

Understanding and forecasting SARS-CoV2 spread and transmission

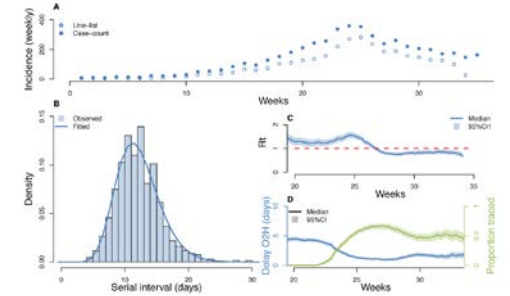
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Sangeeta Bhatia, Anne Cori, Neil Ferguson, Christl Donnelly
and Imperial COVID-19 Team

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About myself

- PhD in quantitative biology (Sussex/Oxford): ant's behaviour, badger population dynamics
- Epidemiology of infectious diseases (Imperial/Sussex):
 - Statistical epidemiology
 - Dynamics of transmission

$$F \approx \frac{\sum_{i=\alpha}^{\omega} e_i F_i}{\sum_{i=\alpha}^{\omega} e_i}, P_j \approx \frac{\sum_{i=1}^{\alpha} e_i P_i}{\sum_{i=1}^{\alpha} e_i}, P_a \approx \frac{\sum_{i=\alpha+1}^{\omega-1} e_i P_i}{\sum_{i=\alpha+1}^{\omega-1} e_i}$$



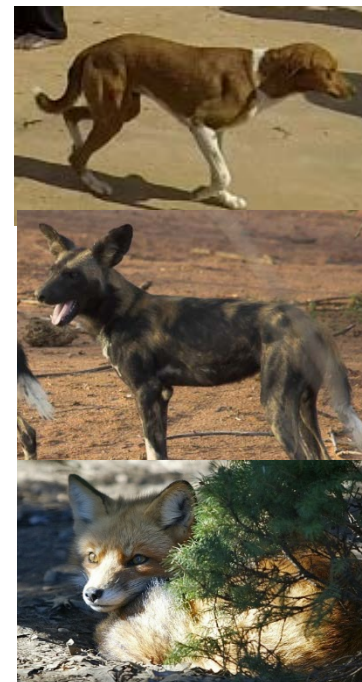
Ecology



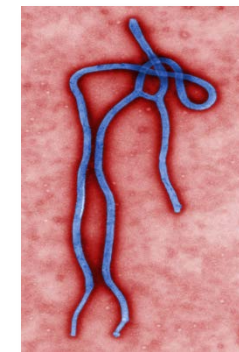
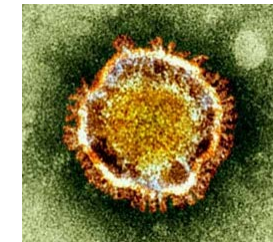
Vector-borne disease and NTDs



Wildlife epidemiology (e.g. rabies)



Emerging diseases and rapid response



- Short-term forecasts of SARS-CoV-2
 - Global forecast of deaths
- Mobility and transmission
 - Correlations between R_t and digital mobility measures
- Variant of concern
 - Estimating transmission advantage of new variant(s) of concern

