Block 2.4: The TSIR model and model validation

Objectives in this section

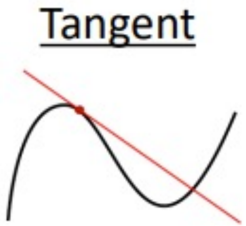
- Models can be used to quantitatively interpret data.
- Data can be used to set parameters in models.
- Probability gives us guiding principles for comparing models and data.
- Incorporating sources of uncertainty into models gives them flexibility but it also gives us a lot of new model considerations.

The TSIR model applied to England and Wales

The TSIR model is a natural modification of the chain-binomial.

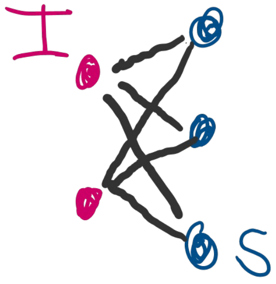
$$
\begin{aligned}
I_t &= \beta_{t-1} S_{t-1} I_{t-1}^{\alpha} \varepsilon_{t-1}, \\
S_t &= S_{t-1} + B_{t-1} - I_t, \\
C_t &\sim \text{Binomial}\{I_t, r_t\}
\end{aligned}
$$

- Finkenstadt and Grenfell 2000 is a key paper introducing this model.
- The choice of time step as 2 weeks is practical based on the data but also related to **equating incidence and prevalence in the model.**

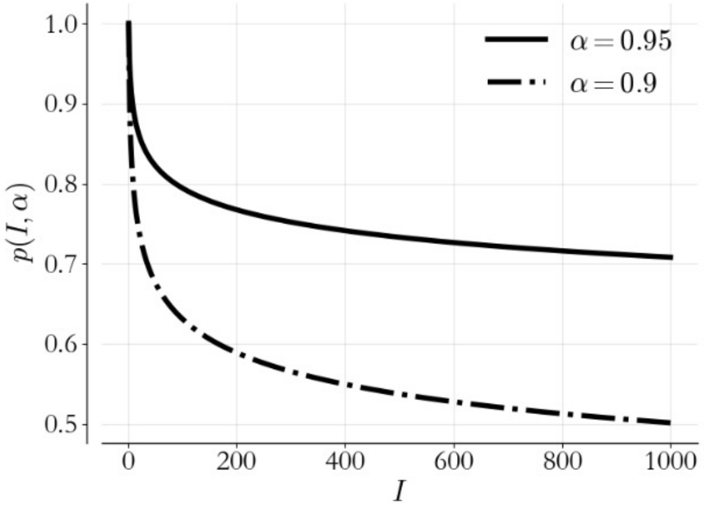


You'll read often that the α **exponent models "network effects"**.

- The exponent is pragmatic – models with it outperform models with α set to 1.

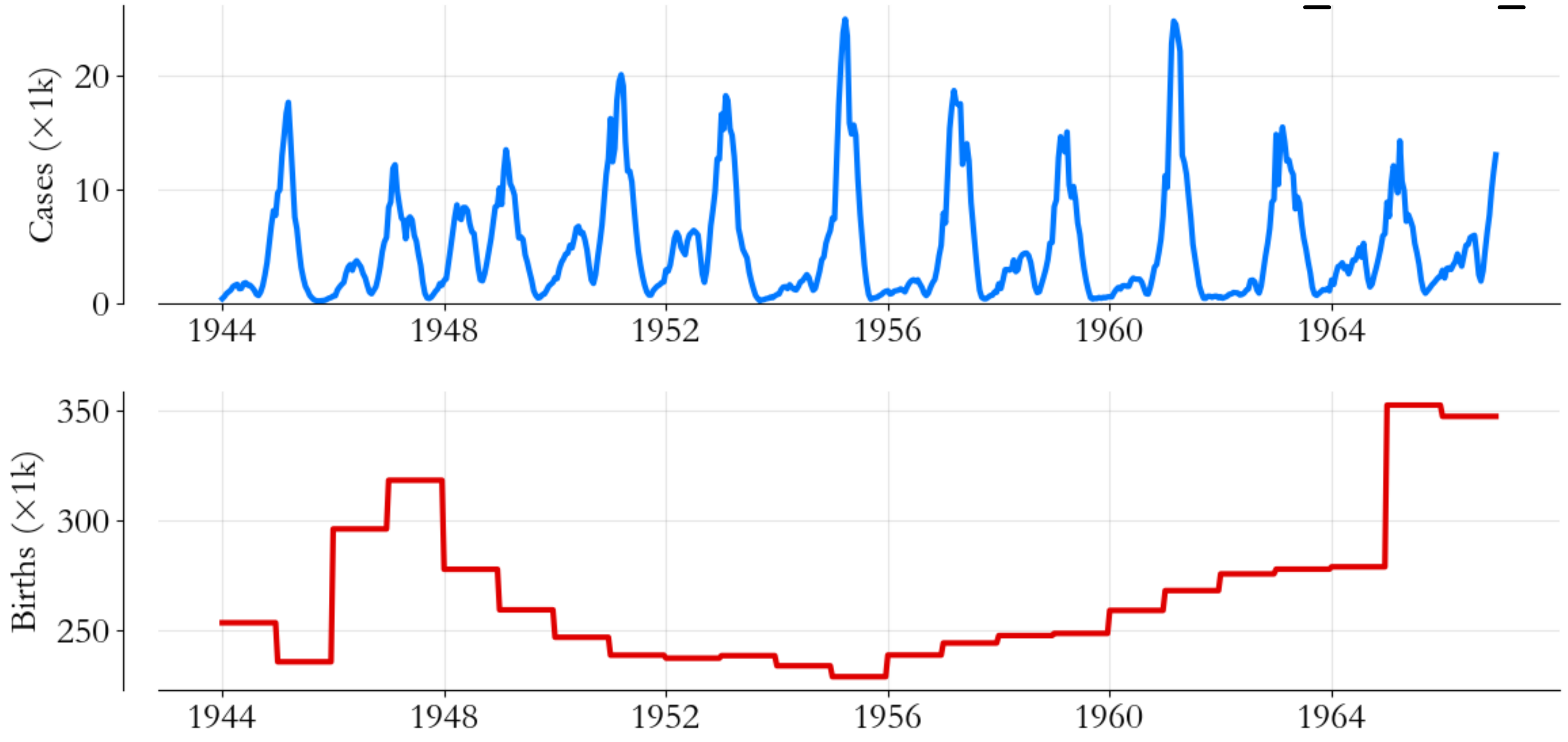


$$
\mathbf{A} = \begin{bmatrix} a_{11} & a_{12} & a_{13} & \dots & a_{1I} \\ a_{21} & a_{22} & a_{23} & \dots & a_{2I} \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ a_{S1} & a_{S2} & a_{S3} & \dots & a_{SI} \end{bmatrix}
$$



- All edge weights a_{ij} = 1 implies $S \times I$ edges.
- If for each j, a_{ij} = 1 with probability p, a_{ij} = 0 otherwise, then we expect $SI \times p$ edges.
- We can choose $p(I, \alpha) = 1/I^{1-\alpha}$

