Department of Mathematics and Statistics
Colloquium Lecture Series

Scott Goddard
Dept. of Statistics, Texas AM University

MOST POWERFUL BAYESIAN TESTING FOR REPRODUCIBLE SCIENCE

Scientific research is validated by reproduction of the results, but efforts to reproduce spurious claims drain resources. I focus on one cause of such failure: false positive statistical test results caused by random variability. Classical statistical methods rely on p-values to measure the evidence against null hypotheses, but Bayesian hypothesis testing produces more easily understood results, provided one can specify prior distributions under the alternative hypothesis. I describe new tests, UMPBTs and RMPBTs, which are Bayesian tests that provide default specification of alternative priors, and show that these tests also maximize statistical power.

I then derive RMPBTs for linear models by restricting the class of possible alternative hypotheses to g-priors. An important feature of the resulting class of tests is that their rejection regions coincide with the rejection regions of usual frequentist F-tests, provided that the evidence thresholds for the Bayesian tests are appropriately matched to the size of the classical tests. This correspondence leads to the definition of default Bayes factors for many common tests of linear hypotheses. I illustrate the use of RMPBTs in the special cases of ANOVA and t-tests, and compare their performance to other Bayesian tests based on g-priors in various examples.

Thursday, February 5, 2015
Chapman 106
1:00 – 1:50 pm
Refreshments after the talk in Chapman 101A