

Biostatistics: Towards near real-time Bayesian inference

Janet van Niekerk

November 28, 2025

QR code for slides



https://github.com/JanetVN1201/SASA_2025

Outline I

- 1 Biostatistics and Bayesian inference
- 2 Survival models as Latent Gaussian models
- 3 The INLA methodology
- 4 Case studies
 - AML survival (using Matern field)
 - Adherence study (Quantile joint model)
 - Dengue risk in Brazil (Non-stationary disease mapping)
 - Dementia study (3D Spatial model)

Disclosure

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I am a Bayesian...

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and it's not that deep...

Modeling pipeline

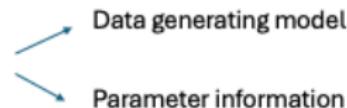
Choose/Develop the model

Data generating model

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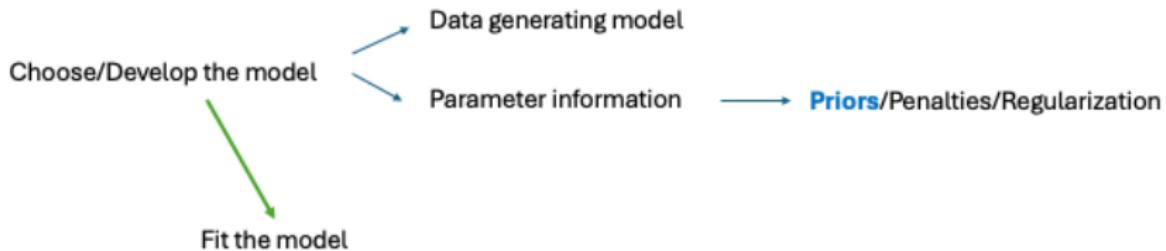


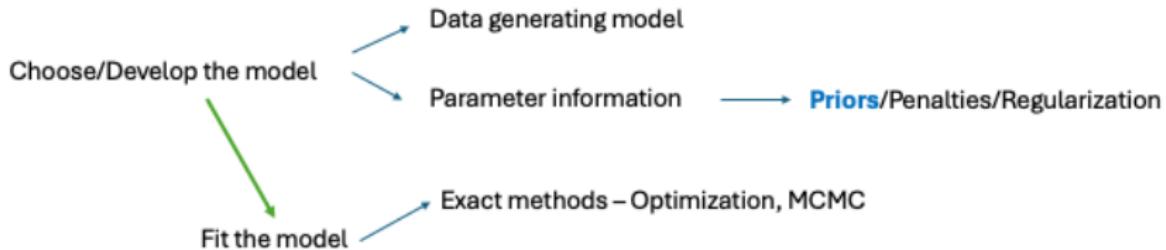
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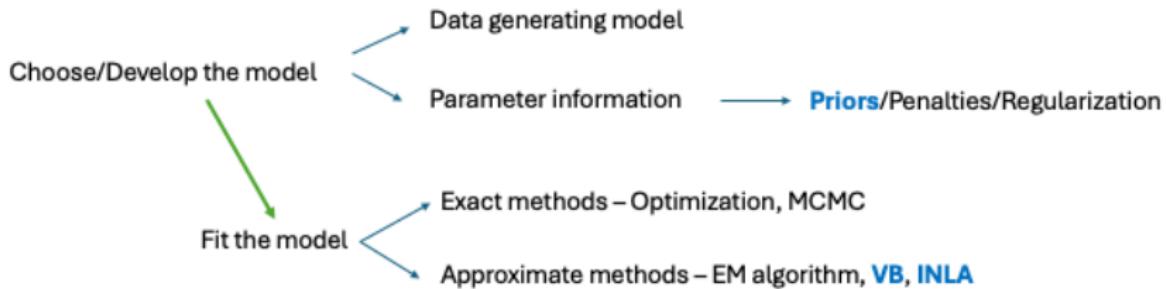


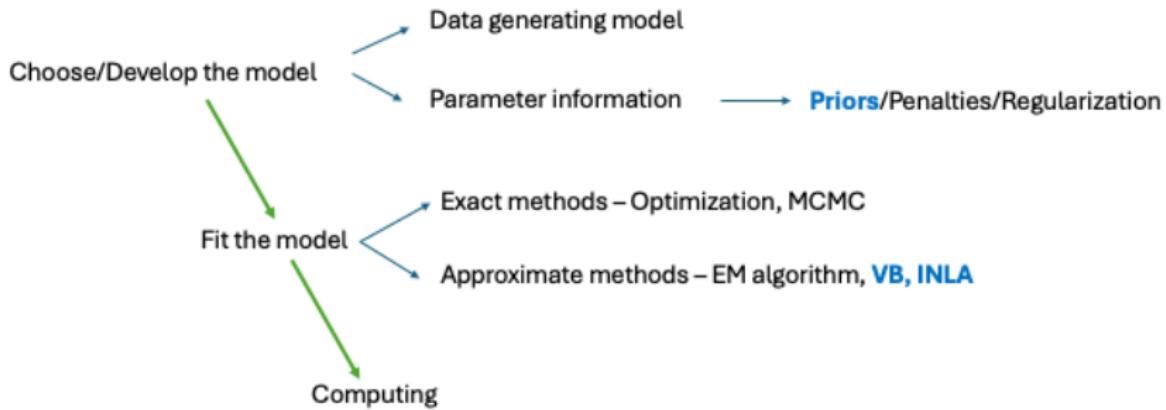
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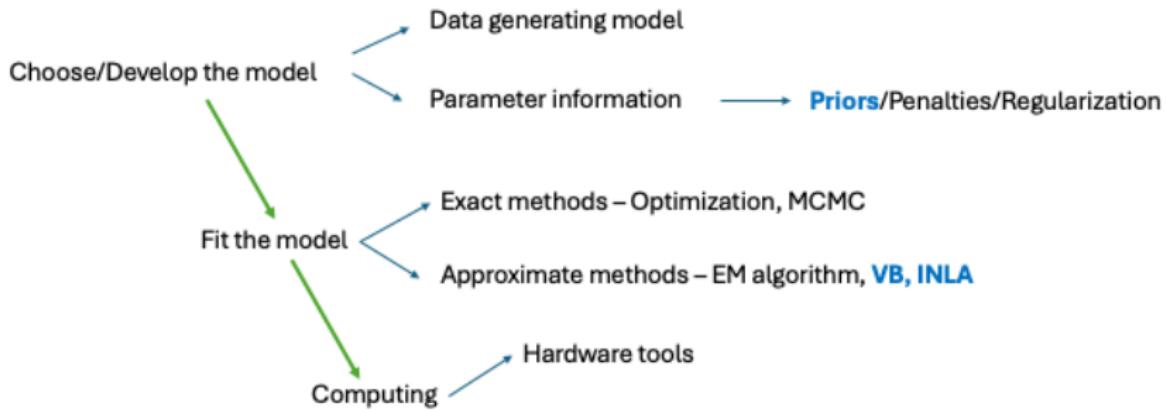