UK_measles_data.csv



$$
\begin{aligned}
I_t &= \beta_{t-1} S_{t-1} I_{t-1}^{\alpha} \varepsilon_{t-1}, \\
S_t &= S_{t-1} + B_{t-1} - I_t, \\
C_t &\sim \text{Binomial}\{I_t, r_t\}
\end{aligned}
$$

If you want to install Python:
https://www.anaconda.com/download

Let’s write some (pseudo)code

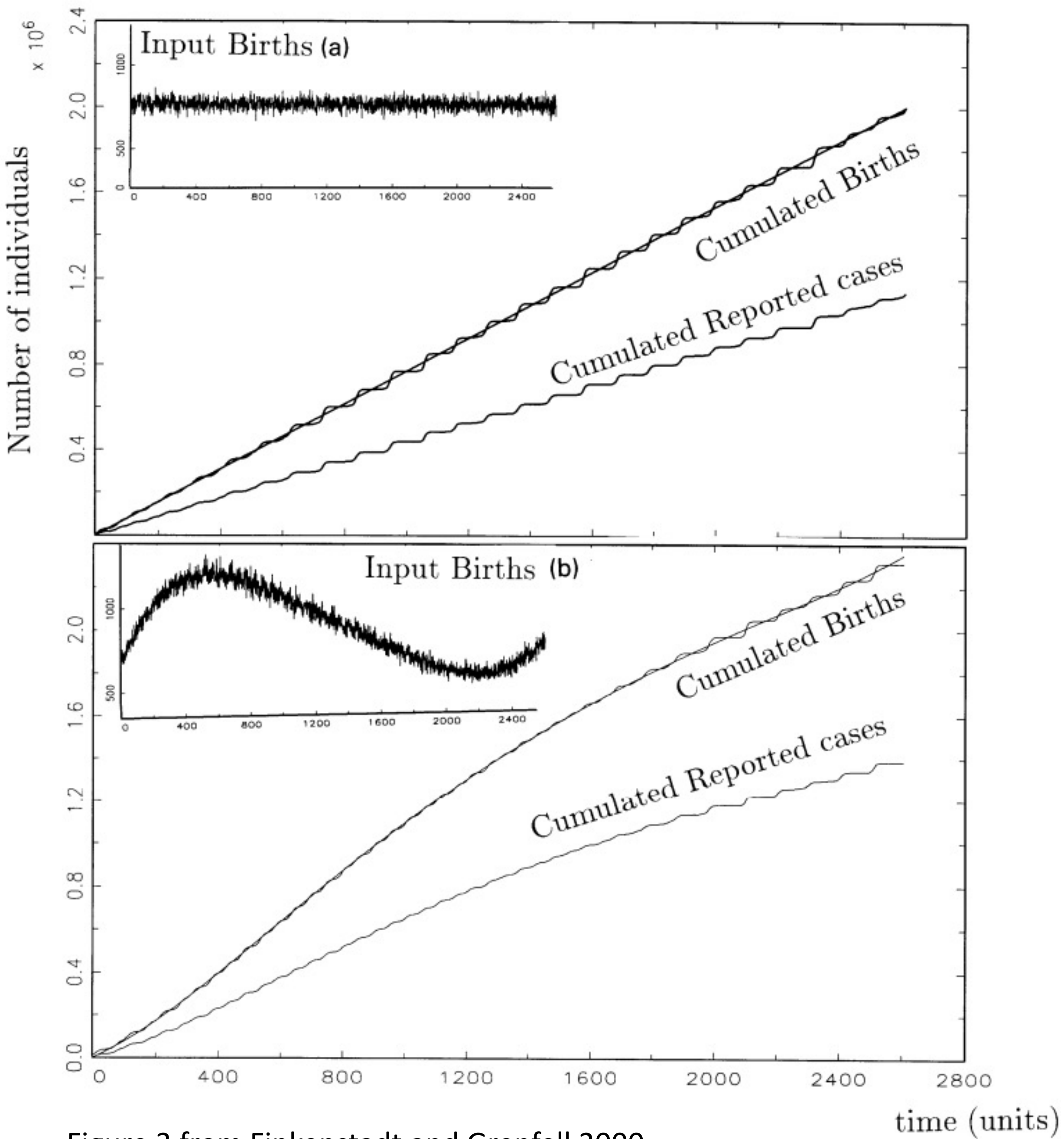


Figure 3 from Finkenstadt and Grenfell 2000

Let's write some (pseudo)code

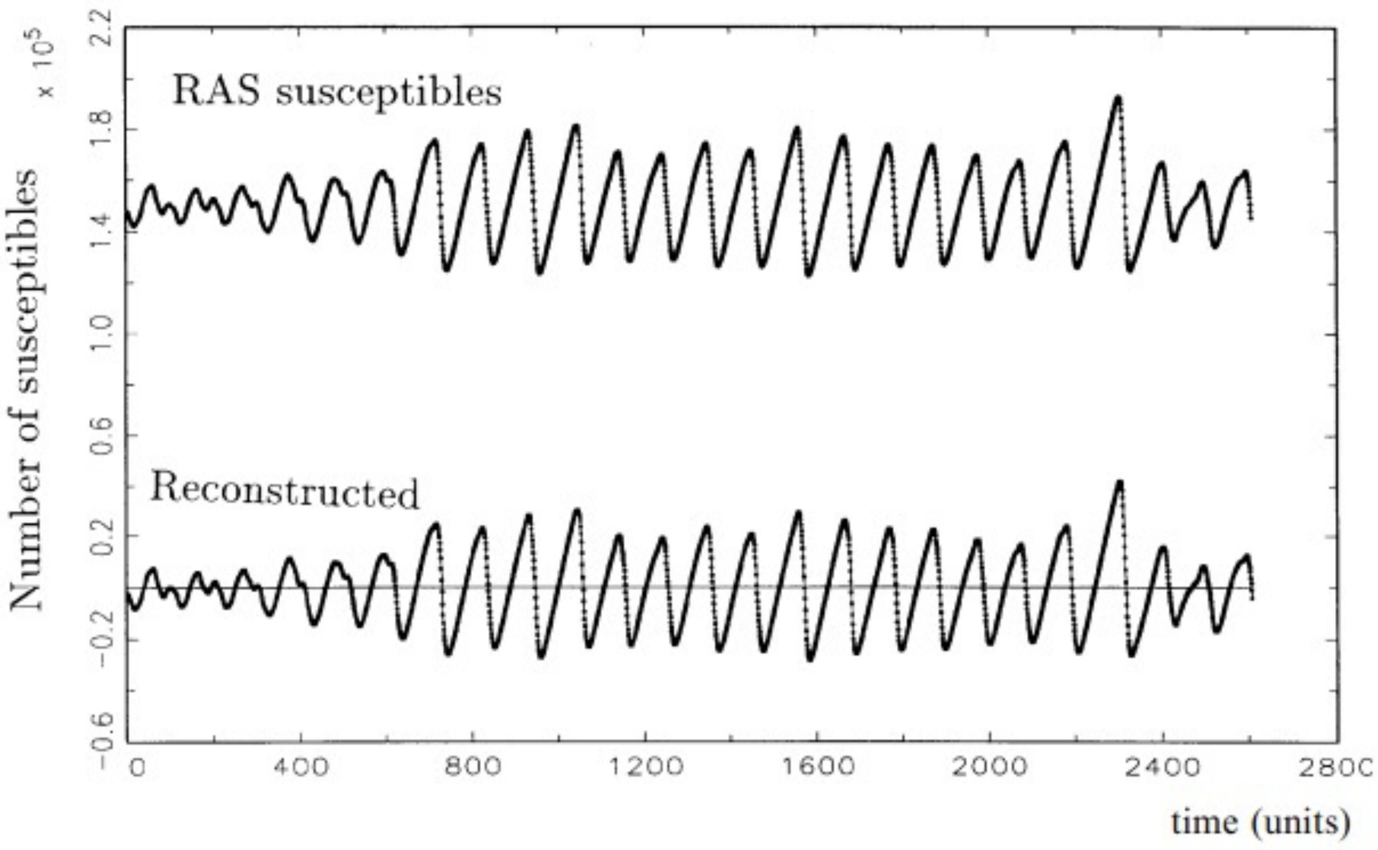
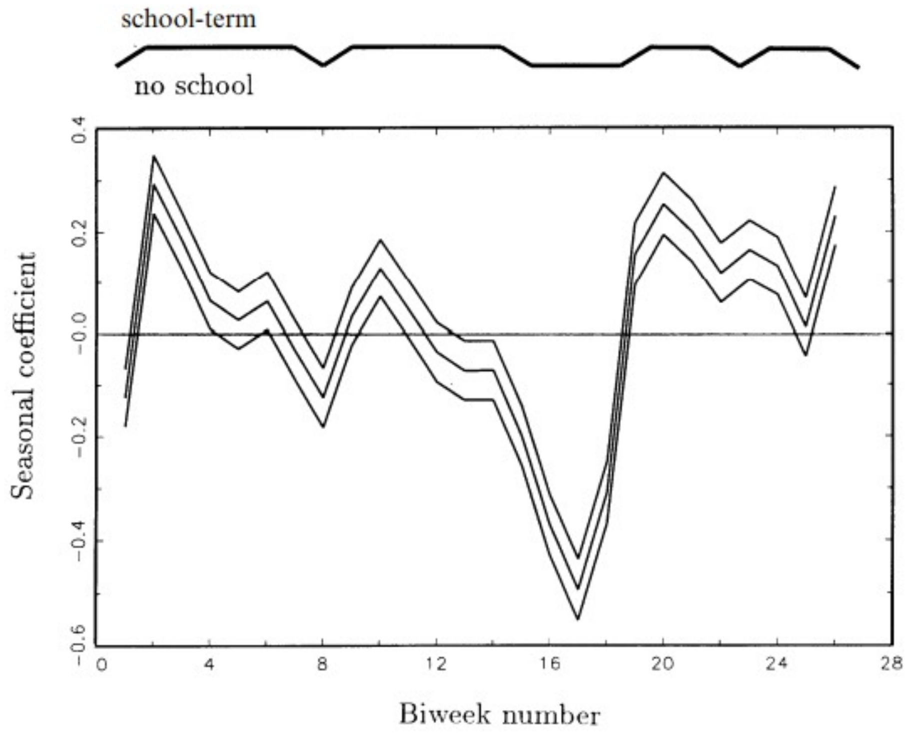
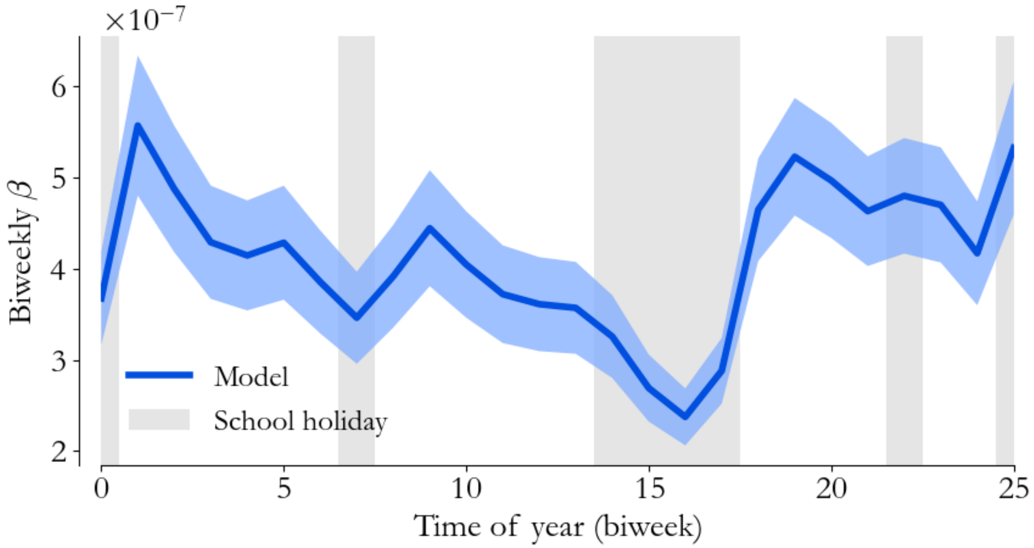
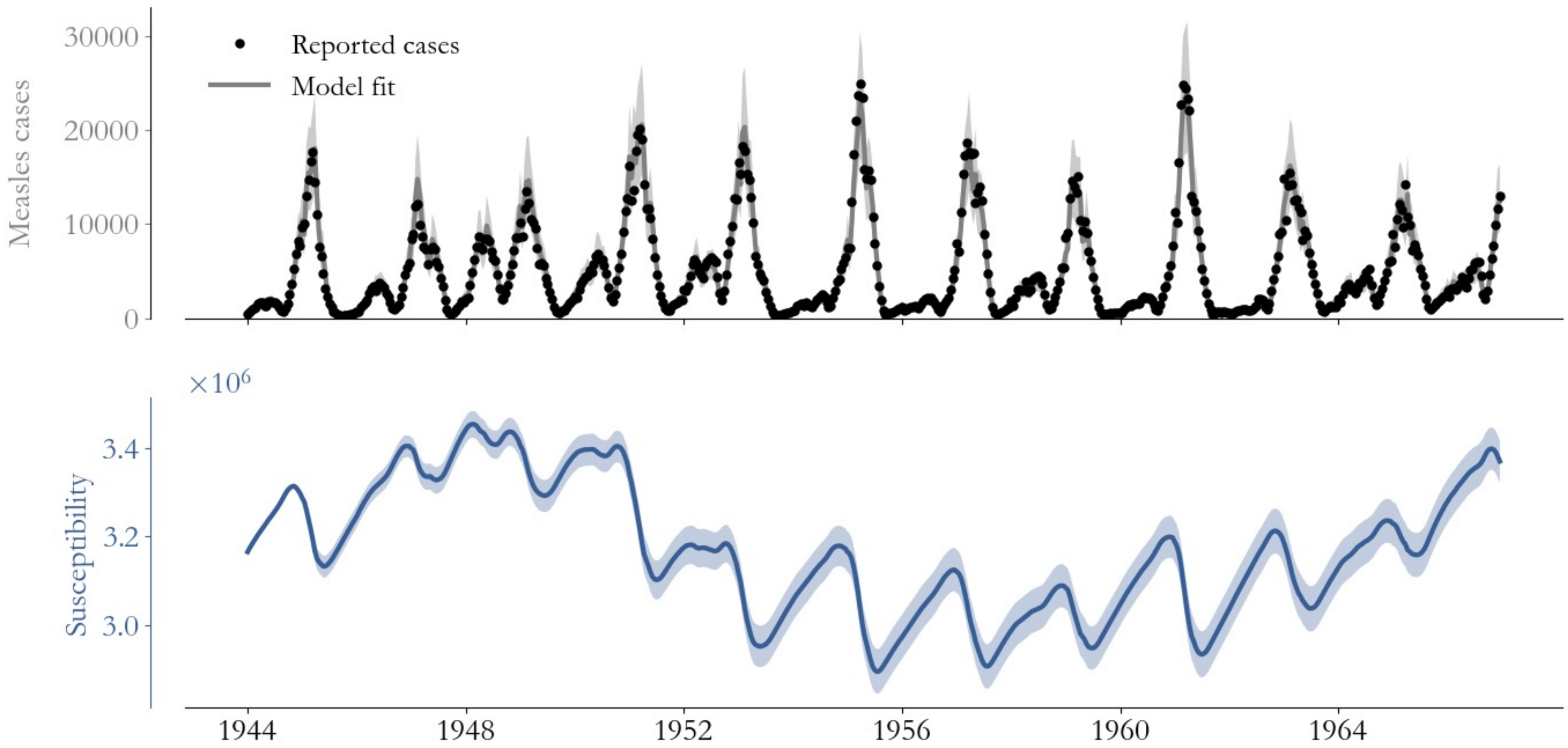


