Week 03: Monte Carlo Hypothesis Testing

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Computational Methods in Statistics and Data Science (Stats 406)

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Monte Carlo Hypothesis Testing

Hypothesis Tests

We'll begin our exploration of **operating characteristics** of statistical procedures with **hypothesis tests**.

A hypothesis test requires stating a **null hypothesis** H_0 and an **alternative hypothesis** H_1. Some examples:

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Goal: Either **accept** the null hypothesis or **reject** the null hypothesis in favor of the alternative.

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Useful framework: pick a **maximum Type I error** α and then pick a test that has **good power**.

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Where does $\mathcal{R}$ come from? How do we pick it?

Distributions for Test Statistics

Recall this key feature of statistics: because $X_1, \ldots, X_n$ are random, **test statistics are also random**!

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To determine what these distributions are, there are typically two methods:

- Analyze $T(X_1, \ldots, X_n)$ under the assumptions of H_0 and H_1 (classical)
- Use Monte Carlo techniques to draw samples of $(X_1, \ldots, X_n)$ and estimate distributions for T

Example: Testing $\mu_0 = 0$ vs. $\mu_0 = 1$

Suppose we assume that

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and want to test:

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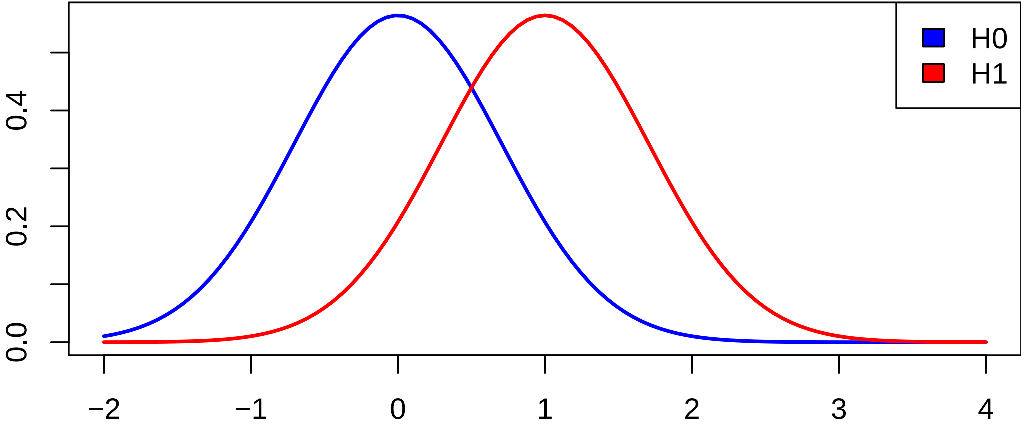
Test Statistic Distribution



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Note: We are will use intervals for simplicity, but the basic ideas apply to more general $\mathcal{R}$.

Example: size and power for $\mu = 0$ vs. $\mu = 1$

Suppose that we use $\mathcal{R} = [0, 0.5]$ for the previously discussed hypothesis test $H_0 : \bar{X} \sim N(0, 1/n)$ vs $H_1 : \bar{X} \sim N(1, 1/n)$.

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> n <- 2; a <- 0; b <- 0.5
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and power (under the alternative):

```
> pnorm(b, mean = 1, sd = 1/sqrt(n)) - pnorm(a, mean = 1, sd = 1/sqrt(n))

[1] 0.1611
```

Limiting Type I error

Since **we pick** $[a, b]$ (or $\mathcal{R}$ more generally), we can limit to $[a, b]$ with the property:

$$P(T \in [a, b] \mid H_0) \leq \alpha$$

We call α the **level** and $P(T \in [a, b] \mid H_0)$ the **size of the test** (i.e., we ensure size is no more than level).

