## Deterministic Bayesian inference methods for the Naomi model

HIV Inference Lab Group Meeting

#### Adam Howes

Imperial College London

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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



#### 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/

#### Why do we use TMB

- 1. It runs quickly
- 2. It is flexible enough to be compatible with the model
- 3. We don't have better viable options

#### What problem we are trying to solve

- Ideally we want exact Bayesian inference: compute the posterior distribution of the parameters of the model given the data
- Computationally this amounts to solving a difficult integral
- We can't solve this, but we can give approximate answers

Goal: approximate this integral for Naomi better than  ${\rm TMB}$  does, without taking too long. In doing so, more accurately reflect uncertainty over hyperparameters

#### Two deterministic methods

- We use two deterministic<sup>1</sup> methods to approximate our integral
- 1. The Laplace approximation
- 2. Quadrature

<sup>&</sup>lt;sup>1</sup>In contrast to the most famous approximate Bayesian inference method, Markov chain Monte Carlo, which is fundamentally stochastic.

#### The Laplace approximation

• If you pretend the posterior distribution is a Gaussian, computation is easy



Figure 3: A Gamma prior with a = 3 and b = 1.



Figure 4: Draw 3 points from Poisson(3), then compute the posterior.

fn <- function(x) dgamma(x, a + sum(y), b + length(y), log = TRUE)</pre>

# # Here we are using numerical derivatives ff <- list( fn = fn, gr = function(x) numDeriv::grad(fn, x), he = function(x) numDeriv::hessian(fn, x) )</pre>

```
opt_bfgs <- aghq::optimize_theta(
    ff, 1, control = aghq::default_control(method = "BFGS")
)</pre>
```

#### Laplace approximation

```
laplace <- posterior +
 stat function(
  data = data.frame(x = c(0, 10)),
   aes(x).
   fun = dnorm.
   n = 500.
   args = list(mean = opt_bfgs$mode, sd = sqrt(1 / opt_bfgs$hessian)),
  col = cbpalette[3]
 ٦
```

#### Laplace approximation



Figure 5: The Laplace approximation in this case is good near the mode but not in the tails.

#### Computation of the Laplace approximation

- This computation was simple, and involved
- 1. Optimising a function
- 2. Taking the mode and the Hessian at the mode

#### The marginal Laplace approximation

- If we don't want to pretend the whole posterior distribution is Gaussian, another option is to pretend some of its marginals are
- This is how TMB works: it's up to the user to choose which parameters should be Gaussian using the random option

#### Which parameters should we treat as Gaussian?

- In spatio-temporal statistics we have data indexed by space and time
- We use random effects also indexed by space and time to model this data
- Spatio-temporal fields can be big
- Willing to make assumptions about how things vary over spacetime

 $\implies$  treat the latent field parameters as Gaussian! That's the majority of the integral done.

#### What about the hyperparameters?

- TMB uses optimisation to find the hyperparameters which maximise the marginal Laplace approximation
- This is the "outer" optimisation loop, where the "inner" is for computation of the Gaussian distribution

Inference for the latent field is based on a single value of the hyperparameters (the mode) – so called empirical Bayes  $\implies$  no uncertainty in the hyperparameters taken into account! How can you sleep at night.

#### Quadrature

- This brings us to our other method for solving integrals deterministically
- Say we have a function, then quadrature has two ingredients
- 1. Nodes: points to evaluate the function at
- 2. Weights: importance of function evaluation at that point
- You evaluate the function at the nodes, then do a weighted sum to calculate your integral

#### Trapezoid rule example

• Let's compute  $\int_0^{\pi} \sin(x) dx = 2$  using quadrature

```
trapezoid_rule <- function(x, spacing) {
    # Assumes nodes are evenly spaced
    w <- rep(spacing, length(x)) # Weights given by space between nodes
    w[1] <- w[1] / 2 # Apart from the first which is halved
    w[length(x)] <- w[length(x)] / 2 # And the last, also halved
    sum(w * x) # Compute the weighted sum
}</pre>
```





Figure 6: With 10 nodes it's 0.02 off.





Figure 7: With 30 nodes it's 0.002 off.





Figure 8: With 100 nodes it's pretty much correct.

