Permutation tests and confidence sets

Release 0.1.alpha5

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May 03, 2019

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CHAPTER

ONE

USER GUIDE

Permutation tests (sometimes referred to as randomization, re-randomization, or exact tests) are a nonparametric approach to statistical significance testing. They were first introduced by R. A. Fisher in 1935 *[Fis35]* and further developed by E. J. G. Pitman *[Pit37][Pit38]*. After the introduction of the bootstrap, the ideas were extended in the 1980's by J. Romano *[Rom88][Rom89]*.

Permutation tests were developed to test hypotheses for which relabeling the observed data was justified by exchangeability [1] of the observed random variables. In these situations, the conditional distribution of the test statistic under the null hypothesis is completely determined by the fact that all relabelings of the data are equally likely. That distribution might be calculable in closed form; if not, it can be simulated with arbitrary accuracy by generating relabelings uniformly at random. In contrast to approximate parametric methods or asymptotic methods, the accuracy of the simulation for any finite (re)sample size is known, and can be made arbitrarily small at the expense of computing time.

More generally, permutation tests are possible whenever the null distribution of the data is invariant under the action of some group (see Appendix [app:def] for background). Then, a subset of outcomes is conditionally equally likely, given that the data fall in a particular *orbit* of the group (all potential observations that result from applying elements of the group to the observed value of the data). That makes it possible to determine the conditional distribution of any test statistic, given the orbit of the data. Since the conditional distribution is uniform on the orbit of the original data, the probability of any event is the proportion of possible outcomes that lie in the event. If tests are performed conditionally at level α regardless of the observed data, the resulting overall test has unconditional level α, by the law of total probability.

1.1 Paired permutation tests

To illustrate the paired two-sample permutation test, consider the following randomized, controlled experiment. You suspect a specific treatment will increase the growth rate of a certain type of cell. To test this hypothesis, you clone 100 cells. Now there are 200 cells composed of 100 pairs of identical clones. For each cloned pair you randomly assign one to treatment, with probability 1/2, independently across the 100 pairs. At the end of the treatment, you measure the growth rate for all the cells. The null hypothesis is that treatment has no effect. If that is true, then the assignment of a clone to treatment amounts to an arbitrary label that has nothing to do with the measured response. So, given the responses within each pair (but not the knowledge of which clone in each pair had which response), it would have been just as likely to observe the same *numbers* but with flipped labels within each pair. We could generate new hypothetical datasets from the observed data by assigning the treatment and control labels for all the cloned pairs independently. This yields a total of 2^{100} total datasets (including the observed data and all the hypothetical datasets

[1] A sequence $X_1, X_2, X_3, \ldots, X_n$ of random variables is *exchangeable* if their joint distribution is invariant to permutations of the indices; that is,

$$p(x_1, \ldots, x_n) = p(x_{\pi(1)}, \ldots, x_{\pi(n)})$$

for all permutations π of $\{1, 2, \ldots, n\}$. It is closely related to the notion of *independent and identically-distributed* random variables. Independent and identically-distributed random variables are exchangeable. However, simple random sampling *without* replacement produces an exchangeable, but not independent, sequence of random variables.

that you generated), all equally likely to have occurred under the null, conditioning on the observed data (but not the labeling).

The standard parametric approach to this problem is the paired t-test, since the cloned cells are presumably more similar to each other than to another randomly chosen cell (and thus more readily compared). The paired t-test assumes that, if the null hypothesis is true, the differences in response between each pair of clones are independently and identically (iid) normally distributed with mean zero and unknown variance. The test statistic is the mean of the differences between each cloned pair divided by the standard error of these differences. Under these assumptions, the test statistic is distributed as a t-distribution with $n - 1$ degrees of freedom. This means you can calculate the test statistic and then read off the from the t-distribution. If the is below some prespecified critical value α, then you reject the null. If the true generative model for the data is not iid normal, however, the probability of rejecting the null hypothesis can be quite different from α even if treatment has no effect.

A permutation version of the t-test can avoid that vulnerability: one can use the t-statistic as the test statistic, but instead of selecting the critical value on the basis of Student's t-distribution, one uses the distribution of the statistic under the permutation distribution. Of course, other test statistics could be used instead; the test statistic should be sensitive to the nature of the alternative hypothesis, to ensure that the test has power against the alternatives the science suggests are relevant.

Regardless of which test statistic you choose for your permutation test, if the problem size is not too large then you enumerate all equally likely possibilities under the null given the observed data. If the problem is too large to feasibly enumerate, then you use a suitably large, iid random sample from the exact distribution just described, by selecting permutations uniformly at random and applying the test statistic to those permutations. As you increase the number of samples, you will get increasingly better (in probability) approximations of the exact distribution of the test statistic under the null. The null conditional probability of any event can be estimated as the proportion of random permutations for which the event occurs, and the sampling variability of that estimate can be characterized exactly, for instance, using binomial tests (since the distribution of the number of times the event occurs is Binomial with n equal to the number of samples and p the unknown probability to be estimated).

1.1.1 Example

We'll generate some fake data to demonstrate the paired two-sample problem. We'll follow the cloned cells example above. The controls have a response that is distributed uniformly between 0 and 10. There is random variation among the cells, so the difference between responses in a pair is normally distributed with 0 mean. In the first case, suppose we give the treatment group an ineffective treatment, so there is no treatment effect. The treated cell is equally likely to have a response that is larger or smaller than it's clone's response.

```
>>> from __future__ import print_function
>>> import numpy as np
>>> from numpy.random import RandomState
>>> from permute.core import one_sample

>>> prng = RandomState(42)
>>> control = prng.uniform(low = 0, high=10, size=100)
>>> ineffective_treatment = control + prng.normal(loc=0, scale=1, size=100)
>>> (p, diff_means) = one_sample(ineffective_treatment, control, stat='mean', seed=prng)
>>> print("P-value: ", p)
P-value:  0.50726
>>> print("Difference in means:", diff_means)
Difference in means: -0.00108036016736
```

Now, suppose we give a new treatment that has a constant effect that increases the cell's response by 1.

```
>>> good_treatment = control + prng.normal(loc=1, scale=1, size=100)
>>> (p, diff_means) = one_sample(good_treatment, control, stat='mean', seed=prng)
>>> print("P-value: ", p)
P-value:  0.0
```

```
>>> print("Difference in means:", diff_means)
Difference in means: 1.08009705107
```

one_sample is written to either take in two arguments and test the difference between pairs as we've done above, or to take in a single argument and test whether that variable is centered around 0. Below, we call *one_sample* in that manner, supplying the difference in response within pairs, and get the same results.

```
>>> paired_differences = good_treatment - control
>>> (p, diff_means) = one_sample(paired_differences, stat='mean', seed = prng)
>>> print("P-value: ", p)
P-value:  0.0
>>> print("Difference in means:", diff_means)
Difference in means: 1.08009705107
```

1.2 Two sample permutation tests

Suppose that we have a completely randomized experiment, where people are assigned to two groups at random. Suppose we have N individuals indexed by $i = 1, \dots, N$. We assign them at random to one of two groups with a random treatment vector Z: if $Z_i = 1$, then individual i receives treatment (for example, a drug) and if $Z_i = 0$, individual i receives no treatment (a placebo). We'd like to test whether or not the drug has an effect on how often catches a cold. The outcome measure is the number of times somebody gets a cold wihin one year of starting to take the drug (for simplicity, assume that this can be measured perfectly). We can measure the difference in outcomes between the two groups with any statistic we'd like. The statistic will be a function of the treatment vector Z and the outcomes, $Y_i(1)$ being the outcome under treatment and $Y_i(0)$ being the outcome under no treatment. We'll use the difference-in-means test statistic:

$$T(Z, Y(1), Y(0)) = \frac{1}{N_t}\sum_{i:Z_i=1} Y_i(1) - \frac{1}{N_c}\sum_{i:Z_i=0} Y_i(0)$$

Here, N_t is the number of treated individuals and N_c is the number of untreated individuals, so $N_t + N_c = N$. If the test statistic is negative, then we may have evidence that the drug reduces colds. Conversely, if the test statistic is positive, we may believe that the drug actually makes people more vulnerable to getting sick. If we have no a priori belief about what the drug may do, we simply want to know if it has any effect at all. How extreme does the statistic need to be to indicate that there is likely an effect?

