UTHealth
The University of Texas Health Science Center at Houston
School of Biomedical Informatics

CPH Seminar in Precision Medicine

"Pushing the limits of low coverage WGS for population genomics"

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The low coverage whole genome sequencing design has been fruitful in cataloging the genetic variation in human genomes. The potential applications include population genomics, and genome-wide association studies. My laboratory has been focusing on addressing several overarching issues for the bioinformatics capabilities. Very recently, we are in the process of scaling the capabilities to cope with the need to study hundreds of thousands of samples. This presentation will provide a flavor of using ultra-low coverage WGS to achieve populational scale studies in biomedical sciences.

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