

Model B: Screening for Clean/Transfused Novel metrics

Table: Sort of P001 Sunderby Hematology Data Update_260326_CM Response: Clean/Transfused Validation: Validation 25_75 by ID
SORTED by Code and Time

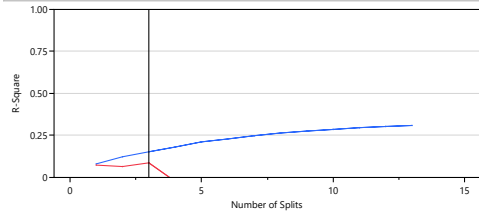
Details

Partition for Clean/Transfused

Validation: Validation 25_75 by ID

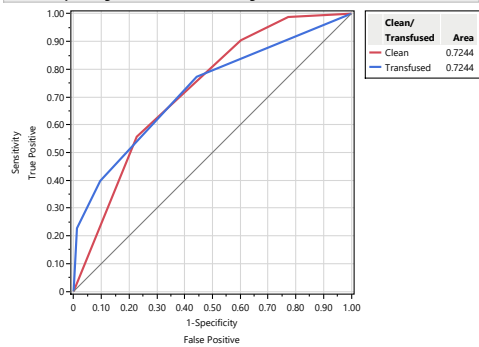
	RSquare	N	Number of Splits
Training	0.153	255	3
Validation	0.087	85	

Split History

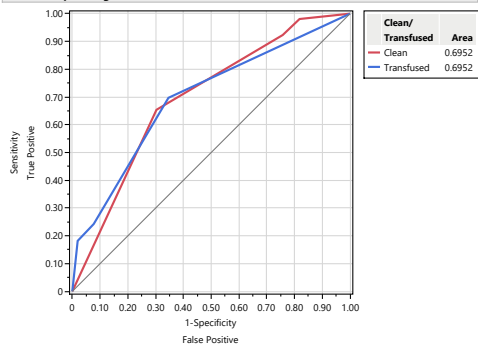


Validation Data in Red

Receiver Operating Characteristic on Training Data



Receiver Operating Characteristic on Validation Data



Bootstrap Forest for Clean/Transfused

Specifications

Target	Clean/Transfused	Training Rows:	255
Validation Column:	Validation 25_75 by ID	Validation Rows:	85
		Test Rows:	0
Number of Trees in the Forest:	100	Number of Terms:	4
Number of Terms Sampled per Split:	3	Bootstrap Samples:	255
		Minimum Splits per Tree:	10
		Minimum Size Split:	5

Overall Statistics

Measure	Training	Validation	Definition
Entropy RSquare	0.3435	0.0859	$1 - \text{Loglike}(\text{model}) / \text{Loglike}(0)$
Generalized RSquare	0.4938	0.1471	$(1 - (L(0)/L(\text{model}))^{2/n}) / (1 - L(0)^{2/n})$
Mean -Log p	0.4230	0.6106	$-\sum \log(p_{ij})/n$
RASE	0.3641	0.4641	$\sqrt{\sum (y_{ij} - p_{ij})^2/n}$
Mean Abs Dev	0.3101	0.3809	$\sum y_{ij} - p_{ij} /n$
Misclassification Rate	0.1608	0.3529	$\sum (p_{ij} \neq \text{pMax})/n$
N	255	85	n

Number of Trees

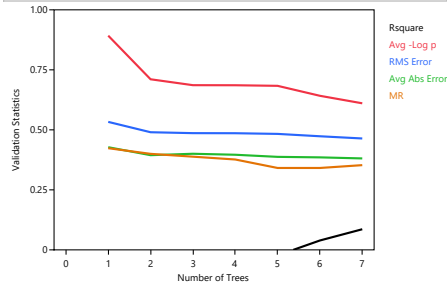
7

Confusion Matrix

Training			Validation		
Actual	Predicted Count		Actual	Predicted Count	
Clean/Transfused	Clean	Transfused	Clean/Transfused	Clean	Transfused
Clean	157	10	Clean	47	5
Transfused	31	57	Transfused	25	8

Actual	Predicted Rate		Actual	Predicted Rate	
Clean/Transfused	Clean	Transfused	Clean/Transfused	Clean	Transfused
Clean	0.940	0.060	Clean	0.904	0.096
Transfused	0.352	0.648	Transfused	0.758	0.242

Cumulative Validation



Per-Tree Summaries

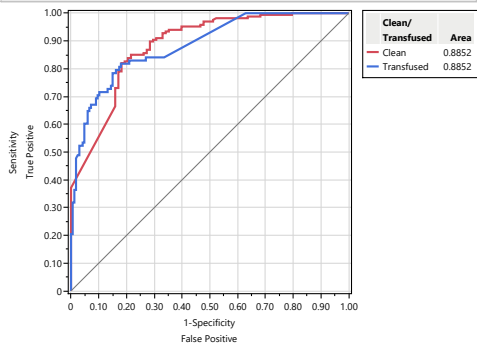
Tree	Splits	Rank	OOB Loss	OOB Loss/N
1	20	4	65.243261	0.7499225
2	24	2	72.752217	0.6674515
3	22	3	58.071423	0.6674876
4	24	6	75.052654	0.7817985
5	20	7	97.413424	0.9940145
6	24	1	66.079174	0.6542493
7	25	5	66.005645	0.7675075