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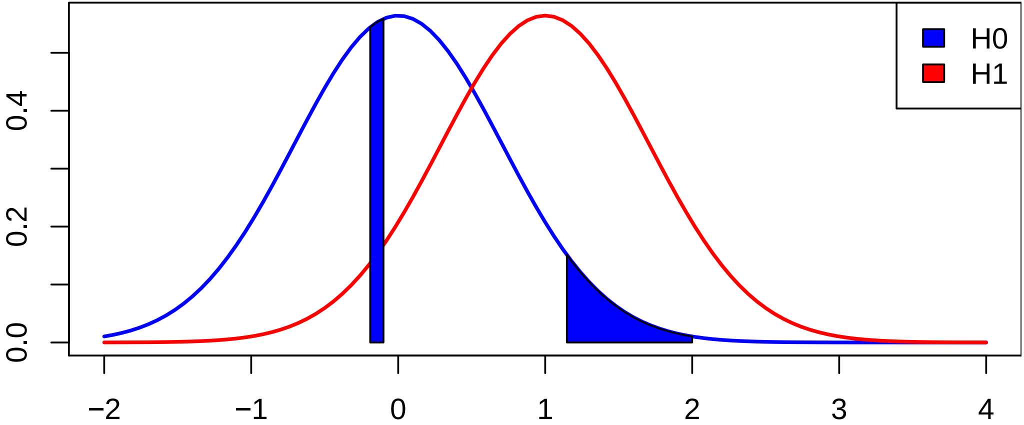
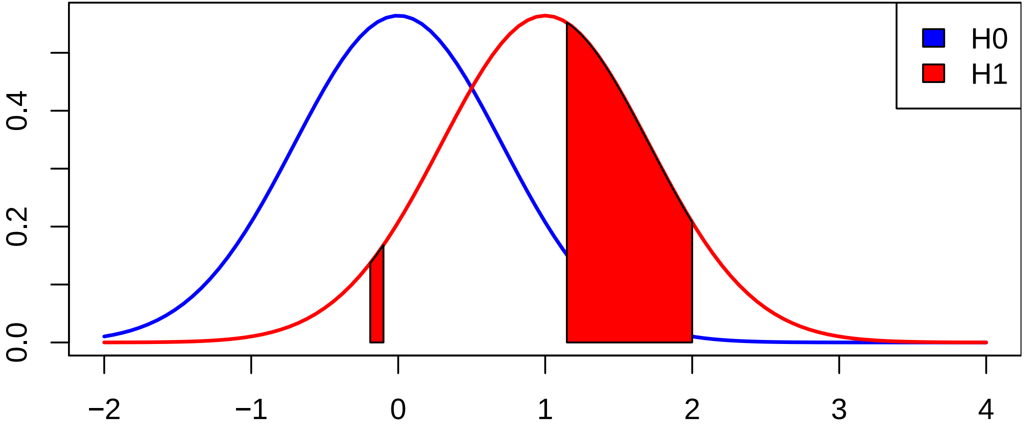
But this is not (usually) unique! Under our null hypothesis ($T \sim N(0, 1/2)$):

```
> n <- 2
> pnorm(-0.1, sd = 1/sqrt(n)) - pnorm(-0.1905725, sd = 1/sqrt(2))
[1] 0.05
> pnorm(2, sd = 1/sqrt(n)) - pnorm(1.147342, sd = 1/sqrt(2))
[1] 0.05
```

Rejection Regions: Size



Rejection Regions: Power



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Computing the power of the test when $H_1 : \mu = 1$:

```
> 1 - pnorm(cutoff, mean = 1, sd = sqrt(1/2))
```

```
[1] 0.294
```

Power Curves

A **power curve** shows how the power of a test changes with respect to another variable (sample size, tuning parameter, alternative hypothesis).

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> sample_sizes <- 2:20
> power_n <- map_dbl(sample_sizes, function(x) {
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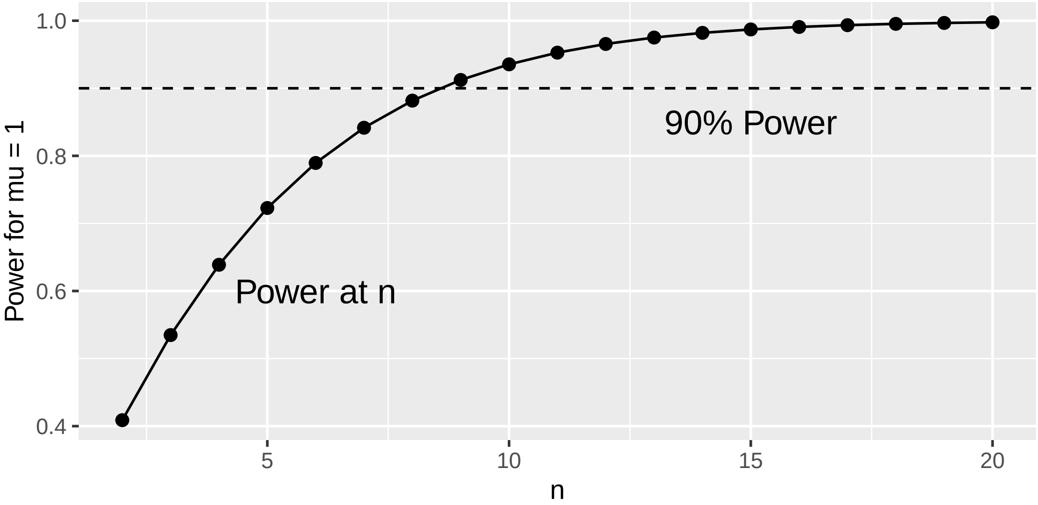
> pc <- ggplot(data.frame(n = sample_sizes, y = power_n),
+              aes(x = n, y = y))  +
+       geom_point(size = 2) + geom_line()
>
```

Power Curve Plot



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- **Rejection region $\mathcal{R}$**: reject H_0 when $T \in \mathcal{R}$ where $\Pr(T \in \mathcal{R} | H_0) \leq \alpha$.
- Good tests will have high $\Pr(T \in \mathcal{R} | H_1)$ (**power**).

MC for Simple v. Simple

Observe that Type I error and power can be written as **expectations**:

$$P(T \in \mathcal{R} \mid H_0) = E(I(T \in \mathcal{R}) \mid H_0), \quad P(T \in \mathcal{R} \mid H_1) = E(I(T \in \mathcal{R}) \mid H_1)$$

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- For rejection region $\mathcal{R}$, **estimate** $P(T \in \mathcal{R})$ with the mean of $I(T_j \in \mathcal{R})$
- Repeat to get **power** by generating samples from F_1.

Example: Binomial Distribution

Suppose we had some IID data that came from a binomial distribution (I'm hiding the θ parameter for now) of 5 trials.

