navicom

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Contents

1 navicom package documentation

The navicom package intends to provide standard methods to visualise high-throughput data in NaviCell web service. It also provide several processing method to get some extra meaning out of the data.

Author

Mathurin Dorel

1.1 Getting started

The communication with NaviCell web service, and data processing are performed by the NaviCom class, which can be initialised with a simple NaviCell map URL.

```
nc = NaviCom(map_url='https://navicell.curie.fr/navicell/maps/cellcycle/master/in
      dex.php')
```

Data and annotations can then be loaded in the NaviCom object.

```
nc.loadData("data/Ovarian_Serous_Cystadenocarcinoma_TCGA_Nature_2011.txt")
```

Two formats are accepted:

- a matrix format where data are represented as matrix, with explicit rows and columns names. The first row has to start by GENE (for data) or NAME (for annotations);
- a set of matrix format where each matrix is separated by a header line expliciting the type of data and starting with M (data) or ANNOTATIONS (annotations).

After being loaded, data and annotations can be easily controlled:

```
nc.listData()
nc.listAnnotations()
```

1.1.1 Display configuration

The displays in the NaviCell map can be easily configured with the DisplayConfig class. It can be provided to the NaviCom class.

```
display_config = DisplayConfig(5, zero_color="000000", na_color="ffffff", na_size
      =0)
nc = NaviCom(map_url='https://navicell.curie.fr/navicell/maps/cellcycle/master/in
      dex.php', display_config)
```

1.1.2 Adding extra data

Data in the NaviCom class are represented in the NaviData format, which is a matrix of data that can be indexed by row and column names. NaviData objects can be created independently and integrated to a NaviCom object:

```
extra_data = NaviData(data_matrix, row_names, col_names)
nc.bindNaviData(extra_data, "extra_data")
```

1.2 Data visualisation

The NaviCom class provides several method to display the data in NaviCell:

- **display** Generic display function to perform any kind of personnalised display
- **displayOmics** Display -omics data as map staining with extra information or data on using the other display modes

2 Class Index

2.1 Class Hierarchy

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

3 Class Index

3.1 Class List

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

4 Class Documentation

4.1 navicom::displayConfig::DisplayConfig Class Reference

DisplayConfig class to set the color gradients configuration in NaviCell.

Public Member Functions

- def __init__

  Initialise a color gradient configuration.

- def **__repr__**

Public Attributes

- **na_color**
- **zero_color**
- **na_size**
- **zero_size**
- **use_absolute_values**
- **step_count**
- **colors**
- **color**

4.1.1 Detailed Description

DisplayConfig class to set the color gradients configuration in NaviCell.

Definition at line 51 of file displayConfig.py.

4.1.2 Member Function Documentation

4.1.2.1 def navicom::displayConfig::DisplayConfig::__init__ (*self*, *step_count* = *3*, *color_gradient* = `["00FF00", ` *FF0000*, *zero_color* = `"ffffff"`, *na_color* = `"ffffff"`, *zero_size* = *0*, *na_size* = *0*, *use_absolute_values* = `False`)

Initialise a color gradient configuration.

Parameters

step_count number of steps for the color gradients. A step for NAs is automatically attributed.

color_gradient a list of colors of length 2 or step_count. If length 2 a gradient is built, if the length is step_count the list is used for the colors.

zero_color an hexadecimal string for the color of the zero, only visible if step_count is odd

Definition at line 60 of file displayConfig.py.

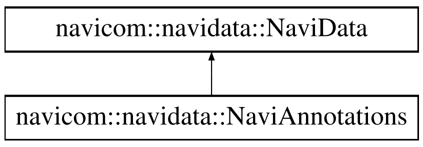
The documentation for this class was generated from the following file:

- navicom/displayConfig.py

4.2 navicom::navidata::NaviAnnotations Class Reference

Enhance NaviData to contain annotations and associate annotations values with samples.

