AlphaFold3: Is it really as good as they claim?

Project outline

AlphaFold3 (AF3) [Abramson et al., 2024] has gained a lot of attention as a modern deep-learning model that is able to predict 3D-structures of individual proteins and protein complexes. However, AF3 also claims to be able to predict the structure of phosphorylated proteins. Phosphorylation is a post-translational modification (PTM) of proteins that can alter the structure and function of the phosphorylated protein. A specific subset of proteins, so-called kinases, are responsible for phosphorylating other proteins. Kinases achieve this by forming a complex with the target protein that they phosphorylate (Wikipedia: Kinase). Together, this gives rise to the question if AF3 is able to predict the 3D binding structures of kinases and phosphorylated target proteins.

Project goal

The steps of the project are:

1. Get familiar with AlphaFold3 and its online implementation (AF3 does not need to be implemented as it is only accessible through an online interface!).
2. Run a given set of kinase-phosphorylated target protein combinations and extract the predicted 3D-structure models.
3. Evaluation of the predicted 3D-structure models (e.g. Computation of the distance between the catalytic site of the kinase and the phosphorylated amino acid of the protein).

Requirements:

- Python or R knowledge
- Basic skills in data analysis

References

Abramson et al. Accurate structure prediction of biomolecular interactions with alphafold 3. *Nature*, 2024. doi: 10.1038/s41586-024-07487-w.