

On-line Table 1: Main MR imaging protocols used in the study across hospitals

MR Imaging Sequence	Data-Acquisition Parameters
Xiangya Hospital/Second Xiangya Hospital	
3T Trio	
T2-weighted TSE	TR/TE = 6400/100 ms, section thickness = 5 mm, matrix size = 128 × 128
T1-weighted SE with gadolinium contrast	TR/TE = 700/10 ms, section thickness = 5 mm, matrix size = 128 × 128
DWI	TR/TE = 5780/60 ms, section thickness = 5 mm, matrix size = 128 × 128
1.5T Avanto	
T2-weighted TSE	TR/TE = 6800/100 ms, section thickness = 5 mm, matrix size = 128 × 128
T1-weighted SE with gadolinium contrast	TR/TE = 683/15 ms, section thickness = 5 mm, matrix size = 128 × 128
DWI	TR/TE = 8000/95 ms, section thickness = 5 mm, matrix size = 128 × 128
Hunan Children's Hospital	
3T Achieva	
T2-weighted TSE	TR/TE = 5260/110 ms, section thickness = 5 mm, matrix size = 256 × 256
T1-weighted SE with gadolinium contrast	TR/TE = 650/10 ms, section thickness = 5 mm, matrix size = 256 × 256
DWI	TR/TE = 8100/92 ms, section thickness = 5 mm, matrix size = 256 × 256
Hunan Provincial People's Hospital	
1.5T Avanto	
T2-weighted TSE	TR/TE = 5540/110 ms, section thickness = 5 mm, matrix size = 128 × 128
T1-weighted SE with gadolinium contrast	TR/TE = 650/15 ms, section thickness = 5 mm, matrix size = 128 × 128
DWI	TR/TE = 8200/94 ms, section thickness = 5 mm, matrix size = 128 × 128

Note:—SE indicates spin-echo.

On-line Table 2: Abbreviations and names of classifiers and feature selection methods

Classifier Acronym	Classifier Name	Feature-Selection Method Acronym	Feature-Selection Method Name
Nnet	Neural network	CHSQ	χ^2 score
DT	Decision tree	ANOVA	Analysis of variance
BST	Boosting	TSCR	T test score
BY	Bayesian	FSCR	Fisher score
BAG	Bagging	RELF	Relief
RF	Random forest	WLCX	Wilcoxon
SVM	Support vector machine	MIFS	Mutual information feature selection
LDA	Linear discriminant analysis	MRMR	Minimum redundancy/Maximum relevance
KNN	k-nearest neighbors	CIFE	Conditional infomax feature selection
GLM	Generalized Linear Model	JMI	Joint mutual information
		CMIM	Conditional mutual information maximization
		ICAP	Interaction capping
		DISR	Double input symmetric relevance
		MIM	Mutual information maximization

On-line Table 3: Stability of classifiers using RSD% of AUC^a

Classifiers	RSD%
GLM	2.22
LDA	2.91
KNN	3.92
DT	6.25
BY	3.30
SVM	9.57
BAG	3.99
Nnet	5.64
RF	3.68
BST	6.29

Note:—RSD% indicates relative SD percentage.

^a Each classifier was trained and tested on different subsamples of the data 100 times, and RSD% was calculated by the SD of AUC divided by the mean of AUC times 100.

On-line Table 4: Comparison of 10 TPOT models for multiclass classification on the training set

Model Index	Parameters	Mirco-Averaged AUC
1	LogisticRegression(LogisticRegression(Normalizer(Binarizer(input_matrix, threshold =1.0), norm=max), C = 5.0, dual=False, penalty=l1), C = 20.0, dual=True, penalty=l2)	0.92
2	LogisticRegression(RobustScaler(input_matrix), C = 20.0, dual=False, penalty=l2)	0.92
3	KNeighborsClassifier(SelectPercentile(MaxAbsScaler(input_matrix), percentile =3), n_neighbors = 7, P = 1, weights=uniform)	0.90
4	LogisticRegression(input_matrix, C = 10.0, dual=False, penalty=l1)	0.88
5	KNeighborsClassifier(MaxAbsScaler(DecisionTreeClassifier(GaussianNB(input_matrix), criterion=gini, max_depth = 10, min_samples_leaf = 13, min_samples_split = 7)), n_neighbors = 11, P = 1, weights=distance)	0.91
6	BernoulliNB(ZeroCount(input_matrix), alpha =0.1, fit_prior=True)	0.87
7	LogisticRegression(DecisionTreeClassifier(input_matrix, criterion=gini, max_depth = 3, min_samples_leaf = 20, min_samples_split = 6), C = 15.0, dual=False, penalty=l1)	0.88
8	LogisticRegression(BernoulliNB(MinMaxScaler(input_matrix),alpha =1.0, fit_prior=False), C = 10.0, dual=False, penalty=l2)	0.93
9	LogisticRegression(MaxAbsScaler(input_matrix), C = 5.0, dual=False, penalty=l2)	0.92
10	BernoulliNB(input_matrix, alpha =0.1, fit_prior=True)	0.87

On-line Table 5: Top 20 radiomics features for models by TPOT for multiclass classification

