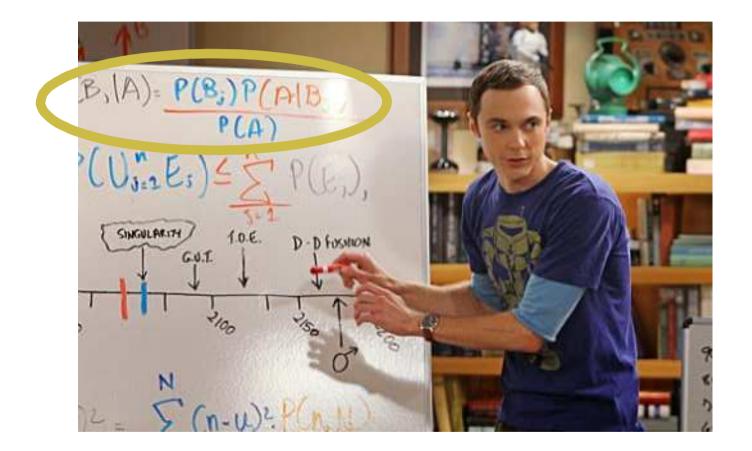
## **Bayesian probability theory**

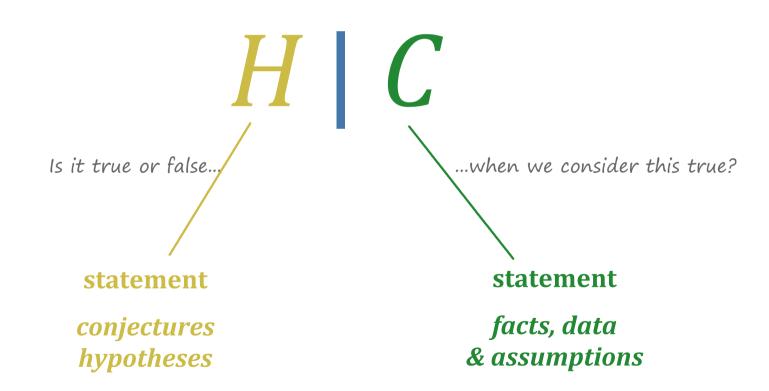


⋇

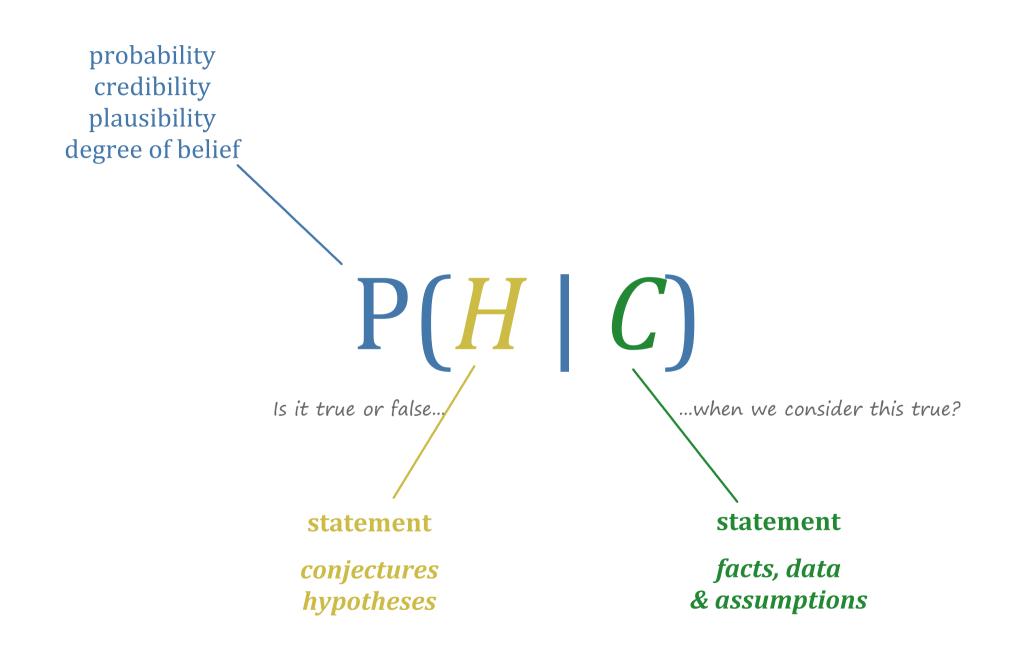
\*

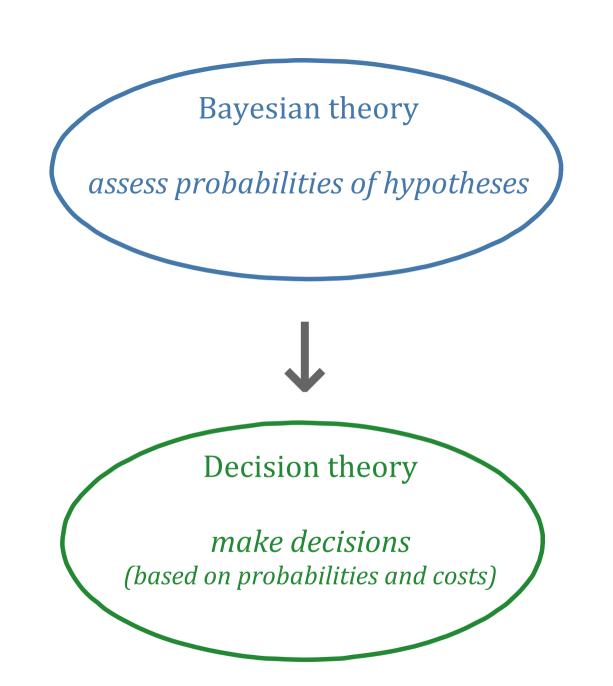
H statement conjectures hypotheses \*

Is it true or false? statement conjectures hypotheses Probability of a statement given another statement

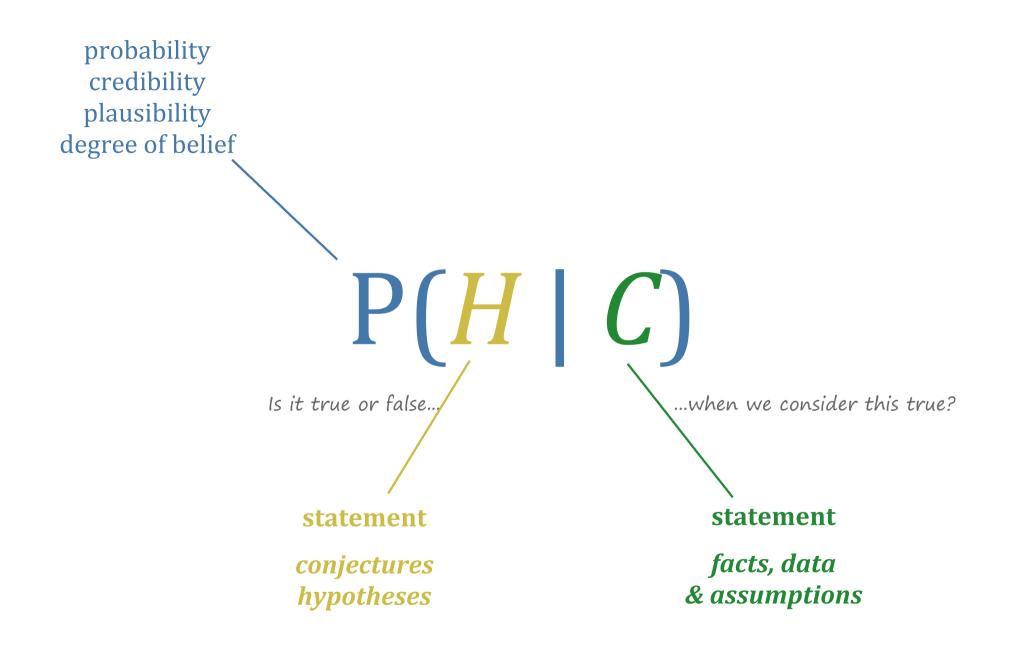


'Probability of statement H given statement C'

