_manager](#) object.

Parameters

<i>result</i> ,:	Path where to write the database
<i>db_file</i> ,:	SQLite db file
<i>fastmode</i> ,:	fastmode flag

Definition at line 25 of file `Sqlite_manager.py`.

6.45.3 Member Function Documentation

6.45.3.1 `def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::commitRetry (self)`

Retry the commit operation.

Returns

: State of the commit

Definition at line 154 of file `Sqlite_manager.py`.

Referenced by `irna::iRNA_stat::Sqlite_manager::Sqlite_manager::setContact()`, `setContact()`, `irna::iRNA_stat::Sqlite_manager::Sqlite_manager::setInteract()`, `setInteract()`, `irna::iRNA_stat::Sqlite_manager::Sqlite_manager::setRNA()`, `setRNA()`, `irna::iRNA_stat::Sqlite_manager::Sqlite_manager::setSoft()`, and `setSoft()`.

6.45.3.2 `def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::connectDB (self)`

Connect to the database.

Definition at line 48 of file `Sqlite_manager.py`.

Referenced by `createSQLdb()`.

6.45.3.3 `def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::createIndexes (self)`

Create index for most use connection.

6.45 irna::iRNA_pred::Sqlite_manager::Sqlite_manager Class Reference 201

Definition at line 531 of file Sqlite_manager.py.

Referenced by getallsRNAname().

6.45.3.4 def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::createSQLdb (self)

Create the database.

Definition at line 34 of file Sqlite_manager.py.

References irna::David2tulip::Sqlite_manager::Sqlite_manager::conn2, conn2, connectDB(), irna::David2tulip::Sqlite_manager::Sqlite_manager::db_file, db_file, irna::David2tulip::Sqlite_manager::Sqlite_manager::db_path, and db_path.

6.45.3.5 def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::disconnectDB (self)

Disconnect the database.

Definition at line 63 of file Sqlite_manager.py.

References irna::David2tulip::Sqlite_manager::Sqlite_manager::conn, conn, irna::David2tulip::Sqlite_manager::Sqlite_manager::conn2, conn2, disconnectDB2(), irna::David2tulip::Files::Files::fastmode, irna::iRNA_pred::Files::Files::fastmode, irna::David2tulip::Sqlite_manager::Sqlite_manager::fastmode, and fastmode.

6.45.3.6 def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::disconnectDB2 (self)

Disconnect the database and copy on to the disk.

Definition at line 74 of file Sqlite_manager.py.

References irna::David2tulip::Sqlite_manager::Sqlite_manager::cur, cur, and setSoft().

Referenced by disconnectDB().

6.45.3.7 def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::getAllmRNAlenbyIntid (self, table_interactid)

Get an mRNA from an interaction.

Parameters

<i>table_interactid.</i>	table of interaction id
--------------------------	-------------------------

Returns

: List of mRNA length

Definition at line 341 of file Sqlite_manager.py.

References getScore().

Referenced by `getAIIrNAidbyIntid()`.

6.45.3.8 `def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::getAIIrNA (self, type_RNA)`

Get all RNA name from one type.

Parameters

<i>type_RNA</i> ,:	Type of RNA
--------------------	-------------

Returns

: list of RNA

Definition at line 240 of file `Sqlite_manager.py`.

References `getrNAlenbyIntid()`.

Referenced by `getidSoftsbyname()`.

6.45.3.9 `def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::getAIIrNALength (self, type_RNA)`

Get all RNA length.

Parameters

<i>type_RNA</i> ,:	Type of RNA
--------------------	-------------

Returns

: list of RNA with their length

Definition at line 228 of file `Sqlite_manager.py`.

References `getRNA()`.

Referenced by `getSoftname()`.

6.45.3.10 `def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::getAIIScore (self, table_interactid)`

Get the score for several interactions.

Parameters

<i>table_ - interactid</i> ,:	list of interaction key
-------------------------------	-------------------------

Returns

: List of score

Definition at line 395 of file Sqlite_manager.py.

References `getmRNAbyIntid()`, and `listit()`.

Referenced by `getNbInteract()`.

6.45.3.11 `def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::getAllSoft (self)`

Get all the software.

Returns

: List of software

Definition at line 409 of file Sqlite_manager.py.

References `irna::David2tulip::Sqlite_manager::Sqlite_manager::listit()`, `listit()`, and `listscore()`.

Referenced by `getInteract()`.

6.45.3.12 `def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::getallsRNA (self)`

Get all sRNA.

Returns

: List of rnaid

Definition at line 474 of file Sqlite_manager.py.

References `IndexMrnaidOnInteract()`.

Referenced by `getmRNAbyIntid()`.

6.45.3.13 `def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::getAllsRNAidbyIntid (self, table_interactid)`

Get an sRNAid from an interaction.

Parameters

<i>interactid,:</i>	Interaction id
---------------------	----------------

Returns

: List of sRNAid

Definition at line 310 of file Sqlite_manager.py.

References getAllmRNAlenbyIntid(), getmRNAbyIntid(), and irna::David2tulip::Sqlite_manager::Sqlite_manager::getmRNAbyIntid().

Referenced by getAllsRNAlenbyIntid().

```
6.45.3.14 def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::getAllsRNAlenbyIntid ( self,
        table_interactid )
```

Get an sRNA length from an interaction.

Parameters

<i>table_ - interactid,:</i>	table of interaction id
----------------------------------	-------------------------

Returns

: list of sRNA length

Definition at line 280 of file Sqlite_manager.py.

References getAllsRNAidbyIntid().

Referenced by getRNA().

```
6.45.3.15 def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::getallsRNAname ( self )
```

Get an sRNA name and unlist.

Returns

: List of rnaid

Definition at line 485 of file Sqlite_manager.py.

References createIndexes(), irna::David2tulip::Sqlite_manager::Sqlite_manager::IndexInteractidOnContact(), IndexInteractidOnContact(), IndexMrnaidOnInteract(), irna::David2tulip::Sqlite_manager::Sqlite_manager::IndexMrnaidOnInteract(), irna::David2tulip::Sqlite_manager::Sqlite_manager::IndexSrnaidOnInteract(), and IndexSrnaidOnInteract().

Referenced by listit().

```
6.45.3.16 def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::getidSoftsbyname ( self,
        name )
```

Get id of softwares corresponding to one name.

6.45 irna::iRNA_pred::Sqlite_manager::Sqlite_manager Class Reference 205

Parameters

<i>name,</i>	name of a software
--------------	--------------------

Returns

: list of softid

Definition at line 216 of file Sqlite_manager.py.

References `getallIRNA()`.

Referenced by `getSoft()`.

```
6.45.3.17 def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::getIntbysRNAid ( self, srnaid )
```

Get the interactid for an sRNA.

Parameters

<i>srnaid,</i>	rna key
----------------	---------

Returns

: List of interactid

Definition at line 497 of file Sqlite_manager.py.

Referenced by `listscore()`.

```
6.45.3.18 def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::getInteract ( self, softid )
```

Get interactions of one software.

Parameters

<i>softid,</i>	soft key
----------------	----------

Returns

: List of interactid

Definition at line 371 of file Sqlite_manager.py.

References `getAllSoft()`, `irna::David2tulip::Sqlite_manager::Sqlite_manager::listscore()`, and `listscore()`.

Referenced by `getmRNAlenbyIntid()`.

6.45.3.19 `def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::getmRNAbyIntid (self,
interactid)`

Get the name of an mRNA from interaction key.

Parameters

<i>interactid</i> ,:	interaction key
----------------------	-----------------

Returns

: name of the mRNA

Definition at line 433 of file `Sqlite_manager.py`.

References `getallsRNA()`.

Referenced by `getAllScore()`, `irna::iRNA_stat::Sqlite_manager::Sqlite_manager::get-
AllsRNAidbyIntid()`, and `getAllsRNAidbyIntid()`.

