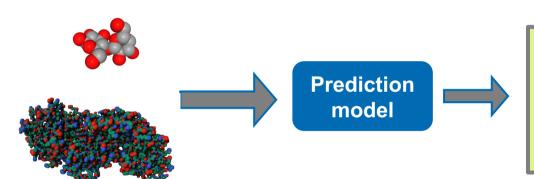




# Predicting protein-small molecule interactions

#### Predicting protein-small molecule interactions

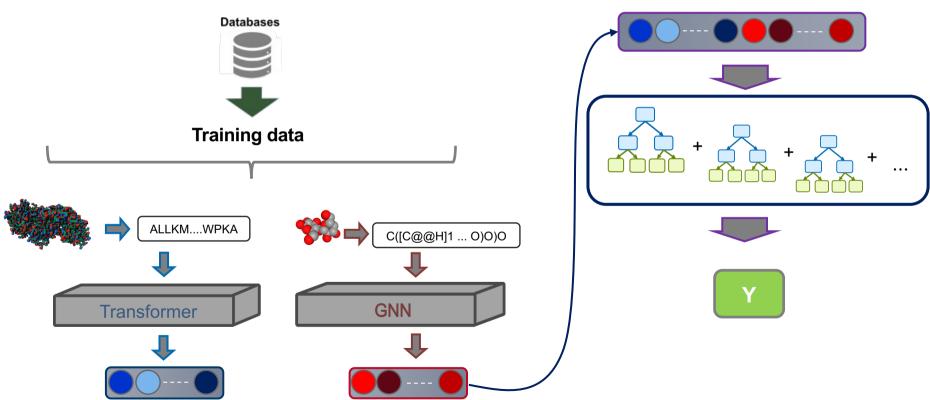




- Enzyme-substrate pairs
- Transporter-substrate pairs
- Michaelis constants K<sub>M</sub>
- Turnover numbers k<sub>cat</sub>
- Drug-Target inhibition
- ...

#### Typical Prediction Pipeline

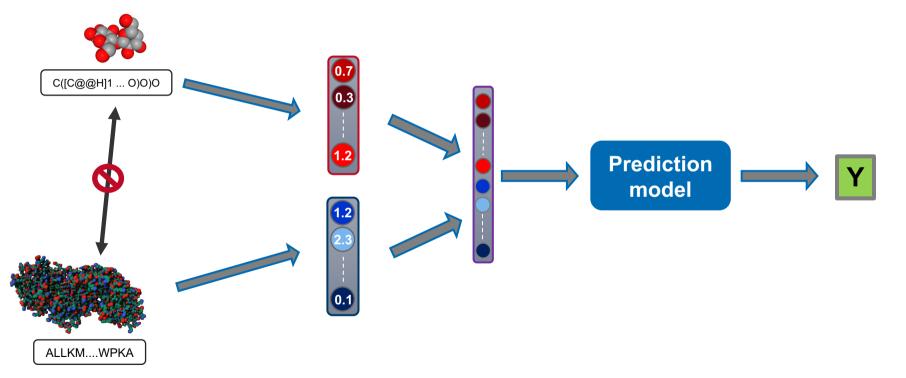




3 hhu.de

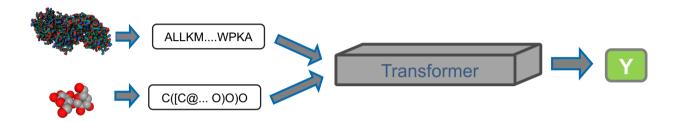
#### Missing Information Exchange





#### Multimodal Transformer Networks (1)





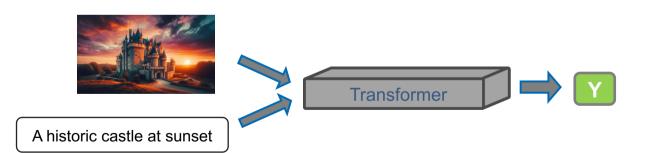


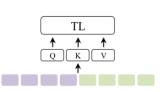
Image generated with DALL-E hhu.de

#### Multimodal Transformer Networks (2)



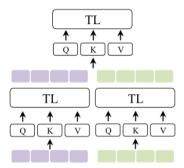
= 1st input type/modality (e.g., text or protein)

= 2nd input type/modality (e.g., image or small molecule)



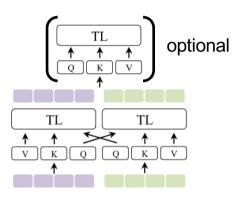
### **Concatenating both initial input sequences**

- Generating a joint vocabulary for tokens of both input types
- Concatenated sequences is input for single Transformer



## Concatenating sequence embeddings after separate processing

- Each input sequence is input of separate Transformer layers
  - Resulting embeddings are used as the input of shared Transformer layers



### **Cross-attention between both sequences**

- Using embeddings from other input type to calculate attention scores
- No self-attention

# ProSmith – Protein-Small Molecule Transformer



