

# 3<sup>rd</sup> International Conference & Exhibition on **Biometrics & Biostatistics**

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## A bivariate model for simultaneous testing in bioinformatics

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The talk will introduce a novel approach for testing treatment effects in high-throughput data (e.g., gene-expression, RNA-seq, metabolomics, etc). Most previous work on this topic focused on testing for differences between the means, but recently it has been recognized that testing for differential variation is probably as important. In this new method the means and variances are modeled as a bivariate response, and are estimated jointly using a parsimonious random-effects model. This method is computationally efficient and scalable, since the number of parameters in the model remains fixed (and small) regardless of the number of tests (corresponding to genes, metabolites, etc.) by “borrowing information” across tests and accounting for both differential mean and differential variation, the new method yields a significant improvement in power over other methods. In particular, it is shown that when the two treatment groups have significantly different variances, the power to detect differential means is substantially higher. The presentation will also demonstrate power and sample size estimation procedures that can be used to design experiments involving thousands of simultaneous tests.

### Biography

Haim Bar has completed his PhD in Statistics from Cornell University, and obtained his MSc in Computer Science from Yale University. His professional interests include statistical modeling, shrinkage estimation, high throughput applications in biology (e.g., genomics, brain imaging), Bayesian statistics, variable selection, and machine learning. He is currently an Assistant Professor at the University of Connecticut.

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