If the drug has no effect on colds, then the number of colds that somebody has would be the same whether he or she received the drug or the placebo. This is the *strong null hypothesis*: the drug has no effect on any individual. Under the strong null, we know both potential outcomes for each individual; namely, their number of colds would be the same regardless of which treatment group they were assigned. In mathematical notation, $Y_i(1) = Y_i(0)$ for all i under the strong null.

The random assignment of people to treatment groups ensures that all possible assignments of N_t people to treatment are equally likely. Thus, we can find the null distribution of the test statistic by calculating $T(Z^*, Y(1), Y(0))$ for all possible treatment assignment vectors Z^*. In general, this would not be possible, because for each individual we observe only $Y_i(1)$ or $Y_i(0)$, but not both. However, the strong null hypothesis allows us to impute the missing potential outcome for each individual.

There are $\binom{N}{N_t}$ possible values of Z^*. In practice, this number is often too large to enumerate all possible values of $T(Z^*, Y(1), Y(0))$. Instead, we simulate the distribution by taking a random subset of B of the Z^*. Then, our estimated p-value for the test is

$$P = 2 \times \min\left(\frac{\#\left\{T(Z^*) <= T(Z)\right\}}{B}, \frac{\#\left\{T(Z^*) >= T(Z)\right\}}{B}\right)$$

1.2.1 Gender bias in student evaluation of teachers

There is growing evidence of gender bias in student evaluations of teaching. To address the question “Do students give higher ratings to male teachers?,” an online experiment was done with two professors, one male and one female cite{macnell2014s}. Each professor taught two sections. In one section, they used a male name. In the other, they used a female name. The students didn’t know the teacher’s real gender. We test whether student evaluations of teaching are biased by comparing the ratings when one of the professors used a male name versus a female name.

As an aside, note that we cannot simply pool the ratings for the two professors when they identified as male and when they identified as female. The “treatment” is the gender the instructor reports, but other things affect the ratings students give. For instance, the two instructors may have different teaching styles, thereby introducing differences in the ratings that are unrelated to their identified gender. This is why we choose to focus on one instructor.

Parametric Approach

First let us consider the parametric two-sample t-test. In this case, our test statistic is

$$t = \frac{\text{mean(rating for M-identified) - mean(rating for F-identified)}}{\sqrt{\text{pooled SD of ratings}}}$$

For the two-sample t-test, the null hypothesis is that the reported/perceived instructor gender has no effect on ratings. The alternative hypothesis is that ratings differ by reported/perceived instructor gender. For the two-sample t-test to be valid, we require the following assumptions:

- Ratings are normally distributed. (But they are on a Likert 1-5 scale, which is definitely not normal.)
- Noise is zero-mean and constant variance across raters. (How should we interpret “noise” in this context? Besides constant variance is not plausible: some raters might give a range of scores, other raters might always give 5.)
- Independence between observations. (Students might talk about ratings with their peers in the class, creating dependence.)

Despite the problematic assumptions we are required to make, let’s temporarily assume they hold and calculate a “p-value” anyway.

```
>>> from __future__ import print_function
>>> import numpy as np
>>> import matplotlib.pyplot as plt
>>> from scipy import stats
```

```
>>> from permute.data import macnell2014
>>> ratings = macnell2014()
>>> prof1 = ratings[ratings.tagender==0]
>>> maleid = prof1.overall[prof1.taidgender==1]
>>> femaleid = prof1.overall[prof1.taidgender==0]
>>> df = len(maleid) + len(femaleid) - 2
>>> t, p = stats.ttest_ind(maleid, femaleid)
>>> print('Test statistic:', np.round(t, 5))
Test statistic: 1.32905
>>> print('P-value (two-sided):', np.round(p, 5))
P-value (two-sided): 0.20043
```

Note that the computed “p-value” is above the standard cut-offs for reporting significance in the literature.

Permutation approach

For the permutation test we can use the same test statistic, but we will compute the p-value by randomly sampling the exact distribution of the test statistics. The null hypothesis is that the ratings are uninfluenced by reported gender—any particular student would assign the same rating regardless of instructor gender. The alternative hypothesis is that the ratings differ by instructor gender—some students would assign different ratings depending on reported instructor gender. The only assumption we need to make is that the random assignment of students to instruction sections is fair and independent across individuals. This can be verified directly from the experimental design.

```
>>> from permute.core import two_sample
>>> p, t = two_sample(maleid, femaleid, stat='t', alternative='two-sided', seed=20)
>>> print('Test statistic:', np.round(t, 5))
Test statistic: 1.32905
>>> print('P-value (two-sided):', np.round(p, 5))
P-value (two-sided): 0.27918
```

```
>>> p, t = two_sample(maleid, femaleid, reps=100, stat='t', alternative='two-sided', seed=20)
>>> print('P-value (two-sided):', np.round(p, 5))
P-value (two-sided): 0.41584
```

Since the permutation test also returns the approximately exact distribution of the test statistic, let's compare the actual distribution with the t-distribution.

```
>>> p, t, distr = two_sample(maleid, femaleid, stat='t', reps=10000,
...                          alternative='greater', keep_dist=True, seed=55)
>>> n, bins, patches = plt.hist(distr, 25, histtype='bar', normed=True)
>>> plt.title('Permutation Null Distribution')
<matplotlib.text.Text object at ...>
>>> plt.axvline(x=t, color='red')
<matplotlib.lines.Line2D object at ...>
>>> x = np.linspace(stats.t.ppf(0.0001, df),
...       stats.t.ppf(0.9999, df), 100)
>>> plt.plot(x, stats.t.pdf(x, df), lw=2, alpha=0.6)
[<matplotlib.lines.Line2D object at ...>]
>>> plt.show()
```

The plot above shows the null distribution generated by 10,000 permutations of the data. The t distribution is superimposed for comparison. The null distribution is much more concentrated around 0 than the t distribution, which has longer tails. Furthermore, it is not perfectly symmetric around zero. This is the source of the difference in p-values between the two tests.

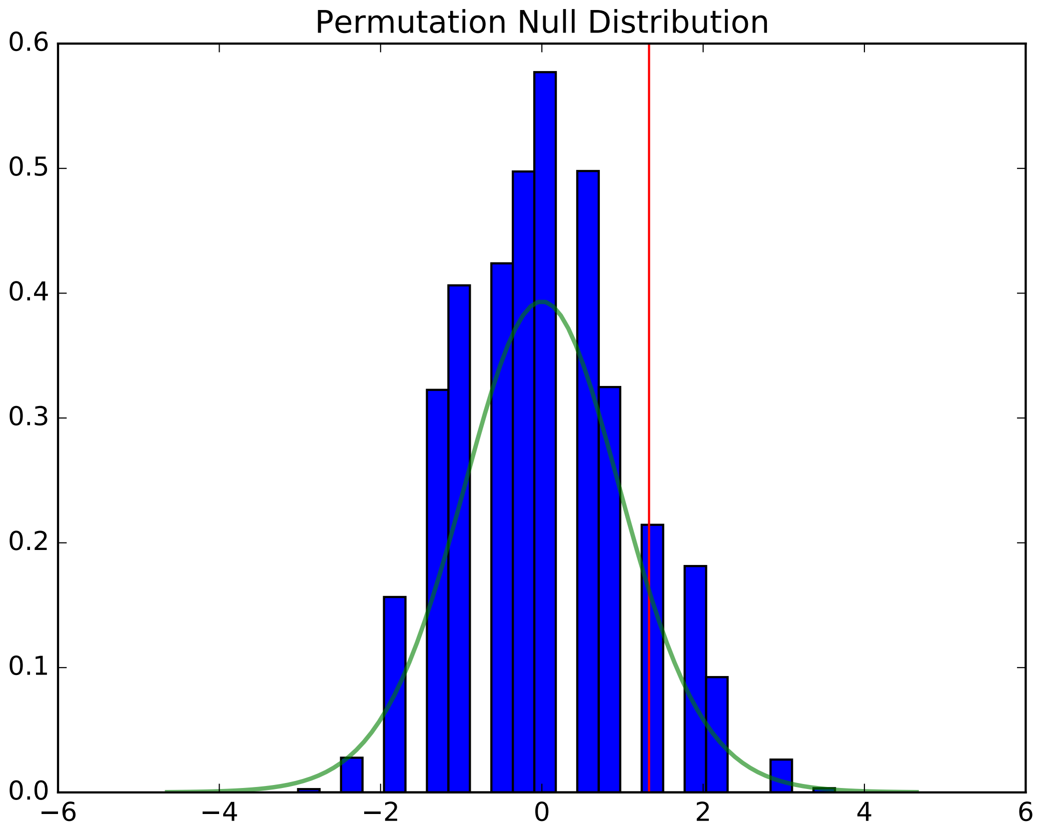
1.2.2 Stratified Spearman correlation permutation test

Some experimental designs have natural groupings. It makes sense to estimate effects within groups, then combine within-group estimates.