```
> (xs <- rbinom(10, size = 5, p = hidden_p))

 [1] 0 1 0 3 2 2 0 2 0 1
```

Let's test the **null hypothesis** that $\theta = 0.5$ against the **alternative** that $\theta = 0.6$.

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Then the **sample mean divided by 5** is a good estimator of θ.

We know that in **large samples**, the sample mean is **approximately normal**, but we only have 10 observations. Is that large enough?

Recall that if $X \sim \text{Binomial}(5, \theta)$, $\mathrm{E}(X) = 5\theta$.

Then the **sample mean divided by 5** is a good estimator of θ.

We know that in **large samples**, the sample mean is **approximately normal**, but we only have 10 observations. Is that large enough?

(We also can figure out that the sample mean is **exactly a scaled binomial** $\bar{X} \sim \frac{1}{10}\textbf{Binomial}(10 \times 5, \theta)$, but let's pretend we don't know that.)

Distribution of T when H_0 is true

Key aspects of the data according to H_0:

- 10 observations, IID
- $X_i \sim \text{Binomial}(5, p = \theta)$
- Test statistic value:

$$T = \frac{1}{5n} \sum_{i=1}^{10} X_i$$

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- 10 observations, IID
- $X_i \sim \text{Binomial}(5, p = \theta)$
- Test statistic value:

$$T = \frac{1}{5n} \sum_{i=1}^{10} X_i$$

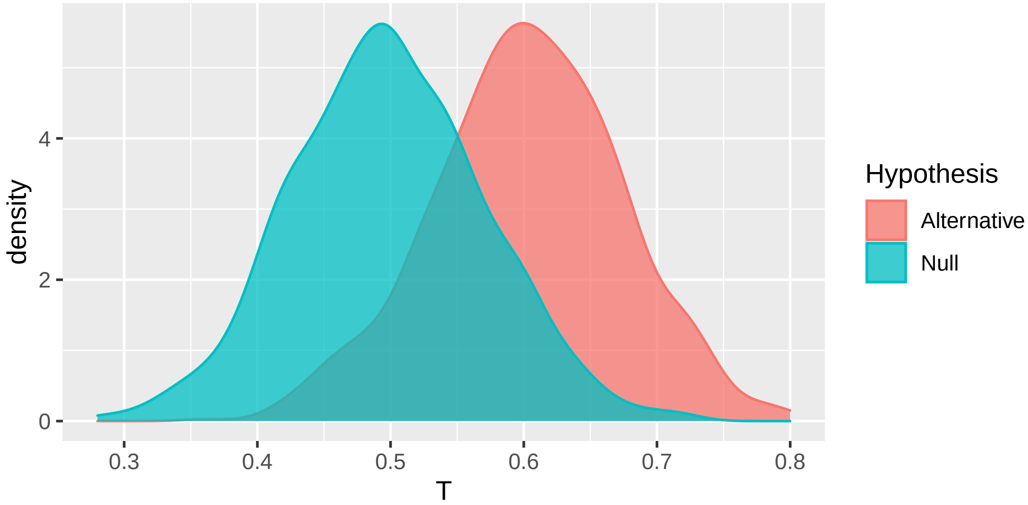
Generate random T values:

```
> k <- 1000
> T_statistic <- function(sample) { mean(sample) / 5 }
> ts_0 <- replicate(k, rbinom(10, size = 5, p = 0.5) %>% T_statistic)
```

Distribution of T when H_1 is true

The only thing that differs is the value of θ:

```
> ts_1 <- replicate(k, rbinom(10, size = 5, p = 0.6) %>% T_statistic)
```


density
4
2
0
0.3
0.4
0.5
0.6
0.7
0.8
T
Hypothesis
Alternative
Null

Picking a rejection region

We want to perform a test with $\alpha = 0.05$. Of any region that has probability of 0.05 under the null, we saw that the **right tail** is probably where most power is:

