

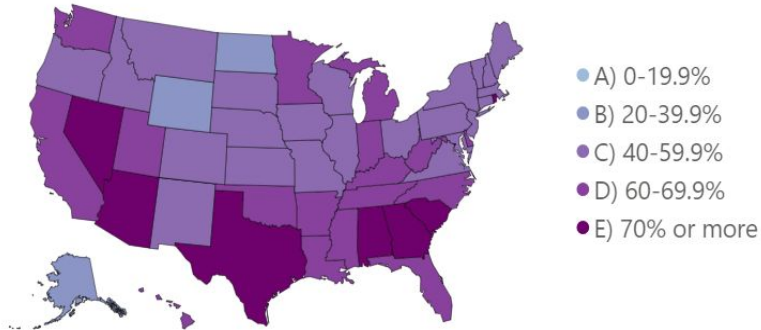
PredictCVID

By Gianna, Vienna, Jessica, Christina, Srihita, Fiona

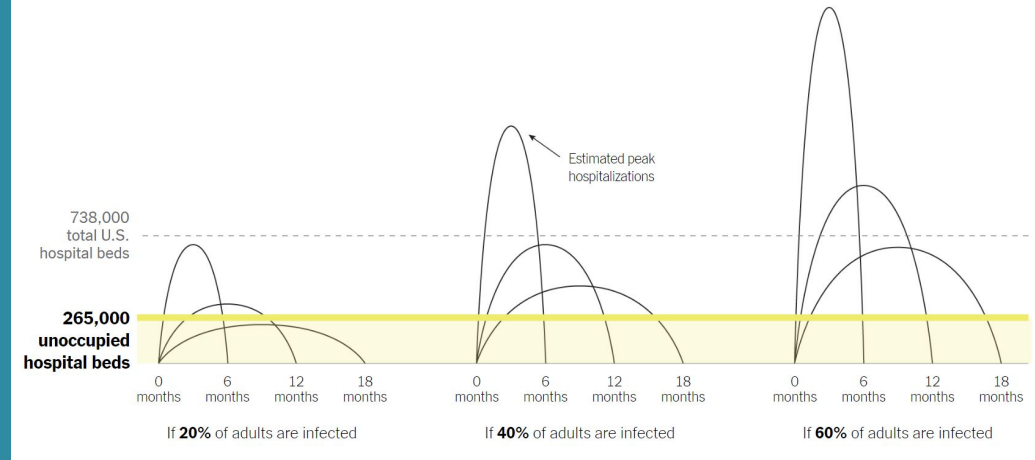
Co-TAs: Alice, Bianca

Infected Patients Overwhelm COVID-19 Testing and ICU Beds

State Representative Estimates for Percentage of ICU Beds Occupied (All Patients)



Source: CDC.gov

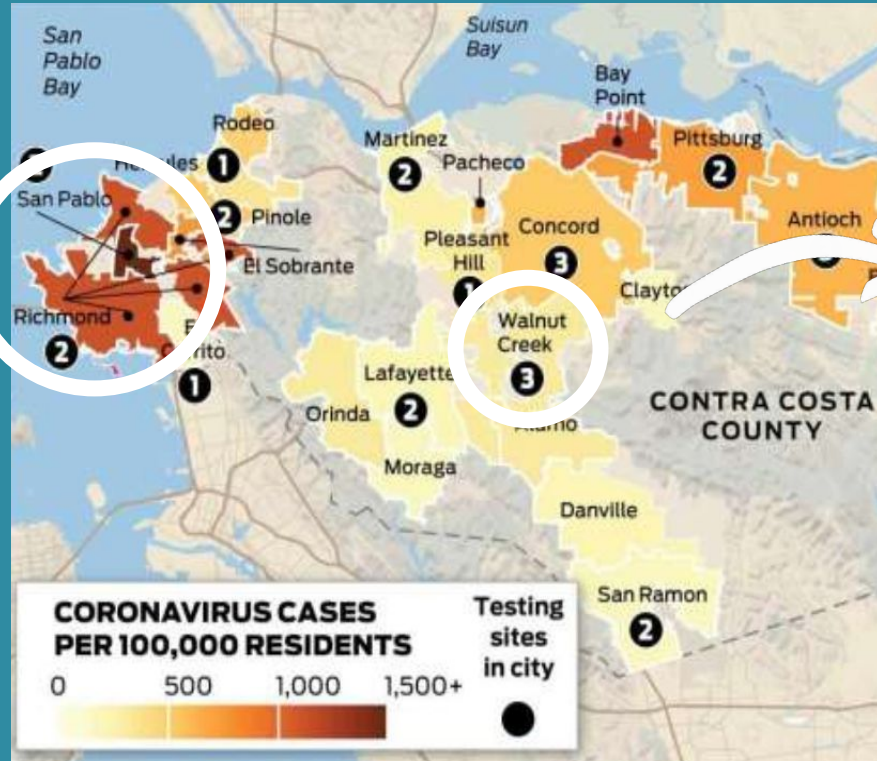


Source: NY Times. Harvard Global Health Institute.

The supply of COVID-19 tests play a big role in controlling the pandemic.

Social Inequalities in Healthcare

Richmond and San Pablo (predominantly Latino, Asian American and Black working-class cities) have some of the highest infection rates in Contra Costa County



But have same number of community testing sites as Walnut Creek (an affluent, mostly white city with half the population)

Drumroll please....

	Patient ID	Patient age quantile	SARS-Cov-2 exam result	Patient admitted to regular ward (1=yes, 0=no)
0	4447775e8169d2	13	negative	0
1	126e9dd13932168	17	negative	0
2	a46b4402a0e5696	8	negative	0
3	f7d619a94f97c45	5	negative	0
4	d9e41465789c2b5	15	negative	0



PredictC-COVID



COVID Status & COVID Severity!

