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# scikit-posthocs Documentation

*Release 0.7.0*

**Maksim Terpilowski**

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# DOCUMENTATION

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**scikit-posthocs** is a Python package which provides post hoc tests for pairwise multiple comparisons that are usually performed in statistical data analysis to assess the differences between group levels if a statistically significant result of ANOVA test has been obtained.

**scikit-posthocs** is tightly integrated with Pandas DataFrames and NumPy arrays to ensure fast computations and convenient data import and storage.

This package will be useful for statisticians, data analysts, and researchers who use Python in their work.



## INTRODUCTION

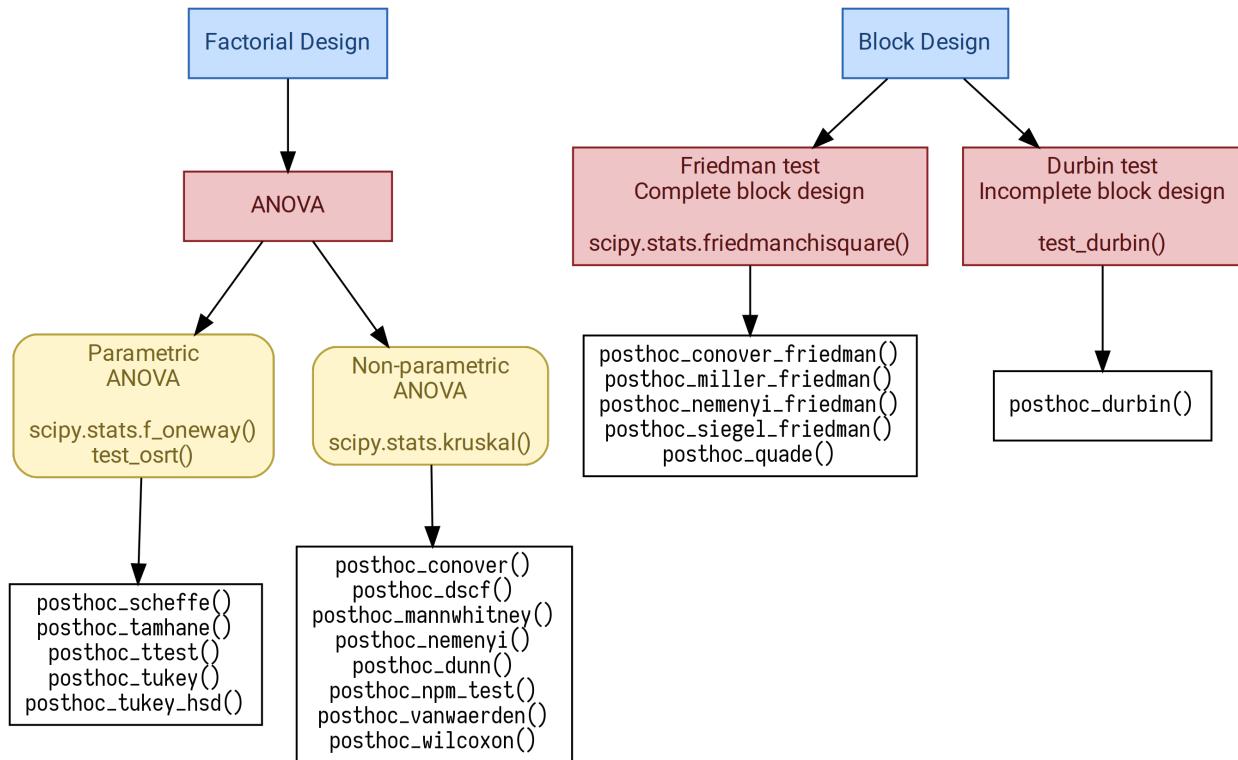
### 1.1 Background

Python statistical ecosystem is comprised of multiple packages. However, it still has numerous gaps and is surpassed by R packages and capabilities.

[SciPy](#) (version 1.2.0) offers *Student*, *Wilcoxon*, and *Mann-Whitney* tests which are not adapted to multiple pairwise comparisons. [Statsmodels](#) (version 0.9.0) features *TukeyHSD* test which needs some extra actions to be fluently integrated into a data analysis pipeline. *Statsmodels* also has good helper methods: `allpairtest` (adapts an external function such as `scipy.stats.ttest_ind` to multiple pairwise comparisons) and `multipletests` (adjusts  $p$  values to minimize type I and II errors). [PMCMRplus](#) is a very good R package which has no rivals in Python as it offers more than 40 various tests (including post hoc tests) for factorial and block design data. [PMCMRplus](#) was an inspiration and a reference for *scikit-posthocs*.

*scikit-posthocs* attempts to improve Python statistical capabilities by offering a lot of parametric and nonparametric post hoc tests along with outliers detection and basic plotting methods.

## 1.2 Features



- *Omnibus* tests:
  - Durbin test (for balanced incomplete block design).
- *Parametric* pairwise multiple comparisons tests:
  - Scheffe test.
  - Student T test.
  - Tamhane T2 test.
  - TukeyHSD test.
- *Non-parametric* tests for factorial design:
  - Conover test.
  - Dunn test.
  - Dwass, Steel, Critchlow, and Fligner test.
  - Mann-Whitney test.
  - Nashimoto and Wright (NPM) test.
  - Nemenyi test.
  - van Waerden test.
  - Wilcoxon test.
- *Non-parametric* tests for block design:
  - Conover test.

- Durbin and Conover test.
- Miller test.
- Nemenyi test.
- Quade test.
- Siegel test.
- Other tests:
  - Anderson-Darling test.
  - Mack-Wolfe test.
  - Hayter (OSRT) test.
- Outliers detection tests:
  - Simple test based on interquartile range (IQR).
  - Grubbs test.
  - Tietjen-Moore test.
  - Generalized Extreme Studentized Deviate test (ESD test).
- Plotting functionality:
  - Significance plots.
  - Critical difference diagrams.

All post hoc tests are capable of p value adjustments for multiple pairwise comparisons.



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**CHAPTER  
TWO**

---

## **INSTALLATION**

The latest version can be installed from PyPi using pip:

```
pip install scikit-posthocs
```

Or from conda-forge repository using conda:

```
conda install -c conda-forge scikit-posthocs
```

You can also use pip to install the development version from GitHub:

```
pip install git+https://github.com/maximtrp/scikit-posthocs.git
```

## **2.1 Dependencies**

Package is compatible with both major versions of Python and has the following dependencies:

- NumPy
- SciPy
- Statsmodels
- Pandas
- Seaborn
- Matplotlib

## **2.2 Bugs**

Please report any bugs using issues tracker on GitHub.



## TUTORIAL

### 3.1 Parametric ANOVA with post hoc tests

Here is a simple example of the one-way analysis of variance (ANOVA) with post hoc tests used to compare *sepal width* means of three groups (three iris species) in *iris* dataset.

To begin, we will import the dataset using statsmodels `get_rdataset()` method.

```
>>> import statsmodels.api as sa
>>> import statsmodels.formula.api as sfa
>>> import scikit_posthocs as sp
>>> df = sa.datasets.get_rdataset('iris').data
>>> df.head()
   Sepal.Length  Sepal.Width  Petal.Length  Petal.Width Species
0            5.1         3.5          1.4         0.2    setosa
1            4.9         3.0          1.4         0.2    setosa
2            4.7         3.2          1.3         0.2    setosa
3            4.6         3.1          1.5         0.2    setosa
4            5.0         3.6          1.4         0.2    setosa
```

Now, we will build a model and run ANOVA using statsmodels `ols()` and `anova_lm()` methods. Columns `Species` and `Sepal.Width` contain independent (predictor) and dependent (response) variable values, correspondingly.

```
>>> lm = sfa.ols('Sepal.Width ~ C(Species)', data=df).fit()
>>> anova = sa.stats.anova_lm(lm)
>>> print(anova)
      df      sum_sq     mean_sq        F      PR(>F)
C(Species)  2.0  11.344933  5.672467  49.16004  4.492017e-17
Residual    147.0  16.962000  0.115388       NaN        NaN
```

The results tell us that there is a significant difference between groups means ( $p = 4.49e-17$ ), but does not tell us the exact group pairs which are different in means. To obtain pairwise group differences, we will carry out a posteriori (post hoc) analysis using `scikits-posthocs` package. Student T test applied pairwisely gives us the following p values:

```
>>> sp.posthoc_ttest(df, val_col='Sepal.Width', group_col='Species', p_adjust='holm')
           setosa    versicolor    virginica
setosa    -1.000000e+00  5.535780e-15  8.492711e-09
versicolor  5.535780e-15 -1.000000e+00  1.819100e-03
virginica   8.492711e-09  1.819100e-03 -1.000000e+00
```

Remember to use a [FWER controlling procedure](#), such as Holm procedure, when making multiple comparisons. As seen from this table, significant differences in group means are obtained for all group pairs.

## 3.2 Non-parametric ANOVA with post hoc tests

If normality and other assumptions are violated, one can use a non-parametric Kruskal-Wallis H test (one-way non-parametric ANOVA) to test if samples came from the same distribution.

Let's use the same dataset just to demonstrate the procedure. Kruskal-Wallis test is implemented in SciPy package. `scipy.stats.kruskal` method accepts array-like structures, but not DataFrames.

```
>>> import scipy.stats as ss
>>> import statsmodels.api as sa
>>> import scikit_posthocs as sp
>>> df = sa.datasets.get_rdataset('iris').data
>>> data = [df.loc[ids, 'Sepal.Width'].values for ids in df.groupby('Species').groups.
-> values()]
```

`data` is a list of 1D arrays containing *sepal width* values, one array per each species. Now we can run Kruskal-Wallis analysis of variance.

```
>>> H, p = ss.kruskal(*data)
>>> p
1.5692820940316782e-14
```

P value tells us we may reject the null hypothesis that the population medians of all of the groups are equal. To learn what groups (species) differ in their medians we need to run post hoc tests. `scikit-posthocs` provides a lot of non-parametric tests mentioned above. Let's choose Conover's test.

```
>>> sp.posthoc_conover(df, val_col='Sepal.Width', group_col='Species', p_adjust = 'holm')
      setosa      versicolor      virginica
setosa    -1.000000e+00  2.278515e-18  1.293888e-10
versicolor  2.278515e-18 -1.000000e+00  1.881294e-03
virginica   1.293888e-10  1.881294e-03 -1.000000e+00
```

Pairwise comparisons show that we may reject the null hypothesis ( $p < 0.01$ ) for each pair of species and conclude that all groups (species) differ in their sepal widths.

## 3.3 Block design

In block design case, we have a primary factor (e.g. treatment) and a blocking factor (e.g. age or gender). A blocking factor is also called a *nuisance* factor, and it is usually a source of variability that needs to be accounted for.

An example scenario is testing the effect of four fertilizers on crop yield in four cornfields. We can represent the results with a matrix in which rows correspond to the blocking factor (field) and columns correspond to the primary factor (yield).

The following dataset is artificial and created just for demonstration of the procedure:

```
>>> data = np.array([[ 8.82, 11.8 , 10.37, 12.08],
                  [ 8.92,  9.58, 10.59, 11.89],
                  [ 8.27, 11.46, 10.24, 11.6 ],
                  [ 8.83, 13.25,  8.33, 11.51]])
```

First, we need to perform an omnibus test — Friedman rank sum test. It is implemented in `scipy.stats` subpackage:

```
>>> import scipy.stats as ss
>>> ss.friedmanchisquare(*data.T)
FriedmanchisquareResult(statistic=8.700000000000003, pvalue=0.03355726870553798)
```

We can reject the null hypothesis that our treatments have the same distribution, because p value is less than 0.05. A number of post hoc tests are available in `scikit-posthocs` package for unreplicated block design data. In the following example, Nemenyi's test is used:

```
>>> import scikit_posthocs as sp
>>> sp.posthoc_nemenyi_friedman(data)
      0         1         2         3
0 -1.000000  0.220908  0.823993  0.031375
1  0.220908 -1.000000  0.670273  0.823993
2  0.823993  0.670273 -1.000000  0.220908
3  0.031375  0.823993  0.220908 -1.000000
```

This function returns a DataFrame with p values obtained in pairwise comparisons between all treatments. One can also pass a DataFrame and specify the names of columns containing dependent variable values, blocking and primary factor values. The following code creates a DataFrame with the same data:

```
>>> data = pd.DataFrame.from_dict({'blocks': {0: 0, 1: 1, 2: 2, 3: 3, 4: 0, 5: 1, 6: 2, 7: 3, 8: 0, 9: 1, 10: 2, 11: 3, 12: 0, 13: 1, 14: 2, 15: 3}, 'groups': {0: 0, 1: 0, 2: 0, 3: 0, 4: 1, 5: 1, 6: 1, 7: 1, 8: 2, 9: 2, 10: 2, 11: 2, 12: 3, 13: 3, 14: 3, 15: 3}, 'y': {0: 8.82, 1: 8.92, 2: 8.27, 3: 8.83, 4: 11.8, 5: 9.58, 6: 11.46, 7: 13.25, 8: 10.37, 9: 10.59, 10: 10.24, 11: 8.33, 12: 12.08, 13: 11.89, 14: 11.6, 15: 11.51}})
>>> data
   blocks  groups      y
0        0       0  8.82
1        1       0  8.92
2        2       0  8.27
3        3       0  8.83
4        0       1 11.80
5        1       1  9.58
6        2       1 11.46
7        3       1 13.25
8        0       2 10.37
9        1       2 10.59
10       2       2 10.24
11       3       2  8.33
12       0       3 12.08
13       1       3 11.89
14       2       3 11.60
15       3       3 11.51
```

This is a *melted* and ready-to-use DataFrame. Do not forget to pass `melted=True`:

```
>>> sp.posthoc_nemenyi_friedman(data, y_col='y', block_col='blocks', group_col='groups', melted=True)
      0         1         2         3
0 -1.000000  0.220908  0.823993  0.031375
1  0.220908 -1.000000  0.670273  0.823993
2  0.823993  0.670273 -1.000000  0.220908
3  0.031375  0.823993  0.220908 -1.000000
```

## 3.4 Data types

Internally, scikit-posthocs uses NumPy ndarrays and pandas DataFrames to store and process data. Python lists, NumPy ndarrays, and pandas DataFrames are supported as *input* data types. Below are usage examples of various input data structures.