```
> (rr <- c(quantile(ts_0, 0.95), 1))
 95%
0.62 1.00
```

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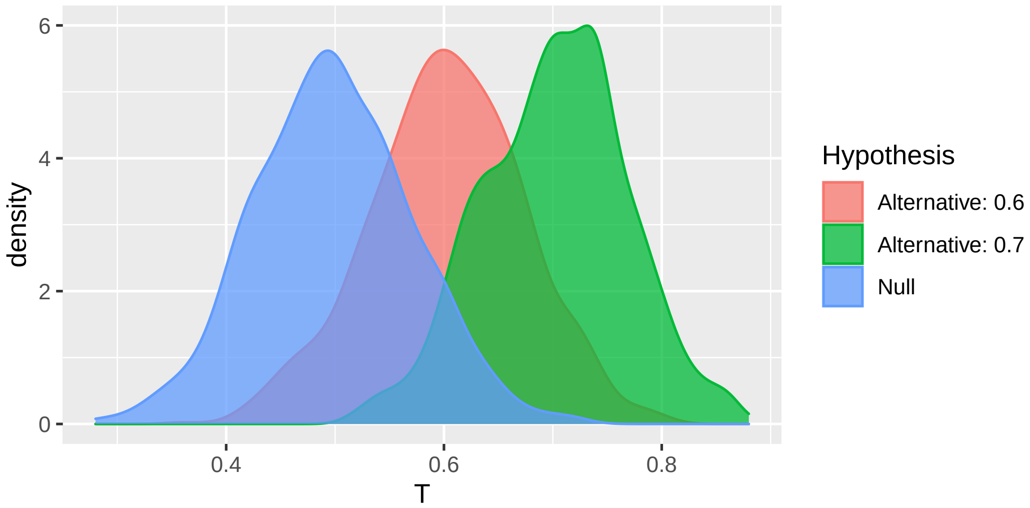
```
> (rr <- c(quantile(ts_0, 0.95), 1))

 95%
0.62 1.00

> T_statistic(xs) # the observed sample

[1] 0.22
```

Since it is less than r_1, **accept (fail to reject)** H_0 **at the** $\alpha = 0.05$ **level**.



density
6
4
2
0
0.4
0.6
0.8
T
Hypothesis
Alternative: 0.6
Alternative: 0.7
Null

Composite Hypotheses

In the previous slide we saw that it seemed for any alternative with $\theta > 0.5$, the best rejection region was in the **right tail of the null distribution**.

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Or in other words, we would pick the same rejection region for any $H_1 : \theta \in (0.5, 1)$.

We call such hypotheses **composite** because they contain many simple hypotheses. For example,

$$H_0 : \theta = \theta_0, \quad H_1 : \theta > \theta_0$$

Composite Null Hypotheses

Null hypotheses can also be composite. We just need to be careful about picking a rejection region that has **proper size for any member hypothesis**.

$$\left[\sup_{\theta_0 \in \Theta_0} P(T \in \mathcal{R} \mid \theta = \theta_0)\right] \leq \alpha$$

(sup is "supremum", which we can think of like "maximum", Θ_0 is the set of all null hypotheses).

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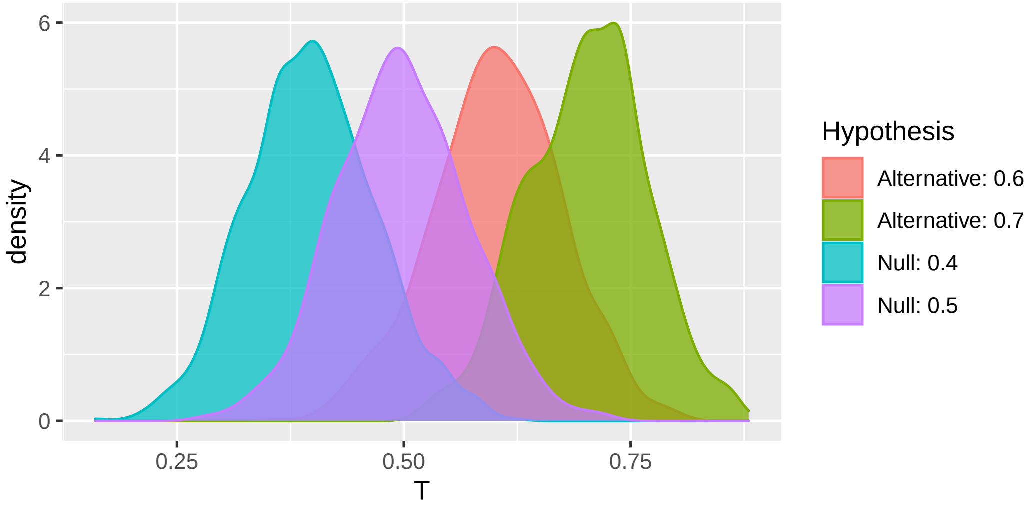
6
4
2
0
density
0.25
0.50
0.75
T
Hypothesis
Alternative: 0.6
Alternative: 0.7
Null: 0.4
Null: 0.5

One Tailed Test for Binomial

For $H_0 : \theta = 0.5 vs. H_1 : \theta = 0.6$, we found a rejection region with good power:

```
> rr

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0.62 1.00
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We saw this region had good power for any $H_1 : \theta > 0.5$ and also had increasingly smaller size for $H_0 : \theta \leq 0.5$.

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We saw this region had good power for any $H_1 : \theta > 0.5$ and also had increasingly smaller size for $H_0 : \theta \leq 0.5$.

