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

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Summary

- Approximate Bayesian inference method using Laplace approximation, adaptive Gauss-Hermite quadrature and principal component analysis
- Motivated by an evidence synthesis model for small-area estimation of HIV indicators in sub-Saharan Africa
- Implemented as a part of the `aghq` package (Stringer 2021), allowing flexible use of the method for any model with a `TMB` C++ user template

The Naomi HIV model

- District-level model of HIV indicators (Eaton et al. 2021) which synthesises data from household surveys, antenatal care (ANC) clinics, and routine service provision of antiretroviral therapy (ART)
  - Combining evidence from multiple data sources helps overcome the limitations of any one
  - Small-area estimation methods to overcome small district-level sample sizes
- Yearly estimation process: model run interactively by country teams using a web-app `naomi.unaids.org`
  - Figure 1 illustrates the seven stages of using the app
- Inference conducted in minutes using empirical Bayes and a Gaussian approximation via Template Model Builder `TMB` (Kristensen et al. 2016)
- It would take days to get accurate answers with MCMC via `tmbstan` (Monnahan and Kristensen 2018), and this is not practical in this setting
- Motivates looking for a fast, approximate approach, that takes uncertainty in hyperparameters into account

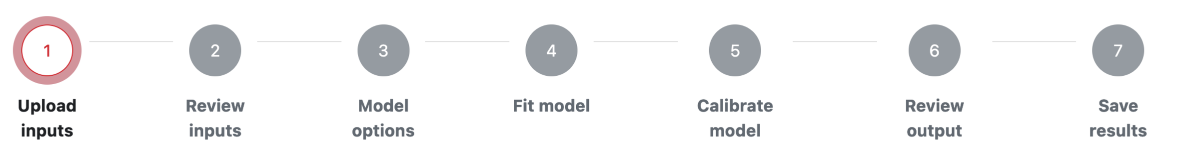

Figure 1: Model fitting occurs interactively in stages.

Extended latent Gaussian models

- Latent Gaussian models (LGMs) (Rue, Martino, and Chopin 2009) are three stage hierarchical models with observations y, Gaussian latent field x and hyperparameters θ
- In an LGM the conditional mean depends on exactly one structured additive predictor $\mu_i = g(\eta_i)$ with $g : \mathbb{R} \to \mathbb{R}$
  - The `R-INLA` implementation of integrated nested Laplace approximations applies only to LGMs, because ELGM precision matrices are not as sparse
- Extended latent Gaussian models (ELGM) remove this requirement such that $\mu_i = g(\eta_{\mathcal{J}_i})$ where $g_i : \mathbb{R}^{|\mathcal{J}_i|} \to \mathbb{R}$ and $\mathcal{J}_i$ is some set of indices
  - Allows a higher degree of non-linearity in the model
- Naomi is an ELGM, not an LGM, because it includes complex dependency structures:
  1. Incidence depends on prevalence and ART coverage
  2. Incidence ane prevalence linked to recent infection
  3. ANC offset from household survey
  4. ART coverage and recent infection are products
  5. Observed data are aggregated finer processes
  6. ART attendance uses the multinomial
  7. Multiple link functions
- We extend work of Stringer, Brown, and Stafford (2022) in this setting to the challenging Naomi ELGM
- Though we focus on Naomi here, the HIV Inference Group (`hiv-inference.org`) works on many other complex models, challenging for existing Bayesian inference methods, which require flexible modelling tools

Inference procedure

- **Laplace approximation** Integrate out variables using a Gaussian approximation to the denominator

$$p(\theta, y) \approx \tilde p_{\texttt{LA}}(\theta, y) = \frac{p(y, x, \theta)}{\tilde p_{\texttt{G}}(x \,|\, \theta, y)}\Big|_{x = \hat x(\theta)}$$

where $\tilde p_{\texttt{G}}(x \,|\, \theta, y) = \mathcal{N}(x \,|\, \hat x(\theta), \mathbf{H}(\theta)^{-1})$
  - Use automatic differentiation via `CppAD` in `TMB`
- **Adaptive Gauss-Hermite Quadrature**

