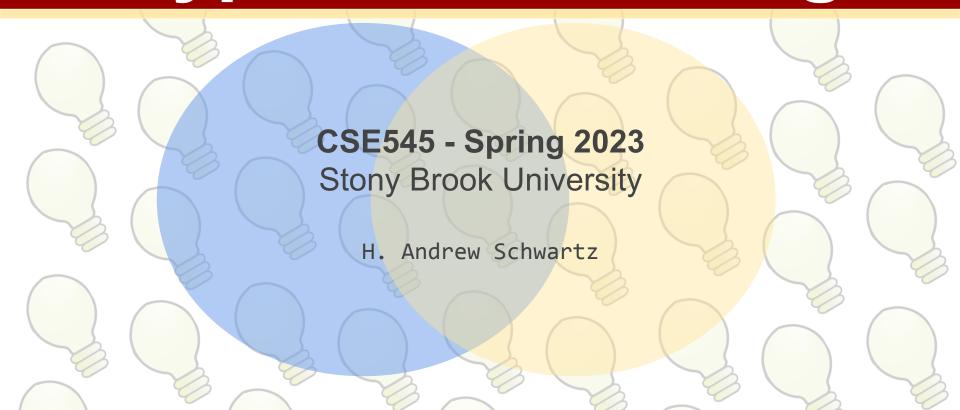
Large Scale Hypothesis Testing



Big Data Analytics, The Class

Goal: Generalizations A *model* or *summarization* of the data.

Data Workflow Systems

Hadoop File System Spark

Streaming

MapReduce Tensorflow

Algorithms and Analyses

Similarity Search Large Scale Hyp. Testing

Link Analysis

Recommendation Systems

Deep Learning

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A model or summarization of the data.

The Data Whisperer

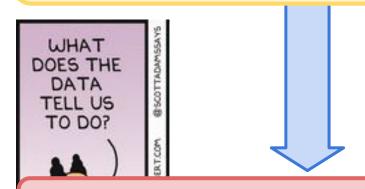
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A model or summarization of the data.





Goal: Generalizations

A *model* or *summarization* of the data.



Data-driven (evidence-based) decision



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A model or summarization of the data.

Discrete Finding(s)

Fis (likely) True



Data-driven (evidence-based) decision

DATA

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A *model* or *summarization* of the data.

Discrete Finding(s)

Fis (likely) True



Data-driven (evidence-based) decision

Blue cell phones cases are selling the most.

The ResImageGenNet model is most accurate.

Those >70 have a greater mortality rate from the viral infection.

DATA

Hypotheses!

Potential findings -- to be tested for happenstance.

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A model or summarization of the data.

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Also known as... "Don't be Dilbert's Boss!"

Hypothesis -- something one asserts to be true.

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Formally, two types:

H_o: null hypothesis -- some "default" value; "null": nothing changes

 H_1 : the alternative -- the opposite of the null => a change or difference

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Thus, we want to know:

Given null, what is the probability of the observation or worse

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H₀: null hypothesis -- some "default" value; "null": nothing changes

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```
observations (i.e. data) level of significance

Input: H<sub>0</sub>, obs, α
```

Output: decision

observations (i.e. data) level of significance

Input: H₀, obs, α

probability of what we observed or worse (i.e. more extreme)

$$p(x)=obs \mid H_{\alpha}$$
) < α

Output: decision

```
Input: H_a, obs, \alpha
if p(x)=obs \mid H_0 > \alpha:
    decision = "Reject H<sub>a</sub>!"
else:
    decision = "Accept H_a."
Output: decision
```

```
Input: H_{\alpha}, obs, \alpha
            Conditional is sometimes evaluated indirectly by first finding the "critical value"
                                 of some measurement such that:
                        if measurement > critical_value then p(obs/HO) < a
if p(x)=obs \mid H_{o} < \alpha:
    decision = "Reject H<sub>a</sub>!"
else:
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Input: H_a, obs, \alpha
if p(x)=obs \mid H_0 > \alpha:
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```
Input: H_{\alpha}, obs, \alpha
                Need to estimate
                                         What is the distribution of values we
                                         would expect if the null was true?
                                         -- the "null distribution"
if p(x)=obs \mid H_0 > \alpha:
    decision = "Reject H<sub>a</sub>!"
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```

X: A mapping from Ω to \mathbb{R} that describes the question we care about in practice.

X is a continuous random variable if it can take on an infinite number of values between any two given values.

X is a discrete random variable if it takes only a countable number of values.

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"sample space", set of all possible outcomes.

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Error of RedImageGenNet Classifier

Amount of sales of a blue case

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X is a *continuous random variable* if there exists a function *fx* such that:

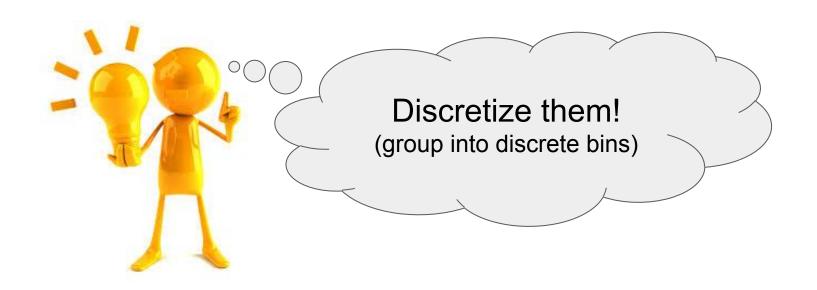
$$f_X(x) \ge 0$$
, for all $x \in X$,
$$\int_{-\infty}^{\infty} f_X(x) dx = 1$$
, and
$$P(a < X < b) = \int_a^b f_X(x) dx$$

