Predictor	Type of prediction	Methodology	Features	Training data	Score range	Cut-off value
CADD	Quantitative	Logistic regression	MSA, sequence, function, other predictors	Simulated variants from the ancestral genome	CADD raw: -28.378 to 25.512; PHRED: 1–99	Not defined, PHRED 10–20 recommended
MetaRNN	Quantitative	Recurrent neural network	MSA, other predictors	ClinVar, gnomAD	0 (benign) to 1 (pathogenic)	>0.5
Envision	Quantitative	Gradient boosting regression	MSA, sequence, structure	DMS/MAVE datasets	0 (pathogenic) to 1 (benign)	Not defined, <0.5 recommended
QAFI	Quantitative	Multiple linear regression models	Sequence, structure	DMS data	0 (pathogenic) to 1 (benign)	<0.81
EVE	Quantitative (binarizable)	Variational autoencoder (unsupervised)	MSA	MSA only	0 (benign) to 1 (pathogenic)	Not defined, <0.5 recommended
AlphaMissense	Binary	Protein Language Modeling	MSA, structure	MSA, population frequency data	0 (benign) to 1 (pathogenic)	>0.5
BayesDel	Binary	Naive Bayes classifier	MSA, other predictors	ClinVar, UniProt	-1.29334 (benign) to 0.75731 (pathogenic)	>0.0692655
REVEL	Binary	Supervised random forest	MSA, other predictors	HGMD	0 (benign) to 1 (pathogenic)	Not defined, <0.5 recommended
VEST4	Binary	Supervised random forest	MSA, sequence, function, structure	HGMD	0 (benign) to 1 (pathogenic)	Not defined

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