Permutation Test
for the Two Sample Problem

- we wish to compare results for two groups of experimental units
- the first group could be some subjects who have been given a treatment, whereas the second group has not
- in some cases we are unable to assume that
  - the two samples of sizes n_1 and n_2 are from normal populations and/or
  - the populations have the same variance
- however we may be able to asssume that the groups were obtained by randomly splitting the subjects $n = n_1 + n_2$ into two groups
- with only this assumption, we are able to base the test on the permutation distribution, described below
- the hypotheses are

$$H_o: \ no\ effect\ of\ the\ treatment$$

$$H_a: \ there\ is\ an\ effect$$

- a reasonable test statistic is

$$T = \bar{X}_1 - \bar{X}_2$$

  which measures the effect of the treatment
- if H_o is true the observed differences in the data are due only to variation among the subjects
- with a different random allocation of subjects, a different value for T would be obtained

- there are exactly
$$\binom{n_1+n_2}{n_1} = \frac{(n_1+n_2)!}{n_1!n_2!}$$
ways of randomly allocating n_1 of the subjects to group 1 and the remaining n_2 to group 2
- each of these is equally likely, and each can lead to a different value of the test statistic T
- the permutation distribution describes the possible values for T for all possible allocations of the subjects
- the P value is the fraction of values for T which are as least as extreme as contrary to the null hypothesis as is the observed value T_{obs}
- for a one-sided alternative the P value is the proportion in one tail of the permutation distribution
- for a two-sided alternative the P value is double the probability in one tail of the permutation distribution
- If the alternative is that the population 2 measurements are smaller than in population 1, and if the test statistic is $T = \bar{X}_1 - \bar{X}_2$, then the p-value is the proportion of possible values of T which are at least as large as T_{obs}. (If your test statistic was $T = \bar{X}_2 - \bar{X}_1$ then the p-value would be the proportion of possible values of T which are at least as small as T_{obs}.)
- If the alternative is that the population 2 measurements are greater than in population 1, and if the test statistic is $T = \bar{X}_1 - \bar{X}_2$, then the p-value is the proportion of possible values of T which are at least as small as T_{obs}. (If your test statistic was $T = \bar{X}_2 - \bar{X}_1$ then the p-value would be the proportion of possible values of T which are at least as large as T_{obs}.)

- If the alternative is two sided - that the distribution in the two populations are different, then the test statistic is $T = |\bar{X}_1 - \bar{X}_2|$, and the p-value is the proportion of possible values of T which are at least as large as T_{obs}.

Example: A simple study has only $n_1 = n_2 = 3$ subjects in each group

Treatment	175	250	260	$\bar{X}_1 = 228.33$
Control	255	275	300	$\bar{X}_2 = 276.67$

Two of the three largest smallest observations are in the treatment group, so it looks as though the treatment may be effective. What is the p-value?

- the test statistic is $T = 228.33 - 276.67 = -48.33$
- there are only $\binom{3+3}{3} = 20$ possible allocations of subjects to the two groups
- these are shown in the table below, along with the value for T

175	250	255	260	275	300	$\bar{X}_1 - \bar{X}_2$	$\lvert\bar{X}_1 - \bar{X}_2\rvert$
1	1	1	2	2	2	-51.67	51.67
1	1	2	1	2	2	-48.33	48.33 (observed)
1	1	2	2	1	2	-38.33	38.33
1	1	2	2	2	1	-21.67	21.67
1	2	1	2	2	1	-18.33	18.33
1	2	1	2	1	2	-35	35
1	2	1	1	2	2	-45	45
1	2	2	1	1	2	-31.67	31.67
1	2	2	2	1	1	-5	5
1	2	2	1	2	1	-15	15
2	1	1	1	2	2	5	5
2	1	1	2	1	2	15	15
2	1	1	2	2	1	31.67	31.67
2	1	2	1	1	2	18.33	18.33
2	1	2	1	2	1	35	35
2	1	2	2	1	1	45	45
2	2	1	1	1	2	21.67	21.67
2	2	1	1	2	1	38.33	38.33
2	2	1	2	1	1	48.33	48.33
2	2	2	1	1	1	51.67	51.67

- For the one sided alternative (treatment leads to smaller observations), $T_{obs} = -48.33$, and there is 1 possible sample (the configuration [1,1,1,2,2,2]) which provides greater evidence against the null hypothesis than T_{obs}. Therefore, the p-value is $2/20 = .1$.
- For the two sided alternative (unspecified difference between treatment and control), $T_{obs} = 48.33$, and there are 4 samples which provide at least as much evidence against H_0 than does T_{obs}, and so the p-value is $4/20 = .2$.