Inheritance diagram for navicom::navidata::NaviAnnotations:


navicom::navidata::NaviData
navicom::navidata::NaviAnnotations

Public Member Functions

- def **__init__**

Public Attributes

- **categoriesPerAnnotation**
- **samplesPerCategory**
- **old_annots**

4.2.1 Detailed Description

Enhance NaviData to contain annotations and associate annotations values with samples. Also reduce continuous data with to many levels to a limited number of interval levels.

Definition at line 210 of file navidata.py.

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

- navicom/navidata.py

4.3 navicom::navicom::NaviCom Class Reference

NaviComm class to handle data and display them in a standardized way on NaviCell maps.

Public Member Functions

- def __init__

  Initialize a Navicell communication object.

- def **listData**
- def **listAnnotations**
- def **__repr__**
- def **nameData**
- def **getDataName**
- def getDataTuple

  Return tuple corresponding to the data name or tuple.

- def getData

  Return the NaviData entity corresponding to the data name or tuple.

- def loadData

  Load data from a .txt or .ncc file containing several datas, or from a .tsv, .ncd or .nca file containing data from one method.

- def bindNaviData

  Bind NaviData to the NaviCom object in order to use it.

- def **defineUniformData**
- def newProcessedData

Update adequate arrays when processed data are generated.

- def quantifyMutations

  Transform the qualitative mutation datas into a quantitative one, where 1 means a mutation and 0 no mutation.

- def defineModules

  Defines the modules to use and which module each gene belongs to.

- def averageModule

  Perform module averaging for every modules for one data type.

- def pcaComp

  Run pca on the data and create a color matrix with the 3 principal components in the three main colors.

- def exportData

  Export data to NaviCell, can be processed data.

- def checkBrowser

  Check if the browser is opened or open it.

- def exportAnnotations

  Export samples annotations to NaviCell.

- def configureDisplay

  Changes the Color and Size Configuration for the datatable to the one precised by the user.

- def display

  Display data on the NaviCell map.

- def resetDisplay

  Reset the data and samples selections in NaviCell.

- def **resetAnnotations**
- def **selectAnnotations**
- def processSampleSelection

  Process a list of samples or groups to a list of samples/groups names exportable to NaviCell or to "all_groups"/"all_samples" for heatmap and barplot, and select the correct groups in NaviCell.

- def processGroupsName

  Process a group selection string and return the names of the individual groups to select and the corresponding values selected.

- def displayMethylome

  Display the methylation data as glyphs or heatmap on the NaviCell map, with mRNA expression of gene CNV as map staining.

- def displayTranscriptome

  Display one transcriptome data as map staining, with optionnaly some extra displays (samples as heatmap or barplot, mutations as glyphs, a glyph for the most highly expressed genes).

- def generateDistributionData

  Compute distribution of values for all genes for one type of data.

- def colorsOverlay

  Create a dataset where values are colors.

- def saveAllData

  Save all data in an .ncc file.

- def saveData

  Save the data in a file that can be exported to NaviCell or imported in NaviCom.

Public Attributes

- **nv**
- **name**
- **exported_annotations**
- **browser_opened**
- **biotypes**
- **display_config**
- **processings**
- **data**
- **exported_data**
- **data_names**
- **associated_data**
- **annotations**
- **modules**
- **associated_modules**
- **hsid**
- **hdid**
- **bid**

4.3.1 Detailed Description

NaviComm class to handle data and display them in a standardized way on NaviCell maps.

Definition at line 28 of file navicom.py.

4.3.2 Member Function Documentation

4.3.2.1 def navicom::navicom::NaviCom::__init__ (*self*, *map_url* = `'https://navicell.curie.fr/navicell/maps/cellcycle/master/index.php'`, *fname* = `""`, *modules_dict* = `""`, *browser_command* = `"firefox %s"`, *display_config* = `DisplayConfig()`)

Initialize a Navicell communication object.

Parameters

- ***map_url*** URL of the NaviCell map
- ***fname*** name of the data file to load
- ***modules_dict*** name of the module definition file (.gmt) to load
- ***browser_command*** command to open the browser

Definition at line 38 of file navicom.py.