### 3.4.1 Lists and arrays

```
>>> x = [[1,2,1,3,1,4], [12,3,11,9,3,8,1], [10,22,12,9,8,3]]
>>> # or
>>> x = np.array([[1,2,1,3,1,4], [12,3,11,9,3,8,1], [10,22,12,9,8,3]])
>>> sp.posthoc_conover(x, p_adjust='holm')
      1          2          3
1 -1.0000000  0.057606  0.007888
2  0.057606 -1.000000  0.215761
3  0.007888  0.215761 -1.000000
```

You can check how it is processed with a hidden function `__convert_to_df()`:

```
>>> sp.__convert_to_df(x)
(
    vals  groups
0      1      1
1      2      1
2      1      1
3      3      1
4      1      1
5      4      1
6     12      2
7      3      2
8     11      2
9      9      2
10     3      2
11     8      2
12     1      2
13    10      3
14    22      3
15    12      3
16     9      3
17     8      3
18     3  'vals', 'groups')
```

It returns a tuple of a DataFrame representation and names of the columns containing dependent (`vals`) and independent (`groups`) variable values.

*Block design* matrix passed as a NumPy ndarray is processed with a hidden `__convert_to_block_df()` function:

```
>>> data = np.array([[ 8.82, 11.8 , 10.37, 12.08],
                   [ 8.92,  9.58, 10.59, 11.89],
                   [ 8.27, 11.46, 10.24, 11.6 ],
                   [ 8.83, 13.25,  8.33, 11.51]])
>>> sp.__convert_to_block_df(data)
(
    blocks  groups       y
```

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0	0	0	8.82
1	1	0	8.92
2	2	0	8.27
3	3	0	8.83
4	0	1	11.80
5	1	1	9.58
6	2	1	11.46
7	3	1	13.25
8	0	2	10.37
9	1	2	10.59
10	2	2	10.24
11	3	2	8.33
12	0	3	12.08
13	1	3	11.89
14	2	3	11.60
15	3	3	11.51, 'y', 'groups', 'blocks')

### 3.4.2 DataFrames

If you are using DataFrames, you need to pass column names containing variable values to a post hoc function:

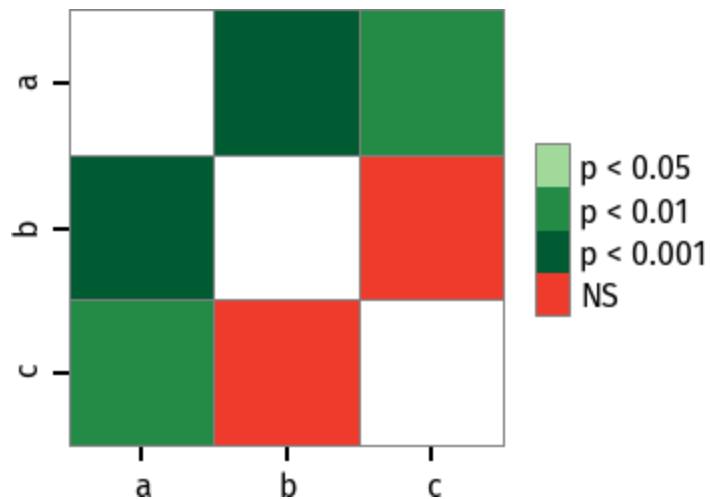
```
>>> import statsmodels.api as sa
>>> import scikit_posthocs as sp
>>> df = sa.datasets.get_rdataset('iris').data
>>> sp.posthoc_conover(df, val_col='Sepal.Width', group_col='Species', p_adjust = 'holm')
```

val\_col and group\_col arguments specify the names of the columns containing dependent (response) and independent (grouping) variable values.

## 3.5 Significance plots

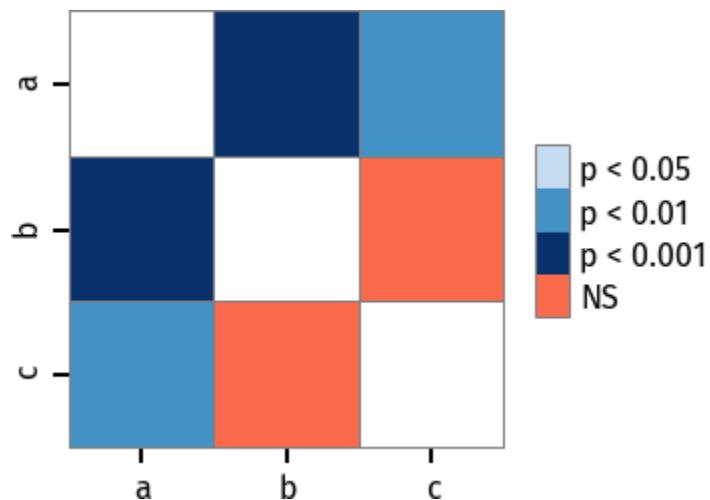
P values can be plotted using a heatmap:

```
pc = sp.posthoc_conover(x, val_col='values', group_col='groups')
heatmap_args = {'linewidths': 0.25, 'linecolor': '0.5', 'clip_on': False, 'square': True,
                'cbar_ax_bbox': [0.80, 0.35, 0.04, 0.3]}
sp.sign_plot(pc, **heatmap_args)
```



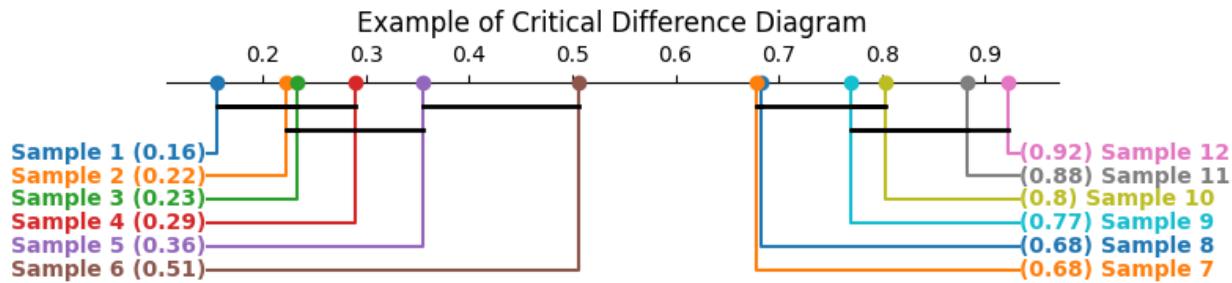
Custom colormap applied to a plot:

```
pc = sp.posthoc_conover(x, val_col='values', group_col='groups')
# Format: diagonal, non-significant, p<0.001, p<0.01, p<0.05
cmap = ['1', '#fb6a4a', '#08306b', '#4292c6', '#c6dbef']
heatmap_args = {'cmap': cmap, 'linewidths': 0.25, 'linecolor': '0.5', 'clip_on': False,
                'square': True, 'cbar_ax_bbox': [0.80, 0.35, 0.04, 0.3]}
sp.sign_plot(pc, **heatmap_args)
```



## 3.6 Critical difference diagrams

Critical difference diagrams are another interesting way of visualizing post hoc test statistics. Firstly, in a block design scenario, the values within each block are ranked, and the average rank across all blocks for each treatment is plotted along the x axis. A crossbar is then drawn over each group of treatments that do not show a statistically significant difference among themselves.



As an example, suppose we have a set of 8 treatments with 30 measurements (blocks) each, as simulated below. It could, for instance, represent scores for eight machine learning models in a 30-fold cross-validation setting.

```
>>> rng = np.random.default_rng(1)
>>> dict_data = {
    'model1': rng.normal(loc=0.2, scale=0.1, size=30),
    'model2': rng.normal(loc=0.2, scale=0.1, size=30),
    'model3': rng.normal(loc=0.4, scale=0.1, size=30),
    'model4': rng.normal(loc=0.5, scale=0.1, size=30),
    'model5': rng.normal(loc=0.7, scale=0.1, size=30),
    'model6': rng.normal(loc=0.7, scale=0.1, size=30),
    'model7': rng.normal(loc=0.8, scale=0.1, size=30),
    'model8': rng.normal(loc=0.9, scale=0.1, size=30),
}
>>> data = (
    pd.DataFrame(dict_data)
    .rename_axis('cv_fold')
    .melt(
        var_name='estimator',
        value_name='score',
        ignore_index=False,
    )
    .reset_index()
)
>>> data
   cv_fold estimator      score
0         0    model1  0.234558
1         1    model1  0.282162
2         2    model1  0.233044
3         3    model1  0.069684
4         4    model1  0.290536
..       ...
235      25    model8  0.925956
236      26    model8  0.758762
237      27    model8  0.977032
238      28    model8  0.829890
```

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```
239      29      model8  0.787381  
[240 rows x 3 columns]
```

The average (percentile) ranks could be calculated as follows:

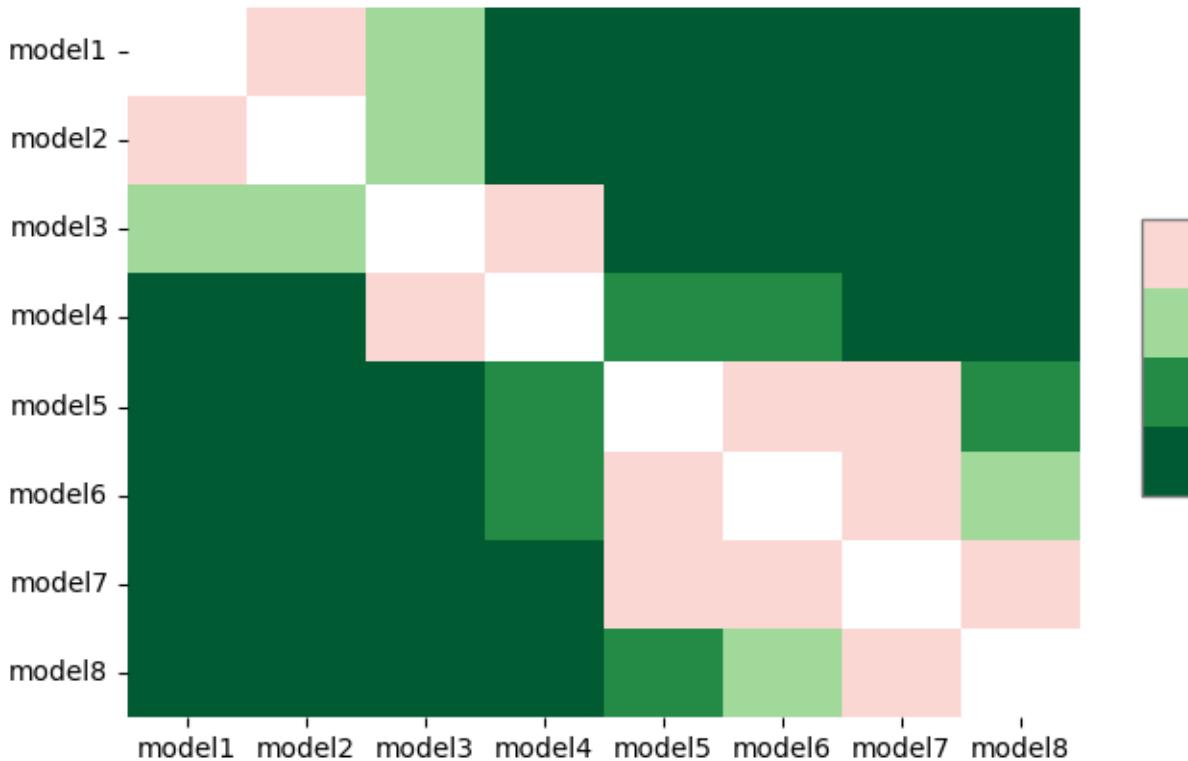
```
>>> avg_rank = data.groupby('cv_fold').score.rank(pct=True).groupby(data.estimator).  
     .mean()  
>>> avg_rank  
  
estimator  
model1    0.208333  
model2    0.191667  
model3    0.366667  
model4    0.495833  
model5    0.708333  
model6    0.737500  
model7    0.850000  
model8    0.941667  
Name: score, dtype: float64
```

Again, the omnibus test result shows we can confidently reject the null hypothesis that all models come from the same distribution and proceed to the post hoc analysis.

