

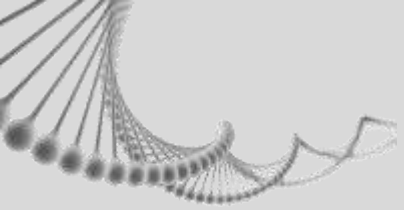
Bioinformatic modelling of SARS-CoV-2 pandemic with a focus on country-specific dynamics

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Goal

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



Study population

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

SIRD (epidemiological modelling at day 300)

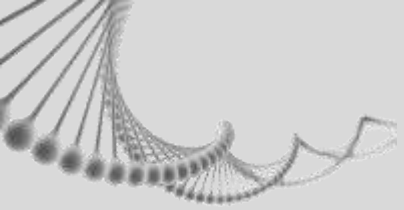


- Susceptible → $S(t) = S(t - 1) - \frac{\alpha}{N} S(t - 1)I(t - 1)$
- Infected → $I(t) = I(t - 1) + \frac{\alpha}{N} S(t - 1)I(t - 1) - \beta I(t - 1) - \gamma I(t - 1)$
- Recovered → $R(t) = R(t - 1) + \beta I(t - 1)$
- Dead → $D(t) = D(t - 1) + \gamma I(t - 1)$



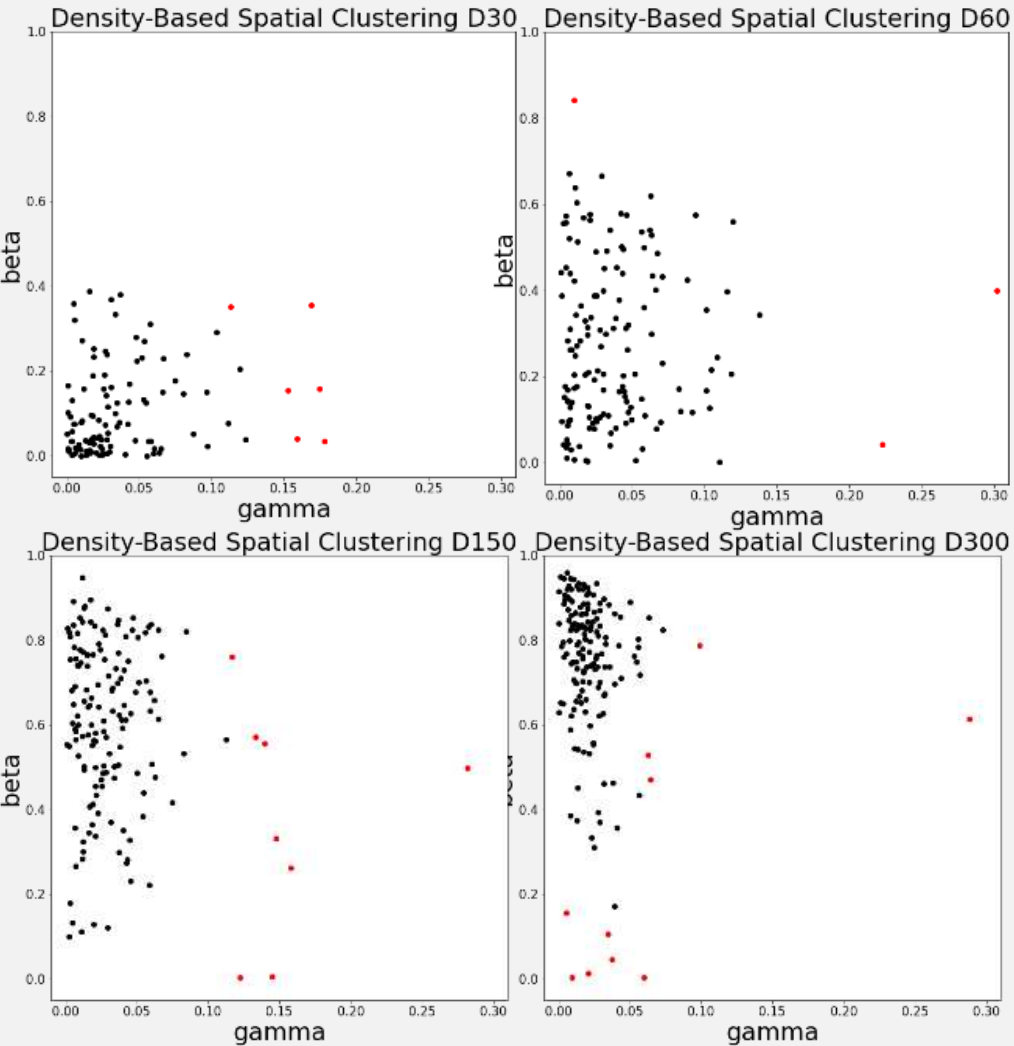
Linear mixture models (general modelling at day 300)