Data Cleaning

Original Dataset

- Patient data from Brazil
- March 28 to April 3
- Samples, laboratory results from hospital visits, COVID tests
- (5644 patients, 111 categories)

Remove Categories

- Threshold = 85% (missing data)
- Remove above threshold (5644 patients, 23 categories)
- Add back important columns (5644 patients, 35 categories)

Process Missing Data

- Divide categorical + numerical data
- Categorical Data:
 - o Change into int (0/1)
 - o Separate columns for missing data
- Numerical Data:
 - o Fill in missing values with mean of each column
- (5644 patients, 72 categories)

Remove all NaN

- Threshold = 95% (missing data)
- Remove features above threshold
- Remove patients with NaN in these categories
- (242 patients, 81 categories) ---> No NaN data

Select Patients

- Split COVID-19 positive + negative patients
- Negative patients with minimal data missing
- Randomly select as many negative as positive COVID-19 patients
- Combine positive (558) + negative (558) patients data
- (1116 patients, 72 categories) ---> Selected data

Status ML Model

NoNaN vs Selected Data Accuracy of Different Classifiers

Classifier	K Nearest Neighbors	Random Forest	Naive Bayes	Gaussian Process	SVM	Decision Tree	QDA	MLP
Accuracy Score (NoNaN data)	89.0%	87.7%	42.5%	92.1%	82.2%	83.6%	78.1%	89.0%
Accuracy Score (Selected data)	88.7%	90.7% (93.0% with feature importance)	92.5%	91.3%	92.8%	93.4%	59.7%	95.5%

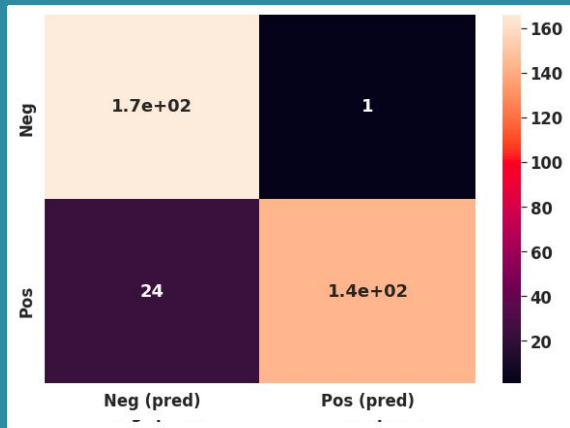
→ The accuracy scores differed with respect to dataset and classifier. Most accuracies increased.

QDA, NB, MLP, Oh My!



QDA

59.7%



NB

02.5%



MLP

95.5%

To have COVID or not to have COVID: Consequences of false negatives vs. false positives

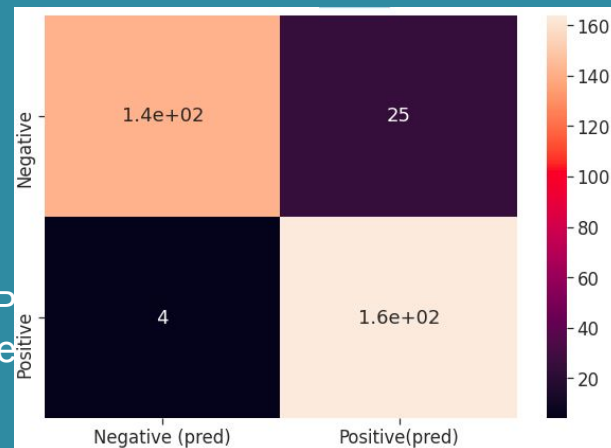
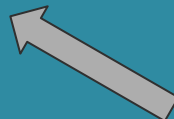
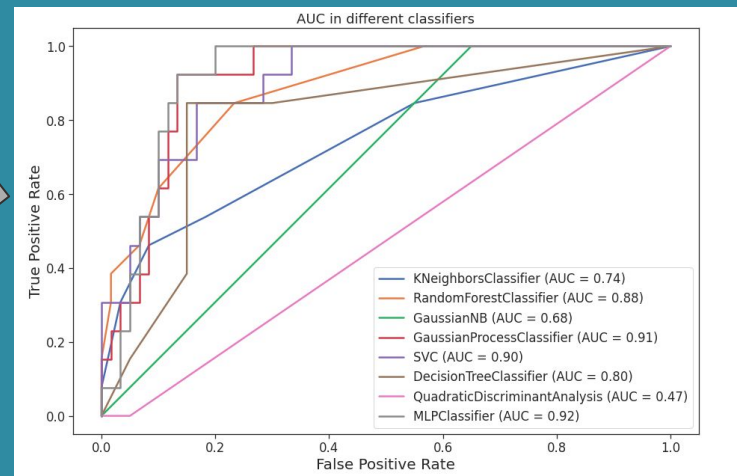
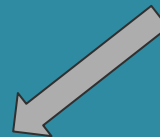
False Negatives	False Positives
<ul style="list-style-type: none">- Not receive treatments in time- Keep spreading COVID-19- Unknowingly infect others around- More severe	<ul style="list-style-type: none">- Take up limited resources- Tests, hospitals, ICU- Small scale → more preferable

Our Status Model Choice

91.3%
Accuracy



**Gaussian
Process**



There are a lot less false negatives from using the GP model. Although the accuracy isn't the highest and we do run the risk of unnecessarily using up resources, we prevent the spread of COVID more.

