Confidence intervals, hypothesis testing, Monte Carlo, and generalized linear models

Roger Levy

9.S918: Quantitative inference in brain and cognitive sciences

19 February 2025

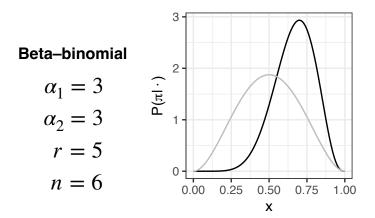
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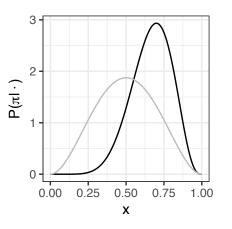
Point estimates we have seen thus far:

$$\alpha_1 = 3$$

$$\alpha_2 = 3$$

$$r = 5$$

$$n = 6$$



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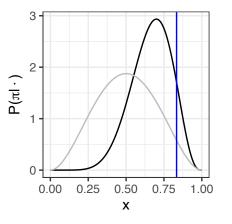
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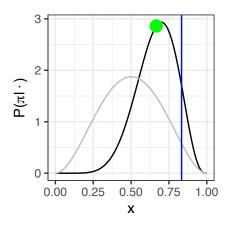
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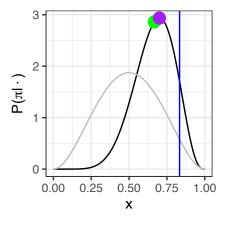
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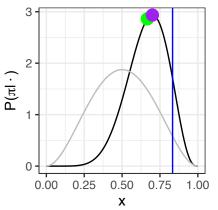
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 All of these point estimates discard a lot of information about the shape of the curve that they come from!

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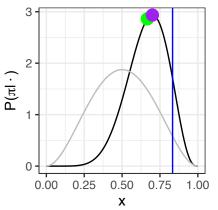
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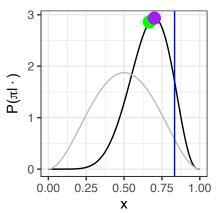
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- Credible intervals (Bayesian) and confidence intervals (frequentist) provide a bit more information about this uncertainty

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• A $(1-\alpha)$ Bayesian credible interval (CI) on parameter π is an interval containing $(1-\alpha)$ of the posterior mass

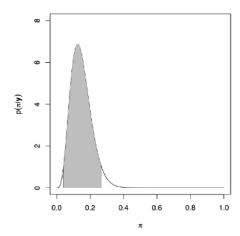
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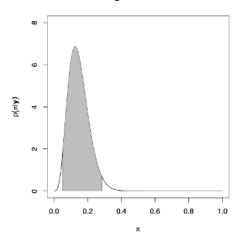
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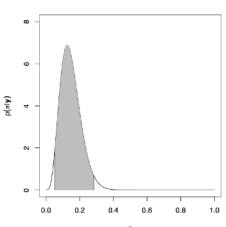


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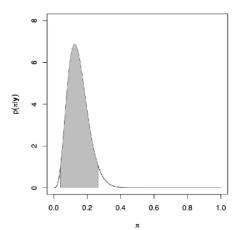


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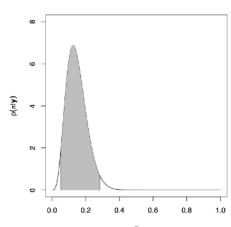
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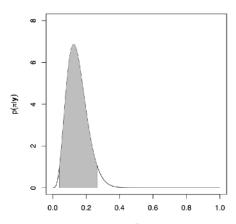


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- Multivariate generalization: interval→region

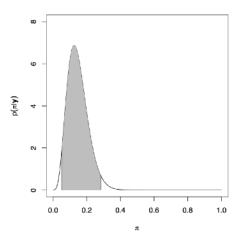
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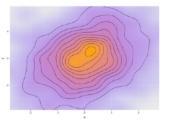
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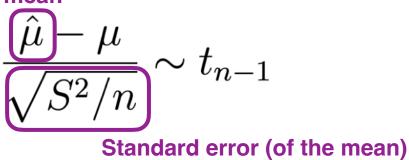
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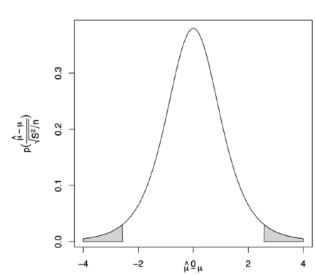
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Bayesian hypothesis testing

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Bayes Factor:
$$\frac{P(\boldsymbol{y}|H)}{P(\boldsymbol{y}|H')}$$

Interpreting Bayes Factors

$$K = \frac{P(\boldsymbol{y}|H)}{P(\boldsymbol{y}|H')}$$

log ₁₀ <i>K</i>	K	Strength of evidence	
0 to 1/2	1 to 3.2	Not worth more than a bare mention	
1/2 to 1	3.2 to 10	Substantial	
1 to 2	10 to 100	Strong	
> 2	> 100	Decisive	

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$$P(\mathbf{y}|H_1) = {6 \choose 4} \pi^4 (1-\pi)^2 = {6 \choose 4} \left(\frac{1}{2}\right)^4 \left(\frac{1}{2}\right)^2 = 0.23$$

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$$P(\mathbf{y}|H_3) = \int_{\pi} P(\mathbf{y}|\pi) P(\pi|H_3) d\pi = \int_0^1 \binom{6}{4} \pi^4 (1-\pi)^2 \frac{P(\pi|H_3)}{1} d\pi = \binom{6}{4} B(5,3) = 0.14$$

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$$\frac{P(\mathbf{y}|H_1)}{P(\mathbf{y}|H_3)} = \frac{0.23}{0.14}$$
$$= 1.64$$

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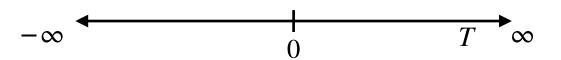
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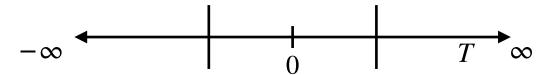


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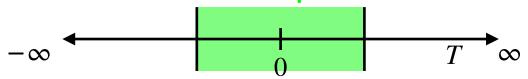


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$$H_0$$
 is... Accept H_0 Reject H_0

True Correct decision (prob. $1-\alpha$) Type I error (prob. α)

False Type II error (prob. β) Correct decision (prob. $1-\beta$)