In other words, we have a test of the composite hypothesis:

$$H_0 : \theta \leq 0.5 \quad \text{v.s.} \quad H_1 : \theta > 0$$

From one tailed to two tailed tests

For a parameter $\theta \in (-\infty, \infty)$, consider a hypothesis test of the form:

$$H_0 : \theta = \theta_0 \quad \text{v.s.} \quad H_1 : \theta \in (-\infty, \theta_0) \cup (\theta_0, \infty)$$

(we often write $\theta \neq \theta_0$ as short hand for H_1)

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For **many test statistics**, we can find good rejection regions of the form:

$$(-\infty, T_0(\alpha/2)) \cup (T_0(1 - \alpha/2), \infty)$$

which we can think of **the union of rejection regions** of two one tailed tests.

Two tailed test for binomial example

Let's test:

$$H_0 : \theta = 0.5 \quad \text{v.s.} \quad H_1 : \theta \neq 0.5$$

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We saw when $H_1 : \theta > 0.5$, our best rejection region was in the upper tail. We will suppose (correctly) that the best rejection region for $H_1 : \theta > 0.5$ is the lower tail.

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Again testing at $\alpha = 0.05$

```
> rr_upper <- quantile(ts_0, 0.975) # cut the alpha level in half
> rr_lower <- quantile(ts_0, 0.025)
> T_statistic(xs) < rr_lower || T_statistic(xs) > rr_upper # do we reject?
```

```
[1] TRUE
```

The "achieved α level": p-value

For the one sided test $H_1 : \theta > 0.5$, we picked our rejection region as $[\,T_0(1-\alpha), 1)$.

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$$\alpha \geq P(T \in [t, 1) \mid H_0)$$

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$$\alpha \geq P(T \in [t, 1) \mid H_0) = P(T \geq t \mid H_0) = p \approx \frac{\sum_{j=1}^{k} I(T_j \geq t)}{k}$$

The “achieved α level”: *p*-value

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Sometimes phrased as, “what proportion of T is more extreme than t?”

Duality between p-values and rejecting hypotheses

The p-value tells us the **smallest α level** that would place t in the rejection region.

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Implication: For any $\alpha > p$, the rejection region would also contain t (reject). For any $\alpha < p$, t would not be in the rejection region (accept).

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Implication: For any $\alpha > p$, the rejection region would also contain t (reject). For any $\alpha < p$, t would not be in the rejection region (accept).

Suppose $\alpha = 0.05$. If $p < 0.05$, then **I would reject that null hypothesis at the 0.05-level**.

The $p-value$ for two-sided tests

We saw for **two sided tests** the rejection region is composed of the union of two one tailed tests.

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$$p^+ = P(T \geq t \mid H_0), p^- = P(T \leq t \mid H_0), p\text{-value} = 2\min(p^+, p^-)$$

We can think about this as looking in both tails, but then penalizing ourselves using our data twice.

Computing the p-value

Observed value of the test statistic:

```
> (observed_t <- T_statistic(xs))
[1] 0.22
```

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```
> (observed_t <- T_statistic(xs))
```

```
[1] 0.22
```

Compute the two one-sided p-values and combine:

```
> p_less    <- mean(ts_0 <= observed_t)
> p_greater <- mean(ts_0 >= observed_t)
> (pvalue <- 2 * min(p_less, p_greater))
```

```
[1] 0
```

Testing $H_0 : \theta = 0.25$

Let's repeat for a different null hypothesis $H_0 : \theta = 0.25$ versus $H_1 : \theta \neq 0.25$.

```
> ts_0.25 <- replicate(10000, T_statistic(rbinom(10, size = 5, p = 0.25)))
> (p_0.25 <- 2 * min(mean(ts_0.25 <= observed_t),
+                     mean(ts_0.25 >= observed_t)))
```

```
[1] 0.7614
```

Testing $H_0 : \theta = 0.25$

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```
> ts_0.25 <- replicate(10000, T_statistic(rbinom(10, size = 5, p = 0.25)))
> (p_0.25 <- 2 * min(mean(ts_0.25 <= observed_t),
+                    mean(ts_0.25 >= observed_t)))
```

```
[1] 0.7614
```

Big reveal: The true θ was 0.25!

Monte Carlo Hypothesis Testing Summary

- Define the **null hypothesis** and **alternative hypothesis** that define distributions for the sample $X_1, \ldots, X_n$.
- Select a **test statistic** $T(X_1, \ldots, X_n)$
- Use the null and alternative hypotheses to draw from $X_1, \ldots, X_n$ and compute T (**null distribution** and **alternative distribution**).
- Find a **rejection region** (subset of support of null distribution) with **size less than specified level**: $P(T \in \mathcal{R} \mid H_0) \leq \alpha$ and good **power**: $P(T \in \mathcal{R} \mid H_1)$
- Compare observed statistic to rejection region or compute a p-value

