Household model

**Methods**

Key assumptions:

* Each household infected once
* Precompute typical household dynamics
* Solve household dynamic
* Transmission rate between household is the same regardless of household size, BUT, larger households are infectious longer.

**Models**

***Deterministic model within household once index case appear:***

With:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Susceptible in household of size ‘i’ |  | Within household transmission | Estimated  Constant throughout |
|  | Exposed in household of size ‘i’ |  | Inverse of mean exposed period | 1/4 |
|  | Infectious (will survive) in household of size ‘i’ |  | Inverse of mean infectious period | 1/4.5 |
|  | Infectious (will die) in household of size ‘i’ |  |  | 0.01 |
|  | Those who will die and are hospitalised in household of size ‘i’  No transmission here  We don’t need to track those hospitalised who survive |  | Hospitalisation period prior to death | 1/(18.5-4-4.5)  18.5: delay infection-death |
|  | recovered in household of size ‘i’ |  |  |  |
|  | deaths in household of size ‘i’ |  |  |  |

***Deterministic model between households:***

Start with I0 infected households:

With:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Susceptible in household of size ‘i’ |  | between households transmission | Estimated  weekly values within interpolation |
|  | Exposed in household of size ‘i’ |  | Inverse of mean exposed period (as for within model) | 1/4 |
|  | Infectious (will survive) in household of size ‘i’ |  | Inverse of mean infectious period of a household | Derived from solving the within household model |
|  | recovered households of size ‘i’ |  |  |  |

From ONS data, household size in UK:

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Household size | 1 | 2 | 3 | 4 | 5 | 6 |
| Number of households | 8197000 | 9609000 | 4287000 | 3881000 | 1254000 | 597000 |

**MCMC**

Fitting the model to:

* Aggregated death data

Allows overdispersion.

Use an MCMC to infer:

* One constant within household transmission rate
* Weekly between household transmission rates (with linear interpolation)

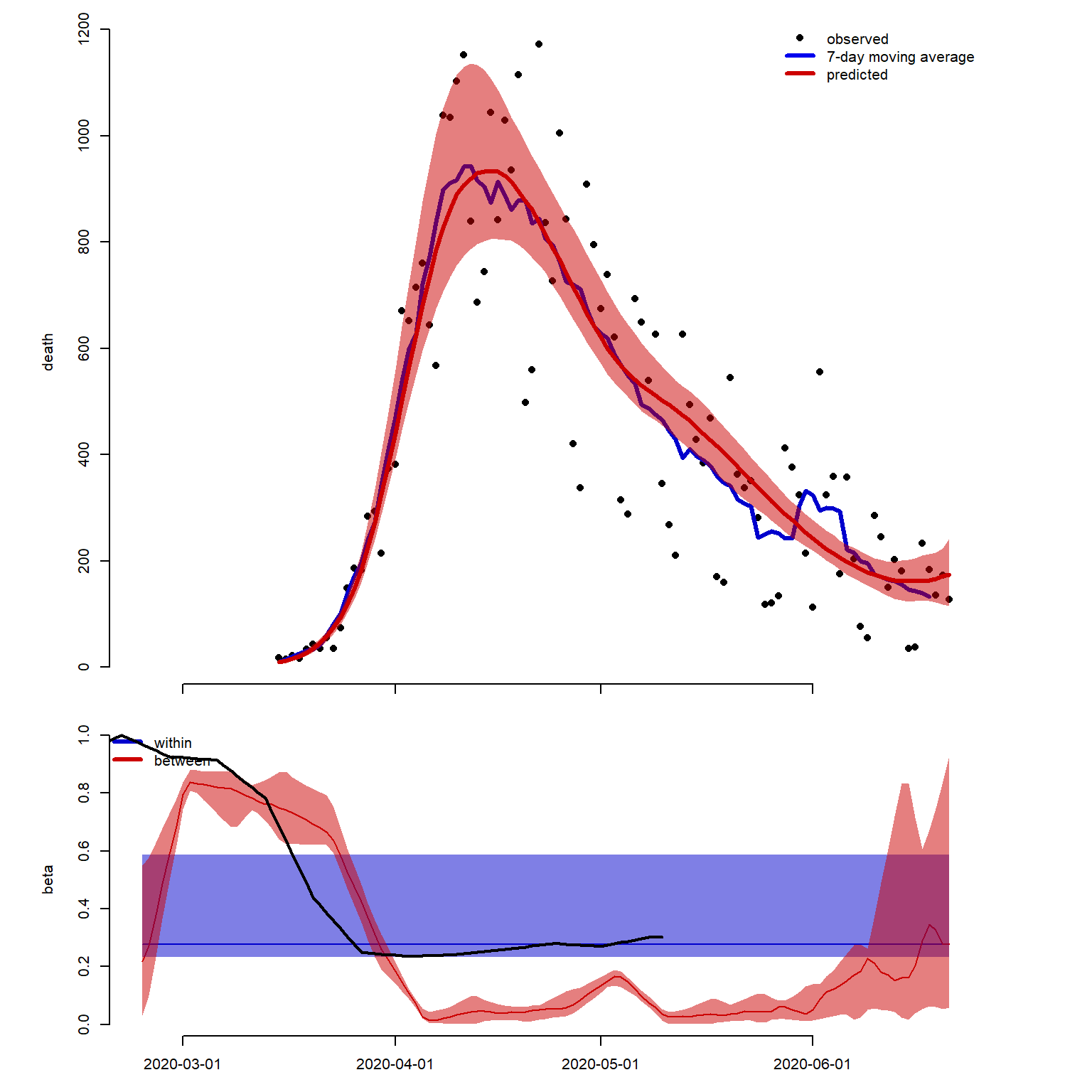


Figure1:

Upper panel: incidence of death in the UK. Black dots: reported deaths, blue line: 7-day moving average, red line/band: predicted incidence and 95%CrI.

Transmission within (blue) and between (red) households (medians and 95%CrIs). Also plotted as an indication in black: google mobility (mobility is not used in the model/inference).

Apparent delay in reduction of between household transmission may reflect too simplistic delay (introducing more compartment to simulate gamma-like distribution might improve this aspect).

*From the framework, we can extract:*

* How many households are affected any time
* The secondary attack rate within household

Every outputs can be specific for household size.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Household size | 2 | 3 | 4 | 5 | 6 |
| Median | 0.63 | 0.59 | 0.56 | 0.54 | 0.52 |
| Lower 2.5% | 0.55 | 0.5 | 0.46 | 0.43 | 0.41 |
| Upper97.5% | 0.92 | 0.91 | 0.91 | 0.91 | 0.91 |

Clearly, we need more info as 2ndary attack rate seems too high?

***Some discussion point:***

In term of model:

* **Need stochasticity?** Perhaps not, given large number of households?
* **Age specific?**
* **Subnational analysis as transmission became much more local during lockdown, and will (hopefully) remain local in the future?**
* **Include care home as a ‘special’ household type?**
* **Break assumption of single index infection per households?**

Implementing all this would almost be equivalent of explicitly modelling each household? Micro-simulation model?

To a large extend, increasing model complexity depend on:

* Question addressed
  + Which in turns, depend on availability of data to fit the model…

In term of data:

* Fit to household sero-surveys? E.g. ONS Infection Survey pilot?