

The univariate analysis showed a significant association of death with absolute neutrophil count (ANC, $p=0.022$), NLR ($p=0.02$), neutrophil-monocyte ratio (NMR, $p<0.0001$), LCR ($p=0.007$), lymphocyte-LDH ratio (LLR, $p<0.0001$), lymphocyte-D-dimer ratio (LDR, $p<0.0001$), lymphocyte-ferritin ratio (LFR, $p<0.0001$), and platelets ($p=0.037$) with mortality. With multivariable logistic regression analysis, the only values that had an odds of survival were high LDR (odds ratio [OR] 1.763; 95% confidence interval [CI], 1.20–2.69), and a high LFR (OR 1.136, CI 1.01–1.34).

We further build up a model which can predict >85% mortality in our cohorts with the utilization of D-dimer (>500 ng/ml), Ferritin (>200 ng/ml), LDR (< 1.6), LFR (< 4) and ANC (>2.5). This new model has a ROC of 0.68 ($p<0.0001$).

Table 1: Analysis of Clinical Characteristic and Demographics

	All Patients (n=303)	Survival (n=214)	Expired (n=89)	p-value
Clinical Characteristic and Demographics				
Age	61.67 ± 15.1	60.08 ± 15.4	65.48 ± 13.7	0.0044
Gender				
• Male	187 (62%)	123 (57%)	64 (72%)	0.0185
• Female	116 (38%)	91 (43%)	25 (28%)	
Ethnicity				
• Hispanic	135 (45%)	97 (45%)	38 (43%)	0.3216
• African American	130 (43%)	92 (43%)	38 (43%)	
• Caucasian	18 (6%)	14 (7%)	4 (4%)	
• Others	20 (6%)	11 (5%)	9 (10%)	
BMI				
• <30	139 (46%)	102 (48%)	37 (42%)	0.4627
• ≥30	164 (54%)	112 (52%)	52 (58%)	
Comorbidities				
• HTN	188 (62%)	135 (63%)	53 (60%)	0.6088
• DM	122 (40%)	80 (37%)	42 (47%)	0.1136
• CAD/CHF	66 (22%)	45 (21%)	21 (24%)	0.254
• CKD/ESRD	60 (20%)	34 (16%)	26 (29%)	0.005
• COPD	32 (11%)	26 (15%)	6 (7%)	0.1641
Need of Mechanical Ventilation	79 (26%)	25 (8%)	54 (61%)	<0.0001

Conclusion: This retrospective cohort study of hospitalized patients with COVID-19 suggests LDR and LFR as potential independent prognostic indicators. A new model with combination of D-dimer, Ferritin, LDR, LFR and ANC, was able to predict >85% mortality in our cohort with ROC of 0.68, it will need to be validated in a prospective cohort study.

Disclosures: Jihad Slim, MD, Abbvie (Speaker's Bureau) Gilead (Speaker's Bureau) Jansen (Speaker's Bureau) Merck (Speaker's Bureau) ViiV (Speaker's Bureau)

61. Using Machine Learning for Prediction of Poor Clinical Outcomes in Adult Patients Hospitalized with COVID-19

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Background: As the ongoing COVID-19 pandemic develops, there is a need for prediction rules to guide clinical decisions. Previous reports have identified risk factors using statistical inference model. The primary goal of these models is to characterize the relationship between variables and outcomes, not to make predictions. In contrast, the primary purpose of machine learning is obtaining a model that can make repeatable predictions. The objective of this study is to develop decision rules tailored to our patient population to predict ICU admissions and death in patients with COVID-19.

Methods: We used a de-identified dataset of hospitalized adults with COVID-19 admitted to our community hospital between March 2020 and June 2020. We

used a Random Forest algorithm to build the prediction models for ICU admissions and death. Random Forest is one of the most powerful machine learning algorithms; it leverages the power of multiple decision trees, randomly created, for making decisions.

