COVID-19 Baseline Risk Score Analysis Report $$_{\rm MockENSEMBLE\ Study}$$

USG COVID-19 Response Biostatistics Team

August 06, 2021

Contents

1	Baseline Risk Score (Proxy for SARS-CoV-2 Exposure)	9
2	Appendix	21

4 CONTENTS

List of Tables

1.1	Variables considered for risk score analysis	(
1.2	All learner-screen combinations (14 in total) used as input to the Superlearner	11
1.3	Weights assigned by Superlearner	15
1.4	Predictors in learners assigned weight > 0.0 by Superlearner	16
1.5	Cases per treatment arm prior to risk score analysis	19
1.6	Cases per treatment arm post risk score analysis	19

List of Figures

1.1	Cross-validated AUC (95% CI) of algorithms for predicting COVID-19 disease status starting 7 days after Day 29	12
1.2	CV-estimated predicted probabilities of COVID-19 disease 7 days after Day 29 by case/control status for top 2 learners, Super-Learner and Discrete SL	13
1.3	ROC curves based off CV-estimated predicted probabilities for the top 2 learners, Superlearner and Discrete SL	14
1.4	Superlearner predicted probabilities of COVID-19 disease in vaccinees 7 days after Day 29 by case/control status	17
1.5	ROC curve based off Superlearner predicted probabilities in vaccinees	18

8 LIST OF FIGURES



Chapter 1

Baseline Risk Score (Proxy for SARS-CoV-2 Exposure)

Table 1.1: Variables considered for risk score analysis.

Variable.Name	Definition	Total.missing.values	Comment
EthnicityHispanic	Indicator ethnicity = Hispanic (1 = Hispanic, 0 = complement)	$0/19501 \ (0.0\%)$	NA
EthnicityNotreported	Indicator ethnicity = Not reported (1 = Not reported, 0 = complement)	$0/19501 \ (0.0\%)$	NA
EthnicityUnknown	Indicator ethnicity = Unknown (1 = Unknown, 0 = complement)	0/19501 (0.0%)	NA
Black	Indicator race = Black (1=Black, 0=complement)	$0/19501 \ (0.0\%)$	NA
Asian	Indicator race = Asian (1=Asian, 0=complement)	$0/19501 \ (0.0\%)$	NA
NatAmer	Indicator race = American Indian or Alaska Native (1=NatAmer, 0=complement)	0/19501 (0.0%)	NA
Multiracial	Indicator race = Multiracial (1=Multiracial, 0=complement)	0/19501 (0.0%)	NA
Notreported	Indicator race = Not reported (1=Notreported, 0=complement)	0/19501 (0.0%)	NA
Unknown	Indicator race = unknown (1=Unknown, 0=complement)	0/19501 (0.0%)	NA
URMforsubcohortsampling	Indicator of under-represented minority (1=Yes, 0=No)	$0/19501 \ (0.0\%)$	NA
HighRiskInd	Baseline covariate indicating >= 1 Co-existing conditions (1=yes, 0=no, NA=missing)	0/19501 (0.0%)	NA
Sex	Sex assigned at birth (1=female, 0=male/undifferentiated/unknown	0/19501 (0.0%)	NA
Age	Age at enrollment in years (integer $>= 18$, NA=missing). Note that the randomization strata included Age 18-59 vs. Age $>= 60$.	0/19501 (0.0%)	NA

10CHAPTER 1. BASELINE RISK SCORE (PROXY FOR SARS-COV-2 EXPOSURE)

Table 1.1: Variables considered for risk score analysis. (continued)

Variable.Name	Definition	Total.missing.values
BMI	MI BMI at enrollment (Ordered categorical 1,2, 3, 4,	
	NA=missing); $1 = \text{Underweight BMI} < 18.5$; $2 =$	
	Normal BMI $18.5 \text{ to} < 25; 3 = \text{Overweight BMI } 25 \text{ to}$	
	< 30; 4 = Obese BMI >= 30	
Country	Country of the study site of enrollment (0=United	$0/19501 \ (0.0\%)$
	States, 1=Argentina,2=Brazil, 3=Chile,4=Columbia,	
	5=Mexico, 6=Peru, 7=South Africa)	
HIVinfection	Indicator HIV infected at enrollment (1=infected,	$0/19501 \ (0.0\%)$
	0=not infected)	
${\bf Calendar Date Enrollment}$	Date variable (used to control for calendar time trends	$0/19501 \ (0.0\%)$
	in COVID incidence). Coded as number of days since	, , ,
	first person enrolled until the ppt is enrolled.	