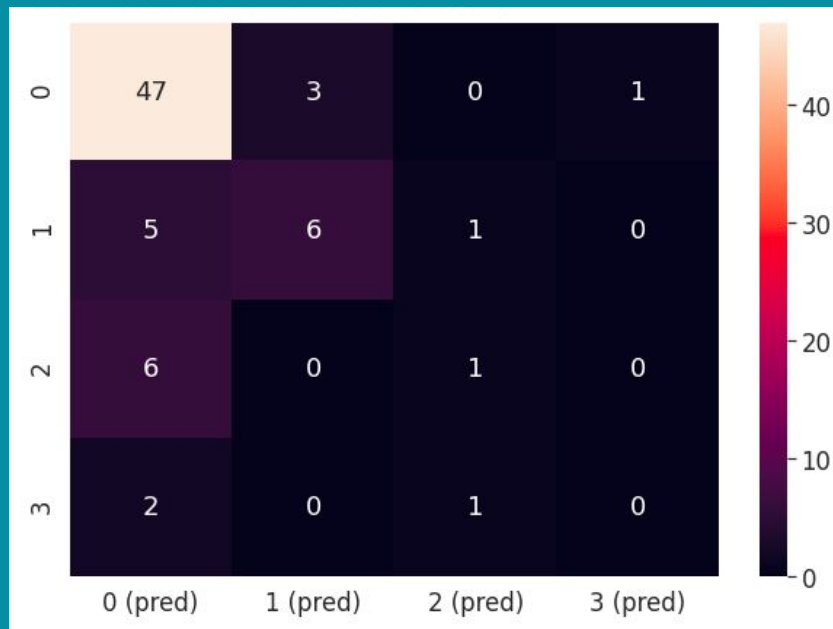
Severity ML Models

Chart of Classifier Values

Classifier	K Nearest Neighbors	Random Forest	Naive Bayes	Gaussian Process	SVM	Decision Tree	QDA	MLP
Accuracy Score (NoNaN data)	72.6%	74.0%	20.5%	69.0%	69.9%	69.9%	68.5%	68.5%

0, 1, 2, 3, which level of treatment is right for me?

0: no treatment
1: regular treatment
2: semi-intensive treatment
3: intensive care unit (ICU)



Random Forest Classifier

Falsely Predicted: 3 Actual: 0	Falsely Predicted: 0 Actual: 3
<ul style="list-style-type: none">- waste resources- takes up limited space (ICU)	<ul style="list-style-type: none">- Not receive treatments in time- Conditions worsen

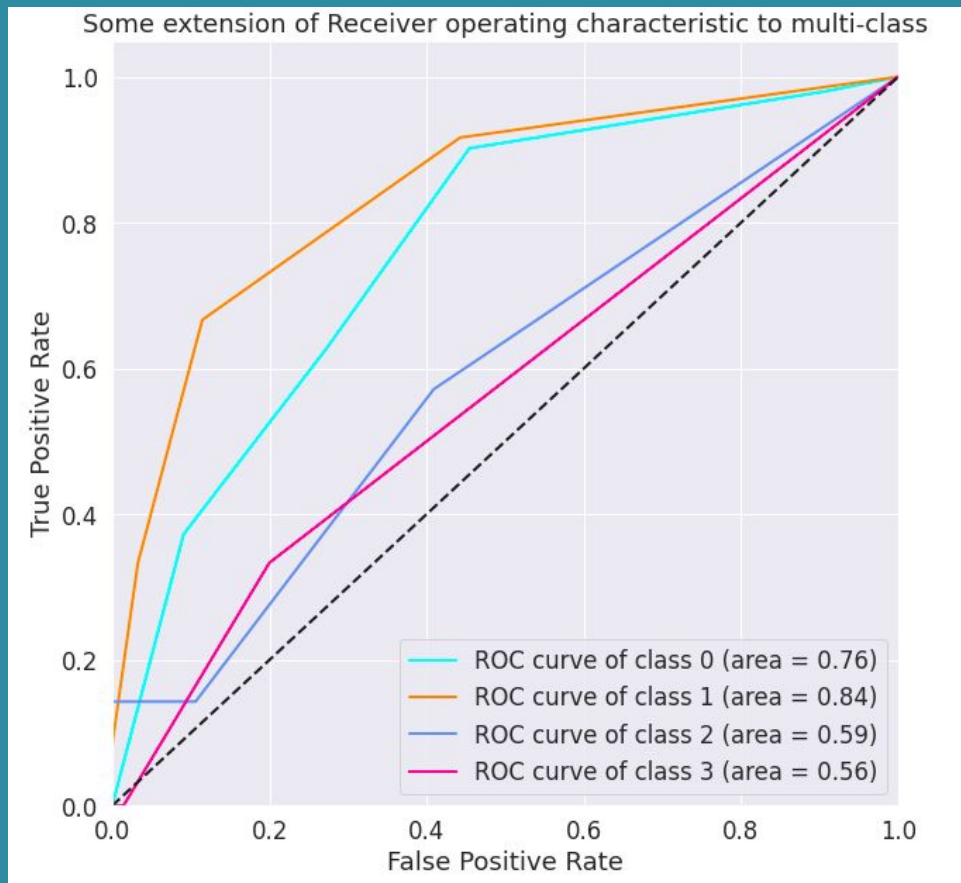
ROC/AUC Graphs for Severity

0: no treatment

1: regular
treatment

2:
semi-intensive
treatment

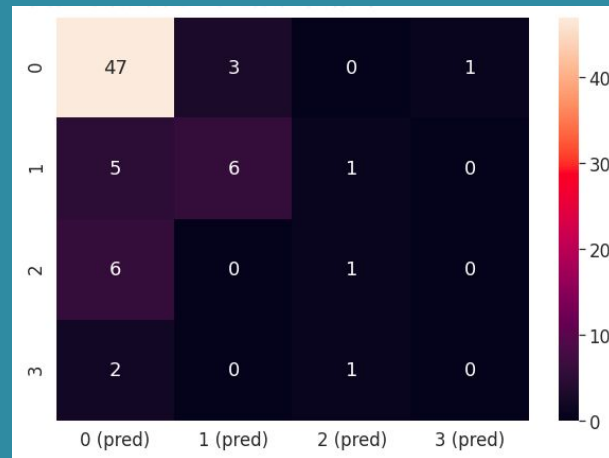
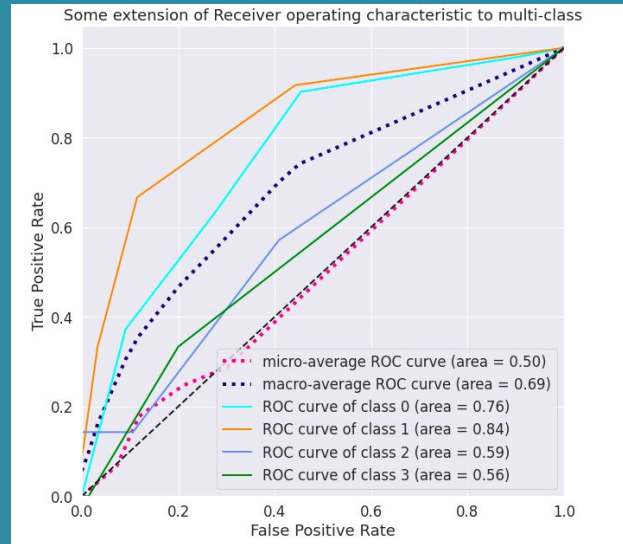
3: intensive care
unit (ICU)



