statsmodels.stats.multitest.multipletests

`statsmodels.stats.multitest.multipletests`(*pvals*, *alpha=0.05*, *method='hs'*, *is_sorted=False*, *returnsorted=False*)[source] [../_modules/statsmodels/stats/multitest.html#multipletests]

Test results and p-value correction for multiple tests

Parameters

pvals : array_like [https://numpy.org/doc/stable/glossary.html#term-array-like], 1-d

uncorrected p-values. Must be 1-dimensional.

alpha : `float` [https://docs.python.org/3/library/functions.html#float]

FWER, family-wise error rate, e.g. 0.1

method : `str` [https://docs.python.org/3/library/stdtypes.html#str]

Method used for testing and adjustment of pvalues. Can be either the full name or initial letters. 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)

is_sorted : bool [https://docs.python.org/3/library/stdtypes.html#bltin-boolean-values]

If False (default), the p_values will be sorted, but the corrected pvalues are in the original order. If True, then it assumed that the pvalues are already sorted in ascending order.

returnsorted : bool [https://docs.python.org/3/library/stdtypes.html#bltin-boolean-values]

not tested, return sorted p-values instead of original sequence

Returns

reject : `ndarray` [https://numpy.org/doc/stable/reference/generated/numpy.ndarray.html#numpy.ndarray], bool [https://docs.python.org/3/library/stdtypes.html#bltin-boolean-values]

true for hypothesis that can be rejected for given alpha

pvals_corrected : `ndarray` [https://numpy.org/doc/stable/reference/generated/numpy.ndarray.html#numpy.ndarray]

p-values corrected for multiple tests

alphacSidak : `float` [https://docs.python.org/3/library/functions.html#float]

corrected alpha for Sidak method

alphacBonf : `float` [https://docs.python.org/3/library/functions.html#float]

corrected alpha for Bonferroni method

Notes

There may be API changes for this function in the future.

Except for ‘fdr_twostage’, the p-value correction is independent of the alpha specified as argument. In these cases the corrected p-values can also be compared with a different alpha. In the case of ‘fdr_twostage’, the corrected p-values are specific to the given alpha, see `fdrcorrection_twostage`.

The ‘fdr_gbs’ procedure is not verified against another package, p-values are derived from scratch and are not derived in the reference. In Monte Carlo experiments the method worked correctly and maintained the false discovery rate.

All procedures that are included, control FWER or FDR in the independent case, and most are robust in the positively correlated case.

fdr_gbs: high power, fdr control for independent case and only small violation in positively correlated case

Timing:

Most of the time with large arrays is spent in *argsort*. When we want to calculate the p-value for several methods, then it is more efficient to presort the pvalues, and put the results back into the original order outside of the function.

Method=’hommel’ is very slow for large arrays, since it requires the evaluation of n partitions, where n is the number of p-values.