Figure 4 from Finkenstadt and Grenfell 2000





Let’s write some (pseudo)code

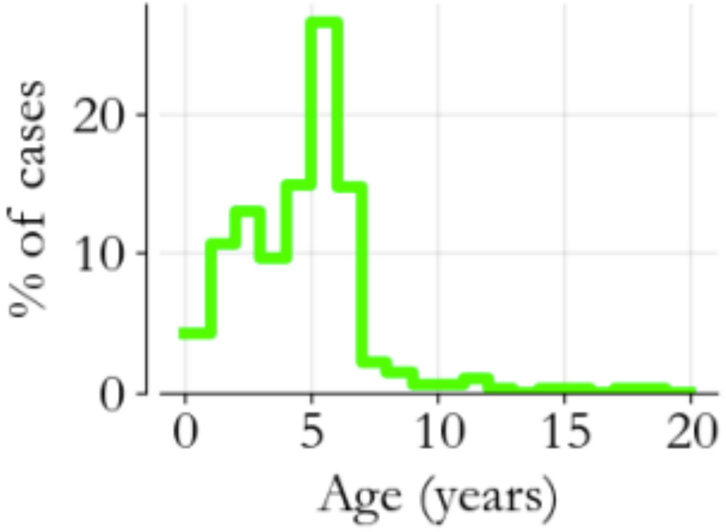


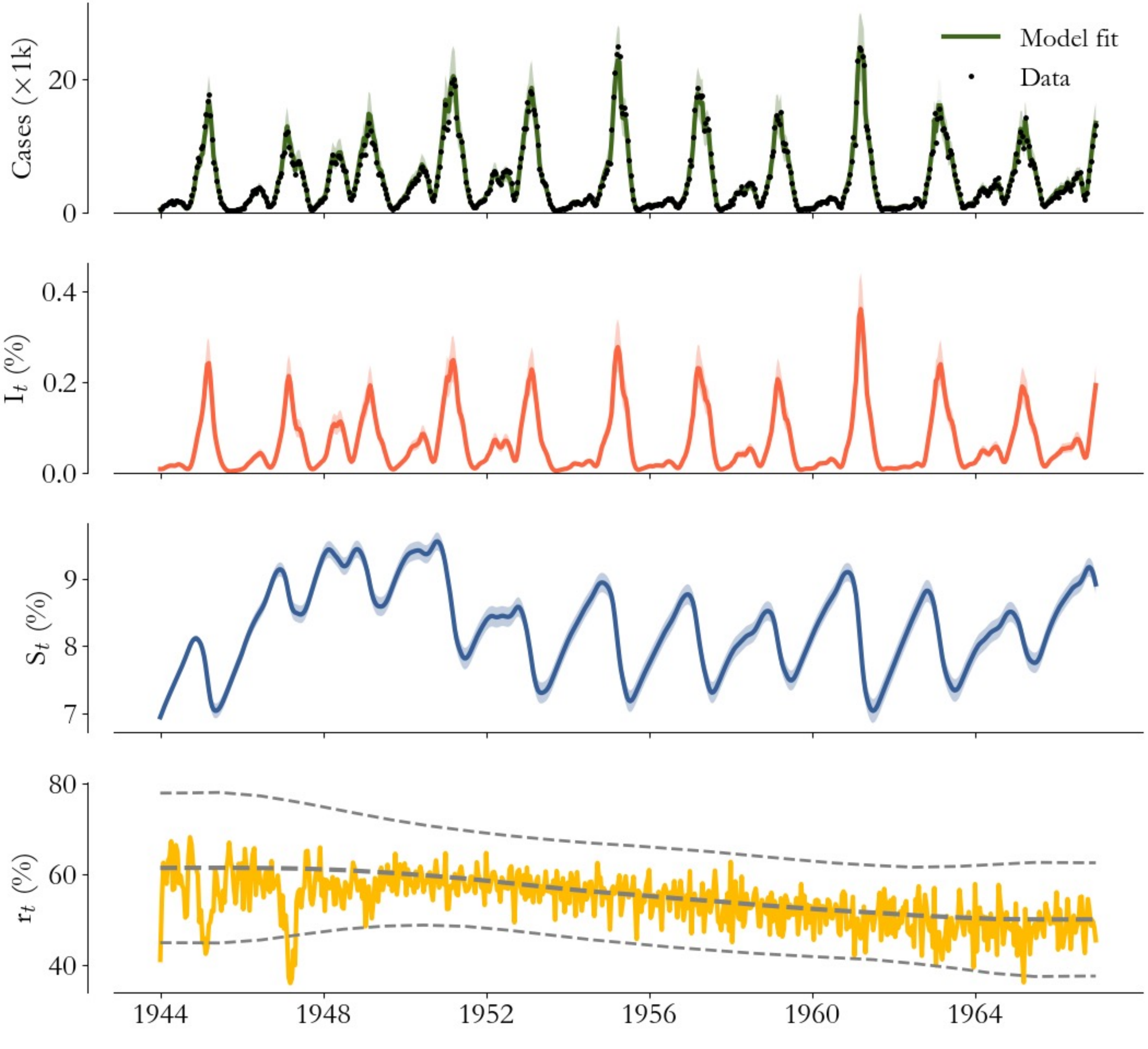
$$I_t = \beta_{t-1} S_{t-1} I_{t-1}^{\alpha} \varepsilon_{t-1},$$
$$S_t = S_{t-1} + B_{t-1} - I_t,$$
$$C_t \sim \text{Binomial}\{I_t, r_t\}$$

How do we validate a model like this?

