



THE UNIVERSITY OF GEORGIA
DEPARTMENT OF STATISTICS

Colloquium Series

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3:45 PM, Thursday, September 3, 2020

Zoom link: <https://zoom.us/j/7979236528>

MAPS: Model-based analysis of long-range chromatin interactions from PLAC-seq and HiChIP

Hi-C and chromatin immunoprecipitation (ChIP) have been combined to identify long-range chromatin interactions genome-wide at reduced cost and enhanced resolution, but extracting information from the resulting datasets has been challenging. Here we describe a computational method, MAPS, Model-based Analysis of PLAC-seq and HiChIP, to process the data from such experiments and identify long-range chromatin interactions. MAPS adopts a zero-truncated Poisson regression framework to explicitly remove systematic biases in the PLAC-seq and HiChIP datasets, and then uses the normalized chromatin contact frequencies to identify significant chromatin interactions anchored at genomic regions bound by the protein of interest. MAPS shows superior performance over existing software tools in the analysis of chromatin interactions from multiple PLAC-seq and HiChIP datasets centered on different transcriptional factors and histone marks. MAPS is freely available at <https://github.com/ijuric/MAPS>.

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