Selected Feature No.	Feature Description	Technique of Feature
31	locInt_3D_Floc_peak_global_scale3	ADC
34	stats_3D_Fstat_skew_scale3	ADC
37	stats_3D_Fstat_min_scale3	ADC
3095	morph_3D_Fmorph_sphericity_scale3	ADC
3098	morph_3D_Fmorph_diam_scale3	TIC
3101	morph_3D_Fmorph_pca_least_scale3	TIC
5201	gldzm_3D_Fdzm_lgze_scale2_algoFBNequal64_bin16	TIC
5265	gldzm_3D_Fdzm_lgze_scale3_algoFBN_bin16	TIC
5278	gldzm_3D_Fdzm_zd_entr_scale3_algoFBN_bin16	TIC
5329	gldzm_3D_Fdzm_lgze_scale3_algoFBNequal64_bin16	TIC
5342	gldzm_3D_Fdzm_zd_entr_scale3_algoFBNequal64_bin16	TIC
5345	gldzm_3D_Fdzm_lgze_scale3_algoFBNequal64_bin32	TIC
5361	gldzm_3D_Fdzm_lgze_scale3_algoFBNequal64_bin64	TIC
5393	gldzm_3D_Fdzm_lgze_scale4_algoFBN_bin16	TIC
5406	gldzm_3D_Fdzm_zd_entr_scale4_algoFBN_bin16	TIC
5409	gldzm_3D_Fdzm_lgze_scale4_algoFBN_bin32	TIC
6159	ngldm_3D_Fngl_lde_scale4_algoFBNequal64_bin64	TIC
6162	ngldm_3D_Fngl_hgce_scale4_algoFBNequal64_bin64	TIC
6165	ngldm_3D_Fngl_hdlge_scale4_algoFBNequal64_bin64	TIC
9193	ngldm_3D_Fngl_dcnu_norm_scale4_algoFBN_bin64	T2WI

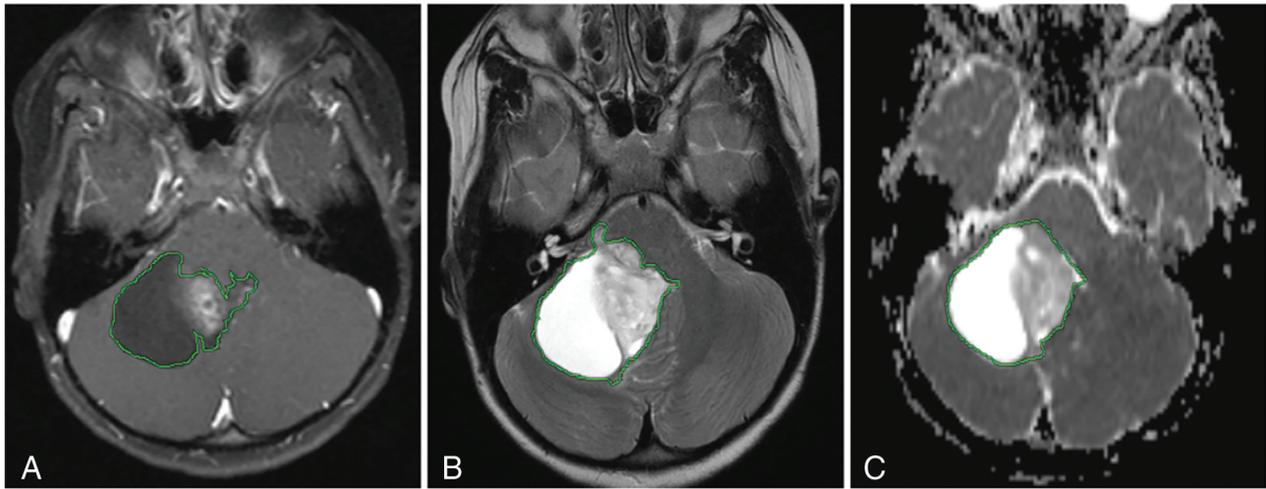
Note:—TIC indicates TIWI contrast-enhanced sequence.

On-line Table 6: Top 20 radiomics features for models by CHSQ and GLM for multiclass classification

Selected Feature No.	Feature Description	Technique of Feature
839	glcm_3Dmrg__Fcm_sum_entr__scale4_algoFBNequal64_bin32	ADC
1373	glrlm_3Dmrg__Frlm_gl_var__scale4_algoFBNequal64_bin32	ADC
1389	glrlm_3Dmrg__Frlm_gl_var__scale4_algoFBNequal64_bin64	ADC
1885	glszm_3D__Fszm_gl_var__scale4_algoFBNequal64_bin32	ADC
1901	glszm_3D__Fszm_gl_var__scale4_algoFBNequal64_bin64	ADC
1981	gldzm_3D__Fdzm_gl_var__scale1_algoFBNequal64_bin8	ADC
2013	gldzm_3D__Fdzm_gl_var__scale1_algoFBNequal64_bin32	ADC
2109	gldzm_3D__Fdzm_gl_var__scale2_algoFBNequal64_bin8	ADC
2125	gldzm_3D__Fdzm_gl_var__scale2_algoFBNequal64_bin16	ADC
2127	gldzm_3D__Fdzm_zd_entr__scale2_algoFBNequal64_bin16	ADC
7264	glrlm_3Dmrg__Frlm_lgre__scale2_algoFBNequal64_bin16	T2WI
8704	ngtdm_3D__Fngt_strength__scale3_algoFBNequal64_bin32	T2WI
8720	ngtdm_3D__Fngt_coarseness__scale4_algoFBN_bin32	T2WI
8816	ngldm_3D__Fngl_lgce__scale1_algoFBNequal64_bin8	T2WI
8832	ngldm_3D__Fngl_lgce__scale1_algoFBNequal64_bin16	T2WI
8848	ngldm_3D__Fngl_lgce__scale1_algoFBNequal64_bin32	T2WI
8864	ngldm_3D__Fngl_lgce__scale1_algoFBNequal64_bin64	T2WI
8960	ngldm_3D__Fngl_lgce__scale2_algoFBNequal64_bin16	T2WI
8976	ngldm_3D__Fngl_lgce__scale2_algoFBNequal64_bin32	T2WI
8992	ngldm_3D__Fngl_lgce__scale2_algoFBNequal64_bin64	T2WI