Model B: Screening for Clean/Transfused Novel metrics

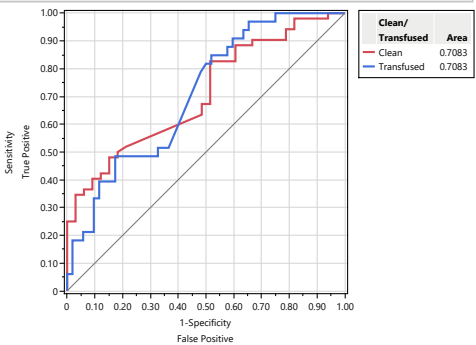
Details

Bootstrap Forest for Clean/Transfused

Receiver Operating Characteristic on Training Data



Receiver Operating Characteristic on Validation Data



Boosted Tree for Clean/Transfused

Specifications

Target	Clean/Transfused	Number of training rows:	255
Validation Column:	Validation 25_75 by ID	Number of validation rows:	85
Number of Layers:	44		
Splits per Tree:	2		
Learning Rate:	0.088		
Overfit Penalty:	0.0001		

Overall Statistics

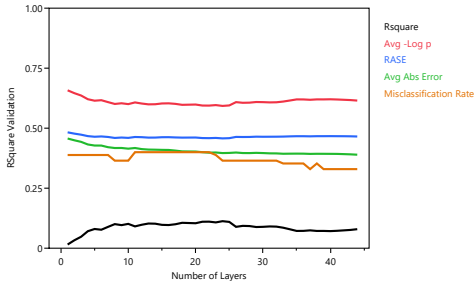
Measure	Training	Validation	Definition
Entropy RSquare	0.2362	0.0792	$1 - \text{Loglike}(\text{model}) / \text{Loglike}(0)$
Generalized RSquare	0.3623	0.1363	$(1 - L(0) / L(\text{model}))^{2/n} / (1 - L(0) / L(2/n))$
Mean -Log p	0.4922	0.6150	$\sum -\text{Log}(p[i]) / n$
RASE	0.4040	0.4654	$\sqrt{\sum (y[i] - p[i])^2 / n}$
Mean Abs Dev	0.3552	0.3895	$\sum y[i] - p[i] / n$
Misclassification Rate	0.2196	0.3294	$\sum (p[i] \neq \text{pMax}) / n$
N	255	85	n

Confusion Matrix

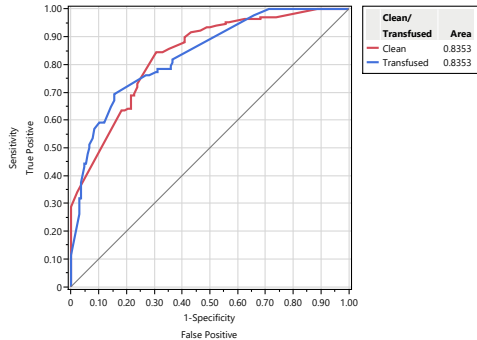
Training			Validation		
Actual	Predicted Count		Actual	Predicted Count	
Clean/ Transfused	Clean	Transfused	Clean/ Transfused	Clean	Transfused
Clean	157	10	Clean	49	3
Transfused	46	42	Transfused	25	8

Actual	Predicted Rate		Actual	Predicted Rate	
Clean/ Transfused	Clean	Transfused	Clean/ Transfused	Clean	Transfused
Clean	0.940	0.060	Clean	0.942	0.058
Transfused	0.523	0.477	Transfused	0.758	0.242

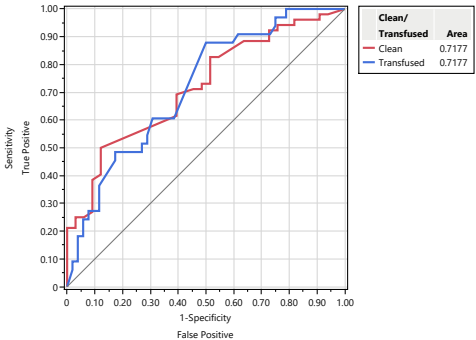
Cumulative Validation



Receiver Operating Characteristic on Training Data



Receiver Operating Characteristic on Validation Data



Model B: Screening for Clean/Transfused Novel metrics

Details

Neural

Validation Column: Validation 25_75 by ID

Model Launch

Hidden Layer Structure

Number of nodes of each activation type

Activation Sigmoid Identity Radial

Layer TanH Linear Gaussian

First 3 0 0

Second 0 0 0

Second layer is closer to X's in two layer models.

Boosting

Fit an additive sequence of models scaled by the learning rate.

