

AMISforInfectiousDiseases: an R package to fit a transmission model to a prevalence map

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Motivation

- For parameter inference of transmission models, simulating from the model can be computationally expensive
- `AMISforInfectiousDiseases` is an R package that allows the user to perform inference on parameters from a **transmission model** at the **sub-national** level, by fitting to a **geostatistical map** of disease prevalence
- To obtain sub-national estimates, output from the transmission model is compared with samples from the geostatistical map to provide each pixel a weight for a given set of model parameters
- The number of simulations from the transmission model scales with the number of parameter samples, and not the number of pixels in the geostatistical map
- The main function from this package is `amis()`, with user-defined arguments including the map(s) of disease prevalence, the transmission model and prior specifications for the model parameters

Algorithm

- Extension of adaptive multiple importance sampling (AMIS) originally developed by Cornuet et al. (2012) that:
 - Applies AMIS to multiple targets simultaneously via the same proposal
 - Works with a “moving” target that changes with each iteration of AMIS
- Notation:
 - $f(p_j)$: probability of having disease prevalence p_j under the geostatistical model
 - $g(p_j)$: probability of having disease prevalence p_j under the transmission model
 - A : set of active pixels (i.e. those pixels for which effective sample size (ESS) is less than a target ESS specified by the user)

Algorithm 1

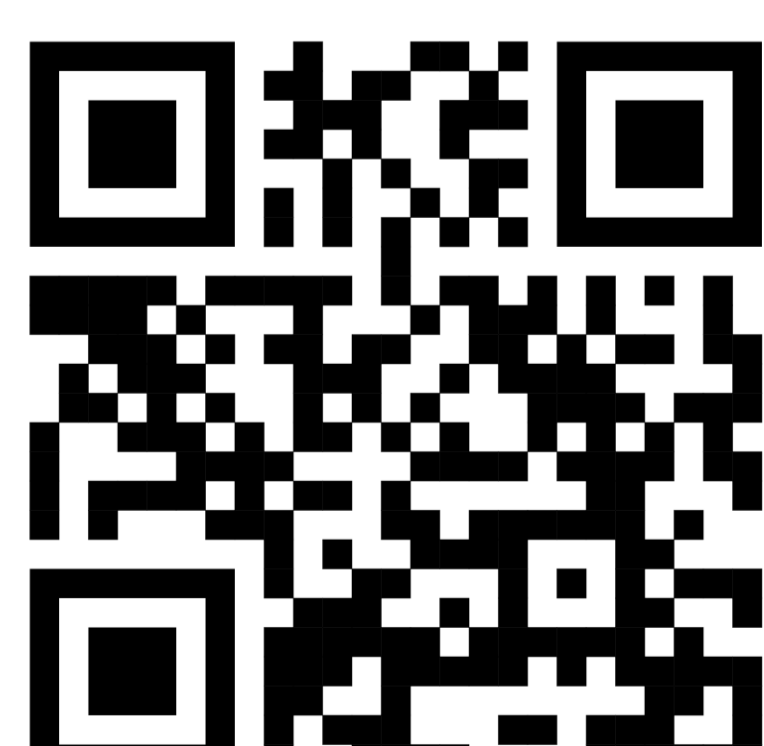
- Initialise $i = 1$, $\phi_1 = \Pi(\theta)$ and $A = \{1, \dots, L = 11369\}$
- While (A is non-empty):
 - Sample $\theta_j, j = \{1, \dots, N\}$ from $\phi_i(\cdot)$
 - Simulate prevalence p_j from transmission model under θ_j for all j
 - Calculate a weight for all pixels in A ,

$$w_{ij}^i = \frac{f_i(p_j)}{g(p_j)} \frac{\Pi(\theta_j)}{\frac{1}{i} \sum_u \phi_u(\theta_j)}$$
 - Normalise weights and calculate ESS for each pixel
 - Update A with pixels for which ESS is less than target ESS
 - Calculate average weight for each j over all pixels to obtain \bar{w}_j , and update $\phi_i(\cdot)$ by fitting a density to the weighted sample $\{\theta_j, \bar{w}_j\}, j = \{1, \dots, N\}$
 - Update $i = i + 1$

- $f(p_j)$ can be defined by the user - if not specified, an empirical estimate is used
- Multiple geostatistical maps at varying time points can also be considered

References

- Poster made with `posterdown` [4].
- [1] CORNUET, J.-M., MARIN, J.-M., MIRA, A., & ROBERT, C. P. (2012). Adaptive Multiple Importance Sampling. *Scandinavian Journal of Statistics*, 39(4), 798–812. doi: 10.1111/j.1467-9469.2011.00756.x
- [2] PULLAN, R. L., SMITH, J. L., JASRASARIA, R. and BROOKER, S. J. (2014). Global numbers of infection and disease burden of soil transmitted helminth infections in 2010. *Parasit. Vectors BioMed. Central*, 7 37. doi: 10.1186/1756-3305-7-37
- [3] RETKUTE, R., TOULOUPOU, P., BASÁÑEZ, M. G., HOLLINGSWORTH, T. D., SPENCER, S. E. F. (2021). Integrating geostatistical maps and infectious disease transmission models using adaptive multiple importance sampling. *The Annals of Applied Statistics*, 15(4), 1980-1998. doi: 10.1214/21-AOAS1486
- [4] THORNE, B. (2019). Posterdown: Generate PDF Conference Posters Using r Markdown. <https://CRAN.R-project.org/package=posterdown>.

