KU Leuven Summer School
Segment 5A
Preferential Sampling and Inferring COVID Lethality

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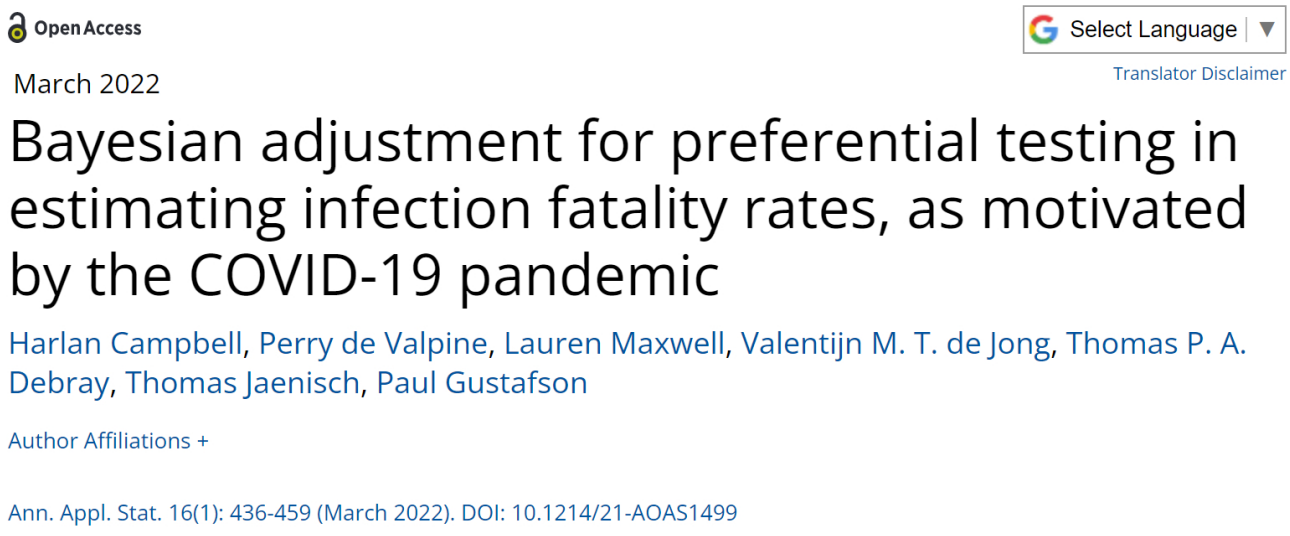
A second "latent variable model in covid times" tale



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Bayesian adjustment for preferential testing in estimating infection fatality rates, as motivated by the COVID-19 pandemic

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(see journal website $\rightarrow$ supplementary material for code/data)

The story begins here

In a given (the k-th) time/place, there are P_k people. Of these:

- C_k get infected by covid
  - and of these D_k die from the infection
- T_k get tested for covid
  - and of these CC_k test positive

Observable: (P_k, D_k, T_k, CC_k). (E.g. ourworldindata.org for country-level)

Latent: C_k.

Can report case fatality rate, $CFR_k = D_k/CC_k$.

Want to report infection fatality rate $IFR_k = D_k/C_k$?

What if testing were done on the basis of random sampling?

E.g., The T_k tested individuals were purely drawn at random from the P_k population members.

Then $\hat{C}_k = (CC_k/T_k)P_k$, hence $\hat{IFR}_k = (D_k/P_k)/(CC_k/T_k)$.

Helpful to think about this for two reasons:

- An anchor - can think about how this $\hat{IFR}_k$ breaks as the process of "who gets tested" deviates from random sampling.
- Then in some instances, testing a random subset of the population did/does happen: "sero-surveys."

Testing of a biased sample

Think of infection rate $IR_k = C_k/P_k$ and infection fatality rate $IFR_k = D_k/C_k$ as parameters.

Generalize from random sampling, $CC_k \sim \text{Bin}(T_k, IR_k)$ to biased sampling:

$$CC_k \sim \text{Bin}(T_k, 1 - (1 - IR_k)^{\phi_k})$$

where $\phi_k > 1$ describes the bias.

Interpretation? $OR(\text{get tested}, \text{are infected}) \approx \phi_k$

Take stock

Have parameters (IR_k, IFR_k, ϕ_k)

Convenient to **collapse:** From $C_k \sim \text{Bin}(P_k, IR_k)$ and $(D_k|C_k) \sim \text{Bin}(C_k, IFR_k)$ down to:

- $D_k \sim \text{Bin}(P_k, (IR_k)(IFR_k))$

Along with (from prev. slide):

- $CC_k \sim \text{Bin}(T_k, 1 - (1 - IR_k)^{\phi_k})$

And then recall we are aiming to draw together information from multiple jurisdictions

$$f(IR_{1:K}, IFR_{1:K}, \phi_{1:K} | P_{1:K}, T_{1:K}, CC_{1:K}, D_{1:K}) \propto$$

$$f(IR_{1:K}, IFR_{1:K}, \phi_{1:K}) \times$$

$$\prod_{k=1}^{K} f(CC_k | T_k, IR_k, \phi_k) f(D_k | P_k, IR_k, IFR_k)$$

Prior distributions (1 of 3): sigh - so much devil in detail

Meta-analysis / random effect idea, e.g.,

$g(IR_1), \ldots, g(IR_K) \sim N(\beta, \sigma^2)$, $(\beta, \sigma^2) \sim$ prior