Number of Models 0

Learning Rate 0.1

Fitting Options

☐ Transform Covariates

Penalty Method Squared

Number of Tours 1

Model NTanH(3)NBoost(2)

Training

Clean/Transfused

Measures	Value
Generalized RSquare	0.0235406
Entropy RSquare	0.0134445
RASE	0.4645258
Mean Abs Dev	0.4052423
Misclassification Rate	0.2987013
-LogLikelihood	96.475759
Sum Freq	154

Confusion Matrix

Actual Clean/ Transfused	Predicted Count	
	Clean	Transfused
Clean	98	5
Transfused	41	10

Confusion Rates

Actual Clean/ Transfused	Predicted Rate	
	Clean	Transfused
Clean	0.951	0.049
Transfused	0.804	0.196

Validation

Clean/Transfused

Measures	Value
Generalized RSquare	0.3905835
Entropy RSquare	0.2606926
RASE	0.3859518
Mean Abs Dev	0.3139779
Misclassification Rate	0.2096774
-LogLikelihood	28.822315
Sum Freq	62

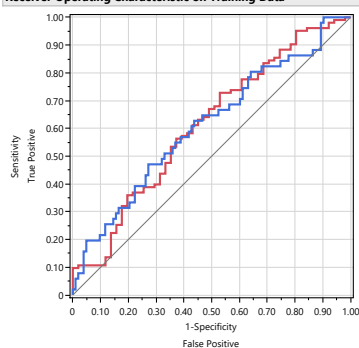
Confusion Matrix

Actual Clean/ Transfused	Predicted Count	
	Clean	Transfused
Clean	42	0
Transfused	13	7

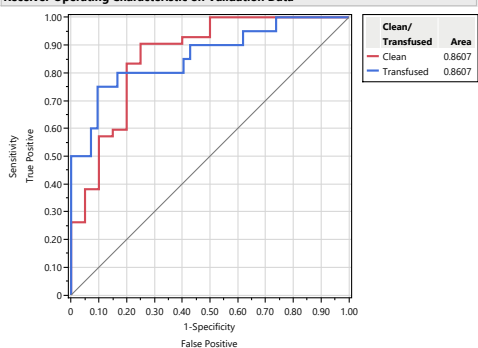
Confusion Rates

Actual Clean/ Transfused	Predicted Rate	
	Clean	Transfused
Clean	1.000	0.000
Transfused	0.650	0.350

Receiver Operating Characteristic on Training Data



Receiver Operating Characteristic on Validation Data



Model B: Screening for Clean/Transfused Novel metrics

Details

Support Vector Machine

Model Comparison

Show	Method	Kernel Function	Cost	Gamma	# SV	Training Misclassification Rate	Validation Misclassification Rate	Validation Generalized RSquare	Probability Threshold	Threshold Validation Misclassification Rate	Best
☒	Model 1	Radial Basis Function	1	0.25	115	0.30519	0.29032	0.34749	0.07434	0.29032	Smallest Misclassification Rate Largest RSquare

Validation Column: Validation 25_75 by ID

Model Launch

Kernel Function

- ☒ Radial Basis Function
☐ Tuning Design

Cost 1
Gamma 0.25

Support Vector Machine Model 1

Model Summary

Response Clean/Transfused
Validation Method Validation Column
Kernel Function Radial Basis Function

Estimation Details

Cost 1
Gamma 0.25

Measure Training Validation

Measure	Training	Validation
Number of rows	154	62
Sum of Frequencies	154	62
Misclassification Rate	0.3051948	0.2903226
Number of Support Vectors	115	115

Fit Details

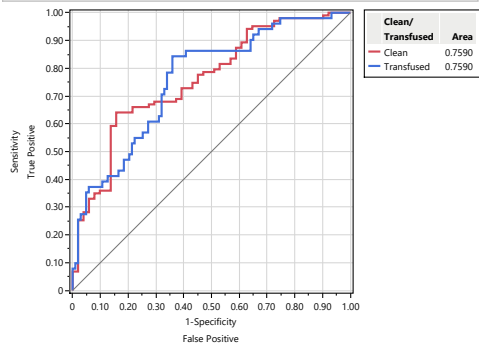
Measure	Training	Validation	Definition
Entropy RSquare	0.1421	0.2274	$1 - \text{Loglike}(\text{model}) / \text{Loglike}(0)$
Generalized RSquare	0.2296	0.3475	$(1 - L(0) / L(\text{model}))^{(2/n)} / (1 - L(0) / L(0))^{(2/n)}$
Mean -Log p	0.5448	0.4858	$\sum -\text{Log}(p[i]) / n$
RASE	0.4267	0.3938	$\sqrt{\sum (y[i] - p[i])^2 / n}$
Mean Abs Dev	0.3668	0.3355	$\sum y[i] - p[i] / n$
Misclassification Rate	0.2727	0.1935	$\sum (p[i] \neq \text{pMax}) / n$
N	154	62	n

