

**Biomedical Informatics Grand Rounds**  
**Wednesday, Dec. 1, 2021, 3:00 pm – 4:00 pm**

**Genomic methods for liquid biopsies in cancer**



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**Remote Access**

**Join Zoom Meeting** <https://stonybrook.zoom.us/j/95617197636?pwd=KytzZ2pVRG9SZGpKZUtpNXJlSjNjZz09>  
Meeting ID: 956 1719 7636 Passcode: 924293

**Bio:** Dr. Andrea Moffitt received her B.S. in Biomedical Engineering from Georgia Tech and a Ph.D. in Computational Biology and Bioinformatics from Duke University, under the mentorship of Dr. Sandeep Dave. Her graduate research focused on understanding the genomic and transcriptomic basis of lymphoma subtypes, including the largest comprehensive characterization of diffuse large B cell lymphoma and the first large-scale genomic studies of hepatosplenic and enteropathy-associated T cell lymphomas. Her graduate studies were supported by a Hertz Foundation Fellowship and a National Science Foundation Graduate Research Fellowship.

Dr. Moffitt is currently a Senior Computational Fellow at Cold Spring Harbor Laboratory, completing her postdoctoral training with Dr. Michael Wigler and Dr. Dan Levy. She is funded by an NCI K99 award, based on her development of an ultra-sensitive method for the detection of residual disease in acute myeloid leukemia. The focus of her independent research program will be the sensitive detection, quantitation, and characterization of residual disease in cancers, with special emphasis on leukemia. Dr. Moffitt is also committed to supporting the next generation of scientists as a mentor for the New York Academy of Sciences 1000 Girls, 1000 Futures program and the Professional Development Chair of the Women in Science group at CSHL.

**Abstract:** Better methods are urgently needed to monitor cancer patients throughout their cancer care. Precise measurements of tumor burden help measure how well a treatment worked and predict patient outcomes. Tumor burden is evaluated in the clinic today primarily through imaging, cytometry, and protein biomarkers. These methods have limits, and better methods for detecting tumor burden will lead to improvements in treatment and survival. Genomic approaches offer a more sensitive method for assessing low levels of disease. When cancer develops, it brings along with it a fingerprint of genetic variants in its DNA that distinguishes it from healthy cells. The levels and patterns of DNA from cancer cells in the blood can serve as a marker for a successful surgery, resistance to therapy, or early relapse. In solid cancers, non-invasive liquid biopsies offer routine monitoring of cancer patients by examining cell-free DNA in the blood; in leukemias, sampling a patient's blood allows for sampling the cancer cells directly. One of the key challenges to developing assays to detect this fingerprint is that the DNA of interest is often present in very low proportions, and is easily obscured by measurement noise created during the sequencing process. I will discuss the strategies we take to obtain excellent quantitation and sensitivity. Using personalized genomic fingerprints, tagging each molecule with a unique barcode, and modeling error rates enable us to improve the limit of detection from 1 in 1000 to 1 in 1 million. I will demonstrate the application of our ultra-sensitive method for the detection of residual disease to acute myeloid leukemia (AML). We also evaluated this strategy to measure cell-free tumor DNA (ctDNA) in the blood of patients with endometrial, ovarian, breast, colorectal, and pancreatic cancers. We detected ctDNA in nearly every patient at presentation and illustrate the use of a genomic test to quantify treatment response over time in pancreatic cancer.

**Educational Objects:** Upon completion, participants should be able to:

- Understand the current state of liquid biopsy technology in cancer.
- Learn how personalized genomic fingerprints can be used to monitor cancer patients.
- Appreciate the impact of sensitivity on the clinical utility of liquid biopsy assays.

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