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	Accept H_0	Reject H_0	Significance level
H_0 is	Correct decision (prob. $1 - \alpha$) Type II error (prob. β)	Type I error (pro Correct decision (

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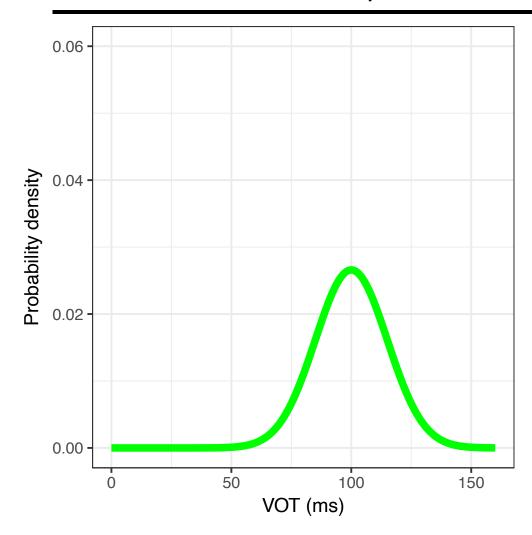
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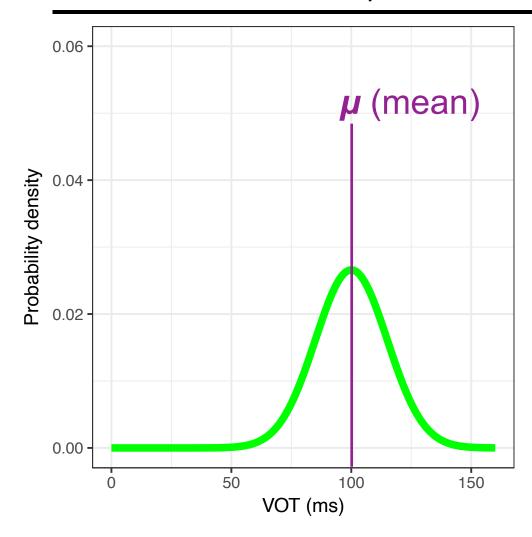
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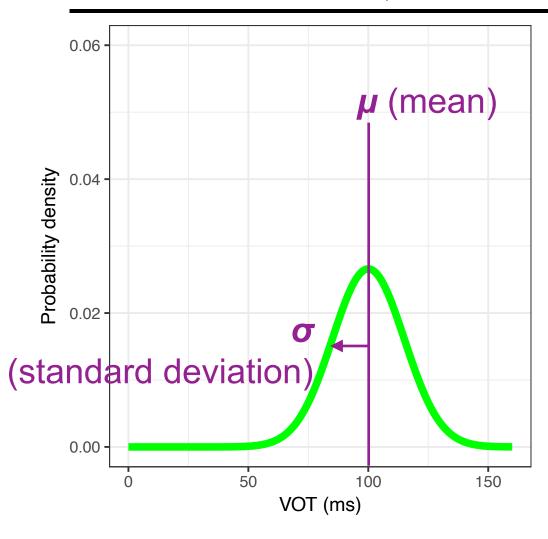
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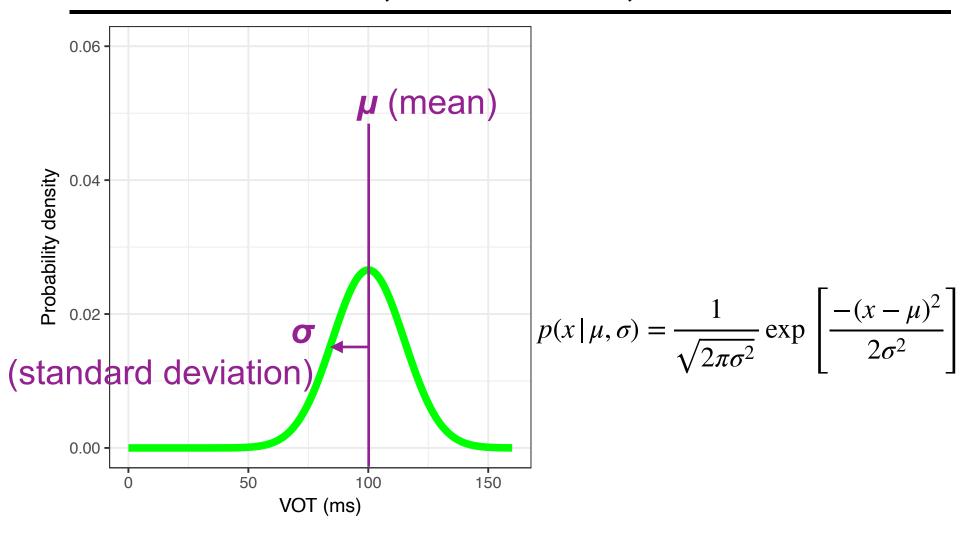