On-line Table 7: Comparison of TPOT models for binary classification of MB versus non-MB, EP versus non-EP, and PA versus non-PA on the training set

Model Index	MB vs Non-MB		EP vs Non-EP		PA vs Non-PA	
	Parameters	AUC	Parameters	AUC	Parameters	AUC
1	BernoulliNB(GaussianNB(MaxAbsScaler(input_matrix), alpha=0.1, fit_prior=False))	0.917	LogisticRegression(MaxAbsScaler(input_matrix), C=0.01, dual=False, penalty=l2)	0.730	BernoulliNB(LogisticRegression(input_matrix, dual=False, penalty=l1), alpha=0.001, fit_prior=True)	0.933
2	BernoulliNB(GaussianNB(Binarizer(input_matrix, threshold=0.2)), alpha=1.0, fit_prior=True)	0.936	DecisionTreeClassifier(input_matrix, criterion=entropy, max_depth=10, min_samples_leaf=18, min_samples_split=14)	0.697	KNeighborsClassifier(SelectFwe(MaxAbsScaler(input_matrix), alpha=0.032), n_neighbors=29, P=2, weights=distance)	0.955
3	BernoulliNB(DecisionTreeClassifier(input_matrix, criterion=entropy, max_depth=7, min_samples_leaf=9, min_samples_split=6), alpha=0.001, fit_prior=False)	0.916	LogisticRegression(MinMaxScaler(input_matrix), C=10.0, dual=False, penalty=l2)	0.789	BernoulliNB(input_matrix, alpha=1.0, fit_prior=True)	0.914
4	KNeighborsClassifier(Binarizer(StandardScaler(input_matrix), threshold=0.15000000000000002), n_neighbors=4, P=1, weights=uniform)	0.931	DecisionTreeClassifier(PCA(input_matrix, iterated_power=8, svd_solver=randomized), criterion=gini, max_depth=4, min_samples_leaf=19, min_samples_split=4)	0.698	MultinomialNB(SelectPercentile(BernoulliNB(MinMaxScaler(input_matrix), alpha=0.01, fit_prior=True), percentile=3)), alpha=100.0, fit_prior=True)	0.921
5	KNeighborsClassifier(MinMaxScaler(input_matrix), n_neighbors=26, P=1, weights=distance)	0.945	BernoulliNB(VarianceThreshold(input_matrix, threshold=0.05), alpha=0.01, fit_prior=True)	0.698	KNeighborsClassifier(MaxAbsScaler(input_matrix), n_neighbors=21, P=2, weights=distance)	0.952
6	BernoulliNB(LogisticRegression(input_matrix, C=0.01, dual=False, penalty=l2), alpha=0.001, fit_prior=True)	0.923	LogisticRegression(MinMaxScaler(BernoulliNB(input_matrix, alpha=1.0, fit_prior=False)), C=20.0, dual=False, penalty=l1)	0.830	BernoulliNB(SelectFwe(input_matrix, alpha=0.045), alpha=0.1, fit_prior=False)	0.915
7	BernoulliNB(VarianceThreshold(input_matrix, threshold=0.0001), alpha=1.0, fit_prior=False)	0.904	KNeighborsClassifier(Binarizer(input_matrix, threshold=1.0), n_neighbors=40, P=1, weights=distance)	0.765	LogisticRegression(StandardScaler(MaxAbsScaler(input_matrix)), C=0.5, dual=False, penalty=l2)	0.963
8	LogisticRegression(MinMaxScaler(input_matrix), C=10.0, dual=False, penalty=l1)	0.972	LogisticRegression(MinMaxScaler(input_matrix), C=20.0, dual=False, penalty=l1)	0.839	BernoulliNB(LogisticRegression(input_matrix, C=20.0, dual=False, penalty=l1), alpha=0.001, fit_prior=True)	0.936
9	LogisticRegression(KNeighborsClassifier(Binarizer(input_matrix, threshold=1.0), n_neighbors=46, P=2, weights=uniform), C=1.0, dual=False, penalty=l1)	0.974	DecisionTreeClassifier(input_matrix, criterion=entropy, max_depth=9, min_samples_leaf=18, min_samples_split=9)	0.697	BernoulliNB(DecisionTreeClassifier(DecisionTreeClassifier(input_matrix, criterion=gini, max_depth=7, min_samples_leaf=12, min_samples_split=14), criterion=gini, max_depth=8, min_samples_leaf=12, min_samples_split=14), alpha=0.1, fit_prior=True)	0.933
10	BernoulliNB(LogisticRegression(input_matrix, C=15.0, dual=False, penalty=l1), alpha=0.001, fit_prior=False)	0.924	KNeighborsClassifier(Binarizer(input_matrix, threshold=0.0), n_neighbors=72, P=1, weights=distance)	0.730	KNeighborsClassifier(Binarizer(input_matrix, threshold=0.15000000000000002), n_neighbors=12, P=1, weights=uniform)	0.954



ON-LINE FIG 1. An example of ROI delineation in a posterior fossa tumor on T1WI contrast-enhanced sequence (A), T2WI (B), and ADC (C).