```
>>> import scipy.stats as ss  
>>> ss.friedmanchisquare(*dict_data.values())  
FriedmanchisquareResult(statistic=186.9000000000001, pvalue=6.787361102785178e-37)
```

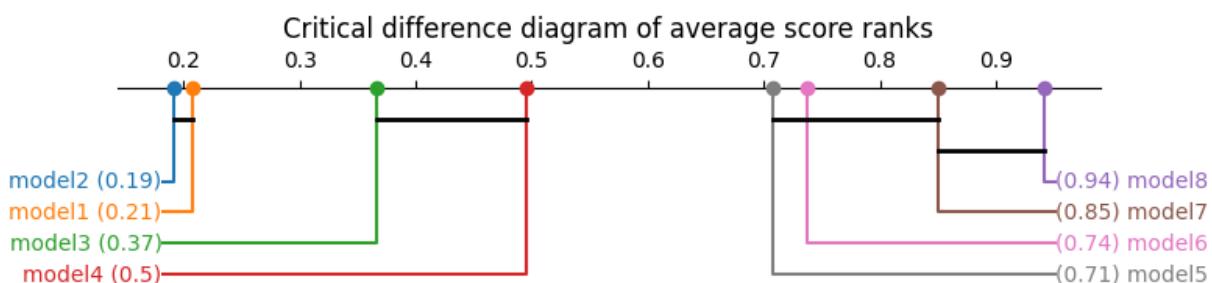
The results of a post hoc Conover test are collected:

```
>>> test_results = sp.posthoc_conover_friedman(  
>>>     data,  
>>>     melted=True,  
>>>     block_col='cv_fold',  
>>>     group_col='estimator',  
>>>     y_col='score',  
>>> )  
>>> sp.sign_plot(test_results)
```



Finally, the average ranks and post hoc significance results can be passed to the `critical_difference_diagram()` function to plot the diagram:

```
>>> plt.figure(figsize=(10, 2), dpi=100)
>>> plt.title('Critical difference diagram of average score ranks')
>>> sp.critical_difference_diagram(avg_rank, test_results)
```



The diagram shows that model 8 is significantly better ranked than all models but model 7, that models 1 and 2 are worse than the others, and that 3 and 4 are also worse ranked than models 5, 6 and 7. Other comparisons, however, do not have sufficient statistical evidence to support them.

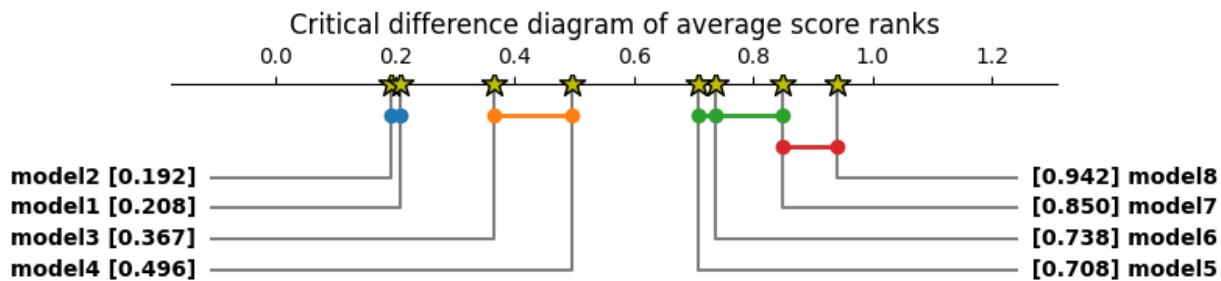
Several style customization options are available:

```
>>> plt.figure(figsize=(10, 2), dpi=100)
```

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```
>>> plt.title('Critical difference diagram of average score ranks')
>>> sp.critical_difference_diagram(
>>>     ranks=avg_rank,
>>>     sig_matrix=test_results,
>>>     label_fmt_left='{label} [{rank:.3f}]',
>>>     label_fmt_right=' [{rank:.3f}] {label}',
>>>     text_h_margin=0.3,
>>>     label_props={'color': 'black', 'fontweight': 'bold'},
>>>     crossbar_props={'color': None, 'marker': 'o'},
>>>     marker_props={'marker': '*', 's': 150, 'color': 'y', 'edgecolor': 'k'},
>>>     elbow_props={'color': 'gray'},
>>> )
```



## GLOBAL TESTS API REFERENCE

<code>global_f_test(p_vals[, stat])</code>	Fisher's combination test for global null hypothesis.
<code>global_simes_test(p_vals)</code>	Global Simes test of the intersection null hypothesis.

### 4.1 scikit\_posthocs.global\_f\_test

`scikit_posthocs.global_f_test(p_vals: List | ndarray, stat: bool = False) → float | Tuple[float, float]`

Fisher's combination test for global null hypothesis.

Computes the combined p value using chi-squared distribution and T statistic:  $-2 * \text{sum}(\log(x))$ <sup>1</sup>.

#### Parameters

- **p\_vals** (*Union[List, ndarray]*) – An array or a list of p values.
- **stat** (*bool*) – Defines if statistic should be returned.

#### Returns

- **p\_value** (*float*) – Global p value.
- **t\_stat** (*float*) – Statistic.

### References

### Examples

```
>>> x = [0.04, 0.03, 0.98, 0.01, 0.43, 0.99, 1.0, 0.002]
>>> sp.global_f_test(x)
```

<sup>1</sup> Fisher RA. Statistical methods for research workers, London: Oliver and Boyd, 1932.

## 4.2 scikit\_posthocs.global\_simes\_test

scikit\_posthocs.**global\_simes\_test**(*p\_vals*: List | ndarray) → float

Global Simes test of the intersection null hypothesis.

Computes the combined p value as  $\min(np(i)/i)$ , where  $p(1), \dots, p(n)$  are the ordered p values<sup>1</sup>.

### Parameters

**p\_vals** (*Union[List, ndarray]*) – An array of p values.

### Returns

**p\_value** – Global p value.

### Return type

float

## References

## Examples

```
>>> arr = [0.04, 0.03, 0.98, 0.01, 0.43, 0.99, 1.0, 0.002]
>>> sp.global_simes_test(arr)
```

---

<sup>1</sup> Simes, R. J. (1986). An improved Bonferroni procedure for multiple tests of significance. Biometrika, 73(3):751-754.

## OMNIBUS API REFERENCE

<code>test_mackwolfe(data[, val_col, group_col, ...])</code>	Mack-Wolfe Test for Umbrella Alternatives.
<code>test_osrt(data[, val_col, group_col, sort])</code>	Hayter's one-sided studentised range test (OSRT)
<code>test_durbin(data[, y_col, block_col, ...])</code>	Durbin's test whether k groups (or treatments) in a two-way balanced incomplete block design (BIBD) have identical effects.

### 5.1 scikit\_posthocs.test\_mackwolfe

```
scikit_posthocs.test_mackwolfe(data: List | ndarray | DataFrame, val_col: str = None, group_col: str = None, p: int = None, n_perm: int = 100, sort: bool = False) → Tuple[float, float]
```

Mack-Wolfe Test for Umbrella Alternatives.

In dose-finding studies one may assume an increasing treatment effect with increasing dose level. However, the test subject may actually succumb to toxic effects at high doses, which leads to decreasing treatment effects<sup>1,2</sup>.

The scope of the Mack-Wolfe Test is to test for umbrella alternatives for either a known or unknown point P (i.e. dose-level), where the peak (umbrella point) is present.

#### Parameters

- **data** (*Union[List, numpy.ndarray, DataFrame]*) – An array, any object exposing the array interface or a pandas DataFrame with data values.
- **val\_col** (*str = None*) – Name of a DataFrame column that contains dependent variable values (test or response variable). Values should have a non-nominal scale. Must be specified if *a* is a pandas DataFrame object.
- **group\_col** (*str = None*) – Name of a DataFrame column that contains independent variable values (grouping or predictor variable). Values should have a nominal scale (categorical). Must be specified if *a* is a pandas DataFrame object.
- **p** (*int = None*) – The a priori known peak as an ordinal number of the treatment group including the zero dose level, i.e.  $p = \{0, \dots, k-1\}$ . Defaults to None.
- **n\_perm** (*int = 100*) – Permutations number.
- **sort** (*bool = False*) – If True, sort data by block and group columns.

<sup>1</sup> Chen, I.Y. (1991) Notes on the Mack-Wolfe and Chen-Wolfe Tests for Umbrella Alternatives. Biom. J., 33, 281-290.

<sup>2</sup> Mack, G.A., Wolfe, D. A. (1981) K-sample rank tests for umbrella alternatives. J. Amer. Statist. Assoc., 76, 175-181.

**Returns**

P value and statistic.

**Return type**

Tuple[float, float]

**References****Examples**

```
>>> x = [[22, 23, 35], [60, 59, 54], [98, 78, 50], [60, 82, 59], [22, 44, 33], [23, 21, 25]]  
>>> sp.posthoc_mackwolfe(x)
```

## 5.2 scikit\_posthocs.test\_osrt

`scikit_posthocs.test_osrt(data: List | ndarray | DataFrame, val_col: str = None, group_col: str = None, sort: bool = False) → Tuple[float, float, int]`

Hayter's one-sided studentised range test (OSRT)

Tests a hypothesis against an ordered alternative for normal data with equal variances<sup>1</sup>.

**Parameters**

- **data** (*Union[List, numpy.ndarray, DataFrame]*) – An array, any object exposing the array interface or a pandas DataFrame with data values.
- **val\_col** (*str = None*) – Name of a DataFrame column that contains dependent variable values (test or response variable). Values should have a non-nominal scale. Must be specified if *a* is a pandas DataFrame object.
- **group\_col** (*str = None*) – Name of a DataFrame column that contains independent variable values (grouping or predictor variable). Values should have a nominal scale (categorical). Must be specified if *a* is a pandas DataFrame object.
- **sort** (*bool = False*) – If True, sort data by block and group columns.

**Returns**

P value, statistic, and number of degrees of freedom.

**Return type**

Tuple[float, float, int]

---

<sup>1</sup> Hayter, A.J.(1990) A One-Sided Studentised Range Test for Testing Against a Simple Ordered Alternative, Journal of the American Statistical Association, 85, 778-785.

## Notes

P values are computed from the Tukey distribution.

## References

## Examples

```
>>> import scikit_posthocs as sp
>>> import pandas as pd
>>> x = pd.DataFrame({"a": [1,2,3,5,1], "b": [12,31,54,62,12], "c": [10,12,6,74,11]}
->)
>>> x = x.melt(var_name='groups', value_name='values')
>>> sp.test_osrt(x, val_col='values', group_col='groups')
```

## 5.3 scikit\_posthocs.test\_durbin

`scikit_posthocs.test_durbin(data: List | ndarray | DataFrame, y_col: str | int = None, block_col: str | int = None, group_col: str | int = None, melted: bool = False, sort: bool = True) → Tuple[float, float, int]`

Durbin's test whether k groups (or treatments) in a two-way balanced incomplete block design (BIBD) have identical effects. See references for additional information<sup>1,2</sup>.

### Parameters

- **data** (`Union[List, np.ndarray, DataFrame]`) – An array, any object exposing the array interface or a pandas DataFrame with data values.  
If `melted` argument is set to False (default), a is a typical matrix of block design, i.e. rows are blocks, and columns are groups. In this case you do not need to specify col arguments.  
If a is an array and `melted` is set to True, `y_col`, `block_col` and `group_col` must specify the indices of columns containing elements of correspondany type.  
If a is a Pandas DataFrame and `melted` is set to True, `y_col`, `block_col` and `group_col` must specify columns names (string).
- **y\_col** (`Union[str, int] = None`) – Must be specified if a is a pandas DataFrame object. Name of the column that contains y data.
- **block\_col** (`Union[str, int] = None`) – Must be specified if a is a pandas DataFrame object. Name of the column that contains block names.
- **group\_col** (`Union[str, int] = None`) – Must be specified if a is a pandas DataFrame object. Name of the column that contains group names.
- **melted** (`bool = False`) – Specifies if data are given as melted columns “y”, “blocks”, and “groups”.
- **sort** (`bool = False`) – If True, sort data by block and group columns.

### Returns

P value, statistic, and number of degrees of freedom.

<sup>1</sup> N. A. Heckert, J. J. Filliben. (2003) NIST Handbook 148: Dataplot Reference Manual, Volume 2: Let Subcommands and Library Functions. National Institute of Standards and Technology Handbook Series, June 2003.

<sup>2</sup> W. J. Conover (1999), Practical nonparametric Statistics, 3rd. edition, Wiley.

**Return type**

Tuple[float, float, int]

**References**

**Examples**

```
>>> x = np.array([[31, 27, 24], [31, 28, 31], [45, 29, 46], [21, 18, 48], [42, 36, 46], [32, 17,
   ↵40]])
>>> sp.test_durbin(x)
```

## OUTLIERS API REFERENCE

<code>outliers_iqr(x[, ret, coef])</code>	Simple detection of potential outliers based on interquartile range (IQR).
<code>outliers_gesd(x[, outliers, hypo, report, alpha])</code>	The generalized (Extreme Studentized Deviate) ESD test is used to detect one or more outliers in a univariate data set that follows an approximately normal distribution [1].
<code>outliers_grubbs(x[, hypo, alpha])</code>	Grubbs' Test for Outliers [1].
<code>outliers_tietjen(x, k[, hypo, alpha])</code>	Tietjen-Moore test [1] to detect multiple outliers in a univariate data set that follows an approximately normal distribution.

### 6.1 scikit\_posthocs.outliers\_iqr

`scikit_posthocs.outliers_iqr(x: List | ndarray, ret: str = 'filtered', coef: float = 1.5) → ndarray`

Simple detection of potential outliers based on interquartile range (IQR). Data that lie within the lower and upper limits are considered non-outliers. The lower limit is the number that lies 1.5 IQRs below (coefficient may be changed with an argument, see Parameters) the first quartile; the upper limit is the number that lies 1.5 IQRs above the third quartile.

#### Parameters

- **x** (*Union[List, np.ndarray]*) – An array, any object exposing the array interface, containing p values.
- **ret** (*str = 'filtered'*) – Specifies object to be returned. Available options are:
  - **filtered**: return a filtered array (default)
  - **outliers**: return outliers
  - **indices**: return indices of non-outliers
  - **outliers\_indices**: return indices of outliers
- **coef** (*float = 1.5*) – Coefficient by which IQR is multiplied.

#### Returns

One of the following objects:

- Filtered array (default) if **ret** is set to **filtered**.
- Array with indices of elements lying within the specified limits if **ret** is set to **indices**.

- Array with outliers if `ret` is set to `outliers`.
- Array with indices of outlier elements if `ret` is set to `outliers_indices`.

**Return type**

numpy.ndarray

**Examples**

```
>>> x = np.array([4, 5, 6, 10, 12, 4, 3, 1, 2, 3, 23, 5, 3])
>>> outliers_iqr(x, ret = 'outliers')
array([12, 23])
```

## 6.2 scikit\_posthocs.outliers\_gesd

`scikit_posthocs.outliers_gesd(x: List | ndarray, outliers: int = 5, hypo: bool = False, report: bool = False, alpha: float = 0.05) → ndarray`

The generalized (Extreme Studentized Deviate) ESD test is used to detect one or more outliers in a univariate data set that follows an approximately normal distribution<sup>1</sup>.