#### Adaptive Gauss-Hermite quadrature

- Gauss-Hermite quadrature is a method for picking nodes and weights based on the theory of polynomial interpolation
- It works especially well for statistical problems where the integrand looks like something multiplied by a Gaussian distribution
- The adaptive part means the nodes and weights are changed depending on the integrand this makes sense, especially when the integrand is also a function of the data
- Implemented by the aghq package (Stringer 2021)



Figure 9: Unadapted points in two dimensions with k = 3.



Figure 10: Add the mean  $z + \hat{\theta}$ .



Figure 11: First option: rotate by the lower Cholesky  $Lz + \hat{\theta}$ .



Figure 12: Second option: rotate using the eigendecomposition  $E\Lambda^{1/2}z + \hat{\theta}$ .

## The plan?

- Write and implement an algorithm for fast approximate Bayesian inference using the Laplace approximation and quadrature for the Naomi model
- Use TMB for writing the model in C++, and implementing the Laplace approximation via automatic differentitation
- Use adaptive Gauss-Hermite quadrature to integrate the hyperparameters



Figure 13: One of Canada's top engineering schools (though ungraded)

#### Long prophecised

My main comment is that several aspects of the computational machineery that is presented by Rue and his colleagues **could benefit from the use of a numerical technique known as automatic differentiation (AD)**... By the use of AD one could obtain a system that is automatic from a user's perspective... the benefit would be a fast, flexible and easy-to-use system for doing Bayesian analysis in models with Gaussian latent variables

– Hans J. Skaug (coauthor of TMB), RSS discussion of Rue, Martino, and Chopin (2009)

#### One challenge

- For Malawi, Naomi has 24 hyperparameters: too many for a dense grid
- One proposed solution is to use principal components analysis (PCA) and keep only the first *s* < 24 dimensions
- We will use k = 3 points per dimension (k = 2 doesn't include the mode)



Figure 14: Illustration of what PCA-AGHQ looks like for the 2D example, keeping only the first principal component, s = 1.



Figure 15: This Scree plot suggests 10 or so dimensions is enough. We use s = 8. Avoiding long computation times is still important.



Figure 16: With 8 dimenions, the covariance matrix is accurately reproduced.

#### Comparison of posterior distributions

- We run HMC for as long as it takes to get a good answer (3 days)
- Compare output of TMB with aghq: which is more similar to HMC?



Figure 17: Histogram of sample draws from each method for one latent field parameter. Which of TMB and aghq is closer to tmbstan? Hard to say.



Figure 18: The empirical cumulative distribution is slightly more enlightening.



Figure 19: The Kolmogorov-Smirnov test statistic is the maximum difference between ECDFs.



Figure 20: Generating the KS test statistic for all latent field parameters, on average aghq does better.

#### Conclusions

- Developed an approximate Bayesian inference method more accurate than TMB and faster than MCMC we're on the Pareto frontier!
- Scaled hyperparameter grid to >20 dimesions using PCA
- Relatively straightforward implementation using aghq R package, compatible with any model that has a TMB template

#### Future work

- More comprehensive inference comparison, particularly of model outputs
  - Maximum mean discrepancy
  - Pareto-smoothed importance sampling
  - Simulation-based calibration
- Extension to Laplace marginals via Wood (2020)
  - May be more accurate, but have to think about computational costs

### 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!

#### Risk group retrospective



### Estimating risk group proportions: informal discussion

A summary, some potentially useful takeaways, and reflections on the paper "Spatio-temporal estimates of HIV risk group proportions for adolescent girls and young women across 13 priority countries in sub-Saharan Africa"



#### Figure 21: Available at athowes.github.io

#### 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. Rue, Håvard, Sara Martino, and Nicolas Chopin. 2009. "Approximate Bayesian inference for latent Gaussian models by using integrated nested Laplace approximations." Journal of the Royal Statistical Society: Series b (Statistical Methodology) 71 (2): 319-92. Stringer, Alex. 2021. "Implementing Approximate Bayesian Inference using Adaptive Quadrature: the aghg Package." https://arxiv.org/abs/2101.04468. Wood, Simon N. 2020. "Simplified Integrated Nested Laplace Approximation."

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