6.45.3.20 `def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::getmRNAlenbyIntid (self,
interactid)`

Get an mRNA from an interaction.

Parameters

<i>interactid</i> ,:	Interaction id
----------------------	--------------------------------

Returns

: mRNA length

Definition at line 327 of file `Sqlite_manager.py`.

References `getInteract()`, and `getNbInteract()`.

Referenced by `getsRNAidbyIntid()`.

6.45.3.21 `def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::getNbInteract (self, softid)`

Count the number of interaction for one software.

Parameters

<i>softid</i> ,:	soft key
------------------	----------

6.45 irna::iRNA_pred::Sqlite_manager::Sqlite_manager Class Reference 207

Returns

: Number of interaction

Definition at line 358 of file Sqlite_manager.py.

References `getAllScore()`, `irna::David2tulip::Sqlite_manager::Sqlite_manager::listscore()`, and `listscore()`.

Referenced by `getmRNAlenbyIntid()`.

```
6.45.3.22 def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::getPositionbyIntid ( self,
                                             interactid )
```

Get position for one interaction.

Parameters

<i>interactid</i> ,:	interact key
----------------------	--------------

Returns

: List of position

Definition at line 463 of file Sqlite_manager.py.

References `IndexInteractidOnContact()`, and `IndexSrnaidOnInteract()`.

Referenced by `getsRNAbyIntid()`.

```
6.45.3.23 def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::getRNA ( self, name,
                                                                           type_RNA )
```

Get an RNA by its name and type.

Parameters

<i>name</i> ,:	RNA name
<i>type</i> ,:	RNA type

Returns

: A rnaid

Definition at line 254 of file Sqlite_manager.py.

References `getAllsRNAlenbyIntid()`.

Referenced by `getallRNAlength()`.

6.45.3.24 `def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::getScore (self, interactid)`

Get the score of an interaction.

Parameters

<i>interactid,:</i>	interaction key
---------------------	-----------------

Returns

: List of score

Definition at line 383 of file Sqlite_manager.py.

References getsRNAbyIntid().

Referenced by getAllmRNAlenbyIntid().

6.45.3.25 `def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::getSoft (self, softid)`

Get if software exist by its id.

Parameters

<i>softid,:</i>	Soft key
-----------------	----------

Returns

: A softid

Definition at line 192 of file Sqlite_manager.py.

References getidSoftsbyname().

Referenced by setContact().

6.45.3.26 `def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::getSoftname (self, softid)`

Get if software exist by its id.

Parameters

<i>softid,:</i>	Soft key
-----------------	----------

Returns

: A software name

Definition at line 204 of file Sqlite_manager.py.

6.45 irna::iRNA_pred::Sqlite_manager::Sqlite_manager Class Reference 209

References `getAllRNAlength()`, `irna::David2tulip::Sqlite_manager::Sqlite_manager::listscore()`, and `listscore()`.

Referenced by `setContact()`.

6.45.3.27 `def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::getsRNAbyIntid (self,
interactid)`

Get the name of an sRNA from interaction key.

Parameters

<i>interactid</i> ,:	interaction key
----------------------	-----------------

Returns

: name of the sRNA

Definition at line 421 of file `Sqlite_manager.py`.

References `getPositionbyIntid()`.

Referenced by `getScore()`, `irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getsRNAlenbyIntid()`, and `getsRNAbyIntid()`.

6.45.3.28 `def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::getsRNAidbyIntid (self,
interactid)`

Get an sRNAid from an interaction.

Parameters

<i>interactid</i> ,:	Interaction id
----------------------	--------------------------------

Definition at line 296 of file `Sqlite_manager.py`.

References `getmRNAlenbyIntid()`.

Referenced by `getsRNAlenbyIntid()`.

6.45.3.29 `def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::getsRNAlenbyIntid (self,
interactid)`

Get an sRNA length from an interaction.

Parameters

<i>interactid</i> ,:	Interaction id
----------------------	--------------------------------

Returns

: sRNA length

Definition at line 266 of file `Sqlite_manager.py`.

References `irna::David2tulip::Sqlite_manager::Sqlite_manager::getsRNAbyIntid()`, `getsRNAbyIntid()`, and `getsRNAidbyIntid()`.

Referenced by `getallRNA()`.

6.45.3.30 `def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::IndexInteractidOnContact (self)`

Create index on interactid for contact.

Definition at line 507 of file `Sqlite_manager.py`.

Referenced by `irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getallsRNAname()`, `getallsRNAname()`, and `getPositionsbbyIntid()`.

6.45.3.31 `def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::IndexMrnaidOnInteract (self)`

Create index on mrnaid for interact.

Definition at line 523 of file `Sqlite_manager.py`.

Referenced by `getallsRNA()`, `irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getallsRNAname()`, and `getallsRNAname()`.

6.45.3.32 `def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::IndexSrnaidOnInteract (self)`

Create index on srnaid for interact.

Definition at line 515 of file `Sqlite_manager.py`.

Referenced by `irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getallsRNAname()`, `getallsRNAname()`, and `getPositionsbbyIntid()`.

6.45.3.33 `def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::listit (self, t)`

Convert fetchall result into list of list.

Returns

: List of list

Definition at line 444 of file `Sqlite_manager.py`.

References `getallsRNAname()`.

Referenced by `getAllScore()`, `irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getAllSoft()`, and `getAllSoft()`.

6.45 irna::iRNA_pred::Sqlite_manager::Sqlite_manager Class Reference 211

6.45.3.34 `def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::listscore (self, score)`

Unlist score.

Returns

: List of score

Definition at line 452 of file `Sqlite_manager.py`.

References `getIntbysRNAid()`, `irna::David2tulip::Sqlite_manager::Sqlite_manager::listscore()`, and `listscore()`.

Referenced by `getAllSoft()`, `irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getInteract()`, `getInteract()`, `irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getNbInteract()`, `getNbInteract()`, `irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getSoftname()`, `getSoftname()`, `irna::iRNA_stat::Sqlite_manager::Sqlite_manager::listscore()`, and `listscore()`.

6.45.3.35 `def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::setContact (self, interactid, tab)`

Insert contacts.

Parameters

<i>interactid</i> ,:	Interaction key
<i>tab</i> ,:	Table of contact

Definition at line 169 of file `Sqlite_manager.py`.

References `irna::David2tulip::Sqlite_manager::Sqlite_manager::commitRetry()`, `commitRetry()`, `getSoft()`, and `getSoftname()`.

Referenced by `setInteract()`.

6.45.3.36 `def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::setInteract (self, sRNAid, mRNAid, softid)`

Insert interaction.

Parameters

<i>sRNAid</i> ,:	sRNA key
<i>mRNAid</i> ,:	mRNA key
<i>softid</i> ,:	soft key

Returns

: Last insert id

Definition at line 137 of file Sqlite_manager.py.

References `commitRetry()`, and `setContact()`.

Referenced by `setRNA()`.

6.45.3.37 `def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::setRNA (self, RNAtab)`

Insert RNA.

Parameters

<i>RNAtab</i> ,:	Table of RNA
------------------	--------------

Definition at line 107 of file Sqlite_manager.py.

References `irna::David2tulip::Sqlite_manager::Sqlite_manager::commitRetry()`, `commitRetry()`, `irna::David2tulip::Sqlite_manager::Sqlite_manager::cur`, `cur`, and `setInteract()`.

Referenced by `setSoft()`.

6.45.3.38 `def irna::iRNA_pred::Sqlite_manager::Sqlite_manager::setSoft (self, name)`

Insert soft name.

Parameters

<i>name</i> ,:	Soft name
----------------	-----------

Returns

: Last insert id

Definition at line 90 of file Sqlite_manager.py.

References `irna::David2tulip::Sqlite_manager::Sqlite_manager::commitRetry()`, `commitRetry()`, and `setRNA()`.

