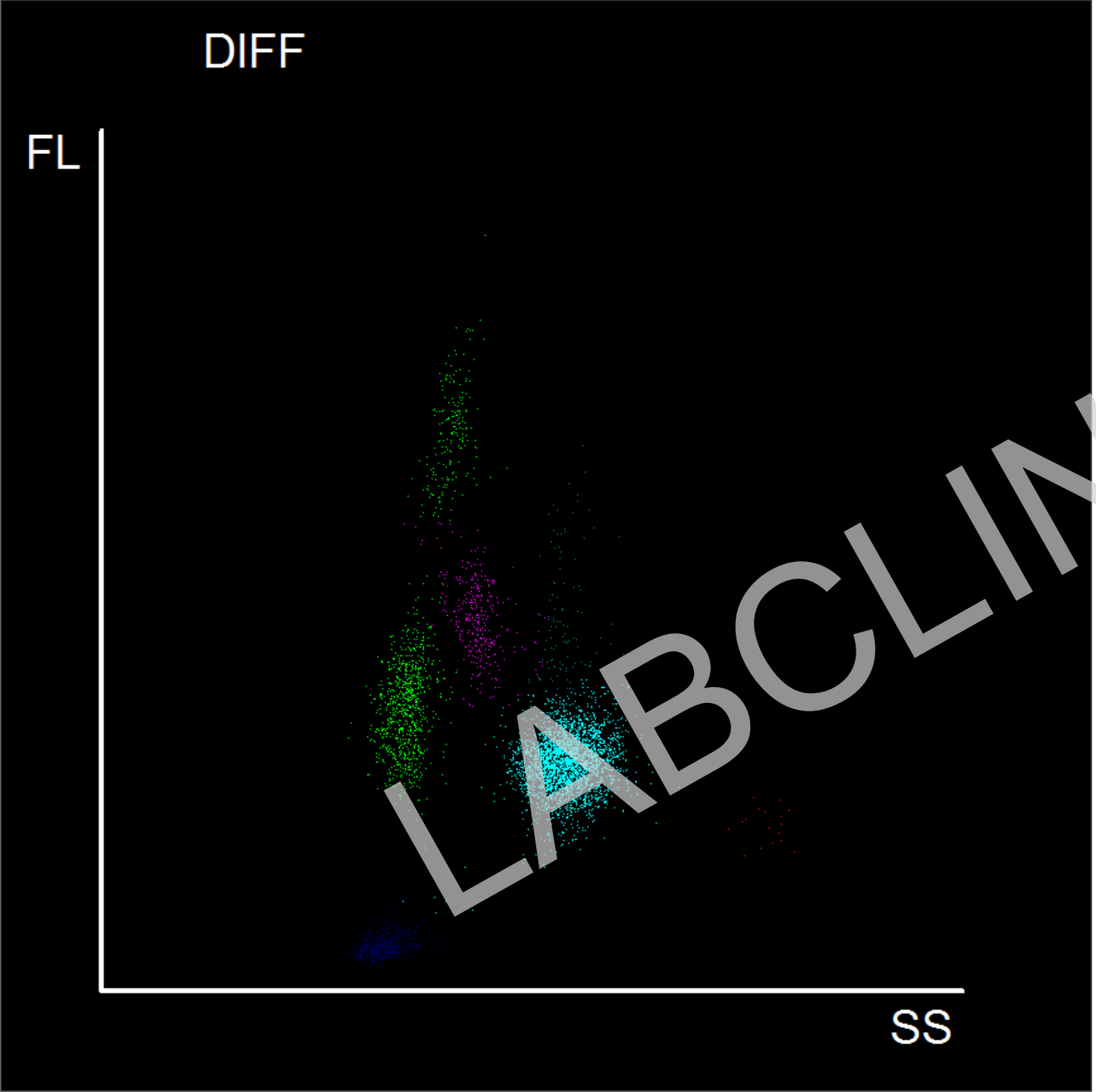

Leukocyte differential and cell population data from Mindray BC6800 Plus analyzer in the discrimination of SARS CoV2 infection

