Kinds of tests

Kinds of tests

By number of samples:

- One-sample: just one sample. Example: testing whether a coin is symmetric (probability of success equals probability of failure).
- Two-sample: two independent samples. Example: A/B testing.
- Paired: two dependent samples. Example: treatment effect, when the same participants are tested more than once.

By hypothesis type:

- Non-parametric: either we know the distribution entirely (goodness-of-fit) or we test its parameters
- Parametric: we know the distribution up to a **parametric** family of distributions

Permutation test

Permutation test

Permutation test is a **non-parametric two-sample** test.

Suppose that we have samples $X = (X_1, \dots, X_n) \sim p(\cdot)$ and $Y = (Y_1, \dots, Y_m) \sim q(\cdot)$. We'd like to test whether the samples come from the same distribution:

$$H_0 : p \equiv q$$

This test works with **any** test statistic $T(\cdot)$. Denote the joined sample $Z = (X_1, \dots X_n, Y_1, \dots, Y_m)$. Intuitively, we would like to asses how likely it is to have the partition of Z into X and Y the way it is observed.

Let's shuffle Z randomly and compute a statistic of the shuffled sample $T(\tilde{Z})$. Let's do so for all possible permutations and collect $(n+m)!$ values of test statistics. Now, the p-value of the test will be simply the fraction of cases with a more extreme value of the statistic:

$$p\text{—value} = \frac{1}{(\mathrm{n}+\mathrm{m})!} \sum_{\text{all permutations } \tilde{\mathrm{Z}} \text{ of } \mathrm{Z}} \mathbb{I}\mathrm{nd}\left(\mathrm{T}(\tilde{\mathrm{Z}}) > \mathrm{T}(\mathrm{Z})\right)$$

- Advantages: non-parametric, any test statistic
- Disadvantages: computationally hard

In [1]:
```
import numpy as np
import itertools as it
from scipy.special import factorial
```

In [2]:
```
X = np.array([0.225, 0.262, 0.217, 0.240, 0.230, 0.229, 0.235, 0.217])
Y = np.array([0.209, 0.205, 0.196, 0.210, 0.202, 0.207, 0.224, 0.223, 0.220, 0.201])
Z = np.concatenate([X, Y])

n, m = len(X), len(Y)

alpha = 0.05
```

In [3]:
```
def T(z):
    x, y = z[:, :n], z[:, n:]
    x_mean, y_mean = np.mean(x, axis=1), np.mean(y, axis=1)
    return np.abs(x_mean - y_mean)
```

In [4]:
```
t_obs = T(np.expand_dims(Z, 0))
```

In [5]:
```
factorial(n + m)
```

Out[5]:
```
6402373705728000.0
```

In [6]:
```
B = 1e6
permutations = []
for i, permutation in enumerate(it.permutations(Z)):
    permutations.append(permutation)
    if i > B: break
statistics = T(np.array(permutations))
pvalue = np.sum(statistics > t_obs) / factorial(B)
print("Rejected" if pvalue < alpha else "Not rejected")
```

```
Rejected
```

Multinomial test

Multinomial test

The multinomial test is the test of the null hypothesis that the parameters of a multinomial distribution equal specified values. It is a **one-sample non-parametric** test.

Suppose that we have sample $X = (X_1, \dots, X_n) \sim Mult(\theta)$ with k categories. We'd like to test whether our parameters θ equal specified values:

$$H_0 : \theta = \theta_0$$

The statistic for the test is simply the multinomial probability:

$$T(X) = n! \sum_{i=1}^{k} \frac{\theta_i^{X_i}}{X_i!}$$

Now, the p-value of the test will be simply the probability of observing a sample (there is a finite number of possible multinomial samples of size n) less likely that the given one:

$$p\text{—value} = \sum_{\mathrm{Y}:\mathrm{T}(\mathrm{Y}) \leqslant \mathrm{T}(\mathrm{X})} \mathrm{T}(\mathrm{Y})$$

- Advantages: non-parametric, simple
- Disadvantages: computationally hard

Likelihood ratio test

Likelihood ratio test

Likelihood ratio test is a **parametric one-sample** test.