	GLM	LDA	KNN	DT	BY	SVM	BAG	Nnet	RF	BST
CHSQ	0.93	0.79	0.90	0.80	0.90	0.92	0.91	0.92	0.90	0.85
ANOVA	0.92	0.87	0.87	0.83	0.90	0.91	0.89	0.92	0.89	0.86
FSCR	0.92	0.87	0.87	0.82	0.90	0.91	0.91	0.92	0.89	0.86
RELf	0.92	0.85	0.89	0.80	0.90	0.92	0.90	0.92	0.89	0.88
WLCX	0.79	0.59	0.67	0.66	0.67	0.71	0.74	0.80	0.69	0.72
MIM	0.84	0.72	0.81	0.69	0.78	0.82	0.82	0.86	0.82	0.78
MIFS	0.88	0.66	0.83	0.73	0.81	0.87	0.84	0.87	0.86	0.81
MRMR	0.88	0.63	0.84	0.71	0.82	0.88	0.87	0.88	0.83	0.84
CIFE	0.87	0.68	0.83	0.77	0.83	0.88	0.85	0.87	0.87	0.81
JMI	0.90	0.74	0.85	0.73	0.78	0.86	0.83	0.91	0.79	0.81
CMIM	0.85	0.75	0.83	0.74	0.80	0.83	0.85	0.86	0.87	0.82
ICAP	0.85	0.75	0.83	0.74	0.80	0.83	0.84	0.86	0.85	0.82
DISR	0.74	0.60	0.63	0.60	0.61	0.60	0.69	0.74	0.73	0.64

A

	GLM	LDA	KNN	DT	BY	SVM	BAG	Nnet	RF	BST
CHSQ	0.92	0.86	0.90	0.83	0.90	0.92	0.88	0.91	0.90	0.86
ANOVA	0.92	0.88	0.88	0.77	0.90	0.91	0.89	0.91	0.89	0.85
FSCR	0.92	0.88	0.88	0.75	0.90	0.90	0.88	0.91	0.90	0.85
RELf	0.92	0.87	0.89	0.76	0.90	0.92	0.88	0.91	0.90	0.84
WLCX	0.70	0.67	0.59	0.58	0.56	0.62	0.70	0.68	0.68	0.63
MIM	0.85	0.81	0.82	0.72	0.81	0.82	0.84	0.85	0.86	0.77
MIFS	0.88	0.79	0.87	0.72	0.85	0.88	0.86	0.88	0.84	0.84
MRMR	0.87	0.79	0.87	0.71	0.87	0.87	0.85	0.87	0.88	0.84
CIFE	0.87	0.81	0.87	0.75	0.85	0.86	0.86	0.87	0.86	0.83
JMI	0.87	0.81	0.78	0.66	0.72	0.80	0.83	0.87	0.84	0.81
CMIM	0.86	0.83	0.85	0.74	0.84	0.85	0.84	0.87	0.86	0.80
ICAP	0.86	0.83	0.85	0.73	0.84	0.84	0.86	0.87	0.85	0.80
DISR	0.75	0.64	0.64	0.61	0.63	0.67	0.72	0.74	0.70	0.68

B

	GLM	LDA	KNN	DT	BY	SVM	BAG	Nnet	RF	BST
CHSQ	0.92	0.90	0.88	0.79	0.89	0.91	0.89	0.92	0.90	0.81
ANOVA	0.89	0.86	0.85	0.75	0.89	0.89	0.85	0.88	0.86	0.81
FSCR	0.89	0.86	0.85	0.74	0.89	0.89	0.85	0.88	0.86	0.80
RELf	0.91	0.91	0.91	0.75	0.90	0.91	0.88	0.90	0.90	0.81
WLCX	0.62	0.56	0.56	0.60	0.58	0.58	0.63	0.59	0.58	0.61
MIM	0.66	0.66	0.64	0.56	0.63	0.64	0.65	0.68	0.64	0.60
MIFS	0.84	0.85	0.81	0.70	0.84	0.78	0.85	0.85	0.84	0.81
MRMR	0.83	0.83	0.80	0.70	0.78	0.81	0.83	0.84	0.82	0.79
CIFE	0.87	0.84	0.84	0.75	0.88	0.87	0.84	0.86	0.87	0.84
JMI	0.85	0.84	0.77	0.68	0.72	0.83	0.82	0.87	0.82	0.77
CMIM	0.84	0.80	0.85	0.68	0.82	0.83	0.82	0.84	0.85	0.78
ICAP	0.84	0.80	0.85	0.68	0.82	0.83	0.84	0.84	0.86	0.78
DISR	0.70	0.71	0.64	0.61	0.63	0.60	0.64	0.72	0.65	0.68

C

	GLM	LDA	KNN	DT	BY	SVM	BAG	Nnet	RF	BST
CHSQ	0.92	0.92	0.90	0.81	0.90	0.91	0.92	0.92	0.90	0.84
ANOVA	0.88	0.88	0.86	0.79	0.88	0.88	0.84	0.88	0.85	0.82
FSCR	0.88	0.88	0.86	0.75	0.88	0.88	0.83	0.88	0.86	0.82
RELf	0.91	0.90	0.89	0.79	0.91	0.90	0.90	0.90	0.89	0.86
WLCX	0.62	0.62	0.56	0.60	0.61	0.60	0.60	0.61	0.61	0.59
MIM	0.67	0.63	0.62	0.58	0.63	0.59	0.63	0.68	0.66	0.66
MIFS	0.62	0.61	0.60	0.54	0.66	0.57	0.58	0.63	0.56	0.59
MRMR	0.64	0.63	0.60	0.52	0.65	0.60	0.58	0.65	0.59	0.61
CIFE	0.80	0.79	0.80	0.68	0.81	0.79	0.82	0.82	0.77	0.78
JMI	0.81	0.82	0.75	0.69	0.72	0.82	0.81	0.81	0.79	0.79
CMIM	0.81	0.78	0.85	0.71	0.80	0.81	0.79	0.81	0.82	0.73
ICAP	0.81	0.78	0.85	0.73	0.80	0.80	0.79	0.81	0.80	0.73
DISR	0.65	0.65	0.67	0.58	0.64	0.64	0.62	0.66	0.65	0.58

D

ON-LINE FIG 2. Heatmap (micro-averaged AUC) of multiclass classification on the training set when 100 (A), 50 (B), 20 (C), and 10 (D) features are selected. WLCX, Wilcoxon. See On-line Table 2 for expansion of other acronyms.