Note:

Variables with more than 5% missing values were dropped from analysis; missing values for other variables values for other variables values are the threshold, such that under the null of not a risk factor there were less the subgroup with value 1 (or 0), were dropped from analysis.

Table 1.2: All learner-screen combinations (14 in total) used as input to the Superlearner.

Learner	Screen*
SL.mean	all
SL.glm	all glmnet univar_logistic_pval highcor_random

Note:

*Screen details:

all: includes all variables

glmnet: includes variables with non-zero coefficients in the standard implementation of SL.glmnet that optimizes the lasso tuning parameter via cross-validation

univar_logistic_pval: Wald test 2-sided p-value in a logistic regression model $<0.10\,$

high cor_random: if pairs of quantitative variables with Spearman rank correlation > 0.90, select one of the variables at random



Figure 1.1: Cross-validated AUC (95% CI) of algorithms for predicting COVID-19 disease status starting 7 days after Day 29.



Figure 1.2: CV-estimated predicted probabilities of COVID-19 disease 7 days after Day 29 by case/control status for top 2 learners, SuperLearner and Discrete SL.



Figure 1.3: ROC curves based off CV-estimated predicted probabilities for the top 2 learners, Superlearner and Discrete SL.

Table 1.3: Weights assigned by Superlearner.

Learner	Screen	Weight
SL.glm	screen_all	0.833
SL.glm	screen_glmnet	0.167
SL.mean	screen_all	0.000
SL.glm	$screen_univariate_logistic_pval$	0.000
SL.glm	screen_highcor_random	0.000



Screen Weight Predictors Coefficient Odds.Ratio Learner SL.glm screen_all 0.833 (Intercept) -19.397 0 0.833 0.964SL.glm $screen_all$ ${\bf Ethnicity Hispanic}$ -0.037 SL.glm 0.833 EthnicityNotreported 0.013 1.013 screen_all $_{\mathrm{SL.glm}}$ 0.833 ${\bf Ethnicity Unknown}$ 0.051.051 $screen_all$ SL.glm screen_all 0.833 Black -0.16 0.852 $_{\mathrm{SL.glm}}$ screen_all 0.833 Asian -0.066 0.936 SL.glm screen_all 0.833 NatAmer -0.056 0.9450.833 Multiracial -0.039 SL.glm screen_all 0.9610.833 SL.glmscreen_all Notreported -1.403 0.2460.833 -0.056 SL.glm $screen_all$ Unknown 0.946URMforsubcohortsampling SL.glm $screen_all$ 0.833 0.063 1.065 SL.glmscreen_all 0.833HighRiskInd0.3791.461SL.glm screen all 0.833 12.071 174754.678 Sex $_{\mathrm{SL.glm}}$ $screen_all$ 0.8330.3541.425SL.glmscreen_all 0.833 вмі -0.046 0.955 $_{\mathrm{SL.glm}}$ 0.833 Country -0.017 0.983 screen_all SL.glm $screen_all$ 0.833HIVinfection 0.0111.011 0.833 ${\bf Calendar Date Enrollment}$ 1.027 SL.glm $screen_all$ 0.027 $_{\mathrm{SL.glm}}$ $screen_glmnet$ 0.167(Intercept) -19.395 0 SL.glm $screen_glmnet$ 0.167 EthnicityNotreported 0.015 1.015 $_{\mathrm{SL.glm}}$ $screen_glmnet$ 0.167 ${\bf Ethnicity Unknown}$ 0.0521.053 SL.glm 0.167 Black -0.136 0.873 screen_glmnet 0.936 SL.glm0.167 Asian -0.067 screen_glmnet SL.glm screen_glmnet 0.167NatAmer-0.055 0.947-0.04 SL.glm $screen_glmnet$ 0.167Multiracial 0.961 $_{\mathrm{SL.glm}}$ screen_glmnet 0.167Notreported -1.403 0.246SL.glm 0.167 Unknown -0.056 0.946 screen_glmnet SL.glm $screen_glmnet$ 0.167 ${\bf URM}$ for subcohort sampling 0.03 1.031 SL.glm 0.167 HighRiskInd 0.379 1.461 screen_glmnet $_{\mathrm{SL.glm}}$ 174555.444 0.167 Sex 12007 screen_glmnet SL.glm screen_glmnet 0.1670.3541.425Age 0.955 SL.glm $_{\mathrm{BMI}}$ -0.046 $screen_glmnet$ 0.167 SL.glm $screen_glmnet$ 0.167 Country -0.013 0.987SL.glm screen_glmnet 0.167HIVinfection 0.011 1.011