Overview

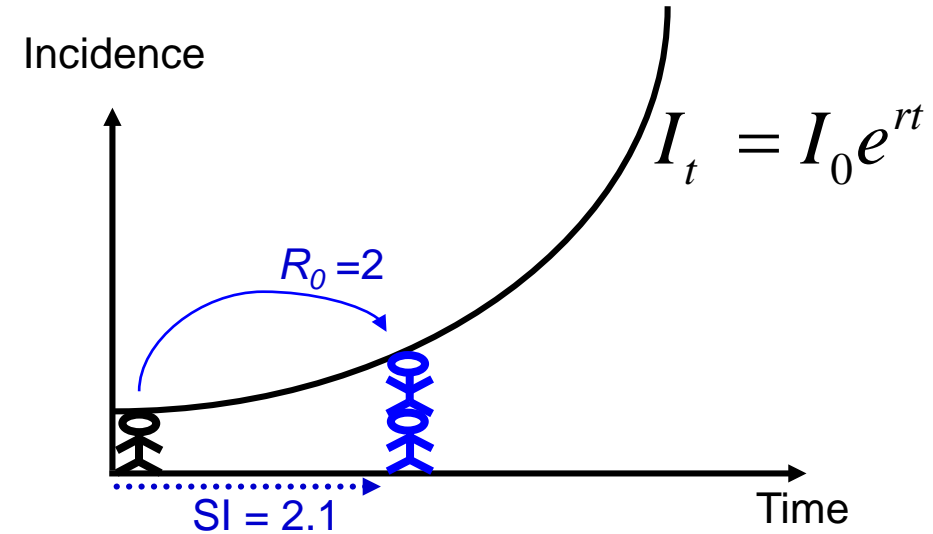
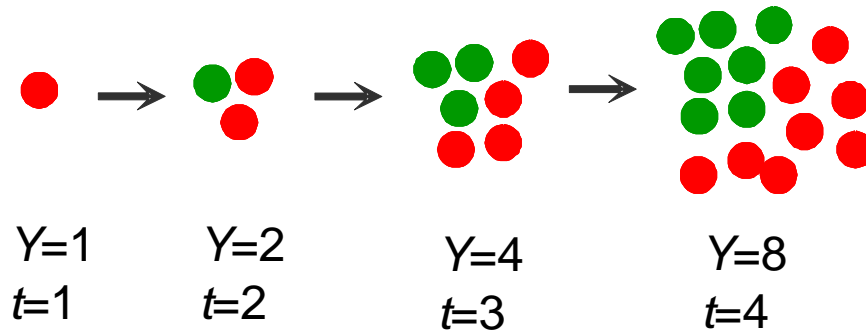
Quantitative Epidemiology: intersection between maths, statistics and ID epidemiology

Characterising the potential transmissibility of a pathogen:

- Basic reproduction number R_0 : average number of secondary cases generated by an index case in a large entirely susceptible population.



