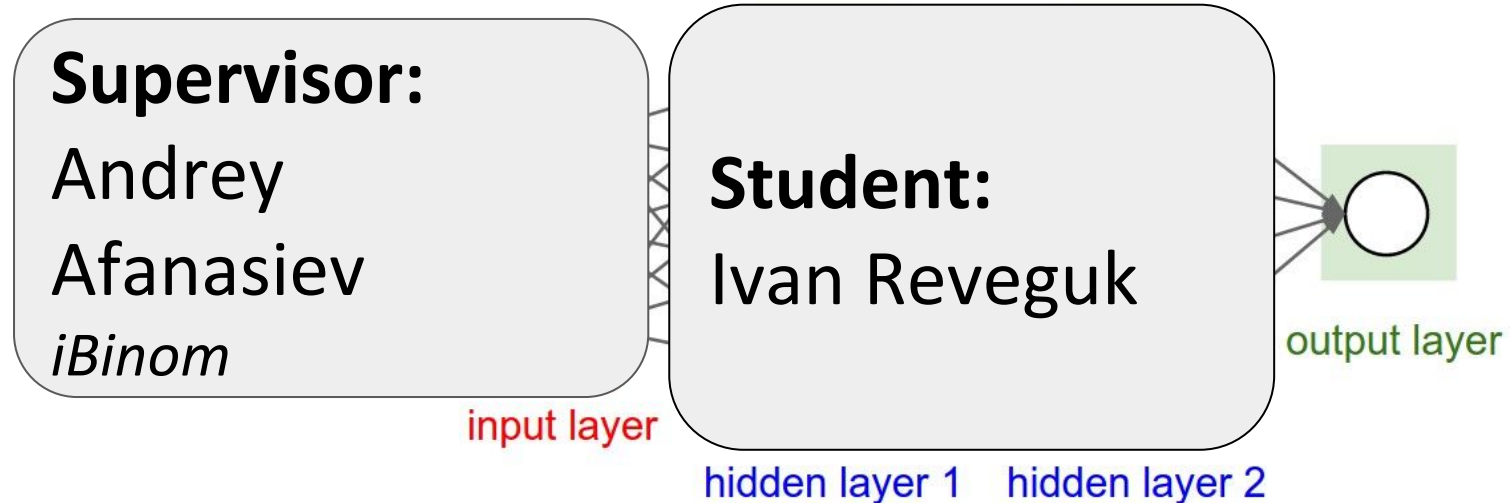


Predicting vital protein features

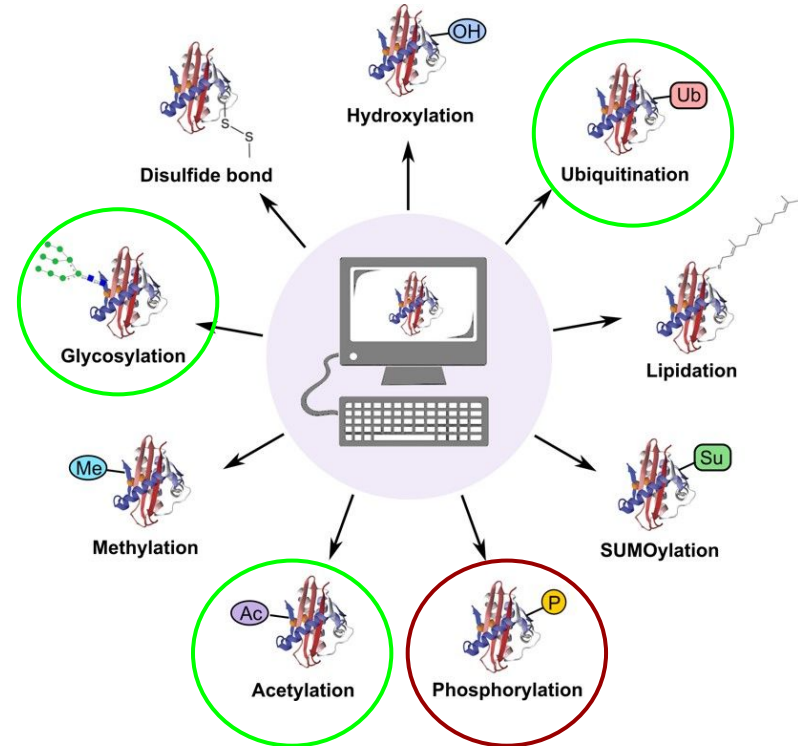


Why vital? What features?