$g(IFR_1), \ldots, g(IFR_K) \sim N(\theta, \tau^2)$, $(\theta, \tau^2) \sim$ prior

- Science: cross-jurisdiction variation in IFR much less than in IR.
- So prior that concentrates τ near zero justified
- In fact, perhaps with addition of covariates, unexplained IFR variation could be *very* low? Getting toward a "biological constant''?
- Interpret $g^{-1}(\theta)$ as target parameter, "typical" IFR.

Prior distributions (2 of 3): refining the previous slide a tad

$$g(IR_i) \quad \sim \quad N(\beta_0 + \beta_1 x_{1i} + \beta_2 x_{2i} + \beta_3 x_{3i}, \sigma^2)$$

$$g(IFR_i) \quad \sim \quad N(\theta_0 + \theta_1 z_{1i} + \theta_2 z_{2i}, \tau^2)$$

All country-specific covariates centred.

So can interpret $g^{-1}(\theta_0)$ as the typical IFR amongst typical jurisdictions.

Prior distributions (3 of 3)

Recall that larger ϕ_k corresponds to more targeted testing (compared to testing a random subset, $\phi_k = 1$).

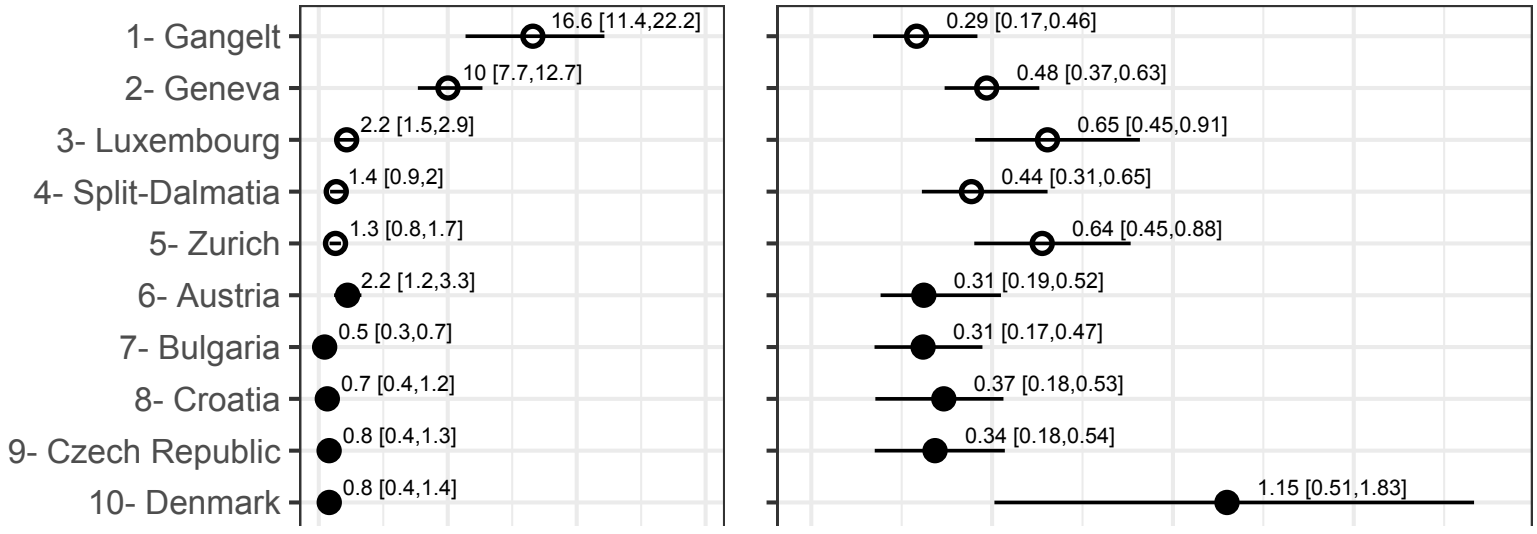
- Countries contributing (P_k, CC_k, T_k, D_k):
  - $\phi_k \sim \text{Unif}(1, 1 + \gamma)$, $\gamma \sim$ prior.
- Sero-surveys contributing (P_k, CC_k, T_k, D_k):
  - $\phi_k \equiv 1$.