Contagion

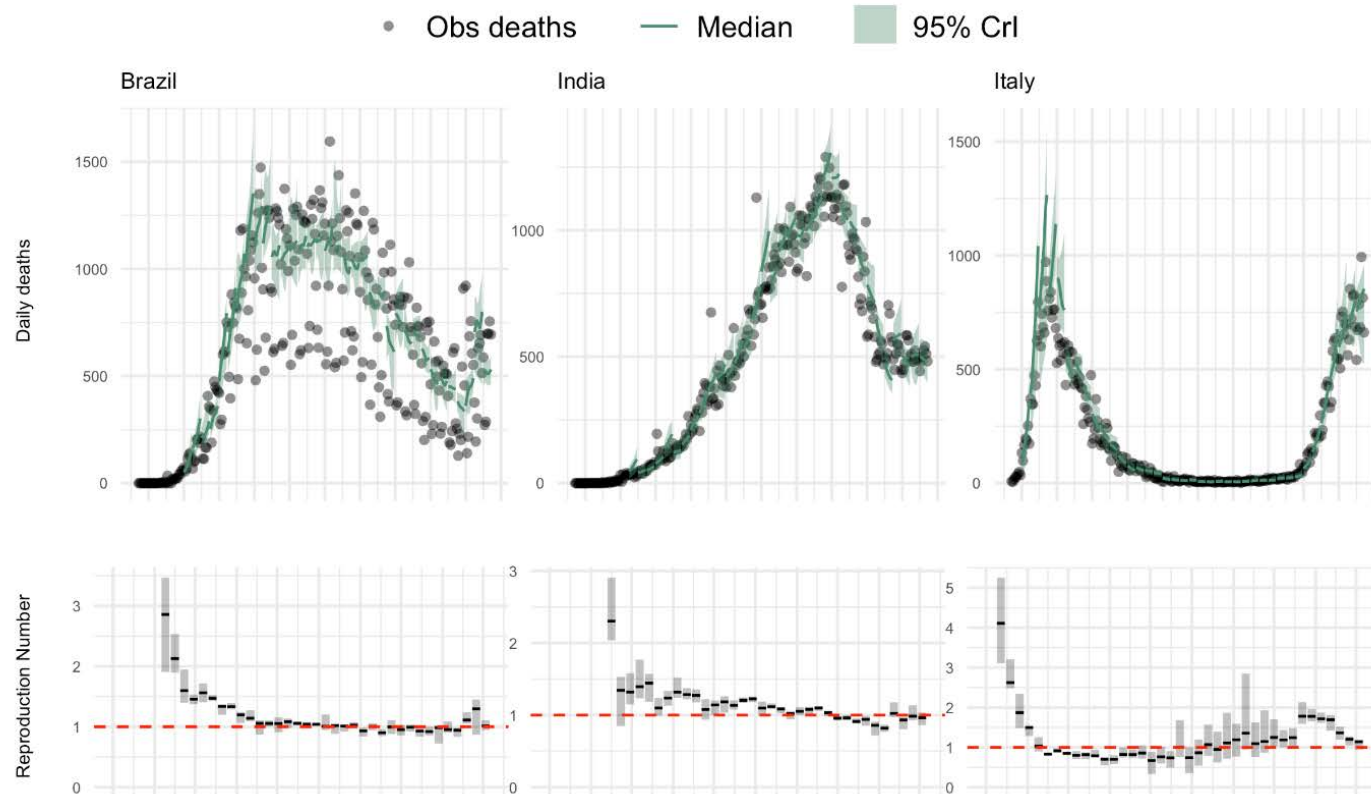


Formally, renewal equation (branching process):

$$I_t = \mathcal{P} \left(R_t \sum_{s=0}^t [I_{t-s} w_s] \right)$$

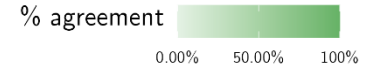
Short-term forecast of SARS-CoV-2

- Weekly report on trends across various countries with sustained transmission;
 - Up to 80 countries included,
 - Releasing since 8th March 2020, contribute to other forecasting effort (Reich Lab, European COVID-19 Forecasting Hub, etc.)