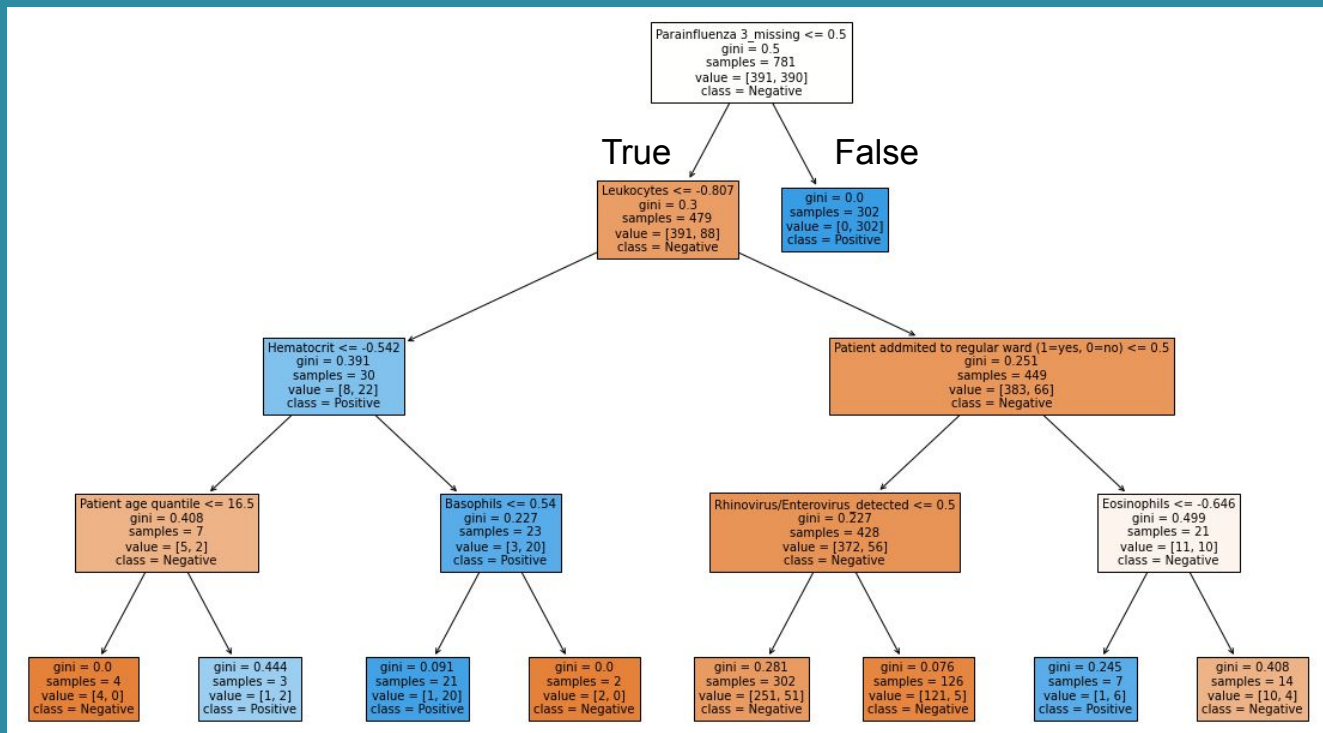
Our Severity Model Choice

74%
Accuracy

**Random
Forest**



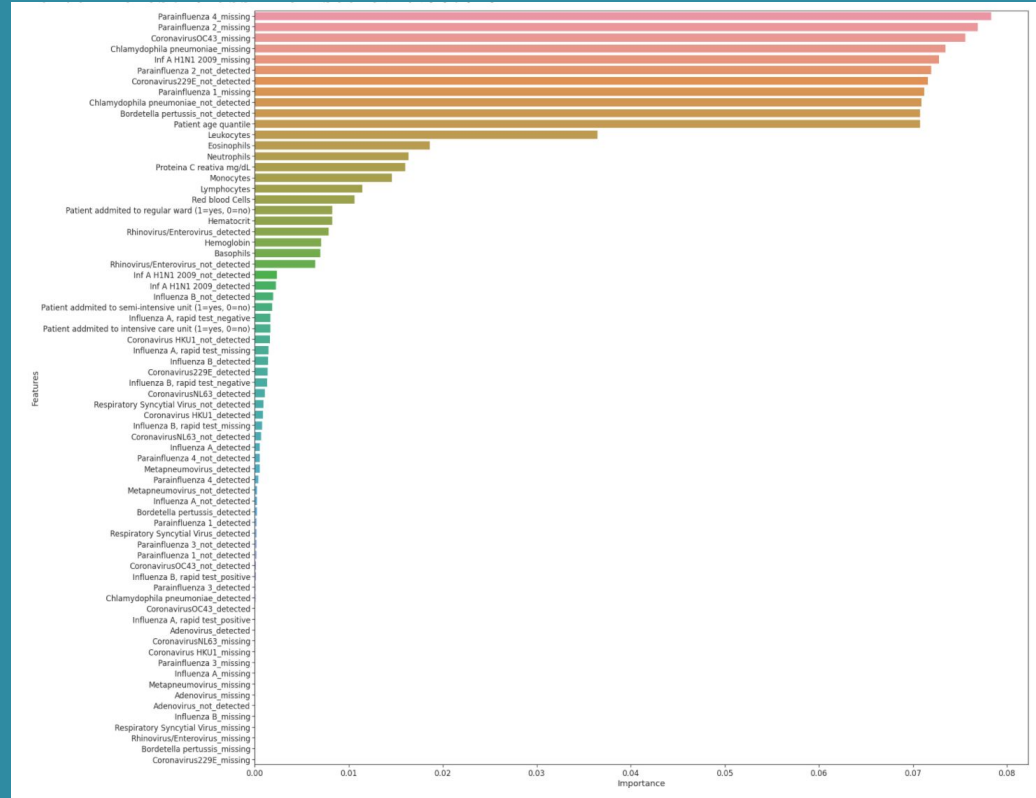
Decision Tree for Selected Data shows that many immune related features are important