To turn this idea into a permutation test, we carry out permutations within groups, then aggregate the test statistics across groups. This helps control for group-level effects.

More on teaching evaluations

We established that one instructor got higher ratings when they used a male name than when they used a female name, but the difference was not significant. Now we may ask, did ratings differ according in this way for either of the two instructors?


Permutation Null Distribution
0.6
0.5
0.4
0.3
0.2
0.1
0.0
−6
−4
−2
0
2
4
6

If there is no gender bias in the ratings, then students should give the same rating to the male instructor regardless of the gender he claims to be and students should give the same rating to the female instructor regardless of the gender she claims to be. However, we don't necessarily believe that students would rate the two instructors the same, since there may be some difference in their teaching styles.

Null hypothesis: student by student, the instructor would receive the same rating regardless of reported gender

Alternative hypothesis: there is at least one student who would rate their instructor higher if they identified as male

The test statistic we use within groups is the Spearman correlation. For each instructor, we compute the correlation between their rating and reported gender, then add the absolute values of the correlations for the instructors. Because reported gender is just a binary indicator, the correlation is equivalent to using the mean rating for male-identified instructors as a test statistic.

```
>>> from permute.stratified import sim_corr
>>> p, rho, sim = sim_corr(x=ratings.overall, y=ratings.taidgender, group=ratings.tagender, seed = 25
>>> n, bins, patches = plt.hist(sim, 40, histtype='bar')
>>> plt.axvline(x=rho, color='red')
<matplotlib.lines.Line2D object at ...>
>>> plt.show()
```

Finally, I plot the simulated distribution of the test statistics under the null conditioned on the observed data in Figure [fig:figure2].

```
>>> print('Test statistic:', np.round(rho, 5))
Test statistic: 0.4459
>>> print('P-value:', np.round(p, 3))
P-value: 0.09
```

At the 10% level, there is a significant difference in ratings between male-identified and female-identified instructors. We could not have computed this p-value with any common distribution, since the null hypothesis assumes some observations (ratings for a single instructor) are exchangeable but others are not.

1.3 Regression

Given n observations of two scalars (x_i, y_i) for $i = 1, 2, \ldots, n$, consider the simple linear regression model

$$y_i = a + bx_i + \epsilon_i.$$

Assume that $\{\epsilon_i\}_{i=1}^n$ are exchangeable.

You are interested in testing whether the slope of the population regression line is non-zero; hence, your null hypothesis is $b = 0$. If $b = 0$, then the model reduces to $y_i = a + \epsilon_i$ for all i. If this is true, the $\{y_i\}_{i=1}^n$ are exchangeable since they are just shifted versions of the exchangeable $\{\epsilon_i\}_{i=1}^n$. Thus every permutation of the $\{y_i\}_{i=1}^n$ has the same conditional probability regardless of the xs. Hence every pairing (x_i, y_j) for any fixed i and for $j = 1, 2, \ldots, n$ is equally likely.

Using the least squares estimate of the slope as the test statistic, you can find its exact distribution under the null given the observed data by computing the test statistic on all possible pairs formed by permuting the y values, keeping the original order of the x values. From the distribution of the test statistic under the null conditioned on the observed data, the is the ratio of the count of the *as extreme* or *more extreme* test statistics to the total number of such test statistics. You might in principle enumerate all $n!$ equally likely pairings and then compute the exact p-value. For sufficiently large n, enumeration becomes infeasible; in which case, you could approximate the exact p-value using a uniform random sample of the equally likely pairings.

A parametric approach to this problem would begin by imposing additional assumptions on the noise ϵ. For example, if we assume that $\{\epsilon_i\}$ are iid Gaussians with mean zero, then the the least squares estimate of the slope normalized by its standard error has a t-distribution with $n - 2$ degrees of freedom. If this additional assumption holds, then we can read the off a table. Note that, unlike in the permutation test, we were only able to calculate the p-value (even with the additional assumptions) because we happened to be able to derive the distribution of this specific test statistic.

1.3.1 Derivation

Given n observations

$$y_i = a + bx_i + \epsilon_i,$$

the least square solution is

$$\min_{a,b} \sum_{i=1}^{n} \left(y_i - a - bx_i\right)^2$$

Taking the partial derivative with respect to a

$$\begin{aligned} \frac{\partial}{\partial b} \sum_{i=1}^{n} \left(y_i - a - bx_i\right)^2 &= -2 \sum_{i=1}^{n} \left(y_i - a - bx_i\right) \\ &= -2 \left(\sum_{i=1}^{n} y_i - na - b \sum_{i=1}^{n} x_i \right) \\ &= -2n \left(\bar{y} - a - b\bar{x}\right). \end{aligned}$$

Setting this to 0 and solving for a yields our estimate $\hat{a}$

$$\hat{a} = \bar{y} - b\bar{x}.$$

Taking the partial derivative with respect to b

$$\begin{aligned} \frac{\partial}{\partial b} \sum_{i=1}^{n} \left(y_i - a - bx_i\right)^2 &= -2 \sum_{i=1}^{n} \left(y_i - a - bx_i\right) x_i \\ &= -2 \left(\sum_{i=1}^{n} y_i x_i - a \sum_{i=1}^{n} x_i - b \sum_{i=1}^{n} x_i x_i \right) \\ &= -2n \left(\overline{xy} - a\bar{x} - b\overline{xx}\right). \end{aligned}$$

Plugging in $\hat{a}$, setting the result to 0, and solving for b yields

$$\hat{b} = \frac{\overline{xy} - \bar{x}\bar{y}}{\overline{xx} - \bar{x}\bar{x}} = \frac{\mathrm{Cov}(x, y)}{\mathrm{Var}(x)} = \mathrm{Cor}(x, y) \left(\frac{\mathrm{Std}(y)}{\mathrm{Std}(x)} \right).$$

Since $\frac{\mathrm{Std}(y)}{\mathrm{Std}(x)}$ is constant under the permutation of y, we can calculate the p-value using the permutation test of the correlation.

```
>>> from __future__ import print_function
>>> import numpy as np

>>> X = np.array([np.ones(10), np.random.random_integers(1, 4, 10)]).T
>>> beta = np.array([1.2, 2])
>>> epsilon = np.random.normal(0, .15, 10)
>>> y = X.dot(beta) + epsilon

>>> from permute.core import corr
>>> t, pv_left, pv_right, pv_both, dist = corr(X[:, 1], y)
>>> print(t)
```

```
0.998692462616
>>> print(pv_both)
0.0007
>>> print(pv_right)
0.0007
>>> print(pv_left)
1.0

>>> t, pv_both, dist = corr(X[:, 1], y)
>>> print(t)
0.103891027265
>>> print(pv_both)
0.765
>>> print(pv_right)
0.3818
>>> print(pv_left)
0.619
```

1.4 Permutation Tests for Complex Data

Examples from "Permutation Tests for Complex Data: Theory, Applications and Software" by F. Pesarin and L. Salmaso.