**Parameters**

- **x** (`Union[List, np.ndarray]`) – An array, any object exposing the array interface, containing data to test for outliers.
- **outliers** (`int = 5`) – Number of potential outliers to test for. Test is two-tailed, i.e. maximum and minimum values are checked for potential outliers.
- **hypo** (`bool = False`) – Specifies whether to return a bool value of a hypothesis test result. Returns True when we can reject the null hypothesis. Otherwise, False. Available options are: 1) True - return a hypothesis test result. 2) False - return a filtered array without an outlier (default).
- **report** (`bool = False`) – Specifies whether to print a summary table of the test.
- **alpha** (`float = 0.05`) – Significance level for a hypothesis test.

**Returns**

Returns the filtered array if alternative hypo is True, otherwise an unfiltered (input) array.

**Return type**

np.ndarray

**Notes****Examples**

```
>>> data = np.array([-0.25, 0.68, 0.94, 1.15, 1.2, 1.26, 1.26, 1.34,
1.38, 1.43, 1.49, 1.49, 1.55, 1.56, 1.58, 1.65, 1.69, 1.7, 1.76,
1.77, 1.81, 1.91, 1.94, 1.96, 1.99, 2.06, 2.09, 2.1, 2.14, 2.15,
2.23, 2.24, 2.26, 2.35, 2.37, 2.4, 2.47, 2.54, 2.62, 2.64, 2.9,
2.92, 2.92, 2.93, 3.21, 3.26, 3.3, 3.59, 3.68, 4.3, 4.64, 5.34,
```

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<sup>1</sup> Rosner, Bernard (May 1983), Percentage Points for a Generalized ESD Many-Outlier Procedure, Technometrics, 25(2), pp. 165-172.

(continued from previous page)

```

5.42, 6.01])
>>> outliers_gesd(data, 5)
array([-0.25,  0.68,  0.94,  1.15,  1.2 ,  1.26,  1.26,  1.34,  1.38,
       1.43,  1.49,  1.49,  1.55,  1.56,  1.58,  1.65,  1.69,  1.7 ,
       1.76,  1.77,  1.81,  1.91,  1.94,  1.96,  1.99,  2.06,  2.09,
       2.1 ,  2.14,  2.15,  2.23,  2.24,  2.26,  2.35,  2.37,  2.4 ,
       2.47,  2.54,  2.62,  2.64,  2.9 ,  2.92,  2.92,  2.93,  3.21,
       3.26,  3.3 ,  3.59,  3.68,  4.3 ,  4.64])
>>> outliers_gesd(data, outliers = 5, report = True)
H0: no outliers in the data
Ha: up to 5 outliers in the data
Significance level:  = 0.05
Reject H0 if Ri > Critical Value (i)
Summary Table for Two-Tailed Test
-----
   Exact      Test      Critical
Number of    Statistic    Value, i
Outliers, i    Value, Ri      5 %
-----
   1          3.119      3.159
   2          2.943      3.151
   3          3.179      3.144 *
   4          2.81       3.136
   5          2.816      3.128

```

## 6.3 scikit\_posthocs.outliers\_grubbs

`scikit_posthocs.outliers_grubbs(x: List | ndarray, hypo: bool = False, alpha: float = 0.05) → ndarray | bool`

Grubbs' Test for Outliers<sup>1</sup>. This is the two-sided version of the test. The null hypothesis implies that there are no outliers in the data set.

### Parameters

- **x** (`Union[List, np.ndarray]`) – An array, any object exposing the array interface, containing data to test for an outlier in.
- **hypo** (`bool = False`) – Specifies whether to return a bool value of a hypothesis test result. Returns `True` when we can reject the null hypothesis. Otherwise, `False`. Available options are:
  - `True`: return a hypothesis test result
  - `False`: return a filtered array without an outlier (default)
- **alpha** (`float = 0.05`) – Significance level for a hypothesis test.

### Returns

Returns a filtered array if alternative hypothesis is true, otherwise an unfiltered array. Returns null hypothesis test result instead of an array if `hypo` argument is set to `True`.

### Return type

`Union[np.ndarray, bool]`

<sup>1</sup> <http://www.itl.nist.gov/div898/handbook/eda/section3/eda35h1.htm>

## Notes

### Examples

```
>>> x = np.array([199.31, 199.53, 200.19, 200.82, 201.92, 201.95, 202.18, 245.57])
>>> ph.outliers_grubbs(x)
array([ 199.31,  199.53,  200.19,  200.82,  201.92,  201.95,  202.18])
```

## 6.4 scikit\_posthocs.outliers\_tietjen

`scikit_posthocs.outliers_tietjen`(*x*: *List* | *ndarray*, *k*: *int*, *hypo*: *bool* = *False*, *alpha*: *float* = 0.05) → *ndarray* | *bool*

Tietjen-Moore test<sup>1</sup> to detect multiple outliers in a univariate data set that follows an approximately normal distribution. The Tietjen-Moore test<sup>2</sup> is a generalization of the Grubbs' test to the case of multiple outliers. If testing for a single outlier, the Tietjen-Moore test is equivalent to the Grubbs' test.

The null hypothesis implies that there are no outliers in the data set.

### Parameters

- **x** (*Union[List, np.ndarray]*) – An array, any object exposing the array interface, containing data to test for an outlier in.
- **k** (*int*) – Number of potential outliers to test for. Function tests for outliers in both tails.
- **hypo** (*bool* = *False*) – Specifies whether to return a *bool* value of a hypothesis test result. Returns *True* when we can reject the null hypothesis. Otherwise, *False*. Available options are:
  - *True*: return a hypothesis test result
  - *False*: return a filtered array without outliers (default).
- **alpha** (*float* = 0.05) – Significance level for a hypothesis test.

### Returns

Returns a filtered array if alternative hypothesis is true, otherwise an unfiltered array. Returns null hypothesis test result instead of an array if *hypo* argument is set to *True*.

### Return type

*Union[numpy.ndarray, bool]*

## Notes

### Examples

```
>>> x = np.array([-1.40, -0.44, -0.30, -0.24, -0.22, -0.13, -0.05, 0.06,
0.10, 0.18, 0.20, 0.39, 0.48, 0.63, 1.01])
>>> outliers_tietjen(x, 2)
array([-0.44, -0.3 , -0.24, -0.22, -0.13, -0.05,  0.06,  0.1 ,  0.18,
0.2 ,  0.39,  0.48,  0.63])
```

<sup>1</sup> Tietjen and Moore (August 1972), Some Grubbs-Type Statistics for the Detection of Outliers, *Technometrics*, 14(3), pp. 583-597.

<sup>2</sup> <http://www.itl.nist.gov/div898/handbook/eda/section3/eda35h2.htm>

## PLOTTING API REFERENCE

<code>sign_array(p_values[, alpha])</code>	Significance array.
<code>sign_table(p_values[, lower, upper])</code>	Significance table.
<code>sign_plot(x[, g, flat, labels, cmap, ...])</code>	Significance plot, a heatmap of p values (based on Seaborn).
<code>critical_difference_diagram(ranks, sig_matrix, *)</code>	Plot a Critical Difference diagram from ranks and post-hoc results.

### 7.1 scikit\_posthocs.sign\_array

`scikit_posthocs.sign_array(p_values: List | ndarray, alpha: float = 0.05) → ndarray`

Significance array.

Converts an array with p values to a significance array where 0 is False (not significant), 1 is True (significant), and -1 is for diagonal elements.

#### Parameters

- **p\_values** (*Union[List, np.ndarray]*) – Any object exposing the array interface and containing p values.
- **alpha** (*float = 0.05*) – Significance level. Default is 0.05.

#### Returns

**result** – Array where 0 is False (not significant), 1 is True (significant), and -1 is for diagonal elements.

#### Return type

`numpy.ndarray`

#### Examples

```
>>> p_values = np.array([[ 1.          ,  0.00119517,  0.00278329],
   ...                   [ 0.00119517,  1.          ,  0.18672227],
   ...                   [ 0.00278329,  0.18672227,  1.          ]])
>>> ph.sign_array(p_values)
array([[1, 1, 1],
       [1, 1, 0],
       [1, 0, 1]])
```

## 7.2 scikit\_posthocs.sign\_table

```
scikit_posthocs.sign_table(p_values: List | ndarray | DataFrame, lower: bool = True, upper: bool = True)
    → DataFrame | ndarray
```

Significance table.

Returns table that can be used in a publication. P values are replaced with asterisks: \* -  $p < 0.05$ , \*\* -  $p < 0.01$ , \*\*\* -  $p < 0.001$ .

### Parameters

- **p\_values** (*Union[List, np.ndarray, DataFrame]*) – Any object exposing the array interface and containing p values.
- **lower** (*bool*) – Defines whether to return the lower triangle.
- **upper** (*bool*) – Defines whether to return the upper triangle.

### Returns

**result** – P values masked with asterisks.

### Return type

*Union[DataFrame, np.ndarray]*

### Examples

```
>>> p_values = np.array([[ -1.          ,  0.00119517,  0.00278329],
   ...           [ 0.00119517, -1.          ,  0.18672227],
   ...           [ 0.00278329,  0.18672227, -1.          ]])
>>> ph.sign_table(p_values)
array([[-', '**', '**'],
       ['**', '-', 'NS'],
       ['**', 'NS', '-']], dtype=object)
```

## 7.3 scikit\_posthocs.sign\_plot

```
scikit_posthocs.sign_plot(x: List | ndarray | DataFrame, g: List | ndarray = None, flat: bool = False, labels:
                           bool = True, cmap: List = None, cbar_ax_bbox: List = None, ax: SubplotBase =
                           None, **kwargs) → SubplotBase | Tuple[SubplotBase, Colorbar]
```

Significance plot, a heatmap of p values (based on Seaborn).

### Parameters

- **x** (*Union[List, np.ndarray, DataFrame]*) – If *flat* is False (default), *x* must be an array, any object exposing the array interface, containing p values. If *flat* is True, *x* must be a *sign\_array* (returned by `scikit_posthocs.sign_array()` function).
- **g** (*Union[List, np.ndarray]*) – An array, any object exposing the array interface, containing group names.
- **flat** (*bool*) – If *flat* is True, plots a significance array as a heatmap using seaborn. If *flat* is False (default), plots an array of p values. Non-flat mode is useful if you need to differentiate significance levels visually. It is the preferred mode.
- **labels** (*bool*) – Plot axes labels (default) or not.

- **cmap** (*list*) – 1) If flat is False (default): List consisting of five elements, that will be exported to ListedColormap method of matplotlib. First is for diagonal elements, second is for non-significant elements, third is for  $p < 0.001$ , fourth is for  $p < 0.01$ , fifth is for  $p < 0.05$ .  
2) If flat is True: List consisting of three elements, that will be exported to ListedColormap method of matplotlib. First is for diagonal elements, second is for non-significant elements, third is for significant ones. 3) If not defined, default colormaps will be used.
- **cbar\_ax\_bbox** (*list*) – Colorbar axes position rect [left, bottom, width, height] where all quantities are in fractions of figure width and height. Refer to *matplotlib.figure.Figure.add\_axes* for more information. Default is [0.95, 0.35, 0.04, 0.3].
- **ax** (*SubplotBase*) – Axes in which to draw the plot, otherwise use the currently-active Axes.
- **kwargs** – Keyword arguments to be passed to seaborn heatmap method. These keyword args cannot be used: cbar, vmin, vmax, center.

**Returns**

- **ax** (*matplotlib.axes.\_subplots.AxesSubplot*) – Axes object with the heatmap.
- **cbar** (*matplotlib.colorbar.Colorbar*) – ColorBar object if *flat* is set to False.

**Examples**

```
>>> x = np.array([[ 1,  1,  1],
   [ 1,  1,  0],
   [ 1,  0,  1]])
>>> ph.sign_plot(x, flat = True)
```

## 7.4 scikit\_posthocs.critical\_difference\_diagram

```
scikit_posthocs.critical_difference_diagram(ranks: dict | Series, sig_matrix: DataFrame, *, ax:
                                             SubplotBase = None, label_fmt_left: str = '{label}
                                             ({rank:.2g})', label_fmt_right: str = '({rank:.2g}) {label}', label_props: dict = None, marker_props: dict = None, elbow_props: dict = None, crossbar_props: dict = None, color_palette: Dict[str, str] | List = {}, text_h_margin: float = 0.01) → Dict[str, list]
```

Plot a Critical Difference diagram from ranks and post-hoc results.

The diagram arranges the average ranks of multiple groups on the x axis in order to facilitate performance comparisons between them. The groups that could not be statistically deemed as different are linked by a horizontal crossbar<sup>1,2</sup>.



(continues on next page)

<sup>1</sup> Demšar, J. (2006). Statistical comparisons of classifiers over multiple data sets. The Journal of Machine learning research, 7, 1-30.

<sup>2</sup> <https://mirkobunse.github.io/CriticalDifferenceDiagrams.jl/stable/>

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|\_\_\_\_\_|  
text\_h\_margin

| ----- | clf5

In the drawing above, the two crossbars indicate that clf1 and clf2 cannot be statistically differentiated, the same occurring between clf3, clf4 and clf5. However, clf1 and clf2 are each significantly lower ranked than clf3, clf4 and clf5.

### Parameters

- **ranks** (*dict or Series*) – Indicates the rank value for each sample or estimator (as keys or index).
- **sig\_matrix** (*DataFrame*) – The corresponding p-value matrix outputted by post-hoc tests, with indices matching the labels in the ranks argument.
- **ax** (*matplotlib.SubplotBase, optional*) – The object in which the plot will be built. Gets the current Axes by default (if None is passed).
- **label\_fmt\_left** (*str, optional*) – The format string to apply to the labels on the left side. The keywords label and rank can be used to specify the sample/estimator name and rank value, respectively, by default '{label} ({rank:.2g})'.
- **label\_fmt\_right** (*str, optional*) – The same, but for the labels on the right side of the plot. By default '{(rank:.2g)} {label}'.
- **label\_props** (*dict, optional*) – Parameters to be passed to pyplot.text() when creating the labels, by default None.
- **marker\_props** (*dict, optional*) – Parameters to be passed to pyplot.scatter() when plotting the rank markers on the axis, by default None.
- **elbow\_props** (*dict, optional*) – Parameters to be passed to pyplot.plot() when creating the elbow lines, by default None.
- **crossbar\_props** (*dict, optional*) – Parameters to be passed to pyplot.plot() when creating the crossbars that indicate lack of statistically significant difference. By default None.
- **text\_h\_margin** (*float, optional*) – Space between the text labels and the nearest vertical line of an elbow, by default 0.01.
- **color\_palette** (*dict, optional*) – Parameters to be passed when you need specific colors for each category

### Returns

Lists of Artists created.