Referenced by `disconnectDB2()`.

6.45.4 Member Data Documentation

6.45.4.1 `irna::iRNA_pred::Sqlite_manager::Sqlite_manager::conn`

Definition at line 48 of file Sqlite_manager.py.

Referenced by `irna::iRNA_stat::Sqlite_manager::Sqlite_manager::disconnectDB()`, and `disconnectDB()`.

6.45.4.2 irna::iRNA_pred::Sqlite_manager::Sqlite_manager::conn2

Definition at line 48 of file Sqlite_manager.py.

Referenced by irna::iRNA_stat::Sqlite_manager::Sqlite_manager::createSQLdb(), createSQLdb(), irna::iRNA_stat::Sqlite_manager::Sqlite_manager::disconnectDB(), and disconnectDB().

6.45.4.3 irna::iRNA_pred::Sqlite_manager::Sqlite_manager::cur

Definition at line 48 of file Sqlite_manager.py.

Referenced by irna::iRNA_stat::Sqlite_manager::Sqlite_manager::disconnectDB2(), disconnectDB2(), irna::iRNA_stat::Sqlite_manager::Sqlite_manager::setRNA(), and setRNA().

6.45.4.4 irna::iRNA_pred::Sqlite_manager::Sqlite_manager::db_file

Definition at line 25 of file Sqlite_manager.py.

Referenced by irna::iRNA_stat::Sqlite_manager::Sqlite_manager::createSQLdb(), and createSQLdb().

6.45.4.5 irna::iRNA_pred::Sqlite_manager::Sqlite_manager::db_path

Definition at line 25 of file Sqlite_manager.py.

Referenced by irna::iRNA_stat::Sqlite_manager::Sqlite_manager::createSQLdb(), and createSQLdb().

6.45.4.6 irna::iRNA_pred::Sqlite_manager::Sqlite_manager::fastmode

Definition at line 25 of file Sqlite_manager.py.

Referenced by irna::iRNA_stat::Sqlite_manager::Sqlite_manager::disconnectDB(), disconnectDB(), and irna::iRNA_stat::Files::Files::getfiles().

The documentation for this class was generated from the following file:

- [/home/amine/workspace/iRNA/irna/iRNA_pred/Sqlite_manager.py](#)

6.46 irna::iRNA_stat::Sqlite_manager::Sqlite_manager Class - Reference

Public Member Functions

- [def __init__](#)

- Instantiate [Sqlite_manager](#) object.*
- def [createSQLdb](#)
Create the database.
- def [connectDB](#)
Connect to the database.
- def [disconnectDB](#)
Disconnect the database.
- def [disconnectDB2](#)
Disconnect the database and copy on to the disk.
- def [setSoft](#)
Insert soft name.
- def [setRNA](#)
Insert RNA.
- def [setInteract](#)
Insert interaction.
- def [commitRetry](#)
Retry the commit operation.
- def [setContact](#)
Insert contacts.
- def [getSoft](#)
Get if software exist by its id.
- def [getSoftname](#)
Get if software exist by its id.
- def [getidSoftsbyname](#)
Get id of softwares corresponding to one name.
- def [getAllRNAlength](#)
Get all RNA length.
- def [getAllRNA](#)
Get all RNA name from one type.
- def [getRNA](#)
Get an RNA by its name and type.
- def [getsRNAlenbyIntid](#)
Get an sRNA length from an interaction.
- def [getAllsRNAlenbyIntid](#)
Get an sRNA length from an interaction.
- def [getsRNAidbyIntid](#)
Get an sRNAid from an interaction.
- def [getAllsRNAidbyIntid](#)
Get an sRNAid from an interaction.
- def [getmRNAlenbyIntid](#)
Get an mRNA from an interaction.
- def [getAllmRNAlenbyIntid](#)
Get an mRNA from an interaction.

- def [getNbInteract](#)
Count the number of interaction for one software.
- def [getInteract](#)
Get interactions of one software.
- def [getScore](#)
Get the score of an interaction.
- def [getAllScore](#)
Get the score for several interactions.
- def [getAllSoft](#)
Get all the software.
- def [getsRNAbyIntid](#)
Get the name of an sRNA from interaction key.
- def [getmRNAbyIntid](#)
Get the name of an mRNA from interaction key.
- def [listit](#)
Convert fetchall result into list of list.
- def [listscore](#)
Unlist score.
- def [getPositionbyIntid](#)
Get position for one interaction.
- def [getallsRNA](#)
Get all sRNA.
- def [getallsRNAname](#)
Get an sRNA name and unlist.
- def [getIntbysRNAid](#)
Get the interactid for an sRNA.
- def [IndexInteractidOnContact](#)
Create index on interactid for contact.
- def [IndexSrnaidOnInteract](#)
Create index on srnaid for interact.
- def [IndexMrnaidOnInteract](#)
Create index on mrnaid for interact.
- def [createIndexes](#)
Create index for most use connection.

Public Attributes

- [db_path](#)
- [db_file](#)
- [fastmode](#)
- [conn2](#)
- [conn](#)
- [cur](#)

6.46.1 Detailed Description

Definition at line 12 of file `Sqlite_manager.py`.

6.46.2 Constructor & Destructor Documentation

6.46.2.1 `def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::__init__(self, result, db_file, fastmode)`

Instantiate [Sqlite_manager](#) object.

Parameters

<i>result</i> ,:	Path where to write the database
<i>db_file</i> ,:	SQLite db file
<i>fastmode</i> ,:	fastmode flag

Definition at line 21 of file `Sqlite_manager.py`.

6.46.3 Member Function Documentation

6.46.3.1 `def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::commitRetry (self)`

Retry the commit operation.

Returns

: State of the commit

Definition at line 150 of file `Sqlite_manager.py`.

Referenced by `setContact()`, `setInteract()`, `setRNA()`, and `setSoft()`.

6.46.3.2 `def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::connectDB (self)`

Connect to the database.

Definition at line 44 of file `Sqlite_manager.py`.

Referenced by `createSQLdb()`.

6.46.3.3 `def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::createIndexes (self)`

Create index for most use connection.

Definition at line 527 of file `Sqlite_manager.py`.

Referenced by `getallsRNAname()`.

6.46.3.4 def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::createSQLdb (*self*)

Create the database.

Definition at line 30 of file Sqlite_manager.py.

References conn2, irna::David2tulip::Sqlite_manager::Sqlite_manager::conn2, irna::iRNA_pred::Sqlite_manager::Sqlite_manager::conn2, connectDB(), db_file, irna::David2tulip::Sqlite_manager::Sqlite_manager::db_file, irna::iRNA_pred::Sqlite_manager::Sqlite_manager::db_file, db_path, irna::David2tulip::Sqlite_manager::Sqlite_manager::db_path, and irna::iRNA_pred::Sqlite_manager::Sqlite_manager::db_path.

6.46.3.5 def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::disconnectDB (*self*)

Disconnect the database.

Definition at line 59 of file Sqlite_manager.py.

References conn, irna::David2tulip::Sqlite_manager::Sqlite_manager::conn, irna::iRNA_pred::Sqlite_manager::Sqlite_manager::conn, conn2, irna::David2tulip::Sqlite_manager::Sqlite_manager::conn2, irna::iRNA_pred::Sqlite_manager::Sqlite_manager::conn2, disconnectDB2(), irna::David2tulip::Files::Files::fastmode, irna::iRNA_stat::Files::Files::fastmode, irna::iRNA_pred::Files::Files::fastmode, fastmode, irna::David2tulip::Sqlite_manager::Sqlite_manager::fastmode, and irna::iRNA_pred::Sqlite_manager::Sqlite_manager::fastmode.

6.46.3.6 def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::disconnectDB2 (*self*)

Disconnect the database and copy on to the disk.

Definition at line 70 of file Sqlite_manager.py.