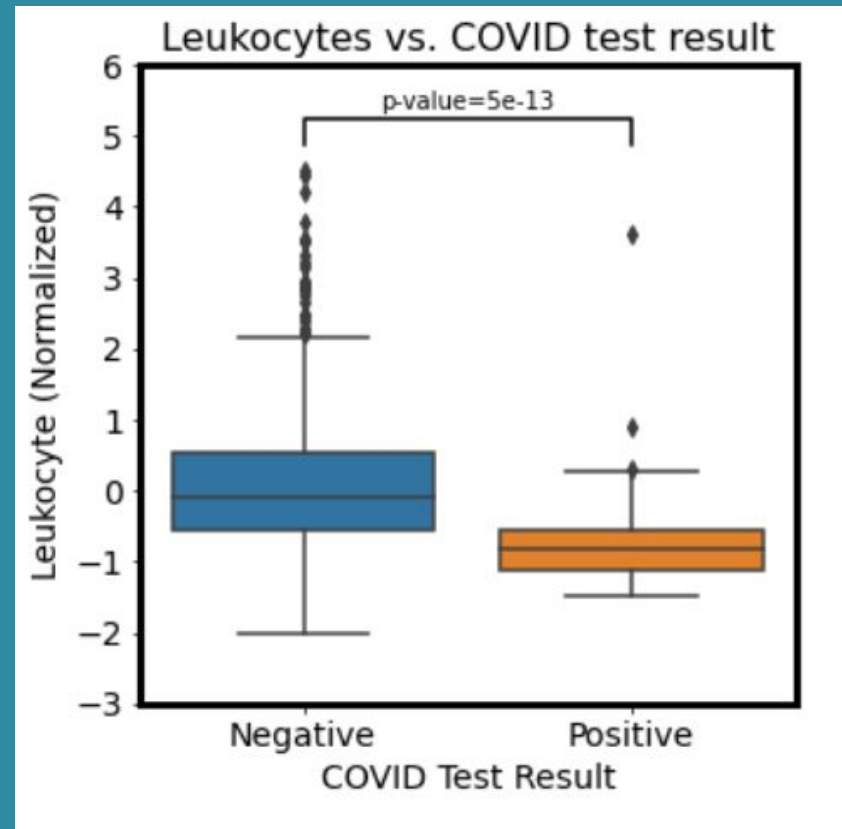
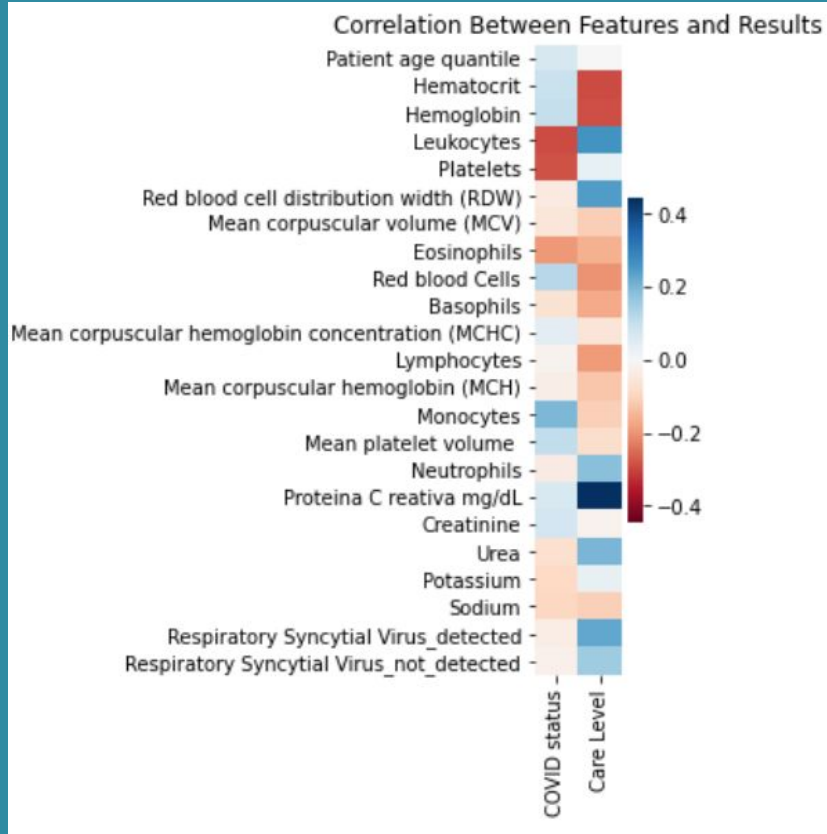
- Leukocytes
- Hematocrit
- Age quantile
- Basophils
- Eosinophils
- Rhinovirus/enterovirus
- Patient admitted to regular ward

