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Title: FLUXIMPLIED: A NOVEL BIOINFORMATIC METHOD INTEGRATES RATE LIMITING STEPS AND DIFFERENTIAL EXPRESSION FOR PATHWAY ANALYSIS

Abstract

Many tools exist to perform a rigorous pathway analysis, though traditional gene set enrichment analysis remains among the most common. While useful for many applications, one common situation where it is less so is the metabolic profiling of bulk omics datasets. Rate limiting steps in more linear pathways are the main determinant of flux through these pathways, but differential expression of the enzymes that catalyze these steps is usually not differentially weighted in pathway analysis. Fluximplied is a free and open source tool built to perform pathway analysis with rate limiting steps in mind to assess the implied flux through several well validated metabolic pathways for use in both bulk and single cell omics analysis.