# Probability & Statistics

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## Overview

- Statistics is the lifeblood of data science
  - You need to learn how to use statistics
  - But the calculations are implemented in two powerful Python modules
    - scipy.stats
    - statsmodels

# Probability

- We concentrate on categorical data
  - Categorical data is discrete: e.g. "not infected", "infected, but no symptoms", "sick", "recovered", "dead"
  - Categorical data can be ordinal :
    - number of cases in Milwaukee County
  - Categorical data can be nominal :
    - Republican, Democrat, Other, Non-affiliated

## Probability Distributions for Categorical Data

- Binomial distribution:
  - Given a binary characteristic (yes/no) and a sample / population of n what is the probability that i have the characteristics
  - If we assume that the presence of the characteristic in one individual is independent of the characteristic of another individual

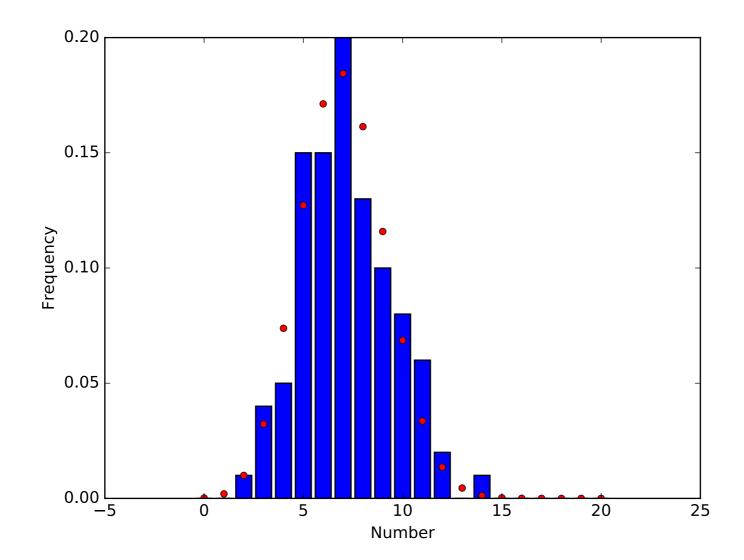
$$p_{binom}(y, n, \pi) = \frac{n!}{y!(y-n)!} \pi^{y} (1-\pi)^{(n-y)}$$

- Let's run an experiment:
  - Select an element of a population with probability p
  - Count how many population member are selected
  - Then normalize to get the probability that x members are selected

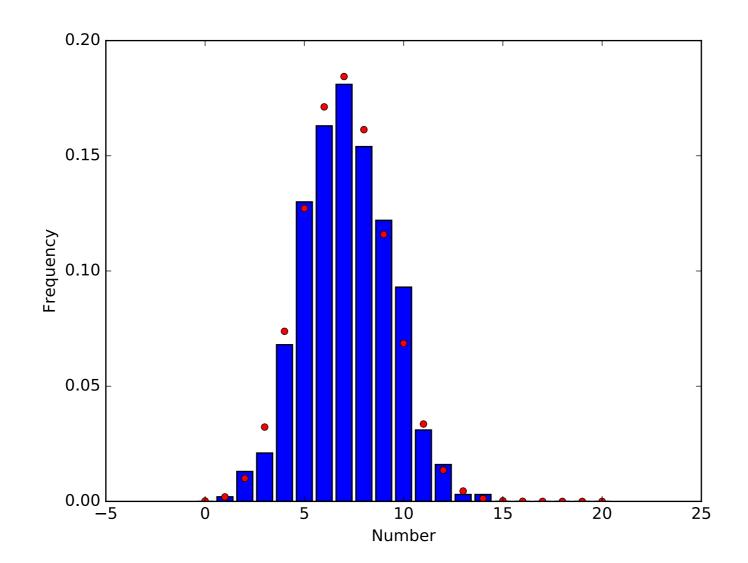
- Then compare with the binomial probability
  - binom.pmf is the probability mass function  $\binom{n}{k} p^k (1-p)^{n-k}$

```
from scipy.stats import binom
results = run_trials(runs, pop_size, p)
xvalues = np.arange(0, len(results))
binom.pmf(xvalues,pop_size, p)
```

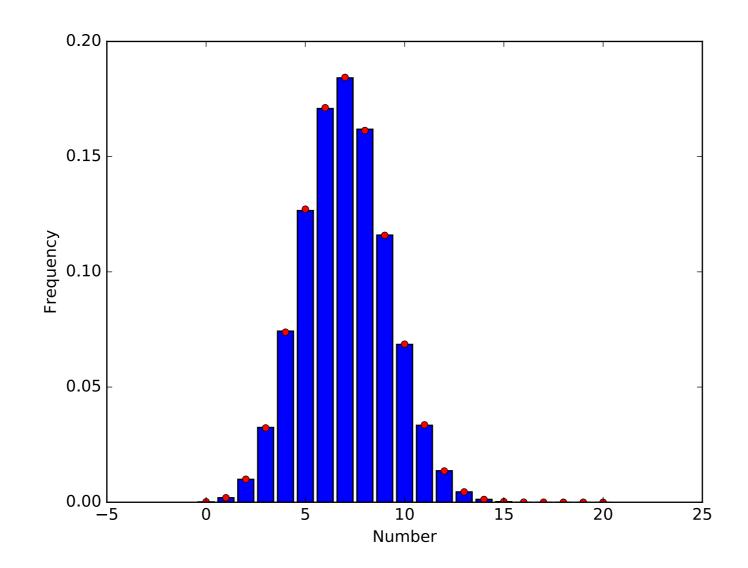
• 100 runs : Prediction and experimental results differ



• 1000 runs: getting better



• 1,000,000 runs



## Morale

• Small numbers means large uncertainty

- For obtaining probabilities experimentally:
  - Need to
    - Estimate confidence
      - Otherwise, you do not know how significant your results are and cannot distinguish between casuality and causality
    - Use enough samples

## Likelihood Estimation

- Problem: Given data, can we say something about the underlying probability distribution
  - Thought experiment: Throw a fair coin 10 times
    - HHHHHHHHH is equally likely than HHTTHTTHHT
    - Why do we think the first one is fishy and the second one not?
    - We use a statistics (number of heads) and assume that coin is fair
    - Observing 10 heads has probability  $2^{-10} = 0.0009765625$ 
      - Observing 5 heads and 5 tails has probability  $\binom{10}{5}(\frac{1}{2})^5(\frac{1}{2})^5 = 0.24609375$

## Likelihood Estimation

- Reversely
  - Given a sample and a putative probability  $\pi$
  - Likelihood:
    - What is the probability given  $\pi$  to observe a statistics on the sample

## Likelihood Estimation

- Assume a binominally distributed random variable
  - How do we estimate  $\pi$  from a sample?
    - Likelihood: Given  $\pi$ , what is the chance to observe what we have seen
    - Observed: *x* out of *n*
    - Probability that this happens is  $\mathscr{L}(x:\pi) = \frac{x!(n-x)!}{n!} \pi^{x} (1-\pi)^{(n-x)}$