 ${\bf Calendar Date Enrollment}$

0.026

1.027

SL.glm

screen_glmnet

0.167

Table 1.4: Predictors in learners assigned weight > 0.0 by Superlearner.

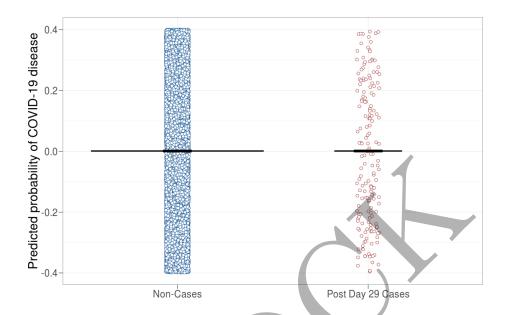


Figure 1.4: Superlearner predicted probabilities of COVID-19 disease in vaccinees 7 days after Day 29 by case/control status.

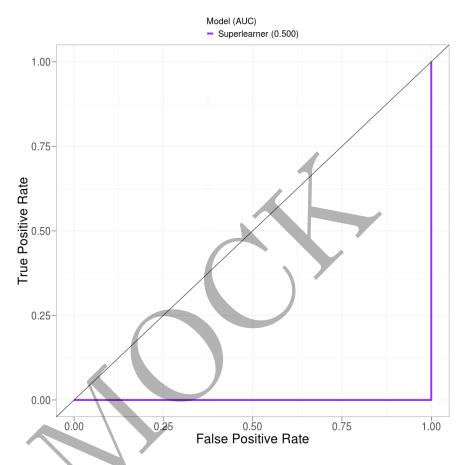


Figure 1.5: ROC curve based off Superlearner predicted probabilities in vaccinees.

Table 1.5: Cases per treatment arm prior to risk score analysis.

29-Cases	Post-Day 29	Non-Cases	Study-Arm
521 170		18756	Placebo
		19198	Vaccine

Table 1.6: Cases per treatment arm post risk score analysis.

Study-Arm	Non-Cases	Post-Day 29-Cases	
Placebo	18756	521	
Vaccine	19198	170	



Chapter 2

Appendix

- This report was built from the CoVPN/correlates_reporting repository with commit hash d4b1ac27b07ce6c1c5ff3f18d0308cc2dfba3c35. A diff of the changes introduced by that commit may be viewed at https://github.com/CoVPN/correlates_reporting/commit/d4b1ac27b07ce6c1c5ff3f18d0308cc2dfba3c35
- The sha256 hash sum of the raw input file, "COVID_ENSEMBLE_practicedata.csv": 186c6fefe0d7ee781c3b0bf5cedee3686398eb67ddc3da19dfa0c9bf3ad88fcc
- The sha256 hash sum of the processed file, "janssen_pooled_mock_data_processed.csv": 168c3beacf95500be32a6d6866656b93759de1680e60d61f8a34341b2a4458a6