### Return type

dict[str, list[matplotlib.Artist]]

## Examples

See the [Tutorial](#).

## References





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 CHAPTER  
**EIGHT**


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## POST-HOCS API REFERENCE

<code>posthoc_conover(a[, val_col, group_col, ...])</code>	Post hoc pairwise test for multiple comparisons of mean rank sums (Conover's test).
<code>posthoc_dunn(a[, val_col, group_col, ...])</code>	Post hoc pairwise test for multiple comparisons of mean rank sums (Dunn's test).
<code>posthoc_nemenyi(a[, val_col, group_col, ...])</code>	Post hoc pairwise test for multiple comparisons of mean rank sums (Nemenyi's test).
<code>posthoc_nemenyi_friedman(a[, y_col, ...])</code>	Calculate pairwise comparisons using Nemenyi post hoc test for unreplicated blocked data.
<code>posthoc_conover_friedman(a[, y_col, ...])</code>	Calculate pairwise comparisons using Conover post hoc test for unreplicated blocked data.
<code>posthoc_siegel_friedman(a[, y_col, ...])</code>	Siegel and Castellan's All-Pairs Comparisons Test for Unreplicated Blocked Data.
<code>posthoc_miller_friedman(a[, y_col, ...])</code>	Miller's All-Pairs Comparisons Test for Unreplicated Blocked Data.
<code>posthoc_npm_test(a[, val_col, group_col, sort])</code>	Calculate pairwise comparisons using Nashimoto and Wright's all-pairs comparison procedure (NPM test) for simply ordered mean ranksums.
<code>posthoc_durbin(a[, y_col, block_col, ...])</code>	Pairwise post hoc test for multiple comparisons of rank sums according to Durbin and Conover for a two-way balanced incomplete block design (BIBD).
<code>posthoc_anderson(a[, val_col, group_col, ...])</code>	Anderson-Darling Pairwise Test for k-samples.
<code>posthoc_quade(a[, y_col, block_col, ...])</code>	Calculate pairwise comparisons using Quade's post hoc test for unreplicated blocked data.
<code>posthoc_vanwaerden(a[, val_col, group_col, ...])</code>	Van der Waerden's test for pairwise multiple comparisons between group levels.
<code>posthoc_tukey_hsd(x, g[, alpha])</code>	Pairwise comparisons with TukeyHSD confidence intervals.
<code>posthoc_ttest(a[, val_col, group_col, ...])</code>	Pairwise T test for multiple comparisons of independent groups.
<code>posthoc_mannwhitney(a[, val_col, group_col, ...])</code>	Pairwise comparisons with Mann-Whitney rank test.
<code>posthoc_wilcoxon(a[, val_col, group_col, ...])</code>	Pairwise comparisons with Wilcoxon signed-rank test.
<code>posthoc_scheffe(a[, val_col, group_col, sort])</code>	Scheffe's all-pairs comparisons test for normally distributed data with equal group variances.
<code>posthoc_tamhane(a[, val_col, group_col, ...])</code>	Tamhane's T2 all-pairs comparison test for normally distributed data with unequal variances.
<code>posthoc_tukey(a[, val_col, group_col, sort])</code>	Performs Tukey's all-pairs comparisons test for normally distributed data with equal group variances.
<code>posthoc_dscf(a[, val_col, group_col, sort])</code>	Dwass, Steel, Critchlow and Fligner all-pairs comparison test for a one-factorial layout with non-normally distributed residuals.
<code>posthoc_dunnett(a[, val_col, group_col, ...])</code>	Dunnett's test [1, 2, 3] for multiple comparisons against a control group, used after parametric ANOVA.

## 8.1 scikit\_posthocs.posthoc\_conover

`scikit_posthocs.posthoc_conover(a: list | ndarray | DataFrame, val_col: str = None, group_col: str = None, p_adjust: str = None, sort: bool = True) → DataFrame`

Post hoc pairwise test for multiple comparisons of mean rank sums (Conover's test). May be used after Kruskal-Wallis one-way analysis of variance by ranks to do pairwise comparisons<sup>1</sup>.

### Parameters

- **a (array\_like or pandas DataFrame object)** – An array, any object exposing the array interface or a pandas DataFrame. Array must be two-dimensional. Second dimension may vary, i.e. groups may have different lengths.
- **val\_col (str, optional)** – Name of a DataFrame column that contains dependent variable values (test or response variable). Values should have a non-nominal scale. Must be specified if *a* is a pandas DataFrame object.
- **group\_col (str, optional)** – Name of a DataFrame column that contains independent variable values (grouping or predictor variable). Values should have a nominal scale (categorical). Must be specified if *a* is a pandas DataFrame object.
- **p\_adjust (str, optional)** – Method for adjusting p values. See `statsmodels.sandbox.stats.multicomp` for details. Available methods are: ‘bonferroni’ : one-step correction ‘sidak’ : one-step correction ‘holm-sidak’ : step-down method using Sidak adjustments ‘holm’ : step-down method using Bonferroni adjustments ‘simes-hochberg’ : step-up method (independent) ‘hommel’ : closed method based on Simes tests (non-negative) ‘fdr\_bh’ : Benjamini/Hochberg (non-negative) ‘fdr\_by’ : Benjamini/Yekutieli (negative) ‘fdr\_tsbh’ : two stage fdr correction (non-negative) ‘fdr\_tsbky’ : two stage fdr correction (non-negative)
- **sort (bool, optional)** – Specifies whether to sort DataFrame by *group\_col* or not. Recommended unless you sort your data manually.

### Returns

**result** – P values.

### Return type

pandas.DataFrame

### Notes

A tie correction are employed according to Conover<sup>1</sup>.

### References

### Examples

```
>>> x = [[1,2,3,5,1], [12,31,54, np.nan], [10,12,6,74,11]]
>>> sp.posthoc_conover(x, p_adjust = 'holm')
```

<sup>1</sup> W. J. Conover and R. L. Iman (1979), On multiple-comparisons procedures, Tech. Rep. LA-7677-MS, Los Alamos Scientific Laboratory.

## 8.2 scikit\_posthocs.posthoc\_dunn

`scikit_posthocs.posthoc_dunn(a: list | ndarray | DataFrame, val_col: str = None, group_col: str = None, p_adjust: str = None, sort: bool = True) → DataFrame`

Post hoc pairwise test for multiple comparisons of mean rank sums (Dunn's test). May be used after Kruskal-Wallis one-way analysis of variance by ranks to do pairwise comparisons<sup>1</sup>,<sup>2</sup>.

### Parameters

- **a (array\_like or pandas DataFrame object)** – An array, any object exposing the array interface or a pandas DataFrame. Array must be two-dimensional. Second dimension may vary, i.e. groups may have different lengths.
- **val\_col (str, optional)** – Name of a DataFrame column that contains dependent variable values (test or response variable). Values should have a non-nominal scale. Must be specified if *a* is a pandas DataFrame object.
- **group\_col (str, optional)** – Name of a DataFrame column that contains independent variable values (grouping or predictor variable). Values should have a nominal scale (categorical). Must be specified if *a* is a pandas DataFrame object.
- **p\_adjust (str, optional)** – Method for adjusting p values. See `statsmodels.sandbox.stats.multicomp` for details. Available methods are: ‘bonferroni’ : one-step correction ‘sidak’ : one-step correction ‘holm-sidak’ : step-down method using Sidak adjustments ‘holm’ : step-down method using Bonferroni adjustments ‘simes-hochberg’ : step-up method (independent) ‘hommel’ : closed method based on Simes tests (non-negative) ‘fdr\_bh’ : Benjamini/Hochberg (non-negative) ‘fdr\_by’ : Benjamini/Yekutieli (negative) ‘fdr\_tsbh’ : two stage fdr correction (non-negative) ‘fdr\_tsby’ : two stage fdr correction (non-negative)
- **sort (bool, optional)** – Specifies whether to sort DataFrame by group\_col or not. Recommended unless you sort your data manually.

### Returns

**result** – P values.

### Return type

pandas.DataFrame

### Notes

A tie correction will be employed according to Glantz (2012).

### References

### Examples

```
>>> x = [[1,2,3,5,1], [12,31,54, np.nan], [10,12,6,74,11]]
>>> sp.posthoc_dunn(x, p_adjust = 'holm')
```

<sup>1</sup> O.J. Dunn (1964). Multiple comparisons using rank sums. *Technometrics*, 6, 241-252.

<sup>2</sup> S.A. Glantz (2012), Primer of Biostatistics. New York: McGraw Hill.

## 8.3 scikit\_posthocs.posthoc\_nemenyi

`scikit_posthocs.posthoc_nemenyi(a: list | ndarray | DataFrame, val_col: str = None, group_col: str = None, dist: str = 'chi', sort: bool = True) → DataFrame`

Post hoc pairwise test for multiple comparisons of mean rank sums (Nemenyi's test). May be used after Kruskal-Wallis one-way analysis of variance by ranks to do pairwise comparisons<sup>1</sup>.

### Parameters

- **a (array\_like or pandas DataFrame object)** – An array, any object exposing the array interface or a pandas DataFrame. Array must be two-dimensional. Second dimension may vary, i.e. groups may have different lengths.
- **val\_col (str, optional)** – Name of a DataFrame column that contains dependent variable values (test or response variable). Values should have a non-nominal scale. Must be specified if *a* is a pandas DataFrame object.
- **group\_col (str, optional)** – Name of a DataFrame column that contains independent variable values (grouping or predictor variable). Values should have a nominal scale (categorical). Must be specified if *a* is a pandas DataFrame object.
- **dist (str, optional)** – Method for determining the p value. The default distribution is “chi” (chi-squared), else “tukey” (studentized range).
- **sort (bool, optional)** – Specifies whether to sort DataFrame by group\_col or not. Recommended unless you sort your data manually.

### Returns

**result** – P values.

### Return type

pandas.DataFrame

### Notes

A tie correction will be employed according to Glantz (2012).

### References

### Examples

```
>>> x = [[1, 2, 3, 5, 1], [12, 31, 54, np.nan], [10, 12, 6, 74, 11]]
>>> sp.posthoc_nemenyi(x)
```

<sup>1</sup> Lothar Sachs (1997), Angewandte Statistik. Berlin: Springer. Pages: 395-397, 662-664.

## 8.4 scikit\_posthocs.posthoc\_nemenyi\_friedman

`scikit_posthocs.posthoc_nemenyi_friedman(a: list | ndarray | DataFrame, y_col: str = None, block_col: str = None, group_col: str = None, melted: bool = False, sort: bool = False) → DataFrame`

Calculate pairwise comparisons using Nemenyi post hoc test for unreplicated blocked data. This test is usually conducted post hoc if significant results of the Friedman’s test are obtained. The statistics refer to upper quantiles of the studentized range distribution (Tukey)<sup>1</sup>,<sup>2</sup>,<sup>3</sup>.

### Parameters

- **a (array\_like or pandas DataFrame object)** – An array, any object exposing the array interface or a pandas DataFrame.  
If *melted* is set to False (default), *a* is a typical matrix of block design, i.e. rows are blocks, and columns are groups. In this case you do not need to specify col arguments.  
If *a* is an array and *melted* is set to True, *y\_col*, *block\_col* and *group\_col* must specify the indices of columns containing elements of correspondancy type.  
If *a* is a Pandas DataFrame and *melted* is set to True, *y\_col*, *block\_col* and *group\_col* must specify columns names (strings).
- **y\_col (str or int)** – Must be specified if *a* is a pandas DataFrame object. Name of the column that contains y data.
- **block\_col (str or int)** – Must be specified if *a* is a pandas DataFrame object. Name of the column that contains blocking factor values.
- **group\_col (str or int)** – Must be specified if *a* is a pandas DataFrame object. Name of the column that contains treatment (group) factor values.
- **melted (bool, optional)** – Specifies if data are given as melted columns “y”, “blocks”, and “groups”.
- **sort (bool, optional)** – If True, sort data by block and group columns.

### Returns

**result** – P values.

### Return type

pandas.DataFrame

### Notes

A one-way ANOVA with repeated measures that is also referred to as ANOVA with unreplicated block design can also be conducted via Friedman’s test. The consequent post hoc pairwise multiple comparison test according to Nemenyi is conducted with this function.

This function does not test for ties.

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<sup>1</sup> J. Demsar (2006), Statistical comparisons of classifiers over multiple data sets, Journal of Machine Learning Research, 7, 1-30.

<sup>2</sup> P. Nemenyi (1963) Distribution-free Multiple Comparisons. Ph.D. thesis, Princeton University.

<sup>3</sup> L. Sachs (1997), Angewandte Statistik. Berlin: Springer. Pages: 668-675.

## References

### Examples

```
>>> # Non-melted case, x is a block design matrix, i.e. rows are blocks
>>> # and columns are groups.
>>> x = np.array([[31,27,24],[31,28,31],[45,29,46],[21,18,48],[42,36,46],[32,17,
-> 40]])
>>> sp.posthoc_nemenyi_friedman(x)
```

## 8.5 scikit\_posthocs.posthoc\_conover\_friedman

`scikit_posthocs.posthoc_conover_friedman(a: list | ndarray | DataFrame, y_col: str = None, block_col: str = None, group_col: str = None, melted: bool = False, sort: bool = False, p_adjust: str = None) → DataFrame`

Calculate pairwise comparisons using Conover post hoc test for unreplicated blocked data. This test is usually conducted post hoc after significant results of the Friedman test. The statistics refer to the Student t distribution<sup>1,2</sup>.