References cur, irna::David2tulip::Sqlite_manager::Sqlite_manager::cur, irna::iRNA_pred::Sqlite_manager::Sqlite_manager::cur, and setSoft().

Referenced by disconnectDB().

6.46.3.7 def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getAllmRNAlenbyIntid (*self*, *table_interactid*)

Get an mRNA from an interaction.

Parameters

<i>table_interactid</i> ,	table of interaction id
---------------------------	-------------------------

Returns

: List of mRNA length

Definition at line 337 of file Sqlite_manager.py.

References `getInteract()`, and `getScore()`.

Referenced by `getAIsRNAidbyIntid()`.

6.46.3.8 `def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getallRNA (self, type_RNA)`

Get all RNA name from one type.

Parameters

<i>type_RNA</i> ,:	Type of RNA
--------------------	-------------

Returns

: list of RNA

Definition at line 236 of file `Sqlite_manager.py`.

References `getsRNAlenbyIntid()`.

Referenced by `getidSoftsbyname()`.

6.46.3.9 `def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getallRNAlength (self, type_RNA)`

Get all RNA length.

Parameters

<i>type_RNA</i> ,:	Type of RNA
--------------------	-------------

Returns

: list of RNA with their length

Definition at line 224 of file `Sqlite_manager.py`.

References `getRNA()`.

Referenced by `getSoftname()`.

6.46.3.10 `def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getAllScore (self, table_interactid)`

Get the score for several interactions.

Parameters

<i>table_ - interactid</i> ,:	list of interaction key
-------------------------------	-------------------------

Returns

: List of score

Definition at line 391 of file Sqlite_manager.py.

References getmRNAbyIntid().

Referenced by getNbInteract().

6.46.3.11 def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getAllSoft (self)

Get all the software.

Returns

: List of software

Definition at line 405 of file Sqlite_manager.py.

References listit(), irna::David2tulip::Sqlite_manager::Sqlite_manager::listit(), irna::iRNA_A_pred::Sqlite_manager::Sqlite_manager::listit(), and listscore().

Referenced by getInteract().

6.46.3.12 def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getallsRNA (self)

Get all sRNA.

Returns

: List of rnaid

Definition at line 470 of file Sqlite_manager.py.

References IndexMrnaidOnInteract(), and IndexSrnaidOnInteract().

Referenced by getmRNAbyIntid().

6.46.3.13 def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getAllsRNAidbyIntid (self, table_interactid)

Get an sRNAid from an interaction.

Parameters

interactid,:	Interaction id
--------------	----------------

Returns

: List of sRNAid

Definition at line 306 of file Sqlite_manager.py.

References getAllmRNAlenbyIntid(), getmRNAbyIntid(), irna::iRNA_pred::Sqlite_manager::Sqlite_manager::getmRNAbyIntid(), and irna::David2tulip::Sqlite_manager::Sqlite_manager::getmRNAbyIntid().

Referenced by getAllsRNAlenbyIntid().

6.46.3.14 `def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getAllsRNAlenbyIntid (self, table_interactid)`

Get an sRNA length from an interaction.

Parameters

<i>table_ - interactid,:</i>	table of interaction id
------------------------------	-------------------------

Returns

: list of sRNA length

Definition at line 276 of file Sqlite_manager.py.

References getAllsRNAidbyIntid().

Referenced by getRNA().

6.46.3.15 `def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getallsRNAname (self)`

Get an sRNA name and unlist.

Returns

: List of rnaid

Definition at line 481 of file Sqlite_manager.py.

References createIndexes(), IndexInteractidOnContact(), irna::David2tulip::Sqlite_manager::Sqlite_manager::IndexInteractidOnContact(), irna::iRNA_pred::Sqlite_manager::Sqlite_manager::IndexInteractidOnContact(), IndexMrnaidOnInteract(), irna::David2tulip::Sqlite_manager::Sqlite_manager::IndexMrnaidOnInteract(), irna::iRNA_pred::Sqlite_manager::Sqlite_manager::IndexMrnaidOnInteract(), IndexSrnaidOnInteract(), irna::David2tulip::Sqlite_manager::Sqlite_manager::IndexSrnaidOnInteract(), and irna::iRNA_pred::Sqlite_manager::Sqlite_manager::IndexSrnaidOnInteract().

Referenced by listit().

6.46 irna::iRNA_stat::Sqlite_manager::Sqlite_manager Class Reference 221

6.46.3.16 `def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getidSoftsbyname (self, name)`

Get id of softwares corresponding to one name.

Parameters

<i>name,</i> :	name of a software
----------------	--------------------

Returns

: list of softid

Definition at line 212 of file Sqlite_manager.py.

References `getallIRNA()`.

Referenced by `getSoft()`.

6.46.3.17 `def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getIntbysRNAid (self, srnaid)`

Get the interactid for an sRNA.

Parameters

<i>srnaid,</i> :	rna key
------------------	---------

Returns

: List of interactid

Definition at line 493 of file Sqlite_manager.py.

Referenced by `listscore()`.

6.46.3.18 `def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getInteract (self, softid)`

Get interactions of one software.

Parameters

<i>softid,</i> :	soft key
------------------	----------

Returns

: List of interactid

Definition at line 367 of file Sqlite_manager.py.

References `getAllSoft()`, `listscore()`, `irna::David2tulip::Sqlite_manager::Sqlite_manager::listscore()`, and `irna::iRNA_pred::Sqlite_manager::Sqlite_manager::listscore()`.

Referenced by `getAllmRNAIdbyIntid()`.

```
6.46.3.19 def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getmRNAbyIntid ( self,
                                     interactid )
```

Get the name of an mRNA from interaction key.

Parameters

<i>interactid</i> ,:	interaction key
----------------------	-----------------

Returns

: name of the mRNA

Definition at line 429 of file `Sqlite_manager.py`.

References `getallsRNA()`.

Referenced by `getAllScore()`, and `getallsRNAIdbyIntid()`.

```
6.46.3.20 def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getmRNAIdbyIntid ( self,
                                     interactid )
```

Get an mRNA from an interaction.

Parameters

<i>interactid</i> ,:	Interaction id
----------------------	--------------------------------

Returns

: mRNA length

Definition at line 323 of file `Sqlite_manager.py`.

References `getNbInteract()`.

Referenced by `getsRNAIdbyIntid()`.

```
6.46.3.21 def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getNbInteract ( self, softid )
```

Count the number of interaction for one software.

Parameters

<i>softid</i> ,:	soft key
------------------	----------

Returns

: Number of interaction

Definition at line 354 of file Sqlite_manager.py.

References `getAllScore()`, `listscore()`, `irna::David2tulip::Sqlite_manager::Sqlite_manager::listscore()`, and `irna::iRNA_pred::Sqlite_manager::Sqlite_manager::listscore()`.

Referenced by `getmRNAlenbyIntid()`.

6.46.3.22 `def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getPositionsbyIntid (self, interactid)`

Get position for one interaction.

Parameters

<i>interactid</i> ,:	interact key
----------------------	--------------

Returns

: List of position

Definition at line 459 of file Sqlite_manager.py.

References `IndexInteractidOnContact()`.

Referenced by `getsRNAbyIntid()`.

6.46.3.23 `def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getRNA (self, name, type_RNA)`

Get an RNA by its name and type.

Parameters

<i>name</i> ,:	RNA name
<i>type</i> ,:	RNA type

Returns

: A rnaid

Definition at line 250 of file Sqlite_manager.py.

References `getAllsRNAlenbyIntid()`.

Referenced by `getAllRNAlength()`.

6.46.3.24 `def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getScore (self, interactid)`

Get the score of an interaction.

Parameters

<i>interactid</i> ,:	interaction key
----------------------	-----------------

Returns

: List of score

Definition at line 379 of file Sqlite_manager.py.

References getsRNAbyIntid().

