Linking the SPDE method with Stan

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Motivation

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Sea urchin (*Loxechinus albus*) is one of the most important benthic resource in Chile ([6][15]). Due to their large-scale spatial metapopulation structure, sea urchin subpopulations are interconnected by larval dispersion, so the recovery of local abundance depends on the distance and hydrodynamic characteristics of their spatial domain. Besides, the population is structured as a metapopulation across a large spatial scale ([17] [18]).

Motivation

Figure: Common structure of the Sea urchin in a "patch". Reference: http://cocinafuturo.net/

....

Motivation

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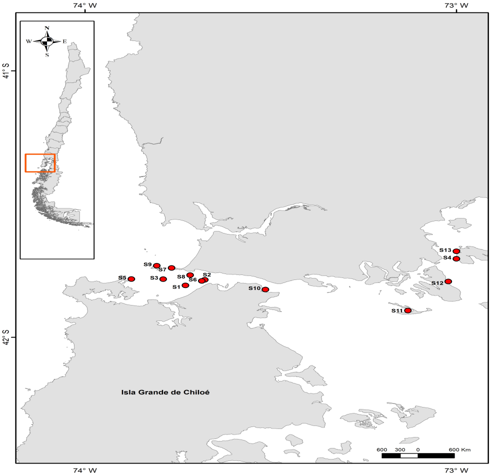

Figure: Sites of fishing of the Sea urchin (*Loxechinus albus*) in the south of Chile

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.... and what is a standardized catch per unit effort?

Catch per unit effort (CPUE) is a crucial variable in fishery science and often assumed proportional to the abundance for a particular fishery resource over time

Motivation

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Methodologies

- Generalized Linear Models (GLM; [16][12])
- Generalized Additive Models (GAM's; [7][23][8])
- Generalized Linear Mixed Models (GLMM; [20][3])

Motivation

Recent methodologies applied

- Delta-GLMM ([22])
- TMB ([9])
- INLA ([4])

Hypothesis

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Research objective

- Obtain the CPUE vector ($\approx$ index of relative abundance) incorporating the spatial and temporal dependence in the observations and compare it with the classical estimation.

Materials and Methods

Gaussian random field (GRF)

Definition

Let s a location in a particular area D and $\boldsymbol{u}(s)$ is a random effect (spatial) at that location. $\boldsymbol{u}(s) \in D$ is a stochastic processes and $\boldsymbol{D} \subset \mathbb{R}^d$ is the spatial domain where are measured the observations. $\boldsymbol{u}\,(s_i)$ is a realization of $\boldsymbol{u}(s)$ where $i = 1, \ldots, n$ locations. We asumme that $\boldsymbol{u}(s)$ has a multivariate Gaussian distribution (GRF), continuous over the space indexed by s and defined by it's mean and covariance ([5])

Note: We consider $s = (s_1, s_2)$ where s_1 and s_2 can be, for example, latitude and longitude respectively.

Materials and Methods

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Solution?

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Solution?

An explicit link between Gaussian fields and Gaussian Markov random fields: the stochastic partial differential equation approach

Finn Lindgren and Håvard Rue

Norwegian University of Science and Technology, Trondheim, Norway

and Johan Lindström

Lund University, Sweden

[11] propose an approximation of the GRF by a GMRF using Stochastic Partial Differential Equations (SPDE)

Materials and Methods

More references about the SPDE method can be found in:

Bayesian Spatial Modelling with R-INLA

Finn Lindgren
University of Bath, United Kingdom

Håvard Rue
Norwegian University of Science and Technology, Norway

Understanding the stochastic partial differential equation approach to smoothing

David L Miller * Richard Glennie* Andrew E Seaton*

Figure: Literature to read about the SPDE method

[10] , [13]

So, how can we express that in a statistical model?

So, how can we express that in a statistical model? $\rightarrow$ Hierarchical model!

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$$
\begin{aligned}
\boldsymbol{\theta} &\sim \boldsymbol{\theta} && \text{Hyperparameters} && (1)\\
\boldsymbol{u} \mid \boldsymbol{\theta} &\sim \mathscr{N}(0, \boldsymbol{Q}(\boldsymbol{\theta})^{-1}) && \text{Latent gaussian field} && (2)\\
y_i \mid \boldsymbol{u}, \boldsymbol{\theta} &\sim \prod_i \pi(y_i \mid \eta_i, \boldsymbol{\theta}) && \text{Observations} && (3)
\end{aligned}
$$

where $\boldsymbol{Q}(\boldsymbol{\theta})$ is the presicion matrix, $\boldsymbol{u}$ is the latent gaussian field and $\eta_i = log(\mu_i) = \text{intercept} + f(\boldsymbol{X}_i) + \boldsymbol{u}_i$, where the matrix $\boldsymbol{X}$ is a set of covariates and $\boldsymbol{u} \sim GMRF(0, \boldsymbol{Q}^{-1})$

How to solve in an efficient way a (spatial) Hierarchical Bayesian model?