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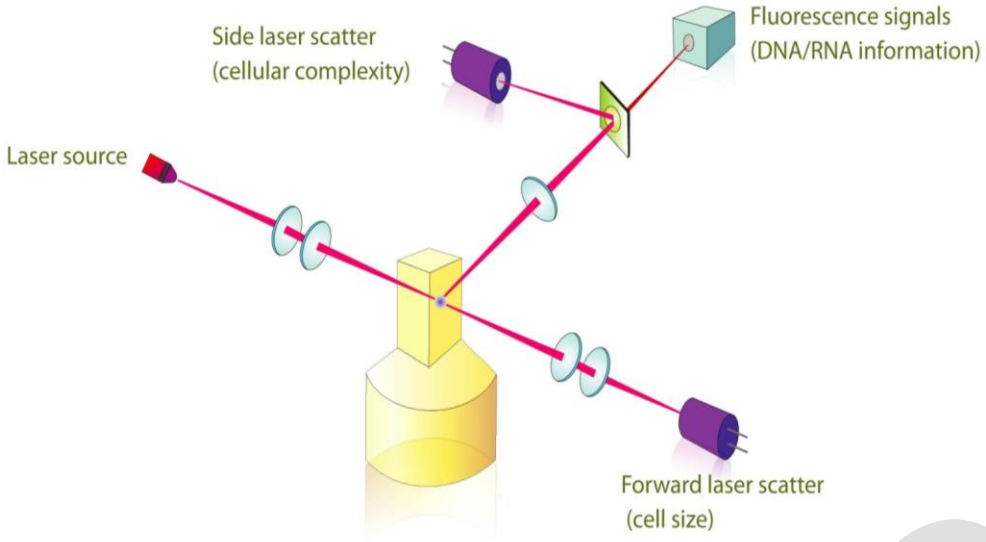
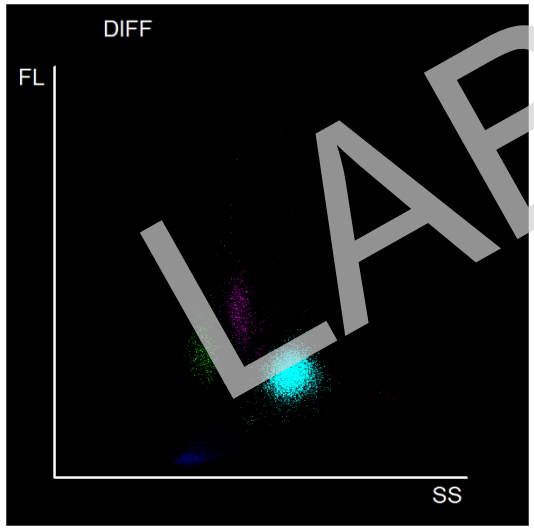
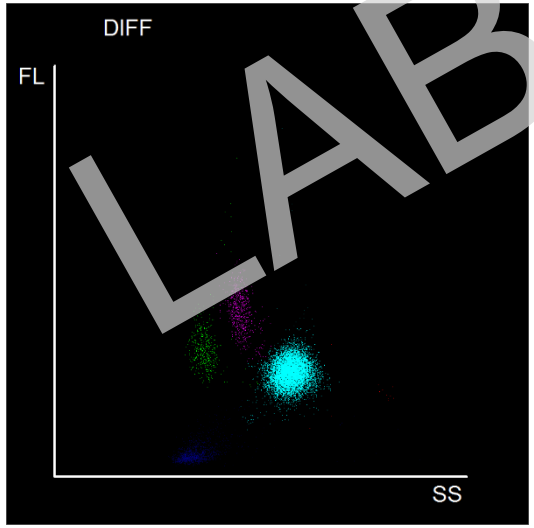
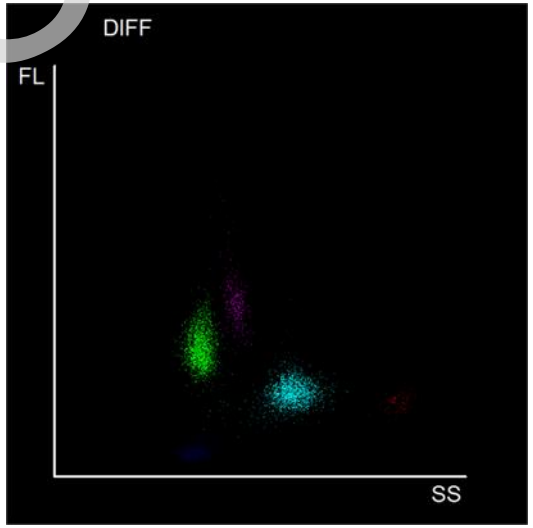


