disaggregation: An R Package for Bayesian Spatial Disaggregation Modelling

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Abstract

Disaggregation modelling, or downscaling, has become an important discipline in epidemiology. Surveillance data, aggregated over large regions, is becoming more common, leading to an increasing demand for modelling frameworks that can deal with this data to understand spatial patterns. Disaggregation regression models use response data aggregated over large heterogeneous regions to make predictions at fine-scale over the region by using fine-scale covariates to inform the heterogeneity. This paper presents the R package **disaggregation**, which provides functionality to streamline the process of running a disaggregation model for fine-scale predictions.

**Keywords:** Bayesian spatial modelling, disaggregation modelling, TMB.

1. Introduction

Methods for estimating high-resolution risk maps from aggregated response data over large spatial regions are becoming increasingly sought after in disease risk mapping (Li, Brown, Gesink, and Rue 2012; Diggle, Moraga, Rowlingson, Taylor et al. 2013; Wilson and Wakefield 2018), especially in malaria mapping (Sturrock, Cohen, Keil, Tatem et al. 2014; Sturrock, Bennett, Midekisa, Gosling, Gething, and Greenhouse 2016). Disaggregation regression, first applied in species distribution modelling in ecology (Keil, Belmaker, Wilson, Unitt, and Jetz 2013; Barwell, Azaele, Kunin, and Isaac 2014) has now become an important method in disease risk mapping (Weiss, Lucas, Nguyen, Nandi, Bisanzio, Battle, Cameron, Twohig, Pfeffer, Rozier et al. 2019; Battle, Lucas, Nguyen, Howes, Nandi, Twohig, Pfeffer, Cameron, Rao, Casey et al. 2019). The aggregation of response data over large heterogeneous regions is problematic for making fine-scale predictions, as relationships learned between variables at one spatial scale may not hold at other scales (Wakefield and Shaddick 2006). However, by using fine-scale information from related covariates we can inform the heterogeneity of the response variable of interest within the aggregated area.

Disaggregation modelling is unorthodox as the predictions are at a different scale to the response data, i.e. the number of rows in the covariate data is different to that of the response data. The spatial modelling software package, **INLA** (Rue, Martino, and Chopin...
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2009), or integrated nested Laplace approximation, has been shown to very useful in a wide variety of circumstances, however it is not flexible enough for the unorthodox nature of the disaggregation problem except in the special case of the linear link function (Wilson and Wakefield 2018). Disaggregation models can be implemented in TMB (Kristensen, Nielsen, Berg, Skaug, and Bell 2016), or template model builder, with a lot of flexibility, however the data manipulation required to format the model objects and construct the model definition in C++ is non-trivial. The disaggregation package allows this process to be streamlined, to make it easy for the user to run disaggregation models at the expense of some flexibility.

2. Disaggregation modelling

Suppose we have response data, \( y_i \), for \( N \) polygons, which corresponds to count data for the property of interest within that polygon. The process that is being counted occurs in continuous space that we model as a high-resolution, square lattice for convenience. The data, \( y_i \), are assumed to be created by the aggregation of the counts over the polygon, i.e. the count data of the polygon is given by the sum of the count data for all the pixels within that polygon. The rate is defined such that the number of cases in this pixel can be calculated by multiplying the rate by the aggregation raster. For example, in epidemiology, we may have as our response the number of people that contract a certain disease in a given period of time (case incidence). Our rate would be the incidence rate of cases per population, where the aggregation raster corresponds to population.