Example: The data below is from the example of soil surface pH which was used to illustrate the (pooled) two sample t test.

Location 1	8.53	8.52	8.01	7.99	7.93
	7.89	7.85	7.82	7.80	
Location 2	7.85	7.73	7.58	7.40	7.35
	7.30	7.27	7.27	7.23	

- the test statistic is

$$T_{obs} = 8.038 - 7.442 = .596$$

- note that only one value (7.85) from Location 2 is larger than two of the values from Location 1
- exchanging this value with one of the smaller values in Location 1 increases the mean for Location 1 and decreases the mean for Location 2, giving a larger $T = \bar{X}_1 - \bar{X}_2$
- the same value for T_{obs} is obtained if the value 7.85 from Location 2 is switched with the value 7.85 from Location 1
- so there are 4 permutations (including the original data) for which T is as large or larger than T_{obs}, and 8 permutations for which T is as extreme or more extreme
- there are

$$\binom{18}{9} = \frac{18!}{9!9!} = 48620$$

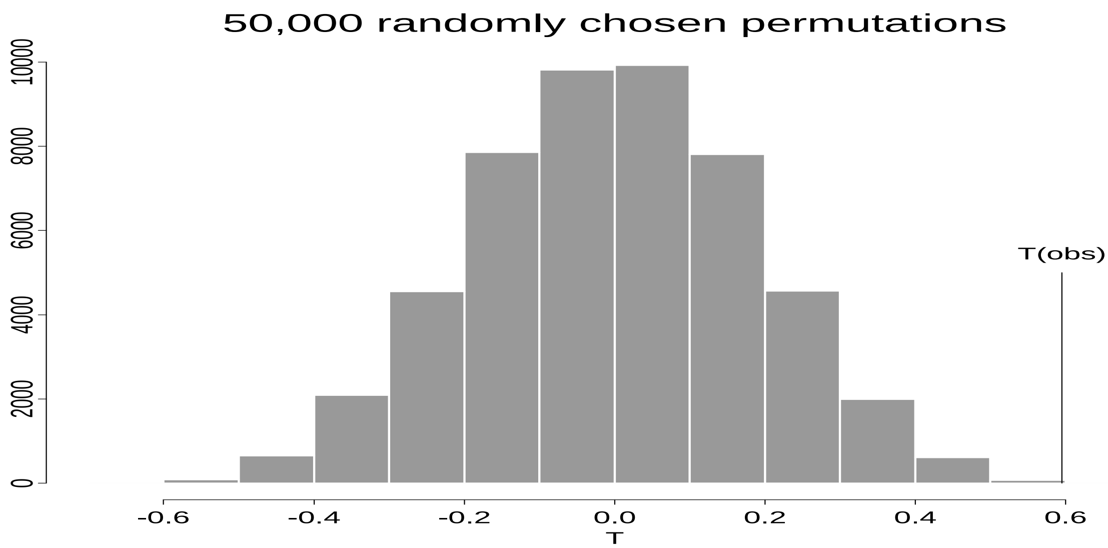
  permutations in total

- if we test the hypotheses

$$\begin{aligned} H_0 &: \ no\ difference\ between\ locations \\ H_a &: \quad there\ is\ a\ difference \end{aligned}$$

  using the permutation test, the P value is $P = 8/48620 = .0001645$

- so there is very strong evidence of a difference in the mean surface soil pH at the two locations
- this is consistent with the result obtained earlier using the t distribution, which requires the assumptions of normality and equal variances
- in this example we are fortunate that it is straightforward to determine how extreme T_{obs} is relative to the permutation distribution
- it would be difficult to list all 48620 possible permutations
- one approach in this situation is to approximate the permutation distribution using random permutations chosen by the computer
- 50,000 such permutations give the following histogram, for this example


50,000 randomly chosen permutations
10000
8000
6000
4000
2000
0
T(obs)
-0.6
-0.4
-0.2
0.0
0.2
0.4
0.6
T

- one can see that there are very few values of T beyond T_{obs}
- the computer found 5 cases as extreme or more extreme
- the approximate P value using this approach is $P = 5/50000 = .0001$
- this is quite close to the exact value