Confusion Matrix

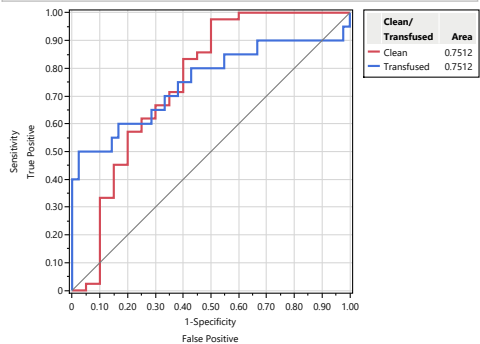
Training					Validation				
Actual		Predicted Rate		Misclassification Rate 0.3052	Actual		Predicted Rate		Misclassification Rate 0.2903
Clean/ Transfused	Clean	Transfused	Clean/ Transfused		Clean	Transfused			
Clean	1.000	0.000	Clean		1.000	0.000			
Transfused	0.922	0.078	Transfused		0.900	0.100			
Actual		Predicted Count			Actual		Predicted Count		
Clean/ Transfused	Clean	Transfused			Clean/ Transfused	Clean	Transfused		
Clean	103	0			Clean	42	0		
Transfused	47	4			Transfused	18	2		

ROC Curve for Clean/Transfused = Clean

Receiver Operating Characteristic on Training Data



Receiver Operating Characteristic on Validation Data



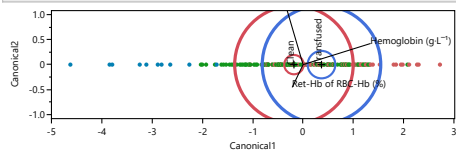
Discriminant Analysis

Discriminant Method: Linear

Classification: Clean/Transfused

Validation: Validation 25_75 by ID

Canonical Plot



Score Summaries

Columns

Hemoglobin (g/L)
Epo (U/L)
Ret-Hb of RBC-Hb (%)

Source	Count	Misclassified	Percent Misclassified	Entropy RSquare	-2LogLikelihood
Training	154	63	40.9091	-0.0322	201.887
Validation	62	12	19.3548	0.17756	

Training			Validation		
Actual	Predicted Count		Actual	Predicted Count	
Clean/Transfused	Clean	Transfused	Clean/Transfused	Clean	Transfused
Clean	59	44	Clean	35	7
Transfused	19	32	Transfused	5	15
Actual	Predicted Rate		Actual	Predicted Rate	
Clean/Transfused	Clean	Transfused	Clean/Transfused	Clean	Transfused
Clean	0.573	0.427	Clean	0.833	0.167
Transfused	0.373	0.627	Transfused	0.250	0.750

Groups

Clean/Transfused

Count
Clean 103
Transfused 51

Model B: Screening for Clean/Transfused Novel metrics

Details

Nominal Logistic Fit for Clean/Transfused

Effect Summary

Source	Logworth	PValue
Hemoglobin (g L ⁻¹)	2.276	0.00530
Ret-Hb of RBC-Hb (%)	0.614	0.24312
Ratio RBC-Hb/Ret-Hb	0.519	0.30245
Epo (UL ⁻¹)	0.492	0.32230

Converged in Gradient, 5 iterations

Iterations

Iter	Objective	Relative Gradient	Norm Gradient
0	106.7446581	5.1211414044	4481.634664
1	92.65610533	1.2292566986	351.62827125
2	91.78301561	0.3481351546	52.187164863
3	91.719792258	0.0235902366	4.3921361479
4	91.719513212	0.0001015747	0.0213552612
5	91.719513207	1.8796387e-9	4.0174099e-7

Whole Model Test

Model	-LogLikelihood	DF	ChiSquare	Prob>ChiSq
Difference	6.070995	4	12.14199	0.0163*
Full	91.719513			
Reduced	97.790508			

RSquare (U)	0.0621
AICc	193.844
BIC	208.624
Observations (or Sum Wgts)	154

Fit Details

Measure	Training	Validation	Definition
Entropy RSquare	0.0621	0.1916	1-Loglike(model)/Loglike(0)
Generalized RSquare	0.1054	0.2992	(1-(L(0)/L(model))^(2/n))/(1-L(0)^(2/n))
Mean -Log p	0.5956	0.5083	$\sum -\log(p_{ij})/n$
RASE	0.4553	0.4071	$\sqrt{\sum (y_{ij}-\hat{p}_{ij})^2/n}$
Mean Abs Dev	0.4129	0.3372	$\sum y_{ij}-\hat{p}_{ij} /n$
Misclassification Rate	0.3247	0.2419	$\sum (p_{ij}-\hat{p}_{ij})/n$
N	154	62	n

Lack Of Fit

Source	DF	-LogLikelihood	ChiSquare
Lack Of Fit	149	91.719513	183.439
Saturated	153	0.000000	Prob>ChiSq
Fitted	4	91.719513	0.0289*

Parameter Estimates

Term	Estimate	Std Error	ChiSquare	Prob>ChiSq
Intercept	-4.0125031	6.4643648	0.39	0.5348
Hemoglobin (g L ⁻¹)	0.07319519	0.0262514	7.77	0.0053*
Epo (UL ⁻¹)	-0.0394519	0.0398605	0.98	0.3223
Ret-Hb of RBC-Hb (%)	-3.8609009	3.3077471	1.36	0.2431
Ratio RBC-Hb/Ret-Hb	-0.0262461	0.0254519	1.06	0.3024