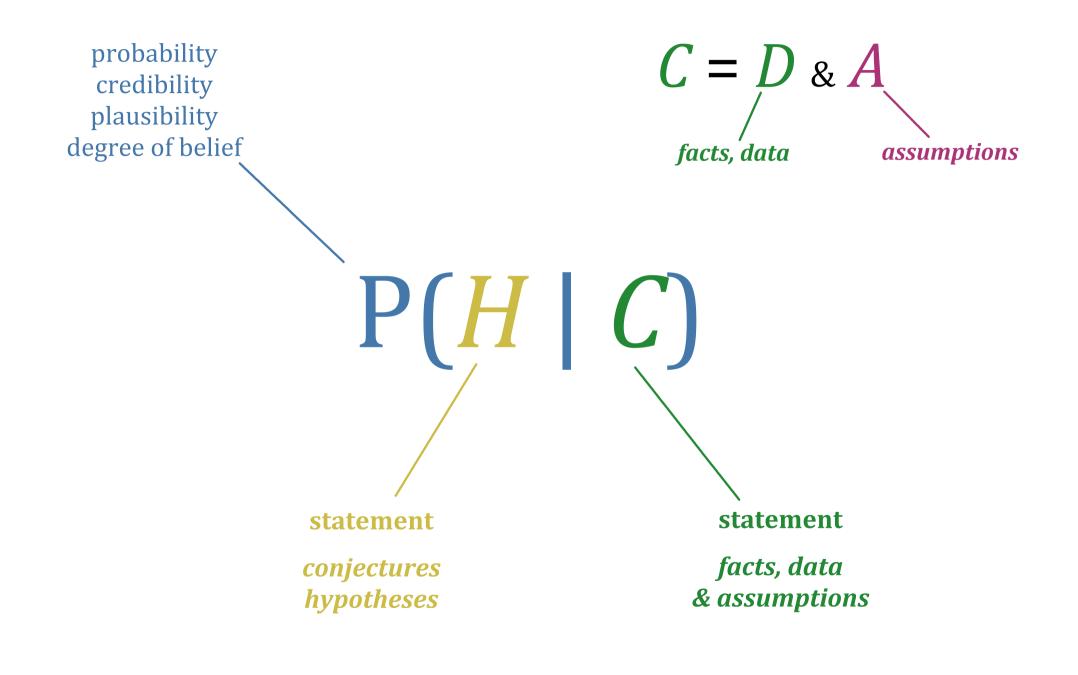




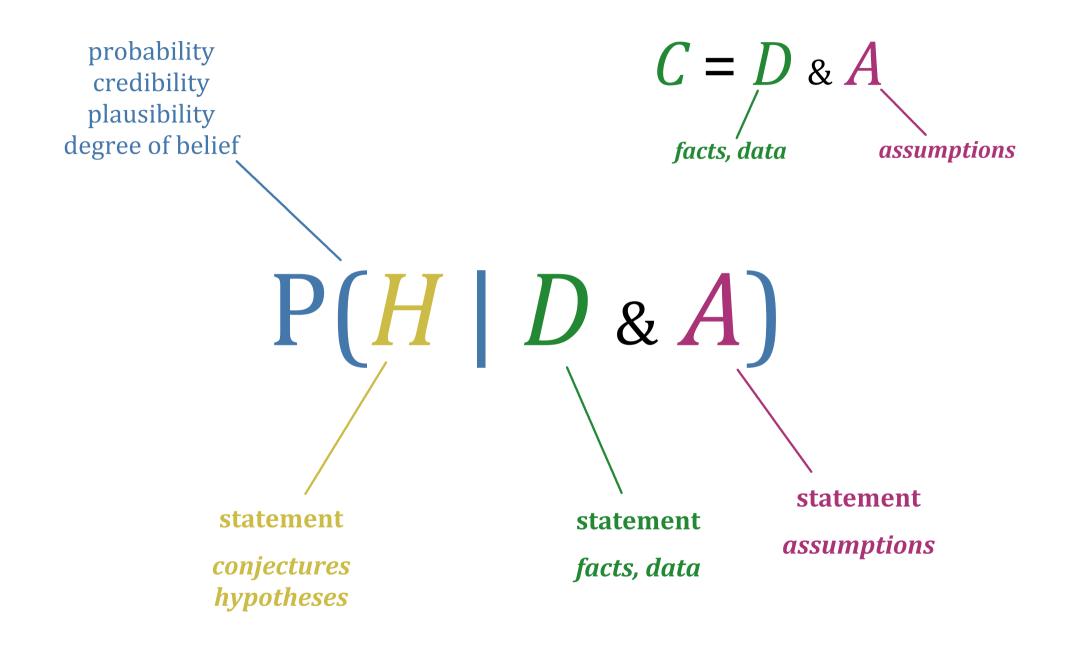












# The three basic rules of the probability calculus $P(not-Q \mid S) = 1 - P(Q \mid S)$ $P(Q \& R \mid S) = P(Q \mid R \& S) \cdot P(R \mid S)$ $P(Q \text{ or } R \mid S) = P(Q \mid S) + P(R \mid S) - P(Q \& R \mid S)$

All probability calculations and results, however complicated they might look, are just the application of the three rules above, over and over and over again

The three basic rules of the probability calculus

## $P(not-Q \mid S) = 1 - P(Q \mid S)$

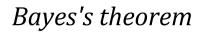
 $P(Q \& R | S) = P(Q | R \& S) \cdot P(R | S)$ 

## $P(Q \text{ or } R \mid S) = P(Q \mid S) + P(R \mid S) - P(Q \& R \mid S)$

#### Rules of Inference: Elementary Valid Argument Forms

Abbreviation	Form	
M.P.	$p \supset q$ p	
M.T.	$p \supset q$	Introduction to
H.S.	$\begin{array}{c} \ddots & \sim p \\ p \supset q \\ q \supset r \end{array}$	LOGIC
D.S.	$\begin{array}{c} \therefore p \supset r \\ p \lor q \\ \sim p \end{array}$	
C.D.	$ \begin{array}{c} \therefore \ q \\ (p \supset q) \bullet (r \supset s) \\ p \lor r \end{array} $	
Abs.	$\therefore q \lor s$ $p \supset q$ $\therefore p \supset (p \bullet q)$	
Simp.	$p \cdot q$	
Conj.	p q	Irving M. Copi Carl Cohen Victor Rodych
Add.	$\begin{array}{c} \cdot \cdot p \bullet q \\ p \\ \cdot \cdot p \lor q \end{array}$	15th edition
	M.P. M.T. H.S. D.S. C.D. Abs. Simp. Conj.	M.P. $p \supset q$ $p$ $\therefore q$ M.T. $p \supset q$ $\sim q$ $\therefore p \supset q$ $q \supset r$ $\therefore p \supset r$ H.S. $p \supset q$ $q \supset r$ $\therefore p \supset r$ D.S. $p \lor q$ $\sim p$ $\therefore q$ C.D. $(p \supset q) \cdot (r \supset s)$ $p \lor r$ $\therefore q \lor s$ Abs. $p \supset q$ $\therefore p \supset (p \cdot q)$ Simp. $p \cdot q$ $\therefore p$ Conj. $p$ $q$ $\therefore p \cdot q$ Add. $p$

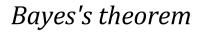




\*

## $P(H_{\#1} \mid D \& A) = \frac{P(D \mid H_{\#1} \& A) \cdot P(H_{\#1} \mid A)}{P(D \mid H_{\#1} \& A) \cdot P(H_{\#1} \mid A) + P(D \mid H_{\#2} \& A) \cdot P(H_{\#2} \mid A) + \dots}$

(sum over all possible hypotheses)



## $P(H_{\#1} \mid D \& A) = \frac{P(D \mid H_{\#1} \& A) \cdot P(H_{\#1} \mid A)}{P(D \mid H_{\#1} \& A) \cdot P(H_{\#1} \mid A) + P(D \mid H_{\#2} \& A) \cdot P(H_{\#2} \mid A) + \dots}$

(sum over all possible hypotheses)

 $P(hypothesis | data \& assumptions) \propto$ 

P(*data* | *hypothesis* & *assumptions*) × P(*hypothesis* | *assumptions*)