Suppose that we have sample $X = (X_1, \dots, X_n) \sim p(\theta)$ and $\theta \in \Theta$. We'd like to test wheter θ belongs to a subset of Θ:

$$H_0 : \theta \in \Theta_0 \subset \Theta$$
$$H_1 : \theta \in \Theta_1 = \Theta \backslash \Theta_0$$

The test statistic is given as follows (most common example, will lead to χ^2 distribution):

$$\lambda(X) = 2 \log \Lambda(X) = 2 \log \left(\frac{\sup_{\theta \in \Theta} L(X, \theta)}{\sup_{\theta \in \Theta_0} L(X, \theta)} \right) = 2 \log \left(\frac{L(X, \hat{\theta}^{MLE})}{L(X, \hat{\theta}_0^{MLE})} \right)$$

We reject the null hypothesis, if $\lambda(X) \leqslant c$, where c is defined from

$$\int_{y:\lambda(y) \leqslant c} L(x, \theta) \leqslant \alpha$$

Many tests can be derived from likelihood ratio test.

Likelihood ratio test: example

Suppose that we have sample $X = (X_1, \dots, X_n) \sim \mathcal{N}(\theta_1, \theta_2^2)$.

$$H_0 : \theta_1 = \theta_0$$
$$H_1 : \theta_1 \neq \theta_0$$

We'l need to compute

$$\Lambda(X) = \frac{L(X, \hat{\theta}^{MLE})}{L(X, \hat{\theta}_0^{MLE})}$$

Numerator:

$$L(X, \theta_1, \theta_2) = \frac{1}{(2\pi)^{n/2} \theta_2^n} \exp\left(-\frac{1}{2\theta_2^2} \sum_{i=1}^{n} (X_i - \theta_1)^2 \right) = \\ = \frac{1}{(2\pi)^{n/2} \theta_2^n} \exp\left(-\frac{n}{2\theta_2^2} \left(s^2 + (\bar{X} - \theta_1)^2\right) \right)$$

MLE estimates are $\hat{\theta}_1 = \bar{X}, \hat{\theta}_2^2 = s^2$. The supremum of likelihood is:

$$\sup_{\theta \in \Theta} L(X, \theta_1, \theta_2) = \left(2\pi e s^2\right)^{-n/2}$$

Likelihood ratio test: example

Denominator:

$$L(X, \theta_1, \theta_2) = \frac{1}{(2\pi)^{n/2} \theta_2^n} \exp\left(-\frac{1}{2\theta_2^2} \sum_{i=1}^{n} (X_i - \theta_0)^2 \right)$$

MLE estimate is

$$\hat{\theta}_2^2 = \frac{1}{n} \sum_{i=1}^{n} (X_i - \theta_0)^2 = s_0^2$$

The supremum of likelihood is:

$$\sup_{\theta \in \Theta} L(X, \theta_1, \theta_2) = \left(2\pi e s_0^2\right)^{-n/2}$$

Likelihood ratio test: example

The statistic for this case will be $\lambda(X) = \Lambda(X)^{-1}$.

$$\lambda(X) = \frac{\left(2\pi e s_0^2\right)^{-n/2}}{\left(2\pi e s^2\right)^{-n/2}} = \left(\frac{s^2 + (\bar{X} - \theta_0)^2}{s^2} \right)^{-n/2}$$

Note that $\bar{X} \sim \mathcal{N}(\theta_0, \frac{\theta_2^2}{n})$, therefore $\frac{\bar{X} - \theta_0}{\theta_2} \sqrt{n} \sim \mathcal{N}(0, 1)$. Therefore,

$$t^2 = \left(\frac{\frac{\bar{X} - \theta_0}{\theta_2} \sqrt{n}}{\sqrt{\frac{\frac{s^2}{\theta_2^2} n}{n-1}}} \right)^2 \sim St(n-1)$$

We have,

$$\lambda(X) = \left(1 + \frac{1}{n-1} t^2\right)^{-n/2} \leqslant c \Leftrightarrow |t| \geqslant \tilde{c}$$

Tests comparison for multinomial data

1. Multinomial test: exact, works best on small samples, hard
2. Likelihood ratio test: not exact, works best on large samples, produces type I errors (false positives), simplier
3. Pearson χ^2 test: not exact, works best on medium-sized samples, produces type I errors (false positives), simplier

Student t-test

Student t-test

It is a **parametric** test. There are all kinds of t-test: one-sample, two-sample, paired test. We'll cover one-sample test for now.