For the disaggregation model we model the rate at pixel level, with the likelihood for the observed data given by aggregating these pixel level rates. The rate in pixel \( j \) of polygon \( i \) at location \( s_{ij} \) is given by:

\[
\text{link}(\text{rate}_{ij}) = \beta_0 + \beta X_{ij} + \text{GP}(s_{ij}) + u_i
\]

where \( \beta \) are regression coefficients, \( X_{ij} \) are covariate values, GP is a Gaussian random field and \( u_i \) is a polygon-specific iid effect. The user-defined link function is typically log, identity and logit for Poisson, Normal and Binomial likelihoods, respectively. The Gaussian random field has a Matern covariance function parameterised by \( \rho \), the range (approximately the distance beyond which correlation is less than 0.1), and \( \sigma \), the marginal standard deviation. As we are working in a Bayesian setting, each of the model parameters and hyperparameters are given a prior, which is discussed later.

The pixel predictions are then aggregated to the polygon level using the weighted sum (via the aggregation raster \( a_{ij} \)):

\[
\text{cases}_i = \sum_{j=1}^{N_i} a_{ij} \text{rate}_{ij}
\]

\[
\text{rate}_i = \frac{\text{cases}_i}{\sum_{j=1}^{N_i} a_{ij}}
\]

The different likelihoods correspond to slightly different models (\( y_i \) is the response count data):

- **Poisson**
  \[ y_i \sim \text{Pois}(\text{cases}_i) \]
• Gaussian

\[ y_i \sim \text{Normal}(\text{cases}_i, \sigma_i) \] (5)

Here \( \sigma_i = \sigma \sqrt{\sum_j a_{ij}^2} \), where \( \sigma \) is the pixel-level dispersion (a parameter learnt by the model).

• Binomial

\[ y_i \sim \text{Binomial}(M_i, \text{rate}_i) \] (6)

In the example of disease mapping, Poisson or Gaussian likelihoods could be used when the quantity observed, \( y_i \), is the total number of cases in a given polygon. The Binomial model could be used when \( y_i \) is the prevalence of a disease in a sample of \( M_i \) people in the polygon.

### 2.1. Priors

For each of the model parameters and hyperparameters we specify priors. The regression parameters and intercept are given Gaussian priors, where the default priors are \( \beta_0 \sim N(0, 2) \) and \( \beta_i \sim N(0, 0.4) \). A penalised complexity prior is placed on the scale and range parameters of the random field (Fuglstad, Simpson, Lindgren, and Rue 2018) such that

\[ P(\rho < \rho_{\text{min}}) = \rho_{\text{prob}} \] (7)

\[ P(\sigma > \sigma_{\text{max}}) = \sigma_{\text{prob}} \] (8)

where the values \( \rho_{\text{min}}, \rho_{\text{prob}}, \sigma_{\text{max}}, \sigma_{\text{prob}} \) are set by the user. This prior shrinks the field towards a base model with zero variance and infinite range, in other words regularising towards a flatter field with smaller magnitude. The polygon-specific effects \( u_1, ..., u_N \) have Gaussian priors centered at 0 with standard deviation \( \sigma_u \) (where the precision \( \tau_u = 1/\sigma_u^2 \)). A penalised complexity prior (Simpson, Rue, Riebler, Martins, Sørbye et al. 2017) is placed on \( \sigma_u \) such that

\[ P(\sigma_u > \sigma_{u,\text{max}}) = \sigma_{u,\text{prob}} \] (9)

which shrinks towards a base model of no polygon-specific effect. The \( \sigma_{u,\text{max}} \) and \( \sigma_{u,\text{prob}} \) are set by the user.

For models that use a Gaussian likelihood, a log gamma prior is set on the log of the precision, \( \log \tau \sim \log \Gamma(\text{shape} = 1, \text{rate} = 5 \times 10^{-5}) \), to regularise the dispersion (\( \sigma = 1/\sqrt{\tau} \)) to take low values. This is the same as the prior set by INLA for the dispersion of the normal likelihood.