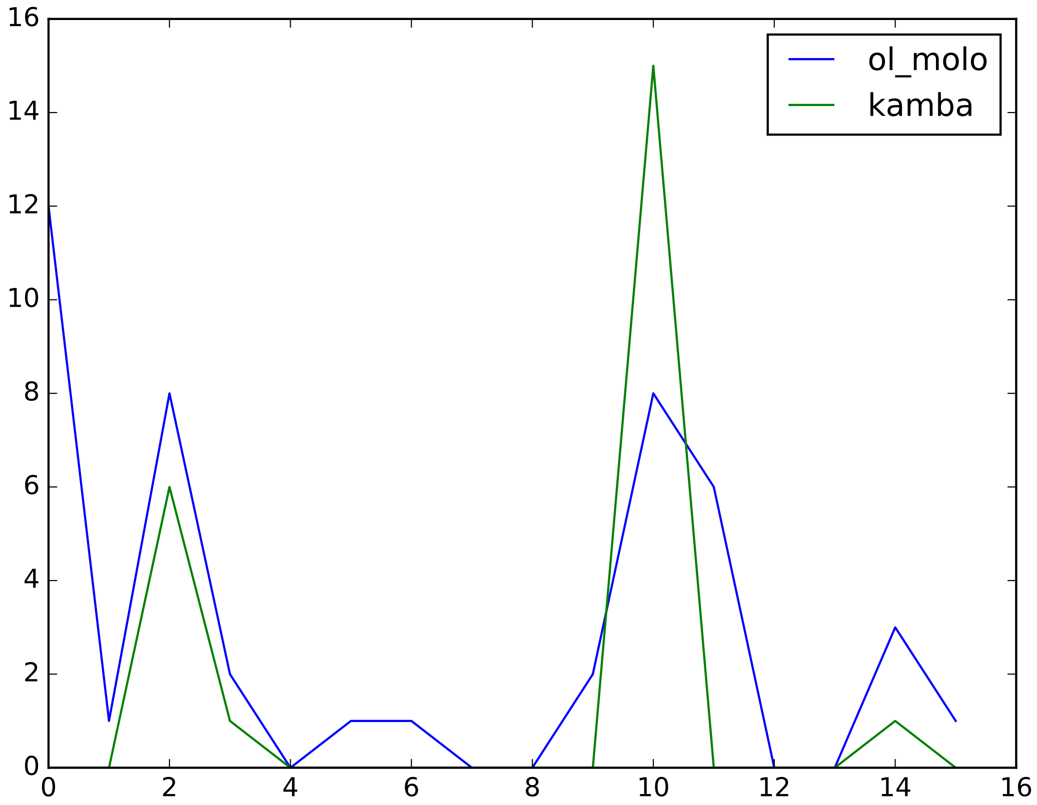
1.4.1 Kenya

The Kenya dataset *[CM77]* contains 16 observations and two variables in total. It concerns an anthropological study on the "Ol Molo" and "Kamba" populations described above. Table 1 shows the sample frequencies of the 16 phenotypic combinations in the samples selected from the two populations.

Given $X_1, X_2, \dots, X_n$ and ...

```
>>> from __future__ import print_function
>>> from matplotlib import mlab
>>> from permute.data import kenya
>>> d = kenya()
>>> print(mlab.rec2txt(d))
   classes   ol_molo   kamba
         1        12       0
         2         1       0
         3         8       6
         4         2       1
         5         0       0
         6         1       0
         7         1       0
         8         0       0
         9         0       0
        10         2       0
        11         8      15
        12         6       0
        13         0       0
        14         0       0
        15         3       1
        16         1       0
```

```
>>> import matplotlib.pyplot as plt
>>> plt.plot(d['ol_molo'])
[<matplotlib.lines.Line2D object at ...>]
>>> plt.plot(d['kamba'])
[<matplotlib.lines.Line2D object at ...>]
>>> plt.legend(['ol_molo', 'kamba'])
<matplotlib.legend.Legend object at ...>
>>> plt.show()
```



1.4.2 Chapter 1-4 examples

IPAT Data

This example is shown in Chapter 1.9, page 33-34.

```
>>> import permute.data as data
>>> from permute.core import one_sample, two_sample
>>> from permute.ksample import k_sample, bivariate_k_sample
>>> from permute.utils import get_prng
>>> import numpy as np
```

```
>>> prng = get_prng(2019426)
>>> ipat = data.ipat()
>>> ipat_res = one_sample(ipat.ya, ipat.yb, stat='mean', alternative='greater', seed=prng)
>>> print("P-value:", round(ipat_res[0], 4))
P-value: 0.0002
```

Job Satisfaction Data

This example is shown in Chapter 1.10.3, page 41-42.

```
>>> job = data.job()
>>> job_res = two_sample(job.x[job.y == 1], job.x[job.y == 2], stat='mean', reps = 10**5, alternative
>>> print("P-value:", round(job_res[0], 4))
P-value: 0.0003
```

Worms Data

This example is shown in Chapter 1.11.12, page 47-48.

```
>>> worms = data.worms()
>>> res = k_sample(worms.x, worms.y, stat='one-way anova', seed=prng)
>>> print("ANOVA p-value:", round(res[0], 4))
ANOVA p-value: 0.0107
```

Testosterone Data

This example is shown in Chapter 2.6.1, page 92-93.

```
>>> testosterone = data.testosterone()
>>> x = np.hstack(testosterone.tolist())
>>> group1 = np.hstack([[i]*5 for i in range(len(testosterone))])
>>> group2 = np.array(list(range(5))*len(testosterone))
>>> print(len(group1), len(group2), len(x))
55 55 55
>>> res = bivariate_k_sample(x, group1, group2, reps=5000, seed=prng)
>>> print("ANOVA p-value:", round(res[0], 4))
ANOVA p-value: 0.0002
```

Massaro-Blair Data

This example is shown in Chapter 4.6, page 240.

```
>>> from permute.npc import npc
>>> mb = data.massaro_blair()
>>> sam1 = mb.y[mb.group == 1]
>>> sam2 = mb.y[mb.group == 2]
>>> first_moment = two_sample(sam1, sam2, alternative='two-sided', reps=5000, keep_dist=True, seed=42
>>> second_moment = two_sample(sam1**2, sam2**2, alternative='two-sided', reps=5000, keep_dist=True,
>>> partial_pvalues = np.array([first_moment[0], second_moment[0]])
>>> print("Partial p-values:", round(first_moment[0], 3), round(second_moment[0], 3))
Partial p-values: 0.017 0.009
```

```
>>> npc_distr = np.vstack([first_moment[2], second_moment[2]]).T
>>> global_p = npc(partial_pvalues, npc_distr, alternatives='two-sided')
>>> print("Global p-value:", round(global_p, 4))
Global p-value: 0.0018
```

Fly Data

This example is shown in Chapter 4.6, page 253.

```
fly = data.fly()
vars = fly.dtype.names[1:]
results = {}
for col in vars:
    sam1 = fly[col][fly.group == 0]
    sam2 = fly[col][fly.group == 1]
    if col == 'x7':
        results[str(col)] = two_sample(sam1, sam2, keep_dist=True, seed=prng, plus1=True, reps=10**4)
    else:
        results[str(col)] = two_sample(sam1, sam2, keep_dist=True, alternative = 'less', seed=prng, p
partial_pvalues = np.array(list(map(lambda col: results[col][0], vars)))
print(np.round(partial_pvalues, 3))
[0.022 0.212 0.    0.337 0.    0.332 0.096]

npc_distr = np.array(list(map(lambda col: results[col][2], vars))).T
npc_distr.shape
000, 7)
alternatives = ['greater']*6 + ['less']*1
fisher = npc(partial_pvalues, npc_distr, alternatives=alternatives)
liptak = npc(partial_pvalues, npc_distr, alternatives=alternatives, combine = 'liptak')
tippett = npc(partial_pvalues, npc_distr, alternatives=alternatives, combine='tippett')
print("Fisher combined p-value:", fisher)
er combined p-value: 0.0
print("Liptak combined p-value:", liptak)
ak combined p-value: 0.0
print("Tippett combined p-value:", tippett)
Tippett combined p-value: 0.0
```

Post-hoc conditional power analysis

These examples come from Chapter 3.2.1, pages 139-141.

```
# IPAT data
alpha = 0.01
prng = get_prng(78943501)
effect_est = ipat_res[1]
print("Estimated difference in means:", effect_est)
Estimated difference in means: 3.1

z = ipat.ya - ipat.yb - effect_est
simulated_pvalues = np.zeros(1000)
for i in range(1000):
    prng.shuffle(z)
    sim_sam = z.copy() + effect_est
    simulated_pvalues[i] = one_sample(sim_sam, stat='mean', alternative='greater', seed=1234, reps=10
power = np.mean(simulated_pvalues <= alpha)
print("Estimated power:", power)
Estimated power: 1.0

# Job data
effect_est = job_res[1]
print("Estimated difference in means:", effect_est)
Estimated difference in means: 17.29166666666667
```

```
xnorm = job.x
xnorm[job.y == 1] = job.x[job.y == 1] - effect_est
simulated_pvalues = np.zeros(1000)
for i in range(1000):
    prng.shuffle(xnorm)
    sim_sam = xnorm.copy()
    sim_sam[job.y==1] = sim_sam[job.y==1] + effect_est
    simulated_pvalues[i] = two_sample(sim_sam[job.y == 1], sim_sam[job.y == 2], stat='mean', reps = 1
power = np.mean(simulated_pvalues <= alpha)
print("Estimated power:", power)
Estimated power: 0.96
```

CHAPTER

TWO

API REFERENCE

2.1 Data sets

Standard test data.