### Parameters

- **a (array\_like or pandas DataFrame object)** – An array, any object exposing the array interface or a pandas DataFrame.  
If *melted* is set to False (default), *a* is a typical matrix of block design, i.e. rows are blocks, and columns are groups. In this case you do not need to specify col arguments.  
If *a* is an array and *melted* is set to True, *y\_col*, *block\_col* and *group\_col* must specify the indices of columns containing elements of correspondany type.  
If *a* is a Pandas DataFrame and *melted* is set to True, *y\_col*, *block\_col* and *group\_col* must specify columns names (strings).
- **y\_col (str or int)** – Must be specified if *a* is a pandas DataFrame object. Name of the column that contains y data.
- **block\_col (str or int)** – Must be specified if *a* is a pandas DataFrame object. Name of the column that contains blocking factor values.
- **group\_col (str or int)** – Must be specified if *a* is a pandas DataFrame object. Name of the column that contains treatment (group) factor values.
- **melted (bool, optional)** – Specifies if data are given as melted columns “y”, “blocks”, and “groups”.
- **sort (bool, optional)** – If True, sort data by block and group columns.
- **p\_adjust (str, optional)** – Method for adjusting p values. See `statsmodels.sandbox.stats.multicomp` for details. Available methods are: ‘bonferroni’ : one-step correction ‘sidak’ : one-step correction ‘holm-sidak’ : step-down method using Sidak adjustments ‘holm’ : step-down method using Bonferroni adjustments ‘simes-hochberg’ : step-up method (independent) ‘hommel’ : closed method based on Simes tests (non-negative) ‘fdr\_bh’ : Benjamini/Hochberg (non-negative) ‘fdr\_by’ : Benjamini/Yekutieli (negative) ‘fdr\_tsbh’ : two stage fdr correction (non-negative) ‘fdr\_tsbky’ : two stage fdr correction (non-negative) ‘single-step’ : uses Tukey distribution for multiple comparisons

<sup>1</sup> W. J. Conover and R. L. Iman (1979), On multiple-comparisons procedures, Tech. Rep. LA-7677-MS, Los Alamos Scientific Laboratory.

<sup>2</sup> W. J. Conover (1999), Practical nonparametric Statistics, 3rd. Edition, Wiley.

**Returns**

**result** – P values.

**Return type**

pandas.DataFrame

**Notes**

A one-way ANOVA with repeated measures that is also referred to as ANOVA with unreplicated block design can also be conducted via the friedman.test. The consequent post hoc pairwise multiple comparison test according to Conover is conducted with this function.

If  $y$  is a matrix, than the columns refer to the treatment and the rows indicate the block.

**References****Examples**

```
>>> x = np.array([[31, 27, 24], [31, 28, 31], [45, 29, 46], [21, 18, 48], [42, 36, 46], [32, 17,
   ↵40]])
>>> sp.posthoc_conover_friedman(x)
```

## 8.6 scikit\_posthocs.posthoc\_siegel\_friedman

`scikit_posthocs.posthoc_siegel_friedman(a: list | ndarray | DataFrame, y_col: str = None, block_col: str = None, group_col: str = None, p_adjust: str = None, melted: bool = False, sort: bool = False) → DataFrame`

Siegel and Castellan's All-Pairs Comparisons Test for Unreplicated Blocked Data. See authors' paper for additional information<sup>1</sup>.

**Parameters**

- **a (array\_like or pandas DataFrame object)** – An array, any object exposing the array interface or a pandas DataFrame.  
If *melted* is set to False (default), *a* is a typical matrix of block design, i.e. rows are blocks, and columns are groups. In this case you do not need to specify col arguments.  
If *a* is an array and *melted* is set to True, *y\_col*, *block\_col* and *group\_col* must specify the indices of columns containing elements of correspondant type.  
If *a* is a Pandas DataFrame and *melted* is set to True, *y\_col*, *block\_col* and *group\_col* must specify columns names (strings).
- **y\_col (str or int)** – Must be specified if *a* is a pandas DataFrame object. Name of the column that contains y data.
- **block\_col (str or int)** – Must be specified if *a* is a pandas DataFrame object. Name of the column that contains blocking factor values.
- **group\_col (str or int)** – Must be specified if *a* is a pandas DataFrame object. Name of the column that contains treatment (group) factor values.

<sup>1</sup> S. Siegel, N. J. Castellan Jr. (1988), Nonparametric Statistics for the Behavioral Sciences. 2nd ed. New York: McGraw-Hill.

- **melted** (*bool, optional*) – Specifies if data are given as melted columns “y”, “blocks”, and “groups”.
- **sort** (*bool, optional*) – If True, sort data by block and group columns.
- **p\_adjust** (*str, optional*) – Method for adjusting p values. See statsmodels.sandbox.stats.multicomp for details. Available methods are: ‘bonferroni’ : one-step correction ‘sidak’ : one-step correction ‘holm-sidak’ : step-down method using Sidak adjustments ‘holm’ : step-down method using Bonferroni adjustments ‘simes-hochberg’ : step-up method (independent) ‘hommel’ : closed method based on Simes tests (non-negative) ‘fdr\_bh’ : Benjamini/Hochberg (non-negative) ‘fdr\_by’ : Benjamini/Yekutieli (negative) ‘fdr\_tsby’ : two stage fdr correction (non-negative) ‘fdr\_tsby’ : two stage fdr correction (non-negative)

**Returns****result** – P values.**Return type**

pandas.DataFrame

**Notes**

For all-pairs comparisons in a two factorial unreplicated complete block design with non-normally distributed residuals, Siegel and Castellan’s test can be performed on Friedman-type ranked data.

**References****Examples**

```
>>> x = np.array([[31, 27, 24], [31, 28, 31], [45, 29, 46], [21, 18, 48], [42, 36, 46], [32, 17,
   -40]])
>>> sp.posthoc_siegel_friedman(x)
```

## 8.7 scikit\_posthocs.posthoc\_miller\_friedman

`scikit_posthocs.posthoc_miller_friedman(a: list | ndarray | DataFrame, y_col: str = None, block_col: str = None, group_col: str = None, melted: bool = False, sort: bool = False) → DataFrame`

Miller’s All-Pairs Comparisons Test for Unreplicated Blocked Data. The p-values are computed from the chi-square distribution<sup>1 2 3</sup>.

**Parameters**

- **a** (*array\_like or pandas DataFrame object*) – An array, any object exposing the array interface or a pandas DataFrame.

If *melted* is set to False (default), *a* is a typical matrix of block design, i.e. rows are blocks, and columns are groups. In this case you do not need to specify col arguments.

If *a* is an array and *melted* is set to True, *y\_col*, *block\_col* and *group\_col* must specify the indices of columns containing elements of correspondant type.

<sup>1</sup> J. Bortz J, G. A. Lienert, K. Boehnke (1990), Verteilungsfreie Methoden in der Biostatistik. Berlin: Springerself.

<sup>2</sup> R. G. Miller Jr. (1996), Simultaneous statistical inference. New York: McGraw-Hill.

<sup>3</sup> E. L. Wike (2006), Data Analysis. A Statistical Primer for Psychology Students. New Brunswick: Aldine Transaction.

If  $a$  is a Pandas DataFrame and  $melted$  is set to True,  $y\_col$ ,  $block\_col$  and  $group\_col$  must specify columns names (strings).

- **`y_col` (*str or int*)** – Must be specified if  $a$  is a pandas DataFrame object. Name of the column that contains  $y$  data.
- **`block_col` (*str or int*)** – Must be specified if  $a$  is a pandas DataFrame object. Name of the column that contains blocking factor values.
- **`group_col` (*str or int*)** – Must be specified if  $a$  is a pandas DataFrame object. Name of the column that contains treatment (group) factor values.
- **`melted` (*bool, optional*)** – Specifies if data are given as melted columns “ $y$ ”, “blocks”, and “groups”.
- **`sort` (*bool, optional*)** – If True, sort data by block and group columns.

#### Returns

`result` – P values.

#### Return type

pandas.DataFrame

#### Notes

For all-pairs comparisons in a two factorial unreplicated complete block design with non-normally distributed residuals, Miller’s test can be performed on Friedman-type ranked data.

#### References

#### Examples

```
>>> x = np.array([[31,27,24],[31,28,31],[45,29,46],[21,18,48],[42,36,46],[32,17,  
...40]])  
>>> sp.posthoc_miller_friedman(x)
```

## 8.8 scikit\_posthocs.posthoc\_npm\_test

`scikit_posthocs.posthoc_npm_test(a: list | ndarray | DataFrame, val_col: str = None, group_col: str = None, sort: bool = False) → DataFrame`

Calculate pairwise comparisons using Nashimoto and Wright’s all-pairs comparison procedure (NPM test) for simply ordered mean ranksums.

NPM test is basically an extension of Nemenyi’s procedure for testing increasingly ordered alternatives<sup>1</sup>.

#### Parameters

- **`a` (*array\_like or pandas DataFrame object*)** – An array, any object exposing the array interface or a pandas DataFrame.
- **`val_col` (*str, optional*)** – Name of a DataFrame column that contains dependent variable values (test or response variable). Values should have a non-nominal scale. Must be specified if  $a$  is a pandas DataFrame object.

<sup>1</sup> Nashimoto, K., Wright, F.T., (2005), Multiple comparison procedures for detecting differences in simply ordered means. Comput. Statist. Data Anal. 48, 291–306.

- **group\_col** (*str, optional*) – Name of a DataFrame column that contains independent variable values (grouping or predictor variable). Values should have a nominal scale (categorical). Must be specified if *a* is a pandas DataFrame object.
- **sort** (*bool, optional*) – If True, sort data by block and group columns.
- **p\_adjust** (*str, optional*) – Method for adjusting p values. See *statsmodels.sandbox.stats.multicomp* for details. Available methods are: ‘bonferroni’ : one-step correction ‘sidak’ : one-step correction ‘holm-sidak’ : step-down method using Sidak adjustments ‘holm’ : step-down method using Bonferroni adjustments ‘simes-hochberg’ : step-up method (independent) ‘hommel’ : closed method based on Simes tests (non-negative) ‘fdr\_bh’ : Benjamini/Hochberg (non-negative) ‘fdr\_by’ : Benjamini/Yekutieli (negative) ‘fdr\_tsbh’ : two stage fdr correction (non-negative) ‘fdr\_tsby’ : two stage fdr correction (non-negative)

**Returns****result** – P values.**Return type**

pandas.DataFrame

**Notes**

The p values are estimated from the studentized range distribution. If the medians are already increasingly ordered, than the NPM-test simplifies to the ordinary Nemenyi test

**References****Examples**

```
>>> x = np.array([[102, 109, 114, 120, 124],
   [110, 112, 123, 130, 145],
   [132, 141, 156, 160, 172]])
>>> sp.posthoc_npm_test(x)
```

## 8.9 scikit\_posthocs.posthoc\_durbin

```
scikit_posthocs.posthoc_durbin(a: list | ndarray | DataFrame, y_col: str = None, block_col: str = None, group_col: str = None, p_adjust: str = None, melted: bool = False, sort: bool = False) → DataFrame
```

Pairwise post hoc test for multiple comparisons of rank sums according to Durbin and Conover for a two-way balanced incomplete block design (BIBD). See references for additional information<sup>1,2</sup>.

**Parameters**

- **a** (*array\_like or pandas DataFrame object*) – An array, any object exposing the array interface or a pandas DataFrame.

If *melted* is set to False (default), *a* is a typical matrix of block design, i.e. rows are blocks, and columns are groups. In this case you do not need to specify col arguments.

<sup>1</sup> W. J. Conover and R. L. Iman (1979), On multiple-comparisons procedures, Tech. Rep. LA-7677-MS, Los Alamos Scientific Laboratory.

<sup>2</sup> W. J. Conover (1999), Practical nonparametric Statistics, 3rd. edition, Wiley.

If  $a$  is an array and  $melted$  is set to True,  $y\_col$ ,  $block\_col$  and  $group\_col$  must specify the indices of columns containing elements of correspondany type.

If  $a$  is a Pandas DataFrame and  $melted$  is set to True,  $y\_col$ ,  $block\_col$  and  $group\_col$  must specify columns names (string).

- **`y_col` (str or int)** – Must be specified if  $a$  is a pandas DataFrame object. Name of the column that contains  $y$  data.
- **`block_col` (str or int)** – Must be specified if  $a$  is a pandas DataFrame object. Name of the column that contains blocking factor values.
- **`group_col` (str or int)** – Must be specified if  $a$  is a pandas DataFrame object. Name of the column that contains treatment (group) factor values.
- **`melted` (bool, optional)** – Specifies if data are given as melted columns “y”, “blocks”, and “groups”.
- **`sort` (bool, optional)** – If True, sort data by block and group columns.
- **`p_adjust` (str, optional)** – Method for adjusting p values. See statsmodels.sandbox.stats.multicomp for details. Available methods are: ‘bonferroni’ : one-step correction ‘sidak’ : one-step correction ‘holm-sidak’ : step-down method using Sidak adjustments ‘holm’ : step-down method using Bonferroni adjustments ‘simes-hochberg’ : step-up method (independent) ‘hommel’ : closed method based on Simes tests (non-negative) ‘fdr\_bh’ : Benjamini/Hochberg (non-negative) ‘fdr\_by’ : Benjamini/Yekutieli (negative) ‘fdr\_tsbh’ : two stage fdr correction (non-negative) ‘fdr\_tsbky’ : two stage fdr correction (non-negative)

#### Returns

`result` – P values.

#### Return type

pandas.DataFrame

## References

## Examples

```
>>> x = np.array([[31,27,24],[31,28,31],[45,29,46],[21,18,48],[42,36,46],[32,17,  
    ↵40]])  
>>> sp.posthoc_durbins(x)
```

## 8.10 scikit\_posthocs.posthoc\_anderson

`scikit_posthocs.posthoc_anderson(a: list | ndarray | DataFrame, val_col: str = None, group_col: str = None, midrank: bool = True, p_adjust: str = None, sort: bool = False) → DataFrame`

Anderson-Darling Pairwise Test for k-samples. Tests the null hypothesis that k-samples are drawn from the same population without having to specify the distribution function of that population<sup>1</sup>.