A lot of them are disease-associated.

break PTM ~ break protein normal function

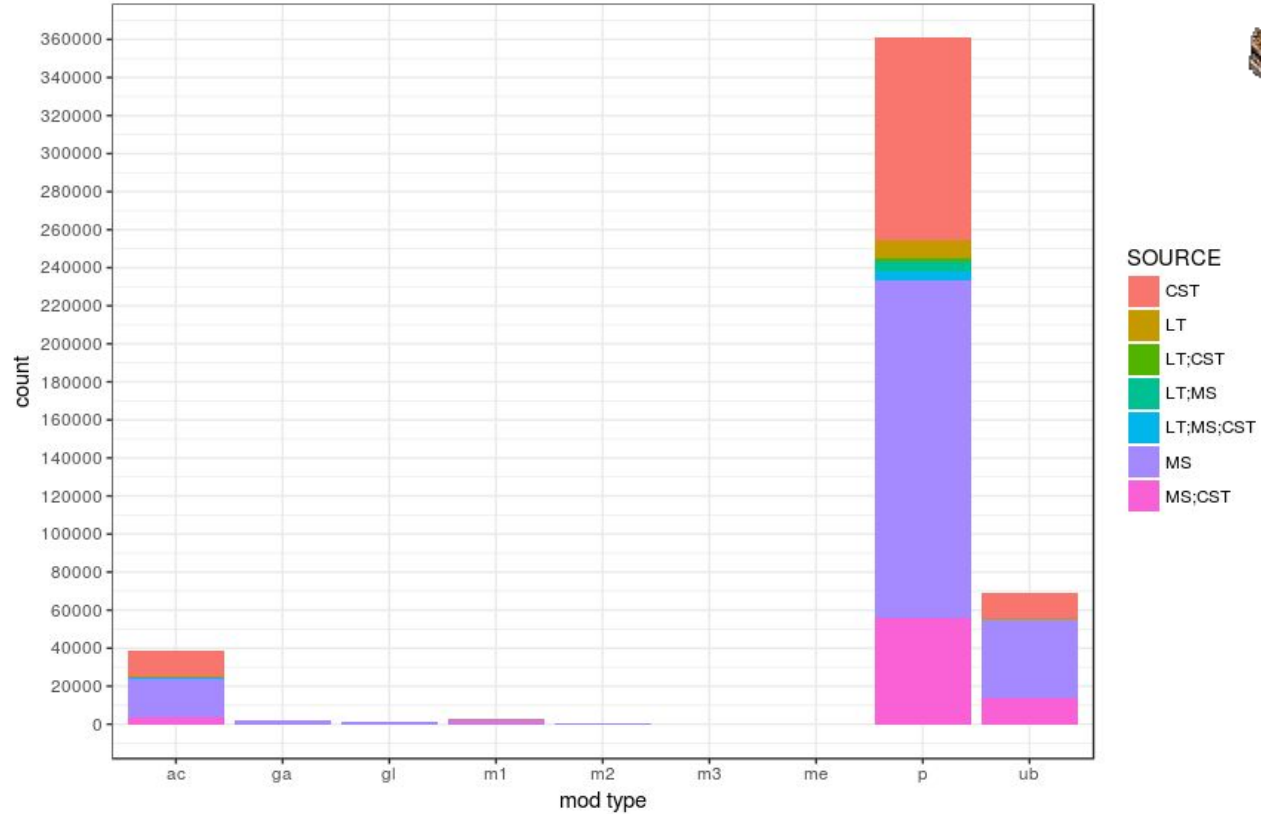
PTM - post-translational modifications.



