

Supplementary Material

SAMPLE SIZE

The need for sample size calculation is for comparison of AUROCs. Before the study, we hypothesized the base model ROC to be 0.60, and the improved model ROC to be 0.88. We set type I error = 0.05, type II error = 0.10. We hypothesized the rank correlation coefficient in the positive and negative groups were 0.5. For various outcomes, the ratio of positive and negative sample size could range from 5 to 33 (corresponding to positive case percentages of 3% to 10%), the number of positive cases required ranges from 13 to 14; and the number of negative case required ranges from 70 to 429 (calculated by MedCalc). If we set type I error = 0.01, the required positive cases ranges from 18 to 20, and negative cases ranges from 100 to 594.

TEST of GOODNESS-OF-FIT

In evaluating different hemoglobin measures' prediction capability for transfusion, we selected multivariate logistic regression. Instead of using other more sophisticated algorithms such as support vector machine, discriminant analysis, we used a simple model to study the utilities of those measures. There were many multivariate logistic regression models built for different outcomes and different variable combinations, adequateness of each model was investigated by Hosmer-Lemeshow goodness of fit test (analyzed by R ResourceSelection package; 10 groups).

Table S1. H-L goodness of fit test for model Base HR + SpHb

Predictor(s): HR + SpHb	X-Squared	p-value
pRBC1-3hr	12.6756	0.1235
pRBC1-6hr	14.2147	0.0763
pRBC1-12hr	10.8932	0.2078

Table S2. H-L goodness of fit test for model Base HR + lab Hb

Predictor(s): HR + lab Hb	X-Squared	p-value
pRBC1-3hr	4.2134	0.8374
pRBC1-6hr	8.5617	0.3806
pRBC1-12hr	13.292	0.1022

Table S3. H-L goodness of fit test for model Base HR + other lab

Predictor(s): HR + other lab	X-Squared	p-value
pRBC1-3hr	5.7438	0.6759
pRBC1-6hr	5.6534	0.6860
pRBC1-12hr	9.8833	0.2733

INTERACTION TERMS

In comparison of the two types of hemoglobin readings in terms of prediction power, we only included the main effects in the models. This allows us to have straightforward way to interpret the coefficients of the main effects, and evaluate their impact on the outcome. Adding the interactions may change the interpretations of coefficients of main effects, and may complicate the comparison. A further reason that we did not include interaction terms is because parsimonious models are generally more robust and further reduce overfitting .

We did examine the effects of interaction terms in those models. For the three models (BaseHR+SpHb, BaseHR+labHb, and BaseHR+otherLab) predicting the pRBC1-3hr (without and with interaction terms), we can observe that the interaction terms are not significant in those models.

Model performance comparison with interaction allowed.

Model:Base(HR)+SpHb: predicting pRBC1-3hr

Without interaction terms:

Deviance Residuals:

Min	1Q	Median	3Q	Max
-0.7249	-0.2823	-0.2470	-0.1460	3.0053

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-4.7734	0.7649	-6.241	4.36e-10 ***
SpHblminPmin	0.1836	0.1267	1.450	0.1472
Gender	1.4897	0.7994	1.863	0.0624 .
Age	0.1848	0.2301	0.803	0.4219
PreH_HR	0.2703	0.2305	1.173	0.2409

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Model:Base(HR)+SpHb: predicting pRBC1-3hr

With interaction terms:

Deviance Residuals:

Min	1Q	Median	3Q	Max
-0.9175	-0.2711	-0.2318	0.0000	2.7210

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-1.493e+02	1.443e+04	-0.010	0.992
SpHblminPmin	6.664e+00	1.176e+03	0.006	0.995
Gender	1.460e+02	1.443e+04	0.010	0.992
Age	3.314e+00	1.021e+04	0.000	1.000
PreH_HR	5.711e+01	5.834e+03	0.010	0.992
SpHblminPmin:vGender	-6.201e+00	1.176e+03	-0.005	0.996
SpHblminPmin:vAge	-5.975e-01	7.799e-01	-0.766	0.444

SpHb1minPmin:vPreH_HR	-4.881e-01	6.381e-01	-0.765	0.444
Gender:vAge	-3.111e+00	1.021e+04	0.000	1.000
Gender:vPreH_HR	-5.723e+01	5.834e+03	-0.010	0.992
Age:vPreH_HR	-5.542e-02	2.406e-01	-0.230	0.818

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Model: Base(HR) + lab Hb: predicting pRBC1-3hr

Without interaction terms:

Deviance Residuals:

Min	1Q	Median	3Q	Max
-0.7518	-0.2709	-0.2245	-0.1476	3.1805

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-5.04562	0.75171	-6.712	1.92e-11 ***
Gender	1.77260	0.77571	2.285	0.0223 *
Age	0.05724	0.22865	0.250	0.8023
PreH_HR	0.33173	0.22429	1.479	0.1391
HGB	-0.52150	0.21546	-2.420	0.0155 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Model: Base(HR) + lab Hb: predicting pRBC1-3hr

With interaction terms:

Deviance Residuals:

Min	1Q	Median	3Q	Max
-0.9161	-0.2695	-0.2020	0.0000	3.1616

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-1.174e+02	8.412e+03	-0.014	0.9889
Gender	1.141e+02	8.412e+03	0.014	0.9892
Age	-9.216e-01	4.181e+03	0.000	0.9998
PreH_HR	4.425e+01	3.377e+03	0.013	0.9895
HGB	2.287e+00	1.836e+03	0.001	0.9990
Gender:vAge	1.128e+00	4.181e+03	0.000	0.9998
Gender:vPreH_HR	-4.407e+01	3.377e+03	-0.013	0.9896
Gender:vHGB	-2.970e+00	1.836e+03	-0.002	0.9987
Age:vPreH_HR	-3.636e-03	2.568e-01	-0.014	0.9887
Age:vHGB	2.904e-01	2.002e-01	1.450	0.1470
PreH_HR:vHGB	3.691e-01	2.068e-01	1.785	0.0742 .

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Model: Base(HR) + other lab: predicting pRBC1-3hr

Without interaction terms:

Deviance Residuals:

	Min	1Q	Median	3Q	Max
	-1.4658	-0.2095	-0.1382	-0.0799	3.1815

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)	
(Intercept)	-5.5376	0.9269	-5.974	2.31e-09	***
PTT	0.3283	0.1272	2.582	0.009831	**
FIBRINOGEN	-1.2295	0.3642	-3.376	0.000735	***
LACTATE	0.4242	0.1540	2.755	0.005876	**
GLUCOSE	0.4933	0.1511	3.264	0.001099	**
Gender	1.2602	0.8969	1.405	0.159985	
Age	0.5312	0.2757	1.927	0.054028	.
PreH_HR	0.1358	0.2325	0.584	0.559016	

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Model: Base(HR) + other lab: predicting pRBC1-3hr

Without interaction terms:

Deviance Residuals:

	Min	1Q	Median	3Q	Max
	-1.36539	-0.16349	-0.09936	0.00000	3.04707

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-5.873e+01	8.100e+03	-0.007	0.994
PTT	9.379e+00	4.521e+03	0.002	0.998
FIBRINOGEN	-9.768e+00	3.321e+03	-0.003	0.998
LACTATE	-6.292e+00	1.442e+04	0.000	1.000
GLUCOSE	1.080e+01	2.958e+03	0.004	0.997
Gender	5.448e+01	8.100e+03	0.007	0.995
Age	-1.250e+01	4.832e+03	-0.003	0.998
PreH_HR	1.237e+01	4.008e+03	0.003	0.998
PTT:FIBRINOGEN	-5.929e-01	5.476e-01	-1.083	0.279
PTT:LACTATE	8.617e-01	5.734e-01	1.503	0.133
PTT:GLUCOSE	4.783e-01	4.267e-01	1.121	0.262
PTT:Gender	-9.406e+00	4.521e+03	-0.002	0.998
PTT:Age	-8.983e-02	4.386e-01	-0.205	0.838
PTT:PreH_HR	5.643e-01	4.974e-01	1.134	0.257
FIBRINOGEN:LACTATE	1.506e-03	3.744e-01	0.004	0.997
FIBRINOGEN:GLUCOSE	-2.199e-01	4.596e-01	-0.478	0.632
FIBRINOGEN:Gender	9.086e+00	3.321e+03	0.003	0.998
FIBRINOGEN:Age	-9.083e-01	5.710e-01	-1.591	0.112
FIBRINOGEN:PreH_HR	5.681e-01	3.688e-01	1.540	0.123
LACTATE:GLUCOSE	-3.563e-02	1.983e-01	-0.180	0.857
LACTATE:Gender	6.671e+00	1.442e+04	0.000	1.000
LACTATE:Age	4.817e-01	3.538e-01	1.362	0.173
LACTATE:PreH_HR	-8.925e-02	2.633e-01	-0.339	0.735
GLUCOSE:Gender	-1.009e+01	2.958e+03	-0.003	0.997

GLUCOSE:Age	-6.940e-01	4.297e-01	-1.615	0.106
GLUCOSE:PreH_HR	1.460e-01	2.803e-01	0.521	0.603
Gender:Age	1.262e+01	4.832e+03	0.003	0.998
Gender:PreH_HR	-1.236e+01	4.008e+03	-0.003	0.998
Age:PreH_HR	-7.571e-02	2.813e-01	-0.269	0.788