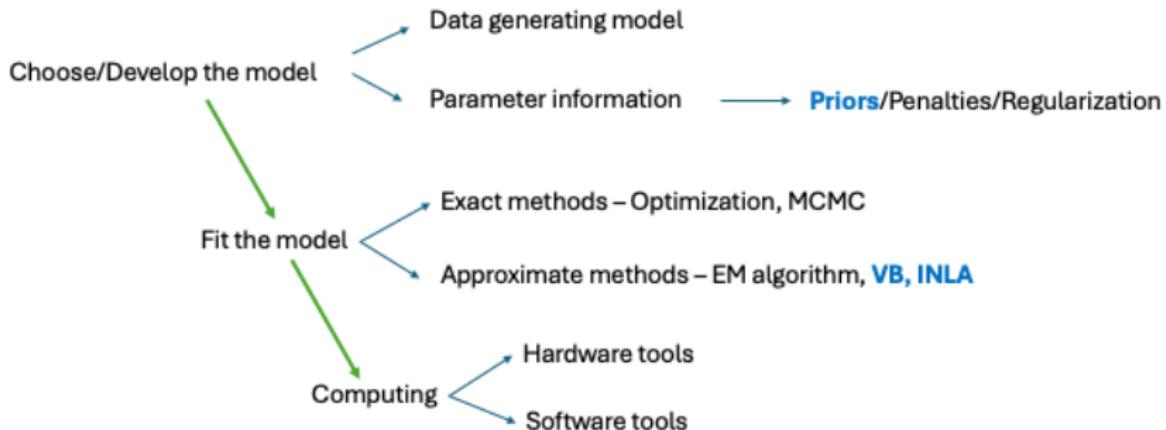


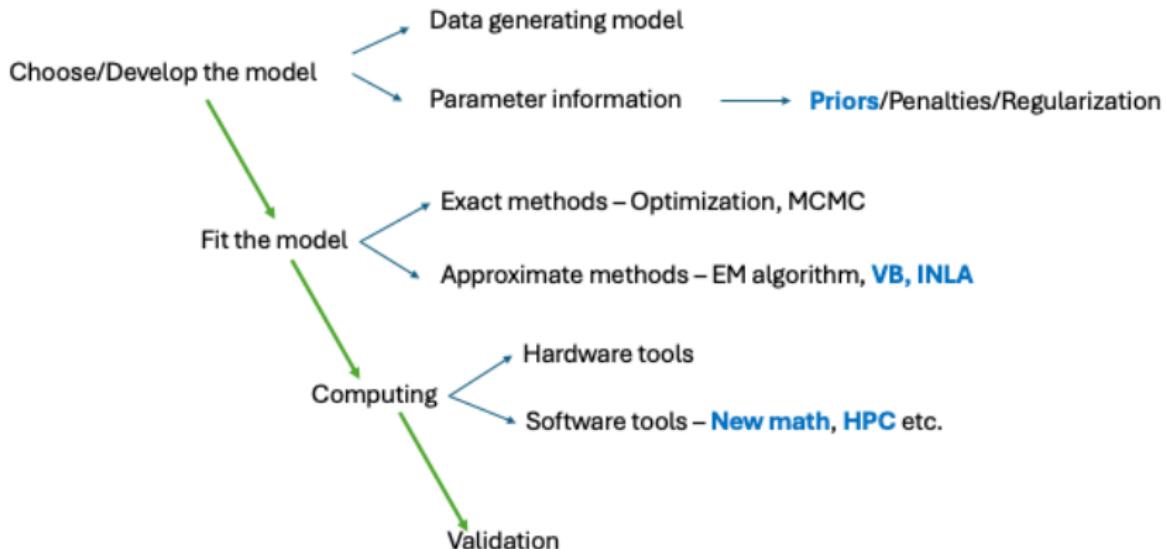


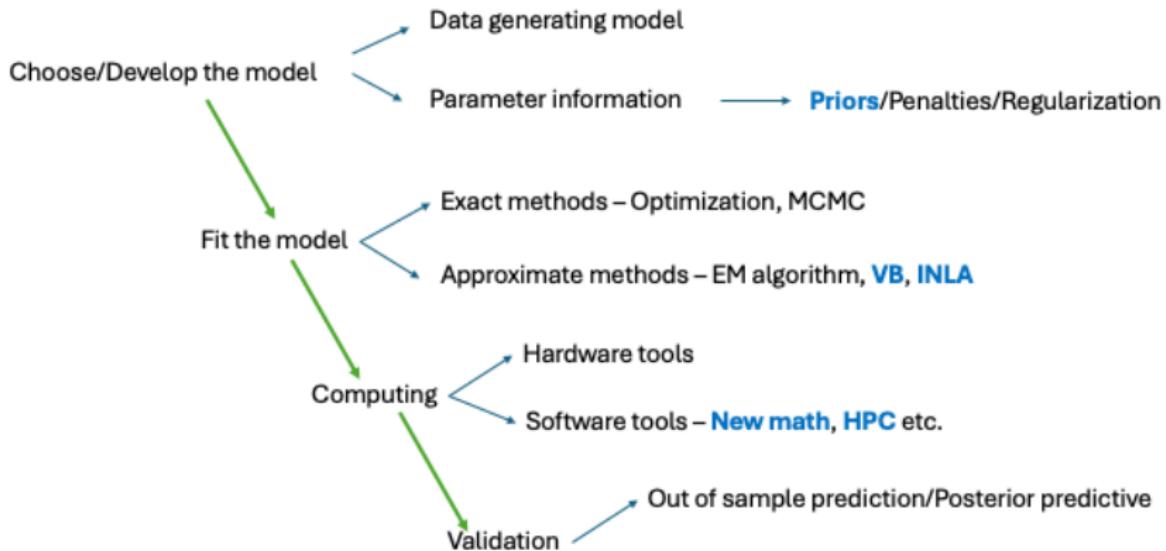


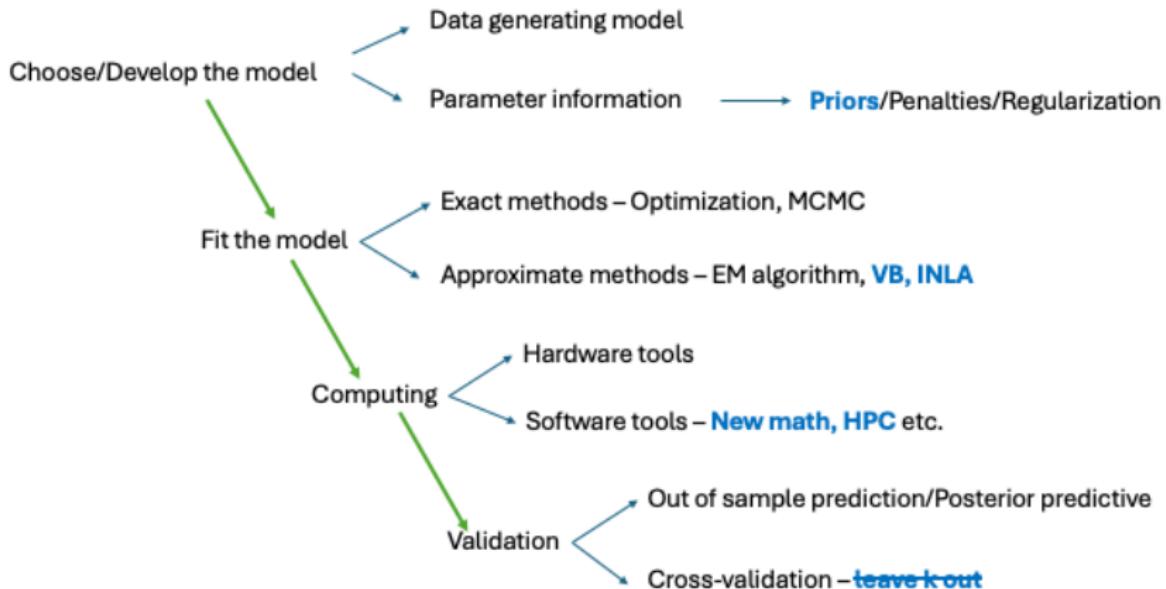












Choose/Develop the model

Data generating model

Parameter information

Priors/Penalties/Regularization

Fit the model

Exact methods – Optimization, MCMC

Approximate methods – EM algorithm, **VB, INLA**

Computing

Hardware tools

Software tools – **New math, HPC** etc.

Validation

Out of sample prediction/Posterior predictive

Cross-validation – **leave k out**

IMPACT!



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Software – R packages (INLA, INLAdjoint, graphpcor), Python packages

Models for Biostatistics

Survival analysis

Models for Biostatistics

Survival analysis

Image analysis

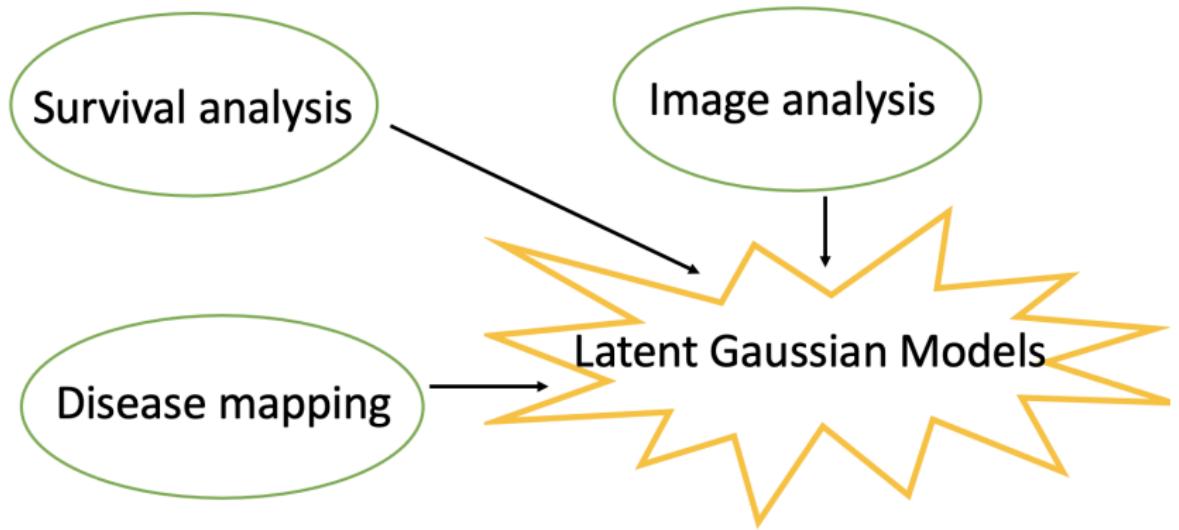
Models for Biostatistics

Survival analysis

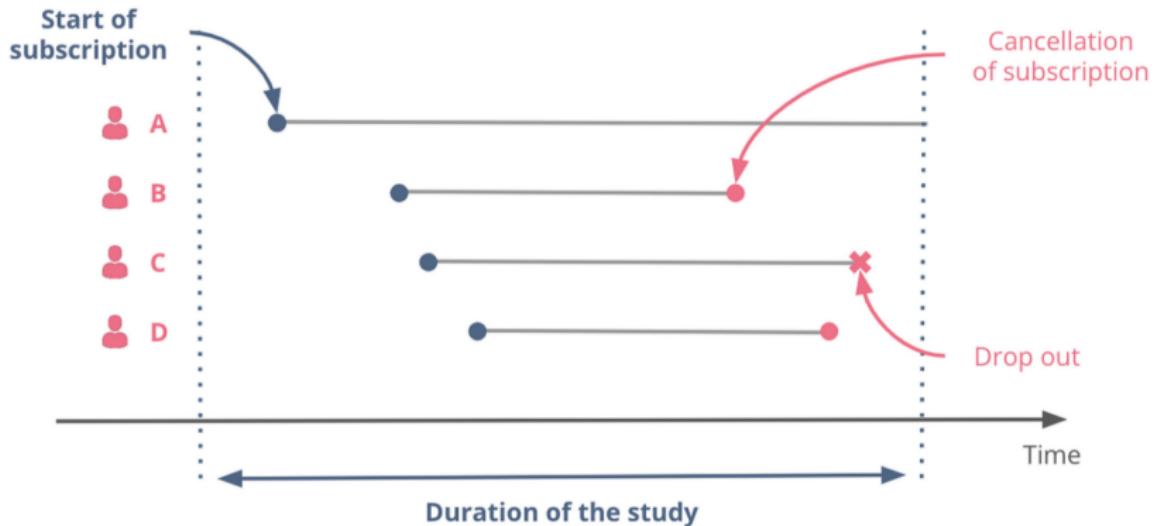
Image analysis

Disease mapping

Models for Biostatistics



Time-to-event data



Hazard rate, Survival probabilities etc.

Bayesian inference for survival analysis

In GLM usually we model the mean with a linear model

$$E(y) = g(\beta_0 + \beta X)$$

But in survival analysis or reliability we usually model the hazard rate or survival function

$$h(t) = g(\beta_0 + \beta X)$$

or

$$S(t) = h(\beta_0 + \beta X)$$

Computational aspects

- Analytical methods - conjugacy (pre-computer era)
- Approximate methods - Laplace (can be inaccurate)
- Exact methods - MCMC (very slow for complex models or large data)

Now, due to computing resources approximate methods are gaining popularity - INLA, VB, EP etc.