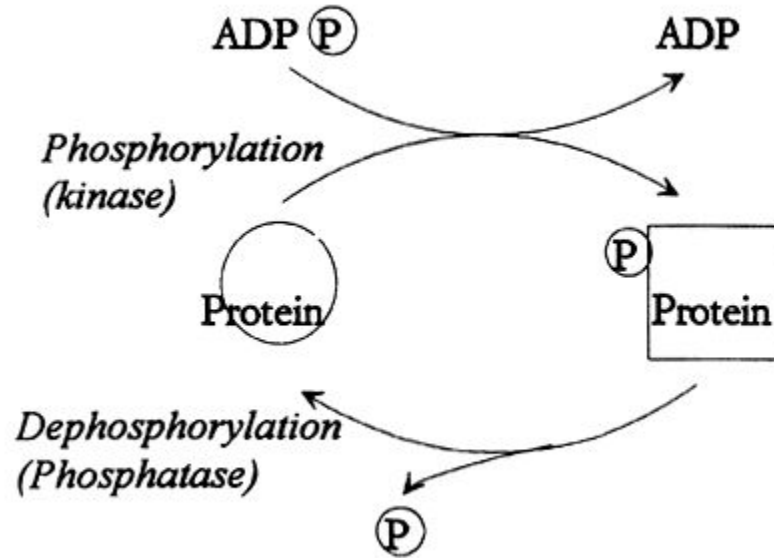
Data used



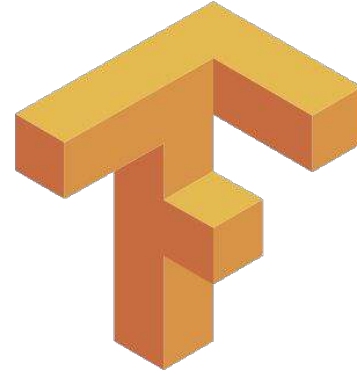
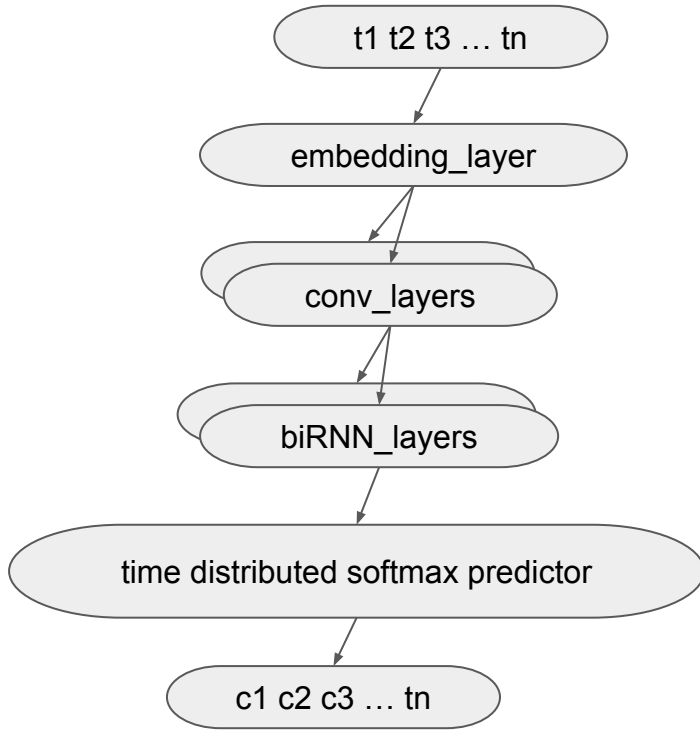
\$ greedisgood