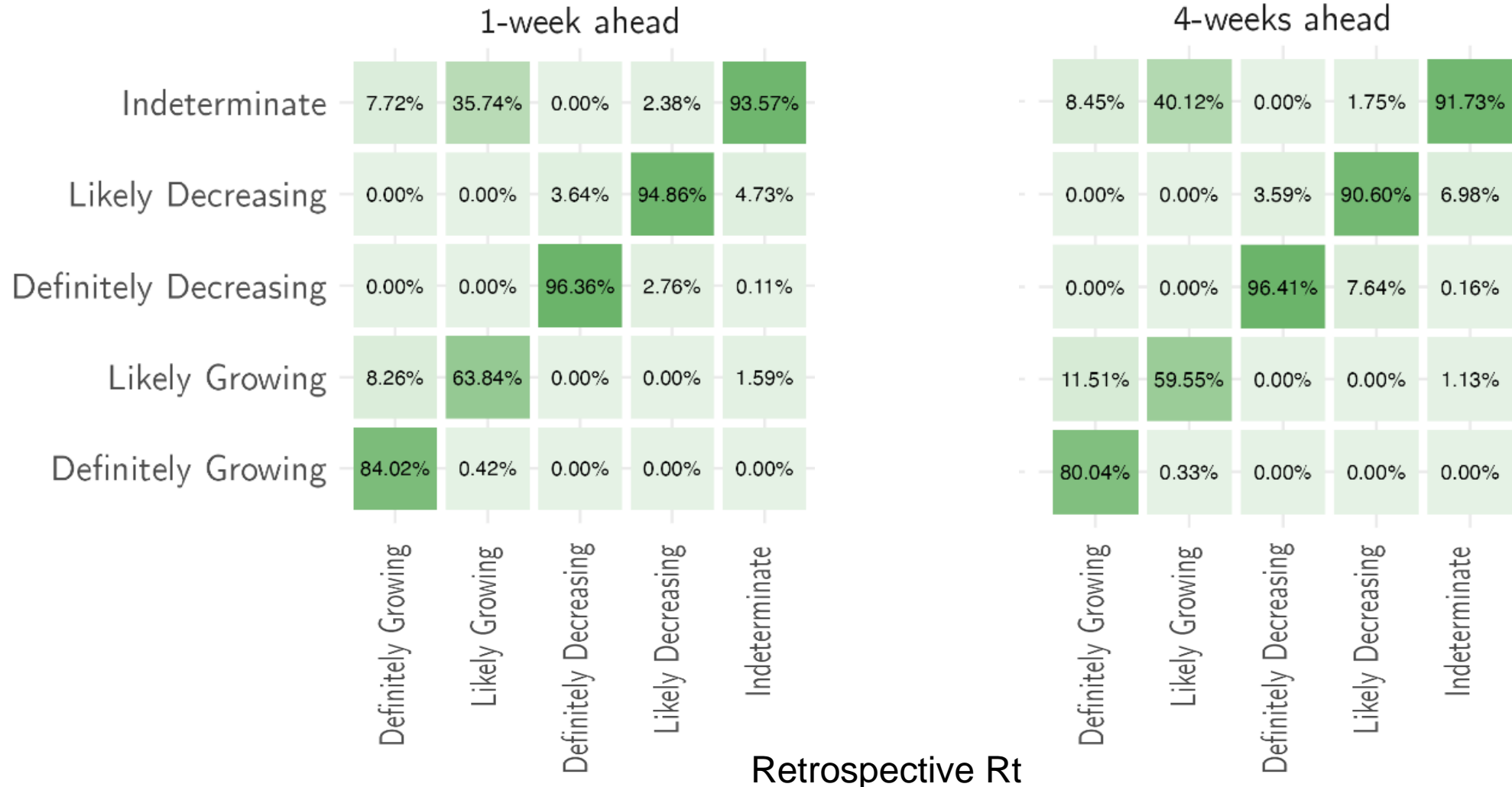


Short-term forecast of SARS-CoV-2

- Can reliably predict the general trends?