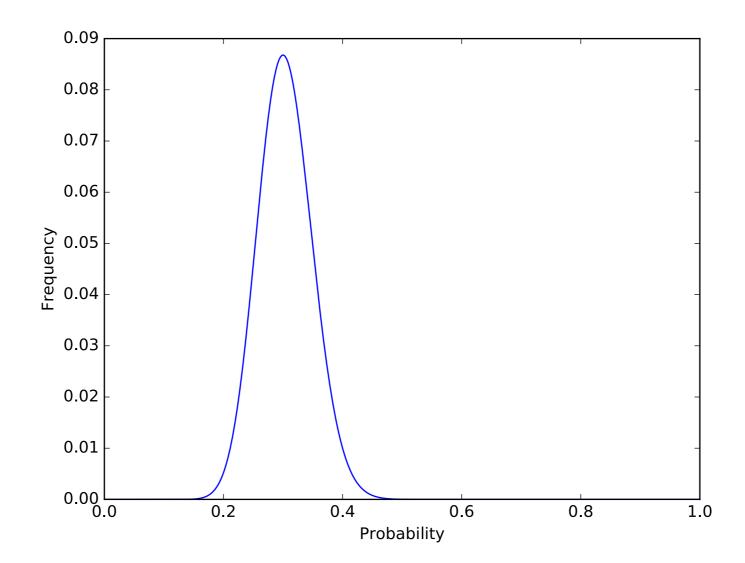
• Example: observed 30 out of 100

```
def likelihood(x, pop_size):
    prob = np.linspace(0,1,1000)
    likelihood = binom.pmf(x, pop size, prob)
```

```
fig = plt.figure()
ax = plt.axes()
```

```
ax.set_xlabel("Probability")
ax.set_ylabel("Frequency")
ax.plot(prob, likelihood)
fig.savefig("{}{}.pdf".format(x,pop size))
```

• Example: observed 30 out of 100



## **Binomial Distribution**

- Likelihood is maximized for  $\pi = 30/100$
- Formally:

•  $\mathcal{L}(x:p) \to \max$ 

- const  $\cdot p^{x}(1-p)^{(n-x)} \to \max$
- which implies by differentiation that
  - $xp^{x-1}(1-p)^{n-x} (n-x)p^x(1-p)^{n-x-1} = 0$

• 
$$x(1-p) = (n-x)p$$

• 
$$p = \frac{x}{n}$$

## **Binomial Distribution**

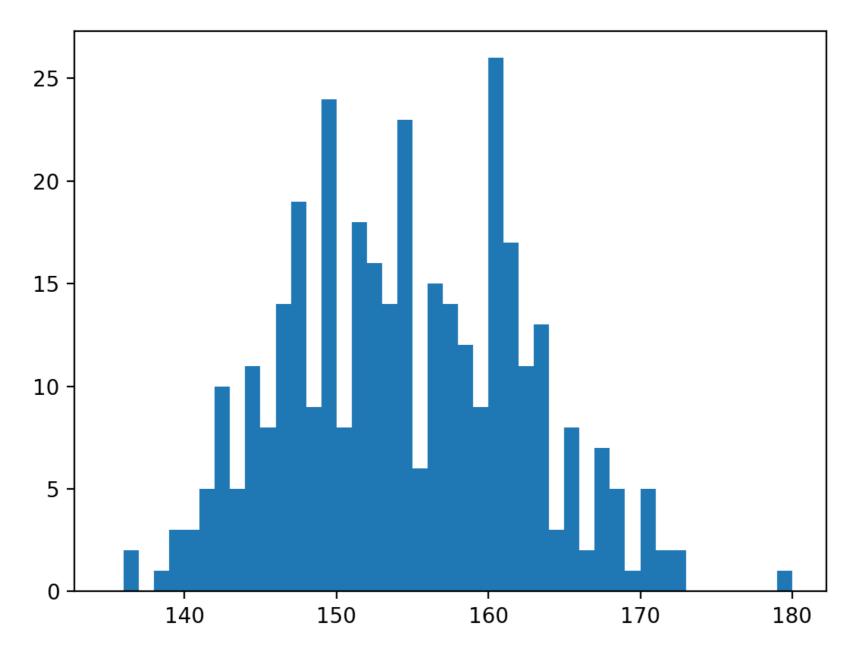
 Therefore: Maximum Likelihood estimator for π given x out of n observations is

 $-\frac{x}{n}$ 

## Getting Statistics

# First Step : Visualize

• Example: Heights



# Second Step: Get Stats

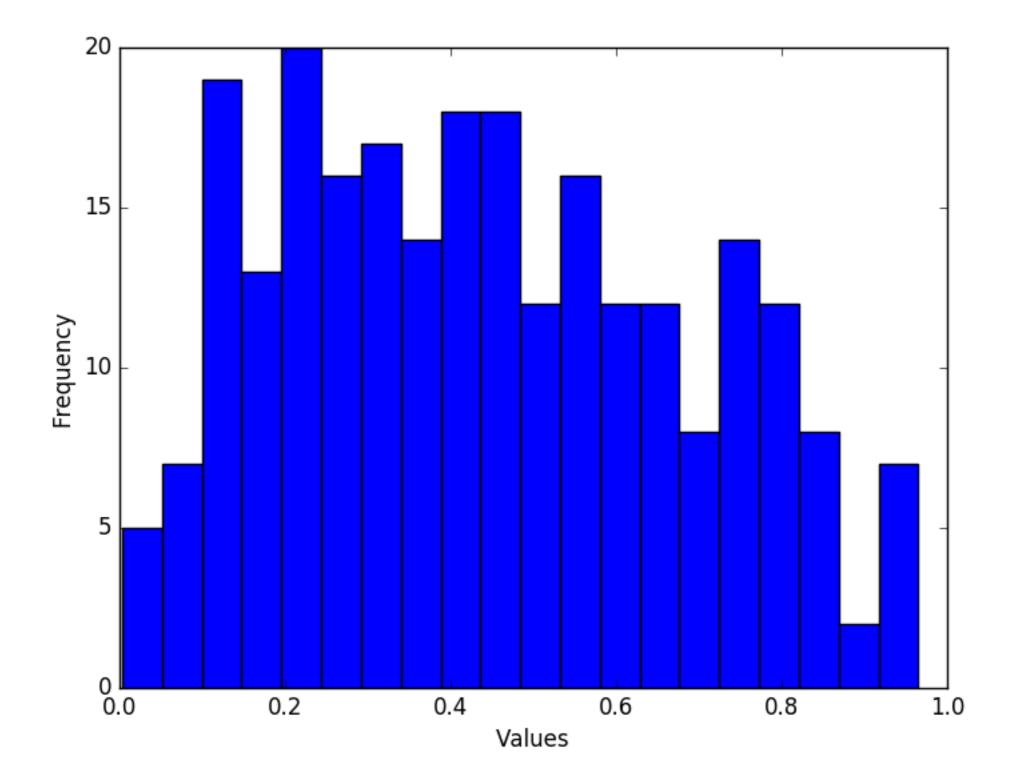
- Statistic: any type of measure taken on a sample
- Implemented in scipy.stats
- Random number generation in np.random

