Bioinformatic modelling of SARS-CoV-2 pandemic

with a focus on country-specific dynamics

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Goal

 Assessment of differences/similarities between countries in the dynamics of SARS-CoV-2 pandemic



Data & Methods

Study population

- Public SARS-CoV-2 Data Repository \rightarrow provided by Johns Hopkins University \rightarrow GitHub
- \circ Cumulative daily numbers of confirmed \rightarrow cases, deaths, recoveries
- Beginning from 21.01.2020
- 191 countries

SIRD (epidemiologiclal modelling at description of time [days] infection rate population

- Susceptible $\rightarrow S(t) = S(t-1) \frac{\alpha}{N} S(t-1) \overline{I(t-1)}$
- Infected $\rightarrow I(t) = I(t-1) + \frac{\alpha}{N}S(t-1)I(t-1) \beta I(t-1) \gamma I(t-1)$
- Recovered $\rightarrow R(t) = R(t-1) + \beta I(t-1)$
- Dead $\rightarrow D(t) = D(t-1) + \gamma I(t-1)$

mortality rate

recovery rate

Linear mixture models (general modelling at day 300)

• Daily number of confirmed cases



Results

SIRD

0.8

0.6

beta

ĕ

0.0

Density-Based Spatial Clustering D30, Density-Based Spatial Clustering D60 Local Outlier Factor D300 - daily confirmed cases Local Qutlier Factor D300 - daily deaths 250 200 m 150 100 300 0.30 0.25 0.00 0.05 0.10 0.15 0.20 0.00 0.05 0.10 0.15 0.20 0.25 0.30 gamma gamma gamma Density-Based Spatial Clustering D150 Density-Based Spatial Clustering D300 - 250 200 mean3 200 175 150 150 125 100 mean1 75 - 100 50 25 250 200 150 n2 160 140 120 100 mean1⁸⁰ 100 60 0.00 0.05 0.10 0.15 0.20 0.25 0.30 0.00 0.05 0.10 0.15 0.20 0.25 0.30 gamma gamma 20 PTBI 2021

Linear mixture models



- Heterogeneity between countries
- Lichtenstein

 \rightarrow a "positive" outlier at D30-D150 \rightarrow low mortality, high recovery

o Yemen

 \rightarrow a "negative" outlier at D30-D60 \rightarrow high mortality, low recovery