

CPH Seminar in Precision Medicine

“Population-specific imputation of gene expression for pharmacogenomics’

Assaf Gottlieb, Ph.D.

Assistant Professor at the Center for Precision Health, School of Biomedical Informatics,
University of Texas Health Science Center at Houston

Our lab is interested in understanding and modeling drugs mode of action and their relation to drug efficacy, adverse reaction and pharmacogenomics. We employ an integrative computational approach, combining multiple types of data and applying methodologies from systems medicine, machine learning and causal inference domains to identify population and patient-level factors associated with drug efficacy and adverse reactions and to suggest candidates for drug repurposing.

In this talk, I will describe my latest project, which involves using the Genome-Tissue Expression project to predict the dose of the anticoagulant warfarin. I will review the current state-of-the-art, PrediXcan, for gene expression imputation and will explain modifications that were required to address the warfarin dose problem. Last, I will expand on my previous work on drug pathway models, which was used in this work.

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rosalinda.molina@uth.tmc.edu

713.500.3912

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