
data_tools Documentation

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Nicolas Palacio

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Collection of Python functions and classes designed to make a Computational Biologist's life easier.

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Contact: nicolaspalacio91@gmail.com

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DEPENDENCIES

In module **data_tools.plots**:

- NumPy
- Matplotlib
- Pandas

In module **data_tools.models**:

- NumPy
- Matplotlib
- Pandas
- Scikit-learn

INSTALLATION

First download/clone `data_tools` from the [GitHub repository](#). From the terminal:

```
git clone https://github.com/Nic-Nic/data_tools.git  
cd data_tools
```

Then you can install it by running `setup.py` as follows:

```
python setup.py sdist
```

Or using `pip`:

```
pip install .
```


REFERENCE

3.1 data_tools.models

Model classes module.

class data_tools.models.Lasso (*Cs=500, cv=10, sampler='skf', solver='liblinear', **kwargs*)
Wrapper class inheriting from `sklearn.linear_model.LogisticRegressionCV` with L1 regularization.

- **Arguments:**

- *Cs* [int]: Optional, 500 by default. Integer or list of float values of regularization parameters to test. If an integer is passed, it will determine the number of values taken from a logarithmic scale between $1e-4$ and $1e4$. Note that the value of the parameter is defined as the inverse of the regularization strength.
- *cv* [int]: Optional, 10 by default. Denotes the number of cross validation (CV) folds.
- *sampler* [str]: Optional, 'skf' by default. Determines which sampling method is used to generate the test and training sets for CV. Methods available are K-Fold ('kf'), Shuffle Split ('ss') and their stratified variants ('skf' and 'sss' respectively).
- *solver* [str]: Optional, 'liblinear' by default. Determines which solver algorithm to use. Note that L1 regularization can only be handled by 'liblinear' and 'saga'. Additionally if the classification is multinomial, only the latter option is available.
- ***kwargs*: Optional. Any other keyword argument accepted by the `sklearn.linear_model.LogisticRegressionCV` class.

Other keyword arguments and functions available from the parent class `LogisticRegressionCV` can be found in [Scikit-Learn's reference](#).

fit_data (*x, y, silent=False*)

Fits the data to the logistic model.

- **Arguments:**

- *x* [pandas.DataFrame]: Contains the values/measurements [float] of the features (columns) for each sample/replicate (rows).
- *y* [pandas.Series]: List or any iterable containing the observed class of each sample (must have the same order as in *x*).
- *silent* [bool]: Optional, False by default. Determines whether messages are printed or not.

plot_coef ()

Plots the non-zero coefficients for the fitted predictor features.

- **Returns:**

- [matplotlib.figure.Figure]: Figure object containing the bar plot of the non-zero coefficients.

plot_score()

Plots the mean score across all folds obtained during CV. The optimum C parameter chosen and its score are highlighted.

- **Returns:**

- [matplotlib.figure.Figure]: Figure object containing the score plot.

3.2 data_tools.plots

Plotting functions module.

`data_tools.plots.volcano(logfc, logpval, thr_pval=0.05, thr_fc=2.0, c=('C0', 'C1'), legend=True, title=None, filename=None, figsize=None)`

Generates a volcano plot from the differential expression data provided.