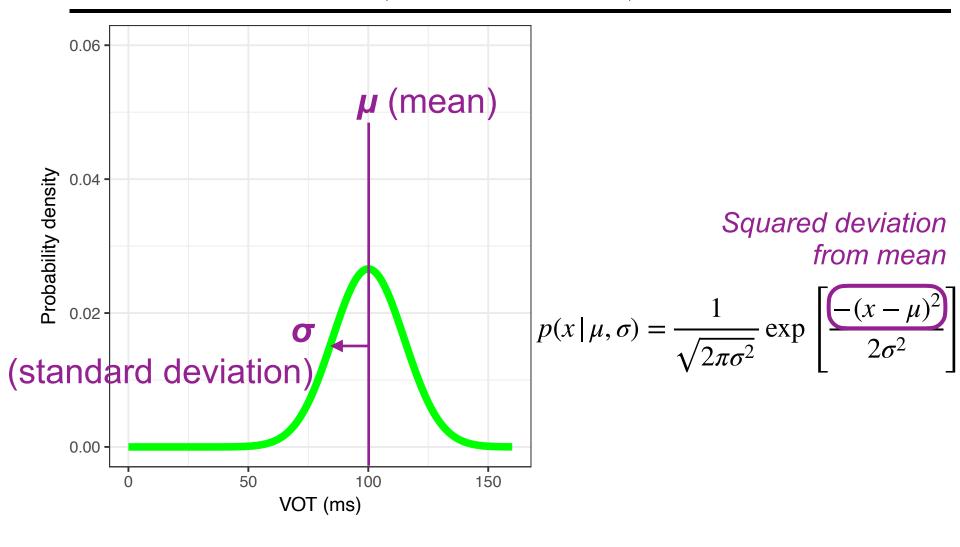
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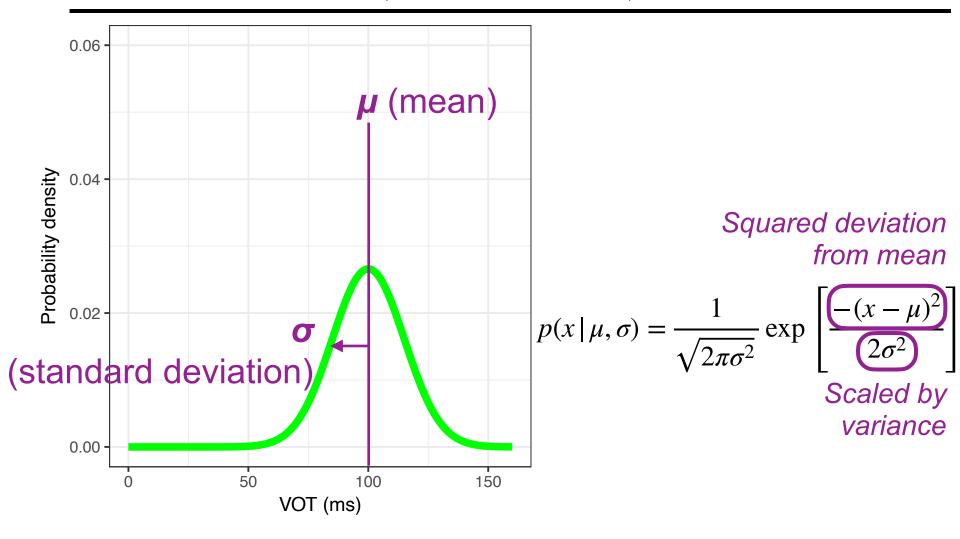


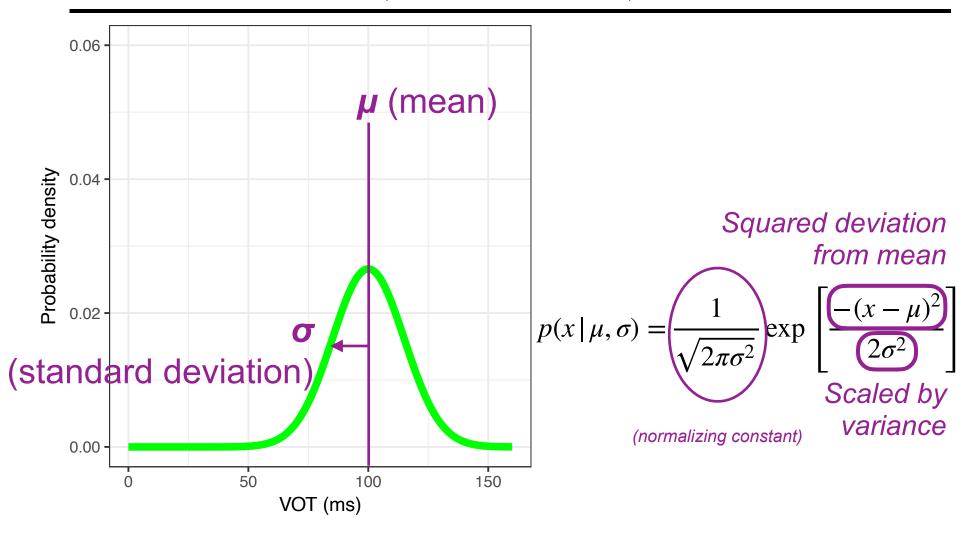


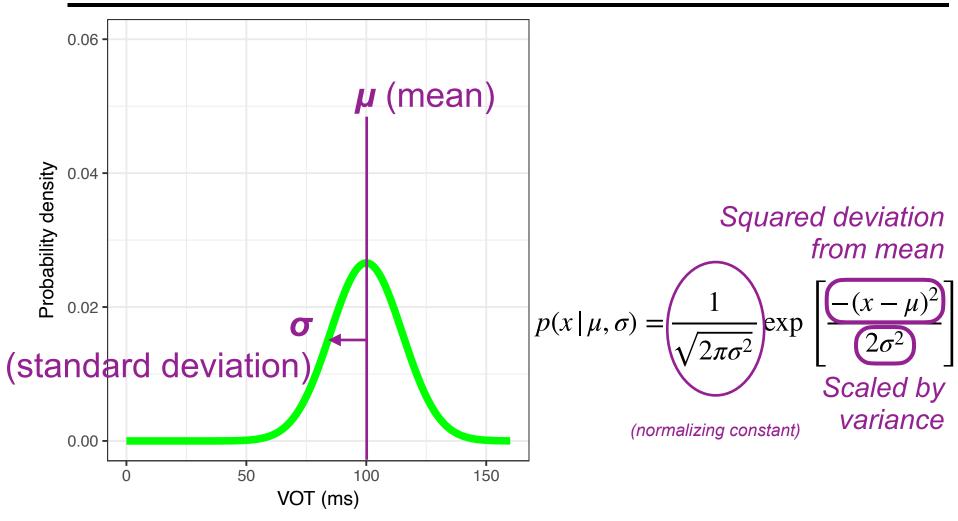








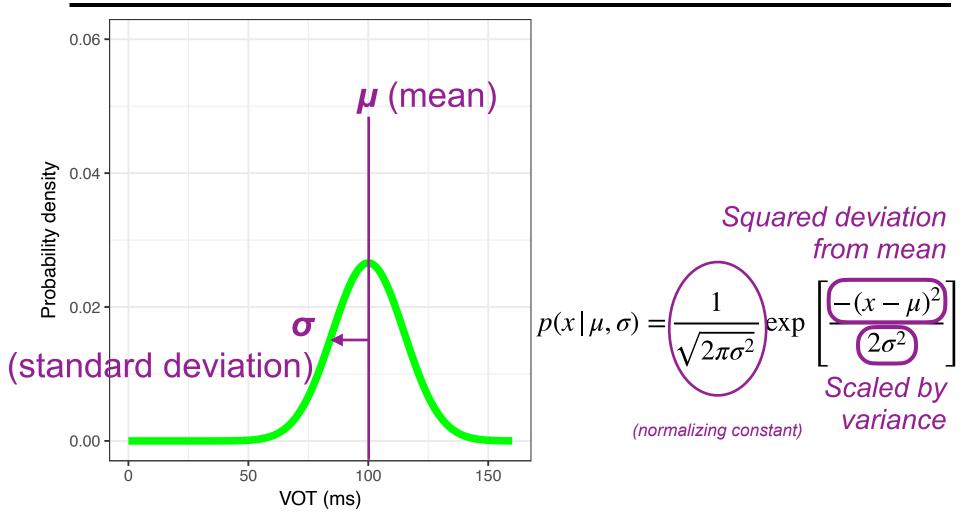




• Unbiased parameter estimates from a size-N sample:

$$\hat{u} = \bar{x}$$

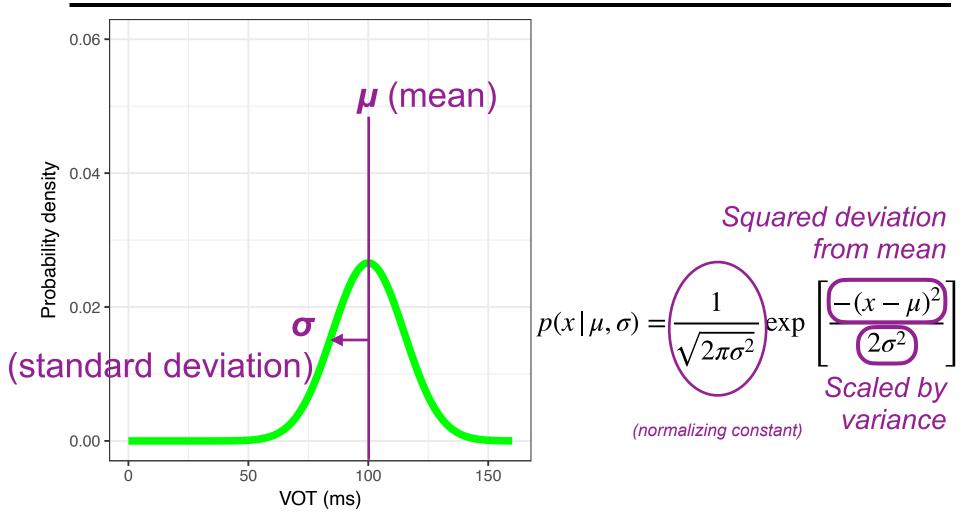
$$\hat{\sigma} = \sqrt{\frac{1}{N-1} \sum_{i=1}^{N} (x_i - \bar{x})^2} \triangleq 1$$



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$$\hat{\mathcal{U}} = \overline{\bar{X}}$$
 Sample mean $\hat{\sigma} = \sqrt{\frac{1}{N-1} \sum_{i=1}^{N} (x_i - \bar{x})^2} \triangleq 1$

The Gaussian, or normal, distribution



• Unbiased parameter estimates from a size-N sample:

$$\hat{\mu} = \overline{\bar{x}}$$
 Sample mean $\hat{\sigma}$

$$r = \sqrt{\frac{1}{N-1} \sum_{i=1}^{N} (x_i - \bar{x})^2} \triangleq s$$
 Sample standard deviation

The *t*-test: three variants

- One sample (Student's) test: Does the underlying population mean of a sample differ from zero?
- Two-sample test (unpaired): do the underlying population means of two samples differ from one another?

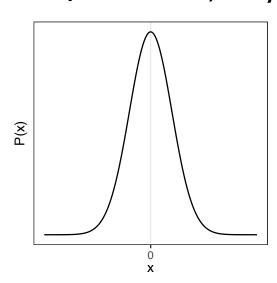
William Sealy Gosset, a.k.a. Student

 Two-sample test (paired): You have a sample of individuals from the population and take measurements from each member of the sample in two different conditions. Do the underlying population means in the two conditions differ from one another?

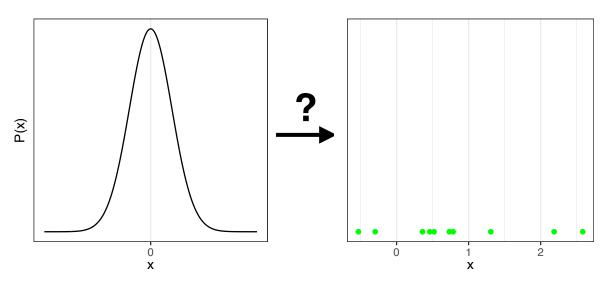
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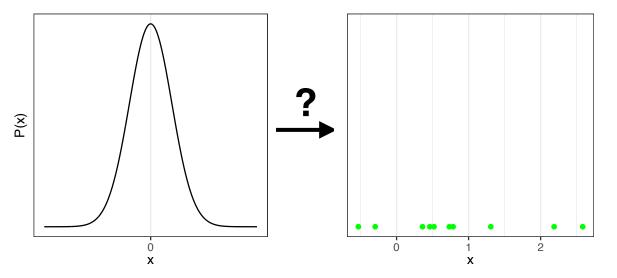
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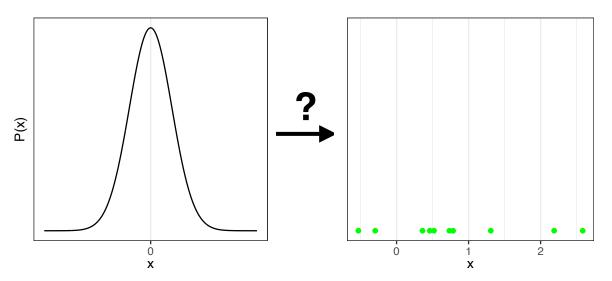