INLA versus MCMC

For small models and data:

	INLA	MCMC/HMC
Method	Deterministic (Mathematical)	Sampling-based
Memory cost	Low	Low
Computational cost	Low	Low

For large models and/or data:

	INLA	MCMC/HMC
Method	Deterministic (Mathematical)	Sampling-based
Memory cost	Low	High
Computational cost	Low	Very high

What is INLA?

INLA - Integrated Nested Laplace Approximations

- Deterministic "nonparametric" approximations instead of sampling
- LGM - Latent Gaussian models
- Three internal strategies - Gaussian, simplified Laplace, Laplace (pre 2021)
- R package "INLA"

Now there is a new default strategy combining Laplace approximations with Variational Bayes.¹ (2024)

¹van Niekerk, J. and Rue, H., 2024. Low-rank variational Bayes correction to the Laplace method. *Journal of Machine Learning Research*, 25(62), pp.1-25.

Why is INLA so accurate and so fast?

- LGM structure
- Sparse precision matrix
- Specialized matrix algebra for sparse matrices
- NEW: VB (low-rank) correction

Use precision matrix instead of covariance matrix → natural occurrence

But what about survival and reliability models (or overall biostatistics)?
Can we use INLA to perform Bayesian inference of such models?

Model definition - GAMM

Suppose we have response data $\mathbf{y}_{n \times 1}$ (conditionally independent) with density function $\pi(y|\mathbf{X}, \boldsymbol{\theta})$ and link function $h(\cdot)$, that is linked to some covariates \mathbf{Z} through linear predictors

$$\boldsymbol{\eta}_n = \beta_0 + \mathbf{Z}_\beta \boldsymbol{\beta} + \sum f^k(\mathbf{Z}_f) = \mathbf{A}\mathbf{X}$$

The inferential aim is to estimate the latent field $\mathbf{X}_m = \{\beta_0, \boldsymbol{\beta}, \mathbf{f}\}$, and $\boldsymbol{\theta}$.

GAMM → LGM

Assume

$$\boldsymbol{X}|\boldsymbol{\theta} \sim N(\boldsymbol{0}, \boldsymbol{Q}(\boldsymbol{\theta})^{-1})$$

where $\boldsymbol{Q}(\boldsymbol{\theta})$ is a sparse matrix (\boldsymbol{X} is a GMRF).

$p(\boldsymbol{X}, \boldsymbol{\theta}) = p(\boldsymbol{X}|\boldsymbol{\theta})p(\boldsymbol{\theta})$ and $p(\boldsymbol{\theta})$ can be non-Gaussian.

INLA is designed to work for LGM's

- ① Data y_i with some likelihood $L(\mathbf{X}, \boldsymbol{\theta} | \mathbf{y}) = \prod_{i=1}^n f(y_i | \eta_i = h(\mathbf{X}, \boldsymbol{\theta}))$
- ② $\eta_i = h(\beta Z + \mathbf{u}(\boldsymbol{\theta}) \mathbf{A})$
- ③ $\mathbf{X} | \boldsymbol{\theta} \sim N(\mathbf{0}, Q(\boldsymbol{\theta})^{-1})$
- ④ $\boldsymbol{\theta} \sim \text{hyperprior}$

Survival models as LGM's

Censoring and Truncation affects the likelihood only. For censoring,

- ① Right : $L_i(t_i|d_i) = S_i(t_i)$
- ② Event : $L_i(t_i|d_i) = S_i(t_i)f_i(t_i)$
- ③ Left : $L_i(t_i|d_i) = 1 - S_i(t_i)$
- ④ Interval : $L_i(t_{1i}, t_{2i}|d_i) = S_i(t_{1i}) - S_i(t_{2i}),$

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Possibilities

- Frailty models - unit-specific or clustered
- Spatial survival models - areal or continuous in space
- Nonlinear effects of covariates using splines
- Joint models with continuous or discrete longitudinal biomarker(s)
- Competing risks or multi-state models
- and many more...

How does INLA work?

Website for R-INLA library



<https://www.r-inla.org/>

Bayesian inference

Data \mathbf{y} (with covariates \mathbf{Z}), depend on \mathbf{X} and $\boldsymbol{\theta}$ such that, $E[Y] = h(\mathbf{A}(\mathbf{Z})\mathbf{X})$.

Bayes' theorem:

$$q(\mathbf{X}, \boldsymbol{\theta} | \mathbf{y}) \propto L(\mathbf{y} | \mathbf{X}, \boldsymbol{\theta}) p(\mathbf{X}, \boldsymbol{\theta})$$

Posterior \propto Likelihood \times Prior

$$\log q(\mathbf{X}, \boldsymbol{\theta} | \mathbf{y}) \propto \log L(\mathbf{y} | \mathbf{X}, \boldsymbol{\theta}) + \log p(\mathbf{X}, \boldsymbol{\theta})$$

\log Posterior \propto \log Likelihood + \log Prior

Posterior approximations by INLA

$$\pi(\boldsymbol{X}, \boldsymbol{\theta}, \boldsymbol{y}) = \pi(\boldsymbol{\theta})\pi(\boldsymbol{X}|\boldsymbol{\theta}) \prod_{i=1}^n \pi(y_i | (\boldsymbol{AX})_i, \boldsymbol{\theta})$$

Posterior approximations by INLA

$$\begin{aligned}\pi(\boldsymbol{X}, \boldsymbol{\theta}, \boldsymbol{y}) &= \pi(\boldsymbol{\theta})\pi(\boldsymbol{X}|\boldsymbol{\theta}) \prod_{i=1}^n \pi(y_i | (\boldsymbol{AX})_i, \boldsymbol{\theta}) \\ \tilde{\pi}(\boldsymbol{\theta}|\boldsymbol{y}) &\propto \frac{\pi(\boldsymbol{X}, \boldsymbol{\theta}, \boldsymbol{y})}{\pi_G(\boldsymbol{X}|\boldsymbol{\theta}, \boldsymbol{y})} \Big|_{\boldsymbol{X}=\mu(\boldsymbol{\theta})}\end{aligned}$$

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$\tilde{\pi}(\boldsymbol{X}_j|\boldsymbol{\theta}, \boldsymbol{y})$ depends on the approximation used, for Gaussian it is straightforward for the Laplace approximation we do another Gaussian approximation to $\tilde{\pi}(\boldsymbol{X}_{-j}|\boldsymbol{\theta}, \boldsymbol{y})$.

Modern INLA

The Gaussian approximation $\pi_G(\boldsymbol{X}|\boldsymbol{\theta}, \boldsymbol{y})$ to $\pi(\boldsymbol{X}|\boldsymbol{\theta}, \boldsymbol{y})$ is calculated from a second order expansion of the likelihood around the mode of $\pi(\boldsymbol{X}|\boldsymbol{\theta}, \boldsymbol{y})$, $\mu(\boldsymbol{\theta})$ as follows

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$$\begin{aligned}\log(\pi(\mathbf{X}|\boldsymbol{\theta}, \mathbf{y})) &\propto -\frac{1}{2}\mathbf{X}^\top \mathbf{Q}(\boldsymbol{\theta})\mathbf{X} + \sum_{i=1}^n \left(b_i(\mathbf{AX})_i - \frac{1}{2}c_i(\mathbf{AX})_i^2 \right) \\ &= -\frac{1}{2}\mathbf{X}^\top (\mathbf{Q}(\boldsymbol{\theta}) + \mathbf{A}^\top \mathbf{D}\mathbf{A})\mathbf{X} - \mathbf{b}^\top \mathbf{AX}\end{aligned}$$

where \mathbf{b} is an n -dimensional vector with entries $\{b_i\}$ and \mathbf{D} is a diagonal matrix with n entries $\{c_i\}$. Note that both \mathbf{b} and \mathbf{D} depend on $\boldsymbol{\theta}$, so the Gaussian approximation is for a fixed $\boldsymbol{\theta}$.

Modern INLA

The process is iterated to find \boldsymbol{b} and \boldsymbol{D} that gives the Gaussian approximation at the mode, $\mu(\boldsymbol{\theta})$, so that

$$\boldsymbol{X}|\boldsymbol{\theta}, \boldsymbol{y} \sim N\left(\boldsymbol{\mu}(\boldsymbol{\theta}), \boldsymbol{Q}_{\boldsymbol{X}}^{-1}(\boldsymbol{\theta})\right).$$

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The graph of the Gaussian approximation consists of two components,

- ① \mathcal{G}_p : the graph obtained from the prior of the latent field through $\boldsymbol{Q}(\boldsymbol{\theta})$
- ② \mathcal{G}_d : the graph obtained from the data based on the non-zero entries of $\boldsymbol{A}^\top \boldsymbol{A}$

Implicit mean correction

Recall that $Q\mu = b$.

Now let's formulate $Q\mu^*$

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So now we solve for,

$$\arg_{\lambda} \min_{p(\mathbf{X}|\mathbf{y}, \boldsymbol{\theta})} \left(E_{p(\mathbf{X}|\mathbf{y}, \boldsymbol{\theta})} \left[- \sum_{i=1}^n \log f(y_i | \mathbf{X}_i, \boldsymbol{\theta}) \right] + \text{KLD}(p || \pi) \right)$$

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where $\mathbf{X}|\mathbf{y}, \boldsymbol{\theta} \sim N(\boldsymbol{\mu}^*, \mathbf{Q}^{-1})$.

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where $\mathbf{X}|\mathbf{y}, \boldsymbol{\theta} \sim N(\mu^*, Q^{-1})$.

Low-rank correction → Only correct some b 's, change to all μ 's.

