

CPH Seminar in Precision Medicine

“Evaluating the Evaluation of Cancer Driver Genes”

Rachel Karchin, PhD

Associate Professor, The Willam R. Brody Faculty Scholar

Department of Biomedical Engineering and Oncology Institute for Computational Medicine

John Hopkins University

Numerous methods have been developed to identify driver genes, but evaluation of the performance of these methods is hindered by the lack of a gold standard. I will discuss an evaluation framework that can be applied to driver gene prediction methods. Most current methods do not adequately account for heterogeneity in the number of mutations expected by chance and consequently have many false positive calls, which is acute for cancers with high mutation rates.

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arlisa.k.ross@uth.tmc.edu

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