Trying to keep score - Need JAGS (or comparable) to encode/compute:

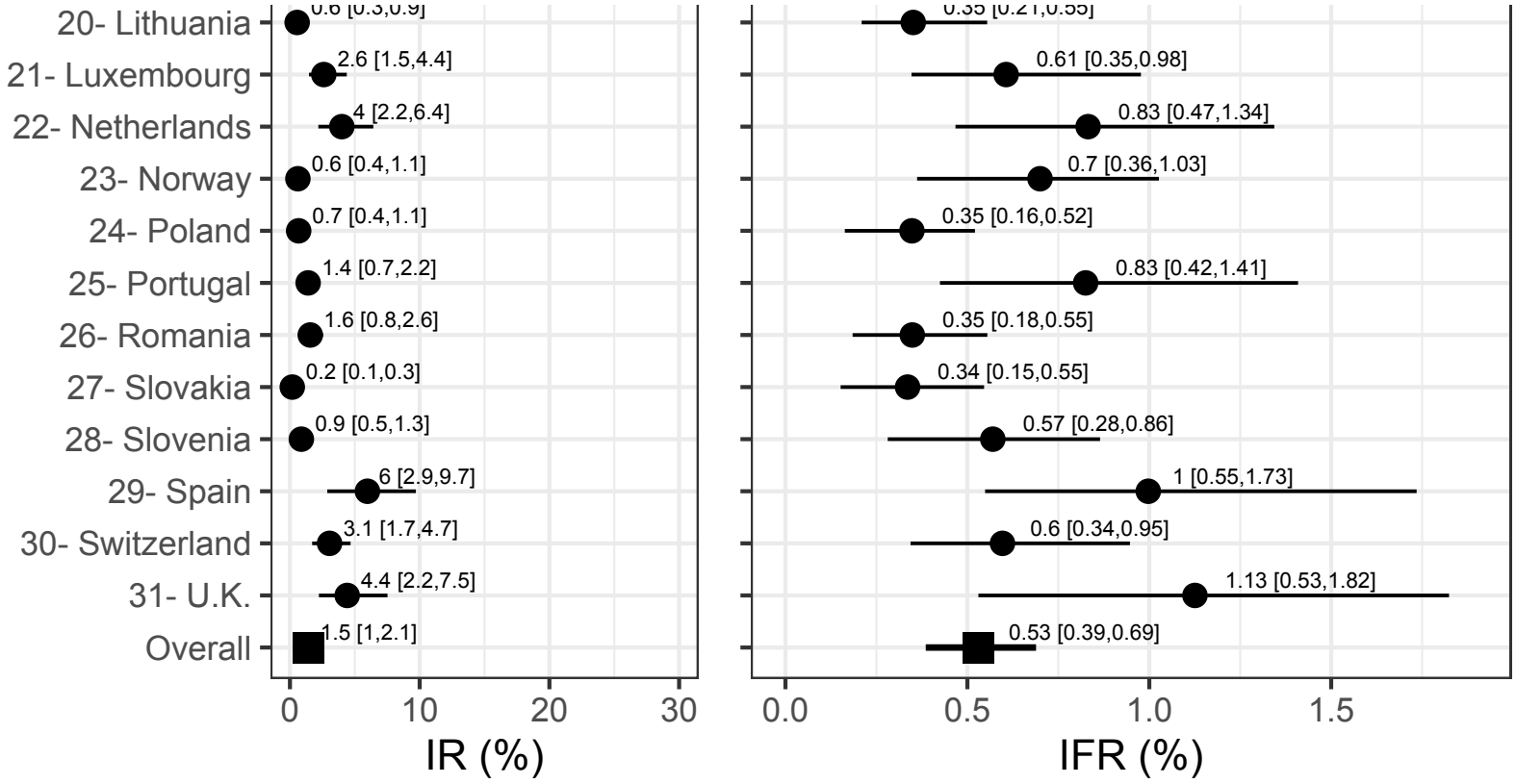
$$f(\gamma, \beta, \sigma^2, \gamma, \tau^2, \{\phi, IR, IFR\}_{1:K} | \{P, T, CC, D\}_{1:K}) \quad \propto$$

$$f(\gamma) f(\beta) f(\sigma^2) f(\gamma) f(\tau^2) \times$$
$$\prod_{k=1}^{K} f(IR_k | X_k, \beta, \sigma^2) \times$$
$$\prod_{k=1}^{K} f(IFR_k | Z_k, \theta, \tau^2) \times$$
$$\prod_{k=1}^{K} f(\phi_k | \gamma) \times$$
$$\prod_{k=1}^{K} f(cc_k | IR_k, \phi_k, T_k) f(d_k | IR_k, IFR_k, P_k)$$

Inference: (head of Fig. 3)



Inference: (tail of Fig. 3)



Second-order issue

We had some high-info datapoints ($\phi_k = 1$ known, sero-surveys), and some lower-info datapoints ($\phi_k \sim$ prior, national statistics), drew them all together in a meta-analysis.

Would it be useless to try to proceed in these sorts of problems with only lower-info data points?

Appendix: A meta-analysis "life hack"

For the sero-surveys, really helps to organize our thinking that a random sample of size T_k produced CC_k confirmed cases (and $T_k - CC_k$ non-cases).

In actuality, the better surveys did something along the lines of:

So in fact we take the data to be the effective T_k and CC_k that would produce this 95% credible interval *assuming* random sampling.