Modern INLA

Next, the marginal conditional posteriors of the elements of \boldsymbol{X} is calculated from the joint Gaussian approximation as

$$\boldsymbol{X}_j | \boldsymbol{\theta}, \boldsymbol{y} \sim N \left((\boldsymbol{\mu}(\boldsymbol{\theta}))_j, (\boldsymbol{Q}_{\boldsymbol{X}}^{-1}(\boldsymbol{\theta}))_{jj} \right).$$

and the marginals

$$\tilde{\pi}(\boldsymbol{X}_j | \boldsymbol{y}) = \int \pi_G(\boldsymbol{X}_j | \boldsymbol{\theta}, \boldsymbol{y}) \tilde{\pi}(\boldsymbol{\theta} | \boldsymbol{y}) d\boldsymbol{\theta} \approx \sum_{k=1}^K \pi_G(\boldsymbol{X}_j | \boldsymbol{\theta}_k, \boldsymbol{y}) \tilde{\pi}(\boldsymbol{\theta}_k | \boldsymbol{y}) \delta_k.$$

Universal tools in R-INLA - also for biostatistical models



- Model selection metrics - WAIC, DIC
- Cross validation (1 and group) and model-based clustering
- Prediction of unobserved areas or new profiles
- Mean or quantile models
- Joint models
- Multiple imputation
- Coregionalization models
- etc..... ask at <https://groups.google.com/g/r-inla-discussion-group?pli=1> or
e-mail help@r-inla.org

Acute Myeloid Leukemia study

Introduction

In this example we are studying the spatial distribution of leukemia mortality to inform public health policies, to gain insights for unmeasured covariates²



²van Niekerk, J. and Rue, H., 2024. Low-rank variational Bayes correction to the Laplace  

Model

In this example we are studying the spatial distribution of leukemia mortality to inform public health policies, to gain insights for unmeasured covariates.

$$\begin{aligned} h(t|\beta, \boldsymbol{u}) &= h_0(t) \exp(\eta(s)) \\ \eta_i(s) &= \beta_0 + \beta_1 \text{Age}_i + \beta_2 \text{WBC}_i + \beta_3 \text{TPI}_i + u(s), \end{aligned}$$

to account for spatial variation we use a Gaussian effect \boldsymbol{u} with a Matérn covariance structure with hyperparameters, marginal variance σ_u^2 and nominal range $r = 2/\kappa$.

Posterior inference - fixed effects

Time used:

Pre = 4.1, Running = 2.58, Post = 0.156, Total = 6.84

Fixed effects:

	mean	sd	0.025quant	0.5quant	0.975quant	mode	kld
(Intercept)	-2.170	0.206	-2.569	-2.173	-1.753	-2.172	0
sex	0.072	0.069	-0.063	0.072	0.208	0.072	0
age	0.033	0.002	0.029	0.033	0.037	0.033	0
wbc	0.003	0.000	0.002	0.003	0.004	0.003	0
tpi	0.025	0.010	0.005	0.025	0.044	0.025	0

Random effects:

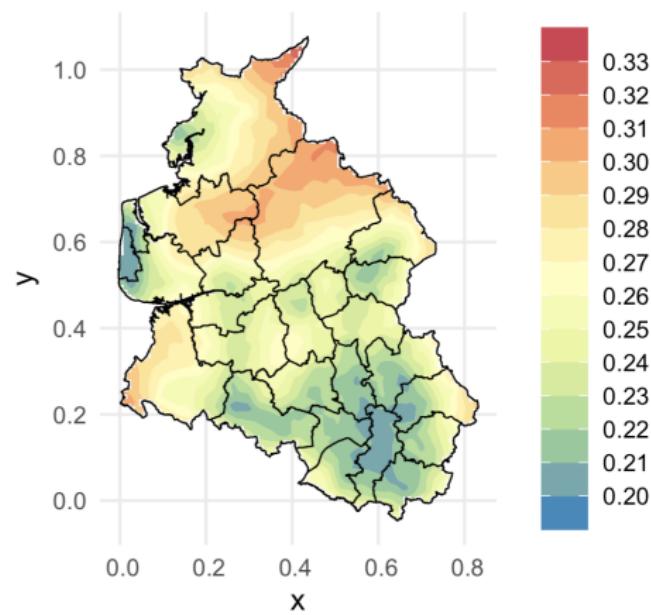
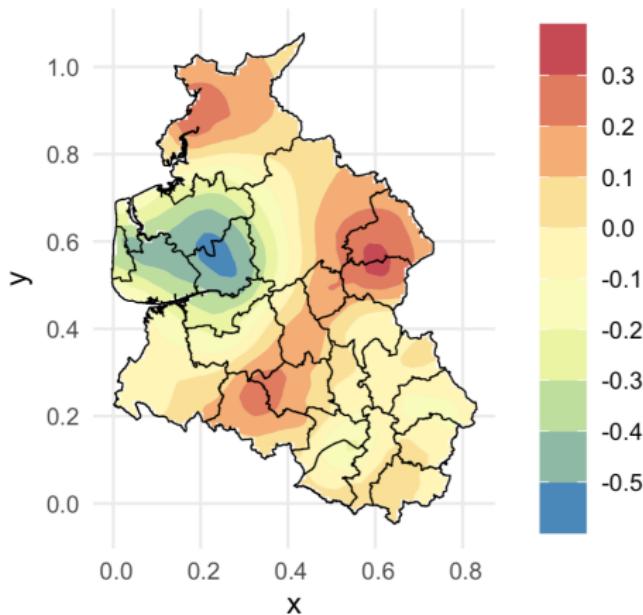
Name Model
spatial SPDE2 model

Model hyperparameters:

	mean	sd	0.025quant	0.5quant	0.975quant	mode
alpha parameter for weibullsurv	0.599	0.016	0.568	0.599	0.631	0.599
Range for spatial	0.310	0.156	0.114	0.276	0.709	0.220
Stdev for spatial	0.293	0.073	0.174	0.284	0.460	0.268

Marginal log-Likelihood: -839.92

Posterior inference - latent spatial field



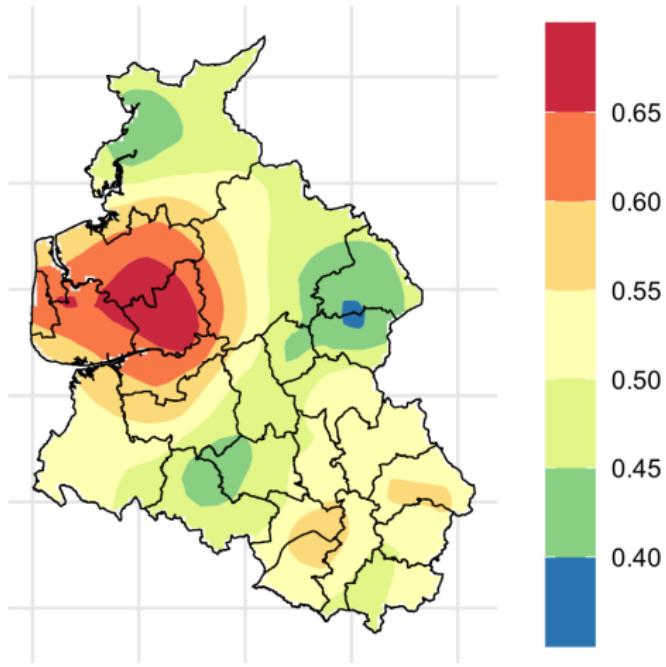
Posterior inference - with MCMC

	HMC	INLA
β_0	-2.189	-2.189
β_1	0.597	0.597
β_2	0.241	0.241
β_3	0.108	0.108
τ	0.340	0.340
σ_u	0.223	0.223
r	0.202	0.202
Time(s)	8214	6.8