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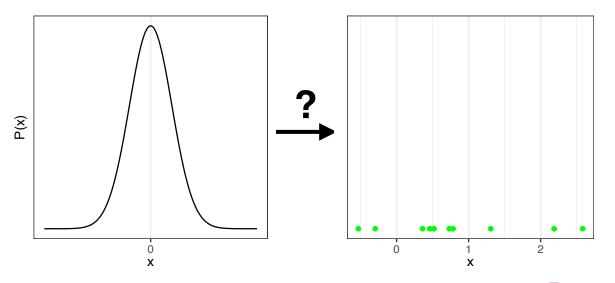
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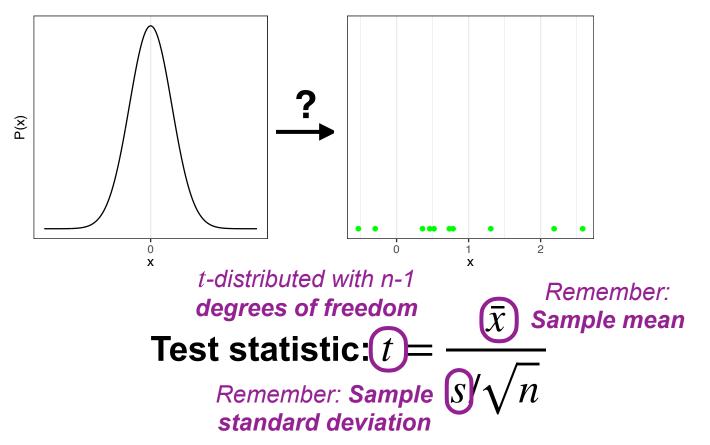
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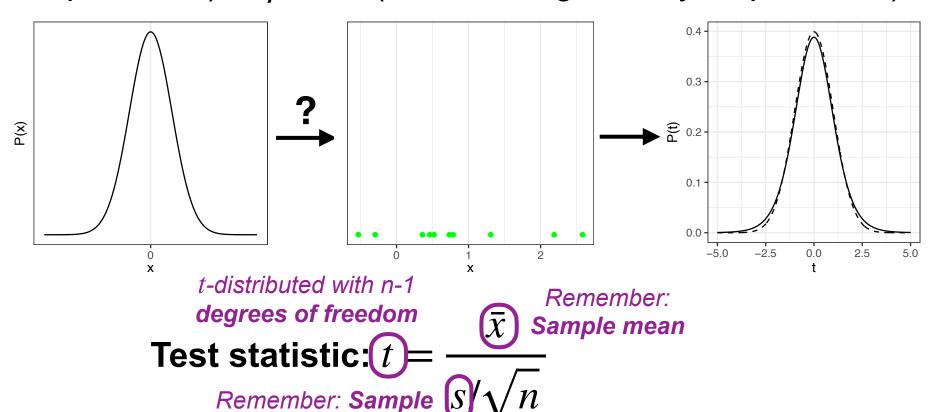
standard deviation

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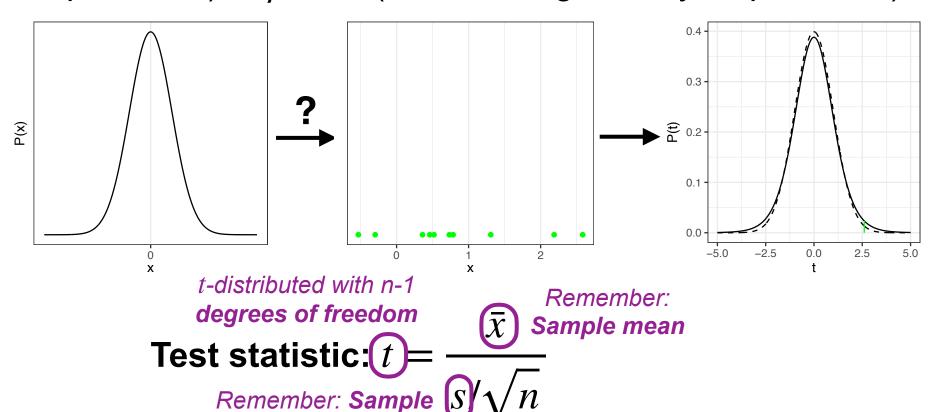
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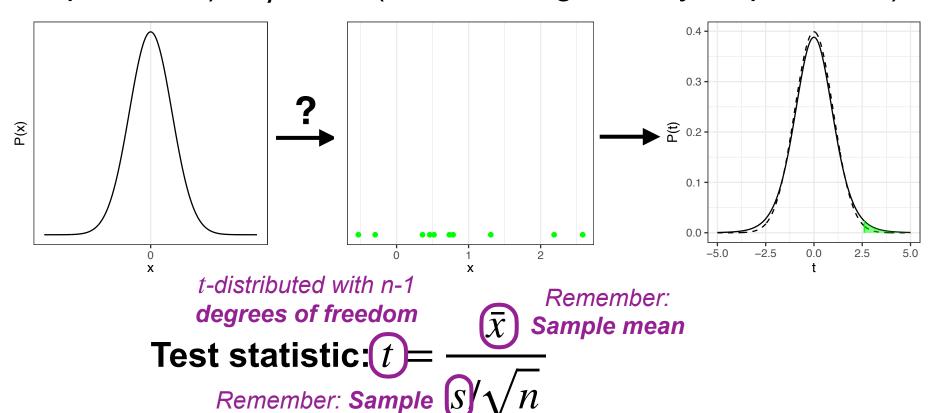
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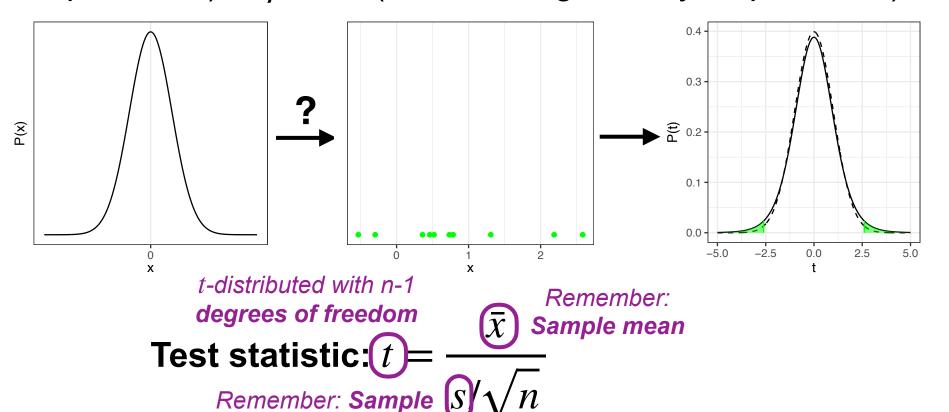
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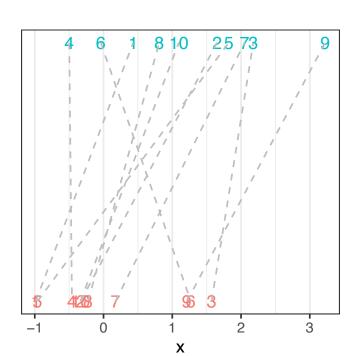
$$= \frac{\bar{x_1} - \bar{x_2}}{\sqrt{s_1^2/n_1 + s_2^2/n_2}}$$
t-distributed with a complex number of degrees of freedom whose formula can easily be looked up