4.3.2.2 def navicom::navicom::NaviCom::colorsOverlay (*self*, *red* = `"uniform"`, *green* = `"uniform"`, *blue* = `"uniform"`, *processing* = `""`)

Create a dataset where values are colors.

The color is calculated according to three datasets.

Parameters

- ***red*** data name or tuple (processing, method)
- ***green*** data name or tuple (processing, method)
- ***blue*** data name or tuple (processing, method)

Definition at line 950 of file navicom.py.

4.3.2.3 def navicom::navicom::NaviCom::defineModules (*self*, *modules_dict* = `""`)

Defines the modules to use and which module each gene belongs to.

Parameters

- ***modules_dict*** Either a dict indexed by module name or a file name with the description of each module (.gmt `file:` tab delimited, first column module name, second column description, then list of entities in the module)

Definition at line 290 of file navicom.py.

4.3.2.4 def navicom::navicom::NaviCom::display (*self*, *perform_list*, *default_samples* = `"all: 1.0"`, *colors* = `""`, *module* = '', *reset* = `True`)

Display data on the NaviCell map.

perform_list (list of 2-tuples): each tuple must contain the name of the data to display and the mode of display ("glyphN_(color|size|shape)", "barplot", "heatmap" or "map_staining"). Barplots and heatmaps cannot be displayed simultaneously. Several data types can be specified for heatmaps. Specifying "glyph" (without number) will automatically select a new glyph for each data using the same properties (shape, color or size) in glyphs (maximum of 5 glyphs).

Parameters

colors range of colors to use (NOT IMPLEMENTED YET) default_samples (str or list of str) : Samples to use. Only the first sample is used for glyphs and map staining, all default_samples from the list are used for heatmaps and barplots. Use 'all_samples' to use all default_samples or ['annot1:...:annotn', 'all_groups'] to use all groups corresponding to the combinations of annot1...annotn.

Definition at line 539 of file navicom.py.

4.3.2.5 def navicom::navicom::NaviCom::displayMethylome (*self*, *samples* = `"all: 1.0"`, *processing* = `"raw"`, *background* = `"mRNA"`, *methylation* = `"glyph"`)

Display the methylation data as glyphs or heatmap on the NaviCell map, with mRNA expression of gene CNV as map staining.

Parameters

background should genes, mRNA or no data be used for the map staining

processing should the processed data be used

Definition at line 836 of file navicom.py.

4.3.2.6 def navicom::navicom::NaviCom::displayTranscriptome (*self*, *dataName*, *group* = `"all: 1.0"`, *samplesDisplay* = `""`, *samples* = `list ()`, *binsNb* = `10`)

Display one transcriptome data as map staining, with optionnaly some extra displays (samples as heatmap or barplot, mutations as glyphs, a glyph for the most highly expressed genes).

- dataName (str or tuple): name or identifier of the data.
- group (str): Identifier of the group to display
- samplesDisplay (str): Channel where the individual samples should be displayed (heatmap or barplot)
- samples (list or str): list of samples to display, or a string specifying how such a list should be built ('quantiles' to get the distribution of values)
- nbOfSamples (int): number of individual samples to display, ignored if samples is a list

Definition at line 877 of file navicom.py.

4.3.2.7 def navicom::navicom::NaviCom::exportData (*self*, *method*, *processing* = `"raw"`, *name* = `""`)

Export data to NaviCell, can be processed data.

Parameters

- ***method*** name of the method to export
- ***processing*** "" to export raw data, processing method to export processed data. See 'averageModule' and 'pcaComponent'

Definition at line 380 of file navicom.py.

4.3.2.8 def navicom::navicom::NaviCom::generateDistributionData (*self*, *dataName*, *group*, *binsNb* = `10`)

Compute distribution of values for all genes for one type of data.

Use the same scale for all genes. The distribution is centered on 0 if it is included, so that it is easy to see if a gene is over- or under-expressed.

Definition at line 896 of file navicom.py.

