

## Leveraging of SARS-CoV-2 PCR cycle thresthold values (Ct) to forecast COVID-19 trends

<u>Nicolas Yin</u>. Sigi Van Den Wijngaert. Leila Mekkaoui. Charlotte Michel. Giulia Zorzi. Dieter Van Cauteren. Marie Hallin. Delphine Martiny. Olivier Vandenberg

LHUB-ULB – department of Microbiology

#### Introduction

- Ct values can be used to assess the infectiousness at the individual level. but:
  - Depends on the quality of the sample

O Negative test

O Positive test

Viral Load

0

Preinfectious

**Positive by PCR** 

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Infectious

- Depends on the timing of the sampling
- Depends on the instrument
- Depends on the target





# **Correlation between the Ct and the epidemic**

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N. Yin. S. Dellicour. V. Daubie. N. Franco. M. Wautier. C. Faes. D. Van Cauteren. L. Nymark. N. Hens. M. Gilbert. M. Hallin and O. Vandenberg



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3

#### How to explain this correlation





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- For a same number of positive tests. the proportion of recently infected people is bigger in the growing phase
  - Furthermore. the recently infected people are known to be more infectious

#### Use of semi-quantitative results

- Since December 2020. the Belgian Risk assessment group recommends the use of a semiquantitative reporting
- The goal is to help with infectiousness assessment

The proposal for reporting and the associated evaluation of contagiousness is as follows:

Semi-quantitative reporting of RT-PCR values in four categories:

- very strongly positive: ≥ 10<sup>7</sup> RNA copies/mL 'the patient is contagious'
- strongly positive: ≥ 10<sup>5</sup> <10<sup>7</sup> RNA copies/mL 'the patient is probably contagious'
- positive:  $\geq 10^3 <10^5 \text{ RNA copies/mL}$

'the patient is potentially contagious, unless there is clinical and/or serological evidence of an old, cleared infection'

weakly positive: < 10<sup>3</sup> RNA copies/mL

'the patient is probably not or no longer contagious if there is also clinical and/or serological evidence of an old, cleared infection'.

#### Lisbon, Portugal 23–26 April 2022



#### **Inter-instrument Ct comparability**

Instrument	10 <sup>7</sup> copies/ml	10 <sup>5</sup> copies/ml	10 <sup>3</sup> copies/ml
Altona RealStar®	16.6	24.2	31.7
Abbott <i>m</i> 2000	6.5	12.7	19
Abbott Alinity	16.7	23.3	29.9
Roche Cobas <sup>®</sup> Liat <sup>®</sup>	14.4	20.1	25.9

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> sbon, Portugal -26 April 2022

#### Methods

- Analysis of results collected from April 2020 to April 2022  $\rightarrow$  attribution of a semi-quantitative evaluation based on Ct values
- Use of 14-day averages to minimize day-to-day and holiday related variations
- Correlation between % of "strong" and "very strong" positive results and N of positive tests from 0-45 days later using Spearmans r<sub>s</sub> rank correlation





#### **Correlation between % of "strong positive" results and number of positive tests**



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#### Conclusions

- Using the SARS-CoV-2 PCR Ct values can add a useful dimension to follow epidemic' dynamic (likely true for all respiratory transmitted viruses)
- Categorizing positive results allows an easier follow-up and the gathering of comparable data between labs and instruments
- Such strategy could be used at a regional level through a laboratory network
- The model is however influenced by the testing policy and can be only followed if it remains stable





### Acknowledgment

LHUB-ULB team and especially the microbiology department for their amazing work for more than 2 years into pandemic