	GLM	LDA	KNN	DT	BY	SVM	BAG	Nnet	RF	BST
CHSQ	0.96	0.83	0.92	0.83	0.91	0.97	0.95	0.96	0.94	0.96
ANOVA	0.97	0.88	0.92	0.82	0.94	0.97	0.93	0.97	0.94	0.93
FSCR	0.97	0.88	0.92	0.81	0.94	0.97	0.93	0.97	0.95	0.93
RELF	0.96	0.86	0.92	0.81	0.94	0.96	0.94	0.95	0.95	0.91
WLCX	0.91	0.72	0.84	0.72	0.83	0.88	0.86	0.90	0.87	0.86
MIM	0.90	0.73	0.86	0.74	0.88	0.87	0.87	0.91	0.85	0.88
MIFS	0.89	0.65	0.84	0.75	0.86	0.89	0.88	0.89	0.86	0.78
MRMR	0.89	0.64	0.86	0.73	0.85	0.90	0.88	0.88	0.87	0.81
CIFE	0.89	0.68	0.84	0.79	0.87	0.89	0.87	0.89	0.90	0.85
JMI	0.91	0.75	0.77	0.70	0.77	0.89	0.84	0.89	0.82	0.87
CMIM	0.90	0.74	0.86	0.72	0.87	0.88	0.88	0.90	0.88	0.91
ICAP	0.90	0.74	0.86	0.74	0.87	0.88	0.85	0.90	0.89	0.91
DISR	0.67	0.56	0.61	0.58	0.57	0.66	0.59	0.69	0.62	0.64

A

	GLM	LDA	KNN	DT	BY	SVM	BAG	Nnet	RF	BST
CHSQ	0.96	0.92	0.93	0.84	0.94	0.97	0.94	0.95	0.93	0.94
ANOVA	0.96	0.94	0.93	0.82	0.94	0.96	0.93	0.96	0.93	0.92
FSCR	0.96	0.94	0.93	0.83	0.94	0.96	0.94	0.96	0.94	0.92
RELF	0.96	0.94	0.94	0.86	0.95	0.97	0.94	0.95	0.94	0.92
WLCX	0.87	0.83	0.78	0.69	0.80	0.83	0.80	0.85	0.86	0.85
MIM	0.90	0.85	0.87	0.72	0.87	0.88	0.85	0.90	0.87	0.91
MIFS	0.90	0.79	0.88	0.65	0.89	0.90	0.86	0.89	0.88	0.81
MRMR	0.89	0.79	0.87	0.69	0.90	0.90	0.86	0.87	0.85	0.84
CIFE	0.90	0.79	0.88	0.70	0.90	0.91	0.86	0.90	0.85	0.81
JMI	0.90	0.85	0.83	0.80	0.78	0.90	0.86	0.90	0.85	0.86
CMIM	0.90	0.86	0.88	0.73	0.89	0.89	0.84	0.92	0.83	0.89
ICAP	0.90	0.86	0.88	0.73	0.89	0.89	0.85	0.92	0.87	0.89
DISR	0.67	0.63	0.56	0.54	0.55	0.69	0.62	0.69	0.58	0.64

B

	GLM	LDA	KNN	DT	BY	SVM	BAG	Nnet	RF	BST
CHSQ	0.96	0.95	0.95	0.82	0.95	0.97	0.92	0.96	0.93	0.93
ANOVA	0.96	0.96	0.90	0.81	0.95	0.96	0.89	0.96	0.90	0.93
FSCR	0.96	0.96	0.90	0.81	0.95	0.96	0.90	0.96	0.91	0.93
RELF	0.97	0.95	0.91	0.83	0.96	0.97	0.92	0.97	0.91	0.92
WLCX	0.73	0.77	0.67	0.64	0.73	0.69	0.78	0.70	0.79	0.74
MIM	0.67	0.71	0.64	0.55	0.67	0.66	0.65	0.68	0.61	0.56
MIFS	0.88	0.87	0.84	0.68	0.84	0.88	0.84	0.88	0.88	0.75
MRMR	0.88	0.88	0.89	0.75	0.87	0.88	0.86	0.89	0.91	0.86
CIFE	0.90	0.87	0.88	0.72	0.87	0.90	0.89	0.90	0.90	0.86
JMI	0.89	0.90	0.85	0.75	0.82	0.90	0.84	0.88	0.88	0.86
CMIM	0.77	0.79	0.74	0.70	0.70	0.77	0.79	0.77	0.74	0.66
ICAP	0.77	0.79	0.74	0.71	0.70	0.77	0.82	0.76	0.73	0.66
DISR	0.56	0.63	0.51	0.50	0.52	0.60	0.57	0.62	0.61	0.63

C

	GLM	LDA	KNN	DT	BY	SVM	BAG	Nnet	RF	BST
CHSQ	0.96	0.96	0.91	0.87	0.96	0.96	0.93	0.96	0.92	0.94
ANOVA	0.96	0.96	0.92	0.79	0.96	0.96	0.91	0.96	0.92	0.92
FSCR	0.96	0.96	0.92	0.80	0.96	0.96	0.92	0.96	0.91	0.92
RELF	0.96	0.96	0.91	0.84	0.96	0.96	0.89	0.96	0.92	0.94
WLCX	0.59	0.59	0.54	0.55	0.61	0.59	0.63	0.57	0.62	0.61
MIM	0.67	0.64	0.63	0.59	0.64	0.64	0.63	0.66	0.61	0.62
MIFS	0.59	0.59	0.57	0.52	0.60	0.45	0.53	0.59	0.54	0.53
MRMR	0.54	0.55	0.41	0.51	0.56	0.53	0.54	0.53	0.49	0.59
CIFE	0.84	0.84	0.82	0.67	0.79	0.85	0.79	0.85	0.79	0.79
JMI	0.83	0.84	0.78	0.70	0.76	0.85	0.76	0.84	0.77	0.68
CMIM	0.77	0.79	0.80	0.67	0.72	0.78	0.80	0.78	0.75	0.63
ICAP	0.77	0.79	0.80	0.70	0.72	0.78	0.77	0.77	0.80	0.63
DISR	0.51	0.63	0.43	0.50	0.51	0.50	0.58	0.51	0.51	0.64

D

ON-LINE FIG 3. Heatmap (AUC) of binary classification of MB versus non-MB on the training set when 100 (A), 50 (B), 20 (C), and 10 (D) features are selected. WLCX, Wilcoxon. See On-line Table 22 for expansion of other acronyms.