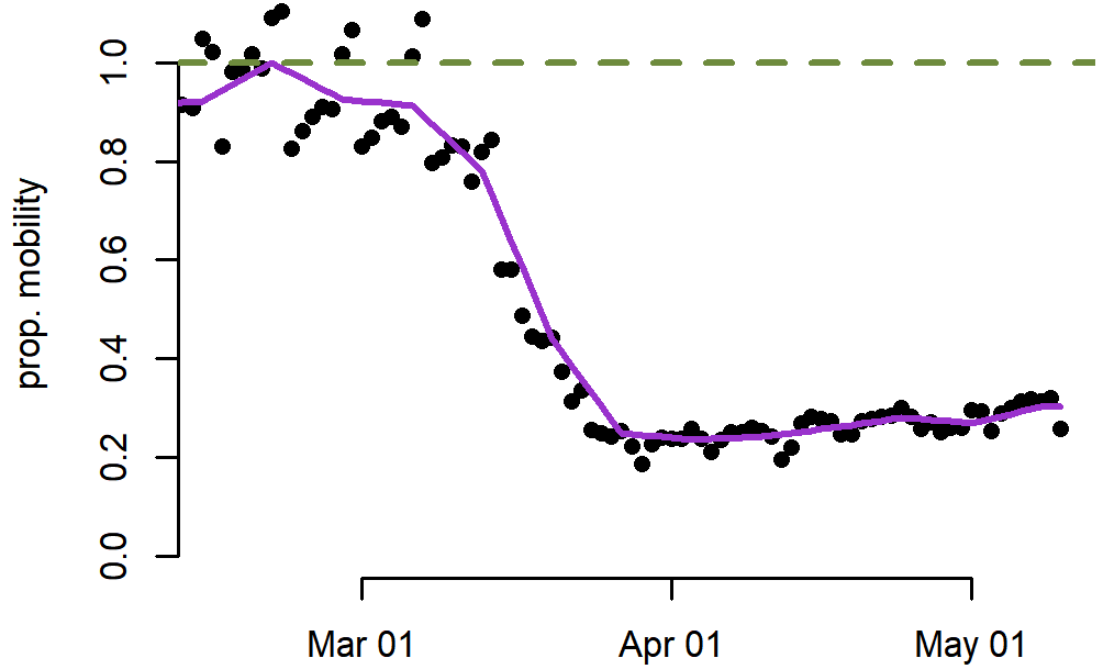
Forecasted Rt



General conclusions

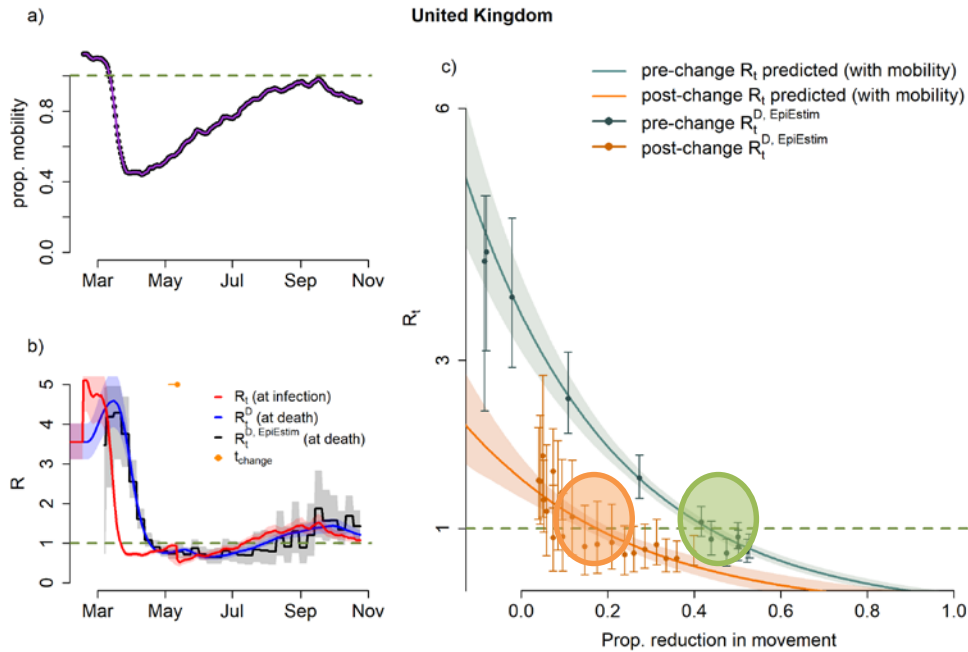
- Simple approach to predictions: allows global analysis
- Applicable to other infectious diseases
- Relatively accurate predictions

