



THE UNIVERSITY OF
CHICAGO

Department of Statistics

DISSERTATION PROPOSAL

ZHENGRONG XING

Department of Statistics
The University of Chicago

Detecting Functional Differences Between Biological Conditions in
Next Generation Sequencing Data

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Eckhart 126, 5734 S. University Avenue

ABSTRACT

With the advent of high throughput sequencing methods and the large amounts of readily available sequencing data, many are interested in the associations between these functional data and certain covariates. We propose approaches aimed at detecting differences in shape and amplitude between sequencing reads for different biological conditions, where condition is a generic term that could be cell types, genotypes, experimental conditions (case vs control) and so on. A multiresolution approach has been developed when we expect the differences to be spatially structured, and a hidden Markov model is currently being implemented for the case where differences might be extremely sparse (that is, non-zero in a small number of regions). We plan to further extend our work to the case of multiple conditions or the scenario where we have multiple data types on the same cell line, and implement our methods in genome-wide settings.

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