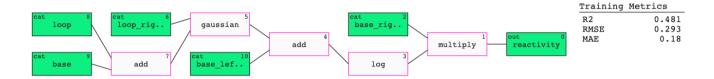
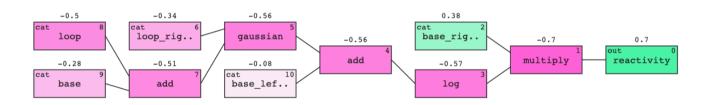
COVID19 mRNA Vaccine Degradation

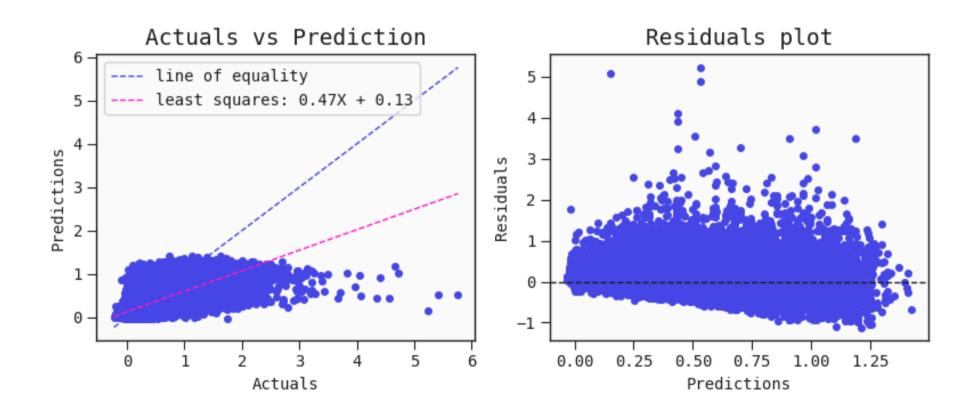
- > Base-model (unconstrained model)
- > Constrained model
- >Three feature model

BASE MODEL



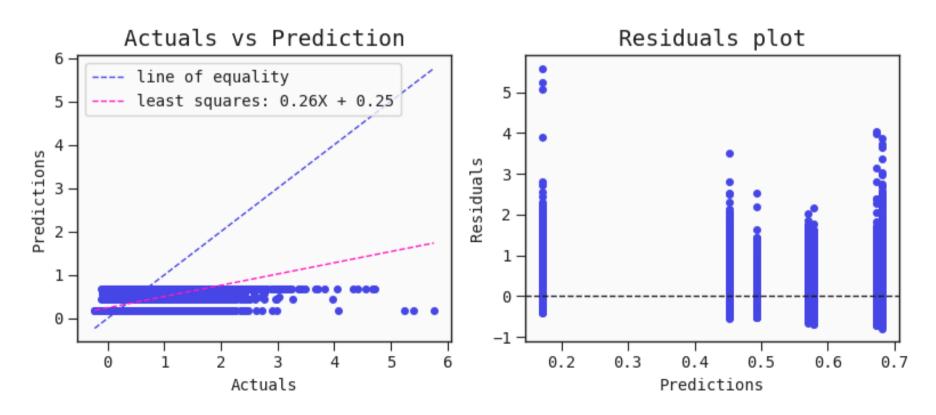


Pearson correlation



The constrained model:





0.258

0.351 0.238

0.284 0.347

0.235

The constrained model:

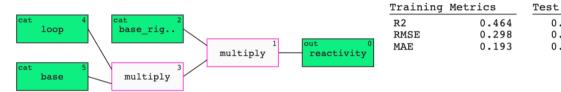
		Training	Metrics
cat 1	out 0 reactivity	R2	0.25
		RMSE	0.35
		MAE	0.23