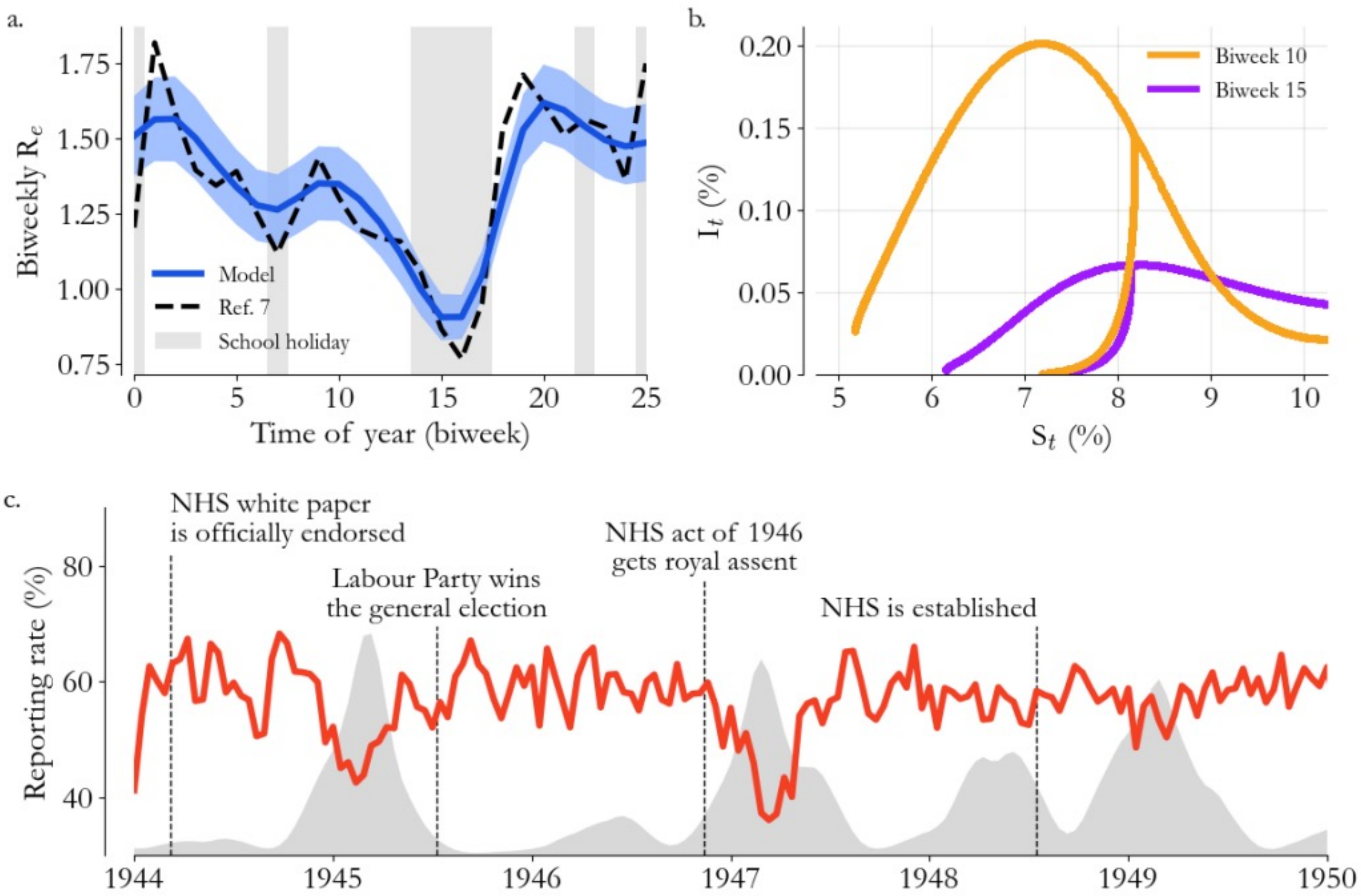
Using a similar approach and some more data we create a more sophisticated model

$$\mathcal{L}(\beta_t, \varepsilon_t, \alpha, r_t, S_0) = \frac{26T-1}{2} \ln \hat{\sigma}_\varepsilon^2 + \frac{(S_0 - \mathrm{E}[S_0])^2}{2\mathrm{V}[S_0]} + \sum_t \frac{(r_t - \mathrm{E}[\tilde{r}_t])^2}{2\mathrm{V}[\tilde{r}_t]}$$