- Daily number of confirmed cases



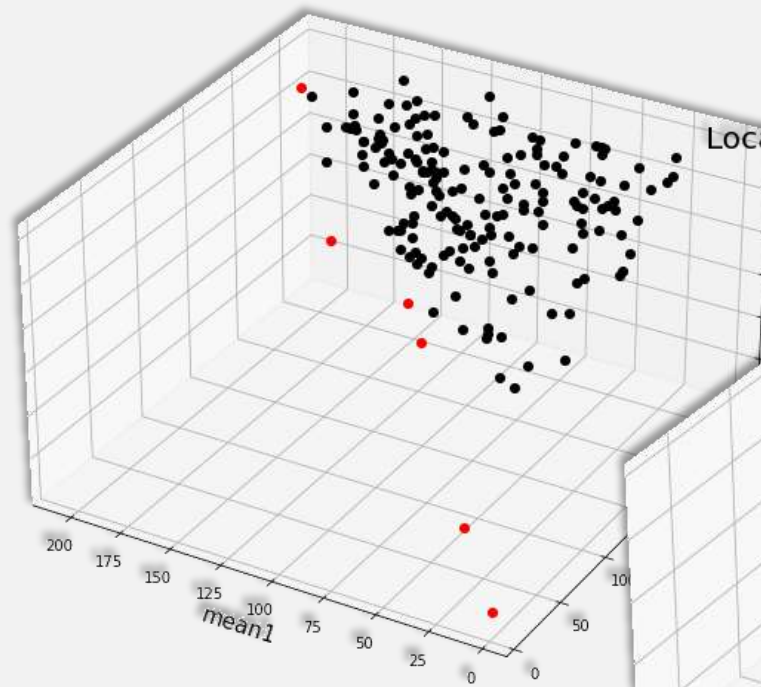
Results

SIRD

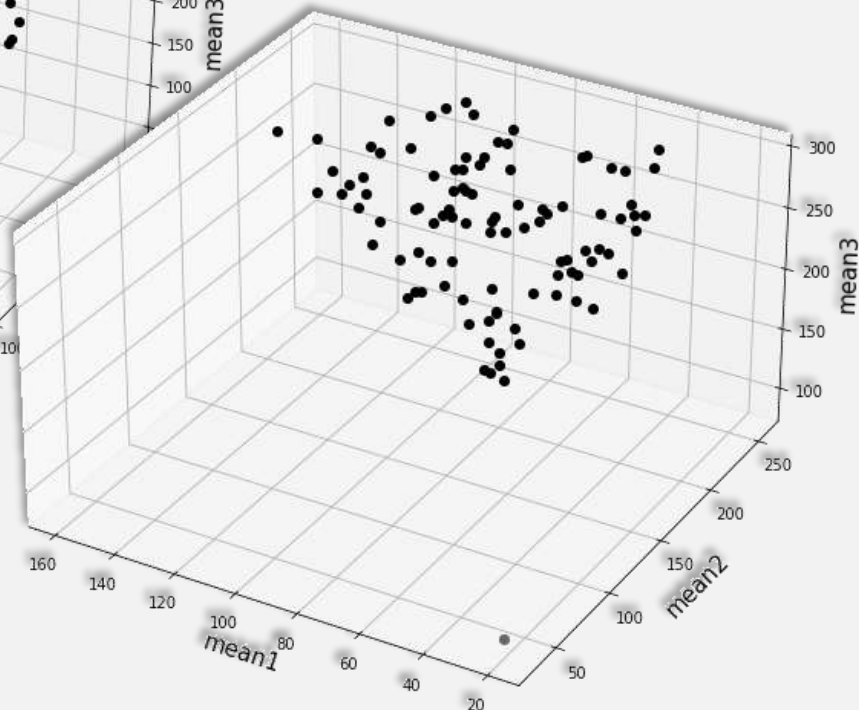


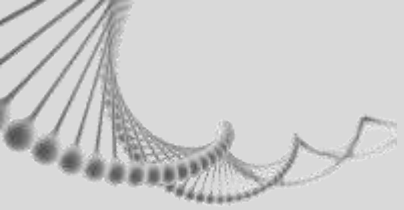
Linear mixture models

Local Outlier Factor D300 - daily confirmed cases



Local Outlier Factor D300 - daily deaths





Conclusions

- Heterogeneity between countries
- Lichtenstein
 - a “positive” outlier at D30-D150 → low mortality, high recovery
- Yemen
 - a “negative” outlier at D30-D60 → high mortality, low recovery