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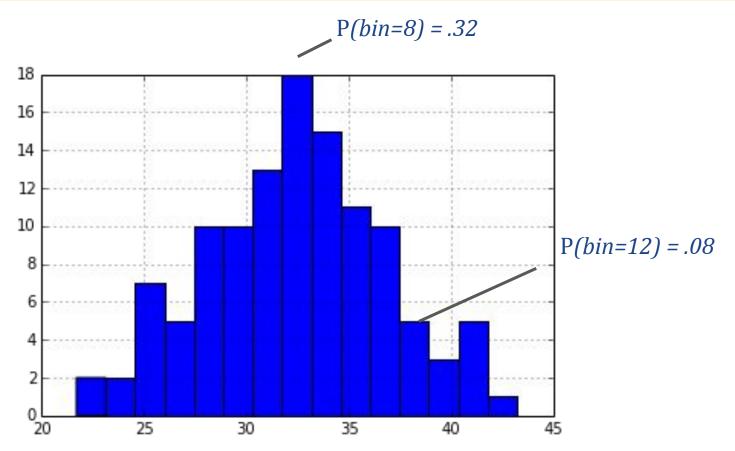
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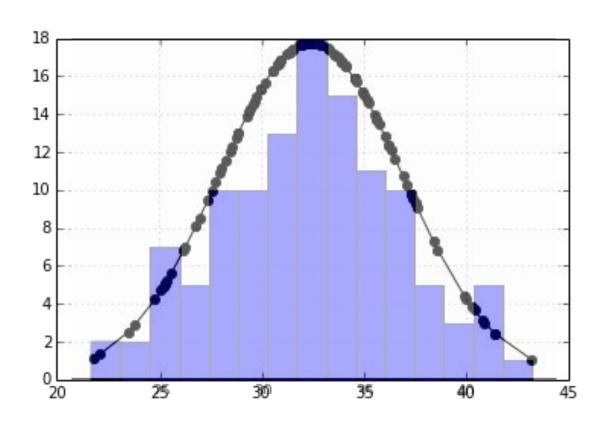
fx: "probability density function" (pdf)

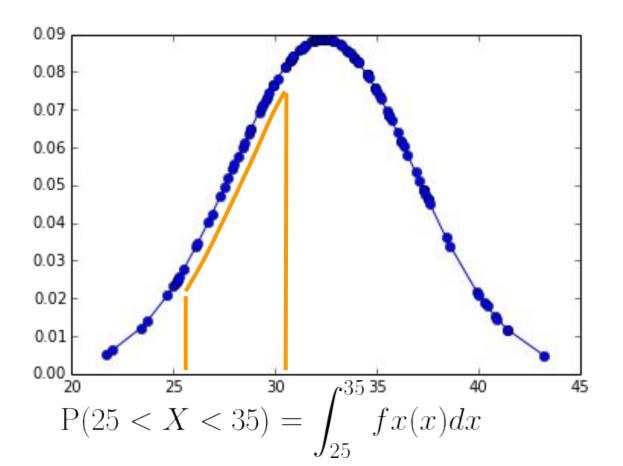


How to model?



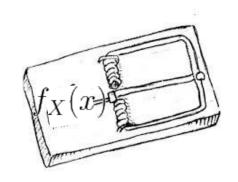
But aren't we throwing away information?





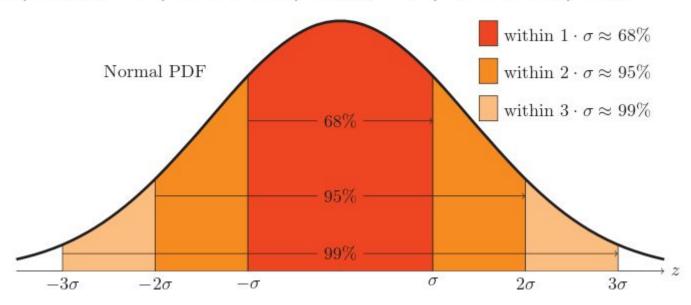
Common Trap

- $f_X(x)$ does not yield a probability
 - $\circ \int_a^b f_X(x) dx$ does
 - \circ *x* may be anything (\mathbb{R})
 - thus, $f_X(x)$ may be > 1



Common *pdf*s: Normal(0, 1)

$$P(-1 \le Z \le 1) \approx .68$$
, $P(-2 \le Z \le 2) \approx .95$, $P(-3 \le Z \le 3) \approx .99$



Common *pdf*s: Normal(0, 1) ("standard normal")

How to "standardize" any normal distribution:

- 1. subtract the mean, μ (aka "mean centering")
- 2. divide by the standard deviation, σ

$$z = (x - \mu) / \sigma$$
, (aka "z score")

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Amount of sales of a blue case

Discrete Random Variables

For a given *discrete* random variable X, *probability mass function (pmf)*, $fx: \mathbb{R} \to [0, 1]$, is defined by:

$$f_X(x) = P(X = x)$$

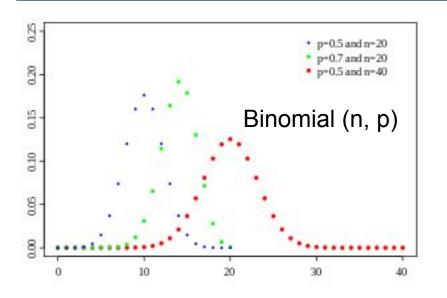
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Was a single sale a blue case: {0, 1}

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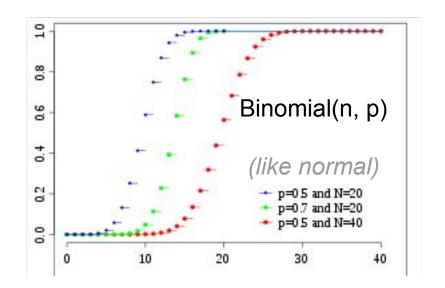
X is a discrete random variable if it takes only a countable number of values.