Mobility analysis

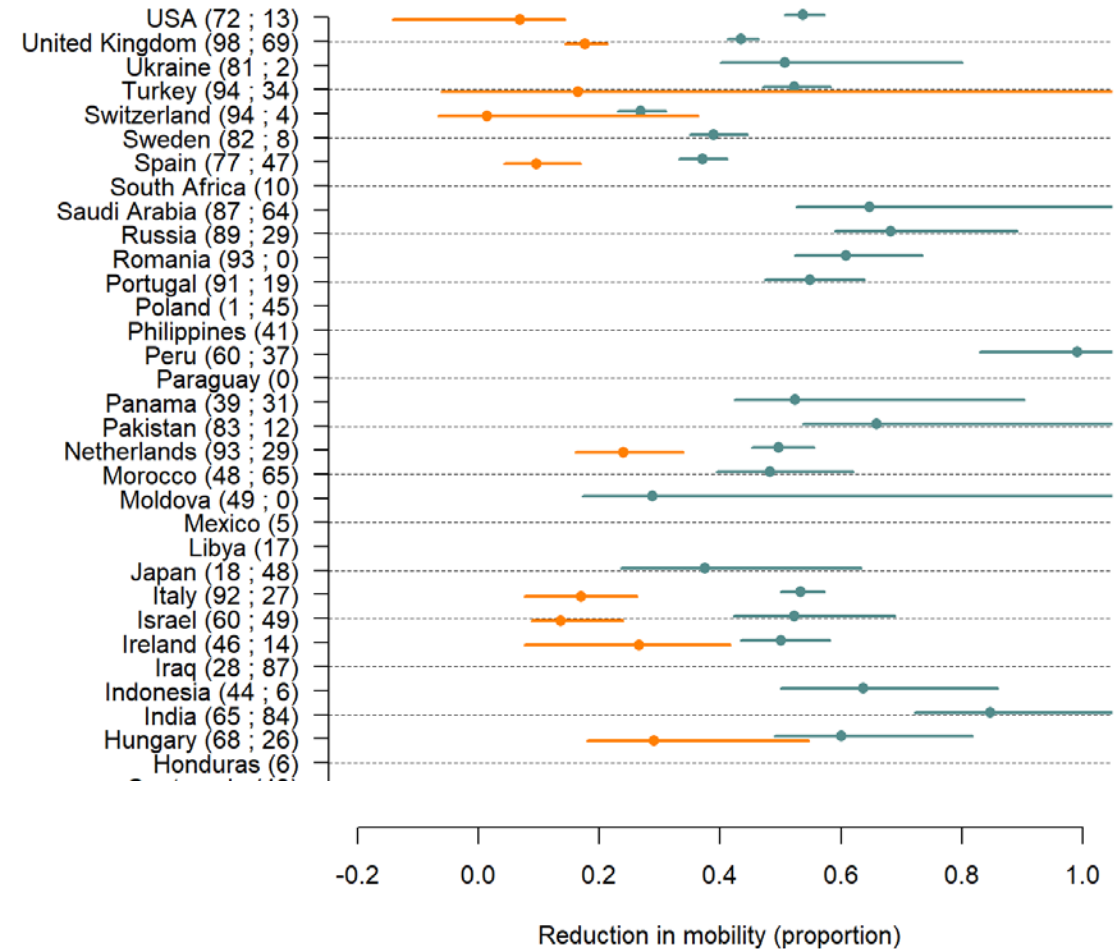


Mobility analysis

- Mobility analysis
 - Correlations R_t and digital mobility measures



Mobility threshold(s)