#### Parameters

<sup>1</sup> F.W. Scholz, M.A. Stephens (1987), K-Sample Anderson-Darling Tests, Journal of the American Statistical Association, Vol. 82, pp. 918-924.

- **a** (*array\_like or pandas DataFrame object*) – An array, any object exposing the array interface or a pandas DataFrame.
- **val\_col** (*str, optional*) – Name of a DataFrame column that contains dependent variable values (test or response variable). Values should have a non-nominal scale. Must be specified if *a* is a pandas DataFrame object.
- **group\_col** (*str, optional*) – Name of a DataFrame column that contains independent variable values (grouping or predictor variable). Values should have a nominal scale (categorical). Must be specified if *a* is a pandas DataFrame object.
- **midrank** (*bool, optional*) – Type of Anderson-Darling test which is computed. If set to True (default), the midrank test applicable to continuous and discrete populations is performed. If False, the right side empirical distribution is used.
- **sort** (*bool, optional*) – If True, sort data by block and group columns.
- **p\_adjust** (*str, optional*) – Method for adjusting p values. See statsmodels.sandbox.stats.multicomp for details. Available methods are: ‘bonferroni’ : one-step correction ‘sidak’ : one-step correction ‘holm-sidak’ : step-down method using Sidak adjustments ‘holm’ : step-down method using Bonferroni adjustments ‘simes-hochberg’ : step-up method (independent) ‘hommel’ : closed method based on Simes tests (non-negative) ‘fdr\_bh’ : Benjamini/Hochberg (non-negative) ‘fdr\_by’ : Benjamini/Yekutieli (negative) ‘fdr\_tsbh’ : two stage fdr correction (non-negative) ‘fdr\_tsby’ : two stage fdr correction (non-negative)

**Returns**

**result** – P values.

**Return type**

pandas.DataFrame

**References****Examples**

```
>>> x = np.array([[2.9, 3.0, 2.5, 2.6, 3.2], [3.8, 2.7, 4.0, 2.4], [2.8, 3.4, 3.7, 2.2, 2.0]])
>>> sp.posthoc_anderson(x)
```

## 8.11 scikit\_posthocs.posthoc\_quade

`scikit_posthocs.posthoc_quade(a: list | ndarray | DataFrame, y_col: str = None, block_col: str = None, group_col: str = None, dist: str = 't', p_adjust: str = None, melted: bool = False, sort: bool = False) → DataFrame`

Calculate pairwise comparisons using Quade's post hoc test for unreplicated blocked data. This test is usually conducted if significant results were obtained by the omnibus test<sup>1 2 3</sup>.

**Parameters**

<sup>1</sup> W. J. Conover (1999), Practical nonparametric Statistics, 3rd. Edition, Wiley.  
<sup>2</sup> N. A. Heckert and J. J. Filliben (2003). NIST Handbook 148: Dataplot Reference Manual, Volume 2: Let Subcommands and Library Functions. National Institute of Standards and Technology Handbook Series, June 2003.  
<sup>3</sup> D. Quade (1979), Using weighted rankings in the analysis of complete blocks with additive block effects. Journal of the American Statistical Association, 74, 680-683.

- **a** (*array\_like or pandas DataFrame object*) – An array, any object exposing the array interface or a pandas DataFrame.  
If *melted* is set to False (default), *a* is a typical matrix of block design, i.e. rows are blocks, and columns are groups. In this case you do not need to specify col arguments.  
If *a* is an array and *melted* is set to True, *y\_col*, *block\_col* and *group\_col* must specify the indices of columns containing elements of correspondany type.  
If *a* is a Pandas DataFrame and *melted* is set to True, *y\_col*, *block\_col* and *group\_col* must specify columns names (string).
- **y\_col** (*str or int, optional*) – Must be specified if *a* is a pandas DataFrame object. Name of the column that contains y data.
- **block\_col** (*str or int*) – Must be specified if *a* is a pandas DataFrame object. Name of the column that contains blocking factor values.
- **group\_col** (*str or int*) – Must be specified if *a* is a pandas DataFrame object. Name of the column that contains treatment (group) factor values.
- **dist** (*str, optional*) – Method for determining p values. The default distribution is “t”, else “normal”.
- **melted** (*bool, optional*) – Specifies if data are given as melted columns “y”, “blocks”, and “groups”.
- **sort** (*bool, optional*) – If True, sort data by block and group columns.
- **p\_adjust** (*str, optional*) – Method for adjusting p values. See statsmodels.sandbox.stats.multicomp for details. Available methods are: ‘bonferroni’ : one-step correction ‘sidak’ : one-step correction ‘holm-sidak’ : step-down method using Sidak adjustments ‘holm’ : step-down method using Bonferroni adjustments ‘simes-hochberg’ : step-up method (independent) ‘hommel’ : closed method based on Simes tests (non-negative) ‘fdr\_bh’ : Benjamini/Hochberg (non-negative) ‘fdr\_by’ : Benjamini/Yekutieli (negative) ‘fdr\_tsby’ : two stage fdr correction (non-negative) ‘fdr\_tsbky’ : two stage fdr correction (non-negative)

**Returns****result** – P values.**Return type**

pandas.DataFrame

**References****Examples**

```
>>> x = np.array([[31,27,24],[31,28,31],[45,29,46],[21,18,48],[42,36,46],[32,17,  
    ↵40]])  
>>> sp.posthoc_quade(x)
```

## 8.12 scikit\_posthocs.posthoc\_vanwaerden

`scikit_posthocs.posthoc_vanwaerden(a: list | ndarray | DataFrame, val_col: str = None, group_col: str = None, sort: bool = False, p_adjust: str = None) → DataFrame`

Van der Waerden's test for pairwise multiple comparisons between group levels. See references for additional information<sup>1,2</sup>.

### Parameters

- **a (array\_like or pandas DataFrame object)** – An array, any object exposing the array interface or a pandas DataFrame.
- **val\_col (str, optional)** – Name of a DataFrame column that contains dependent variable values (test or response variable). Values should have a non-nominal scale. Must be specified if *a* is a pandas DataFrame object.
- **group\_col (str, optional)** – Name of a DataFrame column that contains independent variable values (grouping or predictor variable). Values should have a nominal scale (categorical). Must be specified if *a* is a pandas DataFrame object.
- **sort (bool, optional)** – If True, sort data by block and group columns.
- **p\_adjust (str, optional)** – Method for adjusting p values. See statsmodels.sandbox.stats.multicomp for details. Available methods are: ‘bonferroni’ : one-step correction ‘sidak’ : one-step correction ‘holm-sidak’ : step-down method using Sidak adjustments ‘holm’ : step-down method using Bonferroni adjustments ‘simes-hochberg’ : step-up method (independent) ‘hommel’ : closed method based on Simes tests (non-negative) ‘fdr\_bh’ : Benjamini/Hochberg (non-negative) ‘fdr\_by’ : Benjamini/Yekutieli (negative) ‘fdr\_tsbh’ : two stage fdr correction (non-negative) ‘fdr\_tsbky’ : two stage fdr correction (non-negative)

### Returns

**result** – P values.

### Return type

pandas.DataFrame

### Notes

For one-factorial designs with samples that do not meet the assumptions for one-way-ANOVA and subsequent post hoc tests, the van der Waerden test using normal scores can be employed. Provided that significant differences were detected by this global test, one may be interested in applying post hoc tests according to van der Waerden for pairwise multiple comparisons of the group levels.

There is no tie correction applied in this function.

---

<sup>1</sup> W. J. Conover and R. L. Iman (1979), On multiple-comparisons procedures, Tech. Rep. LA-7677-MS, Los Alamos Scientific Laboratory.

<sup>2</sup> B. L. van der Waerden (1952) Order tests for the two-sample problem and their power, Indagationes Mathematicae, 14, 453-458.

## References

### Examples

```
>>> x = np.array([[10, 'a'], [59, 'a'], [76, 'b'], [10, 'b']])
>>> sp.posthoc_vanwaerden(x, val_col = 0, group_col = 1)
```

## 8.13 scikit\_posthocs.posthoc\_tukey\_hsd

`scikit_posthocs.posthoc_tukey_hsd(x: list | ndarray | DataFrame, g: str, alpha: float = 0.05) → DataFrame`

Pairwise comparisons with TukeyHSD confidence intervals. This is a convenience function to make statsmodels `pairwise_tukeyhsd` method more applicable for further use.

#### Parameters

- `x (array_like or pandas Series object, 1d)` – An array, any object exposing the array interface, containing dependent variable values (test or response variable). Values should have a non-nominal scale. NaN values will cause an error (please handle manually).
- `g (array_like or pandas Series object, 1d)` – An array, any object exposing the array interface, containing independent variable values (grouping or predictor variable). Values should have a nominal scale (categorical).
- `alpha (float, optional)` – Significance level for the test. Default is 0.05.

#### Returns

`result` – DataFrame with 0, 1, and -1 values, where 0 is False (not significant), 1 is True (significant), and -1 is for diagonal elements.

#### Return type

pandas.DataFrame

### Examples

```
>>> x = [[1,2,3,4,5], [35,31,75,40,21], [10,6,9,6,1]]
>>> g = [['a'] * 5, ['b'] * 5, ['c'] * 5]
>>> sp.posthoc_tukey_hsd(np.concatenate(x), np.concatenate(g))
```

## 8.14 scikit\_posthocs.posthoc\_ttest

`scikit_posthocs.posthoc_ttest(a: list | ndarray | DataFrame, val_col: str = None, group_col: str = None, pool_sd: bool = False, equal_var: bool = True, p_adjust: str = None, sort: bool = False) → DataFrame`

Pairwise T test for multiple comparisons of independent groups. May be used after a parametric ANOVA to do pairwise comparisons.

#### Parameters

- `a (array_like or pandas DataFrame object)` – An array, any object exposing the array interface or a pandas DataFrame. Array must be two-dimensional.

- **val\_col** (*str, optional*) – Name of a DataFrame column that contains dependent variable values (test or response variable). Values should have a non-nominal scale. Must be specified if *a* is a pandas DataFrame object.
- **group\_col** (*str, optional*) – Name of a DataFrame column that contains independent variable values (grouping or predictor variable). Values should have a nominal scale (categorical). Must be specified if *a* is a pandas DataFrame object.
- **equal\_var** (*bool, optional*) – If True (default), perform a standard independent test that assumes equal population variances<sup>1</sup>. If False, perform Welch’s t-test, which does not assume equal population variance<sup>2</sup>.
- **pool\_sd** (*bool, optional*) – Calculate a common SD for all groups and use that for all comparisons (this can be useful if some groups are small). This method does not actually call scipy ttest\_ind() function, so extra arguments are ignored. Default is False.
- **p\_adjust** (*str, optional*) – Method for adjusting p values. See statsmodels.sandbox.stats.multicomp for details. Available methods are: ‘bonferroni’ : one-step correction ‘sidak’ : one-step correction ‘holm-sidak’ : step-down method using Sidak adjustments ‘holm’ : step-down method using Bonferroni adjustments ‘simes-hochberg’ : step-up method (independent) ‘hommel’ : closed method based on Simes tests (non-negative) ‘fdr\_bh’ : Benjamini/Hochberg (non-negative) ‘fdr\_by’ : Benjamini/Yekutieli (negative) ‘fdr\_tsbh’ : two stage fdr correction (non-negative) ‘fdr\_tsby’ : two stage fdr correction (non-negative)
- **sort** (*bool, optional*) – Specifies whether to sort DataFrame by group\_col or not. Recommended unless you sort your data manually.

**Returns****result** – P values.**Return type**

pandas.DataFrame

**References****Examples**

```
>>> x = [[1,2,3,5,1], [12,31,54, np.nan], [10,12,6,74,11]]
>>> sp.posthoc_ttest(x, p_adjust = 'holm')
array([[[-1.          ,  0.04600899,  0.31269089],
       [ 0.04600899, -1.          ,  0.6327077 ],
       [ 0.31269089,  0.6327077 , -1.        ]]])
```

<sup>1</sup> [http://en.wikipedia.org/wiki/T-test#Independent\\_two-sample\\_t-test](http://en.wikipedia.org/wiki/T-test#Independent_two-sample_t-test)<sup>2</sup> [http://en.wikipedia.org/wiki/Welch%27s\\_t\\_test](http://en.wikipedia.org/wiki/Welch%27s_t_test)

## 8.15 scikit\_posthocs.posthoc\_mannwhitney

```
scikit_posthocs.posthoc_mannwhitney(a: list | ndarray | DataFrame, val_col: str = None, group_col: str = None, use_continuity: bool = True, alternative: str = 'two-sided', p_adjust: str = None, sort: bool = True) → DataFrame
```

Pairwise comparisons with Mann-Whitney rank test.

### Parameters

- **a (array\_like or pandas DataFrame object)** – An array, any object exposing the array interface or a pandas DataFrame. Array must be two-dimensional.
- **val\_col (str, optional)** – Name of a DataFrame column that contains dependent variable values (test or response variable). Values should have a non-nominal scale. Must be specified if *a* is a pandas DataFrame object.
- **group\_col (str, optional)** – Name of a DataFrame column that contains independent variable values (grouping or predictor variable). Values should have a nominal scale (categorical). Must be specified if *a* is a pandas DataFrame object.
- **use\_continuity (bool, optional)** – Whether a continuity correction (1/2.) should be taken into account. Default is True.
- **alternative(['two-sided', 'less', or 'greater'], optional)** – Whether to get the p-value for the one-sided hypothesis ('less' or 'greater') or for the two-sided hypothesis ('two-sided'). Defaults to 'two-sided'.
- **p\_adjust (str, optional)** – Method for adjusting p values. See statsmodels.sandbox.stats.multicomp for details. Available methods are: 'bonferroni' : one-step correction 'sidak' : one-step correction 'holm-sidak' : step-down method using Sidak adjustments 'holm' : step-down method using Bonferroni adjustments 'simes-hochberg' : step-up method (independent) 'hommel' : closed method based on Simes tests (non-negative) 'fdr\_bh' : Benjamini/Hochberg (non-negative) 'fdr\_by' : Benjamini/Yekutieli (negative) 'fdr\_tsbh' : two stage fdr correction (non-negative) 'fdr\_tsby' : two stage fdr correction (non-negative)
- **sort (bool, optional)** – Specifies whether to sort DataFrame by group\_col or not. Recommended unless you sort your data manually.

