Advanced molecular modelling for improved chromatographic separation

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Description

Demand for affordable, fast to marked vaccines is growing in recent years, the global Covid-19 pandemic of 2020 is a prime example of this. An important bottleneck in speeding up vaccine development is currently downstream processing, which entails a.o. capture and polishing steps.

For the purification of antigen based vaccines, chromatography is the most used technique due to its selectivity[1]. The wide variety in buffer conditions, resin types and additives makes it a versatile technique which can be optimized for specific targets (e.g. antigens). Since many different combinations can be considered, finding optimal/close to optimal purification conditions can be a lengthy process. We aim at developing a computational method to narrow down the viable options by probing the purification landscape using information extracted from atomic models of the target and contaminants.

To achieve this, Quantitative Structure Property relationships (QSPR) and Molecular Dynamics (MD) simulations will be performed[2,3]. In QSPR, features of the protein three dimensional atomic structure, which may contribute to a specific property, are calculated. These features are then used in statistic models to predict this property, in our case retention behavior. MD simulations describe the movement of a molecular system based on Newton's second law. By introducing a protein model to a chromatography resin model, we can calculate the resulting forces which describe the binding affinity.

This project is composed of an experimental component to measure retention behavior of specific host cell proteins and, and a computational component to construct predictive models.

References

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