**Probability of some hypotheses, given data**  $P(H \mid D \& A) \propto P(D \mid H \& A) \cdot P(H \mid A)$ 

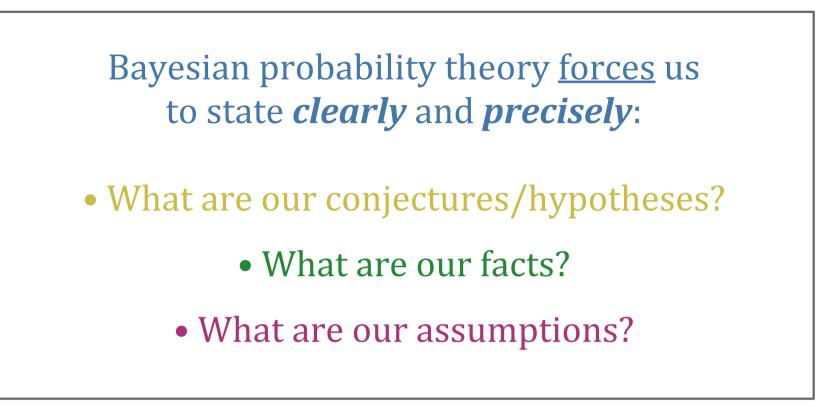
\*

Typical elements of Bayesian analysis

**Probability of some hypotheses, given data**  $P(H \mid D \& A) \propto P(D \mid H \& A) \cdot P(H \mid A)$ 

- Formulate precise hypotheses
- Assess which data we have or need
- Examine which assumptions we need to make
- Assess the probability of the data given each hypothesis
- Assess the pre-data probability of each hypothesis

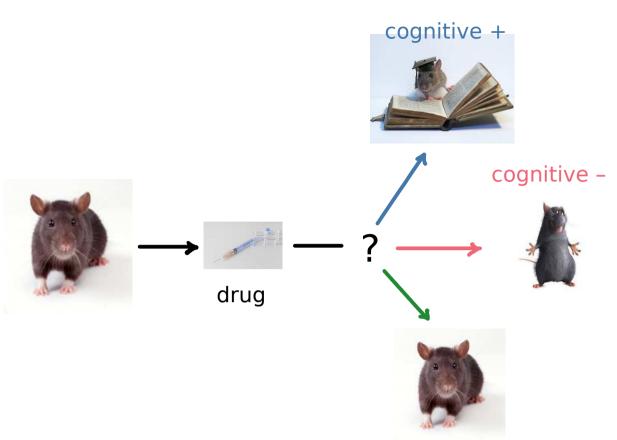




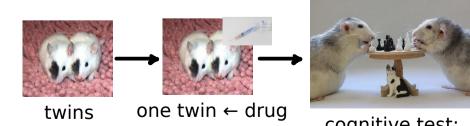


The rats & drug investigation:

approach via Bayesian probability theory



cognitive =



cognitive test: which twin wins?



- Formulate precise hypotheses
- Assess which data we have or need
- Examine which assumptions we need to make
- Assess the probability of the data given each hypothesis
- Assess the pre-data probability of each hypothesis

**Probability of each hypothesis, given the data**  $P(H \mid D \& A) \propto P(D \mid H \& A) \cdot P(H \mid A)$ 

## ► Formulate precise hypotheses

What is our question?
What is the purpose of this study?

- Assess which data we have or need
- Examine which assumptions we need to make
- Assess the probability of the data given each hypothesis
- Assess the pre-data probability of each hypothesis



### Does the drug enhance cognitive abilities?

 $\rightarrow$  Yes, No, Sometimes, It depends, ...



Does the drug enhance cognitive abilities?  $\rightarrow$  Yes, No, Sometimes, It depends, ...

Ultimate question, but too complex

(we'll return to it later)



*Is there a systematic effect?* 

 $\rightarrow$  Yes, No?

#### \*

What are our hypotheses? What are our question & purpose?

Is there a systematic effect?  $\rightarrow$  Yes,

Less complex, but too vague

What do we mean by 'systematic'? If 'systematic' = 'every time' then the answer is No.

We want a question that is

- less categorical
- quantifiable

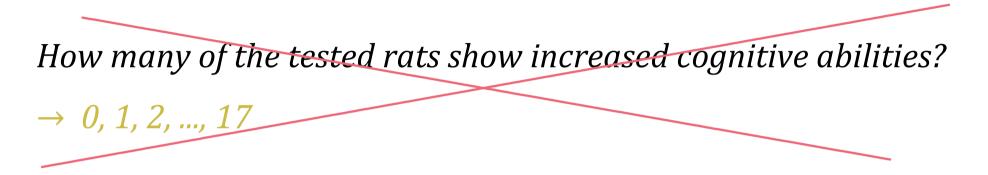


### *How many of the tested rats show increased cognitive abilities?*

→ *0, 1, 2, ..., 17* 

#### \*

What are our hypotheses? What are our question & purpose?



Better! But no probabilities here: after the experiment, we know the exact answer with 100% certainty.

Are we interested in *these specific* 17 rat twins *only*?



## Would the drug lead to a positive result, if tested on a **new** twin pair?

 $\rightarrow$  Yes, No



## Would the drug lead to a positive result, if tested on a **new** twin pair? $\rightarrow$ Yes, No

Good!

We are concretely asking if our study *extrapolates*. This question can be answered also in practice.



## In a **much larger number** of tests, how many positive results? $\rightarrow n = 0, 1, 2, ..., full population N$



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Also good!

Although practically impossible to answer experimentally, this question has clear and unequivocal answers. It quantifies 'how systematic' the effect is.

NB: We need to specify what's the "full population"

The probabilities for the two good questions are often connected:

 $P(New | data) = \sum n/N P(n | data)$ 



## In a **much larger number** of tests, how many a positive results? $\rightarrow n = 0, 1, 2, ..., full population N$

Also good!

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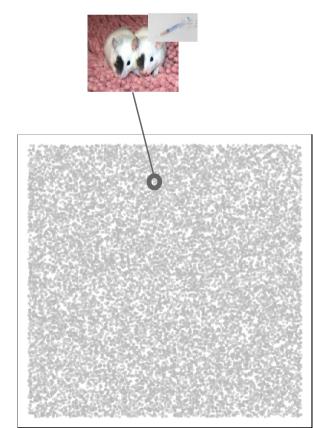
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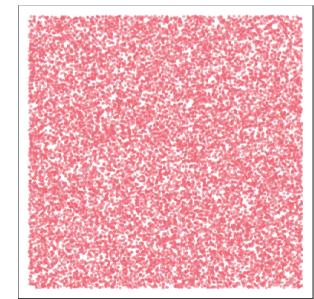






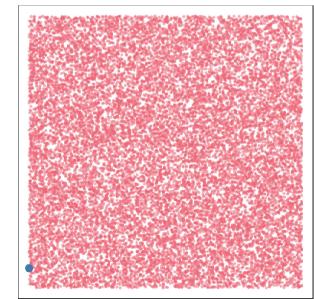


 $H_0$  = 'In 1 billion tests, **no** test yields cognitive+ (all cognitive-)'



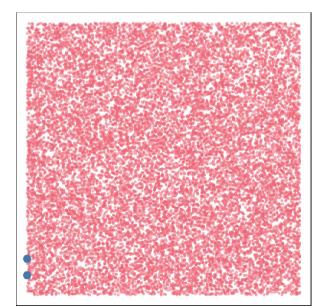


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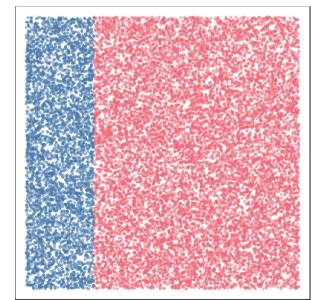


 $H_0$  = 'In 1 billion tests, **no** test yields cognitive+ (all cognitive-)'  $H_{0.000\ 000\ 001}$  = 'In 1 billion tests, **1** test yields cognitive+'  $H_{0.000\ 000\ 002}$  = 'In 1 billion tests, **2** tests yield cognitive+'





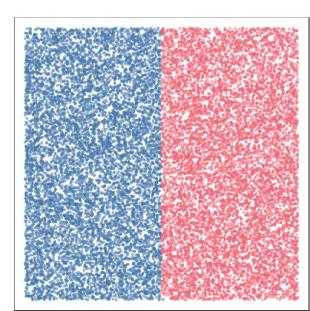
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 $H_0$  = 'In 1 billion tests, **no** test yields cognitive+ (all cognitive-)'  $H_{0.000\ 000\ 001}$  = 'In 1 billion tests, **1** test yields cognitive+'  $H_{0.000\ 000\ 002}$  = 'In 1 billion tests, **2** tests yield cognitive+'

 $H_{0.25}$  = 'In 1 billion tests, 250 000 000 yield cognitive+'





 $H_0 = (In 1 billion tests, no test yields cognitive+ (all cognitive-))$  $H_{0.000\,000\,001}$  = 'In 1 billion tests, 1 test yields cognitive+'  $H_{0.000\,000\,002}$  = 'In 1 billion tests, 2 tests yield cognitive+'  $H_{0.25}$  = 'In 1 billion tests, 250 000 000 yield cognitive+'  $H_{0.5}$  = 'In 1 billion tests, 500 000 000 yield cognitive+' - - - $H_1 =$  'In 1 billion tests, all tests yield cognitive+'

#### \*

#### Let's compare 100000001 concrete hypotheses:

 $H_0$  = 'In 1 billion tests, **no** test yields cognitive+ (all cognitive-)'  $H_{0.000\,000\,001}$  = 'In 1 billion tests, **1** test yields cognitive+'

 $H_1$  = 'In 1 billion tests, **all** tests yield cognitive+'

### $H_f$ = 'In 10000000 tests, a fraction f yield cognitive+'

# f = 0, 1/100000000, 2/100000000, ..., 9999999999/1000000000, 1

(all +)



- Formulate precise hypotheses
- Assess which data we have or need
- Examine which assumptions we need to make
- Assess the probability of the data given each hypothesis
- Assess the pre-data probability of each hypothesis

\*

Which data do we have?