Referenced by getAllmRNAlenbyIntid().

6.46.3.25 `def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getSoft (self, softid)`

Get if software exist by its id.

Parameters

<i>softid</i> ,:	Soft key
------------------	--------------------------

Returns

: A softid

Definition at line 188 of file Sqlite_manager.py.

References getidSoftsbyname().

Referenced by setContact().

6.46.3.26 `def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getSoftname (self, softid)`

Get if software exist by its id.

Parameters

<i>softid</i> ,:	Soft key
------------------	--------------------------

Returns

: A software name

Definition at line 200 of file Sqlite_manager.py.

6.46 irna::iRNA_stat::Sqlite_manager::Sqlite_manager Class Reference 225

References `getallRNAlength()`, `listscore()`, `irna::David2tulip::Sqlite_manager::Sqlite_manager::listscore()`, and `irna::iRNA_pred::Sqlite_manager::Sqlite_manager::listscore()`.

Referenced by `setContact()`.

6.46.3.27 `def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getsRNAbyIntid (self,
interactid)`

Get the name of an sRNA from interaction key.

Parameters

<i>interactid</i> ,:	interaction key
----------------------	-----------------

Returns

: name of the sRNA

Definition at line 417 of file `Sqlite_manager.py`.

References `getPositionbyIntid()`.

Referenced by `getScore()`, and `getsRNAlenbyIntid()`.

6.46.3.28 `def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getsRNAidbyIntid (self,
interactid)`

Get an sRNAid from an interaction.

Parameters

<i>interactid</i> ,:	Interaction id
----------------------	--------------------------------

Definition at line 292 of file `Sqlite_manager.py`.

References `getmRNAlenbyIntid()`.

Referenced by `getsRNAlenbyIntid()`.

6.46.3.29 `def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::getsRNAlenbyIntid (self,
interactid)`

Get an sRNA length from an interaction.

Parameters

<i>interactid</i> ,:	Interaction id
----------------------	--------------------------------

Returns

: sRNA length

Definition at line 262 of file `Sqlite_manager.py`.

References `getsRNAbyIntid()`, `irna::iRNA_pred::Sqlite_manager::Sqlite_manager::getsRNAbyIntid()`, `irna::David2tulip::Sqlite_manager::Sqlite_manager::getsRNAbyIntid()`, and `getsRNAidbyIntid()`.

Referenced by `getallRNA()`.

6.46.3.30 `def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::IndexInteractidOnContact (self)`

Create index on interactid for contact.

Definition at line 503 of file `Sqlite_manager.py`.

Referenced by `getallsRNAname()`, and `getPositionsbbyIntid()`.

6.46.3.31 `def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::IndexMrnaidOnInteract (self)`

Create index on mrnaid for interact.

Definition at line 519 of file `Sqlite_manager.py`.

Referenced by `getallsRNA()`, and `getallsRNAname()`.

6.46.3.32 `def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::IndexSrnaidOnInteract (self)`

Create index on srnaid for interact.

Definition at line 511 of file `Sqlite_manager.py`.

Referenced by `getallsRNA()`, and `getallsRNAname()`.

6.46.3.33 `def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::listit (self, t)`

Convert fetchall result into list of list.

Returns

: List of list

Definition at line 440 of file `Sqlite_manager.py`.

References `getallsRNAname()`.

Referenced by `getAllSoft()`.

6.46.3.34 `def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::listscore (self, score)`

Unlist score.

Returns

: List of score

Definition at line 448 of file `Sqlite_manager.py`.

References `getIntbysRNAid()`, `listscore()`, `irna::David2tulip::Sqlite_manager::Sqlite_manager::listscore()`, and `irna::iRNA_pred::Sqlite_manager::Sqlite_manager::listscore()`.

Referenced by `getAllSoft()`, `getInteract()`, `getNbInteract()`, `getSoftname()`, and `listscore()`.

6.46.3.35 `def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::setContact (self, interactid, tab)`

Insert contacts.

Parameters

<i>interactid</i> ,:	Interaction key
<i>tab</i> ,:	Table of contact

Definition at line 165 of file `Sqlite_manager.py`.

References `commitRetry()`, `irna::iRNA_pred::Sqlite_manager::Sqlite_manager::commitRetry()`, `irna::David2tulip::Sqlite_manager::Sqlite_manager::commitRetry()`, `getSoft()`, and `getSoftname()`.

Referenced by `setInteract()`.

6.46.3.36 `def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::setInteract (self, sRNAid, mRNAid, softid)`

Insert interaction.

Parameters

<i>sRNAid</i> ,:	sRNA key
<i>mRNAid</i> ,:	mRNA key
<i>softid</i> ,:	soft key

Returns

: Last insert id

Definition at line 133 of file `Sqlite_manager.py`.

References `commitRetry()`, `irna::iRNA_pred::Sqlite_manager::Sqlite_manager::commitRetry()`, `irna::David2tulip::Sqlite_manager::Sqlite_manager::commitRetry()`, and `setContact()`.

Referenced by `setRNA()`.

6.46.3.37 `def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::setRNA (self, RNAtab)`

Insert RNA.

Parameters

<i>RNAtab</i> ,:	Table of RNA
------------------	--------------

Definition at line 103 of file `Sqlite_manager.py`.

References `commitRetry()`, `irna::iRNA_pred::Sqlite_manager::Sqlite_manager::commitRetry()`, `irna::David2tulip::Sqlite_manager::Sqlite_manager::commitRetry()`, `cur`, `irna::David2tulip::Sqlite_manager::Sqlite_manager::cur`, `irna::iRNA_pred::Sqlite_manager::Sqlite_manager::cur`, and `setInteract()`.

Referenced by `setSoft()`.

6.46.3.38 `def irna::iRNA_stat::Sqlite_manager::Sqlite_manager::setSoft (self, name)`

Insert soft name.

Parameters

<i>name</i> ,:	Soft name
----------------	---------------------------

Returns

: Last insert id

Definition at line 86 of file `Sqlite_manager.py`.

References `commitRetry()`, `irna::iRNA_pred::Sqlite_manager::Sqlite_manager::commitRetry()`, `irna::David2tulip::Sqlite_manager::Sqlite_manager::commitRetry()`, and `setRNA()`.

Referenced by `disconnectDB2()`.

6.46.4 Member Data Documentation

6.46.4.1 `irna::iRNA_stat::Sqlite_manager::Sqlite_manager::conn`

Definition at line 44 of file `Sqlite_manager.py`.

Referenced by `disconnectDB()`.

6.46.4.2 irna::iRNA_stat::Sqlite_manager::Sqlite_manager::conn2

Definition at line 44 of file Sqlite_manager.py.

Referenced by createSQLdb(), and disconnectDB().

6.46.4.3 irna::iRNA_stat::Sqlite_manager::Sqlite_manager::cur

Definition at line 44 of file Sqlite_manager.py.

Referenced by disconnectDB2(), and setRNA().

6.46.4.4 irna::iRNA_stat::Sqlite_manager::Sqlite_manager::db_file

Definition at line 21 of file Sqlite_manager.py.

Referenced by createSQLdb().

6.46.4.5 irna::iRNA_stat::Sqlite_manager::Sqlite_manager::db_path

Definition at line 21 of file Sqlite_manager.py.

Referenced by createSQLdb().

6.46.4.6 irna::iRNA_stat::Sqlite_manager::Sqlite_manager::fastmode

Definition at line 21 of file Sqlite_manager.py.

Referenced by disconnectDB().

The documentation for this class was generated from the following file:

- /home/amine/workspace/iRNA/irna/iRNA_stat/Sqlite_manager.py

6.47 irna::iRNA_seq::sRNA::sRNA Class Reference

Public Member Functions

- def [__init__](#)
Instantiate name parser object.
- def [readsRNA](#)
Add [sRNA](#) - [sRNA](#) edges based on their similarity.