# Sample Generation

- Use np.random
  - Returns samples for many different distributions
    - E.g.
      - np.random.normal(mean, std, size=1000)
      - np.random.gamma(shape, scale, size=1000)
  - Can use numpy.random.seed(12345)to insure same behavior

- Use scipy.stats
- Has many different distributions
  - scipy.stats.norm is a distribution object
    - Has a pdf, a cdf, ...

```
def stats():
   np.random.seed(6072001)
    sample1 = create beta(alpha = 1.5, beta = 2)
    fig = plt.figure()
    ax = plt.axes()
    ax.set xlabel("Values")
    ax.set ylabel("Frequency")
    ax.hist(sample1, bins = 20)
    fig.savefig('beta15 2')
    print(f'mean is {np.mean(sample1)}')
    print(f'median is {np.median(sample1)}')
    print(f'25% quantile is {scipy.stats.scoreatpercentile(sample1,25)}')
   print(f'75% quantile is {scipy.stats.scoreatpercentile(sample1,75)}')
    print(f'st. dev. is {np.std(sample1)}')
    print(f'skew is {scipy.stats.skew(sample1)}')
    print(f'kurtosis is {scipy.stats.kurtosis(sample1)}')
```



• Many statistical descriptors are available:

mean is 0.44398507464612896
median is 0.42091200120073147
25% quantile is 0.2421793406556383
75% quantile is 0.6277333146506446
st. dev. is 0.24067438845525105
skew is 0.24637036296183917
kurtosis is -0.933113268968349

- Can also fit to distributions
  - Example: Height data
    - Use norm.fit

```
from scipy.stats import norm
pop1 = np.array([151.765, 156.845, 163.83, 168.91,
165.1, 151.13, 163.195, 157.48, 161.29, 146.4,
147.955, 161.925, 160.655, 151.765, 162.8648,
171.45, 154.305, 146.7, ...
```

loc, std = norm.fit(pop1)

- To display the data:
  - Create bins for a histogram

```
bins = np.linspace(135, 180, 46)
```

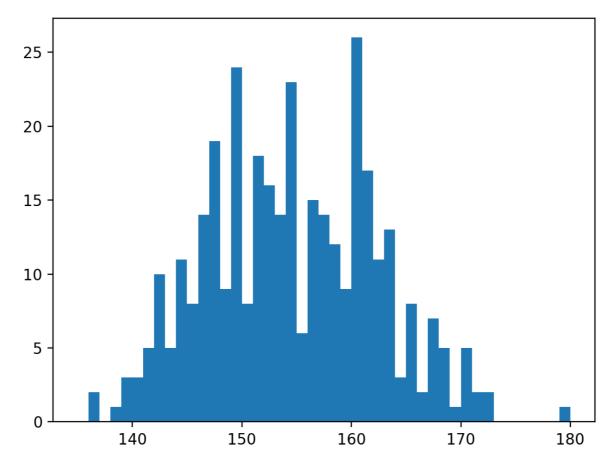
• We need the centers later on

Numpy has a function that calculates a histogram

dt = np.histogram(pop1, bins)[0]

dt contains the number of elements in a bin

3 3 5 10 5 11 8 14 19 9 24 0 1 16 14 23 6 15 14 12 9 26 17 11 13 1 5 2 2 1]



 We now determine mean and standard deviation using the fit function

loc, std = norm.fit(pop1)
print(loc, std)

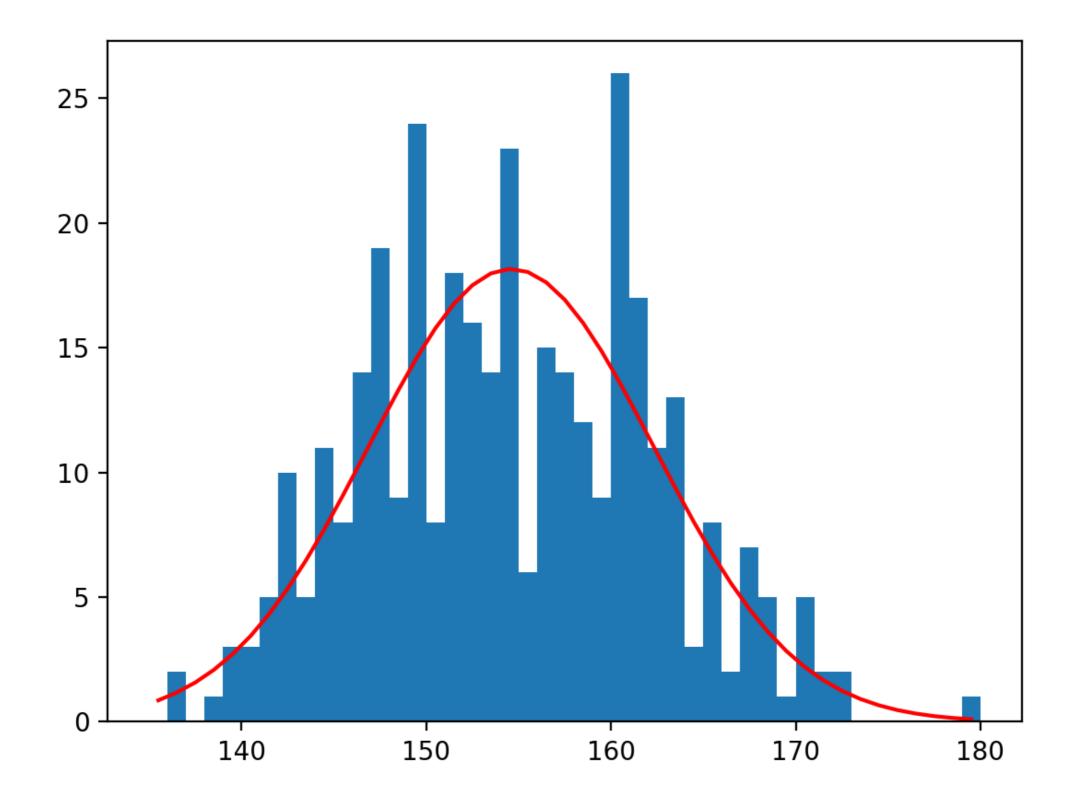
• We could do the same using np.mean and np.std

 We now create a normal distribution object with this mean and this standard deviation