Table: Posterior means from HMC and INLA

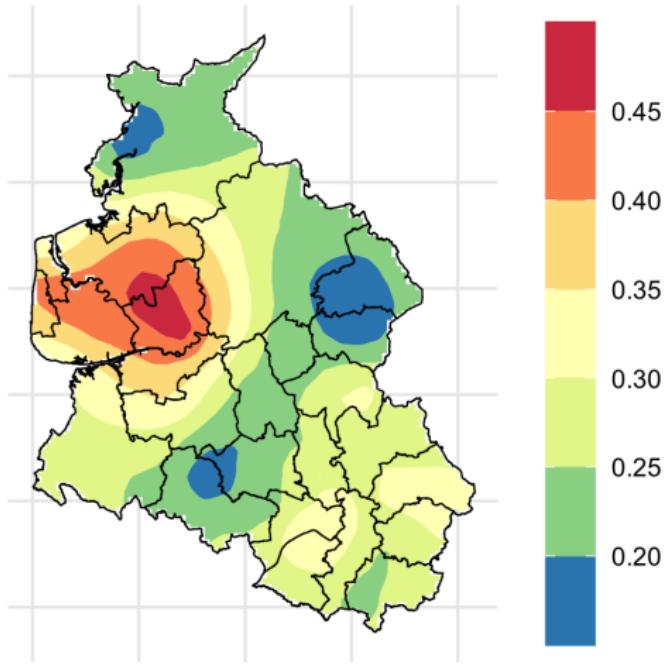
Survival probabilities

Survival function at year 1



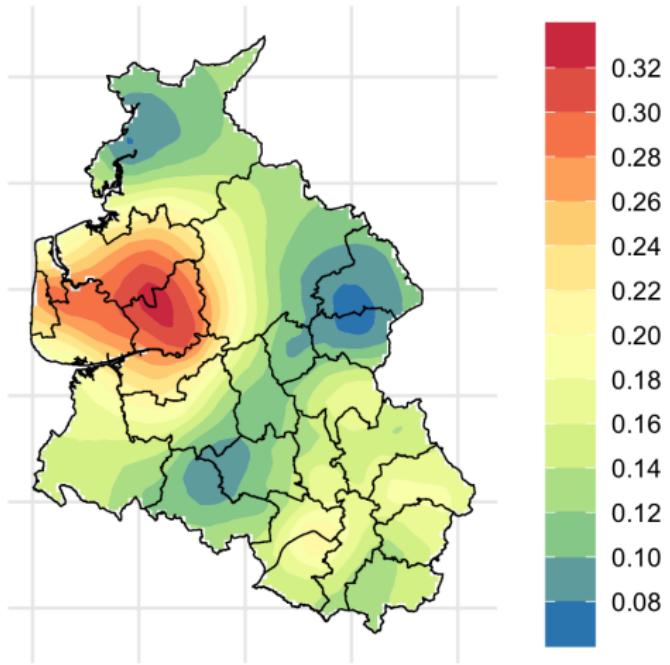
Survival probabilities

Survival function at year 2



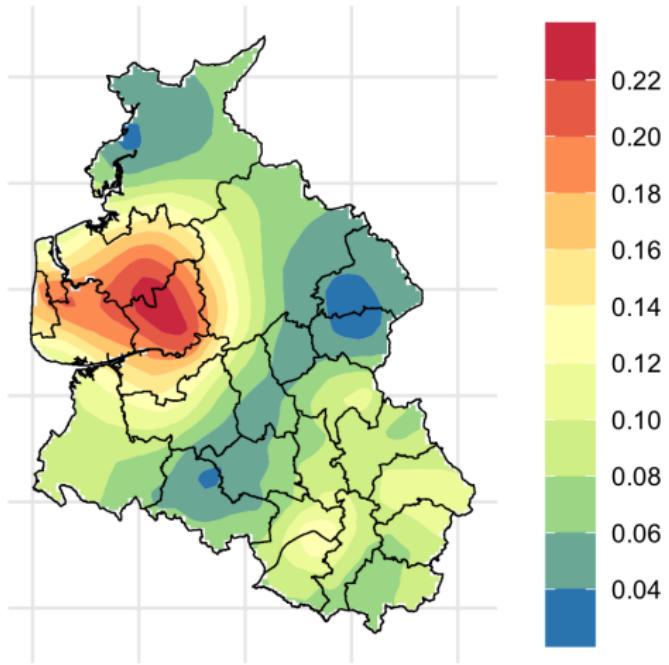
Survival probabilities

Survival function at year 3



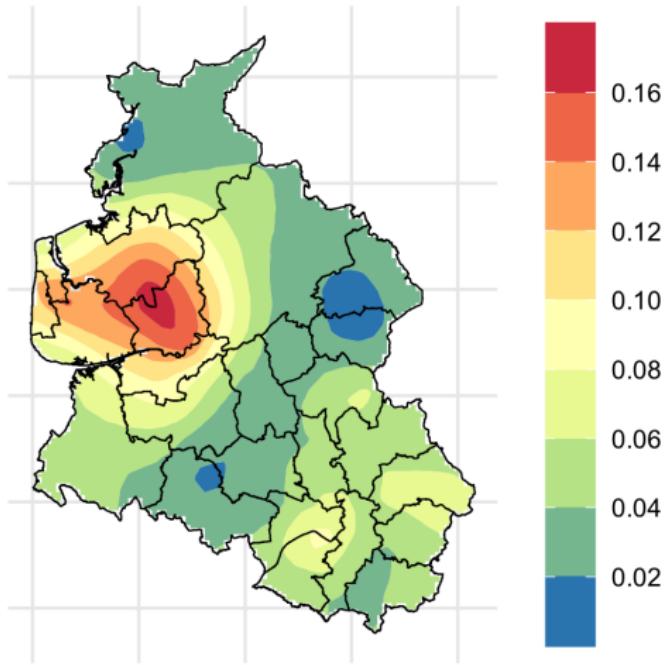
Survival probabilities

Survival function at year 4



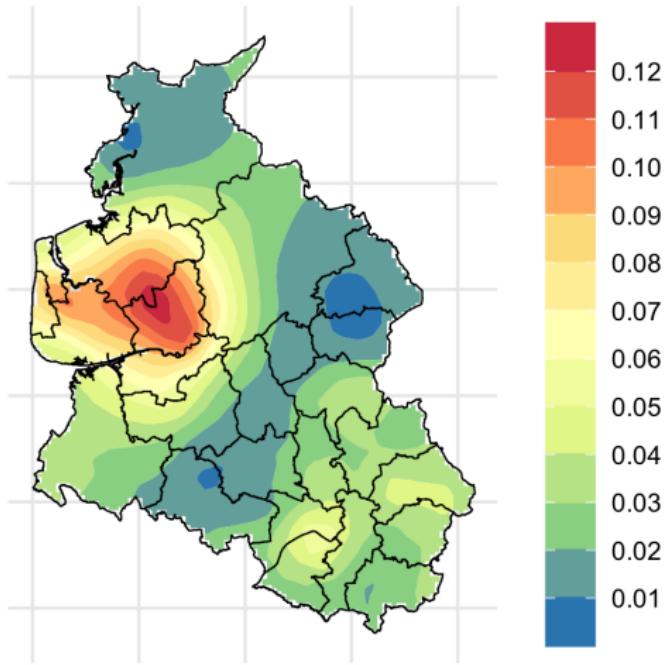
Survival probabilities

Survival function at year 5



Survival probabilities

Survival function at year 6



Medication adherence study

Introduction

From the AARDEX Group - medication adherence and patient persistence is crucial for successful treatment regimes and regularized evaluation³. Adherence is a proportion and persistence is defined based on a set of criteria unique to each drug.

³Burger, D.A., Van der Merwe, S., Van Niekerk, J., Lesaffre, E. and Pironet, A. Joint quantile regression of longitudinal continuous proportions and time-to-event data: application in medication adherence and persistence, *Statistical Methods in Medical Research*, Accepted

Introduction

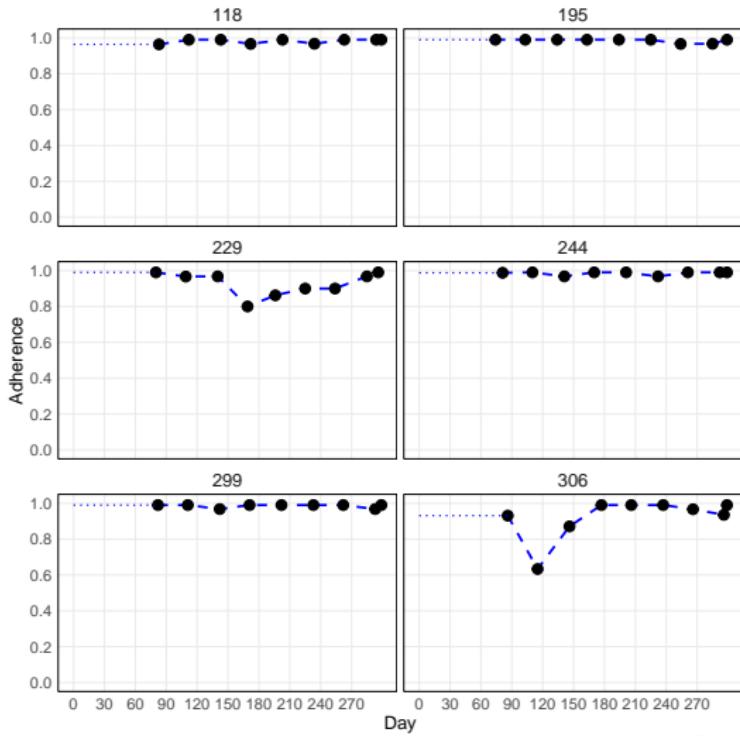
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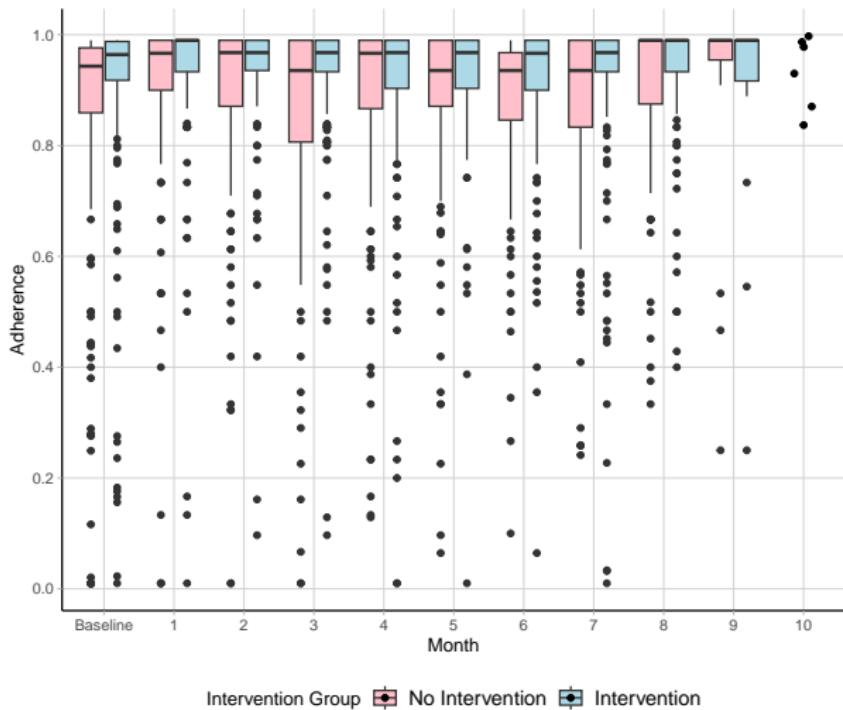
Research problem - outliers in the adherence bias the model, and can cause false positives for intervention.

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Dataset



Dataset



Model

Longitudinal model:

$$f(y_{ij}; \kappa_{q,i}(t_{ij}), \psi) = \alpha_{ij_1} \alpha_2 y_{ij}^{\alpha_{ij_1}-1} \left(1 - y_{ij}^{\alpha_{ij_1}}\right)^{\alpha_2-1},$$

Model

Longitudinal model:

$$\begin{aligned}f(y_{ij}; \kappa_{q,i}(t_{ij}), \psi) &= \alpha_{ij_1} \alpha_2 y_{ij}^{\alpha_{ij_1}-1} \left(1 - y_{ij}^{\alpha_{ij_1}}\right)^{\alpha_2-1}, \\ \kappa_{q,i}(t_{ij}) &= g^{-1}(\eta_{q,i}(t_{ij}))\end{aligned}$$

Model

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$$f(y_{ij}; \kappa_{q,i}(t_{ij}), \psi) = \alpha_{ij_1} \alpha_2 y_{ij}^{\alpha_{ij_1}-1} \left(1 - y_{ij}^{\alpha_{ij_1}}\right)^{\alpha_2-1},$$

$$\kappa_{q,i}(t_{ij}) = g^{-1}(\eta_{q,i}(t_{ij}))$$

$$\eta_{q,i}(t_{ij}) = (\beta_0 + b_{0_i}) + (\beta_{\text{time}} + b_{\text{time}_i} + \mathbf{z}'_i \boldsymbol{\beta}_{\text{tx}}) t_{ij} + \mathbf{x}'_i \boldsymbol{\beta}_{\text{cov}}$$

with $\alpha_{ij_1} = \frac{\log\left(1-(1-q)^{\frac{1}{\alpha_2}}\right)}{\log(\kappa_{q,i}(t_{ij}))}$ and $\alpha_2 = \frac{\log(1-q)}{\log(1-e^{-\psi})}$.