Public Attributes

- [sRNA_obj](#)
- [srnareg](#)

6.47.1 Detailed Description

Definition at line 9 of file sRNA.py.

6.47.2 Constructor & Destructor Documentation

6.47.2.1 `def irna::iRNA_seq::sRNA::sRNA::__init__(self)`

Instantiate name parser object.

Definition at line 14 of file sRNA.py.

6.47.3 Member Function Documentation

6.47.3.1 `def irna::iRNA_seq::sRNA::sRNA::readsRNA(self, sRNA_file)`

Add [sRNA](#) - [sRNA](#) edges based on their similarity.

Parameters

<i>node_ - objects,:</i>	list of node objects
<i>edge_ - objects,:</i>	list of edge objects

Definition at line 23 of file sRNA.py.

6.47.4 Member Data Documentation

6.47.4.1 `irna::iRNA_seq::sRNA::sRNA::sRNA_obj`

Definition at line 23 of file sRNA.py.

6.47.4.2 `irna::iRNA_seq::sRNA::sRNA::srnareg`

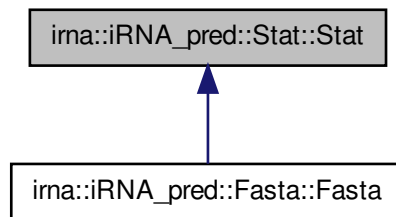
Definition at line 23 of file sRNA.py.

The documentation for this class was generated from the following file:

- `/home/amine/workspace/iRNA/irna/iRNA_seq/sRNA.py`

6.48 irna::iRNA_pred::Stat::Stat Class Reference

Inheritance diagram for irna::iRNA_pred::Stat::Stat:



Public Member Functions

- def [__init__](#)
Stat constructor.
- def [ComputeGC](#)
- def [GetGC](#)
Get the GC percentage.
- def [GetLenSeq](#)
Get the mean length of sequence.
- def [SeqInf](#)
Write Seq Inf data.
- def [openSeqInf](#)
Open seq_inf file and write header.
- def [CloseSeqInf](#)
Close the Seq Inf file.

Public Attributes

- [file](#)

Static Public Attributes

- tuple [seqlen](#) = len(seq)

6.48.1 Detailed Description

Definition at line 9 of file Stat.py.

6.48.2 Constructor & Destructor Documentation

6.48.2.1 `def irna::iRNA_pred::Stat::Stat::_init__ (self)`

[Stat](#) constructor.

Reimplemented in [irna::iRNA_pred::Fasta::Fasta](#).

Definition at line 15 of file Stat.py.

6.48.3 Member Function Documentation

6.48.3.1 `def irna::iRNA_pred::Stat::Stat::CloseSeqInf (self)`

Close the Seq Inf file.

Definition at line 79 of file Stat.py.

Referenced by `openSeqInf()`.

6.48.3.2 `def irna::iRNA_pred::Stat::Stat::ComputeGC (self, name, seq)`

Definition at line 18 of file Stat.py.

6.48.3.3 `def irna::iRNA_pred::Stat::Stat::GetGC (self)`

Get the GC percentage.

Returns

: The GC percentage

Definition at line 44 of file Stat.py.

References `GetLenSeq()`, `irna::iRNA_pred::RanRNA::RanRNA::NbSeq`, and `SeqInf()`.

6.48.3.4 `def irna::iRNA_pred::Stat::Stat::GetLenSeq (self)`

Get the mean length of sequence.

Returns

: Mean length

Definition at line 52 of file Stat.py.

References openSeqInf().

Referenced by GetGC().

6.48.3.5 def irna::iRNA_pred::Stat::Stat::openSeqInf (self)

Open seq_inf file and write header.

Definition at line 67 of file Stat.py.

References CloseSeqInf().

Referenced by irna::iRNA_pred::Fasta::Fasta::ExtractFasta(), and GetLenSeq().

6.48.3.6 def irna::iRNA_pred::Stat::Stat::SeqInf (self, name, seqlen)

Write Seq Inf data.

Definition at line 59 of file Stat.py.

References file.

Referenced by GetGC().

6.48.4 Member Data Documentation**6.48.4.1 irna::iRNA_pred::Stat::Stat::file**

Definition at line 67 of file Stat.py.

Referenced by SeqInf().

6.48.4.2 tuple irna::iRNA_pred::Stat::Stat::seqlen = len(seq) [static]

```
Compute the length and the number of GC
@param name: Name of the sequence
@param seq: RNA sequence
```

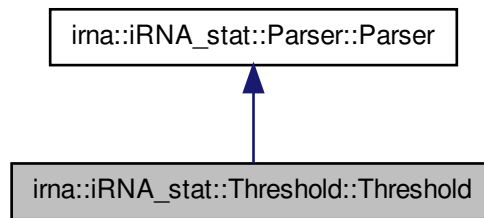
Definition at line 26 of file Stat.py.

The documentation for this class was generated from the following file:

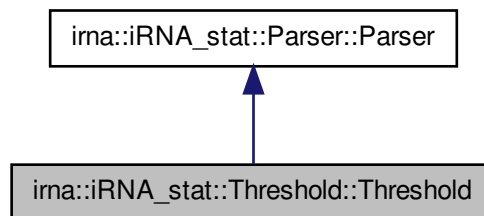
- [/home/amine/workspace/iRNA/irna/iRNA_pred/Stat.py](#)

6.49 ima::iRNA_stat::Threshold::Threshold Class Reference

Inheritance diagram for ima::iRNA_stat::Threshold::Threshold:



Collaboration diagram for ima::iRNA_stat::Threshold::Threshold:



Public Member Functions

- def [__init__](#)
Instantiate soft object.
- def [getThresinf](#)
*Parse *pValue* threshold file.*
- def [getSoftnum](#)

Public Attributes

- [soft](#)

- [threshold](#)

6.49.1 Detailed Description

Definition at line 10 of file Threshold.py.

6.49.2 Constructor & Destructor Documentation

6.49.2.1 `def irna::iRNA_stat::Threshold::Threshold::__init__(self, thres_file)`

Instantiate soft object.

Definition at line 16 of file Threshold.py.

References `getThresinf()`.

6.49.3 Member Function Documentation

6.49.3.1 `def irna::iRNA_stat::Threshold::Threshold::getSoftnum(self, soft)`

Parameters

<i>soft,:</i>	Name of asked software
---------------	------------------------

Definition at line 42 of file Threshold.py.

References `soft`, `irna::iRNA_stat::Rand_data::Rand_data::soft`, and `irna::iRNA_stat::Execute::Execute::soft`.

6.49.3.2 `def irna::iRNA_stat::Threshold::Threshold::getThresinf(self, thres_file)`

Parse [pValue](#) threshold file.

Definition at line 24 of file Threshold.py.

Referenced by `__init__()`.

6.49.4 Member Data Documentation

6.49.4.1 `irna::iRNA_stat::Threshold::Threshold::soft`

Definition at line 24 of file Threshold.py.

Referenced by `getSoftnum()`.

6.49.4.2 `irna::iRNA_stat::Threshold::Threshold::threshold`

Definition at line 24 of file Threshold.py.

The documentation for this class was generated from the following file:

- /home/amine/workspace/iRNA/irna/iRNA_stat/Threshold.py

Chapter 7

File Documentation

7.1 /home/amine/workspace/iRNA/irna/David2tulip/__init__.py File - Reference

Namespaces

- namespace [irna::David2tulip](#)

7.2 /home/amine/workspace/iRNA/irna/iRNA_pred/__init__.py File - Reference

Namespaces

- namespace [irna::iRNA_pred](#)

7.3 /home/amine/workspace/iRNA/irna/iRNA_seq/__init__.py File - Reference

Namespaces

- namespace [irna::iRNA_seq](#)

7.4 /home/amine/workspace/iRNA/irna/iRNA_stat/__init__.py File - Reference

Namespaces

- namespace [irna::iRNA_stat](#)

7.5 /home/amine/workspace/iRNA/irna/David2tulip/David.py File Reference

Classes

- class [irna::David2tulip::David::David](#)

Namespaces

- namespace [irna::David2tulip::David](#)

7.6 /home/amine/workspace/iRNA/irna/David2tulip/David2tulip.py - File Reference

Namespaces

- namespace [irna::David2tulip::David2tulip](#)

Functions

- def [irna::David2tulip::David2tulip::main](#)
Main program ###.

