



# Development of Machine Learning models to predict RT-PCR results for Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) in patients with influenza-like symptoms using only basic clinical data.

*M. Favarato<sup>1</sup>, H. Gay<sup>1</sup>, R. Garberi<sup>1</sup>, F. Villa<sup>1</sup>, A. Zeduri<sup>1</sup>, S. Bragagnolo<sup>1</sup>, A. Molteni<sup>3</sup>, M. Buscema<sup>4</sup>, E. Grossi<sup>5</sup>, R. Giudici<sup>2</sup>, G. Bassi<sup>2</sup>, T. Langer<sup>1,2</sup>, R. Fumagalli<sup>1,2</sup>*

## Background

RT-PCR for SARS-COV-2 diagnosis currently requires quite a long time span. A **quicker and more efficient diagnostic** tool in emergency departments (ED) could improve management during this global crisis.

Our main goal was assessing the accuracy of **artificial intelligence (AI) in predicting the results of RT-PCR for SARS-COV-2**, using basic information at hand in all ED.

## Methods

This is a **retrospective study** carried out between February 22, 2020 and March 16, 2020 in one of the main hospitals in Milan, Italy.

### Inclusion criteria:

- patients admitted to the ED of Niguarda hospital with influenza-like symptoms
- a performed SARS-COV-2 test in ED.

### Exclusion criteria:

- Patients < 12 years old
- absence of leukocyte formula in the ED.

We created a dataset with 74 variables, collected from a combination of **clinical, radiological and routine laboratory** findings upon hospital admission. The RT-PCR results constituted the target variable of the prediction model.

Different Machine Learning algorithms were trained using both the **Training and Testing AB-BA sequence** and the **K-fold cross-validation protocol**.

## Results

Among 199 patients subject to study (median [interquartile range] age 65 [46-78] years; 127 [63.8%] men), 124 [62.3%] resulted positive to SARS-COV-2. The AI model selected 42 out of the 74 collected variables.

The best Machine Learning System reached an **accuracy of 91.4%** with **94.1% sensitivity and 88.7% specificity**. Other AI algorithm had similar results but were less efficient.

| Machine Learning System | Sensitivity | Specificity | Overall accuracy | AUROC       |
|-------------------------|-------------|-------------|------------------|-------------|
| D_FF_Conic (4x12x12x12) | 94.1        | 88.7        | 91.4             | 0.90        |
| D_FF_Conic (6x12x12x12) | 92.5        | 90.2        | 91.3             | 0.91        |
| D_FF_Bp (24)            | 89.2        | 93.0        | 91.1             | 0.93        |
| D_FF_Bp (16x16x16x16)   | 93.2        | 88.7        | 91.0             | 0.92        |
| D_FF_GNet (64)          | 90.7        | 90.2        | 90.5             | 0.90        |
| <b>Mean results</b>     | <b>91.9</b> | <b>90.2</b> | <b>91.1</b>      | <b>0.91</b> |

The following variables hold a **considerable weight in the mathematical model**:

- **Leukocyte**
- **Lymphocyte**
- **Eosinophil**
- **Basophil**
- **Monocyte**
- **Age**
- **Female sex**

## Conclusion

Our exploratory study suggests that properly trained **artificial intelligence algorithms** may be able to **predict correct results in RT-PCR for SARS-COV-2**, using basic clinical data.

If confirmed in larger multicentre studies, this could have important clinical and organizational implications.

### Affiliations

<sup>1</sup> Department of Medicine and Surgery, University of Milan-Bicocca, Monza, Italy;

<sup>2</sup> Department of Anaesthesia and Intensive Care Medicine, Niguarda Ca' Granda, Milan, Italy;

<sup>3</sup> Department of General oncologic and mini-invasive Surgery, Niguarda Ca' Granda, Milan, Italy;

<sup>4</sup> Semeion Research Center of Sciences of Communication, Rome, Italy;

<sup>5</sup> Villa Santa Maria Foundation, Tavernerio, Italy