Model

Longitudinal model:

$$f(y_{ij}; \kappa_{q,i}(t_{ij}), \psi) = \alpha_{ij_1} \alpha_2 y_{ij}^{\alpha_{ij_1}-1} \left(1 - y_{ij}^{\alpha_{ij_1}}\right)^{\alpha_2-1},$$

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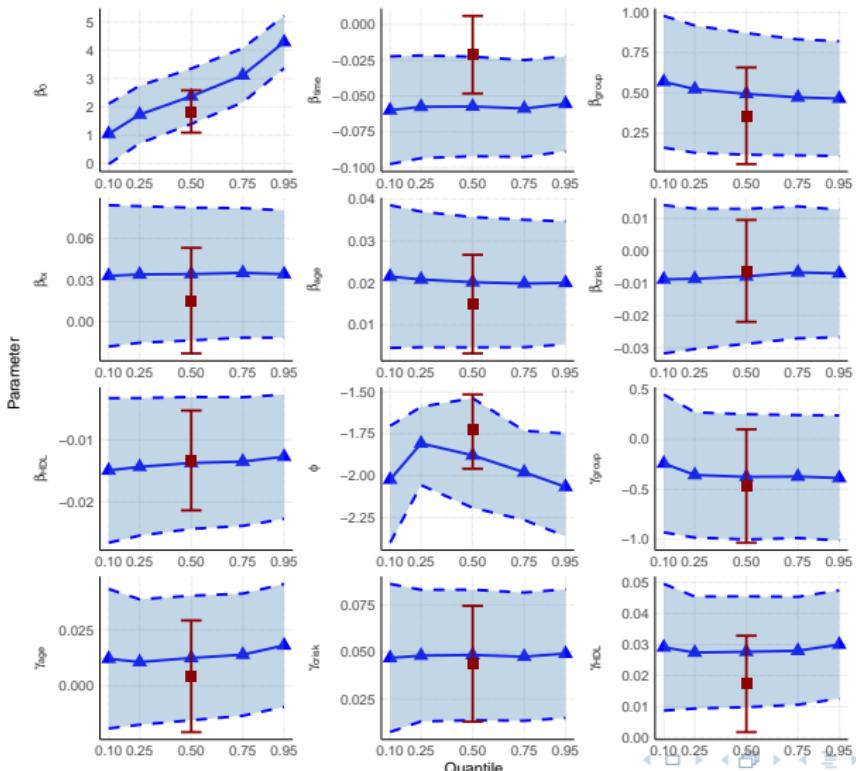
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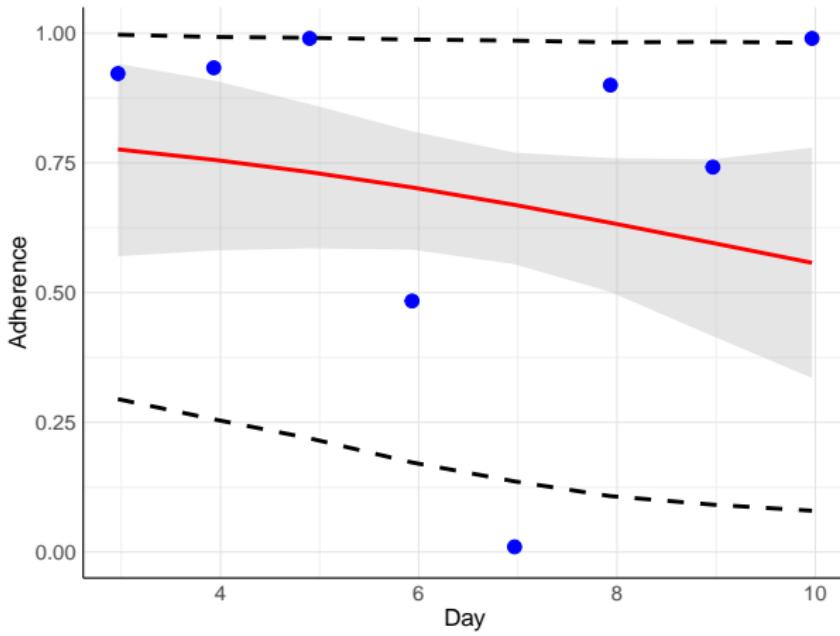
Survival model:

$$h_i(t) = h_0(t) \exp(\phi \eta_i(t) + \mathbf{w}'_i \boldsymbol{\gamma}).$$

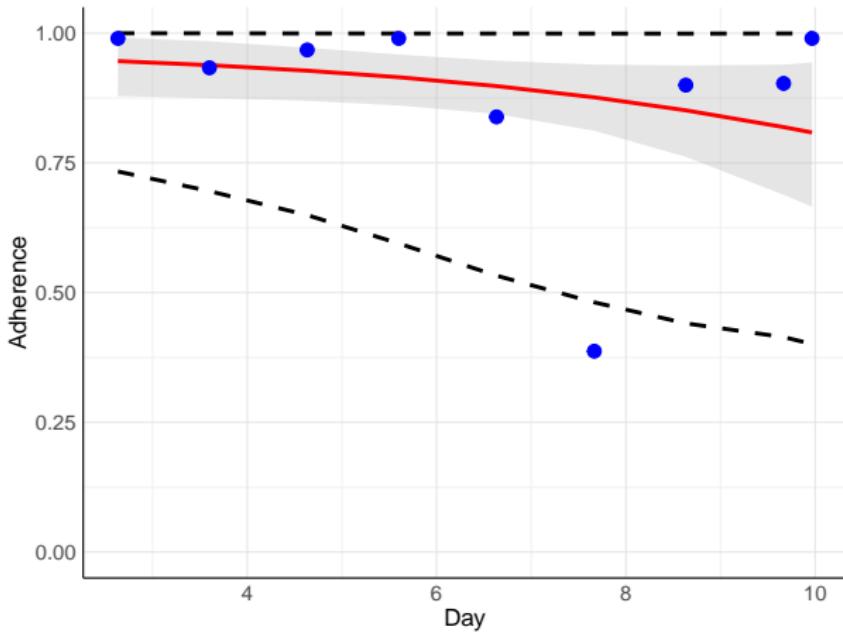
Posterior inference - fixed effects



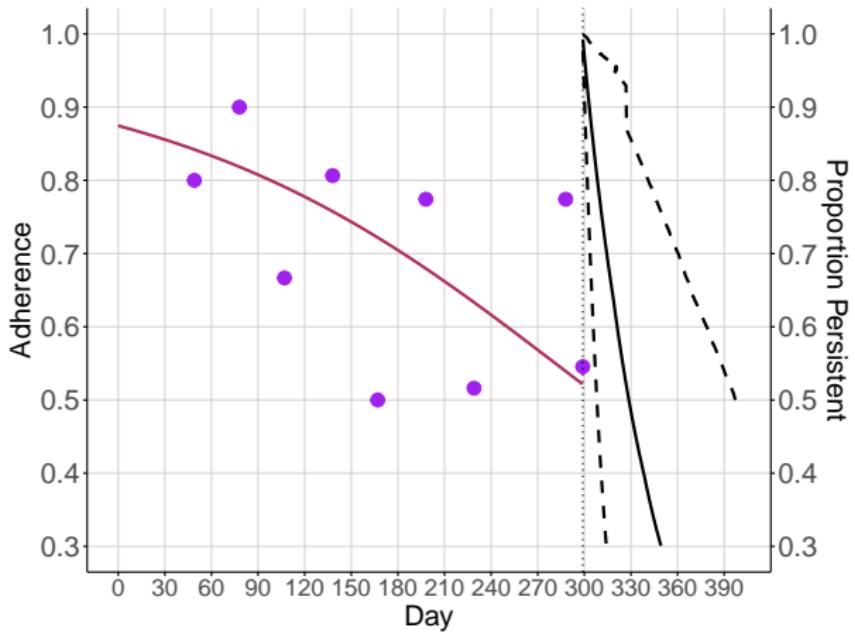
Posterior inference - Patient 46



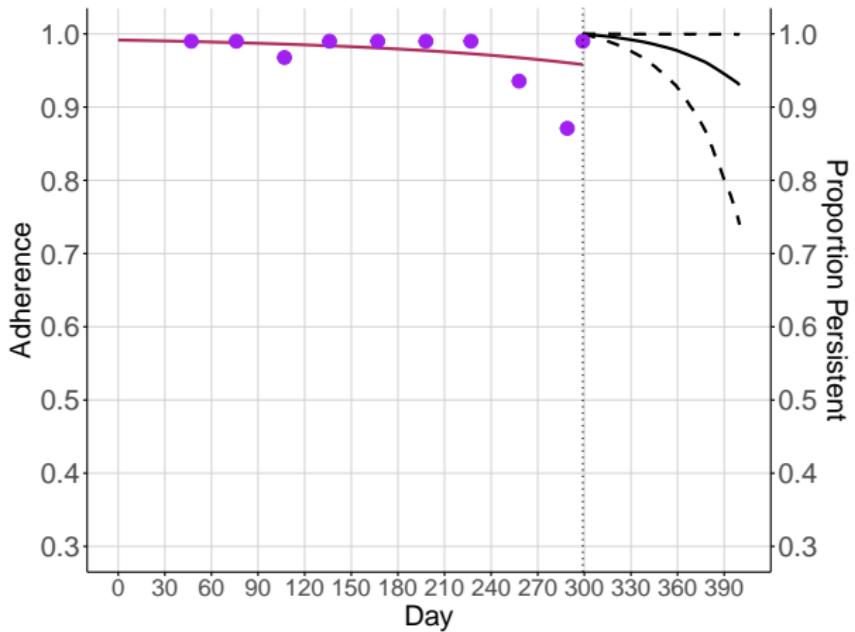
Posterior inference - Patient 56



Dynamic predictions - Patient 27



Dynamic predictions - Patient 10



Dengue risk in Brazil

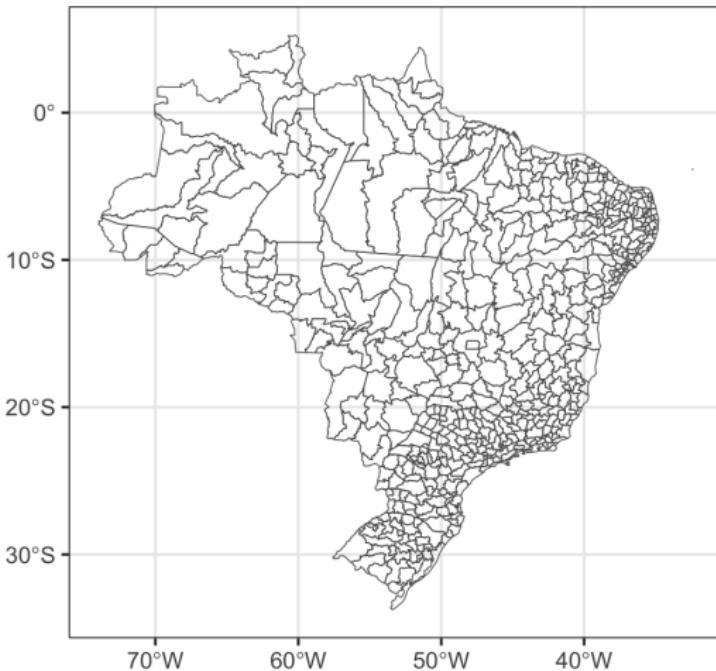
Dengue risk in Brazil

We analyze the effects of hydrometeorological hazards on dengue risk in Brazil. To test the spatial variations in the spread of the virus in different sub-regions of Brazil, we fit dengue counts with a Poisson regression model as follows,

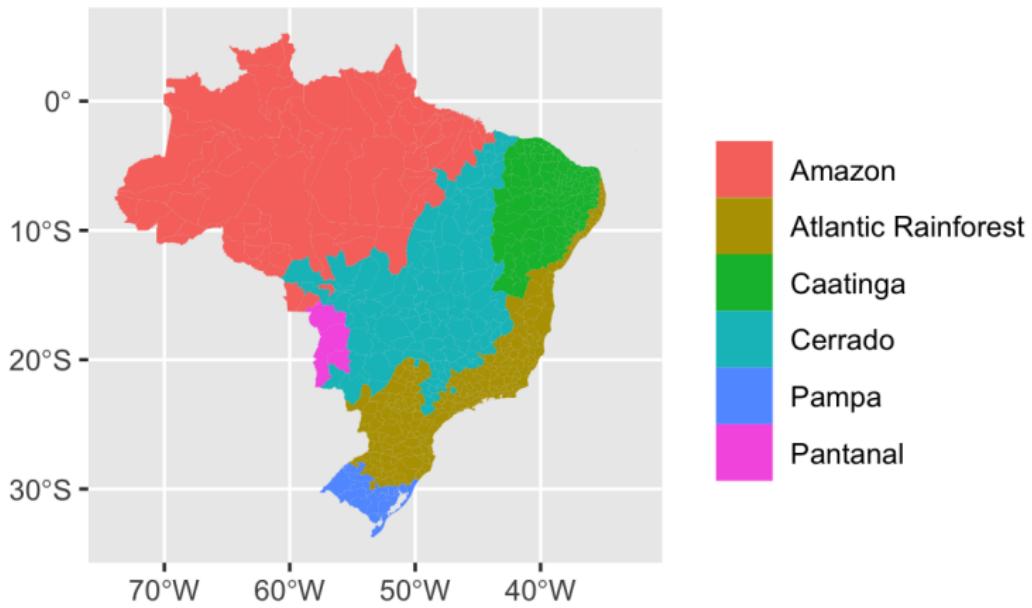
$$\mathbf{y} \sim \text{Poisson}(Ee^{\boldsymbol{\eta}}), \quad \boldsymbol{\eta} = \mathbf{1}^T \boldsymbol{\mu} + \boldsymbol{\alpha}$$

where \mathbf{y} is the observed counts in November of dengue cases, E is the expected number of counts , $\boldsymbol{\eta}$ is the linear predictor, $\boldsymbol{\mu}$ is the overall intercept, and $\boldsymbol{\alpha}$ is the Besag or flexible Besag model over space. We have 561000+ cases for a year.

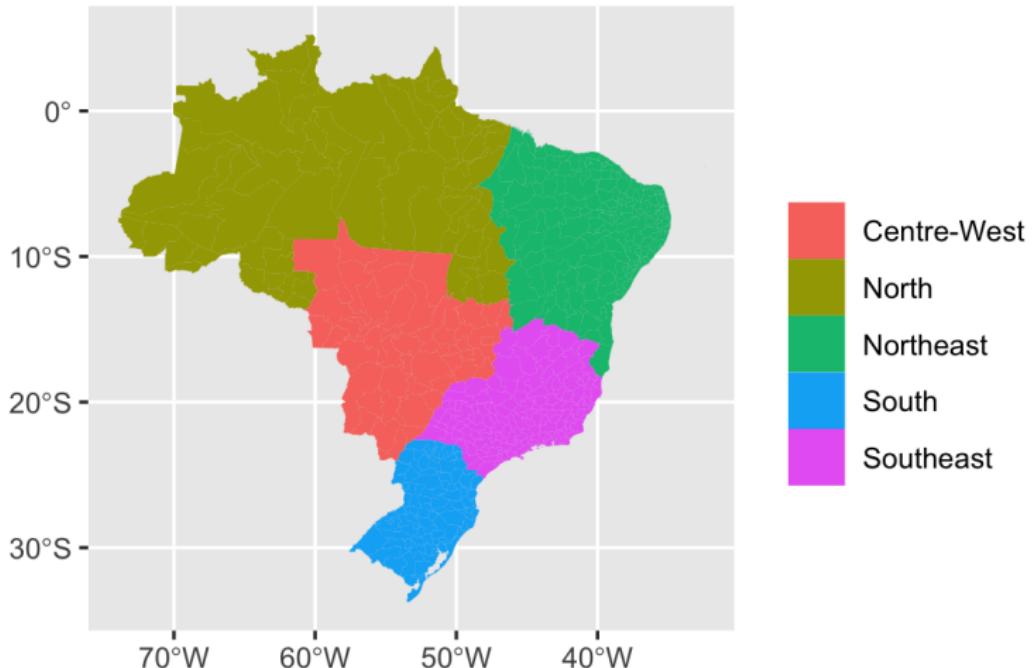
Dengue risk in Brazil



Dengue risk in Brazil



Dengue risk in Brazil



Flexible Besag model⁴

Instead of one precision for the entire area, we define multiple precision parameters, $\tau_1, \tau_2, \dots, \tau_P$, to account for covariance non-stationarity. The conditional density for the spatial effect of area i is

$$x_i | \mathbf{x}_{-i}, \tau_1, \dots, \tau_P \sim N\left(\frac{1}{2} \sum_{\substack{i \text{ in sub-region } k \\ j \text{ in sub-region } l \\ i \sim j}} (\tau_l + \tau_k) \tau_{x_i}^{-1} x_j, \tau_{x_i}^{-1}\right),$$

and

$$\tau_{x_i} = \frac{1}{2} \left(n_i \tau_k + \sum_l n_{il} \tau_l \right).$$

⁴Abdul-Fattah, E., Krainski, E., Van Niekerk, J. and Rue, H., 2024. Non-stationary Bayesian spatial model for disease mapping based on sub-regions. Statistical Methods in Medical Research, p.09622802241244613.

Contraction prior: Non-stationary → stationary

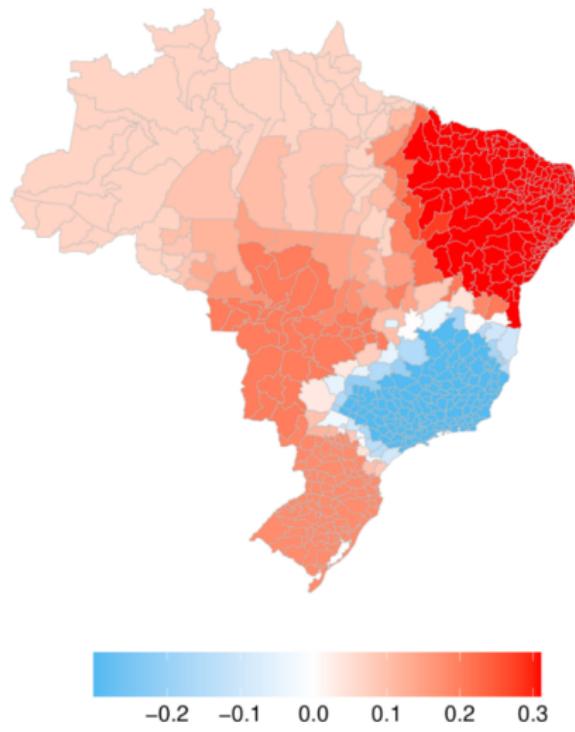
The joint PC prior for $\boldsymbol{\theta} = \log \boldsymbol{\tau}$ can be derived as a convolution of the PC prior for τ from the Besag model, as follows

$$\pi(\boldsymbol{\theta}) = 2^{-(P+2)/2} \pi^{-P/2} \lambda \sigma^{-P} \exp\left(-\frac{1}{2}(\boldsymbol{\theta} - \bar{\boldsymbol{\theta}})^T \tilde{\boldsymbol{\Sigma}}^{-1} (\boldsymbol{\theta} - \bar{\boldsymbol{\theta}}) - \bar{\theta}/2 - \lambda e^{-\bar{\theta}/2}\right),$$