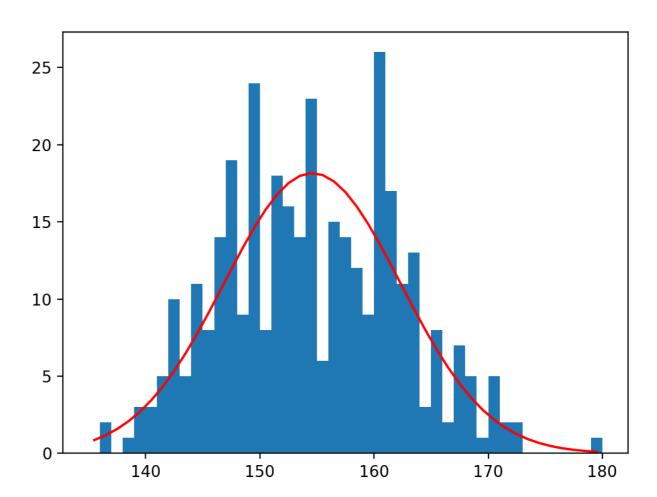
pdf = norm(loc, std).pdf

- Now, we draw both the histogram and the pdf
  - The pdf has an integral of 1, so we multiply with the number of elements in the population

```
plt.figure()
plt.bar(binscenter, dt, width = bins[1]-bins[0])
plt.plot(binscenter, len(pop1)*pdf(binscenter),'red')
plt.show()
```



- Question:
  - Does the red curve fit the blue?
  - Visual inspection is inconclusive
  - So, we use statistical tests



### **Statistical Tests**

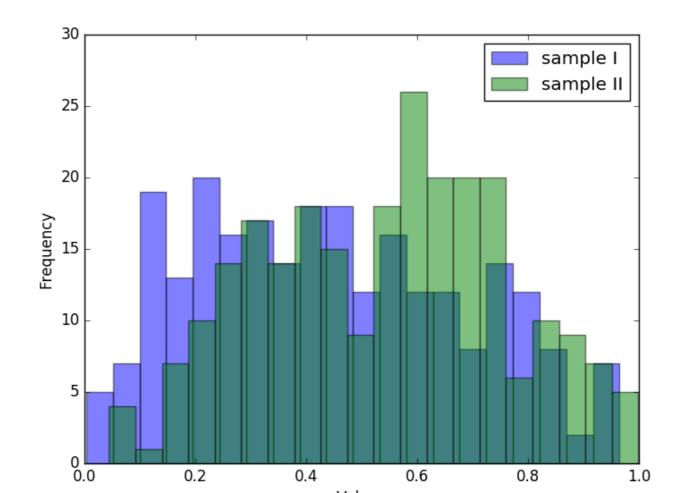
## **Statistical Tests**

- Statistical test calculates a value the test statistics from a sample in order to refute or confirm a hypothesis
  - Formulate a null hypothesis
    - This is usually the boring stuff: two samples from the same distribution, mean is where it is expected to be, ...
  - Calculate the probability that the observed statistics or a more significant result has occurred given the null hypothesis
  - If the probability is small: reject the null hypothesis

## **Statistical Tests**

- Alpha measures the confidence as  $\alpha = 1 \text{confidence}$ 
  - Typical are  $\alpha = 0.05, \ \alpha = 0.01$
- Critical value point at which we start rejecting the null hypothesis
- P-value probability of the observed outcome (or something more significant) under the null hypothesis
- We reject if the p-value is below  $\alpha$
- WARNING: while used, this is somewhat controversial among statisticians

- Create two samples,
  - Beta distributed with  $\alpha = 1.5$  and  $\beta = 2$
  - Normally distributed with  $\mu = 0.5$  and  $\sigma = 0.25$



- To test whether two means are equal:
  - z-test: Assumes two normally / Gaussian distributions with same standard deviation
  - Zero Hypothesis: The means are equal

• z-score is 
$$z = \frac{x - \mu}{\sigma / \sqrt{n}}$$

- Use statsmodels
- WARNING: population should be at least 30

#### • Example:

print('z-score\n',
statsmodels.stats.weightstats.ztest(sample1, x2=None,
value = 0.5))

• Result:

z-score

(-3.672599393379993, 0.00024009571884724942)

• Again, reject zero hypothesis

• Compare the two samples

```
statsmodels.stats.weightstats.ztest(
    sample1,
    sample2,
    value = 0,
    alternative='two-sided'
)
z-score
```

(-4.611040794712781, 4.0065789390516926e-06)

- Student t-test:
  - Assumes Gaussian distribution
  - Works for different variances
  - Can use for smaller samples

• Example: One sample t-test

print(scipy.stats.ttest\_1samp(sample1, 0.5))

Ttest\_1sampResult(statistic=-3.672599393379993, pvalue=0.0002938619482386932)

• Two sample t-test

print(scipy.stats.ttest\_ind(sample1, sample2))

Ttest\_indResult(statistic=-4.611040794712781, pvalue=5.0995747086364474e-06)

• This is just a sample of important tests

- It is much safer to talk with a statistician than drawing conclusions yourself
  - Python makes sure that you make no calculational errors
  - But it cannot assure that you are using the right test
    - E.g. you might be making an assumption that is not warranted
  - Also: interpreting confidence levels is not so simple
    - $\alpha = 0.01$  still means 1% of your results draw the wrong conclusion

- Experiments to measure effects of causes on outcomes
- Example:
  - Test two machine learning algorithm on ten data sets
    - Can we say that classifier 2 is better or could this be chance?

	Correct	Incorrect	Totals
Classifier 1	6	4	10
<b>Classifier 2</b>	5	5	10
Totals	11	9	

- Other example: treatment versus control
  - Does Aspirin help against cardiovascular disease (1988)

	myocardial infarction	none	total
Placebo	189	10845	11034
Aspirin	104	10933	11037
Total	293	21778	

- Usually have
  - explanatory variables (Aspirin)
  - response variables (Disease)

- Type I error:
  - We report an effect when there is none
- Type II error:
  - We do not report an effect even though there is one

- There are many possible statistics
  - More, if the number of observations is high

<ul> <li>Number of different statistical tests</li> <li>Built into statsmodels</li> </ul>			myocar infarcti	non	e total
		Placebo	189	1084	5 11034
		Aspirin	104	1093	3 11037
		Total	293	2177	'8
	Estimate	SE	LCB	UCB ]	p-value
Odds ratio Log odds ratio Risk ratio Log risk ratio	1.818	0.123 0.121	1.433	0.846	0.000 0.000 0.000 0.000

	Odds:		myocardial infarction	none	total
•	Ouus.	Placebo	189	10845	11034
	189	Aspirin	104	10933	11037
	If we take a placebo odds are —	Total	293	21778	
	• In the tarks a placebe, state and 10845				
		04 933			

- The statistic looks at the ratio of the odds:  $\theta = \frac{189 \cdot 10933}{104 \cdot 10845} = 1.832$
- If there would be no influence, then we expect  $\theta = 1$ .