### 3. TMB implementation

The **disaggregation** package is built on template model builder (TMB) Kristensen et al. (2016), which is a tool for flexibly building complex models based on C++. TMB combines the packages CppAD (Bell 2012), for automatic differentiation in C++, Eigen (Guennebaud, Jacob, Avery, Bachrach, Barthelemy et al. 2010), a C++ library for linear algebra, and CHOLMOD (Chen, Davis, Hager, and Rajamanickam 2008), a package for efficient computation of sparse matrices. The use of these packages allows an efficient implementation of the automatic Laplace approximation (Skaug and Fournier 2006) with exact derivatives which gives an approximation to the Bayesian posterior. TMB calculates first and second order
4. Package usage

In this section we show how to use the **disaggregation** package using a dataset of aggregated malaria case counts across Madagascar. Malaria is an infectious disease caused by parasites of the *Plasmodium* group, transmitted by *Anopheles* mosquitoes. Malaria transmission is therefore closely related to mosquito and parasite development. Environmental factors such as temperature, rainfall and elevation have been shown to have significant effect on mosquito survival and development; in general mosquitoes favour warm, humid environments with moderate rainfall. Therefore, such environmental covariates would be useful in a malaria disaggregation model to inform fine-scale distributions. In this model we use the environmental covariates of mean land surface temperature (LST), variation in LST, elevation, and enhanced vegetation index (EVI) to inform spatial heterogeneity in malaria risk. These covariates are obtained from the Moderate Resolution Imaging Spectroradiometer (MODIS), which provides many measurements over the entire Earth’s surface ([https://modis.gsfc.nasa.gov/data/](https://modis.gsfc.nasa.gov/data/)). Malaria incidence rate is often given per thousand cases and given the term annual parasite index (API).

The latest version of **disaggregation** should always be available from the Comprehensive R Archive Network (CRAN) at [http://CRAN.R-project.org/package=disaggregation](http://CRAN.R-project.org/package=disaggregation). Run the following commands to install and load the package.

```r
devtools::install.packages("disaggregation")
library(disaggregation)
```

We then read in the data to use in the **disaggregation** package.

```r
library(raster)

shapes <- shapefile('data/shapes/mdg_shapes.shp')
population_raster <- raster('data/population.tif')
covariate_stack <- getCovariateRasters('data/covariates',
    shape = population_raster)
```

The main functions are **prepare_data**, **fit_model** and **predict**.

Firstly, we use the **prepare_data** function to setup all the data in the format needed in the disaggregation modelling. This function performs various data manipulation tasks to create objects that are necessary for fitting the model. The required input data for the **prepare_data** function are a SpatialPolygonsDataFrame containing the response data and a RasterStack of
covariates to be used in the model. The variable names in the SpatialPolygonsDataFrame of
the response count data and the polygon ID are defined by the user.

An optional aggregation raster can be provided. The aggregation raster defines how the pixels
within each polygon are aggregated. The disaggregation model performs a weighted sum of
the pixel prediction, weighted by the pixel values in the aggregation raster. In this case our
pixel predictions are malaria incidence rate, so we use the population raster to aggregate
pixel incidence rate by summing the number of cases (rate weighted by population). If no
aggregation raster is provided a uniform distribution is assumed, i.e. the pixel predictions are
aggregated to polygon level by summing the pixel values unaltered.

The values of the covariates (as well as the aggregation raster, if given) are extracted at each
pixel within the polygons and stored as a data.frame with a row for each pixel and a column
for each covariate (parallelExtract function). The extraction of each covariate is performed
in parallel over the number of cores defined by the argument ncores. The values extracted
from the aggregation raster are returned as an array of values, one for each pixel.

In order to know which pixels (i.e. which rows) are contained in each polygon, a matrix is
constructed that contains the start and end pixel index for each polygon (getStartendindex
function). Additionally, an INLA mesh is built to use for the spatial field (build_mesh
function). The mesh.args argument allows the user to supply a list of INLA mesh parameters
to control the mesh used for the spatial field. The mesh can take several minutes to construct,
so to prepare the data without building the mesh the user can set the makeMesh flag to FALSE.
However, it would then not be possible to fit the disaggregation model without the mesh.