Goal: phosphorylation site prediction



Architecture



Keras

Results

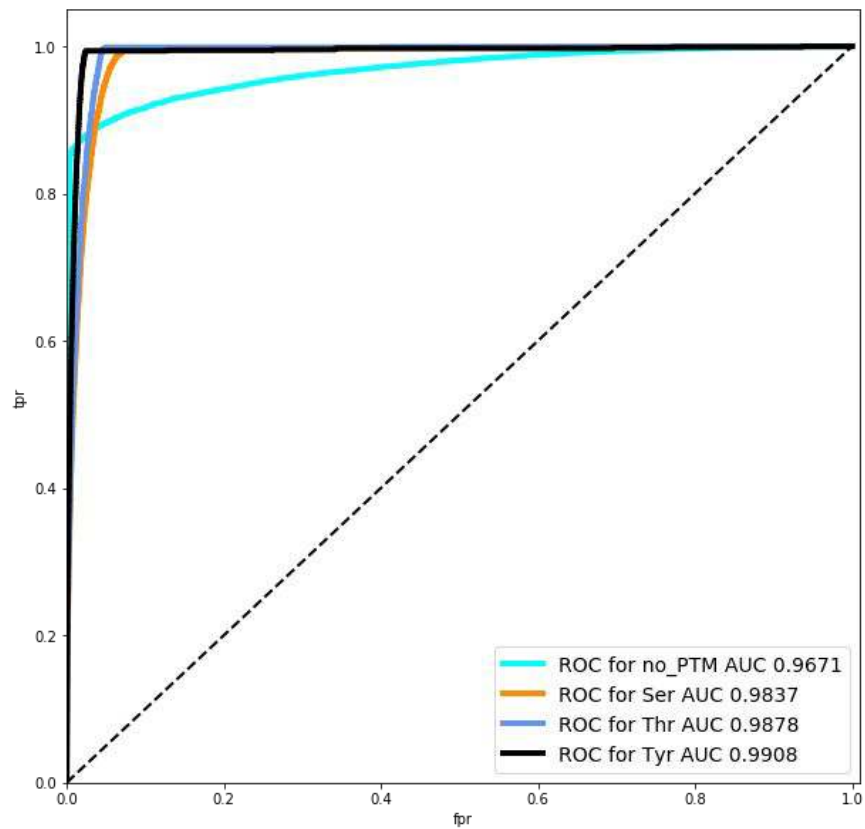
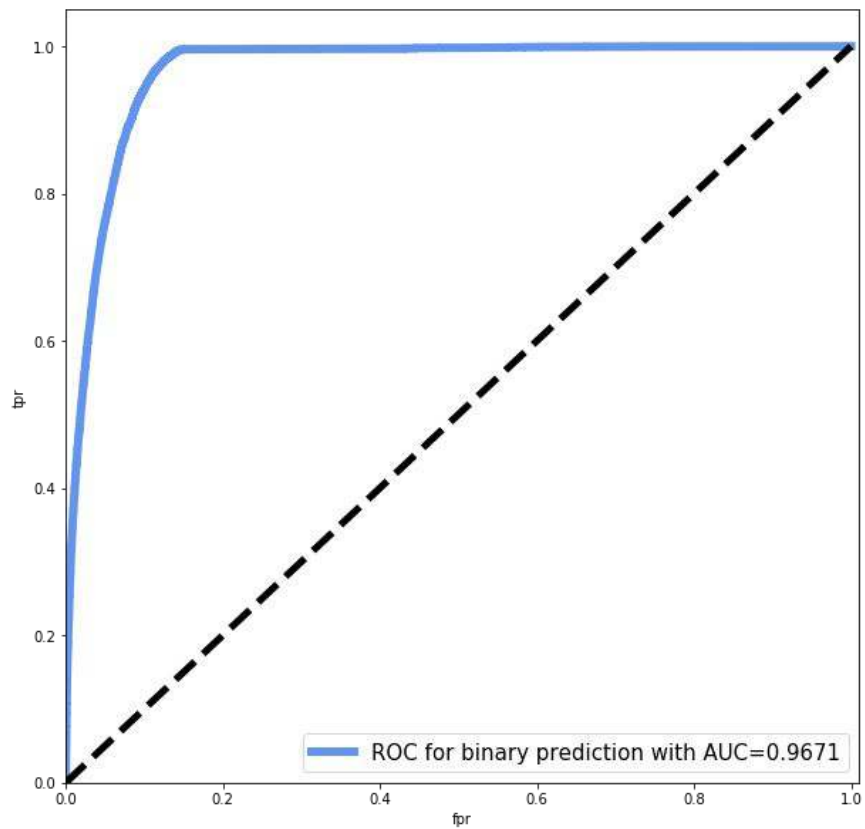
$$Ac = \frac{TP+TN}{TP+FP+TN+FN} \times 100\% \quad \sim 94\%$$

$$Sn = \frac{TP}{TP+FN} \times 100\% \quad \sim 80\%$$

$$Sp = \frac{TN}{TN+FP} \times 100\% \quad \sim 94\%$$

$$\frac{FP}{N} = \frac{FP}{FP+TN} \quad \sim 4\% \quad \mathbf{FNR} \quad \sim 19\%$$

Results



Comparison

	NetPhos3.1 results (%)	MyNet results (%)
Accuracy	90	94
F1-score	20	33
Precision	11	21
Sensitivity	74	80
Specificity	91	94
FPR	9	4
FNR	25	20

Thx for attention!