Materials and Methods

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- `R-INLA` $\Longrightarrow$ ([21], [2], [10], [1])

Materials and Methods

How to solve in an efficient way a (spatial) Hierarchical Bayesian model?

- `R-INLA` $\Longrightarrow$ ([21], [2], [10], [1])
- MCMC ... `Stan`? `How`?

Materials and Methods

Template Model Builder (TMB)

TMB is a frequentist software/package for fitting statistical latent variable models to the data.

The TMB code is essentially written in C++ and there is no need to supply the derivatives of the function to be minimized with respect to the parameters; these are computed automatically using Automatic differentiation.

Materials and Methods

Also,

- The sparsity of the Hessian is detected automatically.
- Automatic bias-corrections are applied when reporting a non-linear function of the random effects.
- The model can be parallelized.

Materials and Methods

How works `TMB`?

- At first intance we need to define the log-likelihood:

$$f(\theta, u) = log(Pr(y \mid \theta_1, u)Pr(u \mid \theta_2)))$$

- Laplace approximation (Taylor series expansion of second order) for the joint log-likelihood:

$$f(u, \theta) \approx f(\hat{u} \mid \theta) + f^{'}(\hat{u} \mid \theta)(\hat{u} - u) + 1/2 * f^{''}(\hat{u} \mid \theta)(\hat{u} - u)^2$$

- Evaluate the Laplace approximation around "inner maximum"

$$\hat{u} = \underset{u}{\operatorname{argmax}}(f(\theta, u))$$

- Aproximate the joint likelihood

$$Pr(y \mid \theta_1, u)Pr(u \mid \theta_2) = e^{f(u|\theta)} \approx e^{f(\hat{u}|\theta) - 1/2 * |f^{''}(\hat{u})|(\hat{u} - u)^2}$$

Materials and Methods

If you want to know more about spatial modeling in `TMB` you can read this very interesting and applied article (it has an example code written in `TMB`!):

A Statistical Introduction to Template Model Builder:
A Flexible Tool for Spatial Modeling

Aaron Osgood-Zimmerman[a,*], Jon Wakefield[a,b]

University of Washington, Seattle

[a] *Department of Statistics*
[b] *Department of Biostatistics*

[19]

Materials and Methods

Ok, but where `Stan` appear?

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tmbstan

The models built in TMB pass their log-density and gradients calculations to the Bayesian samplers in Stan through a R interface. You only need to add the prior distribution on the parameters in your TMB code!

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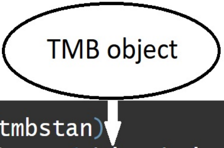
`tmbstan`

The models built in `TMB` pass their log-density and gradients calculations to the Bayesian samplers in `Stan` through a R interface. You only need to add the prior distribution on the parameters in your `TMB` code!




```
library(tmbstan)
fit = tmbstan(Obj, chains = 2, open_progress = FALSE,
              init ='last.par.best',
              control = list(max_treedepth = 10, adapt_delta = 0.8)
              iter = 2000, warmup=1000, seed=483892929)
```

CPUE estimation

Data

- Temporal observations: from 1996 to 2016 ("Year" variable as a "factor").
- Spatial observations: 13 sites of fishing ("sites" as a spatial random effect)
- Covariates: "Depth" (average depth of catches), "Quarter" (season of the year), and the variable "Market" (1 or 2).

CPUE estimation

Table: Proposed models to obtain a relative abundance index

Models	Structure
Lognormal	$(y_i \mid \boldsymbol{\theta}) \sim p(y_i \mid \eta_i, \boldsymbol{\theta})$
Spatial Lognormal	$(y_i \mid \boldsymbol{u}, \boldsymbol{\theta}) \sim p(y_i \mid \eta_i, \boldsymbol{\theta})$
Gamma	$(y_i \mid \boldsymbol{\theta}) \sim p(y_i \mid \eta_i, \boldsymbol{\theta})$
Spatial Gamma	$(y_i \mid \boldsymbol{u}, \boldsymbol{\theta}) \sim p(y_i \mid \eta_i, \boldsymbol{\theta})$

Results

Results

Table: Comparison with `LOO` criterion for each proposed model. The `elpd_diff` measures the difference between each model relative to the best $\widehat{elpd}_n$ (the model in the first row) and `se_diff` is the standard error of the difference in `elpd_diff`.