If there are any NAs in the response or covariate data within the polygons the prepare_data
method will return an error. This can be dealt with using the na.action flag, which is au-
tomatically off. Ideally the NAs in the data would be dealt with by the user beforehand,
however, setting na.action = TRUE will automatically deal with NAs. It removes any poly-
gons that have NAs as a response, sets any aggregation pixels with NA to zero and sets
covariate NAs pixels to the median value for that covariate across all polygons.

```r
dis_data <- prepare_data(polygon_shapefile = shapes,
covariate_rasters = covariate_stack,
aggregation_raster = population_raster,
mesh.args = list(max.edge = c(0.7, 8),
cut = 0.05,
offset = c(1, 2)),
id_var = 'ID_2',
response_var = 'inc',
na.action = TRUE,
ncores = 8)
```

We can see a summary of the data, using the generic summary function, and plot the data.
The summary function returns information on how many pixels and polygons the data con-
tains, how many pixels in the smallest and largest polygons and a summary of the covariate
data. The plot functions plots a map of the polygon response data, the covariate rasters and
the INLA mesh, as shown in Figure 1.
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```r
summary(dis_data)
#
#> They data contains 109 polygons and 28892 pixels
#> The largest polygon contains 867 pixels and the smallest polygon contains 1 pixels
#> There are 4 covariates
#
#> Covariate summary:
#
#> Elevation  EVI  LSTmean
#> Min. :-1.174670  Min. :-2.70028  Min. :-3.33993
#> 1st Qu.:0.848255  1st Qu.:0.73278  1st Qu.:-0.73083
#> Median :0.257381  Median :0.36756  Median :0.23743
#> Mean : 0.009915  Mean : 0.01077  Mean : 0.01572
#> 3rd Qu.: 0.713218  3rd Qu.: 0.59588  3rd Qu.: 0.83374
#> Max. : 4.585433  Max. : 3.14432  Max. : 2.09070
#
#> LSTsd
#> Min. :-2.92708
#> 1st Qu.:0.65033
#> Median :0.09492
#> Mean : 0.03608
#> 3rd Qu.: 0.67376
#> Max. : 3.58093
```

```r
plot(dis_data)
```
Figure 1: Maps of Madagascar showing the data used in the disaggregation model. These plots are produced when calling the plot function on the disag.data object. The plots show: (a) number of malaria cases in each administrative unit, (b) maps of the four covariates used in the model; and (c) inla.mesh object that will be used to make the spatial field.
The `prepare_data` function returns an object of class `disag.data`, which is designed to be used directly in the `fit_model` function.

Now we can fit the disaggregation model using `fit_model`. Here we use a Poisson likelihood for the incident count data with a log link function. Options for the likelihood are Gaussian, Poisson and binomial, and options for the link function are logit, log and identity. The spatial field and iid effect are components of the model by default, they can be turned off using the `field` and `iid` flags. We specify all of the priors for the model in a single list. Hyperpriors for the field are given as penalised complexity priors - specify $\rho_{\text{min}}$ and $\rho_{\text{prob}}$ for the range of the field, where $P(\rho < \rho_{\text{min}}) = \rho_{\text{prob}}$, and $\sigma_{\text{min}}$ and $\sigma_{\text{prob}}$ for the variation of the field, where $P(\sigma > \sigma_{\text{min}}) = \sigma_{\text{prob}}$. Similarly, the user specifies penalised complexity priors for the iid effect. The `iterations` argument specifies the maximum number of iterations the model can run for to find an optimal point. In order to print more verbose output the user can set the `silent` argument to FALSE.