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Was a single sale a blue case: {0, 1}

For a given random variable X, the cumulative distribution function (CDF), $Fx: \mathbb{R} \to [0, 1]$, is defined by:

$$F_X(x) = P(X \le x)$$



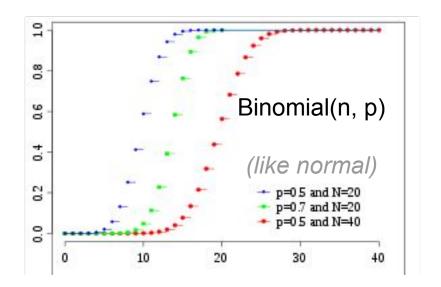
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Amount of sales of a blue case

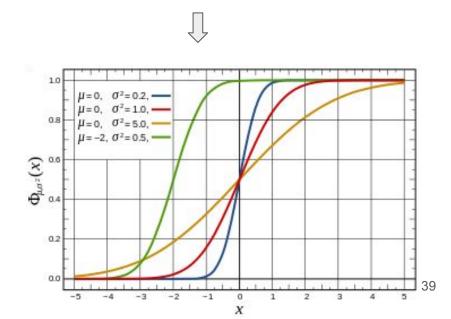
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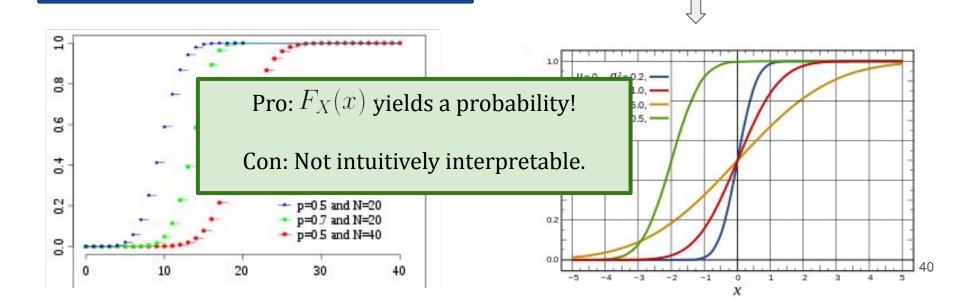
Normal



For a given random variable X, the cumulative distribution function (CDF), $Fx: \mathbb{R} \to [0, 1]$, is defined by:

$$F_X(x) = P(X \le x)$$

Normal



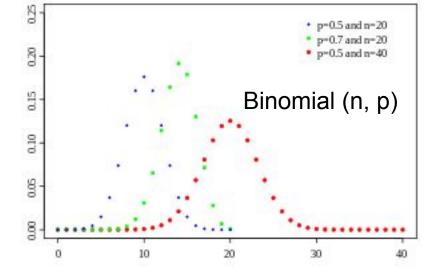
Discrete RVs

For a given random variable X, the cumulative distribution function (CDF), $Fx: \mathbb{R} \to [0, 1]$, is defined by:

$$F_X(x) = P(X \le x)$$

For a given *discrete* random variable X, *probability mass function (pmf)*, $fx: \mathbb{R} \to [0, 1]$, is defined by:

$$f_X(x) = P(X = x)$$



X is a discrete random variable if it takes only a countable number of values.

$$\sum_{i} f_X(x) = 1$$

$$F_X(x) = P(X \le x) = \sum_{x_i \le x} f_X(x)$$

```
Input: H_{\alpha}, observations, \alpha
```

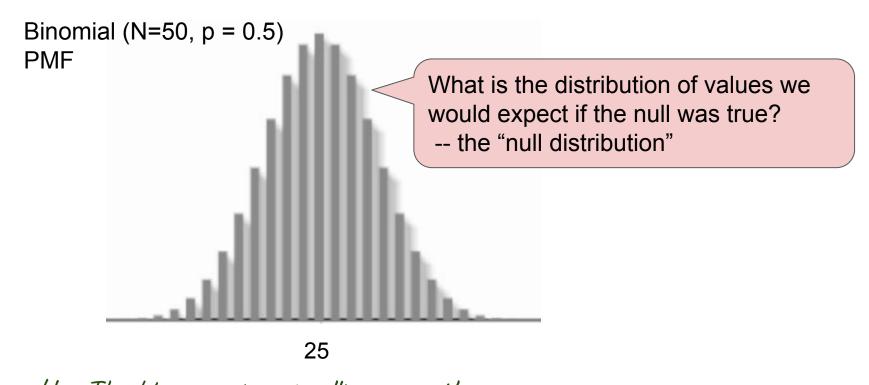
Need to estimate

What is the distribution of values we would expect if the null was true?

