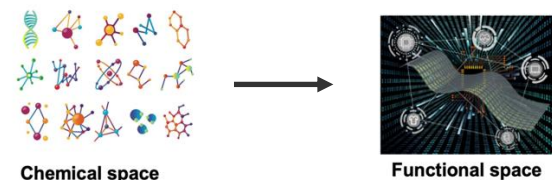
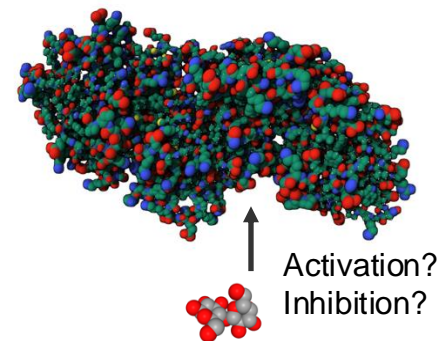


Why do we want to make
predictions for molecules?

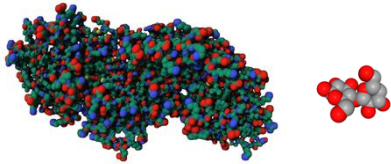
- Molecules are the building blocks of life
 - Understanding their functions and interactions is relevant for many different natural sciences
 - Biology
 - Biochemistry
 - Medicine
 - Environmental Sciences
 - It has also many important industrial applications
 - Designing new materials with desired properties
 - Designing new pathways of chemical reactions for the synthesis of different substances
 - Drugs
 - Biofuels
 - Chemicals



Experimental validation of small molecule-protein interaction

Step 1: Molecule Acquisition

Timeline: 1 – 4+ weeks



Step 2: Assay Selection & Optimization:

Timeline: 1 – 4 weeks



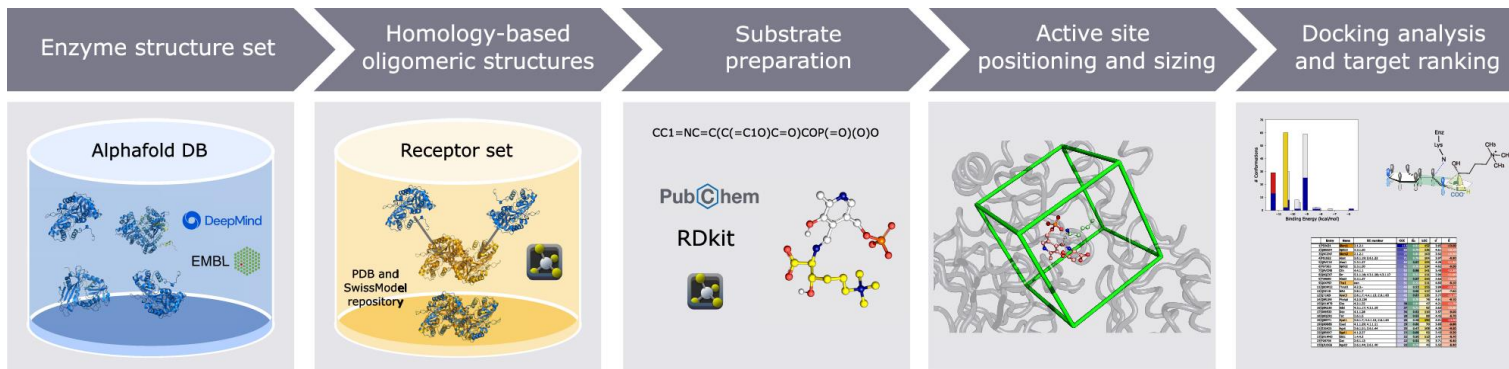
Step 3: Experiment execution:

Timeline: 1 – 2 weeks

Step 4: Results Analysis and Interpretation:

Timeline: Up to 2 weeks

Computational molecular docking analysis



- In molecular docking simulations, we try to place the small molecule into the protein in many different ways by rotating, flipping, and shifting it to see how it fits.
- For each position, the program calculates a score that tells us how good the fit is.

