

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

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Upload inputs

Review inputs

Model options

Fit model

Calibrate model

Review output

Save results

BACK / CONTINUE

Spectrum file (required)

Select new file

Browse

Area boundary file (required)

Select new file

Browse

Population (required)

Select new file

Browse

Household Survey (required)

Select new file

Browse

ART

Select new file

Browse

ANC Testing

Select new file

Browse

BACK / CONTINUE

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.