A systematic framework for gene-transcript-protein-reaction associations of human metabolism

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Alternative splicing plays a significant role in producing different transcripts from a gene, and therefore resulting in various protein isoforms. Here, we show a systematic framework for the production of gene-transcript-protein-reaction associations (GeTPRA) of the human metabolism. This framework generated 11,415 GeTPRAs for 1,106 metabolic genes. The generated GeTPRAs were further evaluated, using a updated human genome-scale metabolic model (GEM), which is biochemically consistent and transcript-level data compatible. Both principal and nonprincipal transcripts of metabolic genes were considered in the framework based on 446 personal RNA-Seq data and 1,784 personal GEMs. The framework and the GeTPRAs are expected to provide better understanding of human metabolism and enable medical applications.