-- the "null distribution"

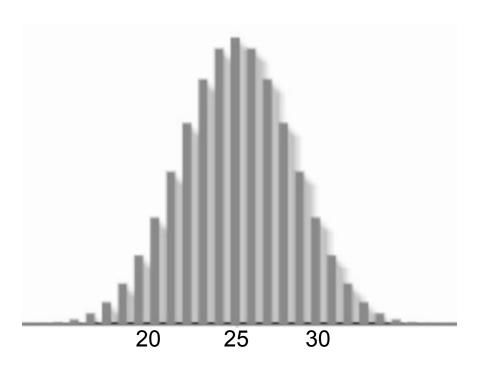
```
if p(x>=obs | H₀) < α:
    decision = "Reject H₀!"
else:
    decision = "Accept H₀."
Output: decision</pre>
```

H: The blue case is not selling more than average.

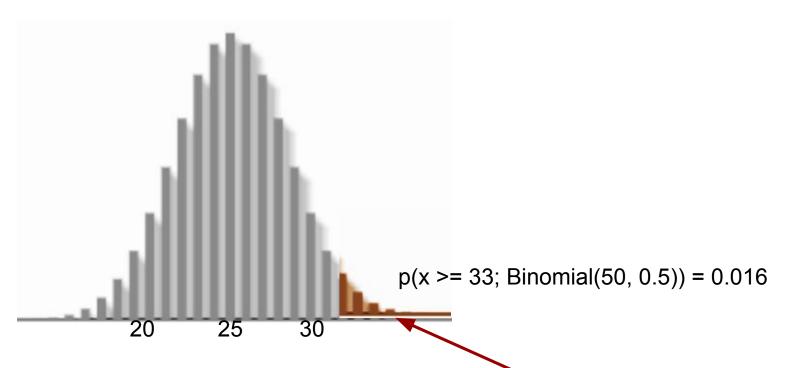


```
Input: H_{\alpha}, obs, \alpha
null_dist = distribution of expected values under Ha
if p(x)=obs | H_{o} > \alpha:
   decision = "Reject H<sub>a</sub>!"
else:
   decision = "Accept H_a."
Output: decision
```

```
Input: H_{\alpha}, obs, \alpha
null_dist = distribution of expected values under Ha
if p(x)=obs | H_{o} > \alpha:
   decision = "Reject H<sub>a</sub>!"
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Output: decision
```



 H_o : The blue case is not selling more than average. **Observed 33 blue sales** 50 sales; 2 colors (blue and red); Thus, average would be 25 blue sales



 H_o : The blue case is not selling more than average. Observed 33 blue sales 50 sales; 2 colors (blue and red); Thus, average would be 25 blue sales

```
Input: H_a, obs, \alpha
null_dist = distribution of expected values under Ha
p(x)=obs \mid H_a = 0
if p(x)=obs \mid H_{o}) < \alpha:
   decision = "Reject H<sub>a</sub>!"
else:
   decision = "Accept H_a."
Output: decision
```

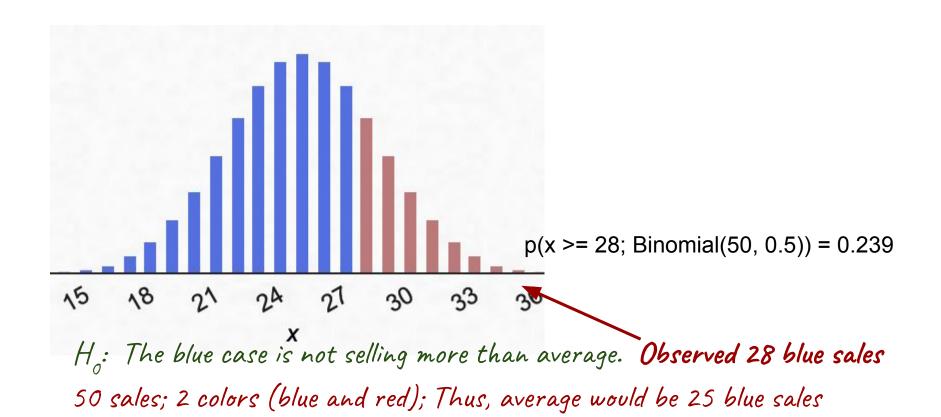
```
Input: H_{\alpha}, obs, \alpha
null dist = distribution of expected values under H_{\alpha}
p(x)=obs \mid H_a = sum(pmf(null_dist, o) for o in range(obs,))
if p(x)=obs \mid H_{\alpha}) < \alpha:
    decision = "Reject H<sub>a</sub>!"
else:
    decision = "Accept H_a."
Output: decision
```

```
Input: H_{\alpha}, obs, \alpha
null dist = distribution of expected values under Ha
p(x>=obs \mid H_a) = 1 - cdf(null\_dist, obs-1)
if p(x)=obs \mid H_{o} < \alpha:
   decision = "Reject H<sub>a</sub>!"
else:
   decision = "Accept H_a."
Output: decision
```

```
Input: H_{\alpha}, obs, \alpha
null_dist = distribution of expected values under Ha
p(x) = obs \mid H_a) = 1 - cdf(null_dist, obs-) = 0.016
if p(x)=obs \mid H_a < \alpha:
   decision = "Reject H<sub>a</sub>!"
else:
   decision = "Accept H_a."
Output: decision
```