Methods to determine molecule properties

■ Experiments

- ➕ Advantage: Usually very accurate
- ➖ Disadvantages: Often time-consuming, difficult, and expensive

■ Non-ML computational methods:

Simulate the behavior of molecules using theoretical principles, empirical data, and statistical analysis

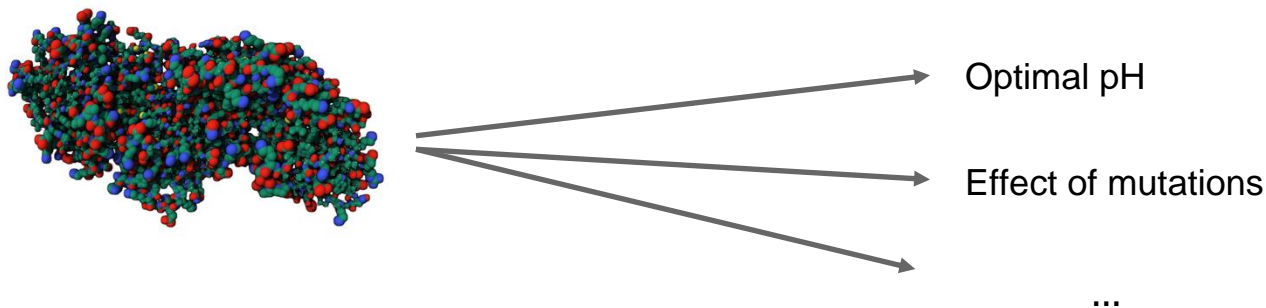
- ➕ Advantages: Speed, Costs, Accessibility
- ➖ Disadvantages: Accuracy, Complexity Limits, Data Requirement

■ Machine Learning models:

- ➕ Advantages: Handling Complexity, Detecting Patterns, Speed, Flexibility
- ➖ Disadvantages: Accuracy, Data Dependency, Overfitting

Examples for predicting molecule properties

■ Protein property prediction:

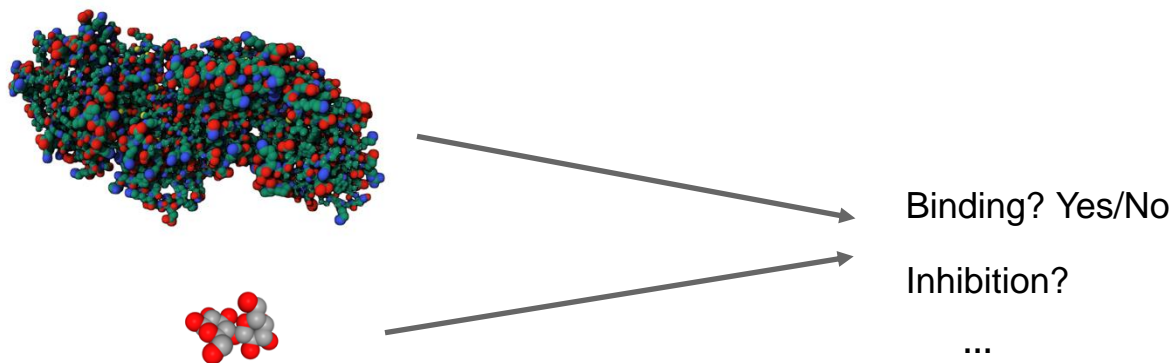


■ Small molecule property prediction:



Examples for predicting molecule properties (2)

- Protein-small molecule interaction predictions:



On what kind of molecules will we focus?

- We will mostly focus on biomolecules:

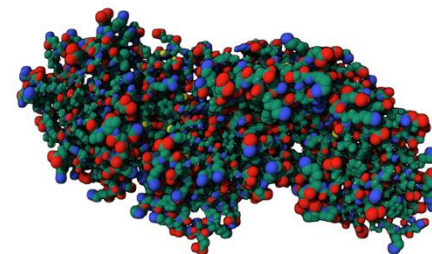
- Micromolecules (Small Molecules):

- Vitamins
 - Amino Acids
 - Monosaccharides
 - Nucleotides



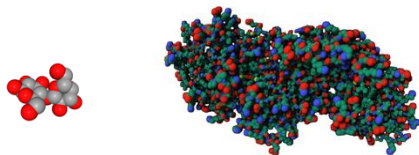
- Macromolecules

- **Proteins**
 - Nucleic Acids (DNA and RNA)
 - Polysaccharides



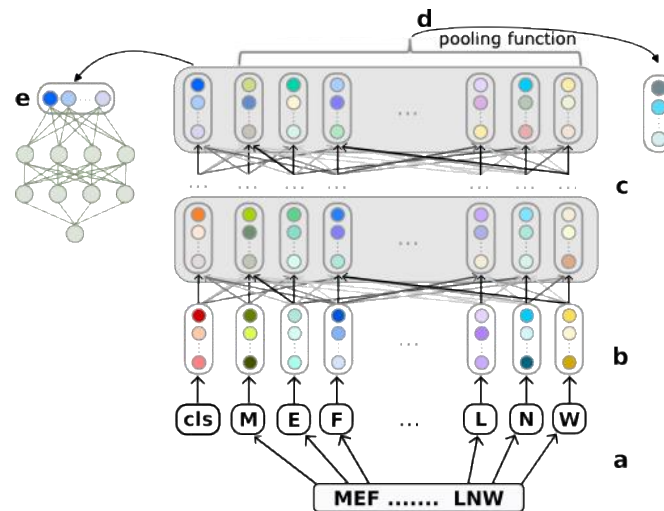
Course content (1)

