# Probability & Statistics

Thomas Schwarz, SJ

#### 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

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

- Let's run an experiment:
  - Select an element of a population with probability p
  - Count how often a population member is selected
  - Then normalize

```
def run_trials(runs, pop_size, p):
    results = np.zeros((pop_size+1))
    for _ in range(runs):
        seen = len([x for x in np.random.rand(pop_size)
        if x < p])
        results[seen]+=1
        return results/runs</pre>
```

- 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



## 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  $\mathscr{L}(x:p) = \frac{x!(n-x)!}{n!} \pi^{x} (1-\pi)^{(n-x)}$

• 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()
```



- 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

- 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

- 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     |
| Classifier 2 | 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</li> </ul>                      |                                  |                | myocaro<br>infarcti              | dial no<br>on                    | ne          | total                            |  |
|--------------------------------------------------------------|----------------------------------|----------------|----------------------------------|----------------------------------|-------------|----------------------------------|--|
| Statistical tests                                            |                                  | Placebo        | 189                              | 108                              | 45          | 11034                            |  |
| <ul> <li>Built into statsmodels</li> </ul>                   |                                  | Aspirin        | 104                              | 109                              | 33          | 11037                            |  |
|                                                              |                                  | Total          | 293                              | 217                              | 78          |                                  |  |
|                                                              | Estimate                         | SE             | LCB                              | UCB                              | p-1         | value                            |  |
| Odds ratio<br>Log odds ratio<br>Risk ratio<br>Log risk ratio | 1.832<br>0.605<br>1.818<br>0.598 | 0.123<br>0.121 | 1.440<br>0.365<br>1.433<br>0.360 | 2.331<br>0.846<br>2.306<br>0.835 | (<br>(<br>( | 000.0<br>0.000<br>0.000<br>0.000 |  |

|                                                        |         | myocardial infarction | none  | total |
|--------------------------------------------------------|---------|-----------------------|-------|-------|
| • Ouus.                                                | Placebo | 189                   | 10845 | 11034 |
| 189                                                    | Aspirin | 104                   | 10933 | 11037 |
| If we take a placebo, odds are —                       | Total   | 293                   | 21778 |       |
| 10845                                                  |         |                       |       |       |
| • If we do not take a placebo, odds are $\frac{1}{10}$ | 04      |                       |       |       |
| 10                                                     |         |                       |       |       |

- 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 |
|   | • Estimate relative risk from observations        | 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

- 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

#### **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=0.154166635843 statistic=2.821146323808743, pvalue=0.2440033896189

• 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

#### 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