For more information, see

- http://www.wiley.com/legacy/wileychi/pesarin/material.html

`permute.data.load(f)`

Load a data file located in the data directory.

Parameters **f** (*string*) – File name.

Returns **x** – Data loaded from permute.data_dir.

Return type ndarray (or Pandas' frame?)

`permute.data.kenya()`

The Kenya dataset contains 16 observations and two variables in total. It concerns an anthropological study on the "Ol Molo" and "Kamba" populations.

2.2 Utility functions

Various utilities and helper functions.

`permute.utils.binom_conf_interval(n, x, cl=0.975, alternative='two-sided', p=None, **kwargs)`

Compute a confidence interval for a binomial p, the probability of success in each trial.

Parameters

- **n** (*int*) – The number of Bernoulli trials.
- **x** (*int*) – The number of successes.
- **cl** (*float in (0, 1)*) – The desired confidence level.
- **alternative** (*{"two-sided", "lower", "upper"}*) – Indicates the alternative hypothesis.
- **p** (*float in (0, 1)*) – Starting point in search for confidence bounds for probability of success in each trial.
- **kwargs** (*dict*) – Key word arguments

Returns lower and upper confidence level with coverage (approximately) 1-alpha.

Return type tuple

Notes

xtol [float] Tolerance

rtol [float] Tolerance

maxiter [int] Maximum number of iterations.

`permute.utils.`**`get_prng`**(*seed=None*)

Turn seed into a np.random.RandomState instance

Parameters **`seed`** (*{None, int, RandomState}*) – If seed is None, return the RandomState singleton used by np.random. If seed is an int, return a new RandomState instance seeded with seed. If seed is already a RandomState instance, return it. Otherwise raise ValueError.

Returns

Return type RandomState

`permute.utils.`**`hypergeom_conf_interval`**(*n*, *x*, *N*, *cl=0.975*, *alternative='two-sided'*, *G=None*, ***kwargs*)

Confidence interval for a hypergeometric distribution parameter G, the number of good objects in a population in size N, based on the number x of good objects in a simple random sample of size n.

Parameters

- **`n`** (*int*) – The number of draws without replacement.
- **`x`** (*int*) – The number of "good" objects in the sample.
- **`N`** (*int*) – The number of objects in the population.
- **`cl`** (*float in (0, 1)*) – The desired confidence level.
- **`alternative`** (*{"two-sided", "lower", "upper"}*) – Indicates the alternative hypothesis.
- **`G`** (*int in [0, N]*) – Starting point in search for confidence bounds for the hypergeometric parameter G.
- **`kwargs`** (*dict*) – Key word arguments

Returns lower and upper confidence level with coverage (at least) 1-alpha.

Return type tuple

Notes

xtol [float] Tolerance

rtol [float] Tolerance

maxiter [int] Maximum number of iterations.

`permute.utils.`**`permute`**(*x*, *seed=None*)

Permute an array in-place

Parameters

- **`x`** (*array-like*) – A 1-d array
- **`seed`** (*RandomState instance or {None, int, RandomState instance}*) – If None, the pseudorandom number generator is the RandomState instance used by *np.random*; If int, seed

is the seed used by the random number generator; If RandomState instance, seed is the pseudorandom number generator

Returns Original array is permuted in-place, nothing is returned.

Return type None

`permute.utils.`**`permute_incidence_fixed_sums`**(*incidence*, *k=1*)

Permute elements of a (binary) incidence matrix, keeping the row and column sums in-tact.

Parameters

- **`incidence`** (*2D ndarray*) – Incidence matrix to permute.
- **`k`** (*int*) – The number of successful pairwise swaps to perform.

Notes

The row and column sums are kept fixed by always swapping elements two pairs at a time.

Returns **permuted** – The permuted incidence matrix.

Return type 2D ndarray

`permute.utils.`**`permute_rows`**(*m*, *seed=None*)

Permute the rows of a matrix in-place

Parameters

- **`m`** (*array-like*) – A 2-d array
- **`seed`** (*RandomState instance or {None, int, RandomState instance}*) – If None, the pseudorandom number generator is the RandomState instance used by *np.random*; If int, seed is the seed used by the random number generator; If RandomState instance, seed is the pseudorandom number generator

Returns Original matrix is permuted in-place, nothing is returned.

Return type None

`permute.utils.`**`permute_within_groups`**(*x*, *group*, *seed=None*)

Permutation of condition within each group.

Parameters

- **`x`** (*array-like*) – A 1-d array indicating treatment.
- **`group`** (*array-like*) – A 1-d array indicating group membership
- **`seed`** (*RandomState instance or {None, int, RandomState instance}*) – If None, the pseudorandom number generator is the RandomState instance used by *np.random*; If int, seed is the seed used by the random number generator; If RandomState instance, seed is the pseudorandom number generator

Returns **permuted** – The within group permutation of x.

Return type array-like

`permute.utils.`**`potential_outcomes`**(*x*, *y*, *f*, *finverse*)

Given observations x under treatment and y under control conditions, returns the potential outcomes for units under their unobserved condition under the hypothesis that x_i = f(y_i) for all units.

Parameters

- **`x`** (*array-like*) – Outcomes under treatment

- **y** (*array-like*) – Outcomes under control
- **f** (*function*) – An invertible function
- **finverse** (*function*) – The inverse function to f.

Returns potential_outcomes – The first column contains all potential outcomes under the treatment, the second column contains all potential outcomes under the control.

Return type 2D array

2.3 Quality assurance

Quality assurance and data cleaning.

`permute.qa.`**`find_consecutive_duplicate_rows`**(*x*, *as_string=False*)

Find rows which are duplicated in x

`permute.qa.`**`find_duplicate_rows`**(*x*, *as_string=False*)

Find rows which are duplicated in x

Notes

If you load a file, for example *nsgk.csv*, as a 2D array, say *x*, then if you found '16,20,2,8' in the list returned by `find_duplicate_rows(x, as_string=True)` you might do something like:

> $ grep -n –context=1 '16,20,2,8' nsgk.csv 12512-16,15,2,8 12513:16,20,2,8 12514-16,45,2,8 – 12532-17,17,2,8 12533:16,20,2,8 12534-17,24,2,8

http://stackoverflow.com/questions/8560440/removing-duplicate-columns-and-rows-from-a-numpy-2d-array

2.4 Core functions

Core.

`permute.core.`**`corr`**(*x*, *y*, *reps=10000*, *seed=None*)

Simulate permutation p-value for Spearman correlation coefficient

Parameters

- **x** (*array-like*) –
- **y** (*array-like*) –
- **reps** (*int*) –
- **seed** (*RandomState instance or {None, int, RandomState instance}*) – If None, the pseudorandom number generator is the RandomState instance used by *np.random*; If int, seed is the seed used by the random number generator; If RandomState instance, seed is the pseudorandom number generator

Returns Returns test statistic, left-sided p-value, right-sided p-value, two-sided p-value, simulated distribution

Return type tuple

`permute.core.`**`one_sample`**`(`*x*, *y=None*, *reps=100000*, *stat='mean'*, *alternative='greater'*, *keep_dist=False*, *seed=None*`)`

One-sided or two-sided, one-sample permutation test for the mean, with p-value estimated by simulated random sampling with reps replications.