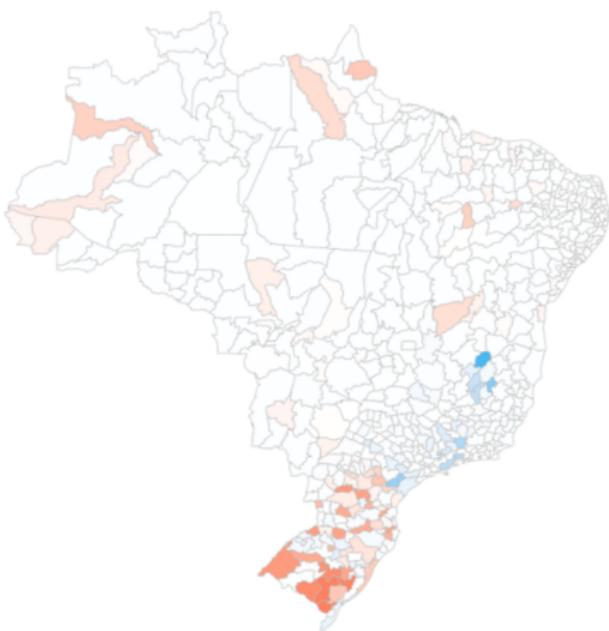
This prior contracts

$$\tau_1, \tau_2, \dots, \tau_P \rightarrow \tau$$

Results

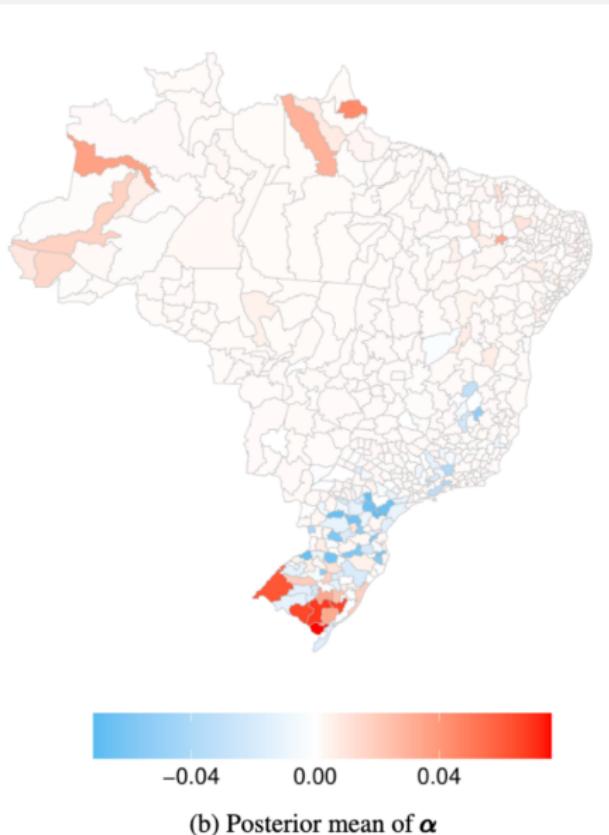


Results

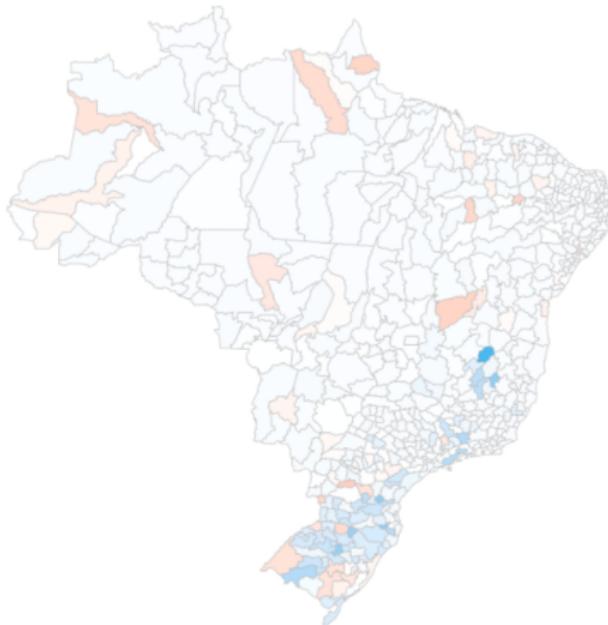


(b) Posterior mean of α

Difference in results

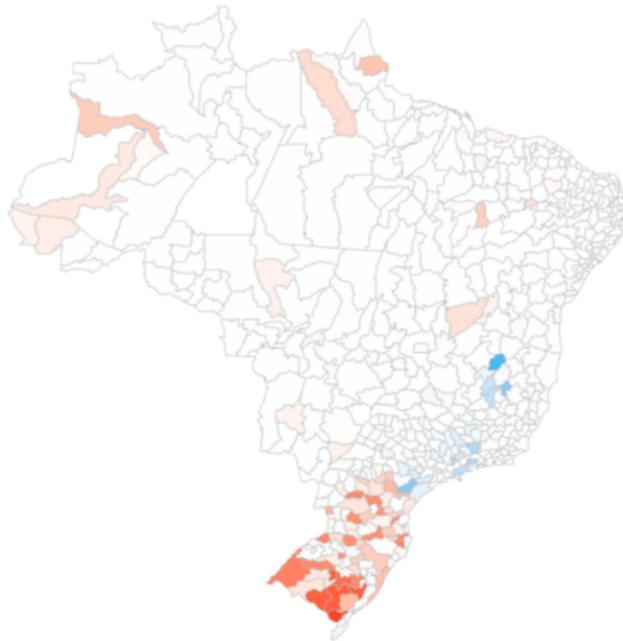


Difference in results



(c) 97.5th percentile of α

Difference in results



(d) 2.5th posterior percentile of α

Dementia study

cs-fMRI model

Functional magnetic resonance imaging (fMRI) is a noninvasive neuro-imaging technique used to localize regions of specific brain activity during certain tasks. For T timepoints and N vertices per hemisphere resulting in data $\mathbf{y}_{TN \times 1}$ with the latent Gaussian model as follows:

$$\begin{aligned}
 \mathbf{y} | \boldsymbol{\beta}, \mathbf{b}, \boldsymbol{\theta} &\sim N(\boldsymbol{\mu}_y, \mathbf{V}), \quad \boldsymbol{\mu}_y = \sum_{k=0}^K \mathbf{X}_k \boldsymbol{\beta}_k + \sum_{j=1}^J \mathbf{Z}_j \mathbf{b}_j \\
 \boldsymbol{\beta}_k &= \boldsymbol{\Psi}_k \mathbf{w}_k \quad (\text{SPDE prior on } \boldsymbol{\beta}_k) \\
 \mathbf{w}_k | \boldsymbol{\theta} &\sim N(\mathbf{0}, \mathbf{Q}_{\tau_k, \kappa_k}^{-1}) \\
 \mathbf{b}_j &\sim N(\mathbf{0}, \delta I) \quad (\text{Diffuse priors for } \mathbf{b}_j) \\
 \boldsymbol{\theta} &\sim \pi(\boldsymbol{\theta}),
 \end{aligned}$$

where we have K task signals and J nuisance signals.⁵

⁵Van Niekerk, J., Krainski, E., Rustand, D. and Rue, H., 2023. A new avenue for Bayesian inference with INLA. Computational Statistics & Data Analysis, 181, p.107692.

cs-fMRI model

The data consists of a 3.5-min fMRI for each subject, consisting of 284 volumes, where each subject performs 5 different motor tasks interceded with a 3 second visual cue. Each hemisphere of the brain contained 32492 surface vertices. From these, 5000 are resampled to use for the analysis. This results in a response data vector \mathbf{y} of size **2 523 624**, with an SPDE model defined on a mesh with 8795 triangles⁶.

⁶Mejia, A.F., Yue, Y., Bolin, D., Lindgren, F. and Lindquist, M.A., 2020. A Bayesian general linear modeling approach to cortical surface fMRI data analysis. *Journal of the American Statistical Association*, 115(530), pp.501-520.

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The inference based on the modern formulation of INLA was computed in **148** seconds.

⁶Mejia, A.F., Yue, Y., Bolin, D., Lindgren, F. and Lindquist, M.A., 2020. A Bayesian general linear modeling approach to cortical surface fMRI data analysis. *Journal of the American Statistical Association*, 115(530), pp.501-520.

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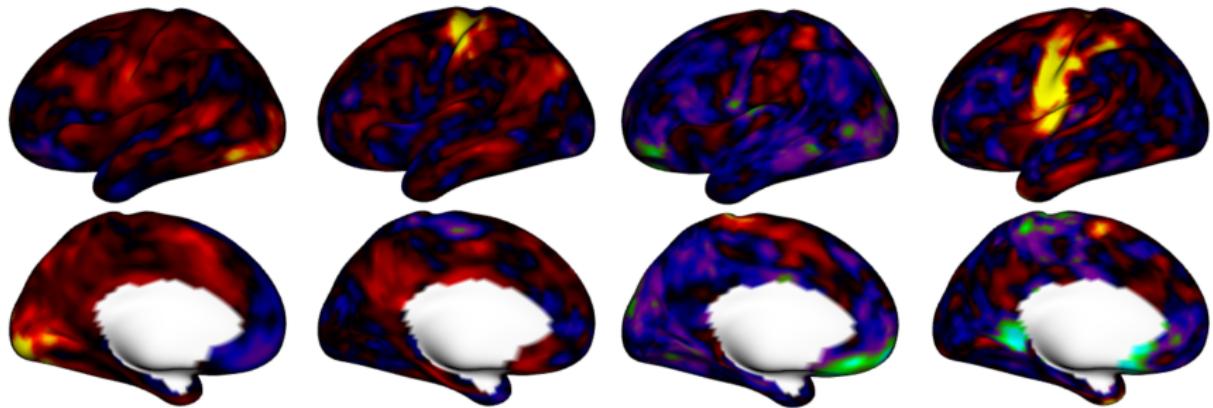


Figure: Activation areas for the different tasks in the left hemisphere - visual cue, right hand motor, right foot motor, tongue motor task (from left to right)

Discussion

- Many biostatistics (and other) problems can be formulated as Latent Gaussian Models

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For references and other projects see [here](#)



شكراً • Thank you



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Science and Technology