

Supplementary Information

AI-QulC Machine Learning for Automated Detection of Misfolded Proteins in Seed Amplification Assays

Kyle D. Howey^{1,2}, Mancı Li^{1,2}, Peter R. Christenson^{1,2}, Peter A. Larsen^{2,3}, and Sang-Hyun Oh^{1,2,*}

¹ Department of Electrical and Computer Engineering, University of Minnesota, Minneapolis, MN 55455, United States

² Minnesota Center for Prion Research and Outreach, University of Minnesota, St. Paul, MN 55108, United States

³ Department of Veterinary and Biomedical Sciences, University of Minnesota, St. Paul, MN 55108, United States

* sang@umn.edu

No Dillution					10-fold Dilution			
Sample	MLP	KMeans M	Human		MLP	KMeans M	Human	Number of Replicates
49G	4	4	4		0	0	0	8
14G	1	1	1		1	1	1	8
92G	0	0	0		5	5	5	8
98G	0	0	0		4	4	4	8

104G	1	1	1		6	6	6	8
121G	4	4	4		3	3	3	8
152G	0	1	1		4	4	4	8
157G	3	3	3		4	4	4	8
158G	2	2	2		4	4	4	8
205G	1	5	5		1	2	2	8
206G	1	5	5		0	0	0	8
212G	0	0	0		4	4	4	8
217G	3	3	3		2	2	2	8
267G	0	0	0		5	5	5	8
379G	3	3	3		0	0	0	8
319G	4	4	4		3	3	3	8
368G	1	1	1		4	4	4	8
321G	0	0	0		4	4	4	8
325G	0	0	0		3	4	4	8

Supplementary Table 1 A Comparison of MLP, K-Means Trained on Metrics Data, and Human Annotations of Ambiguously Labeled Samples

No Dilution					10-fold Dilution			
Sample	SVM Raw	SVM Metric	Human		SVM Raw	SVM Metrics	Human	Number of Replicates
49G	4	4	4		0	0	0	8
14G	1	1	1		0	1	1	8
92G	0	0	0		4	5	5	8
98G	0	0	0		4	4	4	8
104G	1	1	1 or 0		5	6	6	8
121G	4	4	4		3	3	3	8
152G	1	1	1 or 0		4	4	4	8
157G	3	3	3		3	4	4	8
158G	2	2	2		3	4	4	8
205G	3	5	5		1	2	2	8
206G	4	5	5		0	0	0	8
212G	0	0	0		4	4	4	8
217G	3	3	3		2	2	2	8
267G	0	0	0		4	5	5	8
379G	3	3	3		0	0	0	8

319G	4	4	4		3	3	3	8*
368G	1	1	1		3	4	4	8
321G	0	0	0		3	4	4	8
325G	0	0	0		3	4	4 or 3	8

Supplementary Table 2 *A Comparison of SVM Trained on Raw Data, SVM Trained on Metrics Data, and Human Annotations of Ambiguously Labeled Samples*