Alternatively, a permutation test for equality of means of two paired samples.

Tests the hypothesis that x is distributed symmetrically symmetric about 0 (or x and y have the same center) against the alternative that x comes from a population with mean

1.greater than 0 (greater than that of the population from which y comes), if side = 'greater'

2.less than 0 (less than that of the population from which y comes), if side = 'less'

3.different from 0 (different from that of the population from which y comes), if side = 'two-sided'

If `keep_dist`, return the distribution of values of the test statistic; otherwise, return only the number of permutations for which the value of the test statistic and p-value.

Parameters

- **`x`** (*array-like*) – Sample 1
- **`y`** (*array-like*) – Sample 2. Must preserve the order of pairs with x. If None, x is taken to be the one sample.
- **`reps`** (*int*) – number of repetitions
- **`stat`** (*{'mean', 't'}*) – The test statistic. The statistic is computed based on either z = x or z = x - y, if y is specified.

  1. If stat == 'mean', the test statistic is mean(z).
  2. If stat == 't', the test statistic is the t-statistic– but the p-value is still estimated by the randomization, approximating the permutation distribution.
  3. If stat is a function (a callable object), the test statistic is that function. The function should take a permutation of the data and compute the test function from it. For instance, if the test statistic is the maximum absolute value, max_i |z_i|, the test statistic could be written:

     f = lambda u: np.max(abs(u))

- **`alternative`** (*{'greater', 'less', 'two-sided'}*) – The alternative hypothesis to test
- **`keep_dist`** (*bool*) – flag for whether to store and return the array of values of the irr test statistic
- **`seed`** (*RandomState instance or {None, int, RandomState instance}*) – If None, the pseudorandom number generator is the RandomState instance used by *np.random*; If int, seed is the seed used by the random number generator; If RandomState instance, seed is the pseudorandom number generator

Returns

- *float* – the estimated p-value
- *float* – the test statistic
- *list* – The distribution of test statistics. These values are only returned if *keep_dist* == True

`permute.core.`**`two_sample`**`(`*x*, *y*, *reps=100000*, *stat='mean'*, *alternative='greater'*, *keep_dist=False*, *seed=None*`)`

One-sided or two-sided, two-sample permutation test for equality of two means, with p-value estimated by simulated random sampling with reps replications.

Tests the hypothesis that x and y are a random partition of x,y against the alternative that x comes from a population with mean

1.greater than that of the population from which y comes, if side = 'greater'

2.less than that of the population from which y comes, if side = 'less'

3.different from that of the population from which y comes, if side = 'two-sided'

If `keep_dist`, return the distribution of values of the test statistic; otherwise, return only the number of permutations for which the value of the test statistic and p-value.

Parameters

- **`x`** (*array-like*) – Sample 1
- **`y`** (*array-like*) – Sample 2
- **`reps`** (*int*) – number of repetitions
- **`stat`** (*{'mean', 't'}*) – The test statistic.

1. If stat == 'mean', the test statistic is (mean(x) - mean(y)) (equivalently, sum(x), since those are monotonically related)
2. If stat == 't', the test statistic is the two-sample t-statistic– but the p-value is still estimated by the randomization, approximating the permutation distribution. The t-statistic is computed using scipy.stats.ttest_ind
3. If stat is a function (a callable object), the test statistic is that function. The function should take a permutation of the pooled data and compute the test function from it. For instance, if the test statistic is the Kolmogorov-Smirnov distance between the empirical distributions of the two samples, `max_t |F_x(t) - F_y(t)|`, the test statistic could be written:

   f = lambda u: np.max([abs(sum(u[:len(x)]<=v)/len(x)-sum(u[len(x):]<=v)/len(y)) for v in u])

- **`alternative`** (*{'greater', 'less', 'two-sided'}*) – The alternative hypothesis to test
- **`keep_dist`** (*bool*) – flag for whether to store and return the array of values of the irr test statistic
- **`seed`** (*RandomState instance or {None, int, RandomState instance}*) – If None, the pseudorandom number generator is the RandomState instance used by *np.random*; If int, seed is the seed used by the random number generator; If RandomState instance, seed is the pseudorandom number generator

Returns

- *float* – the estimated p-value
- *float* – the test statistic
- *list* – The distribution of test statistics. These values are only returned if *keep_dist* == True

`permute.core.`**`two_sample_conf_int`**(*x*, *y*, *cl=0.95*, *alternative='two-sided'*, *seed=None*, *reps=10000*, *stat='mean'*, *shift=None*)

One-sided or two-sided confidence interval for the parameter determining the treatment effect. The default is the "shift model", where we are interested in the parameter d such that x is equal in distribution to y + d. In general, if we have some family of invertible functions parameterized by d, we'd like to find d such that x is equal in distribution to f(y, d).

Parameters

- **`x`** (*array-like*) – Sample 1

- **y** (*array-like*) – Sample 2
- **cl** (*float in (0, 1)*) – The desired confidence level. Default 0.95.
- **alternative** (*{"two-sided", "lower", "upper"}*) – Indicates the alternative hypothesis.
- **seed** (*RandomState instance or {None, int, RandomState instance}*) – If None, the pseudorandom number generator is the RandomState instance used by *np.random*; If int, seed is the seed used by the random number generator; If RandomState instance, seed is the pseudorandom number generator
- **reps** (*int*) – number of repetitions in two_sample
- **stat** (*{'mean', 't'}*) – The test statistic.

  1. If stat == 'mean', the test statistic is (mean(x) - mean(y)) (equivalently, sum(x), since those are monotonically related)
  2. If stat == 't', the test statistic is the two-sample t-statistic– but the p-value is still estimated by the randomization, approximating the permutation distribution. The t-statistic is computed using scipy.stats.ttest_ind
  3. If stat is a function (a callable object), the test statistic is that function. The function should take a permutation of the pooled data and compute the test function from it. For instance, if the test statistic is the Kolmogorov-Smirnov distance between the empirical distributions of the two samples, max_t **|F_x(t) - F_y(t)|**, the test statistic could be written:

     f = lambda u: np.max([abs(sum(u[:len(x)]<=v)/len(x)-sum(u[len(x):]<=v)/len(y)) for v in u])
- **shift** (*float*) – The relationship between x and y under the null hypothesis.

  1. If None, the relationship is assumed to be additive (e.g. x = y+d)
  2. A tuple containing the function and its inverse (f, finverse), so x_i = f(y_i, d) and y_i = finverse(x_i, d)

Returns the estimated confidence limits

Return type tuple

Notes

xtol [float] Tolerance in brentq

rtol [float] Tolerance in brentq

maxiter [int] Maximum number of iterations in brentq

permute.core.**two_sample_core**(*potential_outcomes_all, nx, tst_stat, alternative='greater', reps=100000, keep_dist=False, seed=None*)

Main workhorse function for two_sample and two_sample_shift

Parameters

- **potential_outcomes_all** (*array-like*) – 2D array of potential outcomes under treatment (1st column) and control (2nd column). To be passed in from potential_outcomes
- **nx** (*int*) – Size of the treatment group x
- **reps** (*int*) – number of repetitions
- **tst_stat** (*function*) – The test statistic

- **alternative** (*{'greater', 'less', 'two-sided'}*) – The alternative hypothesis to test
- **keep_dist** (*bool*) – flag for whether to store and return the array of values of the irr test statistic
- **seed** (*RandomState instance or {None, int, RandomState instance}*) – If None, the pseudorandom number generator is the RandomState instance used by *np.random*; If int, seed is the seed used by the random number generator; If RandomState instance, seed is the pseudorandom number generator

Returns

- *float* – the estimated p-value
- *float* – the test statistic
- *list* – The distribution of test statistics. These values are only returned if *keep_dist* == True

`permute.core.`**`two_sample_shift`**(*x*, *y*, *reps=100000*, *stat='mean'*, *alternative='greater'*, *keep_dist=False*, *seed=None*, *shift=None*)

One-sided or two-sided, two-sample permutation test for equality of two means, with p-value estimated by simulated random sampling with reps replications.