Extended Example: Benford's Law

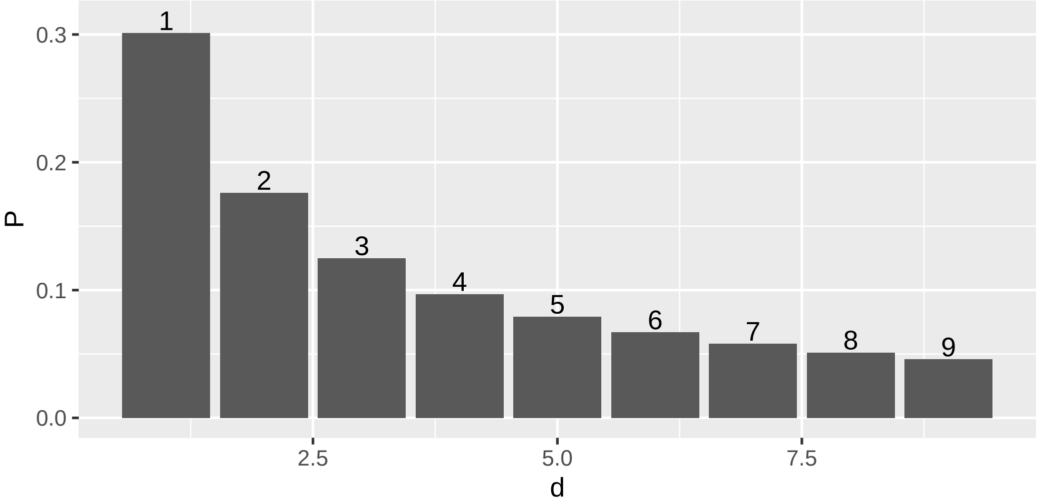
Example: Benford's Law

Benford's Law holds that the distribution of **leading digits** in a collection of numbers spanning several orders of magnitudes will follow the following distribution:

$$\Pr(D = d) = \log_{10}\left(\frac{d+1}{d}\right), \quad d = 1, \dots, 9$$

```
> dbenford <- function(x) {
+     ifelse(x >= 1 & x <= 9, log((x + 1)/ x, base = 10), 0)
+ }
```

$\Pr(D = d)$ under Benford's Law



Using random *D*s

Tam Cho and Gaines (2007) investigated **political contributions between political committees** as reported by the FEC. Here are the digit frequencies for 8,396 contributions in 2004 (Table 1):

```
> pol_digits <- c(23.3, 21.1, 8.5, 11.7, 9.5, 4.2, 3.7, 4.0, 14.1) / 100
```

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```

A typical way to analyze these data would be to use a χ^2 test comparing the **expected** to the **observed counts**. Alternatively, Tam Cho and Gaines suggest the statistic:

```
> distance <- function(v)  { sqrt(sum((v - dbenford(1:9))^2)) }
```

Hypothesis Test

We will test the null hypothesis that Benford's Law holds for political contributions versus the alternative that it does not hold (goodness-of-fit test).

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If the null hypothesis is true, then the observed distance statistic should be close to zero:

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[1] 0.1355
```

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If the null hypothesis is true, then the observed distance statistic should be close to zero:

```
> (observed_dist <- distance(pol_digits))
```

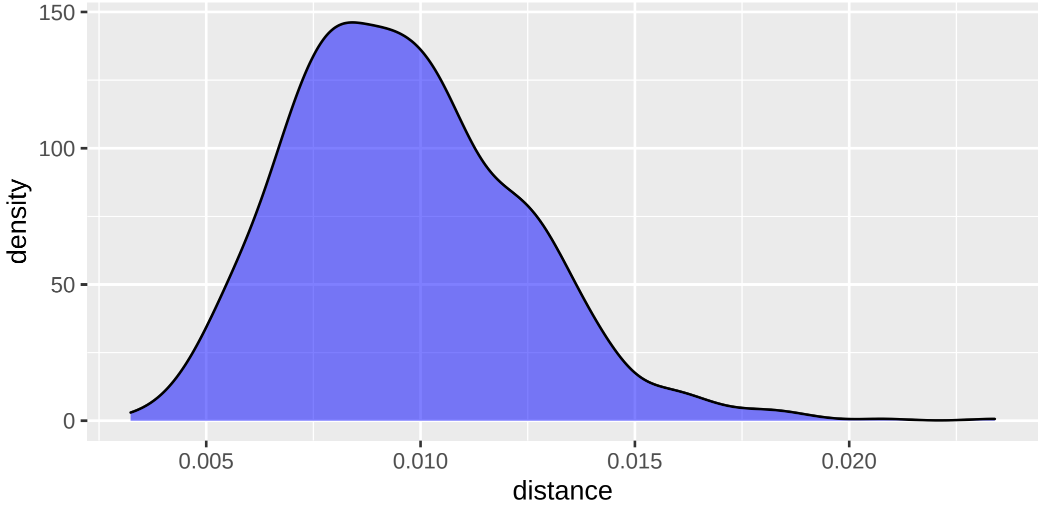
```
[1] 0.1355
```

What is the probability of observing a distance of *at least* 0.1355 if the null hypothesis (Benford's Law) holds?

Distribution of the Test Statistic