For log odds of Transfused/Clean

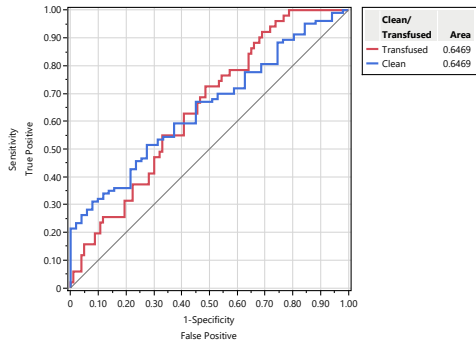
Covariance of Estimates

Cov	Intercept	Hemoglobin (g L ⁻¹)	Epo (UL ⁻¹)	Ret-Hb of RBC-Hb (%)	Ratio RBC-Hb/Ret-Hb
Intercept	41.788	-0.072	-0.005	-17.36	-0.135
Hemoglobin (g L ⁻¹)	-0.072	0.0007	-0.000	-0.014	-0.000
Epo (UL ⁻¹)	-0.005	-0.000	0.0016	-0.002	0.0001
Ret-Hb of RBC-Hb (%)	-17.36	-0.014	-0.002	10.941	0.0810
Ratio RBC-Hb/Ret-Hb	-0.135	-0.000	0.0001	0.0810	0.0006

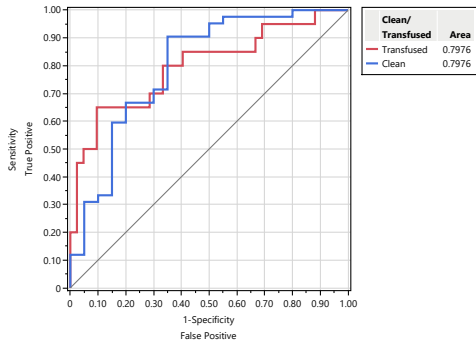
Effect Wald Tests

Source	Nparm	DF	Wald ChiSquare	Prob>ChiSq
Hemoglobin (g L ⁻¹)	1	1	7.77429734	0.0053*
Epo (UL ⁻¹)	1	1	0.97960092	0.3223
Ret-Hb of RBC-Hb (%)	1	1	1.36242535	0.2431
Ratio RBC-Hb/Ret-Hb	1	1	1.06337746	0.3024

Receiver Operating Characteristic on Training Data



Receiver Operating Characteristic on Validation Data



Model B: Screening for Clean/Transfused Novel metrics

Details

Generalized Regression for Clean/Transfused = Transfused

Model Comparison

Show	Response Distribution	Estimation Method	Validation Method	Nonzero Parameters	AICc	BIC	Generalized RSquare	Validation Generalized RSquare
☒	Binomial	Lasso	Validation Column	4	192.91887	204.79822	0.0952731	0.4020199

Model Launch

Response Distribution

Binomial

Estimation Method

Lasso

☐ Adaptive

Validation Method

Validation Column

☐ Early Stopping

Validation Column: Validation 25, 75 by ID

Binomial Lasso with Validation Column

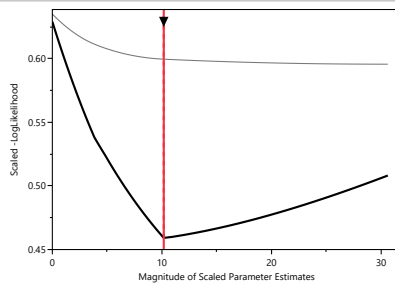
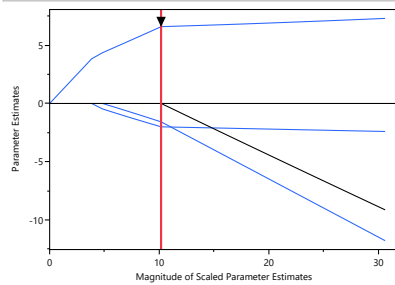
Model Summary

Response	Clean/Transfused	Number of Grid Points	150
Distribution	Binomial	Minimum Penalty Fraction	1e-4
Estimation Method	Lasso	Grid Scale	Square Root
Validation Method	Validation Column		
Probability Model Link	Logit		
Validation Column:	Validation 25, 75 by ID		

Estimation Details

Measure	Training	Validation
Number of rows	154	62
Sum of Frequencies	154	62
-Loglikelihood	92.325207	28.468137
Number of Parameters	4	4
BIC	204.79822	73.444812
AICc	192.91887	65.638029
Generalized RSquare	0.0952731	0.4020199
Lambda Penalty	0.063574	.

Solution Path



Legend
— Validation
— Training

Parameter Estimates for Original Predictors

Term	Estimate	Std Error	Wald ChiSquare	Prob > ChiSquare	Lower 95%	Upper 95%
Intercept	-9.157402	3.0881224	8.7933732	0.0030*	-15.21001	-3.104793
Hemoglobin (g/L ³)	0.0660277	0.0210794	9.8115374	0.0017*	0.0247129	0.1073424
Epo (iU/L ³)	-0.032384	0.0401286	0.6697417	0.4131	-0.111491	0.0458102
Ret-Hb of RBC-Hb (%)	-0.516344	0.7325774	0.4967877	0.4809	-1.952169	0.9194815
Ratio RBC-Hb/Ret-Hb	0	0	0	1.0000	0	0