```r
fitted_model <- fit_model(data = dis_data,
                           iterations = 1000,
                           family = 'poisson',
                           link = 'log',
                           priors = list(priormean_intercept = 0,
                                         priorsd_intercept = 2,
                                         priormean_slope = 0.0,
                                         priorsd_slope = 0.4,
                                         prior_rho_min = 3,
                                         prior_rho_prob = 0.01,
                                         prior_sigma_max = 1,
                                         prior_sigma_prob = 0.01))
```

We can get a summary and plot of the model output. The `summary` function gives the estimate and standard error of the fixed effect parameters in the model, as well as the negative log likelihood and in-sample performance metrics (root mean squared error, mean absolute error, pearson correlation coefficient and spearman rank correlation coefficient). The `plot` function produces two plots: one of the fixed effects parameters and one of the observed data against in-sample predictions, as shown in Figure 2.

```r
summary(fitted_model)
```

| #> Model parameters: | Estimate | Std. Error |
|----------------------|----------|------------|
| #> intercept          | -3.1184394 | 0.2676452 |
| #> slope              | -0.3726411 | 0.1963679 |
| #> slope              | 0.3031676  | 0.2073146  |
| #> slope              | 0.2372611  | 0.2696821  |
| #> slope              | -0.2412063 | 0.2174388  |
| #> iideffect_log_tau  | 1.0981493  | 0.2718976  |
| #> log_sigma          | -3.5489432 | 0.5925067  |
| #> log_rho            | 0.5596955  | 0.2984963  |
The `fit_model` function returns an object of class `fit.result`, which is designed to be used directly in the `predict` function. Therefore, now that we have fitted the model, we are ready to predict the malaria incidence rate across Madagascar.

To predict over a different spatial extent to that used in the model, a RasterStack covering the region to make predictions over can be passed as the `newdata` argument. If this argument is not given, predictions are made over the covariate rasters used in the fit. If the user wants to include the iid effect from the model as a component in the prediction then the `predict_iid` logical flag should be set to TRUE, otherwise, the iid effect will not be predicted.

For the uncertainty calculations, parameter values are sampled from the posterior distribution and summarised. The number of parameter draws used to calculate the uncertainty is set by the user via the `N` parameter (default: 100), and the size of the credible interval (e.g. 75%, 95%) to be calculated when summarising is set via the argument `CI` (default: 0.95).
model_predictions <- predict(fitted_model)

The function predict returns a list of two objects: the mean predictions (of class predictions) and the uncertainty rasters (of class uncertainty). The mean predictions contain a raster of the mean prediction of the incidence rate, as well as rasters of the field, iid (if predicted) and covariate component of the linear predictor. The uncertainty object contains a RasterStack of the prediction realisations and a RasterStack of the upper and lower credible intervals. The plot function can be used on both the predictions and uncertainty objects, as shown in Figures 3 and 4 respectively.

plot(model_predictions$mean_predictions)

Figure 3: Maps of Madagascar showing the fine-scale predictions from the disaggregation model. These maps are produced when calling the plot function on the predictions object. The maps show the (a) mean prediction of malaria incidence rate, (b) covariate contribution to the linear predictor, and (c) field contribution to the linear predictor.

Using three simple functions within the disaggregation package we have been able to fit a Bayesian spatial disaggregation model and predict pixel-level incidence rate across Madagascar using aggregated incidence data and pixel-level environmental covariates.
Figure 4: Maps of Madagascar showing the fine-scale predictions of lower (2.5%) and upper (97.5%) credible intervals of the malaria incidence rate from the disaggregation model. These maps are produced when calling the `plot` function on the `uncertainty_predictions` object.

5. Comparison with Markov chain Monte Carlo (MCMC)