4.3.2.9 def navicom::navicom::NaviCom::loadData (*self*, *fname* = `"data/Ovarian_-Serous_Cystadenocarcinoma_TCGA_Nature_2011.txt"`, *keep_mutations_nan* = `False`)

Load data from a .txt or .ncc file containing several datas, or from a .tsv, .ncd or .nca file containing data from one method.

Parameters

- ***fname*** name of the file from which the data should be loaded
- ***keep_mutations_nan*** whether nan in mutations data should be considered as no mutation (False) or missing value (True)

Definition at line 141 of file navicom.py.

4.3.2.10 def navicom::navicom::NaviCom::quantifyMutations (*self*, *method*, *keep_nan* = `False`)

Transform the qualitative mutation datas into a quantitative one, where 1 means a mutation and 0 no mutation.

Parameters

- ***keep_nan*** Should nan values be converted to O (no mutations) or kept as missing data

Definition at line 267 of file navicom.py.

4.3.2.11 def navicom::navicom::NaviCom::saveAllData (*self*, *folder* = `""`)

Save all data in an .ncc file.

Does not save the distribution nor color data.

Definition at line 1004 of file navicom.py.

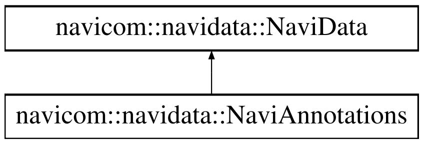
The documentation for this class was generated from the following file:

- navicom/navicom.py

4.4 navicom::navidata::NaviData Class Reference

Custom class to store the data and be able to access rows and columns by name.

Inheritance diagram for navicom::navidata::NaviData:


navicom::navidata::NaviData
navicom::navidata::NaviAnnotations

Public Member Functions

- def **__init__**
- def **__getitem__**
- def **__iter__**
- def **__next__**
- def **__repr__**
- def makeData

  Builds a string suitable for NaviCell Web Service from a python matrix of gene/sample values or a NaviCom object.

- def exportToNaviCell

  Export data to a NaviCell map.

- def saveData

  Save the NaviData datas in a file that can be used in NaviCell, but can also be loaded as NaviData.

Public Attributes

- **processing**
- **method**
- **biotype**
- **data**
- **rows**
- **rows_names**
- **columns**
- **columns_names**
- **inColumns**

- **annotations**
- **annotations_names**
- **inRows**
- **samples**
- **samples_names**
- **genes**
- **genes_names**
- **dType**
- **itermode**
- **index**
- **iter_mode**

4.4.1 Detailed Description

Custom class to store the data and be able to access rows and columns by name. data (list or array) : Values of the data to insert in the NaviData object. Must be convertible into a numpy array.

Parameters

rows_list	names of the rows (samples names)
columns_list	names of the columns (genes names)
processing	name of the computer processing applied to the data
method	name of the experimental method used to get the original ("raw") data
dType	"data" or "annotations", whether the NaviData object contains datas or annotations (Note : this should be left to default, this is used by NaviAnnotations to change some internal variables)

Definition at line 54 of file navidata.py.

4.4.2 Member Function Documentation

4.4.2.1 def navicom::navidata::NaviData::makeData (*self, hugo_map = ""*)

Builds a string suitable for NaviCell Web Service from a python matrix of gene/sample values or a NaviCom object.

Matrix format:

- first line is: GENE word followed by a tab separated list of sample names,
- each line begins with an gene name and must be followed by a tab separated list of gene/sample values.

Remove genes not present in hugo_map if provided.

Definition at line 156 of file navidata.py.

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

- navicom/navidata.py

4.5 navicom::navidata::NaviSlice Class Reference

A slice from a NaviData array.

Public Member Functions

- def **__init__**
- def **__getitem__**
- def **__setitem__**
- def **__iter__**
- def **__repr__**
- def **__add__**

Public Attributes

- **data**
- **ids**

4.5.1 Detailed Description

A slice from a NaviData array.

Definition at line 272 of file navidata.py.

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

- navicom/navidata.py

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