Feature Importance Using Random Forest Classifier

1. Parainfluenza 2_not_detected
2. Coronavirus229E_not_detected
3. Chlamydomphila pneumonia_not_detected
4. Bordetella pertussis_not_detected
5. Patient Age Quantile
6. Leukocytes
7. Eosinophils
8. Neutrophils
9. C Reactive Protein
10. Monocytes



Usage in Clinical Decision Making



Bias and Limitations

Data	Location
<ul style="list-style-type: none">- Missing data- Personal / family medical history- Lifestyle habits- Prior exposures- Specific age- Uneven ratio between COVID negative + positive patient data	<ul style="list-style-type: none">- Hospital Israelita Albert Einstein- São Paulo, Brazil- Date (7 days)- Quarantine- Not full representation of Brazil or the world

Conclusions and Future Directions

- Best Model for Status
 - Gaussian Process Classifier (91.3%)
- Best Model for Severity
 - Random Forest (74% accuracy)
- Important features were highly immune related.
- Future Plans
 - Validate and refine model
 - Include more features such as pre-existing conditions/current medications
 - Run models using data from different hospitals
 - Main goal: implement this model in a hospital

Acknowledgments



EXTRA/UNNECESSARY SLIDES

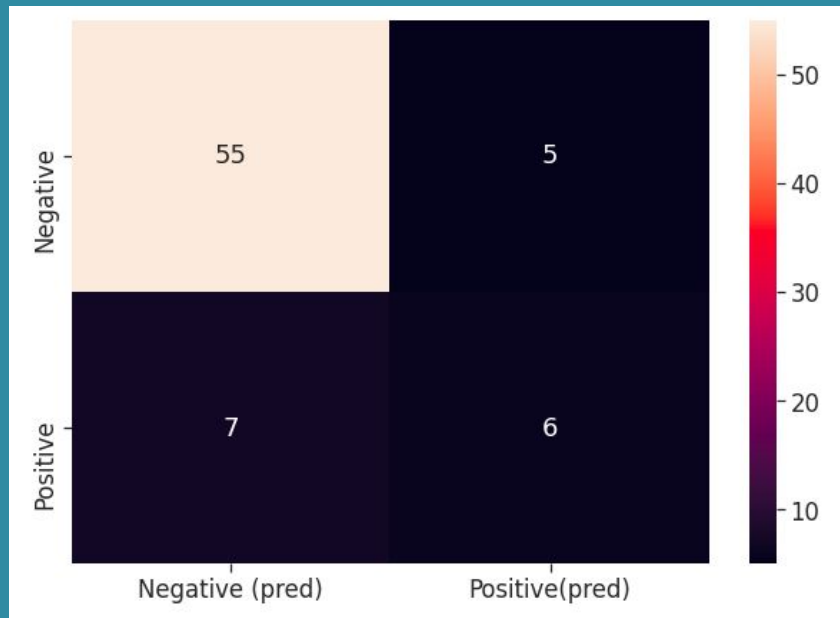
K Nearest Neighbors (KNN)

We used our training data to train the KNN model, using our $K = 5$:

```
from      import
          5
# Train the classifier
# Compute the score (mean accuracy) on test set
print 'KNN score: %f'

⇒ KNN score: 0.835616
```

Our Confusion Matrix can be seen here:

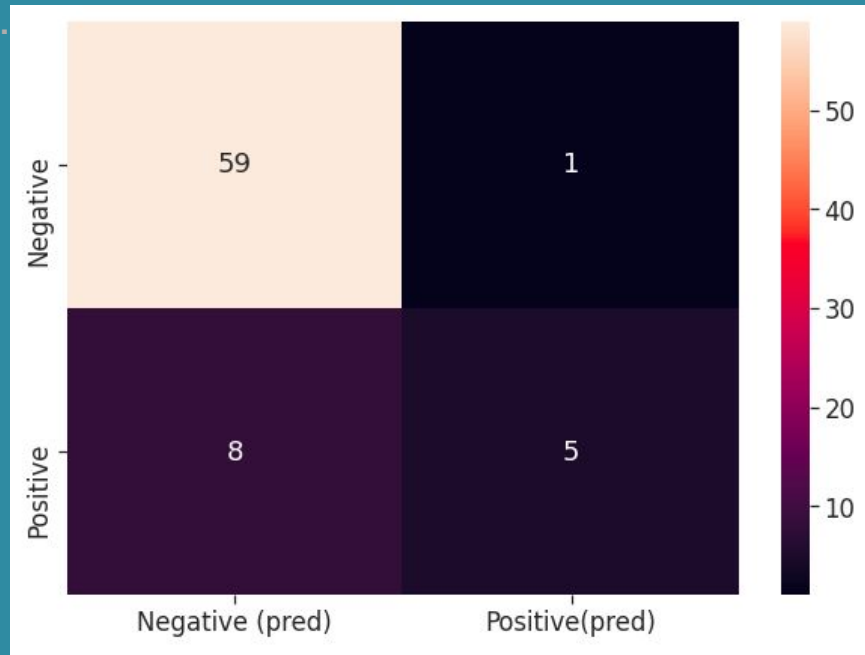


Random Forest Classifier

We did the Random Forest Classifier (RFC), and after trying out different values for `n_estimators` (which indicates the number of trees), we found `n_estimators = 10` to be the most ideal value.