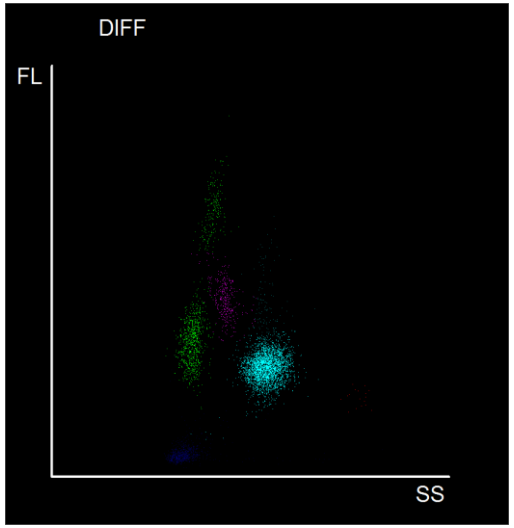


X axis		granules, vacuoles and other cytoplasmic inclusions.
Neu X	neutrophil complexity	
LymX	lymphocyte complexity	
Mon X	monocyte complexity	
Y axis		cellular DNA and RNA
Neu Y	neutrophil fluorescence intensity	
Lym Y	lymphocyte fluorescence intensity	
Mon Y	monocyte fluorescence intensity	
Z axis		abnormal sized cells after staining
Neu Z	neutrophil size	
Lym Z	lymphocyte size	
Mon Z	monocyte size	

Complete Blood counts (CBC) and leukocyte differential present certain features in SARS CoV 2 infected patients, which could be useful for screening and prognostic factors of the patients outcome.
Cell population data (CPD) are reported as part of leukocyte differentials by Mindray BC6800 Plus analyzers, give information of the size, nucleic acid content and internal structure of leukocytes,
CPD values reflect in numbers the functional and morphological changes triggered by infections.
We examine the leukocyte differential and CPD of the patients infected with SARS-CoV-2 virus and other infections of different etiologies when admitted to the Emergency Room. We evaluated these parameters as early laboratory indicators for the detection of COVID-19.
The study group consisted of consecutive patients with fever admitted to the Emergency Department at Galdakao–Usansolo Hospital in the period between 1st of December 2020 and 30th of January 2021. The criterion for inclusion in the validation group was the same as for the study group , consecutive patients with fever admitted to the Emergency Department between 1st of February and 30th of April 2021.
A total of 424 patients with symptoms of infection were recruited at presentation to the Emergency Department. The final study group included 151 COVID-19 cases and 86 patients with other infections (33 viral, 53 bacterial). The reliability of the model was evaluated in a validation group of 187 patients , 115 of them suffering COVID-19.







Statistical analysis

Kolmogorv-Smirnov test was applied to detect normal or skewed distributions.

A preliminary exploratory data analysis was performed medians accompanying with interquartile range (IQR) were displayed for continuous variables; frequencies and percentages for categorical data.

