

PREDICTING THE EFFECT OF MUTATIONS ON A GENOME-WIDE SCALE

by

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Abstract

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Contents

protherm (n = 3602)	100.00	0.03	0.22	0.22	0.31
taipale (n = 1914)	0.05	100.00	52.35	45.19	7.47
humsavar (n = 32252)	0.02	3.11	100.00	49.61	11.97
clinvar (n = 63407)	0.01	1.36	25.23	100.00	11.22
cosmic (n = 357633)	0.00	0.04	1.08	1.99	100.00
	protherm	taipale	humsavar	clinvar	cosmic

Figure 1: Size and overlap between the core and interface predictor datasets.

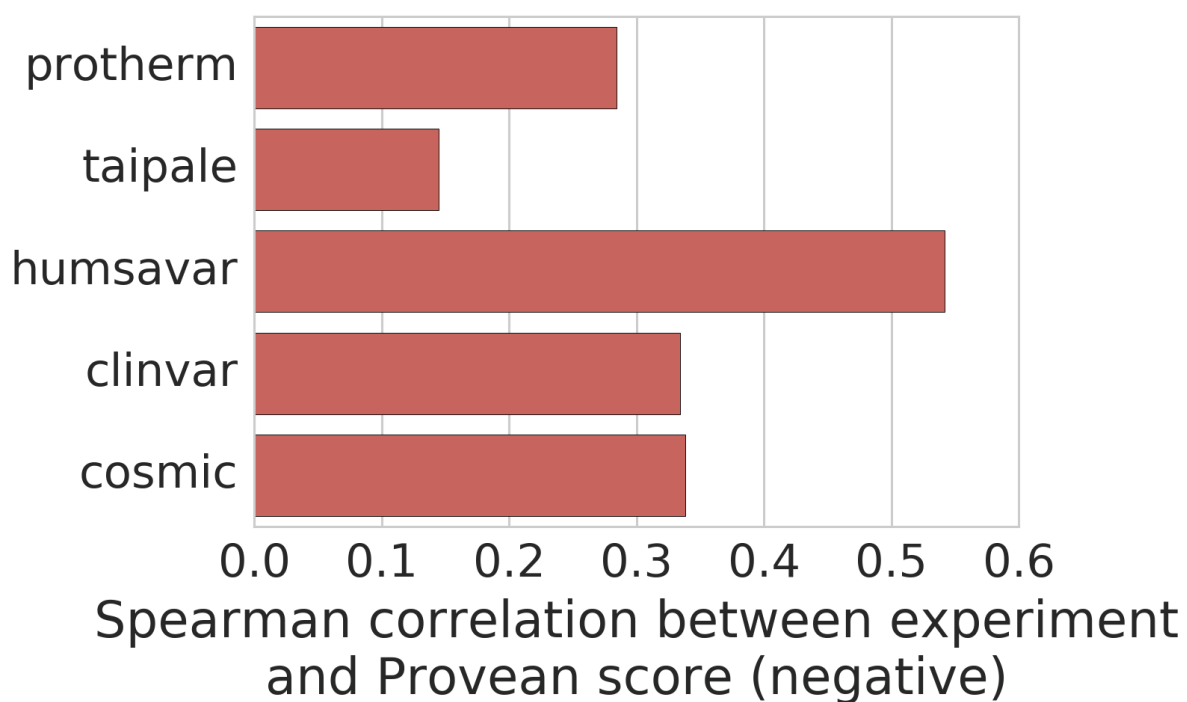
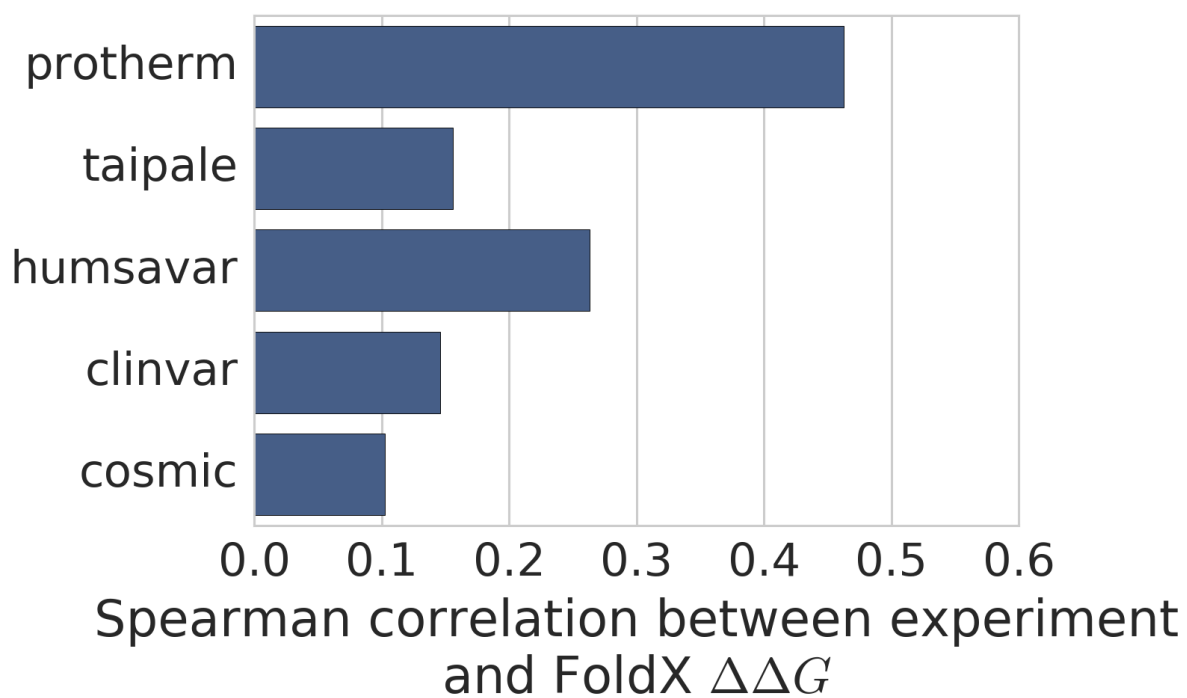


Figure 2: xxx.