- **Arguments:**

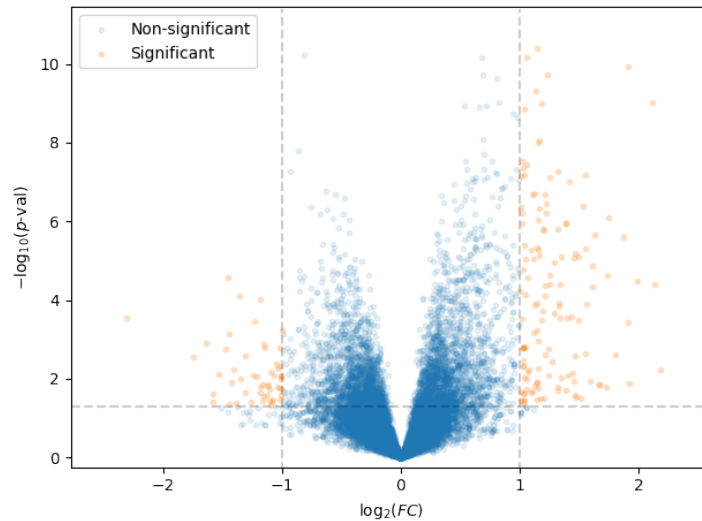
- *logfc* [list]: Or any iterable type. Contains the log (usually base 2) fold-change values. Must have the same length as *logpval*.
- *logpval* [list]: Or any iterable type. Contains the -log p-values (usually base 10). Must have the same length as *logfc*.
- *thr_pval* [float]: Optional, 0.05 by default. Specifies the p-value (non log-transformed) threshold to consider a measurement as significantly differentially expressed.
- *thr_fc* [float]: Optional, 2. by default. Specifies the FC (non log-transformed) threshold to consider a measurement as significantly differentially expressed.
- *c* [tuple]: Optional, ('C0', 'C1') by default (matplotlib default colors). Any iterable containing two color arguments tolerated by matplotlib (e.g.: ['r', 'b'] for red and blue). First one is used for non-significant points, second for the significant ones.
- *legend* [bool]: Optional, True by default. Indicates whether to show the plot legend or not.
- *title* [str]: Optional, None by default. Defines the plot title.
- *filename* [str]: Optional, None by default. If passed, indicates the file name or path where to store the figure. Format must be specified (e.g.: .png, .pdf, etc)
- *figsize* [tuple]: Optional, None by default (default matplotlib size). Any iterable containing two values denoting the figure size (in inches) as [width, height].

- **Returns:**

- [matplotlib.figure.Figure]: Figure object containing the volcano plot.

- **Examples:**

```
>>> volcano(my_log_fc, my_log_pval)
```



`data_tools.plots.piano_consensus` (*df*, *nchar*=40, *boxes*=True, *title*=None, *filename*=None, *figsize*=None)

Generates a GSEA consensus score plot like R package `piano`'s `consensusScores` function, but prettier. The main input is assumed to be a `pandas.DataFrame` whose data is the same as the `rankMat` from the result of `consensusScores`.

- **Arguments:**

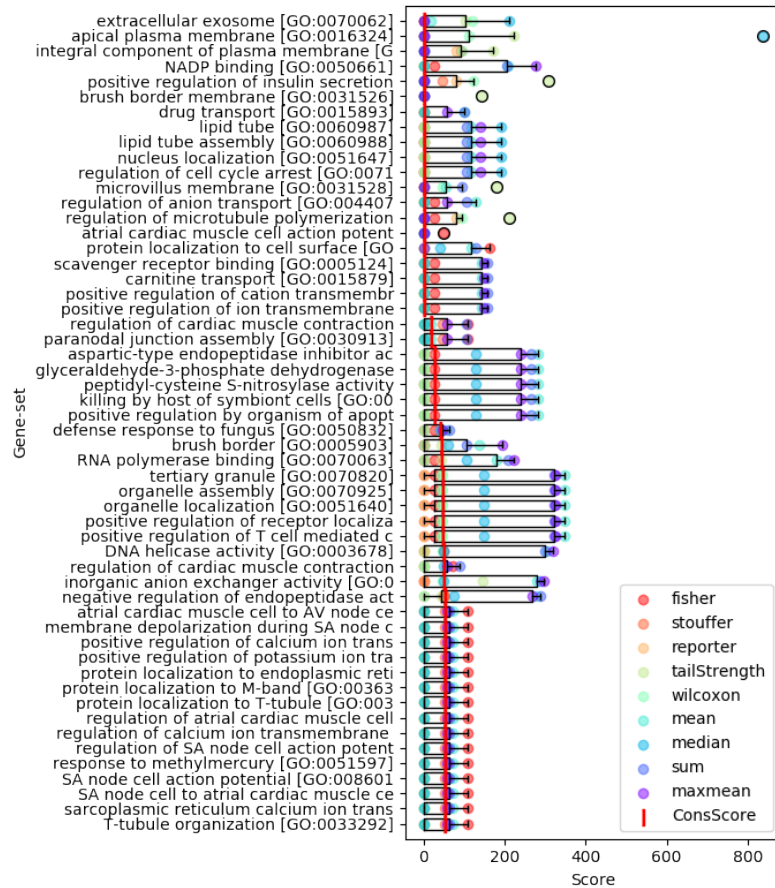
- *df* [`pandas.DataFrame`]: Values contained correspond to the scores of the gene-sets (consensus and each individual methods). Index must contain the gene-set labels. Columns are assumed to be `ConsRank` (ignored), `ConsScore` followed by the individual methods (e.g.: `mean`, `median`, `sum`, etc).
- *nchar* [int]: Optional, 40 by default. Number of string characters of the gene-set labels of the plot.
- *boxes* [bool]: Optional, True by default. Determines whether to show the boxplots of the gene-sets or not.
- *title* [str]: Optional, None by default. Defines the plot title.
- *filename* [str]: Optional, None by default. If passed, indicates the file name or path where to store the figure. Format must be specified (e.g.: `.png`, `.pdf`, etc)
- *figsize* [tuple]: Optional, None by default (default matplotlib size). Any iterable containing two values denoting the figure size (in inches) as [width, height].