Suppose that we have sample $X = (X_1, \dots, X_n) \sim \mathcal{N}(\mu, \sigma^2)$. We'd like to test wheter μ equals a specified value:

$$H_0 : \mu = \mu_0$$
$$H_1 : \mu \neq \mu_0$$

The test statistic is given by

$$T(X) = \frac{\bar{X} - \mu_0}{S / \sqrt{n}} \sim St(n-1)$$

In [7]:
```
from sklearn.datasets import load_wine
import pandas as pd
```

In [8]:
```
wine = load_wine()
df = pd.DataFrame(wine["data"], columns=wine["feature_names"])
```

In [9]:
```
df
```

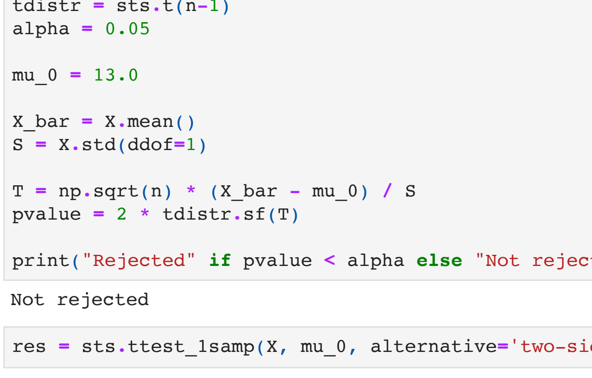
Out[9]:

	alcohol	malic_acid	ash	alcalinity_of_ash	magnesium	total_phenols	flavanoids	nonflavanoid_phenols	proanthocyanins	color_intensity	hue	od280/od315_of_diluted_wi
0	14.23	1.71	2.43	15.6	127.0	2.80	3.06	0.28	2.29	5.64	1.04	
1	13.20	1.78	2.14	11.2	100.0	2.65	2.76	0.26	1.28	4.38	1.05	
2	13.16	2.36	2.67	18.6	101.0	2.80	3.24	0.30	2.81	5.68	1.03	
3	14.37	1.95	2.50	16.8	113.0	3.85	3.49	0.24	2.18	7.80	0.86	
4	13.24	2.59	2.87	21.0	118.0	2.80	2.69	0.39	1.82	4.32	1.04	
...	...	...	...	...	...	...	...	...	...	...	...	
173	13.71	5.65	2.45	20.5	95.0	1.68	0.61	0.52	1.06	7.70	0.64	
174	13.40	3.91	2.48	23.0	102.0	1.80	0.75	0.43	1.41	7.30	0.70	
175	13.27	4.28	2.26	20.0	120.0	1.59	0.69	0.43	1.35	10.20	0.59	
176	13.17	2.59	2.37	20.0	120.0	1.65	0.68	0.53	1.46	9.30	0.60	
177	14.13	4.10	2.74	24.5	96.0	2.05	0.76	0.56	1.35	9.20	0.61	

178 rows × 13 columns

In [10]:
```
df["alcohol"].plot.hist(bins=50)
```

Out[10]:
```
<AxesSubplot:ylabel='Frequency'>
```



In [11]:
```
import scipy.stats as sts
```

In [12]:
```
X = df["alcohol"].values
n = len(X)

tdistr = sts.t(n-1)
alpha = 0.05

mu_0 = 13.0

X_bar = X.mean()
S = X.std(ddof=1)

T = np.sqrt(n) * (X_bar - mu_0) / S
pvalue = 2 * tdistr.sf(T)

print("Rejected" if pvalue < alpha else "Not rejected")
```

```
Not rejected
```

In [13]:
```
res = sts.ttest_1samp(X, mu_0, alternative='two-sided')
```

In [14]:
```
print("Rejected" if res.pvalue < alpha else "Not rejected")
```

```
Not rejected
```