## 17 twins tested: 13 drug $\rightarrow$ cognitive+, 4 drug $\rightarrow$ cognitive-

his was the 17th pair Time to stop.

• Lab#1's stopping rule: test 17

• Lab#2's stopping rule: test until at least four "+" and "-"







- Formulate precise hypotheses
- Assess which data we have or need
- Examine which assumptions we need to make
- Assess the probability of the data given each hypothesis
- Assess the pre-data probability of each hypothesis



Assumptions are necessary for two purposes:

- to assess the probability of the data, given each hypothesis
- to assess the pre-data probability of each hypothesis



• to assess the probability of the data, given each hypothesis

P('In 17 tests, 13 cognitive+' | 'In 1 billion tests, 100 cognitive+' & A)



• to assess the probability of the data, given each hypothesis

P('In 17 tests, 13 cognitive+' | 'In 1 billion tests, 100 cognitive+' & A)

Assumptions:



• to assess the probability of the data, given each hypothesis

P('In 17 tests, 13 cognitive+' | 'In 1 billion tests, 100 cognitive+' & A)

<u>Assumptions</u>:

- The tested rats are part of the larger set of 1 billion tests
- The tested rats are **not specially** chosen from the larger population



• to assess the probability of the data, given each hypothesis

P('In 17 tests, 13 cognitive+' | 'In 1 billion tests, 100 cognitive+' & A)

<u>Assumptions</u>:

- The tested rats are part of the larger set of 1 billion tests
- The tested rats are **not specially** chosen from the larger population

→ If some tested rats were unsystematically exchanged with some in the remaining population, our results would still be valid

We say that the tested rats are *exchangeable* with the full population



• to assess the probability of the data, given each hypothesis

P('In 17 tests, 13 cognitive+' | 'In 1 billion tests, 100 cognitive+' & A)

<u>Assumptions</u>:

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The Annals of Statistics 1981, Vol. 9, No. 1, 45-58

#### THE ROLE OF EXCHANGEABILITY IN INFERENCE<sup>1</sup>

BY D. V. LINDLEY AND MELVIN R. NOVICK

University College London and The University of Iowa

This paper is concerned with basic problems of statistical inference. The thesis is in three parts: (1) that inference is a procedure whereby one passes from a population (or sample) to a new individual; (2) that this connection can be established using de Finetti's idea of exchangeability or Fisher's concept of a subpopulation; (3) in making the connection use must be made of the appropriate probability. These three principles are used in a variety of situations and the topics discussed include analysis of variance and covariance, contingency tables, and calibration. Some comments on randomization are also included.



- Formulate precise hypotheses
- Assess which data we have or need
- Examine which assumptions we need to make
- Assess the probability of the data given each hypothesis
- Assess the pre-data probability of each hypothesis

# Probability of data given hypotheses: Lab#1



$$P(13+4-|H_{0.7} \& A) = \begin{pmatrix} 17\\4 \end{pmatrix} \times 0.7^{13} \times (1-0.7)^4 = 0.1868$$
(This is an approximation to 8 significant digits:

the correct distribution is a hypergeometric one)

# Probability of data given hypotheses: Lab#2



$$P(13+4-|H_{0.7} \& A) = {\binom{16}{3}} \times 0.7^{13} \times (1-0.7)^4 = 0.04395$$

$$\uparrow$$
because of the stopping rule

we couldn't shuffle the last -

# Probability of sequence given hypotheses (same for both labs)

\*

 $P(++++-++++++++) = H_{0.7} \& A = 0.7^{13} \times (1-0.7)^4 = 0.00007848$ 

(Considering the sequences as outcomes would lead to a p-value = 1)



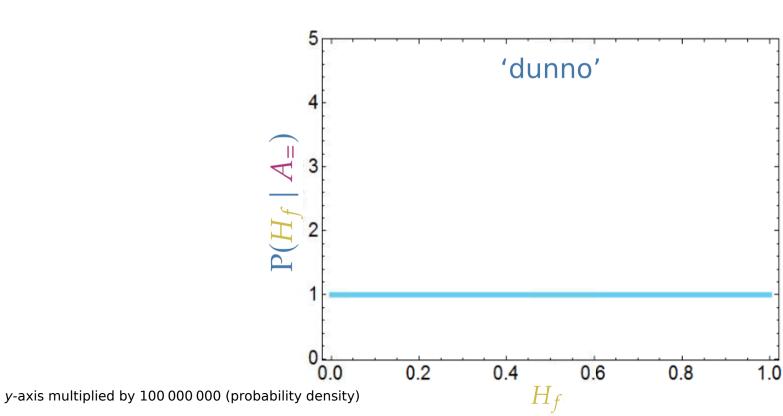
- Formulate precise hypotheses
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- Assess the pre-data probability of each hypothesis

#### \*

# Pre-data probabilities of hypotheses

Let's consider three possible assumptions as examples:

*A*<sub>=</sub> : '*Dunno*', all frequencies equally plausible

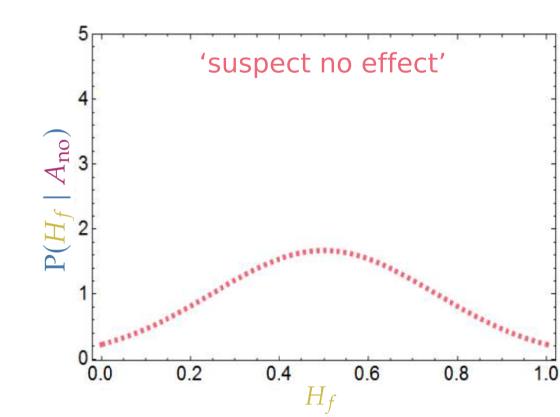


# Pre-data probabilities of hypotheses

Let's consider three possible assumptions as examples:

#### *A*<sub>=</sub> : '*Dunno*', all frequencies equally plausible

Ano : 'Suspect no effect', frequencies f ~ 0.5 slightly more plausible (equal number of + and −)



# Pre-data probabilities of hypotheses

Let's consider three possible assumptions as examples:

#### *A*<sub>=</sub> : '*Dunno*', all frequencies equally plausible

- Ano : 'Suspect no effect', frequencies ~0.5 slightly more plausible (equal number of + and −)
- $A_{\text{ves}}$ : 'Suspect effect', frequencies  $f \sim 0.25$ , 0.75 slightly more plausible (fewer + than - or vice versa) 'suspect effect' Ayes.  $P(H_f |$ 0.2 0.4 0.6 0.8 1.0 0.0 Η



- Formulate precise hypotheses
- Assess which data we have or need
- Examine which assumptions we need to make
- Assess the probability of the data given each hypothesis
- Assess the pre-data probability of each hypothesis

► Probability of each hypothesis, given the data  $P(H | D \& A) \propto P(D | H \& A) \cdot P(H | A)$ 

#### \*

 $P(hypothesis | data \& assumptions) \propto P(data | hypothesis \& assumptions) \cdot P(hypothesis | assumptions)$ 

$$P(H_{f} | D \& A) = \frac{P(D | H_{f} \& A) \cdot P(H_{f} | A)}{P(D | H_{0} \& A) \cdot P(H_{0} | A) + ... + P(D | H_{1} \& A) \cdot P(H_{1} | A)}$$

(1 000 000 001 terms)

