

# Bayesian hypothesis testing (cont.)

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# Outline

- Review of formal Bayesian hypothesis testing
- Likelihood ratio tests
- Jeffrey-Lindley paradox
- $p$ -value interpretation

# Bayes tests = evaluate predictive models

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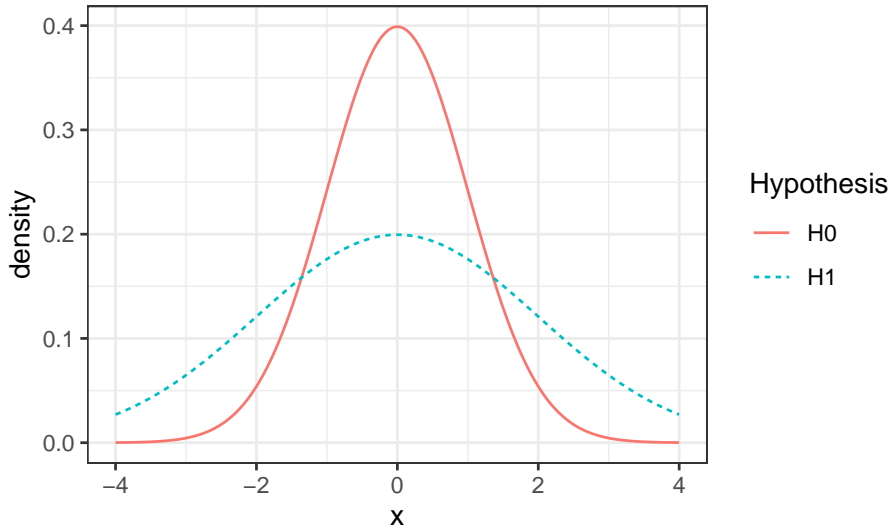
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Now, as  $C \rightarrow \infty$ , our predictions about  $y$  become less sharp.





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where  $\nu$  is the difference between the number of free parameters specified by  $\theta \in \theta_0$  and the number of free parameters specified by  $\theta \in \Theta$ .



## Binomial example

Consider a coin flipping experiment so that  $Y_i \stackrel{iid}{\sim} \text{Ber}(\theta)$  and the null hypothesis  $H_0 : \theta = 0.5$  versus the alternative  $H_1 : \theta \neq 0.5$ .

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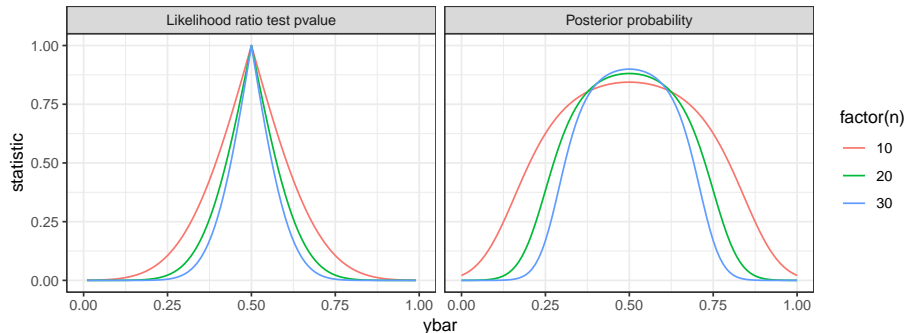
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If  $p\text{-value} < a$ , then we reject  $H_0$  at significance level  $a$ . Typically  $a = 0.05$ .

# Binomial example

$Y \sim \text{Bin}(n, \theta)$  and, for the Bayesian analysis,  $\theta|H_1 \sim \text{Be}(1, 1)$  and  $p(H_0) = p(H_1) = 0.5$ :



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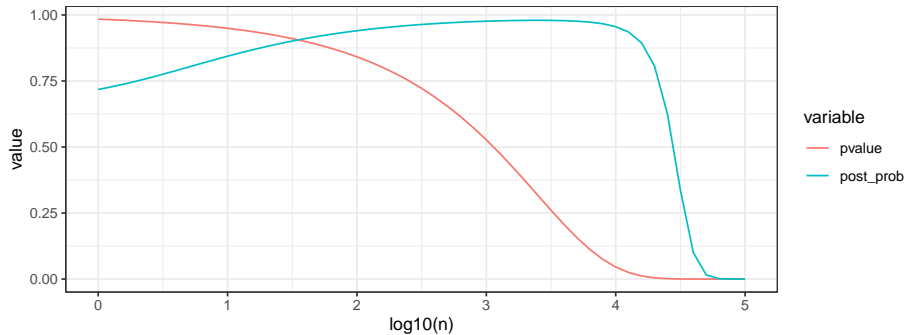
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It appears the Bayesian and LRT  $p$ -value completely disagree!

Binomial  $\bar{y} = 0.49$  with  $n \rightarrow \infty$



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- $H_1$  is relatively diffuse, and
- the prior model odds is  $\approx 1$ .

# Comparison

The test statistic with point null hypotheses:

$$\lambda(y) = \frac{p(y|\theta_0)}{p(y|\hat{\theta}_{MLE})}$$

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- The LRT can be interpreted as a Bayesian point mass prior exactly at the MLE.
- Generally,  $p$ -values provide a measure of lack-of-fit of the data to the null model.
- Bayesian tests compare predictive performance of two Bayesian models (model+prior).

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But, if we reject  $H_0$ , i.e. the  $p$ -value  $< \alpha$ , we should be interested in

$$P(H_0 \text{ true} | \text{reject } H_0)$$



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We can compute a two-sided  $p$ -value via

$$p\text{-value} = 2\Phi(-|y|)$$

where  $\Phi(\cdot)$  is the cumulative distribution function for a standard normal.

Typically, we set our Type I error rate at level  $\alpha$ , i.e.

$$P(\text{reject } H_0 | H_0 \text{ true}) = \alpha.$$

But, if we reject  $H_0$ , i.e. the  $p$ -value  $< \alpha$ , we should be interested in

$$P(H_0 \text{ true} | \text{reject } H_0) = 1 - \text{FDR}$$

where FDR is the False Discovery Rate.

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Then this  $p$ -value app below will calculate (via simulation) the probability the null hypothesis is true.

```
shiny::runGitHub('jarad/pvalue')
```

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Thus, there is nothing Bayesian happening here except that the probability being calculated has the unknown quantity on the left and the known quantity on the right.

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This situation is common enough that it is called The Prosecutor's Fallacy.

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<https://amstat.tandfonline.com/doi/abs/10.1080/00031305.2016.1154108>

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6. By itself, a  $p$ -value does not provide a good measure of evidence regarding a model or hypothesis.