```
> rbenford <- function(n) {
+   sample(1:9, size = n, prob = dbenford(1:9), replace = TRUE)
+ }
> n <- 8396
> compute_test_statistic <- function(ds) {
+     probs <- hist(ds, breaks = 0:9, plot = FALSE)$density
+     distance(probs)
+ }
> null_distances <- replicate(1000,
+                               compute_test_statistic(rbenford(n)))
```

Null Distribution



Understanding power of distance test statistic

In order to **pick a rejection region** and **compute the power** of a test statistic, we need to carefully define an alternative hypothesis.

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One natural choice would be that **digits are uniformly distributed**: $P(D = d) = 1/9$.

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In order to **pick a rejection region** and **compute the power** of a test statistic, we need to carefully define an alternative hypothesis.

One natural choice would be that **digits are uniformly distributed**: $P(D = d) = 1/9$.

Can we add a parameter θ that controls **how close** to either Bedford or uniform a distribution on digits is?

Parameterizing Alternative

Notice that as $\theta \to \infty$,

$$\frac{d+1+\theta}{d+\theta} \to 1$$

which suggests a model like:

$$P(D=d) = \log_{10}\left(a\frac{d+1+\theta}{d+\theta}\right)$$

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$$P(D = d) = \log_{10}\left(a\frac{d+1+\theta}{d+\theta}\right)$$

We need to find the normalizing constant a.

Finding a

To get a,

$$\sum_{d=1}^{9} \log_{10}\left(a\frac{d+\theta+1}{d+\theta}\right) = 1 \Rightarrow a^9 \prod_{d=1}^{9} \frac{d+\theta+1}{d+\theta} = 10$$

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Investigating farther, we see

$$a^9 \frac{(10+\theta)(9+\theta)\cdots(2+\theta)}{(9+\theta)(8+\theta)\cdots(1+\theta)} = a^9 \frac{10+\theta}{1+\theta} = 10$$

so

$$a = \left[\frac{10(1+\theta)}{10+\theta}\right]^{1/9}$$

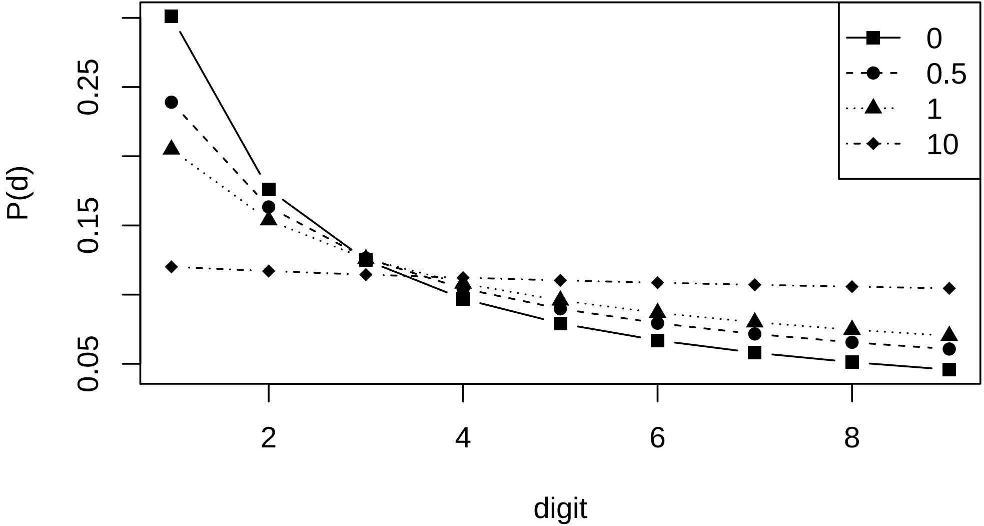
Putting it together

$$P(D = d) = \log_{10}\left(\left[\frac{10(1+\theta)}{10+\theta}\right]^{\frac{1}{9}} \frac{d+\theta+1}{d+\theta}\right), \theta > 0$$

Putting it together

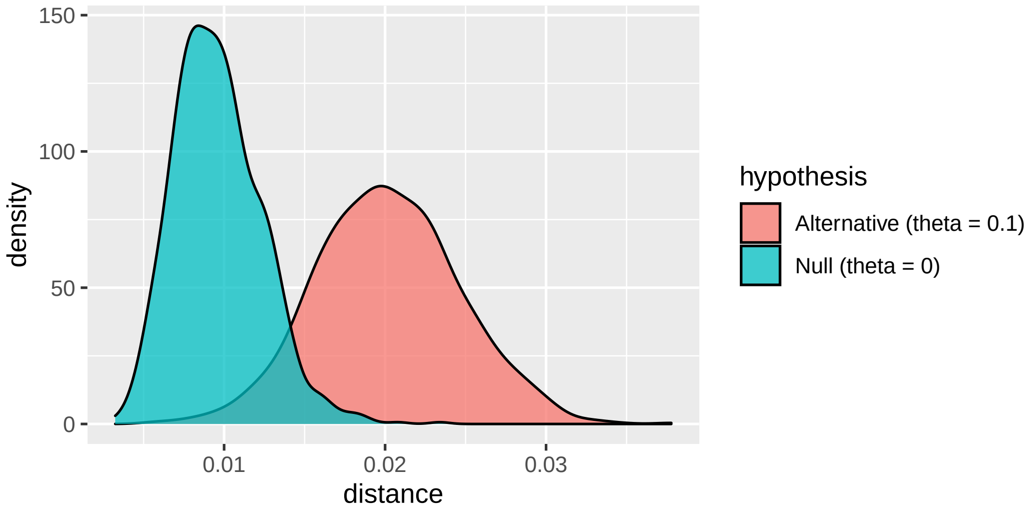
$$P(D = d) = \log_{10}\left(\left[\frac{10(1+\theta)}{10+\theta}\right]^{\frac{1}{9}} \frac{d+\theta+1}{d+\theta}\right), \theta > 0$$

