Fast approximate Bayesian inference for small-area estimation of HIV indicators using the Naomi model

Machine Learning and Global Health Network

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The Naomi model

- Naomi is a complicated spatio-temporal evidence synthesis model
- Used by countries to produce HIV estimates in a yearly process supported by UNAIDS
- Fast inference is important to allow for interactive review and development of estimates
- Inference for Naomi is currently conducted using Template Model Builder (TMB) (Kristensen et al. 2016)



Figure 1: A supermodel

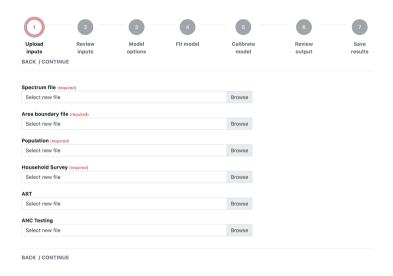


Figure 2: Example of the user interface from https://naomi.unaids.org/

Thanks for listening!

- Working on a paper based on this work called "Fast approximate Bayesian inference for small-area estimation of HIV indicators using the Naomi model" joint with Alex Stringer (Waterloo), Seth Flaxman (Oxford), Jeff Eaton (Imperial)
- Code and notebooks for this project are available at athowes.github.io/elgm-inf

Let me know if you'd be up for being an early reader!

References I

Kristensen, Kasper, Anders Nielsen, Casper W Berg, Hans Skaug, and Bradley M Bell. 2016. "TMB: Automatic Differentiation and Laplace Approximation." *Journal of Statistical Software* 70: 1–21.