H_o: The blue case is not selling more than average. Observed 33 blue sales

50 sales; 2 colors (blue and red); Thus, average would be 25 blue sales



```
Input: H_{\alpha}, obs, \alpha
null_dist = distribution of expected values under Ha
p(x)=obs \mid H_a = 1 - cdf(null_dist, obs-1) = 0.239
if p(x)=obs \mid H_{o}) < \alpha:
    decision = "Reject H<sub>a</sub>!"
else:
   decision = "Accept H<sub>a</sub>."
Output: decision
```

H_o: The blue case is not selling more than average. Observed 28 blue sales

50 sales; 2 colors (blue and red); Thus, average would be 25 blue sales

```
Input: H_{\alpha}, obs, \alpha
null_dist = distribution of expected values under Ha
p(x \le obs \mid H_a) = cdf(null\_dist, obs)
if p(x \le obs \mid H_a) < \alpha:
    decision = "Reject H<sub>a</sub>!"
else:
   decision = "Accept H_a."
Output: decision
```

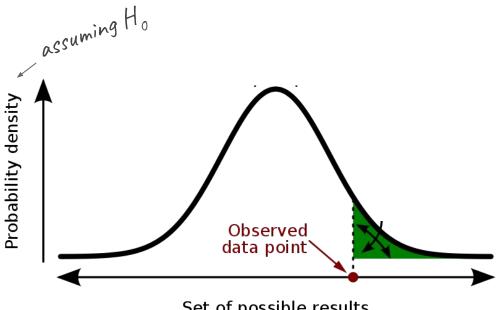
```
Input: H_{\alpha}, obs, \alpha
 null\_dist = distribution of expected obs under H<sub>a</sub>
 p(x \leftarrow obs \mid H_0) = cdf(null\_dist, obs)
 if p(x \le obs \mid H_a) < \alpha:
    decision = "Reject H<sub>o</sub>!"
 else:
    decision = "Accept H_a."
Output: decision
```

```
Input: H_a, obs, \alpha
 obs_ts = test_stat(obs)
 null\_dist = distribution of expected obs under H<sub>a</sub>
 p(x \le obs \mid H_a) = cdf(null\_dist, obs)
 if p(x \le obs \mid H_a) < \alpha:
   decision = "Reject H<sub>o</sub>!"
 else:
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Output: decision
```

```
Input: H_{\alpha}, obs, \alpha
         obs_ts = test_stat(obs)
          null_dist = distribution of expected test_stat under Ha
          p(x \le obs_t = H_a) = cdf(null_dist, obs_t =
          if p(x \leftarrow obs_t = H_a) < \alpha:
                               decision = "Reject H<sub>a</sub>!"
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Output: decision
```

 $P(D|H_0)$: Given null, what is the probability of the observed data or worse?

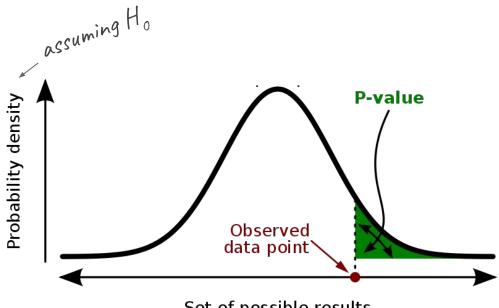
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Set of possible results

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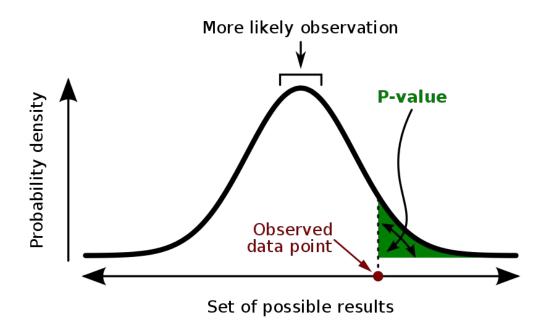


Set of possible results

A **p-value** (shaded green area) is the probability of an observed (or more extreme) result assuming that the null hypothesis is true.

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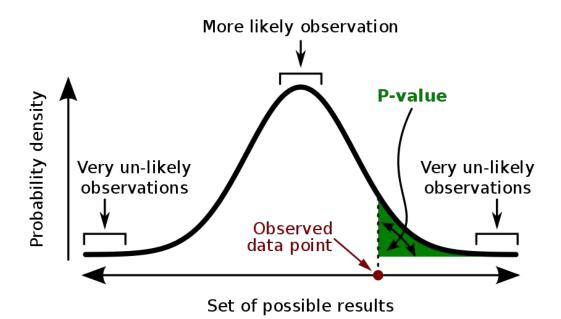
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A **p-value** (shaded green area) is the probability of an observed (or more extreme) result assuming that the null hypothesis is true.

(thanks, Wikipedia)

```
Input: H_{\alpha}, obs, \alpha
         obs_ts = test_stat(obs)
          null_dist = distribution of expected test_stat under Ha
          p(x \le obs_t = H_a) = cdf(null_dist, obs_t =
          if p(x \leftarrow obs_t = H_a) < \alpha:
                               decision = "Reject H<sub>a</sub>!"
          else:
                               decision = "Accept H_a."
Output: decision
```

Why?

Why?

A general framework for answering (yes/no) questions!

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- Are height and baldness related?
- Is my deep predictive model better than the state of the art?

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A general framework for answering (yes/no) questions!

- Are height and baldness related?
- Is my deep predictive model better than the state of the art?
- Is the heat index of a community related to poverty?
- Is the heat index of a community related to poverty controlling for education rates?
- Does my website receive a higher average number of monthly visitors?