Assumptions:

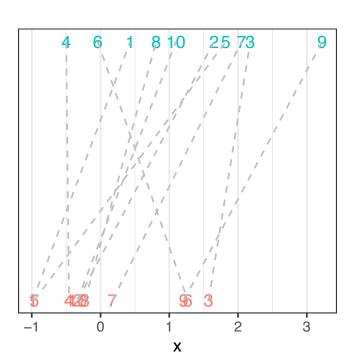
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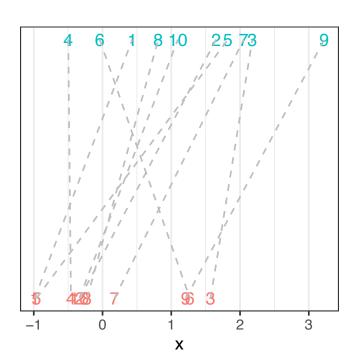
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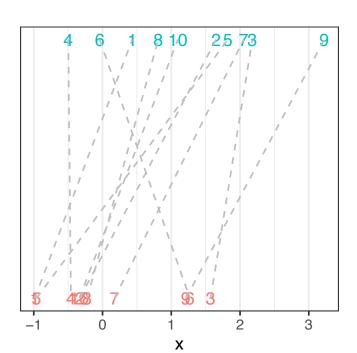
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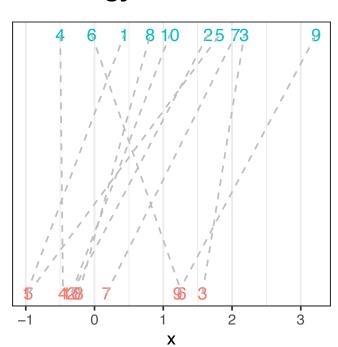
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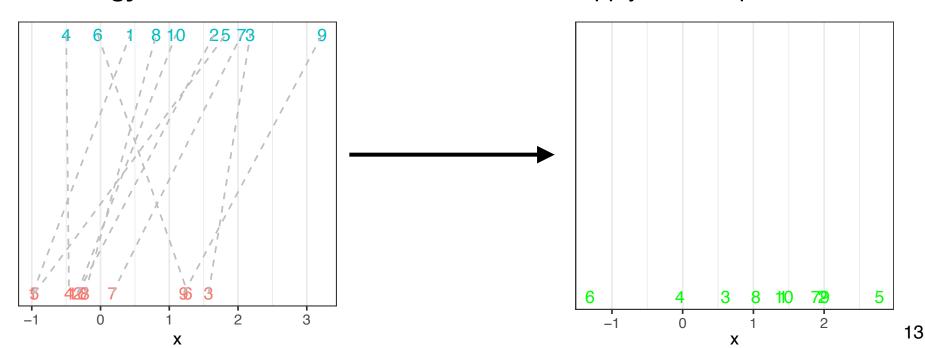
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Data likelihood under MLE of H_0

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Data likelihood under MLE of ${\cal H}_{\!A}$

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Data likelihood under MLE of $\mathcal{H}_{\!\scriptscriptstyle A}$

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$$G^2 \stackrel{\text{def}}{=} -2\log \Lambda^*$$

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$$G^{2} = -2\log \frac{\left(\frac{1}{2}\right)^{30}}{\left(\frac{2}{3}\right)^{20} \left(\frac{1}{3}\right)^{10}} \approx 3.4$$

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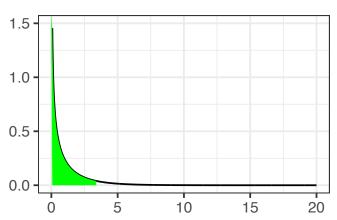
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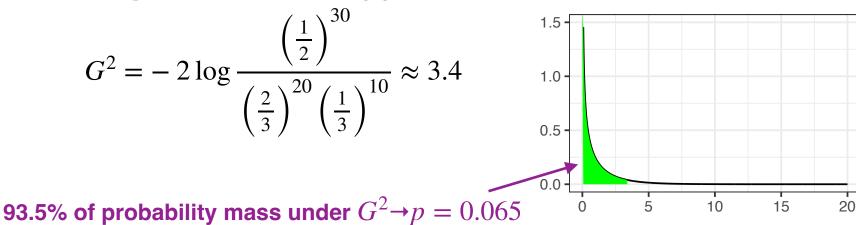
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Data likelihood under MLE of $H_{\scriptscriptstyle A}$

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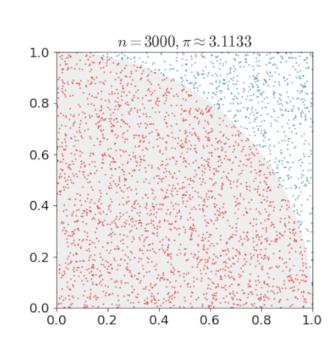
Simulation and approximate computation

Simulation and approximate computation

- All the statistical analysis that I've shown you so far has involved exact computation using analytic expressions
- This is facilitated by:
 - Strong assumptions regarding the data generating process (e.g., iid normal data for t-tests); and/or
 - Conjugate priors for Bayesian inference (e.g., Beta prior for Bernoulli/binomial data)
- But often, exact computation is not possible
- Solution: use more computationally intensive methods that don't rely on these strong assumptions. Examples:
 - Bootstrapped confidence intervals
 - Nonparametric statistical tests
 - Monte Carlo methods (today)

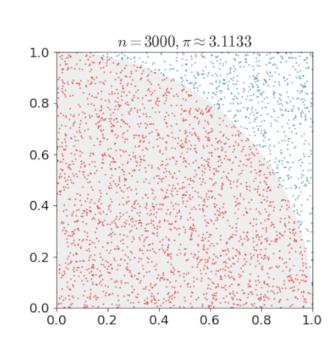
Monte Carlo methods, or "probabilistic simulation"

- Generally speaking:
 - 1. Define a domain of possible inputs
 - 2. Generate *n* iid random inputs from a probability distribution on the domain
 - 3. Perform a deterministic computation on each randomly generated input
 - 4. Aggregate the results of the deterministic computation
- As n grows larger, the simulated result approaches the true value