	GLM	LDA	KNN	DT	BY	SVM	BAG	Nnet	RF	BST
CHSQ	0.71	0.56	0.68	0.58	0.60	0.63	0.72	0.70	0.62	0.71
ANOVA	0.71	0.62	0.61	0.64	0.60	0.64	0.67	0.72	0.66	0.71
FSCR	0.71	0.62	0.61	0.63	0.60	0.64	0.72	0.73	0.68	0.71
RELF	0.78	0.65	0.76	0.64	0.74	0.76	0.68	0.78	0.73	0.70
WLCX	0.691	0.523	0.699	0.502	0.58	0.706	0.594	0.635	0.675	0.614
MIM	0.659	0.55	0.629	0.533	0.581	0.61	0.575	0.617	0.681	0.557
MIFS	0.646	0.458	0.641	0.536	0.621	0.572	0.609	0.657	0.659	0.606
MRMR	0.647	0.499	0.655	0.558	0.616	0.57	0.65	0.641	0.595	0.622
CIFE	0.635	0.511	0.652	0.555	0.583	0.596	0.61	0.645	0.677	0.588
JMI	0.726	0.567	0.704	0.498	0.6	0.731	0.668	0.723	0.755	0.643
CMIM	0.658	0.571	0.631	0.533	0.58	0.575	0.58	0.626	0.648	0.63
ICAP	0.658	0.571	0.631	0.533	0.58	0.575	0.625	0.582	0.633	0.664
DISR	0.656	0.494	0.474	0.556	0.606	0.594	0.619	0.612	0.653	0.578

A

	GLM	LDA	KNN	DT	BY	SVM	BAG	Nnet	RF	BST
CHSQ	0.633	0.55	0.609	0.562	0.528	0.562	0.588	0.666	0.58	0.689
ANOVA	0.621	0.638	0.554	0.593	0.573	0.588	0.659	0.646	0.618	0.671
FSCR	0.621	0.638	0.554	0.596	0.573	0.588	0.639	0.671	0.583	0.671
RELF	0.72	0.654	0.729	0.569	0.742	0.716	0.62	0.747	0.724	0.664
WLCX	0.66	0.662	0.59	0.512	0.568	0.728	0.604	0.596	0.574	0.583
MIM	0.667	0.619	0.675	0.568	0.599	0.634	0.677	0.603	0.74	0.577
MIFS	0.609	0.568	0.686	0.539	0.654	0.572	0.726	0.607	0.65	0.635
MRMR	0.617	0.556	0.712	0.614	0.678	0.576	0.57	0.578	0.663	0.671
CIFE	0.606	0.547	0.652	0.593	0.632	0.563	0.702	0.596	0.722	0.621
JMI	0.776	0.605	0.756	0.635	0.642	0.741	0.638	0.793	0.683	0.672
CMIM	0.678	0.573	0.692	0.533	0.609	0.661	0.594	0.709	0.705	0.643
ICAP	0.678	0.573	0.692	0.54	0.609	0.661	0.615	0.648	0.699	0.617
DISR	0.644	0.582	0.515	0.537	0.609	0.592	0.503	0.62	0.563	0.566

B

	GLM	LDA	KNN	DT	BY	SVM	BAG	Nnet	RF	BST
CHSQ	0.532	0.524	0.569	0.481	0.51	0.492	0.607	0.55	0.623	0.622
ANOVA	0.624	0.621	0.65	0.68	0.584	0.594	0.674	0.628	0.654	0.697
FSCR	0.624	0.621	0.65	0.587	0.584	0.594	0.692	0.621	0.678	0.697
RELF	0.704	0.665	0.699	0.61	0.744	0.711	0.658	0.715	0.686	0.633
WLCX	0.673	0.607	0.568	0.533	0.532	0.69	0.655	0.49	0.631	0.578
MIM	0.71	0.628	0.587	0.543	0.636	0.592	0.583	0.704	0.7	0.581
MIFS	0.628	0.62	0.621	0.626	0.646	0.57	0.716	0.632	0.637	0.715
MRMR	0.588	0.529	0.491	0.559	0.611	0.49	0.625	0.578	0.612	0.631
CIFE	0.63	0.532	0.715	0.519	0.728	0.54	0.718	0.669	0.644	0.648
JMI	0.696	0.635	0.626	0.586	0.589	0.668	0.683	0.711	0.653	0.584
CMIM	0.651	0.63	0.666	0.577	0.571	0.602	0.673	0.659	0.705	0.685
ICAP	0.651	0.63	0.666	0.567	0.571	0.602	0.717	0.645	0.731	0.685
DISR	0.568	0.577	0.523	0.476	0.575	0.67	0.562	0.614	0.562	0.613