Failing to "reject the null" does not mean the null is true.

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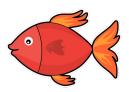
Failing to "reject the null" does not mean the null is true. However, if the sample is large enough, it may be enough to say that the effect size (correlation, difference value, etc...) is not very meaningful.

A general framework for answering (yes/maybe) questions!

- Are height and baldness related?
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General Question: Which fish do cats like?









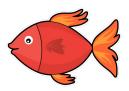




General Question: Which fish do cats like?

N = 50 cats







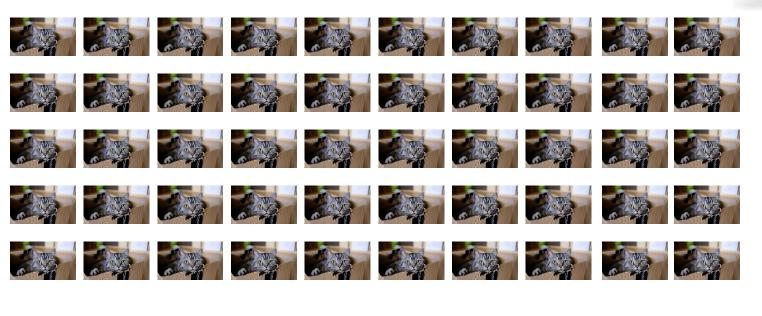




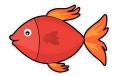


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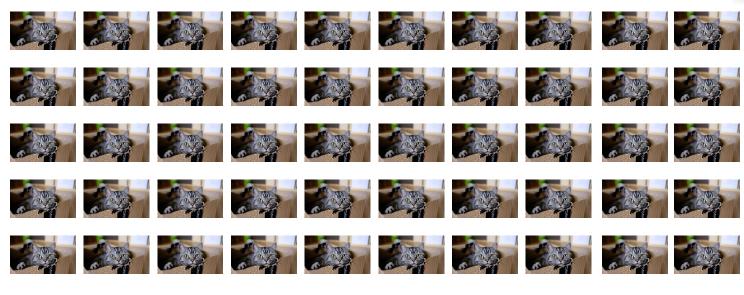






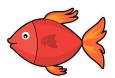
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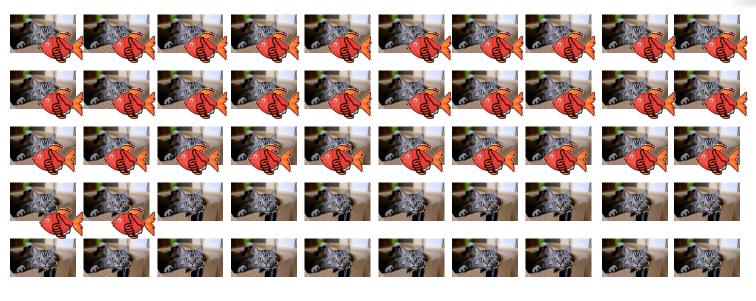






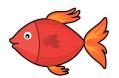
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N = 50 cats; 32 like redfish; p = 0.016







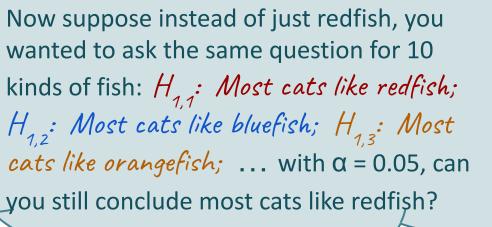






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General Question: Which fish do cats like?

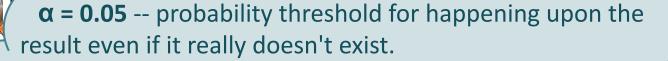
N = 50 cats; 32 like redfish; p = 0.016

Now suppose instead of just redfish, you wanted to ask the same question for 10 kinds of fish: $H_{1,1}$: Most cats like redfish; $H_{1,2}$: Most cats like bluefish; $H_{1,3}$: Most cats like orangefish; ... with $\alpha = 0.05$, can you still conclude most cats like redfish? hint: $P(1 \text{ sig}) = 1 - P(\text{no sig}) = 1 - (1 - 0.05)_{1}^{10} = 0.40$



General Question: Which fish do cats like?

N = 50 cats; 32 like redfish; p = 0.016



What is the probability we happen upon once in ten times?



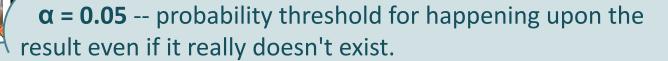






General Question: Which fish do cats like?

N = 50 cats; 32 like redfish; p = 0.016



What is the probability we happen upon once in ten times?

-1 - p(not happening upon the result) = 1 - $(1 - .05)^{10}$

= 1 - 0.599 = .4

don't like redfish.



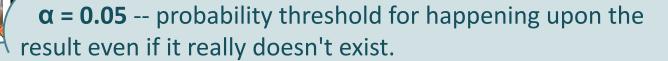




H: Most cas

General Question: Which fish do cats like?

N = 50 cats; 32 like redfish; p = 0.016



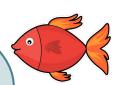
What is the probability we happen upon once in ten times?

-1 - p(not happening upon the result) = $1 - (1 - .05)^{10}$

= 1 - 0.599 = .4

How to fix?