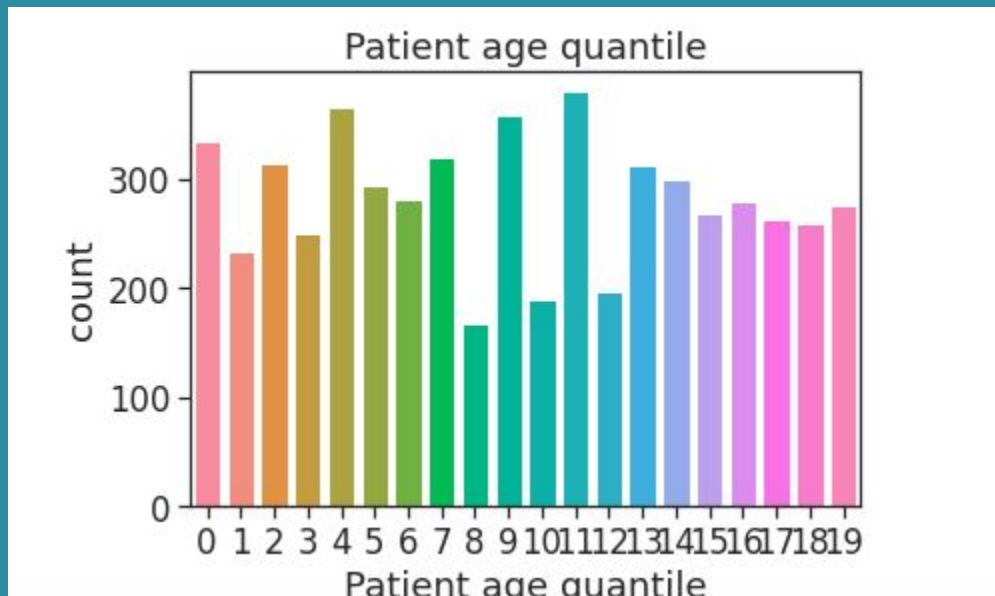
```
Random Forest Classifier score: 0.876712
```

RFC Confusion Matrix can be seen here:



Graphs - seaborn

Matplotlib plotted 23 individual bar plots, so we took measures to beautify our plots, using seaborn (sns):



cleaning our data

To add:

- Graph that shows the percentages of missing data (the different thresholds)
- First vs last category graphs
- The pathway (the process used)
- Distributions
 - Patient age quantile
 - Covid neg/pos !!

Creating our Machine Learning Model

We split our imported dataset (called nonan) into training and testing data:

```
from sklearn.cross_validation import train_test_split
nonan_train, nonan_test, y_train, y_test = train_test_split(
    nonan, nonan['class'], train_size=0.3, random_state=35)
```

From here, we started using different classifiers to test the accuracy of our predicted data outcomes. Some of the classifiers we used include:

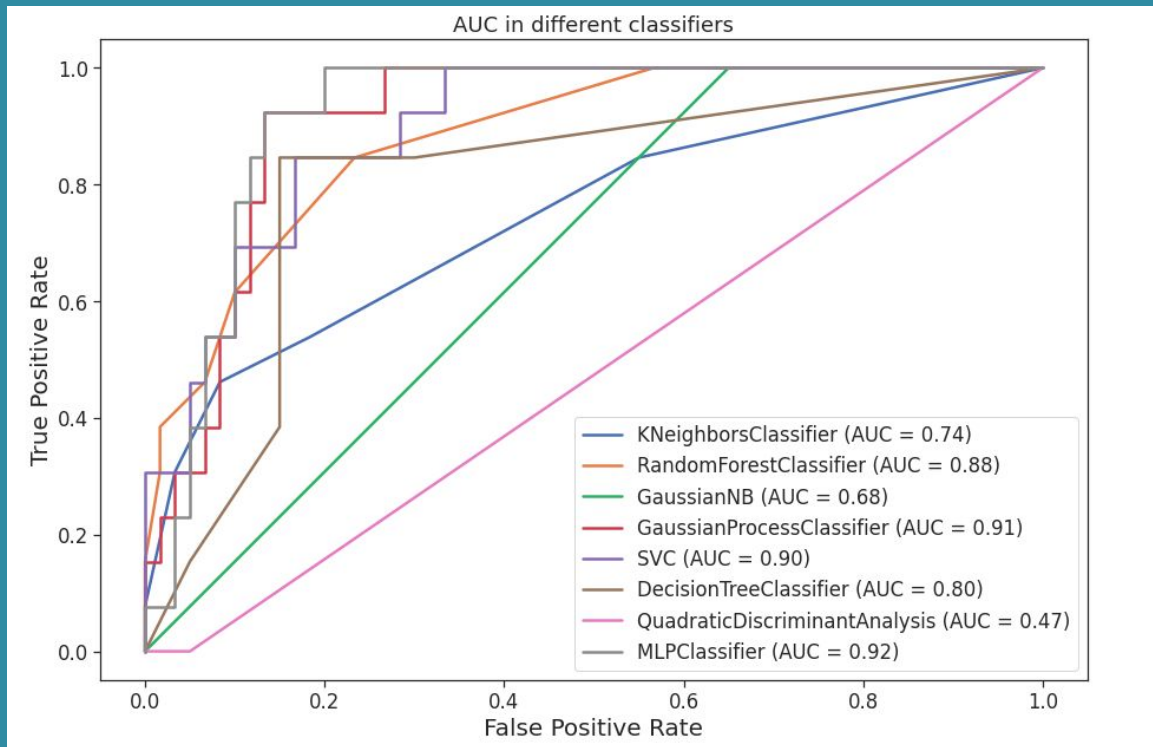
- K Nearest Neighbors
- Random Forest Classifier
- Naive Bayes
- Gaussian
- SVC
- Decision Trees