Mobility analysis

General conclusions

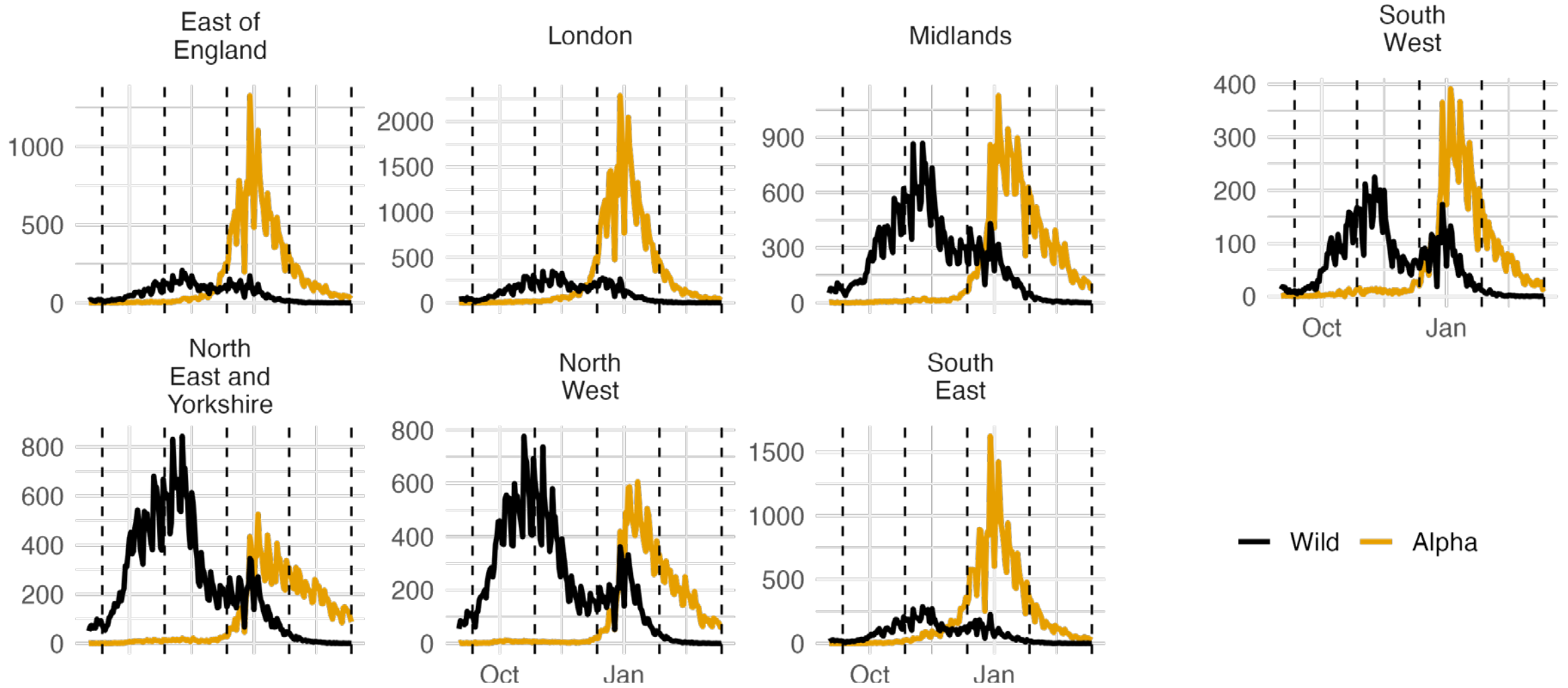
- Strong correlation between transmission and mobility
 - Initially, mobility explained ~75% of variation in R_t
 - Then, observed decoupling/dampening of the correlation
 - ~ the second wave, mobility explained ~30% of variation in R_t
- Allows some predictions of level of mobility restrictions required to achieve control
- Decoupling – dampening of the relationship may reflect:
 - Implementation of alternative control
 - Compliance with social distancing behaviour while increasing mobility
 - Difficulties in using for forecasting purposes as relationship is dynamic

Transmission advantage of variant(s)

- New variants of concern:
 - Alpha, beta, gamma and delta; all appear to have increased transmissibility
- Tool for real-time estimation of transmissibility
 - New extended existing framework to estimate R_t in multiple locations as well as transmission advantage of variant(s)

Transmission advantage of variant(s)