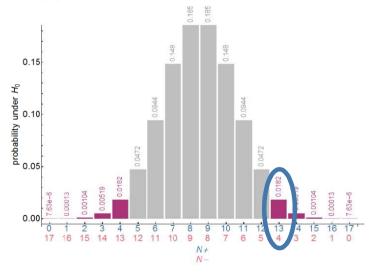
#### $P(hypothesis | data \& assumptions) \propto P(data | hypothesis \& assumptions) \cdot P(hypothesis | assumptions)$

$$P(H_{f} | D \& A) = \frac{P(D | H_{f} \& A) \cdot P(H_{f} | A)}{P(D | H_{0} \& A) \cdot P(H_{0} | A) + ... + P(D | H_{1} \& A) \cdot P(H_{1} | A)}$$

(1 000 000 001 terms)

Bayes's formula:

- is **not** listing outcomes that **could have** happened (but didn't)
- is listing alternative hypotheses



#### \*

# Probability of hypotheses given data: Lab#1

 $P(H_f | data lab#1 \& A) =$ 

 $\mathbf{P}(D \mid H_f \& A) \cdot \mathbf{P}(H_f \mid A)$ 

 $P(D | H_0 \& A) \cdot P(H_0 | A) + \dots + P(D | H_{0.5} \& A) \cdot P(H_{0.5} | A) + \dots + P(D | H_1 \& A) P(H_1 | A)$ 

 $P(H_{f} \mid \text{data lab#1 \& } A) = \begin{pmatrix} 17 \\ 4 \end{pmatrix} \cdot f^{13} \cdot (1 - f)^{4} \cdot P(H_{f} \mid A) \\ \hline \begin{pmatrix} 17 \\ 4 \end{pmatrix} \cdot 0^{13} \cdot 1^{4} \cdot P(H_{0} \mid A) + \dots + \begin{pmatrix} 17 \\ 4 \end{pmatrix} \cdot 0.5^{13} \cdot 0.5^{4} \cdot P(H_{0.5} \mid A) + \dots + \begin{pmatrix} 17 \\ 4 \end{pmatrix} \cdot 1^{13} \cdot 0^{4} \cdot P(H_{1} \mid A)$ 

$$P(H_{f} \mid \text{data lab#1 \& } A) = \begin{pmatrix} 17 \\ 4 \end{pmatrix} \cdot f^{13} \cdot (1 - f)^{4} \cdot P(H_{f} \mid A) \\ \hline \begin{pmatrix} 17 \\ 4 \end{pmatrix} \cdot 0^{13} \cdot 1^{4} \cdot P(H_{0} \mid A) + \dots + \begin{pmatrix} 17 \\ 4 \end{pmatrix} \cdot 0.5^{13} \cdot 0.5^{4} \cdot P(H_{0.5} \mid A) + \dots + \begin{pmatrix} 17 \\ 4 \end{pmatrix} \cdot 1^{13} \cdot 0^{4} \cdot P(H_{1} \mid A)$$

 $P(H_{f} \mid \text{data lab#1 \&} A) = \begin{pmatrix} 17 \\ 4 \end{pmatrix} \cdot f^{13} \cdot (1 - f)^{4} \cdot P(H_{f} \mid A) \\ \hline \begin{pmatrix} 17 \\ 4 \end{pmatrix} \cdot 0^{13} \cdot 1^{4} \cdot P(H_{0} \mid A) + \dots + \begin{pmatrix} 17 \\ 4 \end{pmatrix} \cdot 0.5^{13} \cdot 0.5^{4} \cdot P(H_{0.5} \mid A) + \dots + \begin{pmatrix} 17 \\ 4 \end{pmatrix} \cdot 1^{13} \cdot 0^{4} \cdot P(H_{1} \mid A) \\ = \frac{f^{13} \cdot (1 - f)^{4} \cdot P(H_{f} \mid A)}{0^{13} \cdot 1^{4} \cdot P(H_{0} \mid A) + \dots + 0.5^{13} \cdot 0.5^{4} \cdot P(H_{0.5} \mid A) + \dots + 1^{13} \cdot 0^{4} \cdot P(H_{1} \mid A)}$ 

 $P(H_{f} \mid \text{data } \text{lab#2 \&} A) = \begin{pmatrix} 16 \\ 3 \end{pmatrix} \cdot f^{13} \cdot (1 - f)^{4} \cdot P(H_{f} \mid A) \\ \hline \begin{pmatrix} 16 \\ 3 \end{pmatrix} \cdot 0^{13} \cdot 1^{4} \cdot P(H_{0} \mid A) + \dots + \begin{pmatrix} 16 \\ 3 \end{pmatrix} \cdot 0.5^{13} \cdot 0.5^{4} \cdot P(H_{0.5} \mid A) + \dots + \begin{pmatrix} 16 \\ 3 \end{pmatrix} \cdot 1^{13} \cdot 0^{4} \cdot P(H_{1} \mid A)$ 

\*

we couldn't shuffle the last – because of the stopping rule

$$P(H_{f} \mid \text{data lab#2 \& } A) = \begin{pmatrix} 16 \\ 3 \end{pmatrix} \cdot f^{13} \cdot (1 - f)^{4} \cdot P(H_{f} \mid A) \\ \hline \begin{pmatrix} 16 \\ 3 \end{pmatrix} \cdot 0^{13} \cdot 1^{4} \cdot P(H_{0} \mid A) + \dots + \begin{pmatrix} 16 \\ 3 \end{pmatrix} \cdot 0.5^{13} \cdot 0.5^{4} \cdot P(H_{0.5} \mid A) + \dots + \begin{pmatrix} 16 \\ 3 \end{pmatrix} \cdot 1^{13} \cdot 0^{4} \cdot P(H_{1} \mid A)$$

$$P(H_{f} \mid \text{data lab#2 \&} A) = \begin{pmatrix} 16 \\ 3 \end{pmatrix} \cdot f^{13} \cdot (1 - f)^{4} \cdot P(H_{f} \mid A) \\ \hline \begin{pmatrix} 16 \\ 3 \end{pmatrix} \cdot 0^{13} \cdot 1^{4} \cdot P(H_{0} \mid A) + \dots + \begin{pmatrix} 16 \\ 3 \end{pmatrix} \cdot 0.5^{13} \cdot 0.5^{4} \cdot P(H_{0.5} \mid A) + \dots + \begin{pmatrix} 16 \\ 3 \end{pmatrix} \cdot 1^{13} \cdot 0^{4} \cdot P(H_{1} \mid A) \\ = \frac{f^{13} \cdot (1 - f)^{4} \cdot P(H_{f} \mid A)}{0^{13} \cdot 1^{4} \cdot P(H_{0} \mid A) + \dots + 0.5^{13} \cdot 0.5^{4} \cdot P(H_{0.5} \mid A) + \dots + 1^{13} \cdot 0^{4} \cdot P(H_{1} \mid A)}$$

# Probability of hypotheses given data sequence

 $P(H_f | \text{data sequence } \& A) =$ 

$$\frac{f^{13} \cdot (1-f)^4 \cdot P(H_f \mid A)}{0^{13} \cdot 1^4 \cdot P(H_0 \mid A) + \dots + 0.5^{13} \cdot 0.5^4 \cdot P(H_{0.5} \mid A) + \dots + 1^{13} \cdot 0^4 \cdot P(H_1 \mid A)}$$

 $P(H_{f} \mid \text{data lab#1 & } A) = P(H_{f} \mid \text{data lab#2 & } A) =$   $P(H_{f} \mid \text{data sequence & } A) =$   $f^{13} \cdot (1 - f)^{4} \cdot P(H_{f} \mid A)$   $\overline{0^{13} \cdot 1^{4} \cdot P(H_{0} \mid A) + \dots + 0.5^{13} \cdot 0.5^{4} \cdot P(H_{0.5} \mid A) + \dots + 1^{13} \cdot 0^{4} \cdot P(H_{1} \mid A)}$ 