7.7 /home/amine/workspace/iRNA/irna/David2tulip/Davidconfig.py File Reference

Classes

- class [irna::David2tulip::Davidconfig::Davidconfig](#)

Namespaces

- namespace [irna::David2tulip::Davidconfig](#)

7.8 /home/amine/workspace/iRNA/irna/David2tulip/Edge.py File - Reference

Classes

- class [irna::David2tulip::Edge::Edge](#)
: *Handle interaction*

Namespaces

- namespace [irna::David2tulip::Edge](#)

7.9 /home/amine/workspace/iRNA/irna/David2tulip/Files.py File - Reference

Classes

- class [irna::David2tulip::Files::Files](#)

Namespaces

- namespace [irna::David2tulip::Files](#)

7.10 /home/amine/workspace/iRNA/irna/iRNA_pred/Files.py File - Reference

Classes

- class [irna::iRNA_pred::Files::Files](#)
:

Namespaces

- namespace [irna::iRNA_pred::Files](#)

7.11 /home/amine/workspace/iRNA/irna/iRNA_seq/Files.py File - Reference

Classes

- class [irna::iRNA_seq::Files::Files](#)

Namespaces

- namespace [irna::iRNA_seq::Files](#)

7.12 [/home/amine/workspace/iRNA/irna/iRNA_stat/Files.py](#) File - Reference

Classes

- class [irna::iRNA_stat::Files::Files](#)

Namespaces

- namespace [irna::iRNA_stat::Files](#)

7.13 [/home/amine/workspace/iRNA/irna/David2tulip/Gene_list.py](#) File Reference

Classes

- class [irna::David2tulip::Gene_list::Gene_list](#)
: Handle DAVID enrichment data

Namespaces

- namespace [irna::David2tulip::Gene_list](#)

7.14 [/home/amine/workspace/iRNA/irna/David2tulip/Graph.py](#) File - Reference

Classes

- class [irna::David2tulip::Graph::Graph](#)

7.15 /home/amine/workspace/iRNA/irna/David2tulip/Interact.py File Reference

Namespaces

- namespace [irna::David2tulip::Graph](#)

7.15 /home/amine/workspace/iRNA/irna/David2tulip/Interact.py File Reference

Classes

- class [irna::David2tulip::Interact::Interact](#)

Namespaces

- namespace [irna::David2tulip::Interact](#)

7.16 /home/amine/workspace/iRNA/irna/David2tulip/Multilist.py - File Reference

Classes

- class [irna::David2tulip::Multilist::Multilist](#)

Namespaces

- namespace [irna::David2tulip::Multilist](#)

7.17 /home/amine/workspace/iRNA/irna/David2tulip/Mycarn_data.py File Reference

Classes

- class [irna::David2tulip::Mycarn_data::Mycarn_data](#)

Namespaces

- namespace [irna::David2tulip::Mycarn_data](#)

7.18 /home/amine/workspace/iRNA/irna/David2tulip/Name.py File - Reference

Classes

- class [irna::David2tulip::Name::Name](#)

Namespaces

- namespace [irna::David2tulip::Name](#)

7.19 /home/amine/workspace/iRNA/irna/David2tulip/Node.py File - Reference

Classes

- class [irna::David2tulip::Node::Node](#)
: *Handle RNA information*

Namespaces

- namespace [irna::David2tulip::Node](#)

7.20 /home/amine/workspace/iRNA/irna/David2tulip/Parser.py File - Reference

Classes

- class [irna::David2tulip::Parser::Parser](#)

Namespaces

- namespace [irna::David2tulip::Parser](#)

7.21 /home/amine/workspace/iRNA/irna/iRNA_stat/Parser.py File - Reference

Classes

- class [irna::iRNA_stat::Parser::Parser](#)

7.22 /home/amine/workspace/iRNA/irna/David2tulip/pValue.py File Reference 243

Namespaces

- namespace [irna::iRNA_stat::Parser](#)

7.22 /home/amine/workspace/iRNA/irna/David2tulip/pValue.py File Reference

Classes

- class [irna::David2tulip::pValue::pValue](#)

Namespaces

- namespace [irna::David2tulip::pValue](#)

7.23 /home/amine/workspace/iRNA/irna/iRNA_stat/pValue.py File - Reference

Classes

- class [irna::iRNA_stat::pValue::pValue](#)

Namespaces

- namespace [irna::iRNA_stat::pValue](#)

7.24 /home/amine/workspace/iRNA/irna/David2tulip/Similarity.py File Reference

Classes

- class [irna::David2tulip::Similarity::Similarity](#)

Namespaces

- namespace [irna::David2tulip::Similarity](#)

7.25 /home/amine/workspace/iRNA/irna/David2tulip/Sqlite_manager.py File Reference

Classes

- class [irna::David2tulip::Sqlite_manager::Sqlite_manager](#)
: Handle database connection, disconnection and querying.

Namespaces

- namespace [irna::David2tulip::Sqlite_manager](#)

7.26 /home/amine/workspace/iRNA/irna/iRNA_pred/Sqlite_manager.py File Reference

Classes

- class [irna::iRNA_pred::Sqlite_manager::Sqlite_manager](#)
: Handle database connection, disconnection and querying.

Namespaces

- namespace [irna::iRNA_pred::Sqlite_manager](#)

7.27 /home/amine/workspace/iRNA/irna/iRNA_stat/Sqlite_manager.py File Reference

Classes

- class [irna::iRNA_stat::Sqlite_manager::Sqlite_manager](#)

Namespaces

- namespace [irna::iRNA_stat::Sqlite_manager](#)

7.28 /home/amine/workspace/iRNA/irna/iRNA_pred/Comparison.py File Reference

7.29 /home/amine/workspace/iRNA/irna/iRNA_pred/Fasta.py File Reference 245

Classes

- class [irna::iRNA_pred::Comparison::Comparison](#)
: Create coupled files and the list of comparison

Namespaces

- namespace [irna::iRNA_pred::Comparison](#)

7.29 /home/amine/workspace/iRNA/irna/iRNA_pred/Fasta.py File Reference

Classes

- class [irna::iRNA_pred::Fasta::Fasta](#)
: Write fasta needed for the different software from a multifasta

Namespaces

- namespace [irna::iRNA_pred::Fasta](#)

7.30 /home/amine/workspace/iRNA/irna/iRNA_pred/Interaction.py - File Reference

Classes

- class [irna::iRNA_pred::Interaction::Interaction](#)
: Store information on interaction.

Namespaces

- namespace [irna::iRNA_pred::Interaction](#)

7.31 /home/amine/workspace/iRNA/irna/iRNA_stat/Interaction.py File Reference

Classes

- class [irna::iRNA_stat::Interaction::Interaction](#)

Namespaces

- namespace `irna::iRNA_stat::Interaction`

7.32 /home/amine/workspace/iRNA/irna/iRNA_pred/iRNA_pred.py - File Reference

Namespaces

- namespace `irna::iRNA_pred::iRNA_pred`

Functions

- def `irna::iRNA_pred::iRNA_pred::WriteAllExecTime`
Write execution time.
- def `irna::iRNA_pred::iRNA_pred::saveData`
Save data in a sqlite database.
- def `irna::iRNA_pred::iRNA_pred::main`
: Main program

7.33 /home/amine/workspace/iRNA/irna/iRNA_pred/Merger.py File - Reference

Classes

- class `irna::iRNA_pred::Merger::Merger`
Merge the xml files in a sqlite database.