Kruskal-Wallis test was applied in order to detect statistical differences among patients with different infection types.

Next step was to test the hypothesis that distinct infections could be distinguished into two distinct groups based on their clinical status, the k-means unsupervised clustering method was applied.

This statistical technique maximizes the similarity within each cluster and minimizes the similarities between clusters. Firstly, all the assessed CPD parameters were scaled and normalized by converting into z-scores. After that, the above mentioned statistical method was applied.

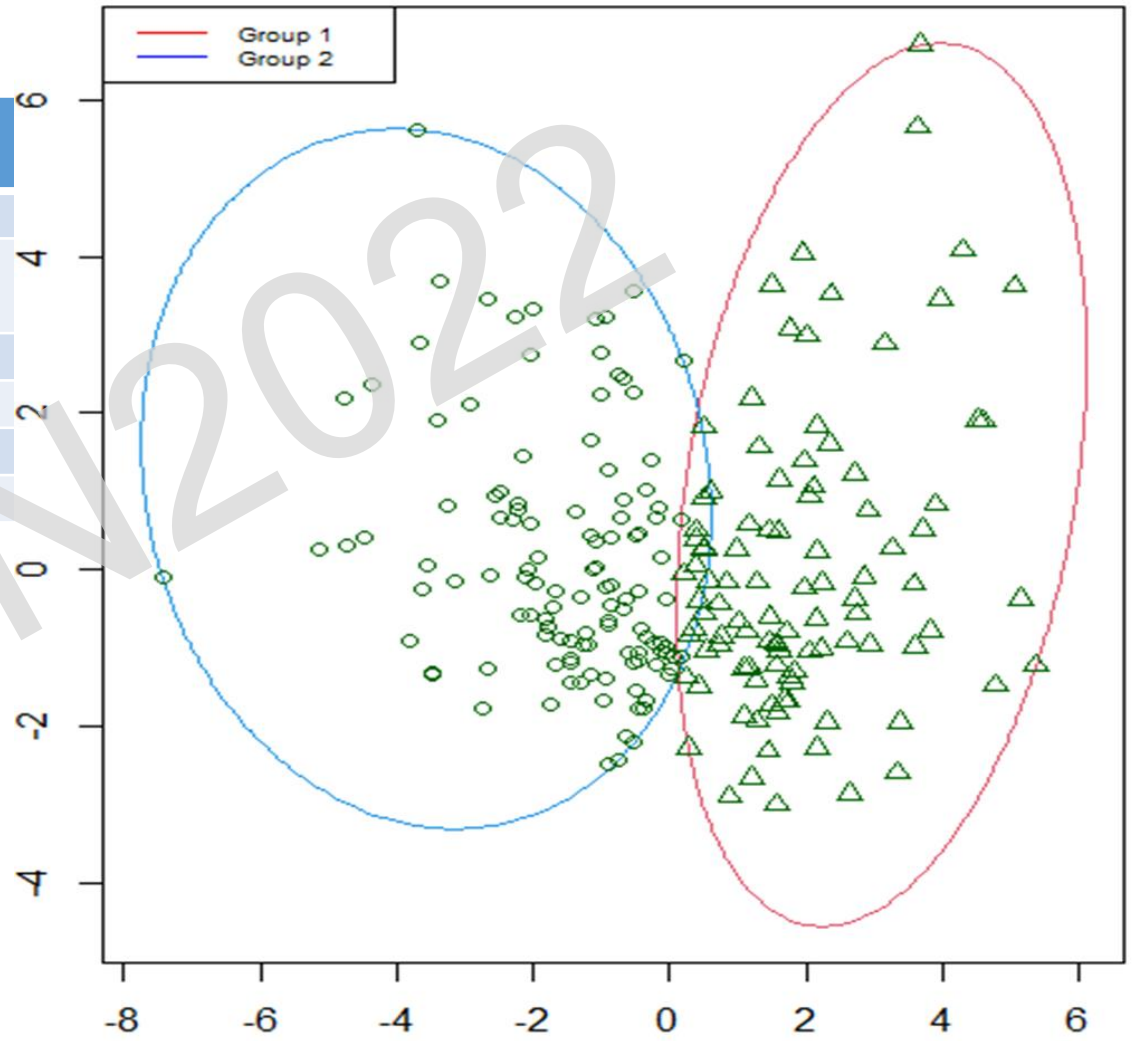
To obtain the optimal cluster number, a set of 30 indices were computed varying all the combinations of number of clusters. In that way, we could decide the best clustering scheme from the different obtained results. Additionally, the Principal component analysis (PCA) was used to validate to the choice of the optimal number of clusters, and to plot data points according the obtained optimal principal components. This was performed in both training and validation sets. Accuracy of the confusion matrix obtained in the test set was computed to assess the performance of the model. An accuracy > 0.8 is considered good performance.