Results: 313 patients were included; 237 patients were used to train each model, 26 were used for testing, and 50 for validation. A total of 16 variables, selected according to their availability in the Emergency Department, were fit into the models. For the survival model, the combination of age >57 years, the presence of altered mental status, procalcitonin ≥3.0 ng/mL, a respiratory rate >22, and a blood urea nitrogen >32 mg/dL resulted in a decision rule with an accuracy of 98.7% in the training model, 73.1% in the testing model, and 70% in the validation model (Table 1, Figure 1). For the ICU admission model, the combination of age < 82 years, a systolic blood pressure of ≤94 mm Hg, oxygen saturation of ≤93%, a lactate dehydrogenase >591 IU/L, and a lactic acid >1.5 mmol/L resulted in a decision rule with an accuracy of 99.6% in the training model, 80.8% in the testing model, and 82% in the validation model (Table 2, Figure 2).

Table 1. Measures of Performance in Predicting Inpatient Mortality

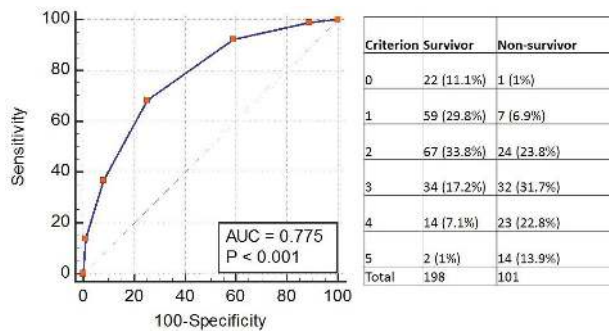
Criterion	Sensitivity	95% CI	Specificity	95% CI	LR	95% CI	PPV	95% CI	NPV	95% CI
00	100	30.4 - 100.0	0	0.0 - 1.8	1	1.0 - 1.0	33.8	33.8 - 33.8	NA	NA
01	98.01	94.6 - 100.0	11.11	7.1 - 16.3	1.11	1.1 - 1.2	36.2	35.0 - 37.5	85.7	75.1 - 99.1
02	92.08	85.0 - 93.5	40.91	34.0 - 49.1	1.58	1.4 - 1.9	44.0	41.1 - 47.5	81	63.6 - 85.3
03	88.37	78.3 - 77.7	74.75	68.1 - 83.6	2.71	2.1 - 3.6	58	51.2 - 64.5	87.2	77.4 - 89.7
04	36.83	27.3 - 49.0	91.92	87.2 - 93.3	4.53	2.7 - 7.7	68.9	57.5 - 79.8	71	70.8 - 79.8
05	15.93	7.8 - 22.2	98.90	95.4 - 99.0	15.77	3.2 - 69.2	87.5	81.6 - 89.8	69.3	67.5 - 73.0

Data are presented as percentage with 95% confidence interval.

Abbreviations: LR, likelihood ratio; NPV, negative predictive value; PPV, positive predictive value. Youden index J 0.4306, Associated criterion >2; Sensitivity 68.32, Specificity 74.75

Conclusion: We created decision rules using machine learning to predict ICU admission or death in patients with COVID-19. Although there are variables previously described with statistical inference, these decision rules are customized to our patient population; furthermore, we can continue to train the models fitting more data with new patients to create even more accurate prediction rules.

Figure 1. Receiver Operating Characteristic (ROC) Curve for Inpatient Mortality



Data are presented as absolute value (percentage). Abbreviations: AUC, area under the curve.

