

American Statistical Association's official statement

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Moving to a World Beyond “ $p < 0.05$ ”

- Don't base your conclusions solely on whether an association or effect was found to be “statistically significant” (i.e., the p -value passed some arbitrary threshold such as $p < 0.05$).
- Don't believe that an association or effect exists just because it was statistically significant.
- Don't believe that an association or effect is absent just because it was not statistically significant.
- Don't believe that your p -value gives the probability that chance alone produced the observed association or effect or the probability that your test hypothesis is true.
- Don't conclude anything about scientific or practical importance based on statistical significance (or lack thereof).

2. Don't Say “Statistically Significant”

We conclude, based on our review of the articles in this special issue and the broader literature, that it is time to stop using the term “statistically significant” entirely. Nor should variants such as “significantly different,” “ $p < 0.05$,” and “nonsignificant” survive, whether expressed in words, by asterisks in a table, or in some other way.

4. Other Approaches

In view of the prevalent misuses of and misconceptions concerning p -values, some statisticians prefer to supplement or even replace p -values with other approaches. These include methods that emphasize estimation over testing, such as confidence, credibility, or prediction intervals; Bayesian methods; alterna-

“ Assuming that the two full-population distributions are probably smooth, we predict:

- The distributions of **future treatment outcomes** will be as in the plots, within uncertainties shown
- Future patients under treatment A** will have on average $X=65$, and $60 < X < 71$ with 95% probability
- Future patients under treatment B** will have on average $X=59$, and $51 < X < 65$ with 95% probability
- The difference between the treatment means will be within $[-0.73, 17]$ with 95% probability
- Variance of X under **treatment A** will be **smaller** than under **treatment B** with 53% probability
- Average X under **treatment B** will be **smaller** than under **treatment A** with 88% probability

These results say that **treatment B** is probably better than **A** at slowing down tumour growth. However, there is still a 10% probability that A could be better than B. If we want to lower this uncertainty to 1% or less, then we need more data.”

Compare the two analyses

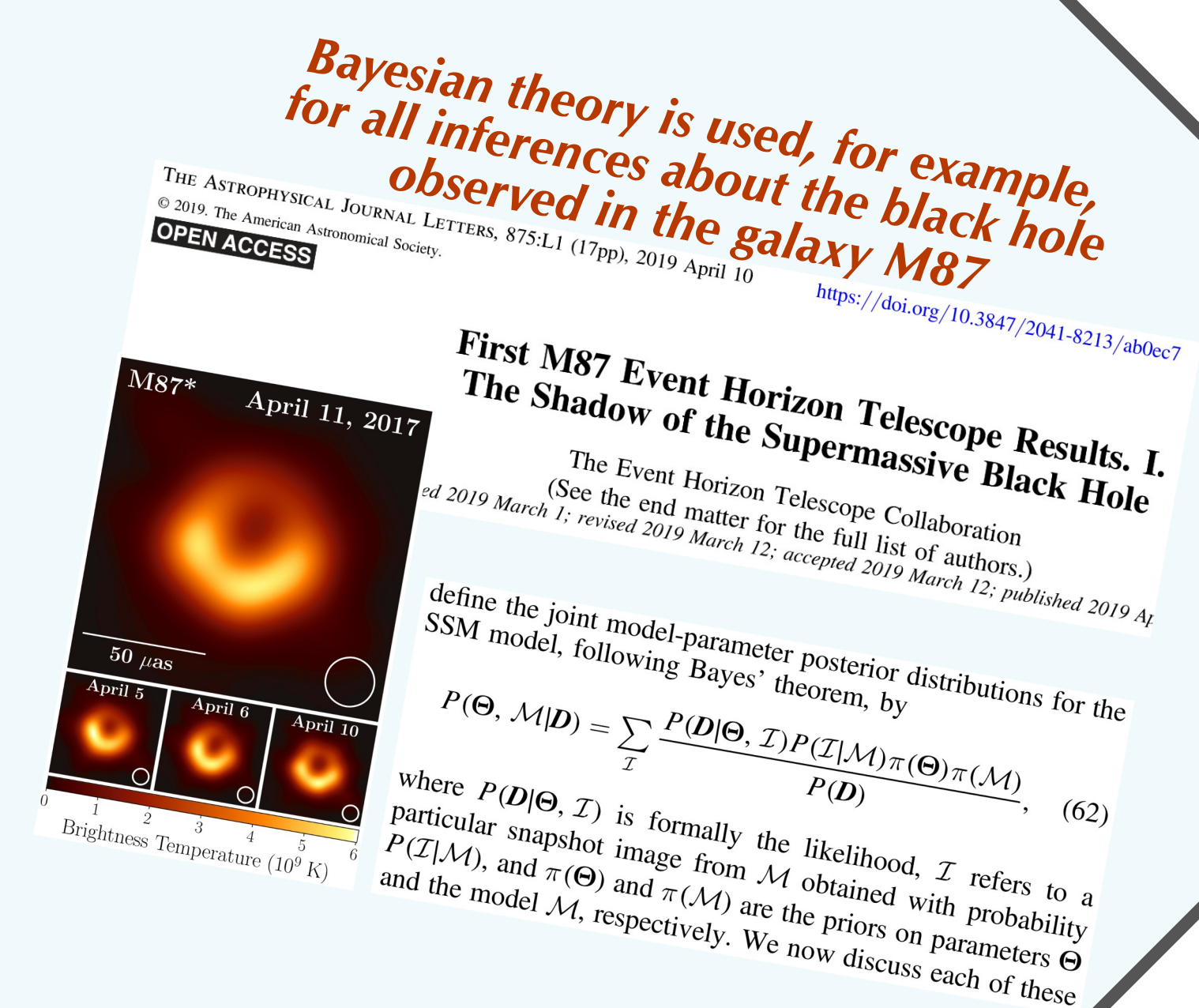
The statements of sampling theory are:

- vague
- obscure or misleading (“significant?”)
- heavily dependent on tacit assumptions
gaussianity, stopping rules, ...
- subject to doubts and corrections
“should I use this test or that test?” “Bonferroni correction?”

The predictions of Bayesian theory are:

- detailed
- quantitative
- easy to interpret and understand
eg: “fraction $x\%$ of population will have effect y ”
- calculated always in the same way
no matter the sample size, no matter how many hypotheses

This was just a simple example. Bayesian theory deals in the same way with multiple hypotheses, variates, and correlation questions



Sounds great, but there's very little friendly software for doing this!

True! That's why we are developing a user-friendly app to do Bayesian analysis on (non-imaging) medical data



The maths will be taken care of under the hood
The software will suggest meaningful questions to be asked (in line with ASA's statement)
Works with mixtures of continuous, integer, categorical variables
– can make predictions about their correlations and relevance
Automatic imputation
No assumptions of gaussianity, linearity or other (ie: nonparametric)
No need to wonder which test or formula to use, no corrections of any kind

We're already using a prototype version for drug-discovery and Alzheimer research

Please get in touch if you want to test it and help us making a great software!

Bibliography

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