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The glycosylation pathway is a highly branched network. Although only a relatively small number of enzymes are involved in the pathway, a multitude of intermediate and terminal glycans can be formed. Each intermediate glycan in the network can be the substrate of subsequent glycosylation steps. In each step, there can be multiple enzymes acting on a single glycan due to overlapping substrate specificity. These enzymes tend to compete with each other to divert the network flux toward a particular branch. Alternation of their relative ratios can result in different glycan profiles. In mammals, such enzymes are distributed in a tissue-specific manner to meet a variety of protein glycosylation requirements. How distinct expression patterns of these enzymes can affect the glycan structures of a protein is not well studied. Understanding the link between these expression patterns and the final glycan profile of a protein will be useful for glycoengineering.

In this study, we develop a mathematical model that incorporates reaction rules for various Golgi-resident glycosylation enzymes. The kinetic information is obtained from *in vitro* enzyme kinetics research. Enzyme levels are estimated from their corresponding transcript levels in various mammalian tissues using public transcriptome data. Insights from this modeling effort will used to predict targets for glycoengineering of mammalian cells.