### Returns

**result** – P values.

### Return type

pandas.DataFrame

### Notes

Refer to *scipy.stats.mannwhitneyu* reference page for further details.

## Examples

```
>>> x = [[1,2,3,4,5], [35,31,75,40,21], [10,6,9,6,1]]
>>> sp.posthoc_mannwhitney(x, p_adjust = 'holm')
```

## 8.16 scikit\_posthocs.posthoc\_wilcoxon

`scikit_posthocs.posthoc_wilcoxon(a: list | ndarray | DataFrame, val_col: str = None, group_col: str = None, method: str = 'auto', zero_method: str = 'wilcox', correction: bool = False, p_adjust: str = None, sort: bool = False) → DataFrame`

Pairwise comparisons with Wilcoxon signed-rank test.

It is a non-parametric version of the paired T-test for use with non-parametric ANOVA.

### Parameters

- **a** (*array\_like or pandas DataFrame object*) – An array, any object exposing the array interface or a pandas DataFrame. Array must be two-dimensional.
- **val\_col** (*str, optional*) – Name of a DataFrame column that contains dependent variable values (test or response variable). Values should have a non-nominal scale. Must be specified if *a* is a pandas DataFrame object.
- **group\_col** (*str, optional*) – Name of a DataFrame column that contains independent variable values (grouping or predictor variable). Values should have a nominal scale (categorical). Must be specified if *a* is a pandas DataFrame object.
- **method** (*{"auto", "exact", "approx"}}, *optional*) – Method to calculate the p-value. Default is “auto”.*
- **zero\_method** (*{"pratt", "wilcox", "zsplit"}, *optional*) – “pratt”: Pratt treatment, includes zero-differences in the ranking process (more conservative) “wilcox”: Wilcox treatment, discards all zero-differences “zsplit”: Zero rank split, just like Pratt, but splitting the zero rank between positive and negative ones*
- **correction** (*bool, optional*) – If True, apply continuity correction by adjusting the Wilcoxon rank statistic by 0.5 towards the mean value when computing the z-statistic. Default is False.
- **p\_adjust** (*str, optional*) – Method for adjusting p values. See `statsmodels.sandbox.stats.multicomp` for details. Available methods are: ‘bonferroni’ : one-step correction ‘sidak’ : one-step correction ‘holm-sidak’ : step-down method using Sidak adjustments ‘holm’ : step-down method using Bonferroni adjustments ‘simes-hochberg’ : step-up method (independent) ‘hommel’ : closed method based on Simes tests (non-negative) ‘fdr\_bh’ : Benjamini/Hochberg (non-negative) ‘fdr\_by’ : Benjamini/Yekutieli (negative) ‘fdr\_tsbh’ : two stage fdr correction (non-negative) ‘fdr\_tsby’ : two stage fdr correction (non-negative)
- **sort** (*bool, optional*) – Specifies whether to sort DataFrame by group\_col and val\_col or not. Default is False.

### Returns

**result** – P values.

### Return type

pandas.DataFrame

## Notes

Refer to `scipy.stats.wilcoxon` reference page for further details<sup>1</sup>.

## References

## Examples

```
>>> x = [[1,2,3,4,5], [35,31,75,40,21], [10,6,9,6,1]]
>>> sp.posthoc_wilcoxon(x)
```

## 8.17 scikit\_posthocs.posthoc\_scheffe

`scikit_posthocs.posthoc_scheffe(a: list | ndarray | DataFrame, val_col: str = None, group_col: str = None, sort: bool = False) → DataFrame`

Scheffe's all-pairs comparisons test for normally distributed data with equal group variances. For all-pairs comparisons in an one-factorial layout with normally distributed residuals and equal variances Scheffe's test can be performed with parametric ANOVA<sup>1 2 3</sup>.

A total of  $m = k(k-1)/2$  hypotheses can be tested.

### Parameters

- **a** (`Union[list, np.ndarray, DataFrame]`) – An array, any object exposing the array interface or a pandas DataFrame.
- **val\_col** (`str, optional`) – Name of a DataFrame column that contains dependent variable values (test or response variable). Values should have a non-nominal scale. Must be specified if *a* is a pandas DataFrame object.
- **group\_col** (`str, optional`) – Name of a DataFrame column that contains independent variable values (grouping or predictor variable). Values should have a nominal scale (categorical). Must be specified if *a* is a pandas DataFrame object.
- **sort** (`bool, optional`) – If True, sort data by block and group columns.

### Returns

**result** – P values.

### Return type

pandas.DataFrame

---

<sup>1</sup> <https://docs.scipy.org/doc/scipy/reference/generated/scipy.stats.wilcoxon.html>

<sup>2</sup> J. Bortz (1993) Statistik für Sozialwissenschaftler. 4. Aufl., Berlin: Springer.

<sup>2</sup>

L. Sachs (1997) Angewandte Statistik, New York: Springer.

<sup>3</sup> H. Scheffe (1953) A Method for Judging all Contrasts in the Analysis of Variance. Biometrika 40, 87-110.

## Notes

The p values are computed from the F-distribution.

## References

## Examples

```
>>> import scikit_posthocs as sp
>>> import pandas as pd
>>> x = pd.DataFrame({"a": [1,2,3,5,1], "b": [12,31,54,62,12], "c": [10,12,6,74,11]})
>>>
>>> x = x.melt(var_name='groups', value_name='values')
>>> sp.posthoc_scheffe(x, val_col='values', group_col='groups')
```

## 8.18 scikit\_posthocs.posthoc\_tamhane

`scikit_posthocs.posthoc_tamhane(a: list | ndarray | DataFrame, val_col: str = None, group_col: str = None, welch: bool = True, sort: bool = False) → DataFrame`

Tamhane's T2 all-pairs comparison test for normally distributed data with unequal variances. Tamhane's T2 test can be performed for all-pairs comparisons in an one-factorial layout with normally distributed residuals but unequal groups variances. A total of  $m = k(k-1)/2$  hypotheses can be tested. The null hypothesis is tested in the two-tailed test against the alternative hypothesis<sup>1</sup>.

### Parameters

- **a** (`Union[list, np.ndarray, DataFrame]`) – An array, any object exposing the array interface or a pandas DataFrame.
- **val\_col** (`str, optional`) – Name of a DataFrame column that contains dependent variable values (test or response variable). Values should have a non-nominal scale. Must be specified if *a* is a pandas DataFrame object.
- **group\_col** (`str, optional`) – Name of a DataFrame column that contains independent variable values (grouping or predictor variable). Values should have a nominal scale (categorical). Must be specified if *a* is a pandas DataFrame object.
- **welch** (`bool, optional`) – If True, use Welch's approximate solution for calculating the degree of freedom. T2 test uses the usual  $df = N - 2$  approximation.
- **sort** (`bool, optional`) – If True, sort data by block and group columns.

### Returns

**result** – P values.

### Return type

pandas.DataFrame

<sup>1</sup> A.C. Tamhane (1979), A Comparison of Procedures for Multiple Comparisons of Means with Unequal Variances. Journal of the American Statistical Association, 74, 471-480.

## Notes

The p values are computed from the t-distribution and adjusted according to Dunn-Sidak.

## References

## Examples

```
>>> import scikit_posthocs as sp
>>> import pandas as pd
>>> x = pd.DataFrame({"a": [1,2,3,5,1], "b": [12,31,54,62,12], "c": [10,12,6,74,11]})
>>>
>>> x = x.melt(var_name='groups', value_name='values')
>>> sp.posthoc_tamhane(x, val_col='values', group_col='groups')
```

## 8.19 scikit\_posthocs.posthoc\_tukey

`scikit_posthocs.posthoc_tukey(a: list | ndarray | DataFrame, val_col: str = None, group_col: str = None, sort: bool = False) → DataFrame`

Performs Tukey's all-pairs comparisons test for normally distributed data with equal group variances. For all-pairs comparisons in an one-factorial layout with normally distributed residuals and equal variances Tukey's test can be performed. A total of  $m = k(k-1)/2$  hypotheses can be tested. The null hypothesis is tested in the two-tailed test against the alternative hypothesis<sup>1,2</sup>.

### Parameters

- **a** (`Union[list, np.ndarray, DataFrame]`) – An array, any object exposing the array interface or a pandas DataFrame.
- **val\_col** (`str, optional`) – Name of a DataFrame column that contains dependent variable values (test or response variable). Values should have a non-nominal scale. Must be specified if *a* is a pandas DataFrame object.
- **group\_col** (`str, optional`) – Name of a DataFrame column that contains independent variable values (grouping or predictor variable). Values should have a nominal scale (categorical). Must be specified if *a* is a pandas DataFrame object.
- **sort** (`bool, optional`) – If True, sort data by block and group columns.

### Returns

`result` – P values.

### Return type

`pandas.DataFrame`

---

<sup>1</sup>

L. Sachs (1997) Angewandte Statistik, New York: Springer.

<sup>2</sup> J. Tukey (1949) Comparing Individual Means in the Analysis of Variance, Biometrics 5, 99-114.

## Notes

The p values are computed from the Tukey-distribution.

## References

## Examples

```
>>> import scikit_posthocs as sp
>>> import pandas as pd
>>> x = pd.DataFrame({"a": [1,2,3,5,1], "b": [12,31,54,62,12], "c": [10,12,6,74,11]})
>>>
>>> x = x.melt(var_name='groups', value_name='values')
>>> sp.posthoc_tukey(x, val_col='values', group_col='groups')
```

## 8.20 scikit\_posthocs.posthoc\_dscf

`scikit_posthocs.posthoc_dscf(a: list | ndarray | DataFrame, val_col: str = None, group_col: str = None, sort: bool = False) → DataFrame`

Dwass, Steel, Critchlow and Fligner all-pairs comparison test for a one-factorial layout with non-normally distributed residuals. As opposed to the all-pairs comparison procedures that depend on Kruskal ranks, the DSCF test is basically an extension of the U-test as re-ranking is conducted for each pairwise test<sup>1,2,3</sup>.

### Parameters

- **a** (`Union[list, np.ndarray, DataFrame]`) – An array, any object exposing the array interface or a pandas DataFrame.
- **val\_col** (`str, optional`) – Name of a DataFrame column that contains dependent variable values (test or response variable). Values should have a non-nominal scale. Must be specified if *a* is a pandas DataFrame object.
- **group\_col** (`str, optional`) – Name of a DataFrame column that contains independent variable values (grouping or predictor variable). Values should have a nominal scale (categorical). Must be specified if *a* is a pandas DataFrame object.
- **sort** (`bool, optional`) – If True, sort data by block and group columns.

### Returns

**result** – P values.

### Return type

pandas.DataFrame

<sup>1</sup> Douglas, C. E., Fligner, A. M. (1991) On distribution-free multiple comparisons in the one-way analysis of variance, Communications in Statistics - Theory and Methods, 20, 127-139.

<sup>2</sup> Dwass, M. (1960) Some k-sample rank-order tests. In Contributions to Probability and Statistics, Edited by: I. Olkin, Stanford: Stanford University Press.

<sup>3</sup> Steel, R. G. D. (1960) A rank sum test for comparing all pairs of treatments, Technometrics, 2, 197-207.

## Notes

The p values are computed from the Tukey-distribution.

## References

## Examples

```
>>> import scikit_posthocs as sp
>>> import pandas as pd
>>> x = pd.DataFrame({"a": [1,2,3,5,1], "b": [12,31,54,62,12], "c": [10,12,6,74,11]})
>>>
>>> x = x.melt(var_name='groups', value_name='values')
>>> sp.posthoc_dscf(x, val_col='values', group_col='groups')
```

## 8.21 scikit\_posthocs.posthoc\_dunnett

`scikit_posthocs.posthoc_dunnett(a: list | ndarray | DataFrame, val_col: str = None, group_col: str = None, control: str = None, alternative: Literal['two-sided', 'less', 'greater'] = 'two-sided', sort: bool = False, to_matrix: bool = True) → Series | DataFrame`

Dunnett's test [1, 2, 3] for multiple comparisons against a control group, used after parametric ANOVA. The control group is specified by the `control` parameter.

### Parameters

- `a (array_like or pandas DataFrame object)` – An array, any object exposing the array interface or a pandas DataFrame. Array must be two-dimensional.
- `val_col (str, optional)` – Name of a DataFrame column that contains dependent variable values (test or response variable). Values should have a non-nominal scale. Must be specified if `a` is a pandas DataFrame object.
- `group_col (str, optional)` – Name of a DataFrame column that contains independent variable values (grouping or predictor variable). Values should have a nominal scale (categorical). Must be specified if `a` is a pandas DataFrame object.
- `control (str, optional)` – Name of the control group within the `group_col` column. Values should have a nominal scale (categorical). Must be specified if `a` is a pandas DataFrame.
- `alternative (['two-sided', 'less', or 'greater'], optional)` – Whether to get the p-value for the one-sided hypothesis ('less' or 'greater') or for the two-sided hypothesis ('two-sided'). Defaults to 'two-sided'.
- `sort (bool, optional)` – Specifies whether to sort DataFrame by `group_col` or not. Recommended unless you sort your data manually.
- `to_matrix (bool, optional)` – Specifies whether to return a DataFrame or a Series. If True, a DataFrame is returned with some NaN values since it's not pairwise comparison. Default is True.

### Returns

`result` – P values.

**Return type**

pandas.Series or pandas.DataFrame

**References**



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