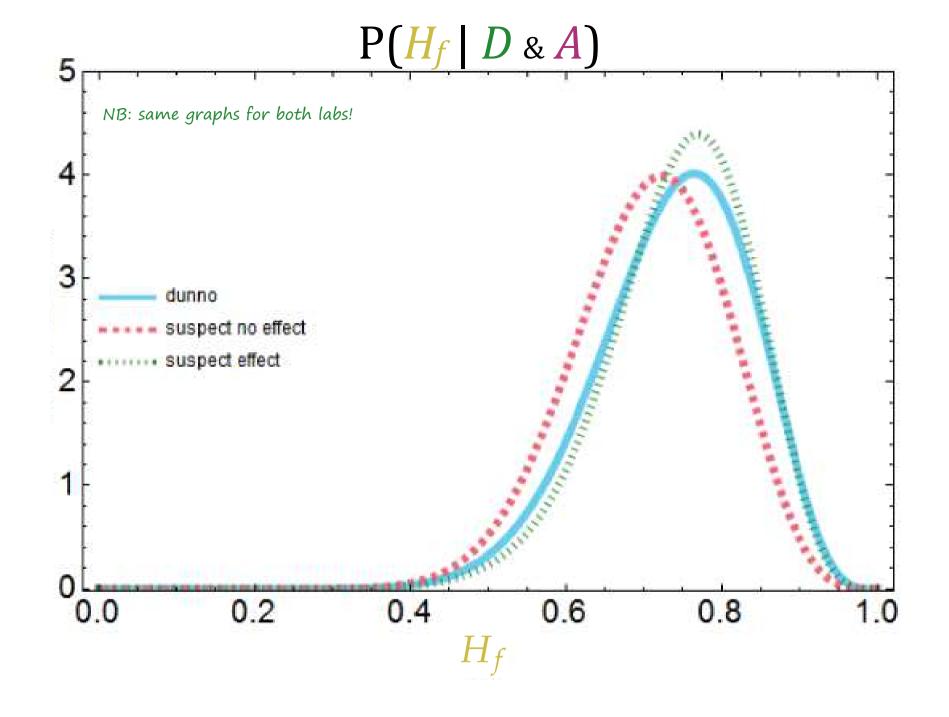
stopping rules don't affect the final probability!

 $P(H_{f} \mid \text{data } \text{lab#1 & } A) = P(H_{f} \mid \text{data } \text{lab#2 & } A) =$   $P(H_{f} \mid \text{data sequence & } A) =$   $f^{13} \cdot (1 - f)^{4} \cdot P(H_{f} \mid A)$   $\overline{0^{13} \cdot 1^{4} \cdot P(H_{0} \mid A) + \dots + 0.5^{13} \cdot 0.5^{4} \cdot P(H_{0.5} \mid A) + \dots + 1^{13} \cdot 0^{4} \cdot P(H_{1} \mid A)}$ 

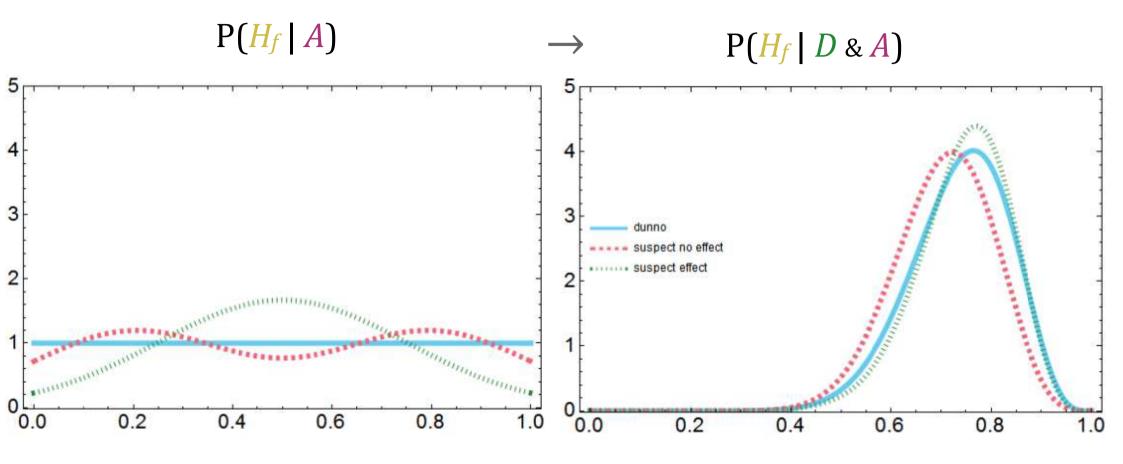
Now let's substitute the pre-data probabilities

 $P(H_f | data lab#1 \& A) = P(H_f | data lab#2 \& A) =$  $P(H_f | \text{data sequence } \& A) =$  $f^{13} \cdot (1-f)^4 \cdot \mathbf{P}(H_f \mid A)$  $\overline{0^{13} \cdot 1^4 \cdot P(H_0 \mid A) + \dots + 0.5^{13} \cdot 0.5^4 \cdot P(H_{0.5} \mid A) + \dots + 1^{13} \cdot 0^4 \cdot P(H_1 \mid A)}$  $\Pr_{\mathbf{N}}(H_f \mid A_{\mathrm{no}})$ 1.0 0.6 0.2 0.4 0.8  $H_{f}$ 

⋇

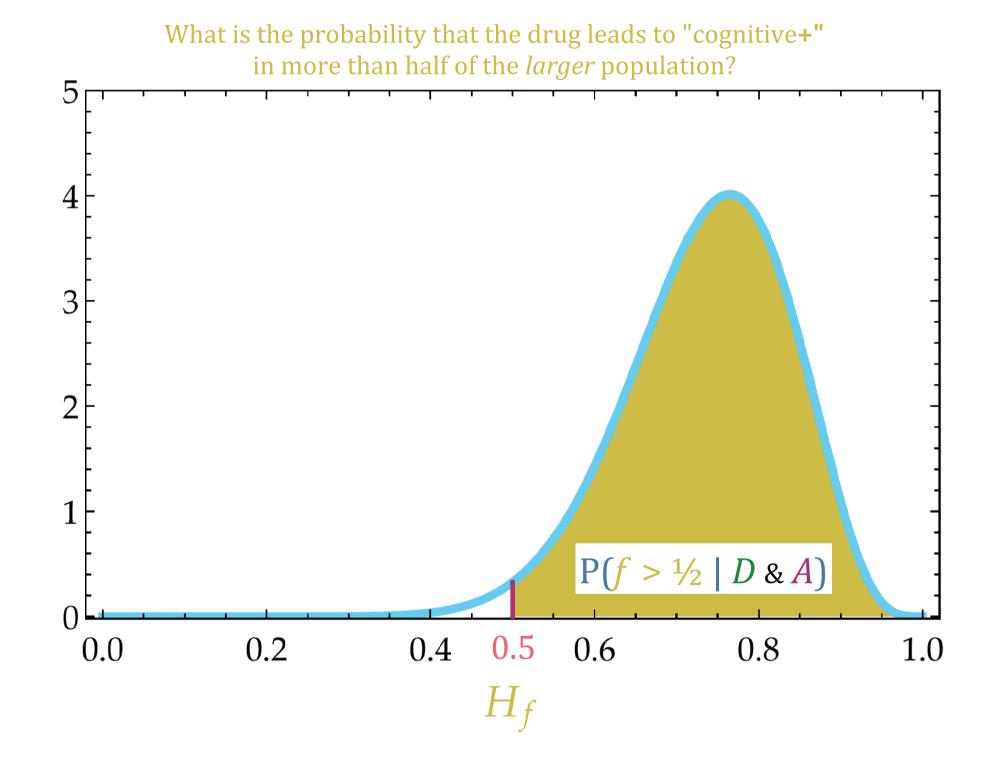






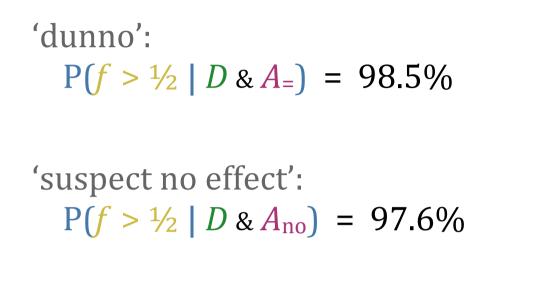


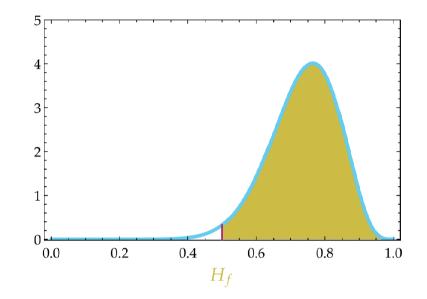
What is the probability that the drug leads to "cognitive+" in more than half of the *larger* population?



⋇

What is the probability that the drug leads to "cognitive+" in more than half of the *larger* population?





'suspect effect':  $P(f > \frac{1}{2} | D \& A_{yes}) = 98.9\%$ 

All three scientists agree that almost surely there is some effect

They are more uncertain about how strong the effect is (as measured by f)

⋇

\*

frequentist paper

"According to a two-tailed test, the data are significant (p = 0.049) at the 0.05 level.