- **Returns:**

- [`matplotlib.figure.Figure`]: the figure object containing a combination of box and scatter plots of the gene-set scores.

- **Examples:**

```
>>> piano_consensus(df, figsize=[7, 8])
```



3.3 data_tools.sets

Set operations module.

`data_tools.sets.in_all(x, N)`

Checks if a vector x is present in all sets contained in a list N .

- **Arguments:**
 - x [tuple]: Or any hashable type as long as is the same contained in the sets of N .
 - N [list]: Or any iterable type containing [set] objects.
- **Returns:**
 - [bool]: True if x is found in all sets of N , False otherwise.
- **Examples:**

```
>>> N = [{(0, 0), (0, 1)}, # <- set A
...      {(0, 0), (1, 1), (1, 0)}] # <- set B
>>> x = (0, 0)
>>> in_all(x, N)
True
>>> y = (0, 1)
```

```
>>> in_all(y, N)
False
```

`data_tools.sets.bit_or(a, b)`

Returns the bit operation OR between two bit-strings *a* and *b*. NOTE: *a* and *b* must have the same size.

- **Arguments:**

- *a* [tuple]: Or any iterable type.
- *b* [tuple]: Or any iterable type.

- **Returns:**

- [tuple]: OR operation between *a* and *b* element-wise.

- **Examples:**

```
>>> a, b = (0, 0, 1), (1, 0, 1)
>>> bit_or(a, b)
(1, 0, 1)
```

`data_tools.sets.multi_union(N)`

Returns the union set of all sets contained in a list *N*.

- **Arguments:**

- *N* [list]: Or any iterable type containing [set] objects.

- **Returns:**

- [set]: The union of all sets contained in *N*.

- **Examples:**

```
>>> A = {1, 3, 5}
>>> B = {0, 1, 2}
>>> C = {0, 2, 5}
>>> multi_union([A, B, C])
set([0, 1, 2, 3, 5])
```

`data_tools.sets.find_min(A)`

Finds and returns the subset of vectors whose sum is minimum from a given set *A*.

- **Arguments:**

- *A* [set]: Set of vectors ([tuple] or any iterable).

- **Returns:**

- [set]: Subset of vectors in *A* whose sum is minimum.

- **Examples:**

```
>>> A = {(0, 1, 1), (0, 1, 0), (1, 0, 0), (1, 1, 1)}
>>> find_min(A)
set([(0, 1, 0), (1, 0, 0)])
```

3.4 data_tools.strings

String operations module.

`data_tools.strings.is_numeric(s)`

Determines if a string can be considered a numeric value. NaN is also considered, since it is float type.

- **Arguments:**

- `s [str]`: String to be evaluated.

- **Returns:**

- `[bool]`: True/False depending if the condition is satisfied.

- **Examples:**

```
>>> is_numeric('4')
True
>>> is_numeric('-3.2')
True
>>> is_numeric('number')
False
>>> is_numeric('NaN')
True
```

`data_tools.strings.join_str_lists(a, b, sep="")`

Joins element-wise two lists (or any 1D iterable) of strings with a given separator (if provided). Length of the input lists must be equal.

- **Arguments:**

- `a [list]`: Contains the first elements [str] of the joint strings.
- `b [list]`: Contains the second elements [str] of the joint strings.
- `sep [str]`: Optional ' ' (non separated) by default. Determines the separator between the joint strings.

- **Returns:**

- `[list]`: List of the joint strings.

- **Example:**

```
>>> a = ['a', 'b']
>>> b = ['1', '2']
>>> join_str_lists(a, b, sep='_')
['a_1', 'b_2']
```


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