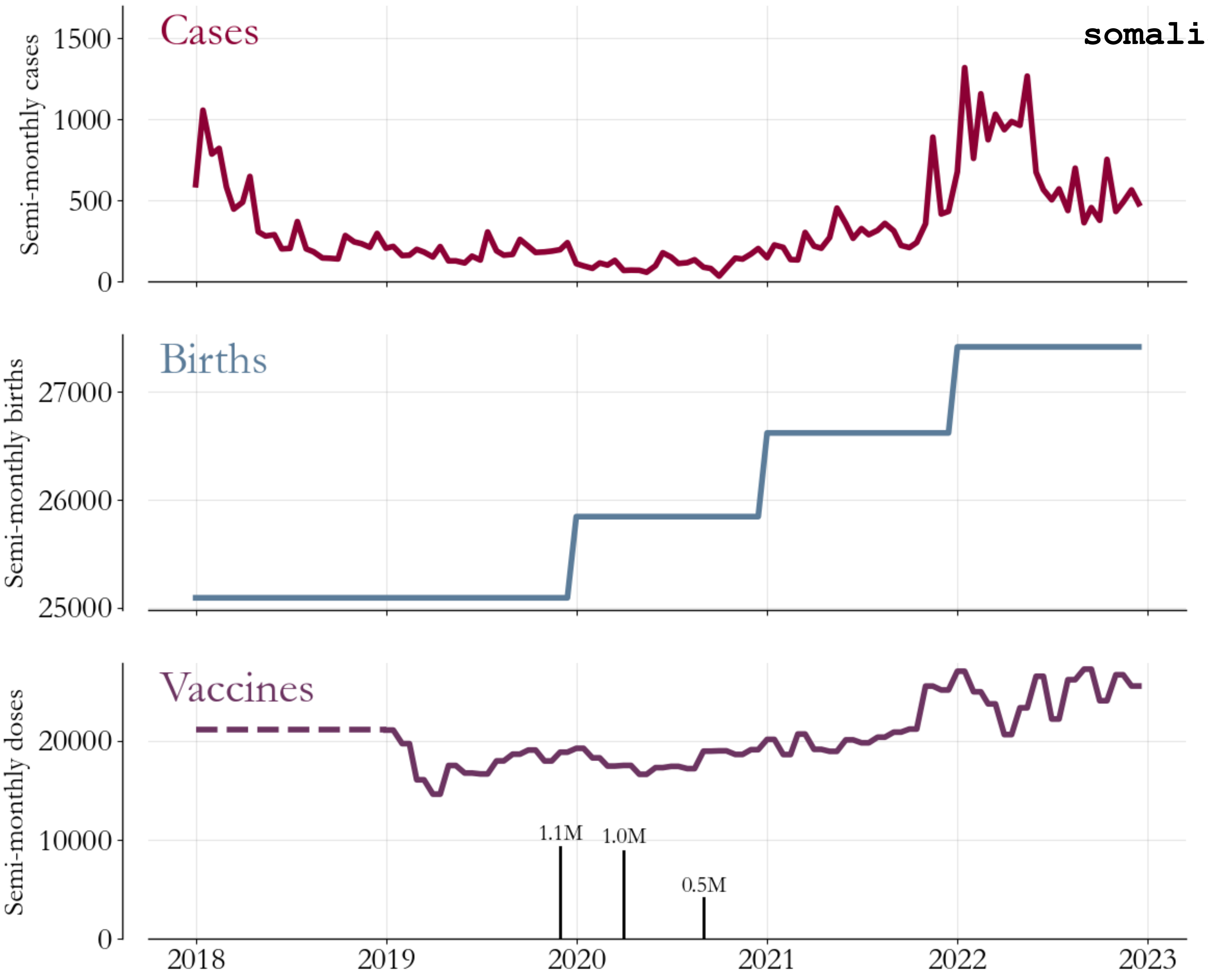
https://arxiv.org/pdf/2202.11222.pdf



Quantities that are difficult to estimate are then difficult to validate!