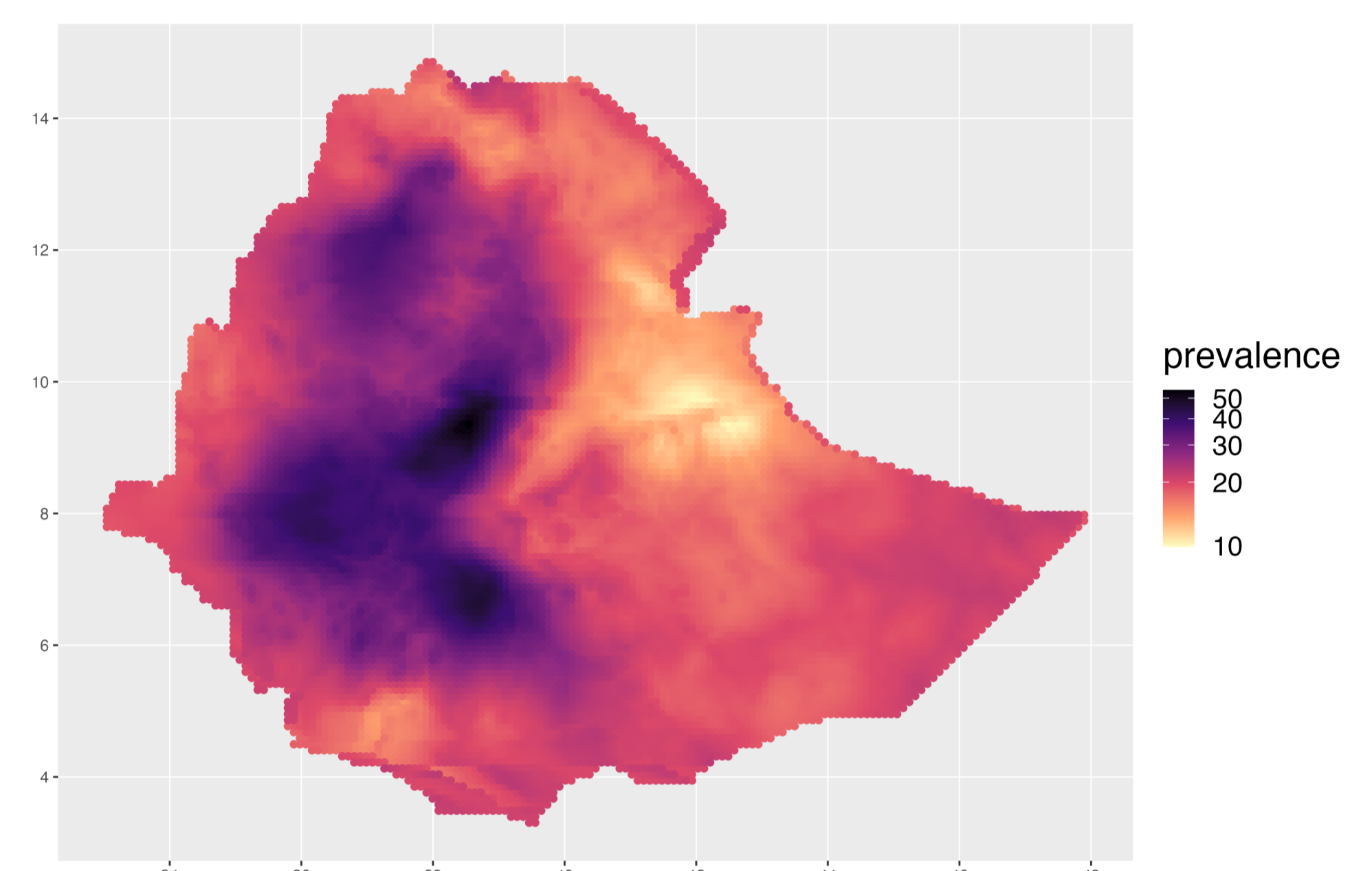


Ascaris in Ethiopia

- Ascaris lumbricoides*, also known as roundworms, are an intestinal nematode
- An estimated 819 million people are infected by *A. lumbricoides* (Pullan et al., 2014)

Geostatistical prevalence map

- Have 100 individual maps from the posterior of a geostatistical model for *Ascaris* prevalence in Ethiopia at 10km × 10km resolution from Retkute et al. (2021)
- Mean prevalence at each pixel below



Transmission model

- From Retkute et al. (2021), the transmission model for *Ascaris* can be described by a relationship between prevalence P and the mean intensity of infection
- Assumes the negative binomial model where $W > 0$ is the mean number of worms per host and k is the worm clumping coefficient

$$P = 1 - \left(1 + \frac{W}{k}\right)^{-k}$$

Priors

- The following priors from Retkute et al. (2021) are placed on $\log(W)$ and k :

$$\log(W) \sim \mathcal{U}\left(\log(0.01), \log(60)\right)$$

$$k|W \sim \mathcal{N}\left(0.3337 + 0.0171 \times W, \sigma(W)^2\right)$$

where $\sigma(W)$ is 5 times the standard error obtained from the Hessian matrix evaluated at W

Results

- The `amis()` function produces a set of weighted samples for each pixel
- Sample 500 parameter sets from all proposals using weights obtained from AMIS for each pixel
- These samples can be used to project into the future under different treatment scenarios