Models	elpd_diff	se_diff
Spatial Gamma	0	0
Spatial Lognormal	-42	23
Lognormal	-88	18
Gamma	-125	28

Results

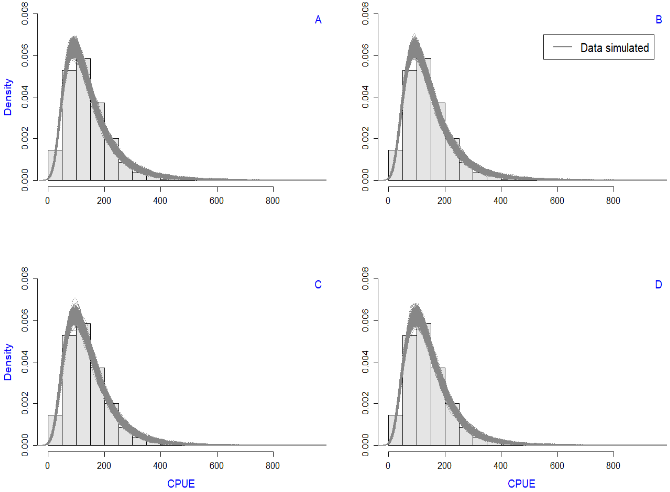


Figure: Observed data (histogram) and density estimates (lines) of 1,000 posterior predictive data simulated from Lognormal model, spatial Lognormal model, Gamma model and spatial Gamma model. See Table 1 for model descriptions.

Results

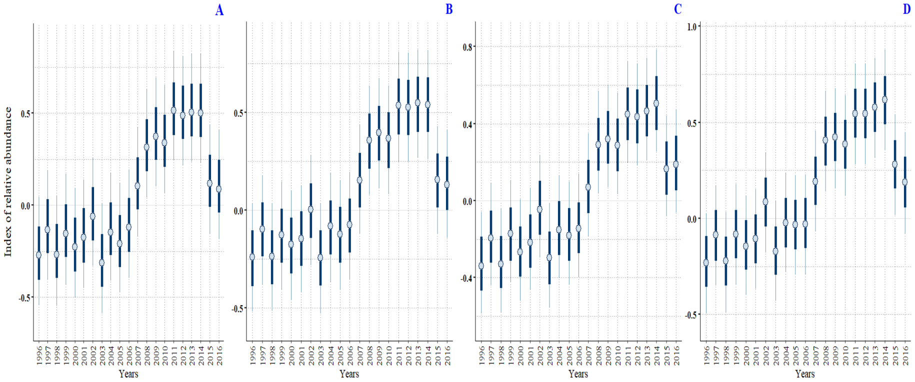


Figure: Comparison of the coefficients (relative abundance indices) estimated with Lognormal model, spatial Lognormal model, Gamma model and spatial Gamma model. The points are the values for the coefficients and the thick bars are uncertainty intervals computed from posterior draws with all chains merged in the MCMC method (90% credible interval).

Results

To assess the potential effects of including sites with only one year of observations we made two additional model comparisons.

Table: Additional comparisons with LOO

Comparison excluding site 1		
Models	elpd_diff	se_diff
Spatial Gamma	0	0
Spatial Lognormal	-15	23
Gamma	-89	18
Lognormal	-95	28

Comparison excluding sites 1, 2, 3 and 8		
Models	elpd_diff	se_diff
Spatial Lognormal	0	0
Spatial Gamma	-5	22
Lognormal	-70	16
Gamma	-81	28

Results

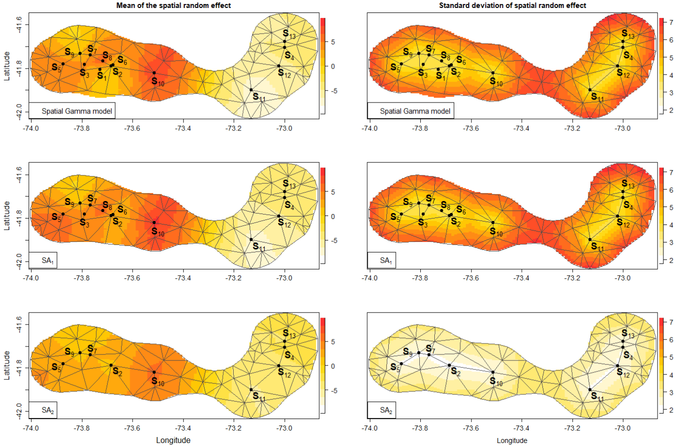


Figure: Mean (left) and standard deviation (right) of the spatial field estimated by the spatial Gamma model, and for the first (SA_1) and second (SA_2) sensitivity analysis respectively.

Conclusions

Conclusions

- Incorporating a spatial random effect to obtain a relative abundance index for sea urchin (L. albus) enabled better statistical performance than models without spatial dependence.
- Although the trends of the estimated indices for our case study with and without spatial effects were similar, statistical diagnostics clearly indicated that the spatial model outperformed the non-spatial version and fit the data better.
- This difference could have important impacts on the estimated status and trend of the stock, and ultimately the catch quota, so assessing the stock with both indices would be valuable.

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Accounting for spatial dependence improves relative abundance estimates in a benthic marine species structured as a metapopulation

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Thank You