A *p-value* <0.05 was deemed to be statistically significant. All the statistical procedures were performed using SAS version 9.4 and R. 3.4.1 release.

	Bacterial (n = 53)	Viral (n = 33)	COVID19 (n =151)	P
WBC, 10^9 /L	12.55 (8.82,16.8)	8.87 (5.77, 12.3)	7.19 (5.13, 9.6)	<0.001
Neut, 10^9 /L	9.92 (5.95,14.0)	3.68 (2.50, 4.6)	5.69 (3.87, 7.8)	<0.001
Lymph, 10^9 /L	1.38 (0.95,1.9)	4.13 (2.78, 5.3)	1.00 (0.68, 1.4)	<0.001
Mono, 10^9 /L	0.69 (0.45,1.0)	0.64 (0.51, 0.8)	0.26 (0.00, 0.5)	<0.001
PLT, 10^9 /L	194 (114,359)	251 (212,370)	222 (176, 302)	0.0286
NLR	8.05 (4.13,12.6)	0.90 (0.47, 1.3)	5.43 (3.79, 8.0)	<0.001
Neu X	376 (351,411)	334 (317, 358)	346 (322, 372)	<0.001
Neu Y	451 (419,469)	409 (399, 442)	428 (412, 448)	<0.001
Neu Z	1821 (1754,1866)	1811 (1781,1859)	1808 (1748, 1876)	0.898
Lym X	90 (86,97)	85 (80, 89)	88 (85, 92)	0.003
Lym Y	664 (630,714)	649 (624, 684)	650 (627, 682)	0.182
Lym Z	957 (936,977)	953 (932, 976)	960 (945, 981)	0.202
Mon X	203 (194,218)	196(188, 200)	200 (193, 209)	0.001
Mon Y	917 (876,976)	960 (892, 994)	933 (887, 990)	0.443
Mon Z	1315 (1273,1341)	1290 (1278,1310)	1343 (1290, 1352)	0.01
IG, 10^9 /L	0.07 (0.02,0.3)	0.01 (0.01, 0.0)	0.01 (0.00, 0.0)	<0.001

	Predicted Cluster		
	cluster 1	cluster 2	Total
Infection group			
Bacteria	23 (56.60)	27 (43.40)	50 (26.74)
Virus	0 (0)	22 (100)	22 (11.76)
COVID-19	105 (91.30)	10 (8.70)	115 (61.50)
			187

The reliability of the model was evaluated in a validation group of 187 patients , 115 of them suffering COVID-19 , 50 bacterial infections and 22 other virus



Conclusions

Early diagnosis of SARS-CoV-2 infection is critical for better caring of patients and to reduce the threat of nosocomial infection for professionals

Abnormalities in white blood cell morphology based on a few cell population data were able to identify COVID-19 etiology.

Leukocyte differential and CPD could assist in a preliminary differential diagnosis of the disease.

Those new peripheral blood biomarkers can help determine the etiology of pneumonia fast and inexpensive