“Systems engineering for enhanced understanding and design of industrially relevant cellular systems”

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In the era of big data, the challenge shifts from acquisition to analysis. This talk will focus on how mathematical models can be used to analyses intracellular metabolic pathways using extracellular data in systems relevant to the bioproduction of protein therapeutics. Specifically, I will present a comparative study between the predictions of generic and cell line-specific genome-scale metabolic models as well as a small-scale metabolic model and experimentally measured growth rates, gene essentialities, amino acid auxotrophies, and 13C intracellular reaction rates. Our results show that while all cell models are able to capture extracellular phenotypes and intracellular fluxes, cell line-specific models better capture gene essentiality and auxotrophy phenotypes, although, in our experience, fail to improve intracellular reaction rate predictions. I will further demonstrate how computational optimisation can be applied to identify strategies that increase resources channelled towards recombinant protein production quickly and efficiently, with select strategies achieving up to 30% increase in specific productivity in the lab.