Training

Method	N	Sum Wgt	Entropy RSquare	Misclassification Rate	AUC	RASE	Generalized RSquare
Bootstrap Forest	255	255.000	0.3435	0.1608	0.8852	0.36408	0.4938
Boosted Tree	255	255.000	0.2362	0.2196	0.8353	0.40395	0.3623
Decision Tree	255	255.000	0.1529	0.2706	0.7244	0.42732	0.2469
Support Vector Machines	154	154.000	0.1421	0.2727	0.7590	0.42674	0.2296
Nominal Logistic	154	154.000	0.0621	0.3247	0.6469	0.45534	0.1054
Generalized Regression Lasso	154	154.000	0.0559	0.3117	0.6269	0.45600	0.0953
Neural Boosted	154	154.000	0.0134	0.2987	0.6118	0.46453	0.0235
Discriminant	154	.	-0.032	0.4091	.	.	.

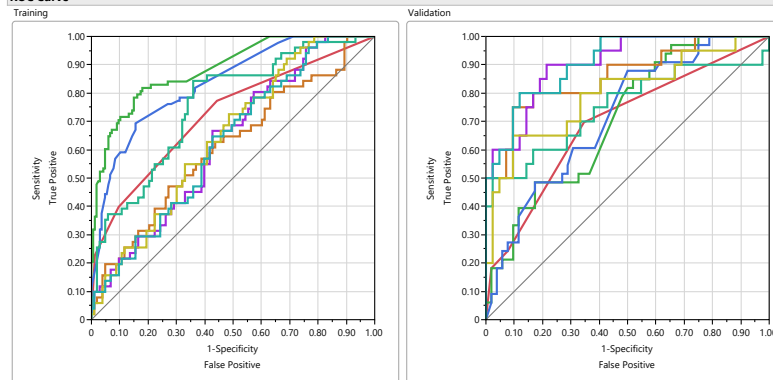
Validation

Method	N	Sum Wgt	Entropy RSquare	Misclassification Rate	AUC	RASE	Generalized RSquare
Generalized Regression Lasso	62	62.0000	0.2698	0.1935	0.9095	0.38252	0.4020
Neural Boosted	62	62.0000	0.2607	0.2097	0.8607	0.38595	0.3906
Support Vector Machines	62	62.0000	0.2274	0.1935	0.7512	0.39382	0.3475
Nominal Logistic	62	62.0000	0.1916	0.2419	0.7976	0.40707	0.2992
Discriminant	62	.	0.1776	0.1935	.	.	.
Decision Tree	85	85.0000	0.0871	0.3412	0.6952	0.45882	0.1490
Bootstrap Forest	85	85.0000	0.0859	0.3529	0.7083	0.46405	0.1471
Boosted Tree	85	85.0000	0.0792	0.3294	0.7177	0.46538	0.1363

† indicates that the method uses validation data to tune model.

Sum Freq is suppressed when it is the same as N.

ROC Curve



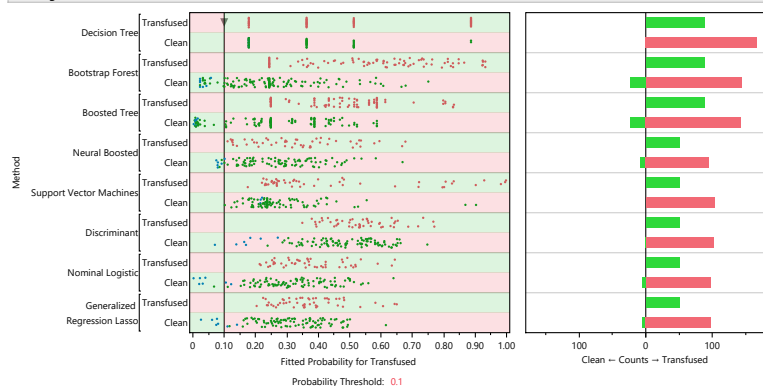
Method	AUC Training	AUC Validation
☒ Decision Tree	0.7244	0.6952
☒ Bootstrap Forest	0.8852	0.7083
☒ Boosted Tree	0.8353	0.7177
☒ Neural Boosted	0.6118	0.8607
☒ Support Vector Machines	0.7590	0.7512
☒ Discriminant	0.6284	0.9048
☒ Nominal Logistic	0.6469	0.7976
☒ Generalized Regression Lasso	0.6269	0.9095