C

	GLM	LDA	KNN	DT	BY	SVM	BAG	Nnet	RF	BST
CHSQ	0.49	0.52	0.59	0.47	0.49	0.49	0.63	0.55	0.64	0.62
ANOVA	0.63	0.63	0.66	0.64	0.59	0.61	0.69	0.65	0.73	0.71
FSCR	0.63	0.63	0.66	0.66	0.59	0.61	0.68	0.64	0.69	0.68
RELF	0.68	0.68	0.68	0.61	0.70	0.68	0.66	0.68	0.67	0.62
WLCX	0.63	0.623	0.621	0.576	0.529	0.586	0.639	0.378	0.606	0.545
MIM	0.666	0.592	0.652	0.642	0.636	0.528	0.69	0.674	0.689	0.632
MIFS	0.407	0.407	0.488	0.496	0.538	0.427	0.528	0.445	0.526	0.502
MRMR	0.407	0.407	0.488	0.496	0.538	0.427	0.527	0.415	0.481	0.502
CIFE	0.611	0.621	0.683	0.597	0.696	0.67	0.659	0.635	0.677	0.627
JMI	0.612	0.679	0.573	0.557	0.604	0.664	0.573	0.629	0.661	0.558
CMIM	0.475	0.561	0.592	0.592	0.462	0.599	0.721	0.52	0.64	0.463
ICAP	0.475	0.561	0.592	0.585	0.462	0.599	0.647	0.541	0.638	0.542
DISR	0.512	0.561	0.653	0.53	0.548					

	GLM	LDA	KNN	DT	BY	SVM	BAG	Nnet	RF	BST
CHSQ	0.95	0.87	0.93	0.83	0.94	0.95	0.94	0.94	0.94	0.95
ANOVA	0.93	0.91	0.90	0.86	0.91	0.92	0.93	0.92	0.93	0.92
FSCR	0.93	0.91	0.90	0.83	0.91	0.92	0.91	0.93	0.93	0.91
RELF	0.94	0.84	0.90	0.88	0.92	0.94	0.95	0.94	0.93	0.90
WLCX	0.90	0.79	0.82	0.74	0.72	0.86	0.89	0.90	0.87	0.88
MIM	0.87	0.74	0.84	0.75	0.81	0.83	0.85	0.88	0.88	0.87
MIFS	0.91	0.75	0.90	0.77	0.89	0.92	0.90	0.91	0.91	0.90
MRMR	0.91	0.78	0.89	0.77	0.90	0.92	0.92	0.92	0.90	0.92
CIFE	0.91	0.76	0.89	0.77	0.90	0.92	0.91	0.91	0.91	0.91
JMI	0.93	0.77	0.85	0.68	0.84	0.87	0.85	0.92	0.91	0.89
CMIM	0.86	0.78	0.84	0.76	0.82	0.84	0.88	0.87	0.88	0.88
ICAP	0.86	0.78	0.84	0.75	0.82	0.84	0.87	0.88	0.85	0.88
DISR	0.79	0.67	0.72	0.70	0.70	0.70	0.74	0.80	0.75	0.74

A

	GLM	LDA	KNN	DT	BY	SVM	BAG	Nnet	RF	BST
CHSQ	0.96	0.86	0.93	0.82	0.94	0.95	0.93	0.96	0.93	0.92
ANOVA	0.93	0.91	0.90	0.86	0.89	0.92	0.92	0.94	0.92	0.91
FSCR	0.93	0.91	0.90	0.87	0.89	0.92	0.94	0.94	0.93	0.91
RELF	0.93	0.89	0.91	0.83	0.92	0.94	0.93	0.92	0.92	0.90
WLCX	0.67	0.69	0.64	0.66	0.63	0.74	0.74	0.68	0.70	0.77
MIM	0.87	0.85	0.85	0.78	0.86	0.85	0.87	0.88	0.87	0.90
MIFS	0.91	0.88	0.93	0.78	0.90	0.92	0.90	0.90	0.93	0.90
MRMR	0.90	0.85	0.95	0.78	0.90	0.92	0.90	0.91	0.92	0.93
CIFE	0.91	0.87	0.92	0.78	0.91	0.92	0.91	0.91	0.92	0.89
JMI	0.87	0.83	0.78	0.69	0.80	0.81	0.79	0.89	0.78	0.77
CMIM	0.87	0.83	0.87	0.75	0.84	0.87	0.88	0.89	0.88	0.88
ICAP	0.87	0.83	0.87	0.77	0.84	0.87	0.88	0.89	0.88	0.88
DISR	0.73	0.72	0.68	0.61	0.69	0.69	0.72	0.74	0.70	0.72