■ Biological / chemical background



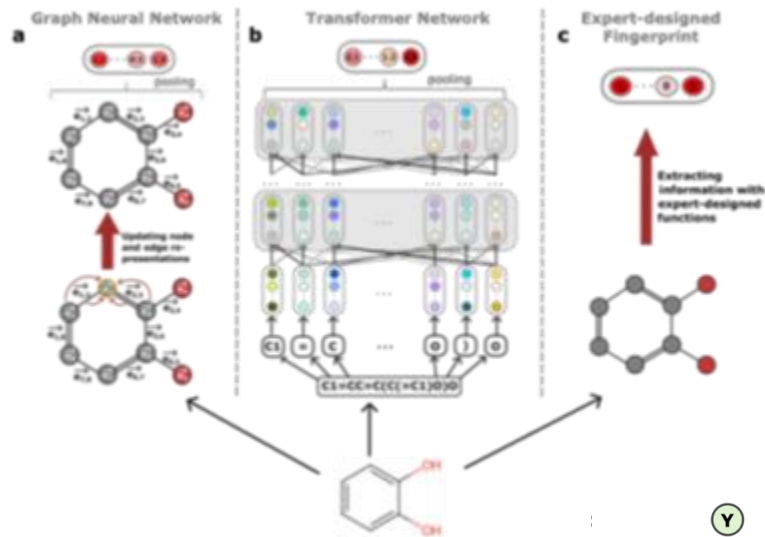
■ Transformer Networks

- Architecture
 - Training
 - Self-Supervised
 - Supervised: Fine-tuning pre-trained models
- ## ■ Transformer Networks for proteins (large molecules)

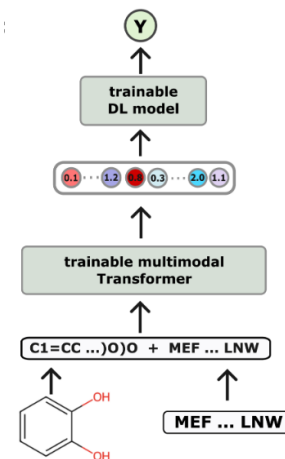


Course content (2)

- Encoding small molecules
 - Transformer networks
 - Graph neural networks (GNNs)
 - Traditional methods

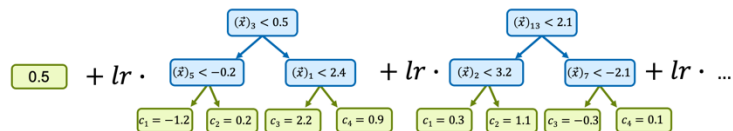


- Multimodal Transformer Networks:
 - Applying a single Transformer to multiple types of input data
 - Predicting interactions between proteins and small molecule

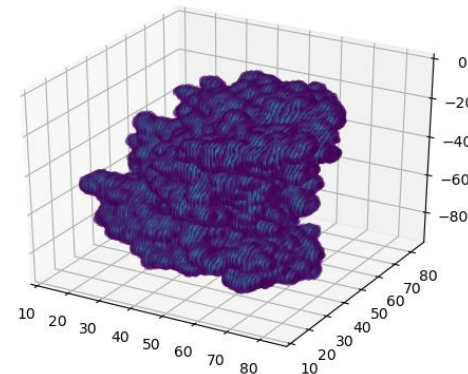


Course content (3)

- Visualizing what Transformer Networks learn
- Gradient Boosting decision tree models

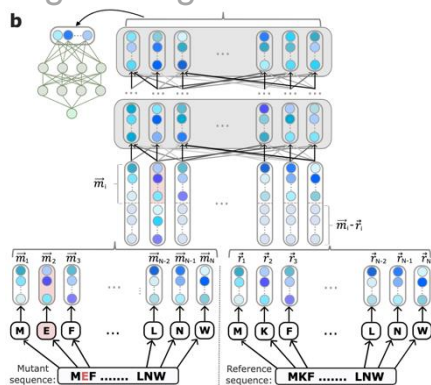


- Utilizing protein 3D structures to predict protein function
 - Protein structure prediction methods
 - Encoding protein structure with
 - Graph Neural Networks
 - 3D Convolutional Neural Networks



Course content (4)

■ Protein engineering methods



- Challenges and best practices
- Optimizing large language models

google-research/
tuning_playbook

A playbook for systematically maximizing the performance of deep learning models.



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Contributors

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Issues

9

Discussions

28k

Stars

2k

Forks

