

JAMES FRANCIS HANNAN LECTURE SERIES

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Some Examples of Statistical Inference in Genomics

Thursday, Sept 6, 2012
BPS1400, 10:20 a.m. - 11:10 a.m.
Refreshments: 10:00 a.m.

Abstract

I shall talk about two examples of how substantive biological questions posed to us by our collaborators in the ENCODE and modENCODE consortia led to major new statistical problems, a model for randomness in the genome and a way of assessing reliability without knowing ground truth.

This talk is based on joint work in various parts with: J.B. Brown, H. Huang, Q. Li, N. Zhang, and N.P. Boley.

References:

1. Bickel, P. Boley, N.P., Brown, J.P. Huang, H., and Zhang, N. (2010). Subsampling methods for genomic inference. *Ann. App. Statist.*, **4**, 1660–1697.
2. Qunhua, L., Brown, J.P., Huang, H., and Bickel, P. (2011). Measuring reproducibility by high throughput experiment. *Ann. App. Statist.*, **5**, 1752–1779.

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