H: Most caus

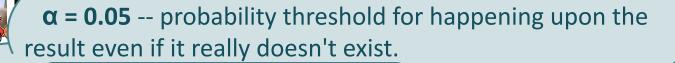






General Question: Which fish do cats like?

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Is there a way we could adjust alpha to keep it low enough?

pon once in ten times?

$$= 1 - (1 - .05)^{10}$$

$$= 1 - 0.599 = .4$$

How to fix? 1- $(1 - adjust(.05))^{10} < .05$



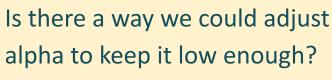






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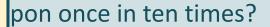


The Bonferroni correction:

$$\alpha_{bonf} = \alpha / |h|$$

How to fix? 1- $(1 - adjust(.05))^{10} < .05$

happening upon the



$$= 1 - (1 - .05)^{10}$$

$$= 1 - 0.599 = .4$$



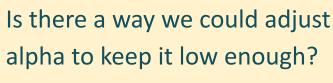






General Question: Which fish do cats like?

N = 50 cats; 32 like redfish; p = 0.016



The Bonferroni correction:

$$\alpha_{bonf} = \alpha / |h|$$

How to fix? $1 - (1 - (.05/10))^{10} = .0488$

H₁: Most cac

happening upon the



$$= 1 - (1 - .05)^{10}$$

$$= 1 - 0.599$$







Type I, Type II Errors

		True state of nature		
		H_0	H_A	
Our	Reject H_0	Type I error	correct decision	
decision	'Accept' H_0	correct decision	Type II error	
	F	36 38	(0.1.66.0.0)	

significance level ("p-value") = P(type I error) = $P(Reject H_0 | H_0)$ (probability we are incorrect)

	H_0	H_A	
Reject H_0	P(Reject H ₀ H ₀)		

		True state of nature		
		H_0	H_A	
Our	Reject H_0	Type I error	correct decision	
decision	'Accept' H_0	correct decision	Type II error	
	-		(Orloff & Bloom, 2014)	

```
significance level ("p-value") = P(type I error) = P(Reject H_0 | H_0) (probability we are incorrect)
```

power = 1 - P(type II error) = $P(Reject H_0 | H_1)$ (probability we are correct)

$$\begin{array}{|c|c|c|c|}\hline & H_0 & H_A \\\hline \hline \text{Reject } H_0 & \text{P(Reject } H_0 | H_0) & \text{P(Reject } H_0 | H_A) \\\hline \end{array}$$

		True state of nature		
		H_0	H_A	
Our	Reject H_0	Type I error	correct decision	
decision	'Accept' H_0	correct decision	Type II error	

FWER: Family-wise error rate (Bonferroni Corrects)

The probability of making >=1 type 1 error.

$$FWER = Pr(type1s>0) = 1 - Pr(type1s=0) = 1 - (1 - a)^m$$

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$$1 - (1 - (.05/10))^{10} = .0488$$

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FDR: False discovery rate (Benjamini-Hochberg corrects) type1s / (type1s + correctRejects)

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FWER: Family-wise error rate (Bonferroni corrects) The probability of making >=1 type 1 error. $FWER = Pr(type1s>0) = 1 - Pr(type1s=0) = 1 - (1 - a)^m$

FDR: False discovery rate (Benjamini-Hochberg corrects) type1s / (type1s + correctRejects)

Proportion of false positives among *all* significant results.

The Hypothesis Test "Algorithm"

```
Input: H_{\alpha}, obs, \alpha
 obs ts = test stat(obs)
 null_dist = distribution of expected test_stat under Ha
 p(x < = obs_ts \mid H_a) = cdf(null_dist, obs_ts)
 if p(x < = obs_t = | H_a) < \alpha:
   decision = "Reject H<sub>a</sub>!"
 else:
   decision = "Accept H_a."
Output: decision
```

The Multi-test "Algorithm"

```
Input: H_{\alpha}s, obs, \alpha
decisions = []
\alpha_{adj} = adjust(\alpha)
for H<sub>a</sub> in H<sub>a</sub>s
   obs ts = test stat(obs)
   null dist = distribution of expected test_stat under Ha
    p(x < obs_ts \mid H_0) = cdf(null_dist, obs_ts)
   if p(x <= obs_ts \mid H_a) < \alpha_adj:
      decisions.append("Reject Ha!")
    else:
      decisions.append("Accept H<sub>a</sub>.")
Output: decisions
```

The Multi-test "Algorithm"

```
Input: H_{\alpha}s, obs, \alpha
decisions = []
\alpha_adj = adjust(\alpha) #e.g. adjust(\alpha) = \alpha/len(H_{\alpha}s)
for H<sub>a</sub> in H<sub>a</sub>s
   obs_ts = test_stat(obs)
   null dist = distribution of expected test_stat under Ha
    p(x < obs_ts \mid H_0) = cdf(null_dist, obs_ts)
   if p(x <= obs_ts \mid H_a) < \alpha_adj:
       decisions.append("Reject Ha!")
    else:
       decisions.append("Accept H<sub>a</sub>.")
Output: decisions
```

Multi-test "Algorithm" Alternative

```
Input: H_{\alpha}s, obs, \alpha
decisions = []
for H<sub>a</sub> in H<sub>a</sub>s
   obs ts = test stat(obs)
   null dist = distribution of expected test_stat under Ha
   p(x \le obs_ts | H_a) = cdf(null_dist, obs_ts)
   p_adj = inverse_adjust(p(x<=obs_ts|Ha))#e.g. p*len(Has)</pre>
   if p adj < \alpha:
      decisions.append("Reject Ha!")
   else:
      decisions.append("Accept H<sub>a</sub>.")
Output: decisions
```