Tests the hypothesis that x and y are a random partition of x,y against the alternative that x comes from a population with mean

1.greater than that of the population from which y comes, if side = 'greater'

2.less than that of the population from which y comes, if side = 'less'

3.different from that of the population from which y comes, if side = 'two-sided'

If `keep_dist`, return the distribution of values of the test statistic; otherwise, return only the number of permutations for which the value of the test statistic and p-value.

Parameters

- **x** (*array-like*) – Sample 1
- **y** (*array-like*) – Sample 2
- **reps** (*int*) – number of repetitions
- **stat** (*{'mean', 't'}*) – The test statistic.

1. If stat == 'mean', the test statistic is (mean(x) - mean(y)) (equivalently, sum(x), since those are monotonically related)
2. If stat == 't', the test statistic is the two-sample t-statistic– but the p-value is still estimated by the randomization, approximating the permutation distribution. The t-statistic is computed using scipy.stats.ttest_ind
3. If stat is a function (a callable object), the test statistic is that function. The function should take a permutation of the pooled data and compute the test function from it. For instance, if the test statistic is the Kolmogorov-Smirnov distance between the empirical distributions of the two samples, max_t **|F_x(t) - F_y(t)|**, the test statistic could be written:

   f = lambda u: np.max([abs(sum(u[:len(x)]<=v)/len(x)-sum(u[len(x):]<=v)/len(y)) for v in u])

- **alternative** (*{'greater', 'less', 'two-sided'}*) – The alternative hypothesis to test
- **keep_dist** (*bool*) – flag for whether to store and return the array of values of the irr test statistic

- **seed** (*RandomState instance or {None, int, RandomState instance}*) – If None, the pseudorandom number generator is the RandomState instance used by *np.random*; If int, seed is the seed used by the random number generator; If RandomState instance, seed is the pseudorandom number generator
- **shift** (*float*) – The relationship between x and y under the null hypothesis.

1. A constant scalar shift in the distribution of y. That is, x is equal in distribution to y + shift.
2. A tuple containing the function and its inverse (f, finverse), so x_i = f(y_i) and y_i = finverse(x_i)

Returns

- *float* – the estimated p-value
- *float* – the test statistic
- *list* – The distribution of test statistics. These values are only returned if *keep_dist* == True

2.5 Stratified testing

Stratified permutation tests.

permute.stratified.**corrcoef**(*x*, *y*, *group*)

Calculates sum of Spearman correlations between x and y, computed separately in each group.

Parameters

- **x** (*array-like*) – Variable 1
- **y** (*array-like*) – Variable 2, of the same length as x
- **group** (*array-like*) – Group memberships, of the same length as x

Returns The sum of Spearman correlations

Return type float

permute.stratified.**sim_corr**(*x*, *y*, *group*, *reps=10000*, *seed=None*)

Simulate permutation p-value of stratified Spearman correlation test.

Parameters

- **x** (*array-like*) – Variable 1
- **y** (*array-like*) – Variable 2, of the same length as x
- **group** (*array-like*) – Group memberships, of the same length as x
- **reps** (*int*) – Number of repetitions
- **seed** (*RandomState instance or {None, int, RandomState instance}*) – If None, the pseudorandom number generator is the RandomState instance used by *np.random*; If int, seed is the seed used by the random number generator; If RandomState instance, seed is the pseudorandom number generator.

Returns

- *float* – the left (lower) p-value
- *float* – the right (upper) p-value
- *float* – the two-sided p-value

- *float* – the observed test statistic
- *list* – the null distribution

`permute.stratified.`**`stratified_permutationtest`**(*group*, *condition*, *response*, *reps=100000*, *testStatistic=<function stratified_permutationtest_mean>*, *seed=None*)

Stratified permutation test based on differences in means.

The test statistic is

$$\sum_{g \in \text{groups}} [f(mean(\text{response for cases in group :math:`g` assigned to each condition}))].$$

The function f is the difference if there are two conditions, and the standard deviation if there are more than two conditions.

There should be at least one group and at least two conditions. Under the null hypothesis, all assignments to the two conditions that preserve the number of cases assigned to the conditions are equally likely.

Groups in which all cases are assigned to the same condition are skipped; they do not contribute to the p-value since all randomizations give the same contribution to the difference in means.

Parameters

- **`group`** (*array-like*) – Group memberships
- **`condition`** (*array-like*) – Treatment conditions, of the same length as group
- **`response`** (*array-like*) – Responses, of the same length as group
- **`reps`** (*int*) – Number of repetitions
- **`testStatistic`** (*function*) – Function to compute test statistic. By default, stratified_permutationtest_mean
- **`seed`** (*RandomState instance or {None, int, RandomState instance}*) – If None, the pseudorandom number generator is the RandomState instance used by *np.random*; If int, seed is the seed used by the random number generator; If RandomState instance, seed is the pseudorandom number generator

Returns

- *float* – the left (lower) p-value
- *float* – the right (upper) p-value
- *float* – the two-sided p-value
- *float* – the observed test statistic
- *list* – the null distribution

`permute.stratified.`**`stratified_permutationtest_mean`**(*group*, *condition*, *response*, *groups=None*, *conditions=None*)

Calculates variability in sample means between treatment conditions, within groups.

If there are two treatment conditions, the test statistic is the difference in means, aggregated across groups. If there are more than two treatment conditions, the test statistic is the standard deviation of the means, aggregated across groups.

Parameters

- **`group`** (*array-like*) – Group memberships
- **`condition`** (*array-like*) – Treatment conditions, of the same length as group

- **response** (*array-like*) – Responses, of the same length as group
- **groups** (*array-like*) – Group labels. By default, it is the unique values of group
- **conditions** (*array-like*) – Condition labels. By default, it is the unique values of condition

Returns **tst** – The observed test statistic

Return type float

2.6 Nonparametric combination of tests

permute.npc.**fisher**(*pvalues*)

Apply Fisher's combining function

$$2\sum_i \log(p_i)$$

Parameters **pvalues** (*array_like*) – Array of p-values to combine

Returns Fisher's combined test statistic

Return type float

permute.npc.**inverse_n_weight**(*pvalues*, *size*)

Compute the test statistic

$$-\sum_{s=1}^{S} \frac{p_s}{\sqrt{N_s}}$$

Parameters

- **pvalues** (*array_like*) – Array of p-values to combine
- **size** (*array_like*) – The $i$th entry is the sample size used for the $i$th test

Returns combined test statistic

Return type float

permute.npc.**liptak**(*pvalues*)

Apply Liptak's combining function

$$\sum_i \Phi^{-1}(1-p_i)$$

where Φ^{-1} is the inverse CDF of the standard normal distribution.

Parameters **pvalues** (*array_like*) – Array of p-values to combine

Returns Liptak's combined test statistic

Return type float

permute.npc.**npc**(*pvalues*, *distr*, *combine='fisher'*, *alternatives='greater'*)

Combines p-values from individual partial test hypotheses H_{0i} against H_{1i}, $i = 1, \dots, n$ to test the global null hypothesis

$$\cap_{i=1}^{n} H_{0i}$$

against the alternative

$$\cup_{i=1}^{n} H_{1i}$$

using an omnibus test statistic.

Parameters

- **pvalues** (*array_like*) – Array of p-values to combine
- **distr** (*array_like*) – Array of dimension [B, n] where B is the number of permutations and n is the number of partial hypothesis tests. The $i$th column of distr contains the simulated null distribution of the $i$th test statistic under H_{0i}.
- **combine** (*{'fisher', 'liptak', 'tippett'}*) – The combining function to use. Default is "fisher" TODO: allow user to pass in their own combining function; check that it satifies the correct monotonicity. Describe the monotonicity!
- **alternatives** (*array_like*) – Optional, an array containing the alternatives for each partial test ('greater', 'less', 'two-sided') or a single alternative, if all tests have the same alternative hypothesis. Default is "greater".

Returns A single p-value for the global test

Return type float

`permute.npc.`**`t2p`**(*stat*, *distr*, *alternative='greater'*)

Use the empirical distribution of a test statistic to compute its p-value.