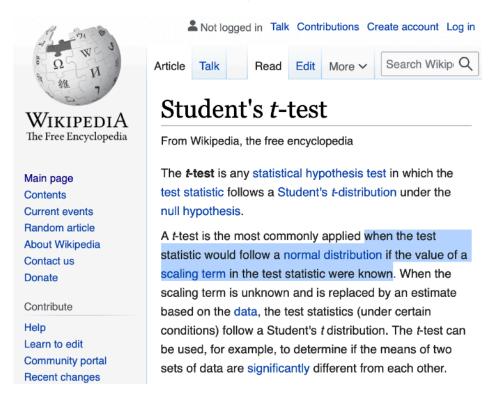
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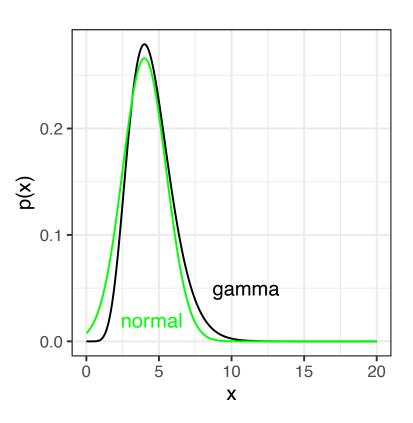
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Simple example of Monte Carlo

 Suppose I want to do a two-sample t-test but my data aren't normally distributed





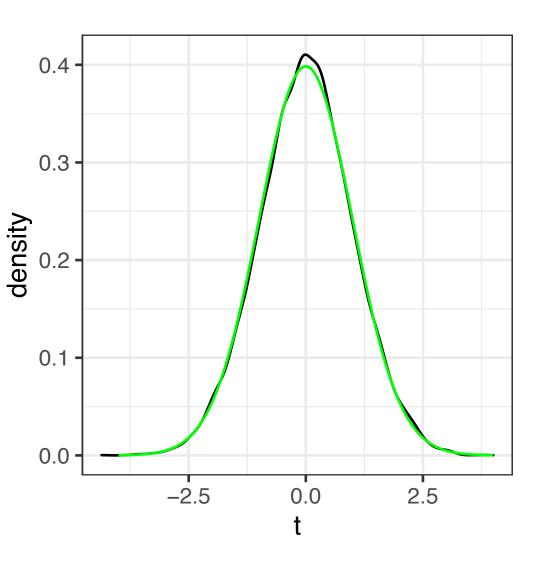
How bad will this be for my t-test????