Decision Thresholds

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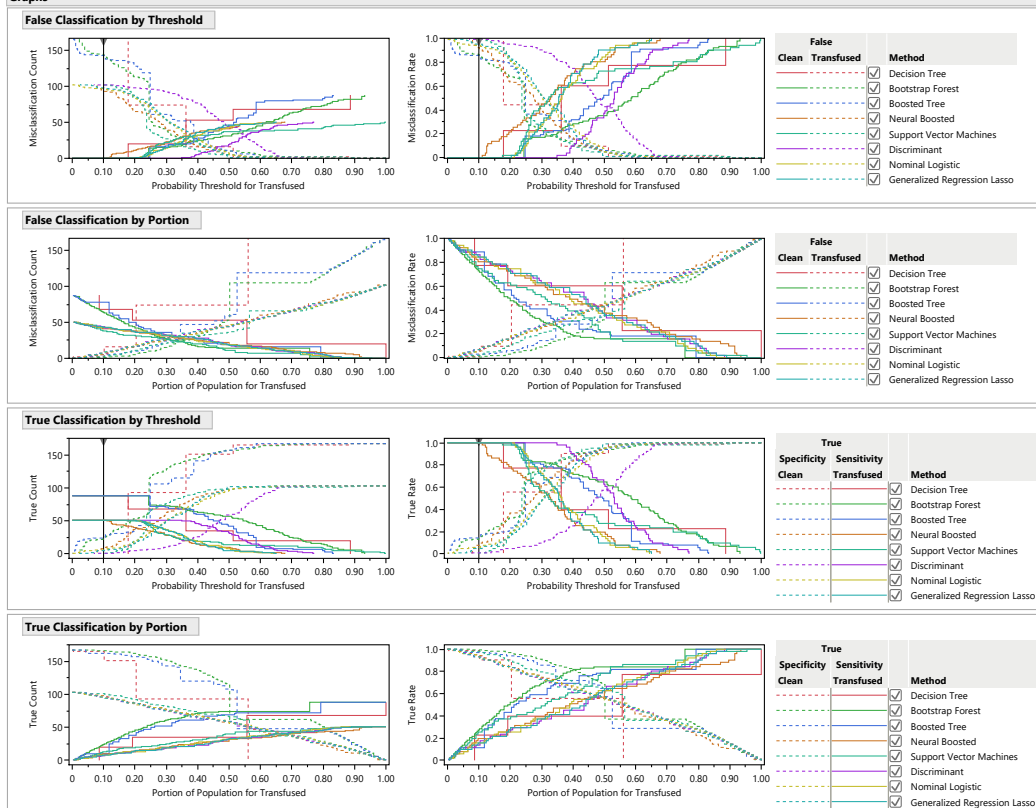
Decision Thresholds

Training



Method	Actual	Predicted		Rates	
		Clean	Transfused	Clean	Transfused
Decision Tree	Transfused	0	88	0.000	1.000
	Clean	0	167	0.000	1.000
Bootstrap Forest	Transfused	0	88	0.000	1.000
	Clean	23	144	0.138	0.862
Boosted Tree	Transfused	0	88	0.000	1.000
	Clean	24	143	0.144	0.856
Neural Boosted	Transfused	0	51	0.000	1.000
	Clean	8	95	0.078	0.922
Support Vector Machines	Transfused	0	51	0.000	1.000
	Clean	0	103	0.000	1.000
Discriminant	Transfused	0	51	0.000	1.000
	Clean	1	102	0.010	0.990
Nominal Logistic	Transfused	0	51	0.000	1.000
	Clean	6	97	0.058	0.942
Generalized Regression Lasso	Transfused	0	51	0.000	1.000
	Clean	5	98	0.049	0.951

Graphs

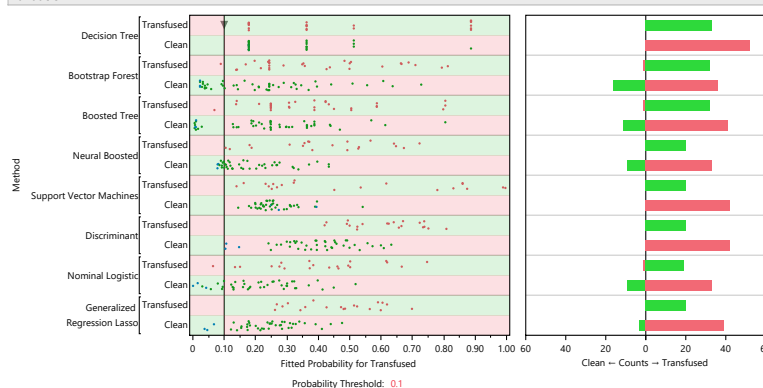


Metrics

Method	TP	FN	FP	TN	Sensitivity	Specificity	Precision	Accuracy	F1	MCC
Decision Tree	88	0	167	0	1.0000	0.0000	0.3451	0.3451	0.5131	
Bootstrap Forest	88	0	144	23	1.0000	0.1377	0.3793	0.4353	0.55	0.2286
Boosted Tree	88	0	143	24	1.0000	0.1437	0.381	0.4392	0.5517	0.234
Neural Boosted	51	0	95	8	1.0000	0.0777	0.3493	0.3831	0.5178	0.1647
Support Vector Machines	51	0	103	0	1.0000	0.0000	0.3312	0.3312	0.4976	
Discriminant	51	0	102	1	1.0000	0.0097	0.3333	0.3377	0.5	0.0569
Nominal Logistic	51	0	97	6	1.0000	0.0583	0.3446	0.3701	0.5126	0.1417
Generalized Regression Lasso	51	0	98	5	1.0000	0.0485	0.3423	0.3636	0.51	0.1289