$$\int_\Theta p(\theta) \mathrm{d}\theta \approx |L| \sum_{z \in \mathcal{Q}(m,k)} p(\hat\theta + Lz)\omega(z)$$

where the Gauss-Hermite quadrature rule $z \in \mathcal{Q}(m, k)$ with $m = \dim(\theta)$ and k points per dimension is adapted based upon
  - The mode $\hat\theta = \text{argmax}_{\theta \in \Theta} p(\theta)$
  - A matrix decomposition $LL^\top = -\partial_\theta^2 \log p(\theta)|_{\theta = \hat\theta}$
- Keep first $s < m$ **principal components** to get size k^s grid

Application to Malawi data

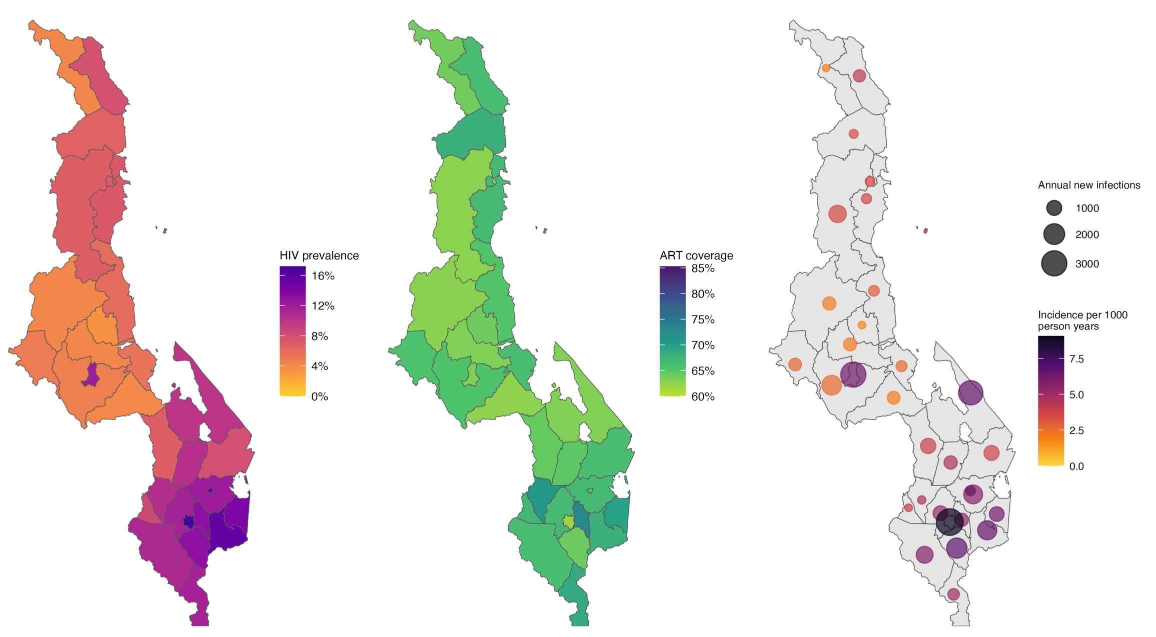

Figure 2: District-level model outputs for adults 15-49 in January 2016. Adapted from Eaton et al. 2021.

- Relatively small country but still a large model: latent field $\dim(x) = 491$, hyperparameters $\dim(\theta) = 24$
- Fit three inference methods (using one C++ template):
  - TMB (2 mins)
  - PCA-AGHQ (1 mins): $k = 3, s = 8$
  - NUTS (3.3 days): 4 chains of 100,000 thinned by 40 (required for good diagnostics)
- Figure 2 illustrates example model outputs: HIV prevalence, ART coverage, HIV incidence, and number of new infections, at the district level
- Compare hyperparameter, latent field, and output posteriors based on Kolmogorov-Smirnov tests, Pareto-smoothed importance sampling, and maximum mean discrepancy

Future directions

- Laplace marginals with matrix algebra approximations (Wood 2020) to speed up latent field marginal calculations
- Further methods for allocation of effort to important dimensions

Interested? Working notebooks and R code available from `github.com/athowes/elgm-inf`. Or get in touch:

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