Simple Linear Regression
$$Y_i = \beta_0 + \beta_1 X_i + \epsilon_i$$
 where $\mathbf{E}(\epsilon_i|X_i) = 0$ and $\mathbf{V}(\epsilon_i|X_i) = \sigma^2$

expected variance

Estimated intercept and slope

$$\hat{r}(x) = \hat{eta}_0 + \hat{eta}_1 x$$
 $\hat{Y}_i = \hat{r}(X_i)$
Residual: $\hat{\epsilon}_i = Y_i - \hat{Y}_i$

Suppose we have multiple *X* that we'd like to fit to *Y* at once:

$$Y_i = \beta_0 + \beta_1 X_{i1} + \beta_2 X_{i2} + \dots + \beta_m X_{m1} + \epsilon_i$$

If we include and $X_{oi} = 1$ for all i (i.e. adding the intercept to X), then we can say:

$$Y_i = \sum_{i=0} \beta_j X_{ij} + \epsilon_i$$

Suppose we have multiple *X* that we'd like to fit to *Y* at once:

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If we include and $X_{oi} = 1$ for all i, then we can say:

$$Y_i = \sum_{j=0}^{m} \beta_j X_{ij} + \epsilon_i$$

Or in vector notation across all i:

$$Y = X\beta + \epsilon$$
 where β and ϵ are vectors and X is a matrix.

Suppose we have multiple *X* that we'd like to fit to *Y* at once:

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 where β and ϵ are vectors and X is a matrix.

Estimating β :

$$\hat{\beta} = (X^T X)^{-1} X^T Y$$

Suppose we have multiple independent variables that we'd like to fit to our dependent variable: $Y_i = \beta_0 + \beta_1 X_{i1} + \beta_2 X_{i2} + ... + \beta_m X_{m1} + \epsilon_i$

If we include and $X_{oi} = 1$ for all *i*. Then we can say:

$$Y_i = \sum_{j=0}^{m} \beta_j X_{ij} + \epsilon_i$$

To test for significance of individual coefficient, *j*:

$$t = \frac{\hat{\beta}_j}{SE(\hat{\beta}_j)} = \frac{\hat{\beta}_j}{\sqrt{\frac{s^2}{\sum_{j=1}^{n} (\mathbf{Y}_j - \bar{\mathbf{Y}}_j)^2}}}$$

Or in vector notation across all i: $Y = X\beta + \epsilon$

Where β and ϵ are vectors and X is a matrix.

Estimating β :

$$\hat{\beta} = (X^T X)^{-1} X^T Y$$

Significance Testing

$$Y_i = \beta_0 + \beta_1 X_{i1} + \beta_2 X_{i2} + \dots + \beta_m X_{m1} + \epsilon_i$$

$$r^2 = \frac{RSS}{df}$$

To test for significance of individual coefficient, *j*:

$$t = \frac{\hat{\beta}_{j}}{SE(\hat{\beta}_{j})} = \frac{\hat{\beta}_{j}}{\sqrt{\frac{\hat{\beta}_{j}}{\sum_{i=1}^{n} (X_{ij} - \bar{X}_{j})^{2}}}}$$

T-Test for significance of hypothesis:

- 1) Calculate t
- 2) Calculate degrees of freedom:

$$df = N - (m+1)$$

3) Check probability in a *t* distribution:

$$\begin{array}{c} 0.40 \\ 0.35 \\ 0.30 \\ 0.25 \\ \hline 0.20 \\ 0.15 \\ 0.10 \\ 0.05 \\ 0.00 \\ \hline \end{array}$$

To test for significance of individual coefficient,
$$j$$
:
$$df = N - (m+1)$$

1) Calculate
$$t$$

2) Calculate degrees of freedom: of
$$df = N - (m+1)$$

T-Test for significance of hypothesis:

Summary: Hypothesis Testing

Hypothesis Testing:

A framework for deciding which differences/relationships matter.

- Random Variables
- Distributions
- Hypothesis Testing Framework

Comparing Variables:

Metrics to quantify the difference or relationship between variables.

- Simple Linear Regression, Correlation, Multiple Linear Regression,
- Comparing Variables and Hypothesis Testing
- Regularized Linear Regression (for supervised ML)
- Multiple Hypothesis Testing

Statistical Standards

- Correct for multiple tests (Bonferonni's Principle)
- Average multiple models (ensemble techniques)
- 3. Smooth data
- 4. "Plot" data (or figure out a way to look at a lot of it "raw")
- 5. Interact with data

Statistical Standards

- Correct for multiple tests (Bonferonni's Principle)
- Average multiple models (ensemble techniques)
- 3. Smooth data
- 4. "Plot" data (or figure out a way to look at a lot of it "raw")
- 5. Interact with data

- 6. Know your "real" sample size
- 7. Correlation is not causation
- 8. Define metrics for success (set a baseline)
- 9. Share code and data
- 10. The problem should drive solution

Large-Scale Hypothesis Testing

- Findings and Uncertainty
- Hypothesis Testing
- Bonferroni's Cats
- Multi-test Corrections
 - Family-wise Error Rate
 - False-Discovery Rate
- Correlation Metrics
 - Effect Size (coefficient)
 - Significance (whether p-value is below significance level)