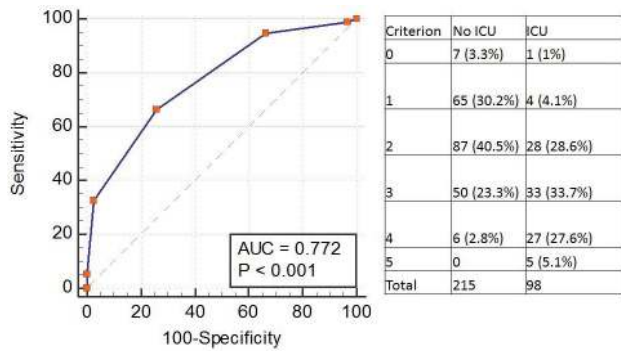
Table 2. Measures of Performance in Predicting Intensive Care Unit Admission

Criteria	Sensitivity	95% CI	Specificity	95% CI	LR	95% CI	PPV	95% CI	NPV	95% CI
00	100	98.3 - 100.0	0	0.0 - 1.7	1	1.0 - 1.0	31.3	31.3 - 31.3	NA	NA
01	88.68	84.4 - 100.0	3.20	1.3 - 6.6	1.32	1.0 - 1.1	31.8	31.1 - 32.5	87.0	40.9 - 98.2
02	81.9	66.6 - 89.3	33.48	27.2 - 40.2	1.43	1.3 - 1.8	39.4	38.9 - 41.8	83.5	65.7 - 97.2
03	63.33	58.1 - 75.6	73.66	67.5 - 79.7	2.55	2.0 - 3.3	53.7	47.1 - 60.2	82.0	70.3 - 86.5
04	39.66	25.6 - 47.5	97.21	94.6 - 99.0	11.7	5.1 - 27.1	84.2	69.7 - 90.5	78	73.4 - 79.5
05	5.1	1.7 - 11.5	100	98.3 - 100.0	NA	NA	100	NA	69.8	68.9 - 70.0

Data are presented as percentage with 95% confidence interval.

Abbreviations: LR, likelihood ratio; NPV, negative predictive value; PPV, positive predictive value. Youden index J 0.4028, Associated criterion >2; Sensitivity 66.33, Specificity 73.95.

Figure 2. Receiver Operating Characteristic (ROC) Curve for Intensive Care Unit Admission



Data are presented as absolute value (percentage).
Abbreviations: AUC, area under the curve; ICU, intensive care unit

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62. Association Between Influenza Co-infection and Poor Outcomes in Patients Hospitalized with COVID-19

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Session: O-12. COVID-19 Clinical Calls and Indicators 2

Background: In December 2019, a novel coronavirus (COVID-19) infection emerged in Wuhan, China, establishing itself as a deadly pathogen leading to an ongoing pandemic. The incidence of co-infection of COVID-19 and Influenza has not been widely reported. Both infections have been known to share similar mechanisms of transmission, however currently, there is no evidence regarding the relationship between co-infection between these viruses and worsening outcomes. Once social distancing measures are eased, and daily activities resumed, there is a possibility for a second wave of cases. Given the incidence of influenza is higher during winter, a higher co-infection rate is expected in these months.

Methods: In this study, the aim was to assess the association of influenza co-infection with outcomes in patients diagnosed with COVID-19 in a hospital-based case-control study in Bronx, New York. 19 patients with Influenza co-infection were found in total. 1 patient did not meet inclusion/exclusion criteria. Charts were reviewed from 18 confirmed cases of influenza and COVID-19 patients. Controls were selected from the remaining pool of patients with COVID-19 in the same period. Cases were matched for age, sex and underlying comorbidities (Hypertension, Diabetes Mellitus, liver disease, cardiovascular disease, HIV status, immunocompromised state other than HIV). The measured outcomes were: in-hospital mortality, need for mechanical ventilation, need for vasopressors and need for renal replacement therapy. For each outcome, Chi Square test and Odds ratio were obtained.

Results: After statistical analysis, no significant difference was found in the following variables: in-hospital mortality [Odds ratio (OR) 0.769; 95% confidence interval (CI): 0.185–3.191; p value= 0.717], need for mechanical ventilation (OR 1.3; 95% CI: 0.313–5.393; p value= 0.717), need for vasopressors (OR 1.923; 95% CI: 0.383–9.646; p value= 0.423), need for renal replacement therapy (OR 1.0; 95% CI: 0.208–4.814; p value= 1.0).