The TSIR model applied to SIA impact estimation in Somalia

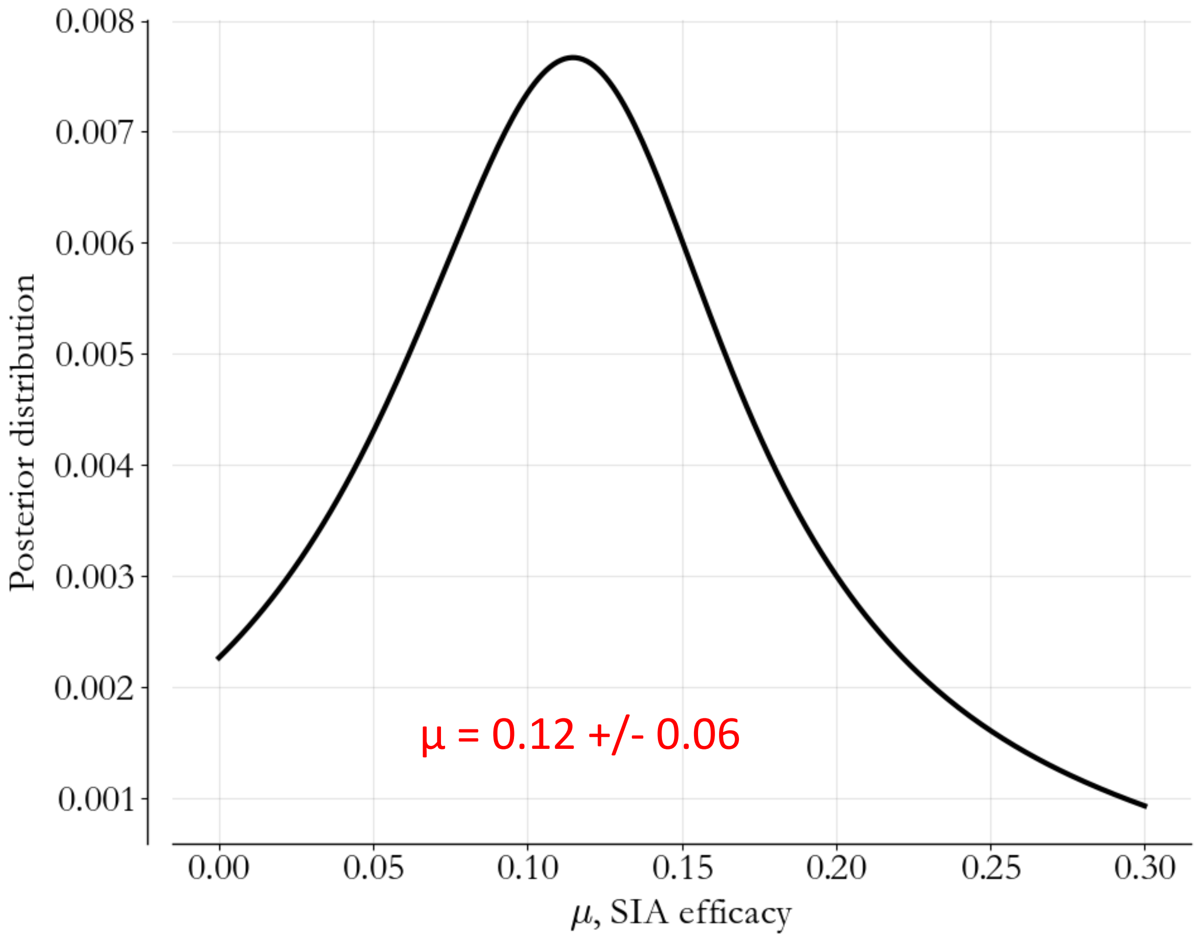
`somalia_synthetic_dataset.csv`

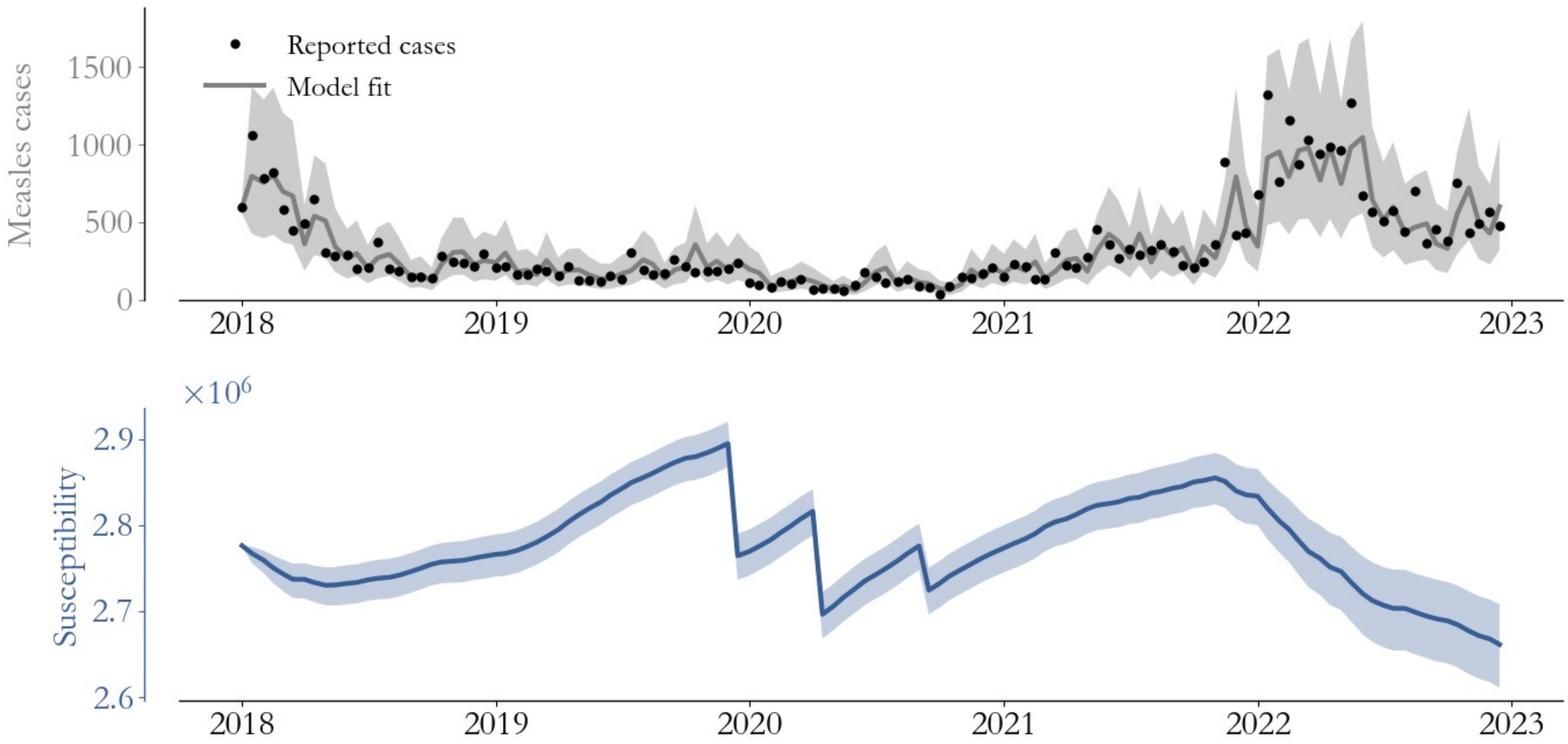


$$I_t = \beta_{t-1} S_{t-1} I_{t-1}^{\alpha} \varepsilon_{t-1},$$
$$S_t = S_{t-1} + B_{t-1} - I_t,$$
$$C_t \sim \text{Binomial}\{I_t, r_t\}$$

How do we incorporate the 2 sources of vaccine?

