



Biomedical Informatics

Grand Rounds

Wednesday, April 30, 2025

3:00 pm – 4:00 pm

Improvements in Compartment Deconvolution for Precision Medicine

Alisa Yurovsky, Ph.D.

*Faculty Member, Department of Biomedical
Informatics, Stony Brook University*

Remote Access

Join Zoom Meeting <https://stonybrook.zoom.us/j/95617197636?pwd=KytzZ2pVRG9SZGpKZUtpNXJISjNjZz09>

Meeting ID: 956 1719 7636 Passcode: 924293

Bio: Dr. Yurovsky is a new faculty member at the Department of Biomedical Informatics at Stony Brook University. Previously, she was a postdoctoral researcher in the same department under the supervision of Richard Moffitt. Dr. Yurovsky completed her PhD in Computer Science at Stony Brook University under the supervision of Steve Skiena. During her research focused Masters, she worked with Bernard Moret at EPFL. Her undergraduate degree in Computer Science is from Carnegie Mellon University. Dr. Yurovsky is a computational biologist who works at the intersection of computer science, genetics, and statistics. She is interested in the development of new algorithms and computational methods that aid in the advances of precision medicine, with the potential to address existing racial disparities in health data. Her current research projects include precise compartment deconvolution and weight estimation of mixed tissue samples, analysis of spatial transcriptomics data, methods for small size differential expression studies, and applied machine learning.

Abstract: Studies on bulk RNA-seq of tumor biopsies can yield incorrect results because varying proportions of non-tumor tissues in the samples obscure the true signal and impact the accuracy of survival and differential expression analyses. This talk will begin by introducing the problem of mixed samples in RNA profiling experiments, and how compartment deconvolution can be used to improve inference from common samples. I will describe our work improving the stability of non-negative matrix factorization, a common compartment deconvolution approach. Next, I will describe our work on sample-specific tissue deconvolution and its applications for improving survival and differential expression analysis. The third portion of the talk will focus on our current research into integrating survival information directly into non-negative matrix factorization objective function. I will conclude with future directions.

Educational Objectives:

After participating in this lecture, attendees will be able to:

1. Gain understanding of the compartment deconvolution problem in the context of tumor biopsies.
2. Discuss how non-negative matrix factorization works.
3. Recognize the benefits of sample-specific deconvolution.

Disclosure Statement: The faculty and planners have no relevant financial relationship with ineligible companies, whose primary business is producing, marketing, selling, reselling, or distributing health care products used by or on patients.

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