\*

## "According to a two-tailed test, the data are significant (p = 0.049) at the 0.05 level.

(alright, but what does this mumbo-jumbo concretely mean?)

"According to a two-tailed test, the data are significant (p = 0.049) at the 0.05 level.

Bayesian paper

"Given the data, the assumption that our sample is exchangeable in a much larger population, and an initial assumption of uniform ignorance about the future frequency of positive test results, we predict:

- With 98% credibility, more than 1/2 of future tests will respond positively to the drug.
- With 90% credibility, the average of future positive responses lies between 0.56 and 0.88.

"According to a two-tailed test, the data are significant (p = 0.049) at the 0.05 level.

Bayesian paper

Given the data, the assumption that our sample is exchangeable in a much larger population, and an initial assumption of uniform ignorance about the future frequency of positive test results, we predictAssumptions behind the conclusions are plainly stated

- With 98% credibility, more than 1/2 of future tests will respond positively to the drug.
- With 90% credibility, the average of future positive responses lies between 0.56 and 0.88.

"According to a two-tailed test, the data are significant (p = 0.049) at the 0.05 level.

Bayesian paper

"Given the data, the assumption that our sample is exchangeable in a much larger population, and an initial assumption of uniform ignorance about the future frequency of positive test results, we predict:

• With 98% credibility, more than 1/2 of future tests will respond positively to the drug. The results are <u>concrete</u> predictions (no vague "significant" bullshit)

• With 90% credibility, the average of future positive responses lies between 0.56 and 0.88.

"According to a two-tailed test, the data are significant (p = 0.049) at the 0.05 level.

Bayesian paper

Given the data, the assumption that our sample is exchangeable in a much larger population, and an initial assumption of uniform ignorance about the future frequency of positive test results, we predict:

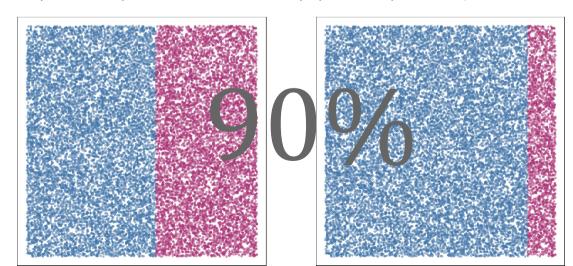
- With 98% credibility, more than 1/2 of future tests will respond positively to the drug. This says that we're almost certain that there is <u>some</u> positive effect
- With 90% credibility, the average of future positive responses lies between 0.56 and 0.88.

"According to a two-tailed test, the data are significant (p = 0.049) at the 0.05 level.

Bayesian paper

"Given the data, the assumption that our sample is exchangeable in a much larger population, and an initial assumption of uniform ignorance about the future frequency of positive test results, we predict:

- With 98% credibility, more than 1/2 of future tests will respond positively to the drug.
- With 90% credibility, the average of future positive responses lies between 0.56 and 0.88. This reports our predictions about the <u>population percentage</u> of the effect



"According to a two-tailed test, the data are significant (p = 0.049) at the 0.05 level.

Bayesian paper

"Given the data, the assumption that our sample is exchangeable in a much larger population, and an initial assumption of uniform ignorance about the future frequency of positive test results, we predict:

- With 98% credibility, more than 1/2 of future tests will respond positively to the drug.
- With 90% credibility, the average of future positive responses lies between 0.56 and 0.88.

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Bayesian paper

Given the data, the assumption that our sample is exchangeable in a much larger population, and an initial assumption of uniform ignorance about the future frequency of positive test results, we predict:

- With 98% credibility, more than 1/2 of future tests will respond positively to the drug.
- With 90% credibility, the average of future positive responses lies between 0.56 and 0.88.

The paper could also add the results from different assumptions:

A strongly sceptical pre-data probability leads to:

- 92%: more than 1/2 of future tests will be positive
- 90%: average will be between 0.48 and 0.74

THE ASTROPHYSICAL JOURNAL LETTERS, 875:L1 (17pp), 2019 April 10

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**OPEN ACCESS** 

## First M87 Event Horizon Telescope Results. I. The Shadow of the Supermassive Black Hole

The Event Horizon Telescope Collaboration (See the end matter for the full list of authors.) Received 2019 March 1; revised 2019 March 12; accepted 2019 March 12; published 2019 April 10

We used two distinct <u>Bayesian-inference</u> <u>algorithms</u> and demonstrate that such crescent models are statistically preferred over other comparably complex geometric models that we have explored.

Our quantitative modeling approach seeks to estimate the posterior distribution  $P(\Theta|D)$  of some parameters  $\Theta$  within the context of a model and conditioned on some data D,

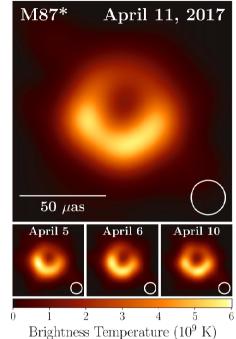
$$P(\boldsymbol{\Theta}|\boldsymbol{D}) = \frac{P(\boldsymbol{D}|\boldsymbol{\Theta})P(\boldsymbol{\Theta})}{P(\boldsymbol{D})} \equiv \frac{\mathcal{L}(\boldsymbol{\Theta})\pi(\boldsymbol{\Theta})}{\mathcal{Z}}.$$
 (7)

Here,  $\mathcal{L}(\Theta) \equiv P(D|\Theta)$  is the likelihood of the data given the model parameters,  $\pi(\Theta) \equiv P(\Theta)$  is the prior probability of the model parameters, and

$$\mathcal{Z} \equiv P(\mathbf{D}) = \int \mathcal{L}(\mathbf{\Theta}) \pi(\mathbf{\Theta}) d\mathbf{\Theta}$$
(8)

is the Bayesian evidence.

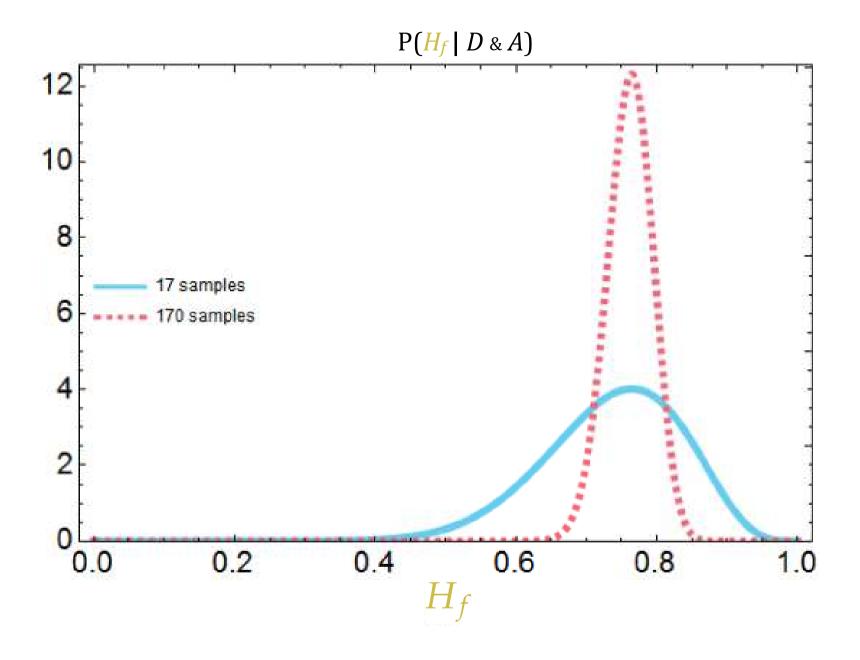
https://doi.org/10.3847/2041-8213/ab0ec7





How many samples, if we want a pre-established credibility?

How many samples, if we want a pre-established credibility?