```
> alt_dist <- function(theta) {
+   a <- (10 * (1 + theta) / (10 + theta))^(1/9)
+   log10(a * (1:9 + theta + 1) / (1:9 + theta))
+ }
```


0
0.5
1
10
P(d)
0.05
0.15
0.25
2
4
6
8
digit

Alternative distribution $\theta = 0.1$

```
> alt_0.1 <- replicate(1000, {
+     a_sample <- sample(1:9, size = n, replace = TRUE,
+                        prob = alt_dist(0.1))
+     compute_test_statistic(a_sample)
+ })
>
```


150
100
50
0
density
0.01
0.02
0.03
distance
hypothesis
Alternative (theta = 0.1)
Null (theta = 0)

p-value for the hypothesis test

```
> (p_value <- mean(null_distances >= observed_dist)) # P(T > t)
[1] 0
```

The observed test statistic was larger than any sample we generated (so the p-value was zero) and is 47 standard deviations from the mean of the null distribution.

p-value for the hypothesis test

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> (p_value <- mean(null_distances >= observed_dist)) # P(T > t)
[1] 0
```

The observed test statistic was larger than any sample we generated (so the *p*-value was zero) and is 47 standard deviations from the mean of the null distribution.

With *extremely high confidence*, we can reject the null hypothesis that these data were a sample from a population that follows Benford's Law.

Power at $\alpha = 0.001$ and $\theta = 0.1$

First, we need to find the 99% quantile under the null:

```
> (rejection_cutoff <- quantile(null_distances, 0.999))

 99.9%
0.0208

> mean(alt_0.1 >= rejection_cutoff)

[1] 0.438
```

Power Curves

We saw power at one particular point $\theta = 0.1$. What about **other values of θ**?

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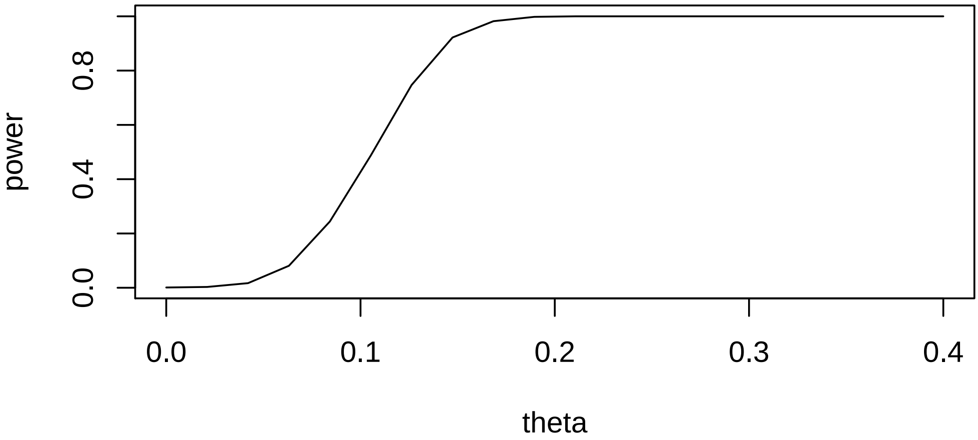
We saw power at one particular point $\theta = 0.1$. What about **other values of θ**?

We can compute power for many values of θ (holding our α level fixed) to see how it changes.

```
> thetas <- seq(0, 0.4, length.out = 20)
> power_curve <- map_dbl(thetas, function(theta) {
+     alt <- replicate(1000, {
+         a_sample <- sample(1:9, size = n,
+                            replace = TRUE, prob = alt_dist(theta))
+         compute_test_statistic(a_sample)
+     })
+     mean(alt >= rejection_cutoff)
+ })
```


power
0.0
0.4
0.8
0.0
0.1
0.2
0.3
0.4
theta

Future Directions and More on Benford's Law

In this analysis, we considered one possible alternative and one test statistic:

- Why would contributions not follow Benford's law? How could this be turned into an alterantive distribution?
- What other test statistics are possible? What would the power of those statistics be?

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- What other test statistics are possible? What would the power of those statistics be?

If you are interested in learning more about Benford's Law,

- A Simple Explanation of Benford's Law by R. M. Fewster.
- Breaking the (Benford) Law: Statistical Fraud Detection in Campaign Finance by Wendy Tam Cho and Brian Gaines