- Example of England; wild type and invasion of alpha variant

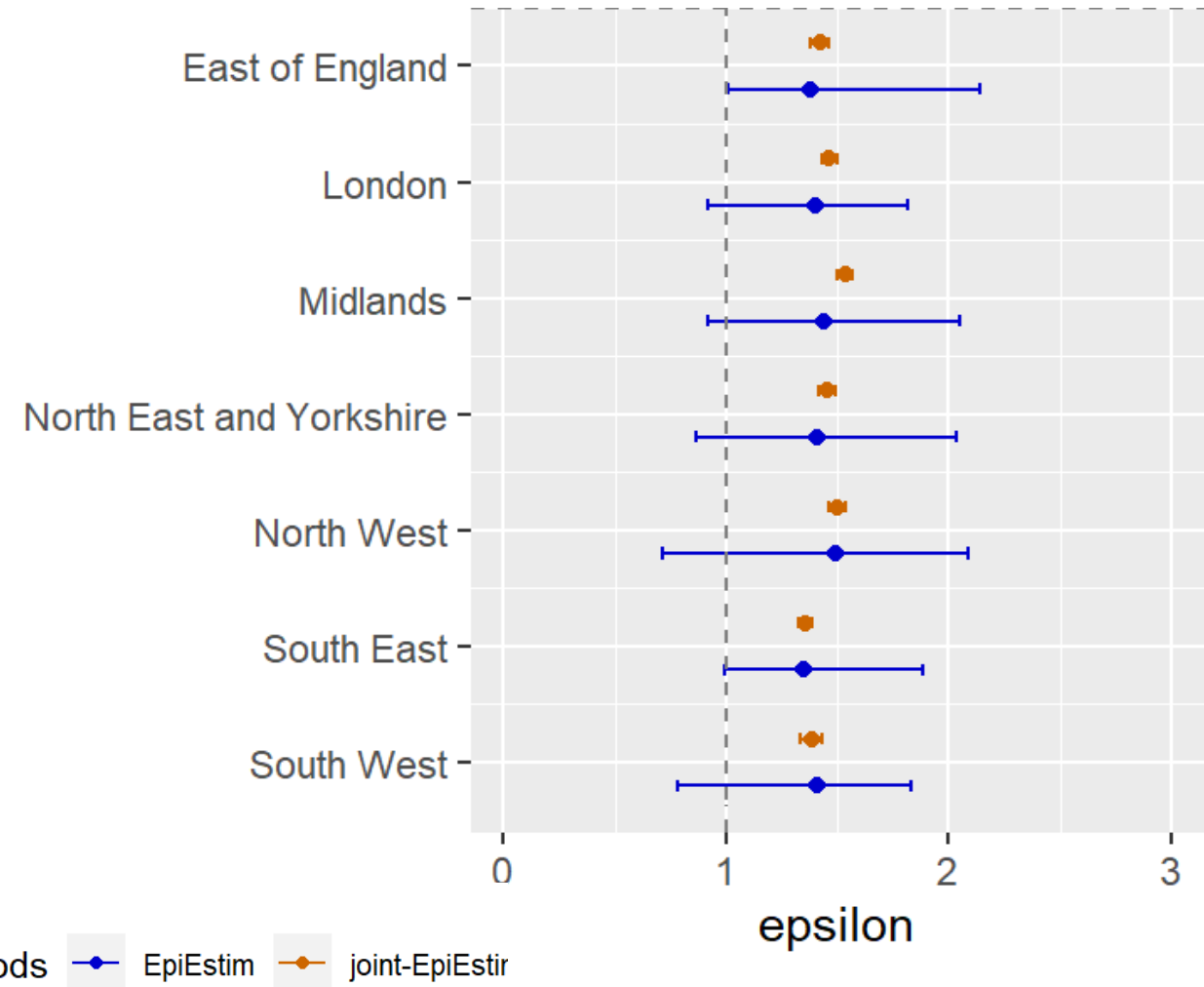


Transmission advantage of variant(s)

- Example of England; wild type and invasion of alpha variant

- MV-Epiestim

- Bring real-time estimation within a single framework
- Pool information by assuming common a local trend in transmissibility within locations, common transmission advantage across locations



Transmission advantage of variant(s)

- Example of England wild type and invasion of alpha variant
- Tool for real-time estimation of transmissibility
 - Takes advantage of pooling information
 - Applicable to multiple variants co-circulating (wild + >1 variants)
 - Applicable in real-time
 - Applicable to other infections with recurrent variants' emergence
- E.g. was applied to estimate delta variant transmission in England, as well as wild, alpha and beta/gamma variants in France.

Thanks