- Log odds
  - The statistics for odds are heavily skewed
  - Easier to use  $\log(\theta)$  which can be approximated with a normal distribution

- Relative risk
  - $\pi_1$  probability of success for group one
  - $\pi_2$  probability of success for group two

• Relative risk is 
$$\frac{\pi_1}{\pi_2}$$

• Depends on how we define success because in general  $\frac{\pi_1}{\pi_2} \neq \frac{1-\pi}{1-\pi_2}$ 

• Example:		myocardial infarction	none	total
	Placebo	189	10845	11034
<ul> <li>Estimate relative risk from observations</li> </ul>	Aspirin	104	10933	11037
	Total	293	21778	
• $\tau = \frac{189/11034}{104/11037} = 1.817802$				

• Again, log of risk is easier to approximate

- statsmodels.Table2x2 gives all four values together with a p-value
- The risk and log risk ratio statistics are not symmetric, so by transposing, you get different values

import numpy as np import matplotlib.pyplot as plt from statsmodels.stats.contingency\_tables import Table2x2

ct = Table2x2([ [25, 280], [45, 405]])
print(ct.summary())

	Estimate	SE	LCB	UCB	p-value
Odds ratio Log odds ratio	0.804		0.482 -0.731		0.403 0.403
Risk ratio	0.820		0.514	1.307	0.404
Log risk ratio	-0.199	0.238	-0.666	0.268	0.404

- For small samples, we should use Fisher's exact test
  - If there is no influence of the explanatory variables, then the numbers in the cells are distributed according to a hyper-geometric distribution
  - With Python, we can apply this even to larger samples
- Use fisher\_exact in scipy.stats

• Calling Fisher's exact method

```
scipy.stats.fisher_exact(table))
```

• Output is value of the statistics and the p-value

(1.8320539419087136, 5.032835599791868e-07)

 Again, we conclude that the difference between Aspirin and Placebo are unlikely to have happened by chance

	Lung Cancer Cases	Controls
Smoker	688	650
Non-smoker	21	59

			Lung Can	cer Cases	Co	ontrols		
	Smoker		6	88		650		
	Non-smoker		21			59		
		Est	imate	SE	LCB	UCB	p-va	lue
Log c Risk	ratio odds ratio ratio isk ratio		1.959		0.580	2.839	0.	000 000 000 000

\_\_\_\_\_\_

	<b>Right Handed</b>	Left Handed
Male	43	9
Female	44	4

	Estimate	SE	LCB	UCB	p-value
Odds ratio Log odds ratio Risk ratio Log risk ratio	-0.834 0.902	0.638	0.124 -2.084 0.776 -0.254	0.417 1.049	0.191 0.191 0.181 0.181

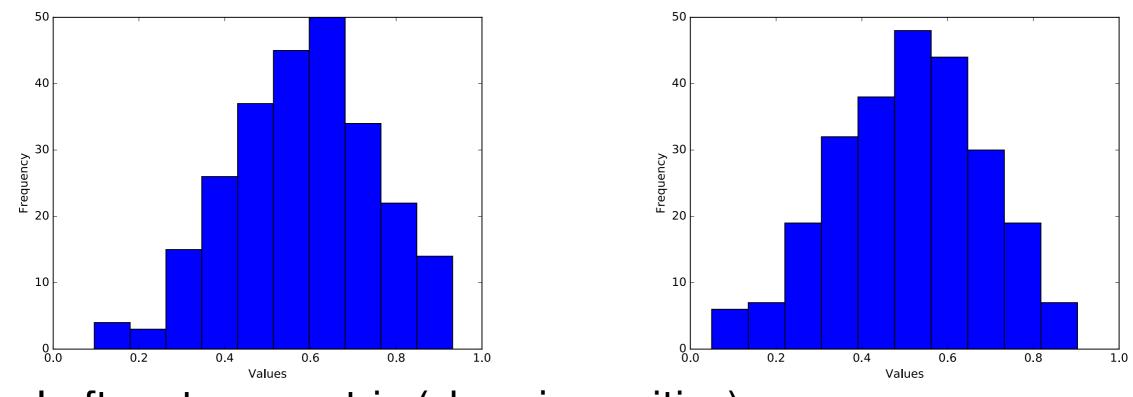
#### **Testing for Normality**

- A large number of models assume that data is or close to normally distributed
  - If data comes from normal distribution:
    - Lots of statistical tricks available
  - If data comes from another distribution:
    - Maybe use "non-parametic" methods
- Use tests to determine whether a given set of data is likely to come from a normal distribution
- Step 1:
  - Use a histogram or scatter-plot of the data

- I created two arrays of length 250
  - With my birth date as the seed for reproducability
- First, I create histograms (with default settings)

```
def show(array, name):
    fig = plt.figure()
    ax = plt.axes()
    ax.set_xlabel("Values")
    ax.set_ylabel("Frequency")
    ax.hist(array)
    fig.savefig(name)
```

• Results are:



- Left: not symmetric (skew is positive)
- Right: shape does not look quite right (kurtosis)

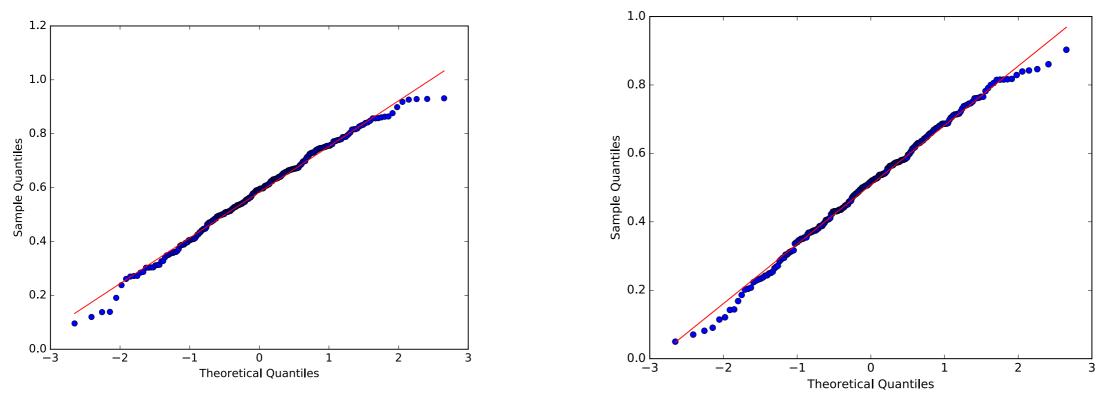
- Quantile-Quantile Plot
  - Quantile q: Proportion q of the data set fall below the point
  - Example: 30% or 0.3 quantile: 30% of the points are below, 70% of the points are above
- Plot two data-sets to compare whether they come from the same distribution
- Plot one data-set. If linear: suggests normal distribution

- QQ-Plot part of statsmodels package
  - Used with numpy, scipy, or pandas and pyplot

import statsmodels.api as sm

- def showqq(array, name):
   fig = sm.qqplot(np.array(array), line='s')
   fig.savefig(name)
  - line will draw a 45° line to compare with normal distribution