Conclusion: There was no difference in the outcome in COVID-19 patients co-infected with influenza compared to non co-infected patients, however, a larger sample of cases will be needed for further assessment of these outcomes.

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63. Prognosis of COVID-19 Patients with Diabetic Ketoacidosis with or Without Hyperosmolar Hyperglycemic State

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Session: O-12. COVID-19 Clinical Calls and Indicators 2

Background: One of the risk factors for poor outcome with SARS-CoV-2 infection is diabetes mellitus; diabetic ketoacidosis (DKA) and hyperosmolar hyperglycemic state (HHS) are the most serious complications of diabetes mellitus. We aimed to explore the clinical characteristics and outcomes of COVID-19 patients presenting with isolated DKA or combined DKA/HHS to our institution.

Methods: A retrospective, hospital based observation case series was performed on patients with SARS-CoV-2 admitted to Intensive Care Unit between 03/20/20 and

04/20/20. Inclusion criteria were: 1) Blood Glucose >250mg/dL; 2) Serum bicarbonate < 18 mmol/L; 3) Anion Gap >10; 4) serum pH < 7.3; 4) ketonemia or ketonuria; and 5) positive SARS-CoV-2 RT-PCR. Hyperosmolality, on the other hand, was defined as an effective/calculated plasma osmolality >304 mOsm/kg.

Results: A total of 87 patients with COVID-19 were admitted to the ICU during the study period, 12 of them had either isolated DKA or DKA/HHS. Baseline demographics, lab values and outcome are summarized in Table 1. Six of the patients had isolated DKA and six had combined DKA and HHS. The median age for the patient was 49.5 years old (range from 19 to 62 years old). The male to female ratio was 5:1. Of the 12 patients, 10 patients (83%) had a history of DM, nine were type 2 and only one type 1; two patients were newly diagnosed DM, presenting as DKA, presumptively precipitated by COVID-19. Five patients (42%) had a BMI >30 kg/m2. As for ethnicity; seven were Hispanic (59%), four African American (33%), and one Caucasian (8%).

Patients with combined DKA/HHS, higher BMI, higher HbA1c, severe acidosis tended to have higher mortality. The striking feature was that isolated DKA or combined DKA/HHS was the initial presentation for COVID-19 for most of the cases.

Table 1: Demographic characteristic, inflammatory markers and outcome.

Case	Age	Sex	Ethnicity	BMI	HbA1c	African Am.	pH	Bicarb	Anion Gap	BHOB	Calcium ionized	CRP	LDH	B-Brain	Parvitis	Outcome
1	51	M	Hispanic	28.6	11.1	31%	7.31	18	15	0.4	2.0	4.5	181	10.4	7.15	Stable
2	51	M	Hispanic	34	17.5	90%	6.9	3.5	50	0.4	2.0	4.6	468	18.0	7.02	Stable
3	45	M	Caucasian	36.1	8.9	2%	6.9	16	31	0.6	2.0	4.7	300	10.1	7.0	Stable
4	51	M	AA	41.7	17.5	8%	7.5	9	21	0.4	2.0	4.7	251	5.6	1.9	Stable
5	48	M	AA	25.3	17.6	100%	7.2	9.1	35	0.4	2.0	4.7	303	4.30	6.0	Stable
6	52	M	AA	23.6	12.1	0%	7.31	1	21	0.4	2.0	4.7	491	12.0	3.05	Stable
7	52	M	Hispanic	73	14	4%	7.32	15	24	0.4	2.0	4.8	751	17.15	4.0	Stable
8	19	M	AA	48.0	10.9	11%	7.1	5	32	0.4	2.0	4.8	495	12.5	3.28	Degrade
9	58	M	Hispanic	24.2	30.8	100%	6.77	4	20	0.4	2.0	4.6	272	8.4	1.07	Degrade
10	62	M	Hispanic	34.9	11	2%	7.23	14	18	0.5	2.0	4.7	300	9.7	2.0	Degrade
11	62	M	Hispanic	24.1	12.2	0%	7	6	21	0.6	2.0	4.7	222	12.2	2.05	Degrade
12	62	M	Hispanic	22.8	30.8	8%	6.83	6.6	20	0.4	2.0	4.8	358	8.4	8.4	Degrade
Average	49.5			31.3	14.2	69.5	7.06	9.2	24.9	0.4	2.0	4.7	458	10.26	3.95	
Median	49.5			28.5	12.1	69.5	7.06	9.1	21	0.4	2.0	4.7	306	12.27	3.95	

