



BIOINFORMATICS 2017 Spring SEMINAR SERIES

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<http://bioinformatics.udel.edu/Seminars/Current>

MONDAY, February 27, 2017
3:30pm
DBI Room 102

Non-Bisulfite Epigenetic Profiling of DNA Methylation Enables Patient Stratification Biomarker Discovery

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ABSTRACT:

DNA methylation is commonly assessed via bisulfite conversion methods and next generation sequencing (NGS). However, resulting nucleotide mutagenesis reduces sequencing efficiency and interferes with genomic variant call analyses. My lab has developed a novel computational platform for high-resolution, quantitative DNA methylation profiles based on a simple, non-destructive preparation of genomic DNA for NGS (Illumina HiSeq X10). Our methylation metrics are sensitive, highly repeatable (low variance) and one sequence run can be used to derive both methylation and variant call profiles simultaneously. This novel epigenetic biomarker discovery platform enables new diagnostic solutions with high sensitivity and statistical discrimination of disease vs. healthy samples in blood serum (Parkinson's disease patients) and in solid tumors (triple-negative breast cancer). We demonstrate how this diagnostic platform has great utility for CDx applications via a recent use-case involving patients with acute myeloid leukemia that shows high confidence in separating responders and non-responders to a hypomethylating drug therapy in pre-treatment bone marrow biopsies.