B

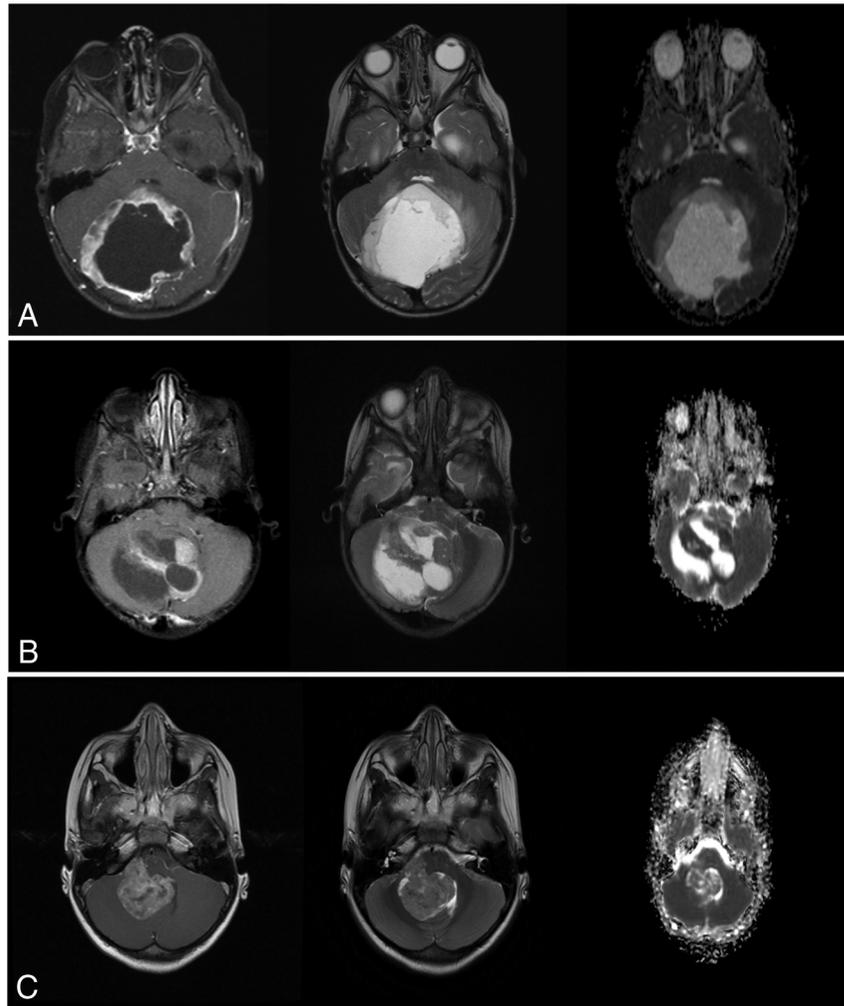
	GLM	LDA	KNN	DT	BY	SVM	BAG	Nnet	RF	BST
CHSQ	0.96	0.94	0.92	0.86	0.94	0.95	0.93	0.96	0.94	0.93
ANOVA	0.93	0.91	0.91	0.81	0.91	0.92	0.93	0.94	0.92	0.92
FSCR	0.93	0.91	0.91	0.82	0.91	0.92	0.93	0.94	0.92	0.92
RELF	0.93	0.91	0.92	0.88	0.92	0.94	0.94	0.92	0.92	0.92
WLCX	0.52	0.54	0.50	0.58	0.55	0.58	0.53	0.53	0.59	0.61
MIM	0.48	0.60	0.58	0.53	0.50	0.54	0.58	0.61	0.57	0.52
MIFS	0.87	0.88	0.87	0.81	0.88	0.88	0.90	0.88	0.86	0.89
MRMR	0.91	0.90	0.90	0.77	0.92	0.91	0.89	0.90	0.93	0.85
CIFE	0.90	0.90	0.87	0.73	0.90	0.88	0.88	0.91	0.91	0.88
JMI	0.77	0.76	0.71	0.61	0.72	0.72	0.75	0.79	0.69	0.68
CMIM	0.79	0.82	0.76	0.67	0.70	0.77	0.83	0.84	0.79	0.77
ICAP	0.79	0.82	0.76	0.72	0.70	0.77	0.78	0.83	0.74	0.77
DISR	0.70	0.67	0.60	0.66	0.67	0.67	0.71	0.71	0.68	0.69

C

	GLM	LDA	KNN	DT	BY	SVM	BAG	Nnet	RF	BST
CHSQ	0.96	0.95	0.92	0.88	0.95	0.95	0.92	0.96	0.93	0.94
ANOVA	0.94	0.92	0.92	0.80	0.93	0.94	0.92	0.94	0.92	0.93
FSCR	0.94	0.92	0.92	0.82	0.93	0.94	0.93	0.94	0.94	0.93
RELF	0.94	0.93	0.89	0.83	0.93	0.94	0.93	0.93	0.91	0.91
WLCX	0.42	0.44	0.43	0.49	0.52	0.51	0.45	0.48	0.47	0.43
MIM	0.49	0.52	0.50	0.53	0.52	0.59	0.58	0.62	0.56	0.55
MIFS	0.41	0.50	0.52	0.52	0.56	0.59	0.54	0.48	0.55	0.51
MRMR	0.58	0.58	0.68	0.57	0.57	0.62	0.70	0.60	0.72	0.60
CIFE	0.73	0.79	0.71	0.67	0.76	0.72	0.78	0.76	0.80	0.83
JMI	0.70	0.67	0.63	0.58	0.69	0.68	0.69	0.73	0.65	0.71
CMIM	0.75	0.77	0.72	0.63	0.74	0.74	0.77	0.78	0.76	0.67
ICAP	0.75	0.77	0.72	0.63	0.74	0.74	0.77	0.78	0.73	0.68
DISR	0.70	0.69	0.66	0.63	0.64	0.68	0.70	0.71	0.69	0.69

D

ON-LINE FIG 5. Heatmap (AUC) of binary classification of PA versus non-PA on the training set when (A), 50 (B), 20 (C), and 10 (D) features are selected. WLCX, Wilcoxon. See On-line Table 2 for expansion of other acronyms.



ON-LINE FIG 6. Examples of agreement or disagreement between the automatic machine learning TPOT model and expert review in the multi-class classification of posterior fossa tumors. *A*, An example of a posterior fossa tumor that was correctly predicted by both the automatic TPOT model and 2 experts. The example presented is a pilocytic astrocytoma showing a characteristic appearance of a cystic cerebellar lesion with a thick enhanced wall. *B*, An example of a posterior fossa tumor that was correctly predicted by the automatic TPOT model, but incorrectly by 2 experts. The example presented is a medulloblastoma showing a mixed cystic/solid enhancing mass in the cerebellum; the solid part is hypointense on ADC. *C*, An example of a posterior fossa tumor that was incorrectly predicted by an automatic TPOT model, but correctly predicted by 2 experts. The example presented is an ependymoma with a heterogeneously enhancing mass in the inferior fourth ventricle. Note extension toward the right cerebellopontine angle cistern.