• Results:



Some outliers are normal

- Statistical tests:
  - Takes data and calculates a test statistics
    - Calculates the probability of the test value assuming that a null hypothesis is true
    - If the probability is too small, concludes that the null hypothesis is false
  - In Scipy:
    - Null hypothesis: "Distribution is normal"
    - Returns a p-value
    - If p-value is smaller than  $\alpha$  : reject the Null Hypothesis, otherwise see it supported by data

• Shapiro Wilk Test:

Calculates a test statistics  $W = \frac{(\sum_{i=1}^{n} a_i x_i)^2}{\sum_{i=1}^{n} (x_i - \bar{x})^2}$ 

where  $x_i$  ordered sample values

 $a_i$  constants from covariance, variance, mean of sample

- For small samples, not so good
- W-distribution is calculated via Monte-Carlo simulation

- Use scipy.stats.shapiro
  - Input is the data
  - Output is the W-value and the p-value

```
import scipy.stats
```

```
def getshapiro(array):
    return scipy.stats.shapiro(array)
```

• Results:

(0.9899240732192993, 0.08035389333963394) (0.9923275709152222, 0.22104869782924652)

• Looks valid, normalcy cannot be rejected at the 0.05 level

- D'Agostino's  $k^2$  test:
  - Looks at skew and curtosis of the normal distribution
  - Implemented in scipy.stats as normaltest

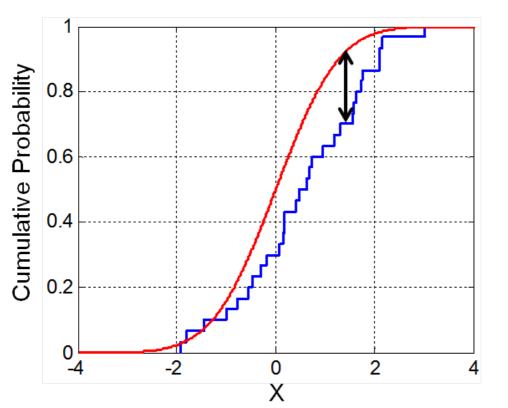
def get\_dagostino(array):
 return scipy.stats.normaltest(array)

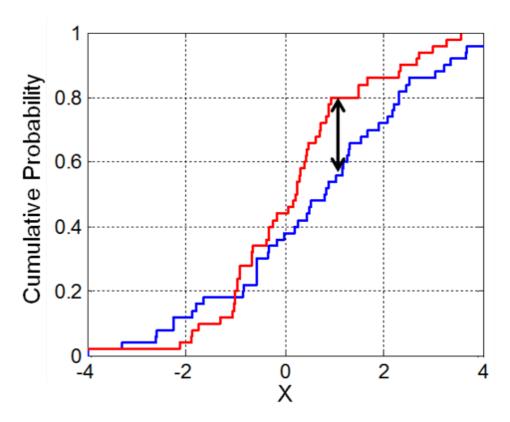
#### • Results:

statistic=3.7394424212691764, pvalue=0.15416663584307644
statistic=2.821146323808743, pvalue=0.24400338961897727)

• Null hypothesis cannot be rejected

- Anderson Darling
  - Comes from the Kolmogorov Smirnov test
    - KS tests for the distance between the cumulative probability of two samples or one sample with a reference distribution



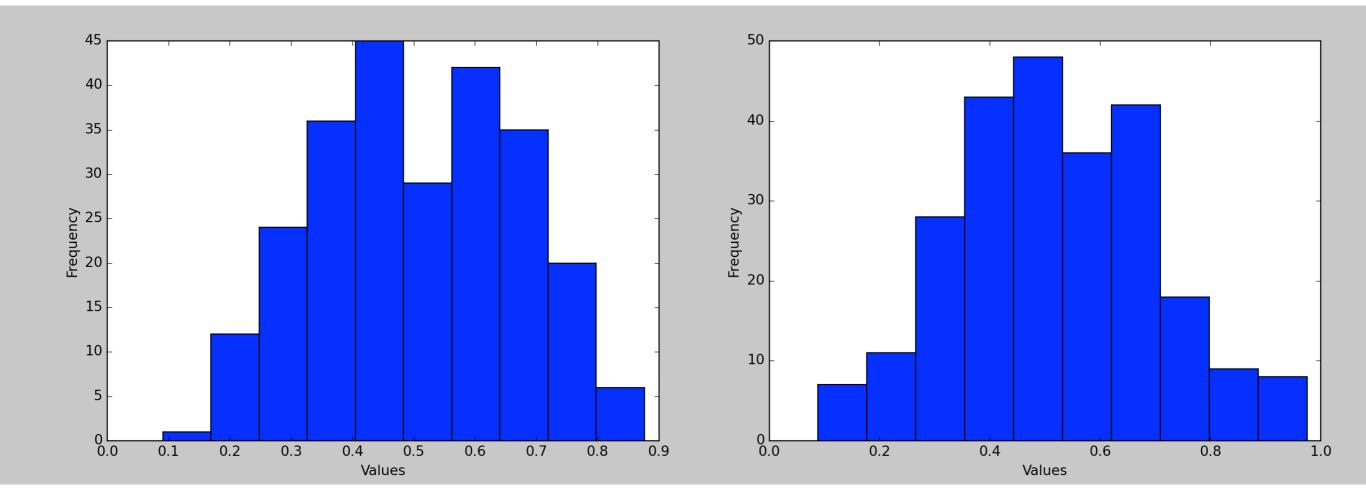


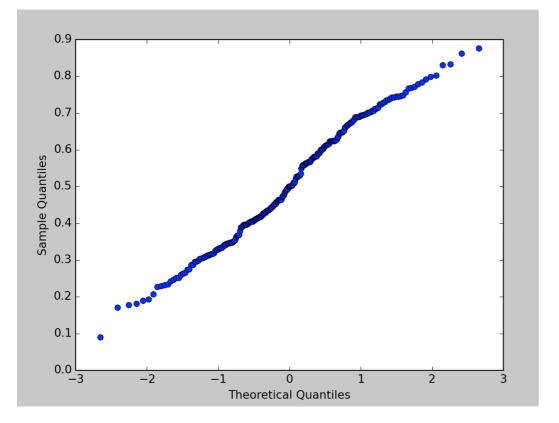
- Prints out statistics with different significance levels

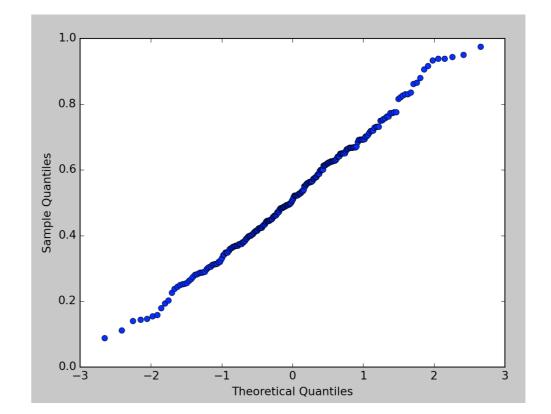
Anderson Darling: AndersonResult(statistic=1.998061561955467, critical\_values=array([0.567, 0.646, 0.775, 0.904, 1.075]), significance\_level=array([15., 10., 5., 2.5, 1.])) Anderson Darling: AndersonResult(statistic=1.0717930773325293, critical\_values=array([0.567, 0.646, 0.775, 0.904, 1.075]), significance\_level=array([15., 10., 5., 2.5, 1.]))