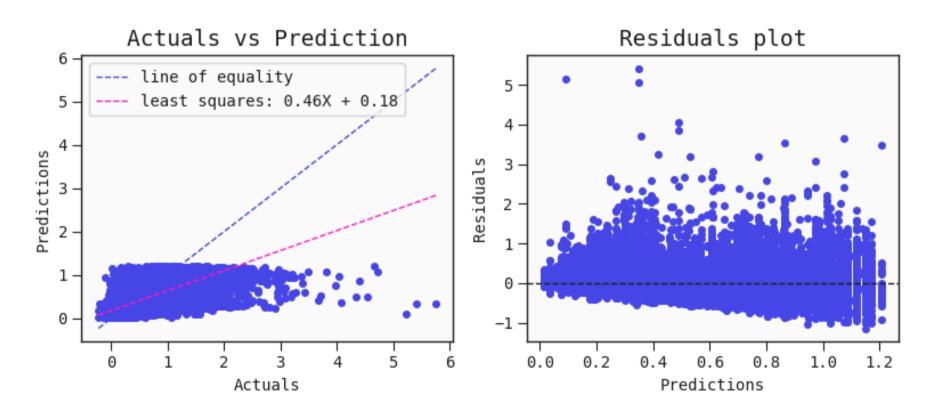
-	Actuals vs Prediction			Residuals plot					
5 -	line of equality least squares: 0.27X + 0.2	24	4 -						•
Predictions	least squares: 0.27X + 0.2	.4	Residuals					•	
0 -	0 1 2 3 4 Actuals	5	-1 -	0.2	0.3	0.4 Predict:	0.5	0.6	0.7

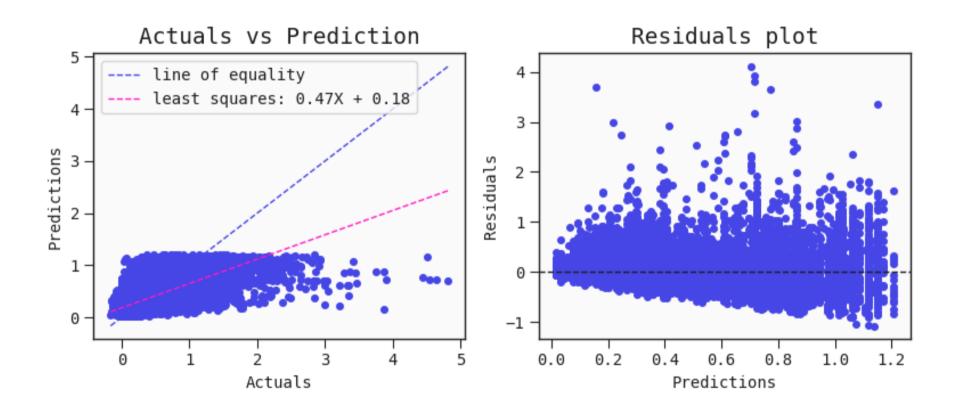
0.479

0.296

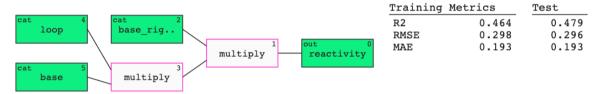
The three feature model:

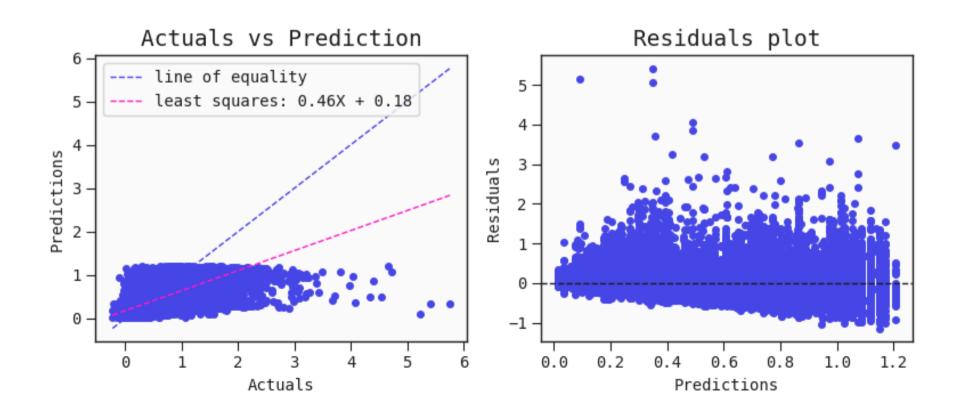


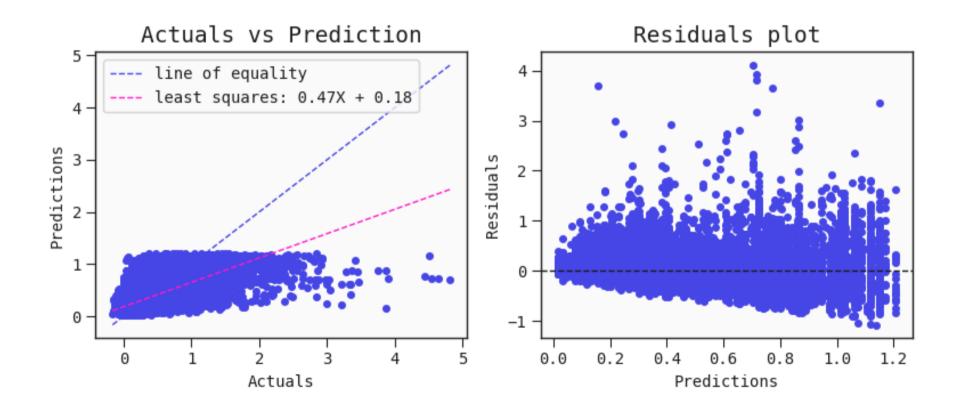




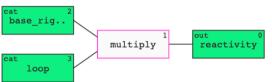
The three feature model:



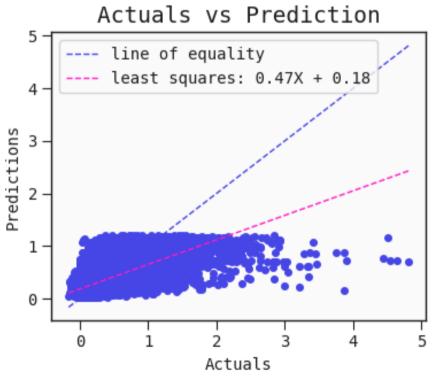


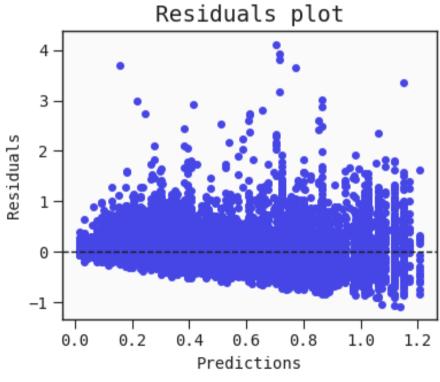


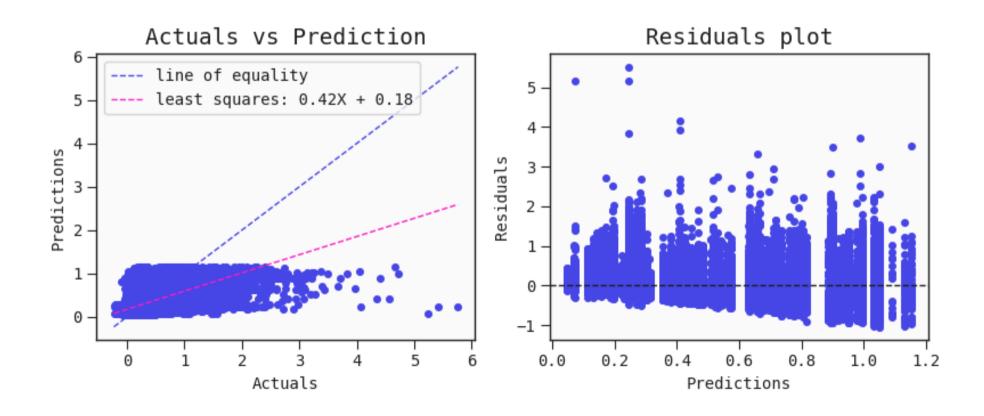
The two feature model:



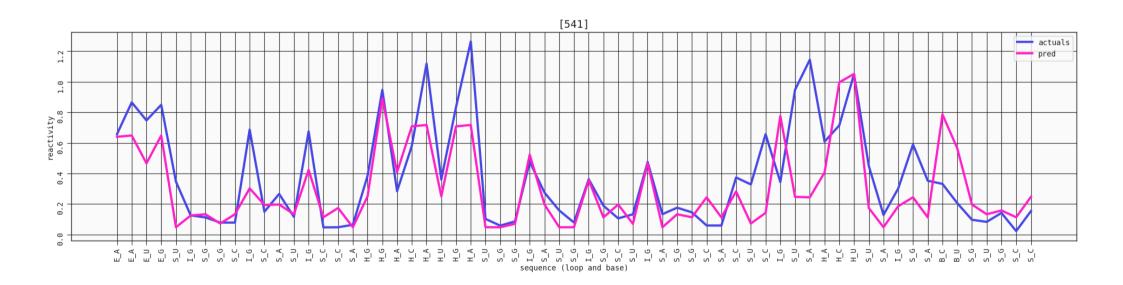
Training	Metrics	Test		
R2	0.423	0.444		
RMSE	0.309	0.306		
MAE	0.199	0.197		



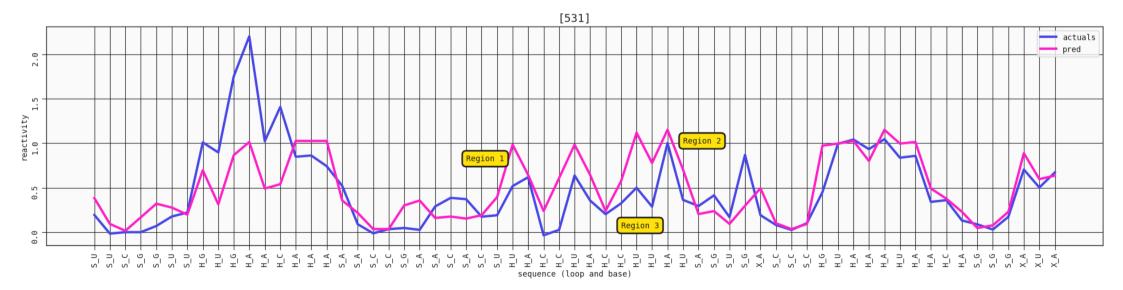




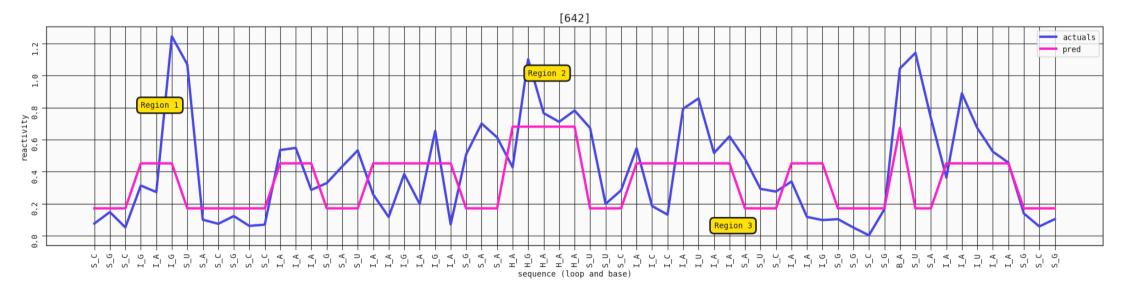
TWO FEATURE MODEL



THREE FEATURE MODEL



CONSTRAINED MODEL



BASE MODEL

