Incubation and latency time estimation for SARS-CoV-2

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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.

Contents

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
CrI	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)