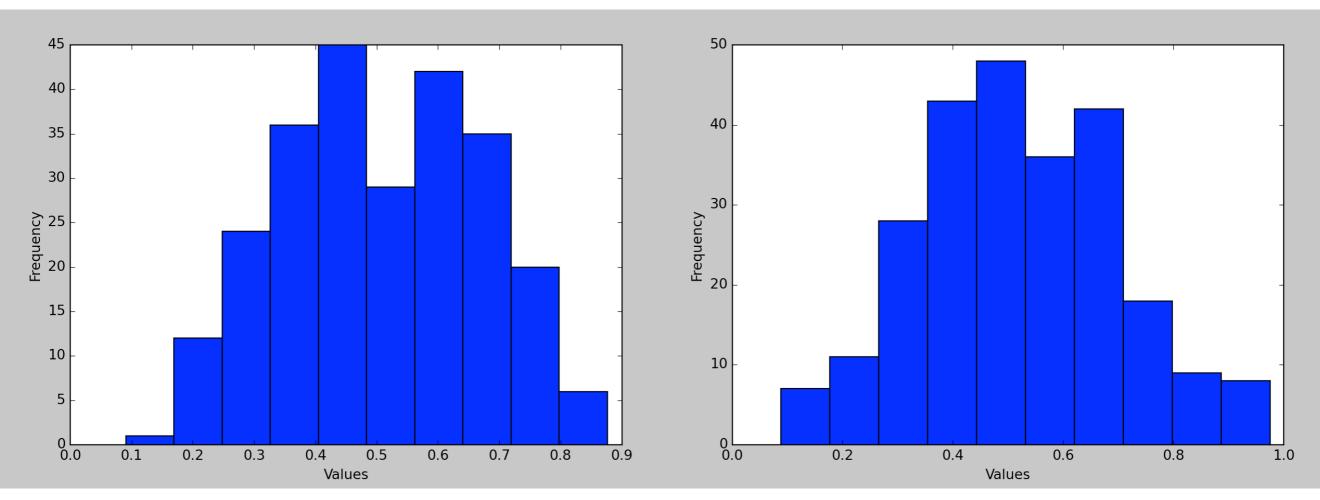
 Sample 2: the two statistics are smaller than the critical values and the null hypothesis cannot be rejected

- Sample 1 was however **not** normally distributed
- Sample 2 was generated with a cut-off normal distribution that prevented samples below 0 and above 1
- This is typical, there was insufficient information to reject the thesis of normality





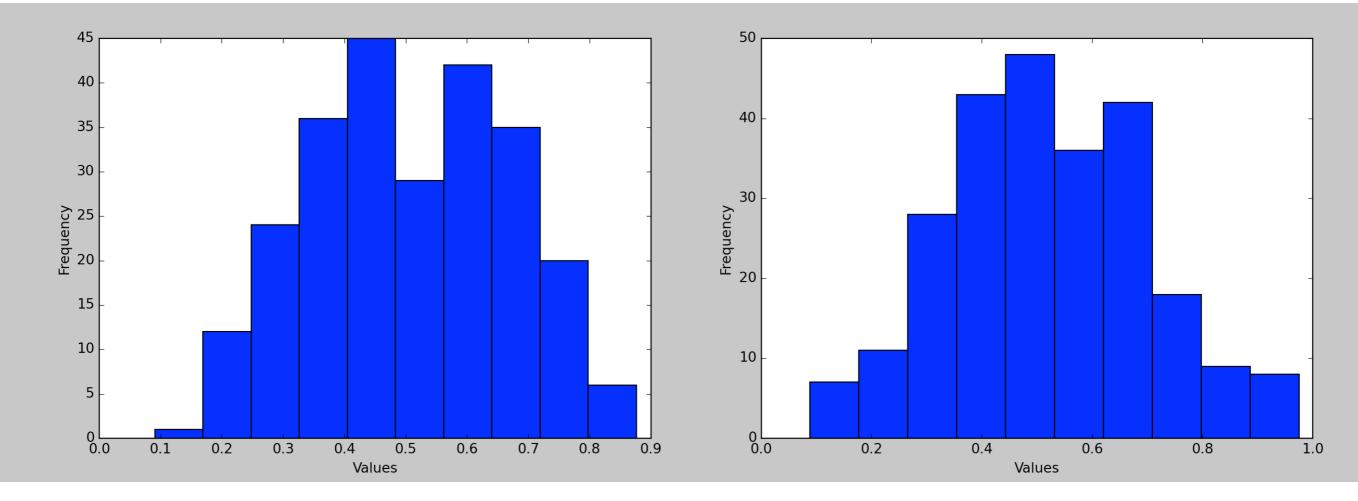




Shapiro Wilk

pvalue=0.005319

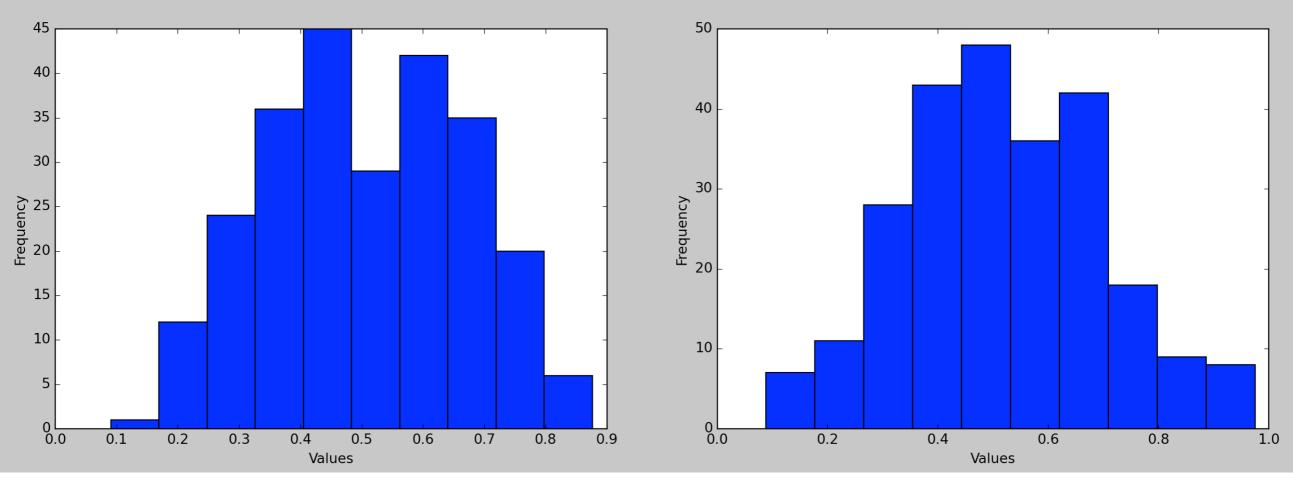
pvalue=0.2683



d'Agostino:

p-value 2.944 e -05

p-value 0.346



Anderson Darling

statistic=1.3877,

statistic=0.3377

critical\_values= 1.075,
1% significance

#### Limitations

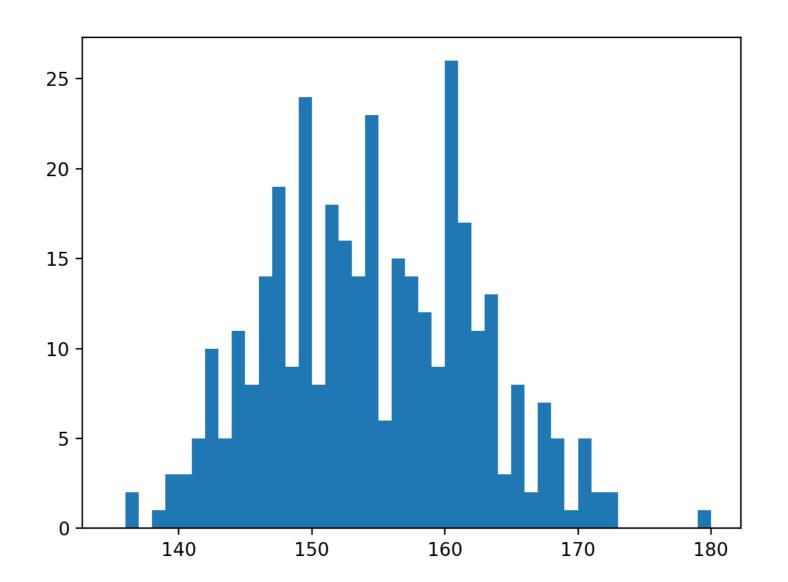
#### Limitations

- With a p value of 0.05, one in twenty tests is likely to give us a false positive
- Rate of false negatives is also around that

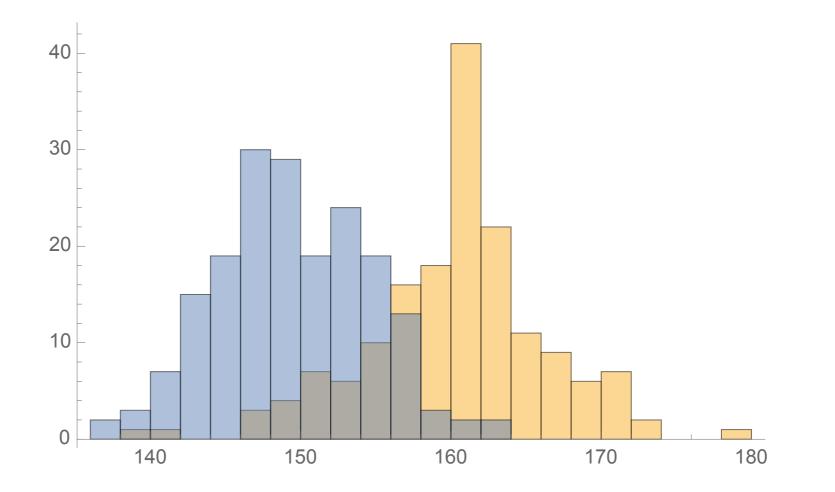
#### Limitations

 Not being able to reject the zero hypothesis does not mean that the hypothesis is wrong

• Height data



- Gender is an important factor for height
- If we know the heights, the distribution looks more normal

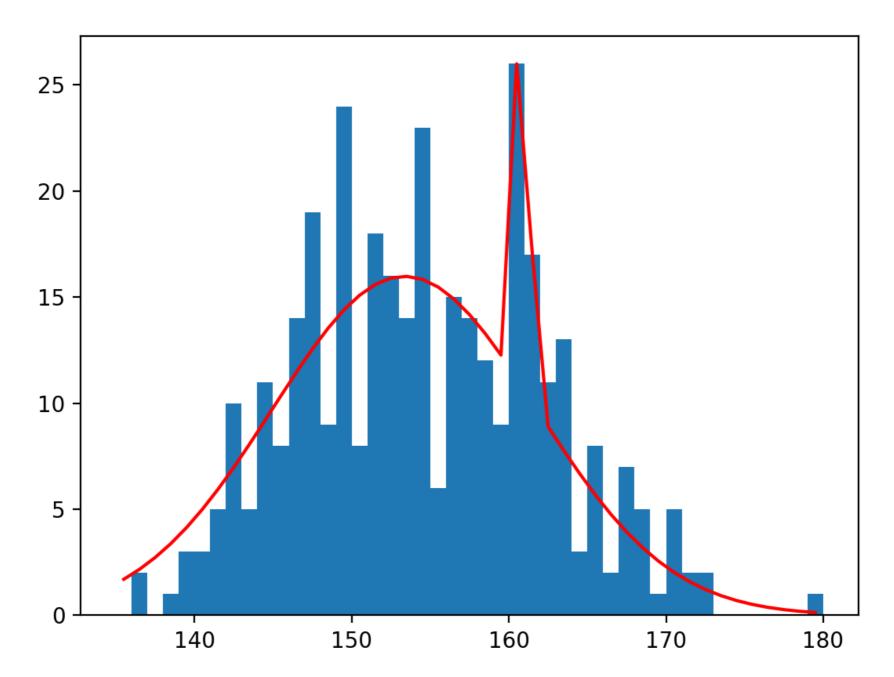


- When we apply normality tests:
  - Female is normally distributed
  - Male is not normally distributed according to Anderson
  - Complete population is normally distributed

- Can we recover the two distributions?
  - Let's try to fit a combination of two normal distributions to the binned data
- def func(t, a, b, m1, s1, m2, s2):
   return a\*norm(m1, s1).pdf(t) + b\*norm(m2, s2).pdf(t)

plt.figure()
plt.bar(binscenter, dt, width = bins[1]-bins[0])
plt.plot(binscenter, func(binscenter, \*params),'red')
#plt.plot(binscenter, len(pop1)\*pdf(binscenter),'red')
plt.show()

• Spectacular failure



### Conclusions

- Numpy has a very broad selection of random number generators
- Scipy.stats has a very good set of implementations for many standard statistical tests
  - Which cannot overcome limitations in the data

## Readings

• Scipy Lecture notes p.195ff