Namespaces

- namespace `irna::iRNA_pred::Merger`

7.34 /home/amine/workspace/iRNA/irna/iRNA_pred/Mpi.py File - Reference

Classes

- class `irna::iRNA_pred::Mpi::Mpi`
*: Manage *Mpi* run*

Namespaces

- namespace [irna::iRNA_pred::Mpi](#)

7.35 /home/amine/workspace/iRNA/irna/iRNA_stat/Mpi.py File - Reference

Classes

- class [irna::iRNA_stat::Mpi::Mpi](#)
: *Manage [Mpi](#) run*

Namespaces

- namespace [irna::iRNA_stat::Mpi](#)

7.36 /home/amine/workspace/iRNA/irna/iRNA_pred/Parse.py File - Reference

Classes

- class [irna::iRNA_pred::Parse::Parse](#)
: *[Parse](#) data from the different software.*

Namespaces

- namespace [irna::iRNA_pred::Parse](#)

7.37 /home/amine/workspace/iRNA/irna/iRNA_pred/RanRNA.py - File Reference

Classes

- class [irna::iRNA_pred::RanRNA::RanRNA](#)

Namespaces

- namespace [irna::iRNA_pred::RanRNA](#)

Variables

- tuple `irna::iRNA_pred::RanRNA::generator` = `RanRNA(0.41728640,141,100,"/home/amine/workspace/-Mycarn_old/data/test/")`

7.38 /home/amine/workspace/iRNA/irna/iRNA_pred/Stat.py File - Reference

Classes

- class `irna::iRNA_pred::Stat::Stat`

Namespaces

- namespace `irna::iRNA_pred::Stat`

7.39 /home/amine/workspace/iRNA/irna/iRNA_seq/Genbank.py File Reference

Classes

- class `irna::iRNA_seq::Genbank::Genbank`

Namespaces

- namespace `irna::iRNA_seq::Genbank`

7.40 /home/amine/workspace/iRNA/irna/iRNA_seq/iRNA_seq.py - File Reference

Namespaces

- namespace `irna::iRNA_seq::iRNA_seq`

Functions

- def `irna::iRNA_seq::iRNA_seq::main`
Main program function.

7.41 /home/amine/workspace/iRNA/irna/iRNA_seq/Sequences.py File Reference 249

7.41 /home/amine/workspace/iRNA/irna/iRNA_seq/Sequences.py File Reference

Classes

- class [irna::iRNA_seq::Sequences::Sequences](#)

Namespaces

- namespace [irna::iRNA_seq::Sequences](#)

7.42 /home/amine/workspace/iRNA/irna/iRNA_seq/sRNA.py File - Reference

Classes

- class [irna::iRNA_seq::sRNA::sRNA](#)

Namespaces

- namespace [irna::iRNA_seq::sRNA](#)

7.43 /home/amine/workspace/iRNA/irna/iRNA_stat/Analysis.py File Reference

Classes

- class [irna::iRNA_stat::Analysis::Analysis](#)

Namespaces

- namespace [irna::iRNA_stat::Analysis](#)

7.44 /home/amine/workspace/iRNA/irna/iRNA_stat/Communication.py File Reference

Classes

- class [irna::iRNA_stat::Communication::Communication](#)
: Empty object used for mpi communication

Namespaces

- namespace [irna::iRNA_stat::Communication](#)

7.45 /home/amine/workspace/iRNA/irna/iRNA_stat/Computer.py - File Reference

Classes

- class [irna::iRNA_stat::Computer::Computer](#)

Namespaces

- namespace [irna::iRNA_stat::Computer](#)

7.46 /home/amine/workspace/iRNA/irna/iRNA_stat/Draw_data.py - File Reference

Classes

- class [irna::iRNA_stat::Draw_data::draw_data](#)

Namespaces

- namespace [irna::iRNA_stat::Draw_data](#)

Variables

- tuple [irna::iRNA_stat::Draw_data::graphics](#) = `importtr('graphics')`
- tuple [irna::iRNA_stat::Draw_data::grdevices](#) = `importtr('grDevices')`
- tuple [irna::iRNA_stat::Draw_data::base](#) = `importtr('base')`
- tuple [irna::iRNA_stat::Draw_data::stats](#) = `importtr('stats')`
- tuple [irna::iRNA_stat::Draw_data::pROC](#) = `importtr('pROC')`
- tuple [irna::iRNA_stat::Draw_data::Cairo](#) = `importtr('Cairo')`

7.47 /home/amine/workspace/iRNA/irna/iRNA_stat/Ecdf.py File Reference

Classes

- class [irna::iRNA_stat::Ecdf::Ecdf](#)

7.48 /home/amine/workspace/iRNA/irna/iRNA_stat/Execute.py File Reference 251

Namespaces

- namespace [irna::iRNA_stat::Ecdf](#)

7.48 /home/amine/workspace/iRNA/irna/iRNA_stat/Execute.py File Reference

Classes

- class [irna::iRNA_stat::Execute::Execute](#)

Namespaces

- namespace [irna::iRNA_stat::Execute](#)

7.49 /home/amine/workspace/iRNA/irna/iRNA_stat/Exp_data.py File Reference

Classes

- class [irna::iRNA_stat::Exp_data::Exp_data](#)

Namespaces

- namespace [irna::iRNA_stat::Exp_data](#)

7.50 /home/amine/workspace/iRNA/irna/iRNA_stat/iRNA_stat.py - File Reference

Namespaces

- namespace [irna::iRNA_stat::iRNA_stat](#)

Functions

- def [irna::iRNA_stat::iRNA_stat::usage](#)
Test correct usage of arguments.
- def [irna::iRNA_stat::iRNA_stat::main](#)
Determine les fichiers fournis en arguments def getArguments(): "" Determine the argument.

7.51 /home/amine/workspace/iRNA/irna/iRNA_stat/NormScore.py - File Reference

Classes

- class [irna::iRNA_stat::NormScore::NormScore](#)

Namespaces

- namespace [irna::iRNA_stat::NormScore](#)

7.52 /home/amine/workspace/iRNA/irna/iRNA_stat/Pickling.py File Reference

Classes

- class [irna::iRNA_stat::Pickling::Pickling](#)

Namespaces

- namespace [irna::iRNA_stat::Pickling](#)

7.53 /home/amine/workspace/iRNA/irna/iRNA_stat/pValue_selection.py File Reference

Classes

- class [irna::iRNA_stat::pValue_selection::pValue_selection](#)

Namespaces

- namespace [irna::iRNA_stat::pValue_selection](#)

7.54 /home/amine/workspace/iRNA/irna/iRNA_stat/Rand_data.py File Reference

Classes

- class [irna::iRNA_stat::Rand_data::Rand_data](#)

7.55 /home/amine/workspace/iRNA/irna/iRNA_stat/Regression.py File Reference 253

Namespaces

- namespace [irna::iRNA_stat::Rand_data](#)

7.55 /home/amine/workspace/iRNA/irna/iRNA_stat/Regression.py - File Reference

Classes

- class [irna::iRNA_stat::Regression::Regression](#)

Namespaces

- namespace [irna::iRNA_stat::Regression](#)

7.56 /home/amine/workspace/iRNA/irna/iRNA_stat/Soft.py File - Reference

Classes

- class [irna::iRNA_stat::Soft::Soft](#)

Namespaces

- namespace [irna::iRNA_stat::Soft](#)

7.57 /home/amine/workspace/iRNA/irna/iRNA_stat/Threshold.py - File Reference

Classes

- class [irna::iRNA_stat::Threshold::Threshold](#)

Namespaces

- namespace [irna::iRNA_stat::Threshold](#)