

An Unified Framework of Personalized Network Recovery and Detection

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Abstract: The Genotype-Tissue Expression Project (GTEx) aims to study how genes are differentially expressed across tissues to lead to human diseases. Whether and how human cells perform commoner unique functions across tissues are determined not only by genes individually but also through their co-expression network; however, inferring the tissue specificity of gene regulatory networks represents a substantial challenge. We address this challenge by developing a unified framework for assembling genomic data from multiple tissues into informative networks, importantly, adjusted for potential risk factors (e.g., gender, race). This framework utilize quasi-dynamic ordinary differential equations to recover tissue- and individual-specific gene networks with bi-directional, signed, and weighted interactions. This work provides a tool to compile, curate, and catalogue comprehensive encyclopedias for personalized gene regulatory networks, facilitating the translation of the GTEx data into clinical practice.