Table 1: Demographic characteristic, inflammatory markers and outcome.

F: Female; M: Male; BMI: Body Mass Index; HbA1c: Glycated Hemoglobin A1c, normal range 4.5-5.9%; BG: Blood glucose, normal range 70-140 mg/dL; pH: normal range 7.34-7.44; Bicarb: Bicarbonate, normal range 20-31 mmol/L; CRP: C-reactive protein, normal range 0-8 mg/dL; LDH: Lactate Dehydrogenase, normal range 122-222 U/L; D-dimer: 0-506 ng/mL; Ferritin: 24-336 ng/dL; Anion gap: 8-15 mmol/L; BHOB: beta hydroxybutyrate, normal range 0.02-0.27 mmol/L; Serum osmolality: 278-305 mOsm/kg; MV: Mechanical Ventilation; N/A: not available

Conclusion: Our observational retrospective case series reinforces the need to watch for new onset DM and monitor blood sugar closely in those with known diabetes mellitus during SARS-CoV-2 infection, in order to avoid such serious complications as DKA and HHS.

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64. Metagenomic Sequencing to Identify Alternative Infections and Co-infections in Persons Under Investigation for covid-19

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Background: Broad testing for respiratory viruses among persons under investigation (PUI) for SARS-CoV-2 is performed inconsistently, limiting our understanding of alternative infections and co-infections in these patients. Here, we used unbiased metagenomic next-generation sequencing (mNGS) to assess the frequencies of 1) alternative viral infections in SARS-CoV-2 RT-PCR negative PUIs and 2) viral co-infections in SARS-CoV-2 RT-PCR positive PUIs.

Methods: A convenience sample set was selected from PUIs who were tested for SARS-CoV-2 in the Emory Healthcare system during the first 2 months of the pandemic from 02/26-04/23/20. Laboratory results were extracted by chart review; Flu/RSV and multiplex respiratory pathogen PCRs had been performed at the discretion of treating physicians. Excess nasopharyngeal swab samples were retrieved within 72 hours of collection and underwent RNA extraction and SARS-CoV-2 testing by triplex RT-PCR. mNGS was performed by DNase treatment, random primer cDNA synthesis, Nextera XT tagmentation, and high-depth Illumina sequencing. Reads underwent taxonomic classification by KrakenUniq, as implemented in viral-ngs.

Results: 53 PUIs were included, 30 negative and 23 positive for SARS-CoV-2 by RT-PCR. Among SARS-CoV-2 negative PUIs, 28 (93%) underwent clinical testing for alternative infections, and 8 (29%) tested positive for another respiratory virus. In all cases, mNGS identified the same virus (Table 1). In another 3 PUIs, mNGS identified two viruses that were not tested for and one that was missed by routine testing. No SARS-CoV-2 was detected by mNGS among RT-PCR negative PUIs. Among SARS-CoV-2 RT-PCR positive PUIs, 18 (69%) underwent clinical testing for co-infections, and none were detected. mNGS did not identify any viral co-infections but did detect SARS-CoV-2 in all 23 PUIs.