Where Transfused is considered Positive. Probability Threshold: 0.100

Validation



Method	Actual	Predicted		Rates	
		Clean	Transfused	Clean	Transfused
Decision Tree	Transfused	0	33	0.000	1.000
	Clean	0	52	0.000	1.000
Bootstrap Forest	Transfused	1	32	0.030	0.970
	Clean	16	36	0.308	0.692
Boosted Tree	Transfused	1	32	0.030	0.970
	Clean	11	41	0.212	0.788
Neural Boosted	Transfused	0	20	0.000	1.000
	Clean	9	33	0.214	0.786
Support Vector Machines	Transfused	0	20	0.000	1.000
	Clean	0	42	0.000	1.000
Discriminant	Transfused	0	20	0.000	1.000
	Clean	0	42	0.000	1.000
Nominal Logistic	Transfused	1	19	0.050	0.950
	Clean	9	33	0.214	0.786
Generalized Regression Lasso	Transfused	0	20	0.000	1.000
	Clean	3	39	0.071	0.929

Graphs

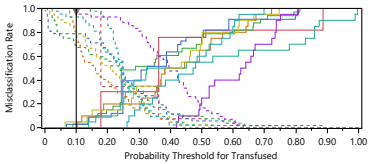
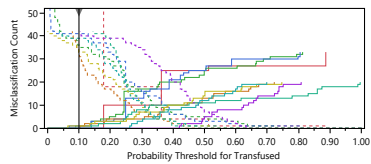
Model B: Screening for Clean/Transfused Novel metrics

Decision Thresholds

Validation

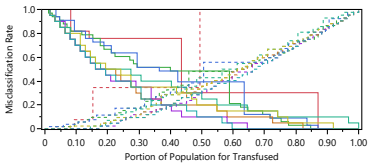
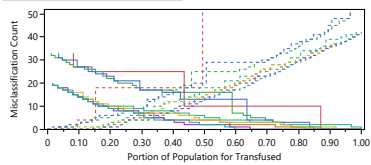
Graphs

False Classification by Threshold



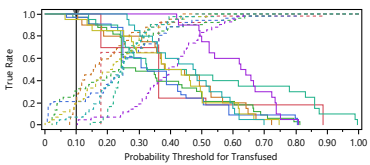
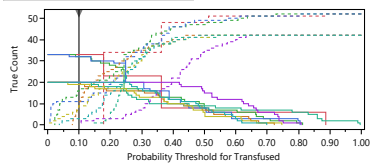
False		Method
Clean	Transfused	
☒	☒	Decision Tree
☒	☒	Bootstrap Forest
☒	☒	Boosted Tree
☒	☒	Neural Boosted
☒	☒	Support Vector Machines
☒	☒	Discriminant
☒	☒	Nominal Logistic
☒	☒	Generalized Regression Lasso

False Classification by Portion



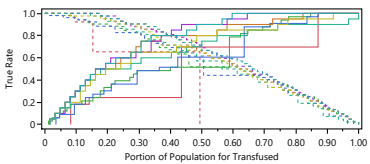
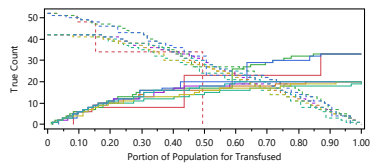
True		Method
Specificity	Sensitivity	
☒	☒	Decision Tree
☒	☒	Bootstrap Forest
☒	☒	Boosted Tree
☒	☒	Neural Boosted
☒	☒	Support Vector Machines
☒	☒	Discriminant
☒	☒	Nominal Logistic
☒	☒	Generalized Regression Lasso

True Classification by Threshold



True		Method
Specificity	Sensitivity	
☒	☒	Decision Tree
☒	☒	Bootstrap Forest
☒	☒	Boosted Tree
☒	☒	Neural Boosted
☒	☒	Support Vector Machines
☒	☒	Discriminant
☒	☒	Nominal Logistic
☒	☒	Generalized Regression Lasso

True Classification by Portion



True		Method
Specificity	Sensitivity	
☒	☒	Decision Tree
☒	☒	Bootstrap Forest
☒	☒	Boosted Tree
☒	☒	Neural Boosted
☒	☒	Support Vector Machines
☒	☒	Discriminant
☒	☒	Nominal Logistic
☒	☒	Generalized Regression Lasso

Metrics

Method	TP	FN	FP	TN	Sensitivity	Specificity	Precision	Accuracy	F1	MCC
Decision Tree	33	0	52	0	1.0000	0.0000	0.3882	0.3882	0.5593	
Bootstrap Forest	32	1	36	16	0.9697	0.3077	0.4706	0.5647	0.6337	0.338
Boosted Tree	32	1	41	11	0.9697	0.2115	0.4384	0.5059	0.6038	0.2537
Neural Boosted	20	0	33	9	1.0000	0.2143	0.3774	0.4677	0.5479	0.2844
Support Vector Machines	20	0	42	0	1.0000	0.0000	0.3226	0.3226	0.4878	
Discriminant	20	0	42	0	1.0000	0.0000	0.3226	0.3226	0.4878	
Nominal Logistic	19	1	33	9	0.9500	0.2143	0.3654	0.4516	0.5278	0.2088
Generalized Regression Lasso	20	0	39	3	1.0000	0.0714	0.339	0.371	0.5063	0.1556

Where Transfused is considered Positive. Probability Threshold: 0.100