Parameters

- **stat** (*float*) – Test statistic
- **distr** (*array_like*) – Empirical distribution of statistic
- **alternative** (*{'greater', 'less', 'two-sided'}*) – The alternative hypothesis to test (default is 'greater')

Returns the estimated p-vlaue

Return type float

`permute.npc.`**`tippett`**(*pvalues*)

Apply Tippett's combining function

$$\max_i \{1 - p_i\}$$

Parameters **pvalues** (*array_like*) – Array of p-values to combine

Returns Tippett's combined test statistic

Return type float

2.7 Interrater reliability

A stratified permutation test for multi-rater inter-rater reliability.

There are S strata. There are N_s items in stratum s. There are $N = \sum_{s=1}^{S} N_s$ items in all.

There are C non-exclusive categories to which each of the N items might belong; an item might belong to none of the categories. That is, each item might be "labeled" with any of the 2^C subsets of the C labels, including the empty set.

There are R "raters," each of whom labels each of the N items with zero or more elements of C.

Define $L_{s,i,c,r} = 1$, if rater r assigns label c to item i in stratum s; and $L_{s,i,c,r} = 0$ if not.

We observe $\{L_{s,i,c,r}\}$ for $s = 1...S$; $i = 1, ..., N_s$; $c = 1, ..., C$; and $r = 1, ..., R$.

We want to know whether the categorizations are "reliable," in the sense that agreement among the raters is higher than would be expected "by chance." The reliability of each category c is of interest, rather than an overall rating for all C categories.

Fix c, since we are considering only one category at a time.

The null hypothesis for category c is that, for each rater r, and each stratum s, the values $\{L_{s,i,c,r}\}$ are exchangeable; that for each rater r, the values $\{L_{s,i,c,r}\}$ for different strata s are independent; and that the values are independent across raters.

Our test conditions on the sets of labels each rater assigns within each stratum, but not on the items to which those labels are assigned. The null distribution involves permuting the assignments each given rater makes of category c to items within each stratum s, permuting independently across across raters and across strata.

The test statistic within stratum s is

$$\rho_s \equiv \frac{1}{N_s \binom{R}{2}} \sum_{i=1}^{N_s} \sum_{r=1}^{R-1} \sum_{v=r+1}^{R} 1(L_{s,i,r} = L_{s,i,v}) = \frac{1}{N_s R(R-1)} \sum_{i=1}^{N_s} (y_{si}(y_{si}-1) + (R - y_{si})(R - y_{si} - 1)).$$

That is, within each stratum, we count the number of concordant pairs of assignments. If all R raters agree whether item i in stratum s belongs to category c, that contributes a term $\binom{R}{2}$ to the sum. If only half agree, the term for item i contributes $2\binom{N/2}{2}$ to the sum. The normalization makes perfect agreement within stratum s correspond to $\rho_s = 1$.

To combine the results across strata to get an overall p-value, we could use any of the methods we've discussed, or the NPC (nonparametric combination of test) methods described in Pesarin and Salmaso, based on the p-values in different strata. For instance, Fisher's combination statistic is

$$\lambda = -\sum_{s=1}^{S} w_s \log \hat{p}_s,$$

where the nonnegative weights $\{w_s\}$ are chosen in some sensible manner (e.g., $w_s = N_s^{-1/2}$ would be reasonable).

`permute.irr.`**`compute_ts`**(*ratings*)

Compute the test statistic

$$\rho_s \equiv \frac{1}{N_s \binom{R}{2}} \sum_{i=1}^{N_s} \sum_{r=1}^{R-1} \sum_{v=r+1}^{R} 1(L_{s,i,r} = L_{s,i,v}) = \frac{1}{N_s R(R-1)} \sum_{i=1}^{N_s} (y_{si}(y_{si}-1) + (R - y_{si})(R - y_{si} - 1)).$$

Parameters **`ratings`** (*array_like*) – Input array of dimension [R, Ns] Each row corresponds to the ratings given by a single rater; columns correspond to items rated.

Returns **rho_s** – concordance of the ratings, where perfect concordance is 1.0

Return type float

`permute.irr.`**`simulate_npc_dist`**(*perm_distr*, *size*, *obs_ts=None*, *pvalues=None*)

Simulates the permutation distribution of the combined NPC test statistic for S matrices of ratings `ratings` corresponding to S strata. The distribution comes from applying `simulate_ts_dist` to each of the S strata.

If obs_ts is not null, computes the reference value of the test statistic before the first permutation. Otherwise, uses the value `obs_ts` for comparison.

If `keep_dist`, return the distribution of values of the test statistic; otherwise, return only the number of permutations for which the value of the irr test statistic is at least as large as `obs_ts`.

Parameters

- **perm_distr** (*array_like*) – Input array of dimension [B, S] Column s is the permutation distribution of `rho_s`, for s=1,...,S
- **size** (*array_like*) – Input array of dimension S Each entry corresponds to the number of items, Ns, in the s-th stratum.
- **obs_ts** (*float*) – if `None`, `obs_npc` is calculated as the value of the test statistic for the original data
- **pvalues** (*array_like*) – Input array of dimension S Each entry corresponds to the p-value for `rho_s`, the concordance for the s-th stratum.

Returns

A dictionary containing:

obs_npc [float] observed value of the test statistic for the input data, or the input value of `obs_ts` if `obs_ts` was given as input

leq [int] number of iterations for which the NPC test statistic was less than or equal to `obs_npc`

num_perm [int] number of permutations

Return type dict

`permute.irr.`**`simulate_ts_dist`**(*ratings*, *obs_ts=None*, *num_perm=10000*, *keep_dist=False*, *seed=None*)

Simulates the permutation distribution of the irr test statistic for a matrix of ratings `ratings`

If `obs_ts` is not `None`, computes the reference value of the test statistic before the first permutation. Otherwise, uses the value `obs_ts` for comparison.

If `keep_dist`, return the distribution of values of the test statistic; otherwise, return only the number of permutations for which the value of the irr test statistic is at least as large as `obs_ts`.

Parameters

- **ratings** (*array_like*) – Input array of dimension [R, Ns]
- **obs_ts** (*float*) – if None, `obs_ts` is calculated as the value of the test statistic for the original data
- **num_perm** (*int*) – number of random permutation of the elements of each row of ratings
- **keep_dist** (*bool*) – flag for whether to store and return the array of values of the irr test statistic
- **seed** (*RandomState instance or {None, int, RandomState instance}*) – If None, the pseudorandom number generator is the RandomState instance used by *np.random*; If int, seed is the seed used by the random number generator; If RandomState instance, seed is the pseudorandom number generator

Returns

A dictionary containing:

obs_ts [int] observed value of the test statistic for the input data, or the input value of `obs_ts` if `obs_ts` was given as input

geq [int] number of iterations for which the test statistic was greater than or equal to `obs_ts`

num_perm [int] number of permutations

pvalue [float] geq / num_perm

dist [array-like] if `keep_dist`, the array of values of the irr test statistic from the `num_perm` iterations. Otherwise, `None`.

Return type dict

`permute` provides permutation tests and confidence intervals for a variety of nonparametric testing and estimation problems, for a variety of randomization designs.

- Stratified and unstratified tests
- Test statistics in each stratum
- Methods of combining tests across strata
- Nonparametric combinations of tests

2.8 Problems/Methods:

1. The 2-sample problem
2. The *n*-sample problem
3. Tests for the slope in linear regression
4. Tests for quantiles
5. Tests of independence and association: runs tests, permutation association
6. Tests of exchangeability
7. Tests of symmetry: reflection, spherical
8. Permutation ANOVA
9. Goodness of fit tests

2.9 Confidence sets

1. Constant shifts
2. Proportional shifts
3. Monotone shifts

2.10 Links

UC Berkeley's Statistics 240: Nonparametric and Robust Methods.

- 2015 course website
- Philip Stark's lecture notes

"Permutation Tests for Complex Data: Theory, Applications and Software" by Fortunato Pesarin, Luigi Salmaso

- Publisher's website
- Supplementary Material (i.e., code and data)
- NPC test code

"Stochastic Ordering and ANOVA: Theory and Applications with R" by Basso D., Pesarin F., Salmaso L., Solari A.

- R code

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[Pit38] Edwin JG Pitman. Significance tests which may be applied to samples from any populations: iii. the analysis of variance test. *Biometrika*, pages 322–335, 1938.

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PYTHON MODULE INDEX

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