ROC/AUC Graphs

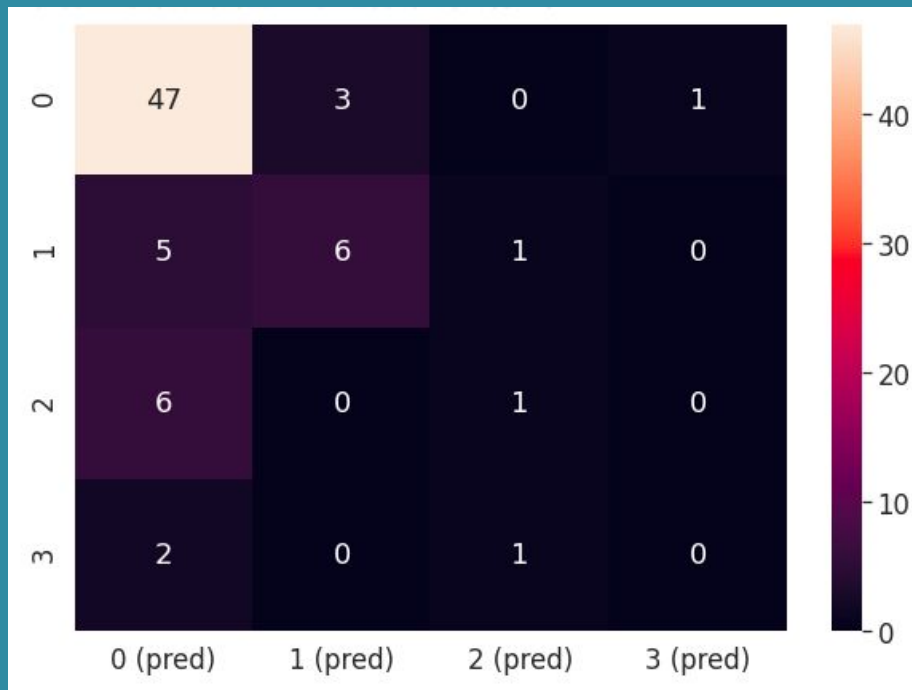
ROC: Receiver Operating Characteristic & **AUC:** Area Under Curve

The higher the area under the curve, the better the model's performance is.

Ideally, the AUC should be above 0.5.

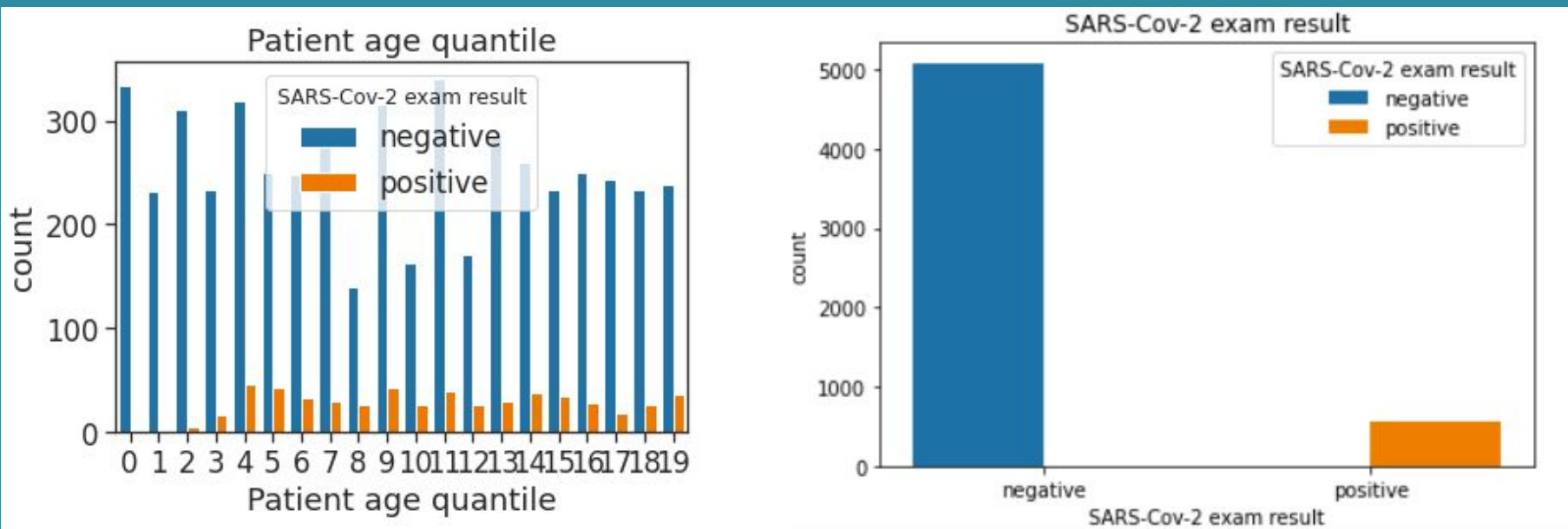


Random Forest for Severity



Graphs - legends

So next, we plotted our graphs with a legend, specific to SARS-Cov-2 exam results: either positive or negative.



The Solution

On average % of people get tested for COVID.

- Using machine learning models, accurately + efficiently predict
 - COVID-19 patient status
 - COVID-19 patient severity
- Prevent further spread of COVID
- Help hospitals distribute beds + ICU spaces

Table of Contents (Task List)

- 1) Background (Gianna)
- 2) Data Cleaning (done)
- 3) Status Model (done)
 - a) Comparing Accuracies (done)
 - b) Confusion Matrices (done)
 - c) ROC/AUC graph comparison (done)
 - d) Our Choice (Jessica)
 - e) False positive / negative consequences (done)
- 4) Severity Model (done)
 - a) Comparing Accuracies (Vienna)
 - b) Our Choice (Vienna)
 - c) ROC/AUC graph (Vienna)
- 5) Bias and Limitations (Christina)
- 6) Important Features (Gianna)
 - a) Decision Tree
- 7) Usage in Clinical Decision making (Srihita)
- 8) Conclusion (Fiona)
- 9) Acknowledgements

Presentation Slide Distribution

4) Gianna?

14) Vienna

5) Gianna

15) Vienna + Christina

6)

16) Vienna

7) Christina + Srihita

17) Vienna

8) Srihita

18) Christina

9) Srihita

19) Jessica

10) Jessica

20)Gianna

11) Jessica + Srihita

21) Gianna

12) Jessica

22) Fiona

13) Vienna

23) Fiona