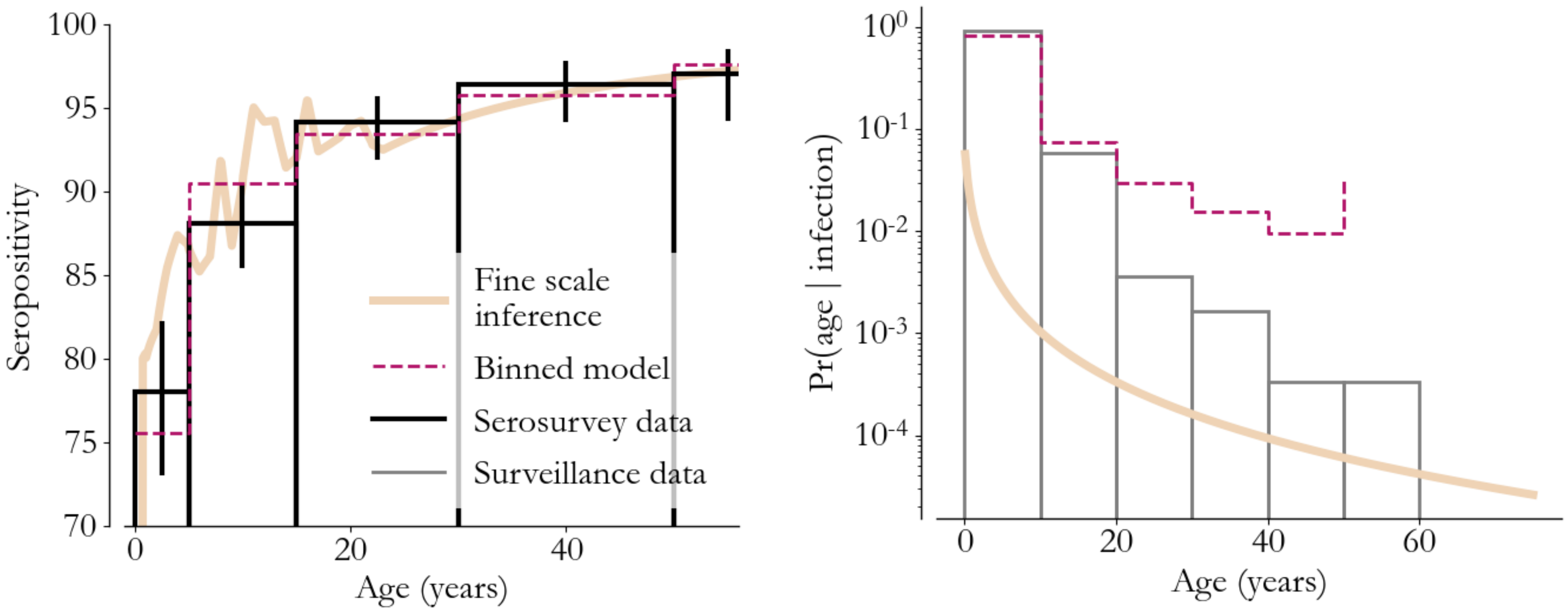
Let’s write some (pseudo)code





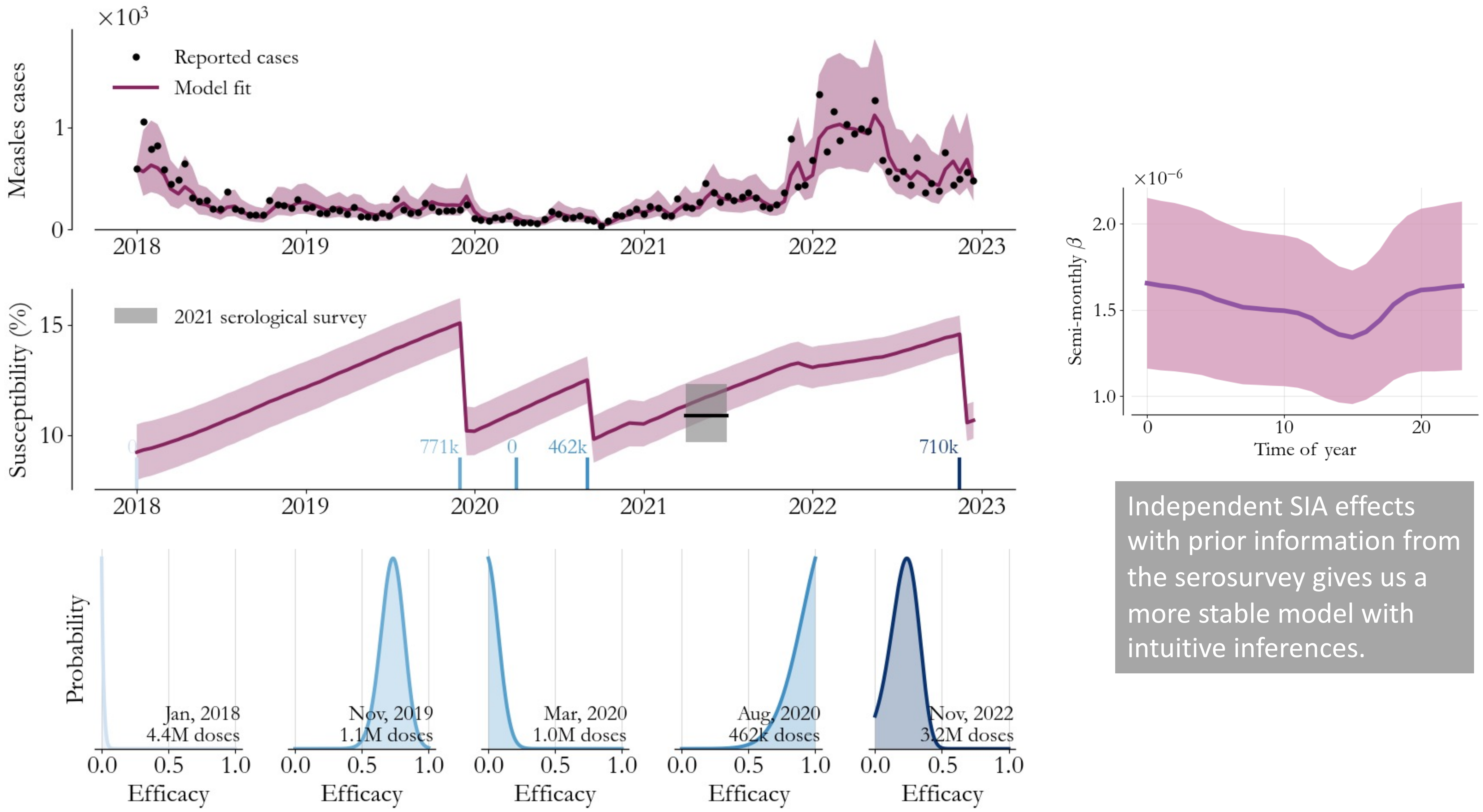
How do we validate a model like this?

We can again incorporate age information, this time from a serological survey in 2021



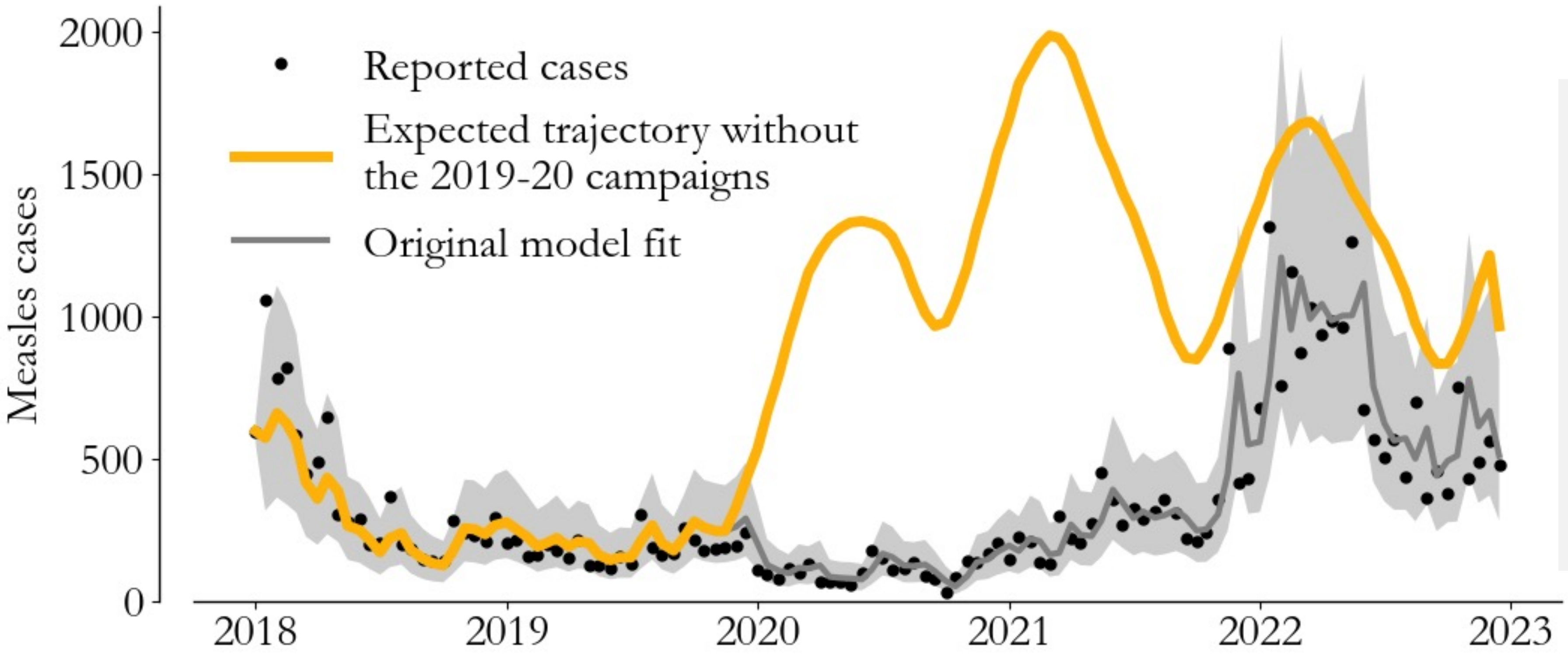
p(sero +) = p(vaccinated before infection)

+ p(infected and not vaccinated)



Independent SIA effects with prior information from the serosurvey gives us a more stable model with intuitive inferences.

To illustrate the importance of the 2019-2020 SIAs, we can **simulate epidemics in their absence**.



Comparing the model with and without the 2019-2020 SIAs, **we estimate that the campaigns prevented 64 thousand (52 to 77 95% interval) measles case reports**, corresponding to 1.3 million (1.1 to 1.6 95% interval) measles infections.

Examples in this block