University of California, Irvine
Statistics Seminar

Bayesian Inference in a Post p-value World

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(Bldg. #314 on campus map)

The article "Redefine Statistical Significance" recommends changing the default p-value threshold for statistical significance from 0.05 to 0.005 for claims of new discoveries to address the lack of reproducibility of statistical findings. Even with the new "brightline" there is still a question of appropriate post-decision or post-selection inference, such as point and interval estimation that account for the decision to accept a hypothesis. In fields such as genetic epidemiology where multiple hypotheses are routinely tested, the adaption of thresholds for p-values significantly lower than 0.005 has not necessarily prevented the problem of the "Winner's curse" in replication studies for validation of the original discovery; a related problem of post-selection inference. In this talk I will discuss Bayesian alternatives for hypothesis testing/selection, issues with adoption of Bayesian hypothesis testing, and the role of p-values for quantifying evidence in a Bayesian world. I will discuss how full Bayesian propagation of uncertainty combined with decision theory can address the problem of inference post-selection, as well as, methods to approximate this solution using p-values and summaries that could be acceptable to investigators who are more comfortable with the traditional point-null hypothesis setting. Finally, I will return to the problem of combining discovery studies and validation data using an example from the ovarian cancer consortium.