**Surrodash by Just: a Capstone Project**

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Many biotechnology companies have moved from experimental probes to simulated mechanistic models to identify the molecular and process parameters that give the highest yield and purity for affordable manufacturing of biologic targets. While these mechanistic models have sped up the process of molecular and process design compared to bench-top science, these models can be slow and computationally expensive to consistently run. Our team has developed a surrogate modeling Python package that cleans data generated from Just--Evotec Biologics’ mechanistic model and trains four ML models (deterministic linear regression, probabilistic linear regression, deterministic NN, probabilistic NN) to predict yield and purity for a set of molecular interaction parameters and operating conditions in a faster and less computationally expensive way. This package loads our pretrained models, explores the input data, provides visualizations and comparisons of the model accuracy, and validates the training process using an interactive Dash app in order to speed the prediction of ideal molecular and process design parameters.

Zoom Meeting Link: <https://washington.zoom.us/j/92176739291>