Student t-test

Suppose that we have samples $X = (X_1, \dots, X_n) \sim \mathcal{N}(\mu_1, \sigma_1^2)$ and $Y = (Y_1, \dots, Y_m) \sim \mathcal{N}(\mu_2, \sigma_2^2)$. We'd like to test whether the distributions of these samples share the same means:

$$H_0 : \mu_1 = \mu_2$$
$$H_1 : \mu_1 \neq \mu_2$$

The test statistic is given by

$$T(X) = \frac{\bar{X} - \bar{Y}}{\sqrt{\frac{S_1^2}{n} + \frac{S_2^2}{m}}} \sim St\left(\frac{\left(\frac{S_1^2}{n} + \frac{S_2^2}{m}\right)^2}{\left(\frac{S_1^2}{n}\right)^2 \frac{1}{n-1} + \left(\frac{S_2^2}{m}\right)^2 \frac{1}{m-1}} \right)$$

In [15]:
```
X = np.array([0.225, 0.262, 0.217, 0.240, 0.230, 0.229, 0.235, 0.217])
Y = np.array([0.209, 0.205, 0.196, 0.210, 0.202, 0.207, 0.224, 0.223, 0.220, 0.201])

alpha = 0.05
```

In [16]:
```
res = sts.ttest_ind(X, Y, equal_var=False)
print("Rejected" if res.pvalue < alpha else "Not rejected")
```

```
Rejected
```

Wilcoxon signed-rank test

Wilcoxon signed-rank test

It is a **non-parametric paired** test.

Suppose that we have samples $X = (X_1, \dots, X_n) \sim p(\cdot)$ and $Y = (Y_1, \dots, Y_n) \sim q(\cdot)$. We'd like to test whether the distributions of these samples share the same means:

$$H_0 : \mu_1 = \mu_2$$
$$H_1 : \mu_1 \neq \mu_2$$

The statistic is:

$$W(X, Y) = \sum_{i=1}^{N_r} R_i \cdot \mathrm{sgn}(\mathrm{y_i} - \mathrm{x_i})$$

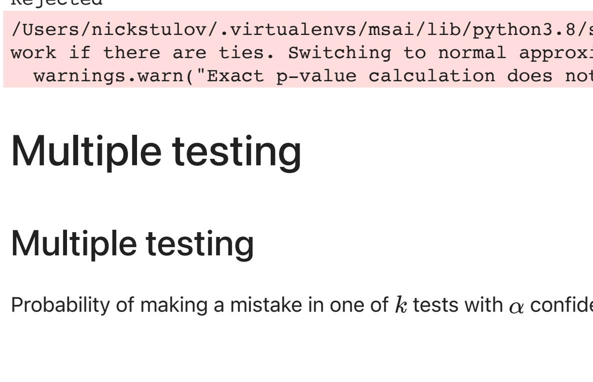
where $\mathrm{sgn}(\cdot)$ is signum function, N_r is the corrected sample size (without samples with equal measurements), R_i is the rank of the difference in ascending order.

It follows a tabulated distribution.

In [17]:
```
X = np.array([176, 163, 152, 155, 156, 178, 160, 164, 169, 155, 122, 144])
Y = np.array([168, 215, 172, 200, 191, 197, 183, 174, 176, 155, 115, 163])
```

In [18]:
```
pd.DataFrame({"X": X, "Y": Y}).plot.hist(bins=20, alpha=0.3)
```

Out[18]:
```
<AxesSubplot:ylabel='Frequency'>
```



In [19]:
```
alpha = 0.05
```

In [20]:
```
res = sts.wilcoxon(X, Y)
print("Rejected" if res.pvalue < alpha else "Not rejected")
```

```
Rejected
```

```
/Users/nickstulov/.virtualenvs/msai/lib/python3.8/site-packages/scipy/stats/morestats.py:3141: UserWarning: Exact p-value calculation does not work if there are ties. Switching to normal approximation.
  warnings.warn("Exact p-value calculation does not work if there are "
```

Multiple testing

Multiple testing

Probability of making a mistake in one of k tests with α confidence level:

$$1 - (1 - \alpha)^k$$

In [22]:
```
alpha = 0.05
print(1 - (1 - alpha) ** 10)
print(1 - (1 - alpha / 10) ** 10)
```

```
0.4012630607616213
0.048889869534228136
```