In this section we show performance comparisons between modelling using the Laplace approximation provided by the `disaggregation` package, based on `TMB`, and using MCMC. Given a function to evaluate the probability density of a distribution at any given point in parameter space, MCMC algorithms construct markov chains to generate samples from this distribution. These algorithms are often slow, particularly in high-dimensional settings, as it can take a long time to converge to and effectively sample from the stationary distribution. The density is evaluated at each step, so this problem is compounded when evaluating this density is computationally expensive. In contrast, the `disaggregation` package approximates using a Laplace approximation to the posterior to generate posterior samples. This only requires the posterior to be maximised to find the posterior mode and therefore involves relatively few evaluations of the posterior density compared to MCMC techniques, although potentially at the expense of less accurate posterior samples. Here we compare the time and performance of the two techniques.

The model described in Section 4 for malaria in Madagascar has been optimised using the `disaggregation` package. Here we fit the same model by running MCMC using the `tmbstan` package, with the NUTS (no-u-turn sampler) algorithm (Hoffman and Gelman 2014) using four chains. It is important to note that this is a useful feature of the `disaggregation` package, to be able to create the `TMB` model object (using the `fit_model` function with one iteration) and pass it directly to `tmbstan`. The model is fitted by running the MCMC algorithm for 8000 iterations with 2000 of those as warmup, which took 94 hours. This number of iterations was chosen by running the MCMC algorithm repeatedly, starting at 1000 iterations, doubling
the number of iterations each time until the value of the MCMC convergence statistic, $\hat{R}$, dropped below 1.05 for all model parameters. In contrast, fitting the model using the Laplace approximation via TMB within the disaggregation package took 56 seconds. Fitted parameter values for both of these methods are given in Table 1.

The trace of the MCMC parameter values is given in Figure 5. It can be seen that the MCMC algorithm has been run for long enough to get sufficient chain mixing. The disaggregation package produces similar results to the MCMC algorithm. However the model fitting using the disaggregation package took 56 seconds in contrast to the 94 hours taken for the MCMC run. Therefore, it can be seen that the disaggregation package provides a quick and simple way to run disaggregation models, that can be prohibitively slow using MCMC.

6. Conclusions

Disaggregation modelling, which involves fitting models at fine-scale resolution using areal data over heterogeneous regions, has become widely used in fields such as epidemiology and ecology. The disaggregation package implements Bayesian spatial disaggregation modelling with a simple, easy to use R interface. The package includes simple data preparation, fitting
and prediction functions that allow some user-defined model flexibility. In this paper we have presented an application of the package, predicting malaria incidence rate across Madagascar from aggregated count data and environmental covariates.

The modelling framework is implemented using the Laplace approximation and automatic differentiation within the TMB package. This allows fast, optimised calculations in C++. These disaggregation models are computationally intensive and take a long time using MCMC optimisation techniques. Using TMB, the models are much faster and produce similar results. Future work could be done extending the disaggregation package to include spatio-temporal disaggregation models. This would require a spatio-temporal field as well as dynamic covariates, and would be significantly more computationally intensive. Additionally, tools for cross-validation could be included within the package. Cross-validation of spatial models is non-trivial due to the spatial autocorrelation in the data.

The disaggregation package provides a simple, useful interface to perform spatial disaggregation modelling, with reasonable flexibility, as well as having the scope to be extended to more complex disaggregation models.

### Computational details

The results in this paper were obtained using R 3.6.1 with the TMB 1.7.15 package. R itself and all packages used are available from the Comprehensive R Archive Network (CRAN) at [https://CRAN.R-project.org/](https://CRAN.R-project.org/), apart from INLA, which can be installed in R using the command:

```r
install.packages("INLA",
    repos = c(getOption("repos"),
      INLA="https://inla.r-inla-download.org/R/stable"),
    dep=TRUE)
```
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Figure 5: Trace of the fixed effects parameters for MCMC using NUTS sampling, running the algorithm for 94 hours. It was run for 8000 iterations with 2000 of those as warmup.

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References

Barwell LJ, Azaele S, Kunin WE, Isaac NJ (2014). “Can Coarse-Grain Patterns in Insect Atlas Data Predict Local Occupancy?” Diversity and Distributions, 20(8), 895–907.

Battle KE, Lucas TC, Nguyen M, Howes RE, Nandi AK, Twohig KA, Pfeffer DA, Cameron
E, Rao PC, Casey D, et al. (2019). “Mapping the Global Endemicity and Clinical Burden of Plasmodium Vivax, 2000–17: A Spatial and Temporal Modelling Study.” The Lancet, 394.

Bell BM (2012). “CppAD: A Package for C++ Algorithmic Differentiation.” Computational Infrastructure for Operations Research, 57, 10.

Chen Y, Davis TA, Hager WW, Rajamanickam S (2008). “Algorithm 887: CHOLMOD, Supernodal Sparse Cholesky Factorization and Update/downdate.” ACM Transactions on Mathematical Software (TOMS), 35(3), 22.

Diggle PJ, Moraga P, Rowlingson B, Taylor BM, et al. (2013). “Spatial and Spatio-Temporal Log-Gaussian Cox Processes: Extending the Geostatistical Paradigm.” Statistical Science, 28(4), 542–563.

Fuglstad GA, Simpson D, Lindgren F, Rue H (2018). “Constructing Priors That Penalize the Complexity of Gaussian Random Fields.” Journal of the American Statistical Association, pp. 1–8.

Griewank A, Walther A (2008). Evaluating Derivatives: Principles and Techniques of Algorithmic Differentiation, volume 105. Siam.

Guennebaud G, Jacob B, Avery P, Bachrach A, Barthelemy S, et al. (2010). “Eigen V3.”

Hoffman MD, Gelman A (2014). “The No-U-Turn Sampler: Adaptively Setting Path Lengths in Hamiltonian Monte Carlo.” Journal of Machine Learning Research, 15(1), 1593–1623.

Keil P, Belmaker J, Wilson AM, Unitt P, Jetz W (2013). “Downscaling of Species Distribution Models: A Hierarchical Approach.” Methods in Ecology and Evolution, 4(1), 82–94.

Kristensen K, Nielsen A, Berg CW, Skaug H, Bell BM (2016). “TMB: Automatic Differentiation and Laplace Approximation.” Journal of Statistical Software, 70(5), 1–21. doi: 10.18637/jss.v070.i05.

Li Y, Brown P, Gesink DC, Rue H (2012). “Log Gaussian Cox Processes and Spatially Aggregated Disease Incidence Data.” Statistical methods in medical research, 21(5), 479–507.

Rue H, Martino S, Chopin N (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), 319–392.

Simpson D, Rue H, Riebler A, Martins TG, Sørbye SH, et al. (2017). “Penalising Model Component Complexity: A Principled, Practical Approach to Constructing Priors.” Statistical Science, 32(1), 1–28.

Skaug HJ, Fournier DA (2006). “Automatic Approximation of the Marginal Likelihood in Non-Gaussian Hierarchical Models.” Computational Statistics & Data Analysis, 51(2), 699–709.

Sturrock HJ, Bennett AF, Midekisa A, Gosling RD, Gething PW, Greenhouse B (2016). “Mapping Malaria Risk in Low Transmission Settings: Challenges and Opportunities.” Trends in Parasitology, 32(8), 635–645.
Sturrock HJ, Cohen JM, Keil P, Tatem AJ, et al. (2014). “Fine-Scale Malaria Risk Mapping from Routine Aggregated Case Data.” *Malaria journal*, 13(1), 421.

Wakefield J, Shaddick G (2006). “Health-Exposure Modeling and the Ecological Fallacy.” *Biostatistics*, 7(3), 438–455.

Weiss DJ, Lucas TC, Nguyen M, Nandi AK, Bisanzio D, Battle KE, Cameron E, Twohig KA, Pfeffer DA, Rozier JA, et al. (2019). “Mapping the Global Prevalence, Incidence, and Mortality of *Plasmodium Falciparum*, 2000–17: A Spatial and Temporal Modelling Study.” *The Lancet*, 394.

Wilson K, Wakefield J (2018). “Pointless Spatial Modeling.” *Biostatistics*.

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