

# **Incubation and latency time estimation for SARS-CoV-2** Arntzen, V.H.

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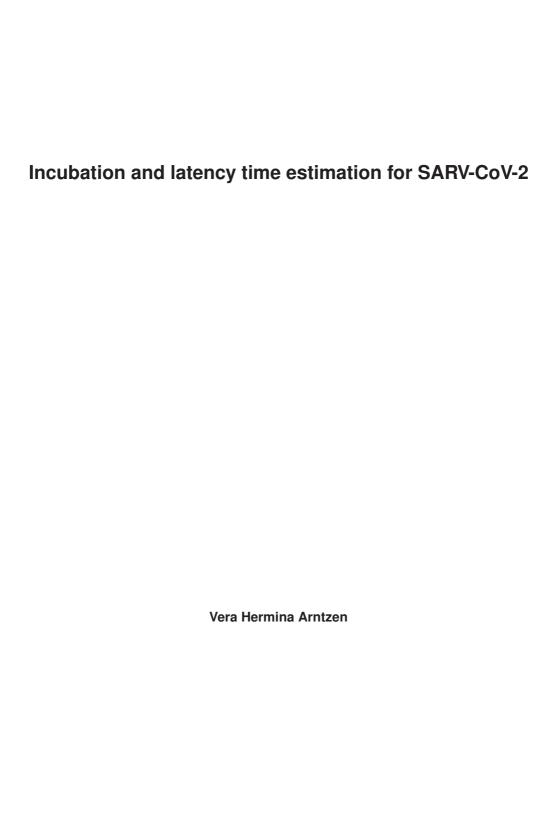
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## Incubation and latency time estimation for SARV-CoV-2

#### **Proefschrift**

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to curiosity

# **Preface**

When the work for the thesis in front of you started, the SARS-CoV-2 pandemic had been ongoing for a couple of months already. Suddenly, the novel coronavirus confronted many of us with incredible losses, whether these were lives, health, the proximity to our loved ones, the fearlessness of living in a world free of pandemics or trust in science. At the same time, the world saw how researchers developed the first mRNA-based vaccines against SARS-CoV-2 and rapid antigen tests, and how many countries reduced transmission levels with public health measures.

Humans are a creative and resilient species, yet viruses are so, stressing the importance of continuously extending our knowledge of pathogens. This thesis focuses on estimating the distribution of two critical quantities of an infectious disease to inform public health measures: incubation and latency time.

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# List of Abbreviations

AIC . . . . . . . . Akaike information criterion (goodness-of-fit, frequentist paradigm)

AIDS . . . . . . . acquired immunodeficiency syndrome

**BRCA** . . . . . breast (and ovarian) cancer associated (genes)

CI . . . . . . . . . Confidence Interval (uncertainty bounds, frequentist paradigm)

Covid-19 . . . . . coronavirus disease CRC . . . . . . . colorectal cancer

Crl . . . . . . . Credible Interval (uncertainty bounds, Bayesian paradigm)

DAG . . . . . . directed acyclic graph

**GWAS** . . . . . . Genome Wide Association Studies **HIV** . . . . . . . human immunodeficiency virus

**LOO IC** . . . . . leave-one-out information criterion (goodness-of-fit, Bayesian paradigm)

MLE . . . . . . . Maximum Likelihood Estimator

MSE . . . . . . . mean squared error

**NP(MLE)** . . . . nonparametric Maximum Likelihood Estimator **PCR** . . . . . . . Polymerase Chain Reaction (laboratory method)

PG(M) . . . . . . penalized Gaussian mixture

PRS . . . . . . . polygenic risk score

reBias . . . . . relative Bias

RNA . . . . . . ribonucleic acid (genetic material)

SARS . . . . . . severe acute respiratory syndrome (lung infection due to SARS-CoV)

SARS-CoV-2 . . . severe acute respiratory syndrome coronavirus 2

SE . . . . . . . Standard Error

**SNP** . . . . . . . Single Nucleotide Polymorphism (genetic variant)