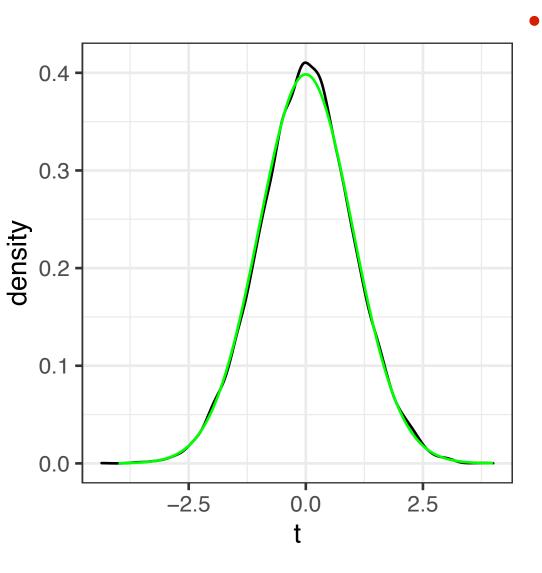
```
library(ggplot2)
 2
    library(tidyverse)
 3
 4
    # Manually compute Student t-statistic
 5 \cdot f \leftarrow function(seed, N=100, shape=9, scale=0.5)
      set.seed(seed)
 6
      y1 <- rgamma(N, shape=shape, scale=scale)
 8
      y2 <- rgamma(N, shape=shape, scale=scale)
      s_p \leftarrow sqrt((var(y1) + var(y2)) / 2)
      t_{statistic} \leftarrow (mean(y1) - mean(y2)) / (s_p*sqrt(2/N))
10
      return(t_statistic)
11
12 - }
13
14
    N <- 100
15
    Ts <- sapply(1:10000,f)
16
17
    t_reference \leftarrow tibble(x=seq(-4,4,by=0.01),t=dt(x,df=2*(N-1)))
18
19
    qaplot(data=tibble(t=Ts),aes(x=t)) +
20
      geom_density() +
21
      geom_line(data=t_reference,aes(x=x,y=t),color="green",linetype="dashed")
```

```
library(ggplot2)
 2
    library(tidyverse)
 3
 4
    # Manually compute Student t-statistic
    f <- function(seed, N=100, shape=9, scale=0.5) {
      set.seed(seed)
 6
                                                                Reproducibility!
      y1 <- rgamma(N, shape=shape, scale=scale)
 8
      y2 <- rgamma(N, shape=shape, scale=scale)
      s_p \leftarrow sqrt((var(y1) + var(y2)) / 2)
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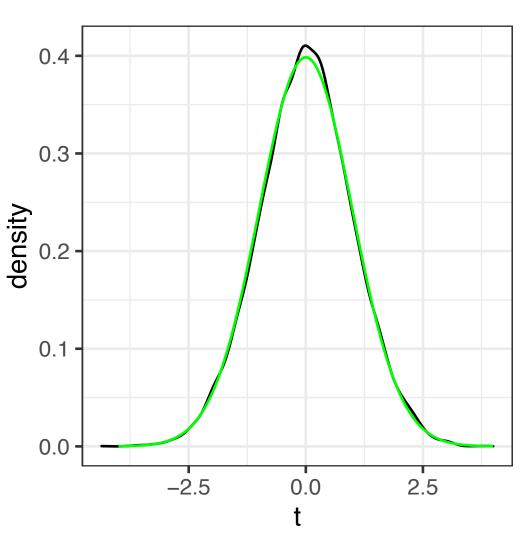
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10
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11
12 - }
13
                            Monte Carlo simulation
14
    N < -100
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10
11
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12 - }
13
                            Monte Carlo simulation
14
    N < -100
15
   Ts <- sapply(1:10000,f)
                                           Compare against Student's t distribution
16
    (t_reference <- tibble(x=seq(-4,4,by=0.01),t=dt(x,df=2*(N-1)))
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19
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 The t distribution is still a pretty good approximation of the distribution of the t statistic, even when the underlying distribution is gamma!



- The t distribution is still a pretty good approximation of the distribution of the t statistic, even when the underlying distribution is gamma!
- This exemplifies what is meant when people say that the t test is robust to deviations from normality

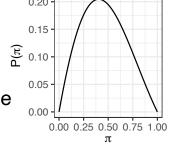
Our motivation: Bayesian posterior inference

$$P(\theta | \mathbf{y}, I) = \frac{P(\mathbf{y} | \theta, I)P(\theta | I)}{P(\mathbf{y} | I)}$$

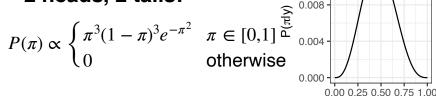
• Sometimes P(y | I) can't be calculated exactly. Example

Bernoulli data with non-conjugate prior:

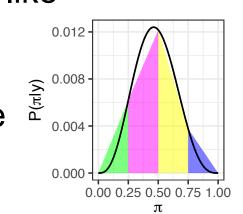
$$P(\pi) \propto \begin{cases} \pi(1-\pi)e^{-\pi^2} & \pi \in [0,1] \end{cases}$$
0 otherwise



Posterior after observing 2 heads, 2 tails:



In simple cases like this, we can numerically approximate the integral:



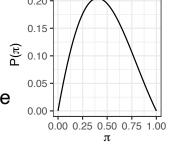
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 Model parameters

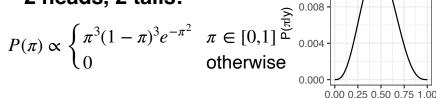
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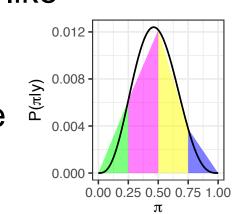
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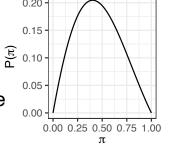
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 Background knowledge

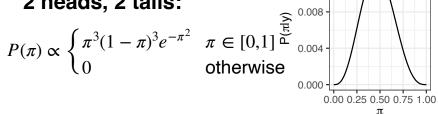
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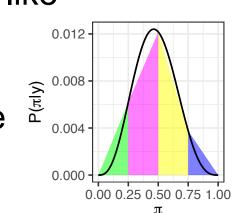
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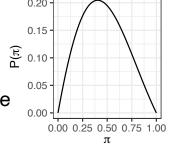
Observed data $P(\theta | \mathbf{y}, I) = \frac{P(\mathbf{y} | \theta, I)P(\theta | \mathbf{I})}{P(\mathbf{y} | I)}$ Model parameters

Background knowledge

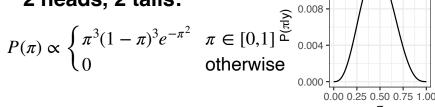
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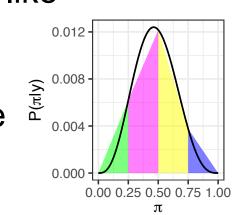
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Posterior after observing 2 heads, 2 tails:



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Our motivation: Bayesian posterior inference

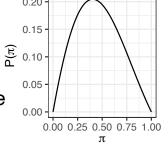
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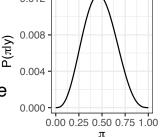
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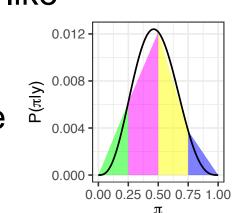
Posterior after observing 2 heads, 2 tails:

$$P(\pi) \propto \begin{cases} \pi^3 (1-\pi)^3 e^{-\pi^2} & \pi \in [0,1]^{\frac{2}{6}} \\ 0 & \text{otherwise} \end{cases}$$

No closed form!

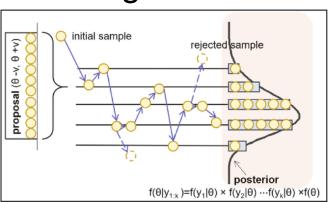


In simple cases like this, we can numerically approximate the integral:



Markov chain Monte Carlo

- However, we can often take samples from the posterior even when we can't compute normalized probabilities
- One general and widely used approach: Markov chain Monte Carlo (MCMC)
- MCMC is a mathematically principled random walk on a non-negative function, directed toward regions where the function takes on a larger value

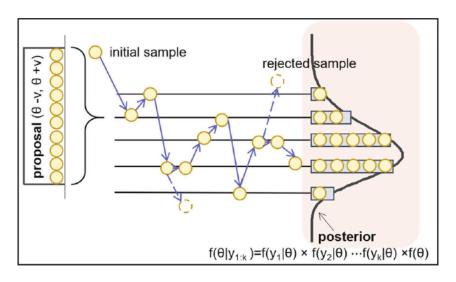


 Asymptotically, the random walk gives us samples from in proportion to the height of the function

MCMC for posterior sampling

We use the unnormalized form of the posterior:

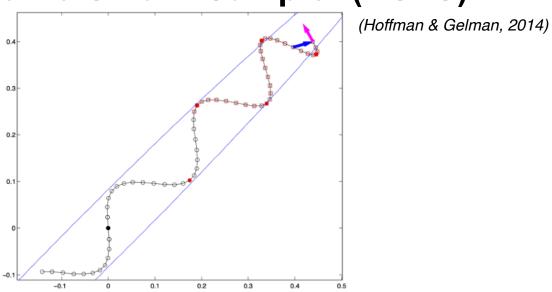
$$P(\theta \mid \mathbf{y}, I) \propto P(\mathbf{y} \mid \theta, I)P(\theta \mid I)$$



- We run MCMC and then treat the chain of values as samples from the posterior
- The full set of samples is not iid (nearby values on the chain are correlated), but methods exist for estimating "effectively" how many independent samples we have

Stan, HMC, and NUTS

- There are many different MCMC algorithms (e.g., Metropolis, Gibbs Sampling)
- We will use the probabilistic programming language Stan for Bayesian inference about model parameters
- Stan uses an algorithm called Hamiltonian Monte Carlo (HMC) with the No U-Turn Sampler (NUTS)



 This algorithm tends to be particularly efficient for many problems we'll face

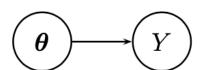
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