\*

⋇

```
clear
                                            Example Matlab script to calculate the post-data distributions
%% Data:
                                           and to output the final probability that f > 0.5
positive = 13:
negative = 4;
%% Parameters for pre-data distribution (mean and standard deviation):
mean = 0.5;
sd = 0.2;
betaShape1 = ((1 - mean) * mean/sd<sup>2</sup> - 1) * mean; % shape-parameters of beta distribution
betaShape2 = betaShape1 * (1 - mean)/mean;
%% Pre-data distribution (represented by a beta distribution, <a href="https://mathworld.wolfram.com/BetaDistribution.html">https://mathworld.wolfram.com/BetaDistribution.html</a>):
predata = @(f) betapdf(f, betaShape1, betaShape2);
%% Final distribution, numerator and denominator of Bayes's formula:
numerator = @(f) nchoosek(positive+negative, positive) .* f.^positive .* (1-f).^negative .* predata(f);
denominator = integral(numerator, 0, 1); % integral approximates sum
%% Plot the two distributions:
fgrid = 0:(1/1000):1; % create a grid of f-coordinates
plot(fgrid, numerator(fgrid)/denominator);
                                                                             45
                                                                                   given data
hold on
                                                                                  initial assumption
plot(fgrid, predata(fgrid), '--');
hold off
                                                                             3.5
grid on
                                                                             3
set(gca, 'XAxisLocation', 'origin');
set(gca, 'YAxisLocation', 'origin');
                                                                           probability
5.2
5
xlabel('f');
ylabel('probability');
                                                                             1.5
legend('given data', 'initial assumption', 'Location', 'northwest')
%% Print probability for f > 0.5, given the data:
disp('probability for f > 0.5:');
                                                                             0.5
disp(integral(numerator, 0.5, 1)/denominator);
% gives 0.9758658
                                                                                  0.1
                                                                                      0.2
                                                                                          0.3
                                                                                               0.4
                                                                                                   0.5
                                                                                                        0.6
                                                                                                            0.7
                                                                                                                0.8
                                                                                                                     0.9
                                                                              0
```

```
Example R script to calculate the post-data distributions
library('ggplot2')
                                                    and to output the final probability that f > 0.5
## Data:
positive <- 13
negative <- 4
## Parameters for pre-data distribution (mean and standard deviation):
mean <-0.5
sd <- 0.2
betaShape1 <- ((1 - mean) * mean/sd^2 - 1) * mean # shape-parameters of beta distribution</pre>
betaShape2 <- betaShape1 * (1 - mean)/mean</pre>
## Pre-data distribution (represented by a beta distribution, <a href="https://mathworld.wolfram.com/BetaDistribution.html">https://mathworld.wolfram.com/BetaDistribution.html</a>):
predata <- function(f) dbeta(f, betaShape1, betaShape2)</pre>
## Final distribution, numerator and denominator of Bayes's formula:
numerator <- function(f) choose(positive+negative, negative) * f^positive * (1-f)^negative * predata(f)</pre>
denominator <- integrate(numerator, 0, 1)$value # integral approximates sum</pre>
                                                                                             given - data - initial assumption
## Plot the two distributions:
fgrid <- seg(0, 1, length.out=1000) # create a grid of f-coordinates</pre>
toPlot <- rbind(data.table(f=fgrid,</pre>
                                                                                  4
                              probability=predata(fgrid),
                              given='initial assumption'),
                 data.table(f=fgrid,
                              probability=numerator(fgrid)/denominator,
                                                                                  3-
                              given='data'))
                                                                                probability
gplot(x=f, y=probability, data=toPlot, geom='line',
      color=given, lty=given, lwd=I(1.5)) + theme(legend.pos='top')
## Print probability for f > 0.5, given the data:
print('probability for f > 0.5:')
                                                                                  1.
print(integrate(numerator, 0.5, 1)$value/denominator)
# gives 0.9758658
```

0.00

0.25

0.50

0.75

1.00

What are our hypotheses? What are our question & purpose?

## Does the drug enhance cognitive abilities?

 $\rightarrow$  Yes, No, Sometimes, It depends, ...

What are our hypotheses? What are our question & purpose?

Does the drug enhance cognitive abilities?

 $\rightarrow$  Yes, No, Sometimes, It depends, ...

P('In 17 tests, 13 cognitive+' | 'The drug enhances cognitive abilities' & A)



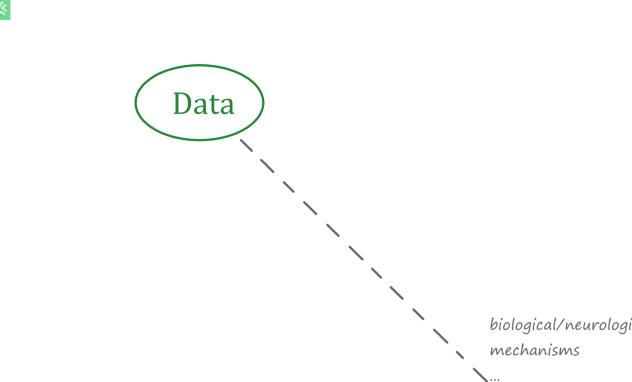
What are our hypotheses? What are our question & purpose?

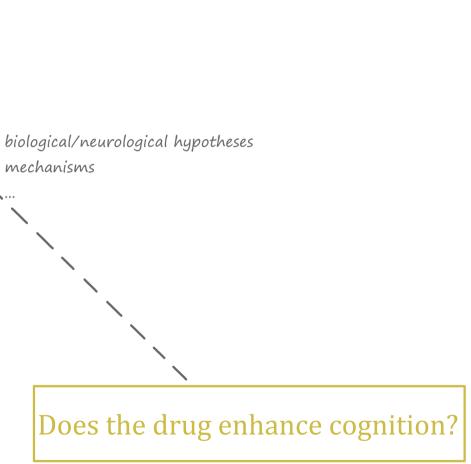
Does the drug enhance cognitive abilities?

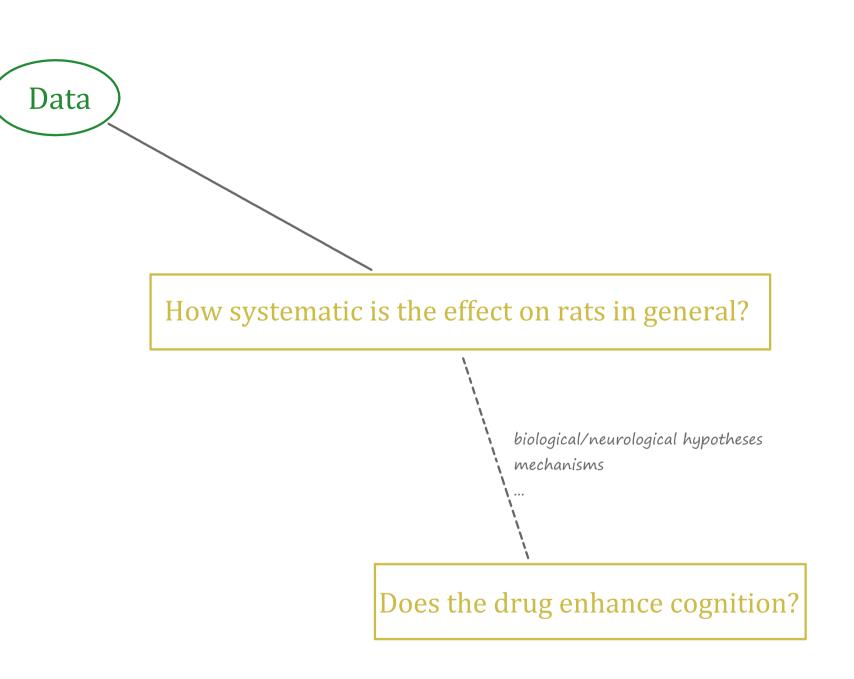
 $\rightarrow$  Yes, No, Sometimes, It depends, ...

What do we need to assume?

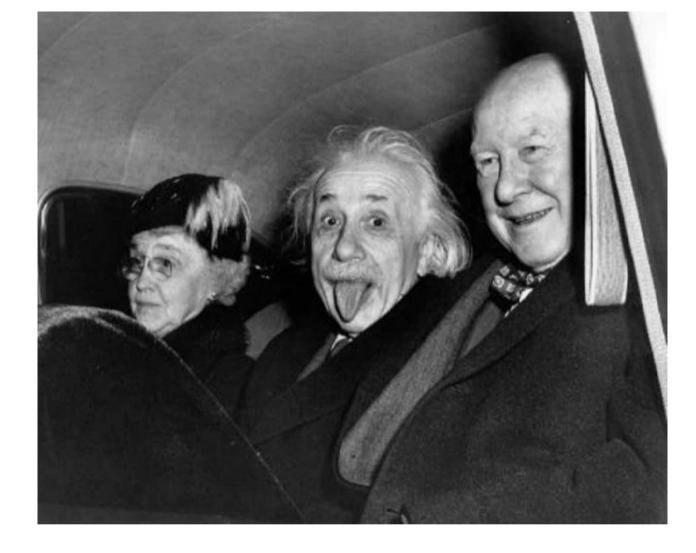
P('In 17 tests, 13 cognitive+' | 'The drug enhances cognitive abilities' & A)











## Thank you!