A comparative study of Integrated nested Laplace approximation and Markov chain Monte Carlo methods: a case study in tree breeding models

Ingelin Steinsland & Andrew Finley

April 21, 2010

Use Bayesian models that include both genetic and spatial dependences.
Inference:

- MCMC: flexible, but slow.
- INLA: less flexible, but fast(er).

Conclusion: For this kind of models INLA can take us very fare.

Outline

- Data
- Model
- INLA and MCMC
- INLA and spatial animal model.
- Results and discussion

Work in progress.

Background

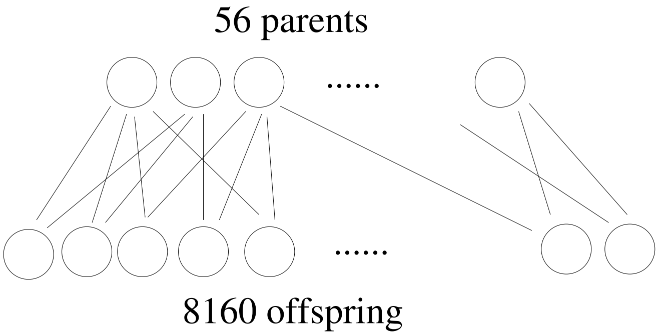
- A. Findley, S. Banerjee, P. Waldmann & T. Ericson, *Hierarchical Spatial Modelling of Additive and Dominance Genetic Variance for Large Spatial Trail Dataset* , Biometrics 2009.
- I. Steinsland & H. Jensen, *Utilizing Gaussian Markov Random Field Properties of Bayesian Animal Models* Biometrics 2010
- H. Rue, S. Martino & N. Chopin *Approximate Bayesian inference for latent Gaussian models by using integrated nested Laplace approximations*, Journal of the Royal Statistical Society -Series B, 2009

Scots Pine Data

Pedigree 56 unrelated parents, partial diallel design. Original 8160 seedlings.

Spatial location 2.2×2.2m grid, two trail sites.

Data Hight and bad(1) / good(0) branch angle of 4970 26-years-old scots pine.



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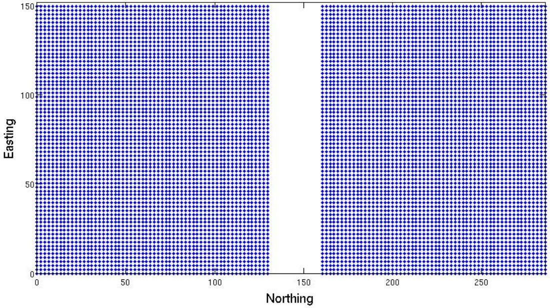

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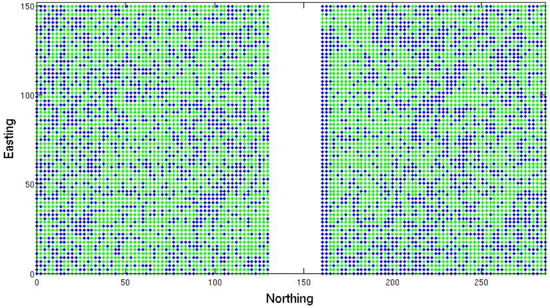

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Provided by Tore Ericsson, Skogforsk, Sweden

Model, hight

Genetic and spatial model:

- Genetic effects
  - Additive, a
  - Dominant, d
- Spatial structure, w

For one tree:

$$y_i = \beta_0 + a_i + d_i + w(s_i) + \epsilon_i$$

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For a population:

$$Y = \beta_0 + Za + Zd + w + E$$

$$\begin{aligned}
\text{Additive: } & a \sim N(0, \sigma_a^2 A), \\
\text{Dominance: } & d \sim N(0, \sigma_d^2 D) \\
\text{Space: } & w \sim N(0, \sigma_w^2 R(\phi)) \\
\text{Random effect: } & E \sim N(0, \tau I)
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\text{Space:}\quad & w \sim N(0, \sigma_w^2 R(\phi))\; n_w = 4970 \\
\text{Random effect:}\quad & E \sim N(0, \tau I)\; n_e = 4970
\end{aligned}$$

Model, branch angle

Genetic and spatial model:

- Genetic effects
  - Additive, a
  - Dominant, d
- Spatial structure, w

For one tree:

$$y_1 = bin(p_i, 1)$$
$$p_i = logit(\eta)$$
$$\eta_i = \beta_0 + a_i + d_i + w(s_i) + \epsilon_i$$

Model, branch angle

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For one tree:

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Additive: $a \sim N(0, \sigma_a^2 A)$,
Dominance: $d \sim N(0, \sigma_d^2 D)$
Space: $w \sim N(0, \sigma_w^2 R(\phi))$
Random effect: $E \sim N(0, \tau I)$ fix τ to a small value

Inference methods

Markov Chain Monte Carlo, MCMC

- Run a Markov chain to get samples from $\pi(x, \theta | y)$
- Can find posterior for any parameter(s) / variable(s) or function of variables
- But 1: Need many iterations / takes a long time.
- But 2: Burn-in and mixing problems, hard to detect.

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Finley et al, 2009:

- Many clever tricks
- C-code
- 15.000 iterations took 24 hours.

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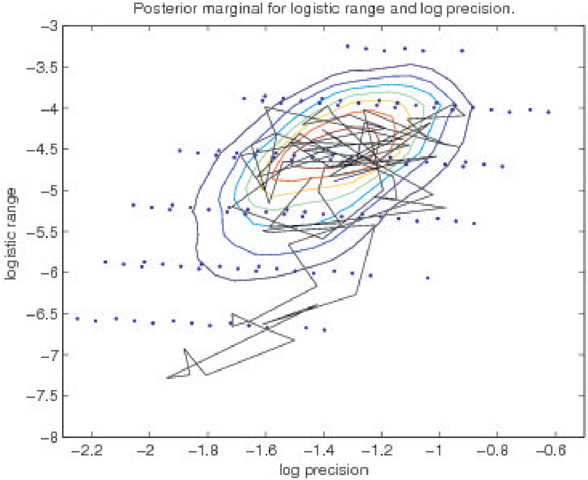
Integrated Nested Laplace Approximations, INLA

- Non-sampling based numerical method.
- Fast(er)
- But 1: For *latent Gaussian Markov Random Field (GMRF) models* with max. 6 non-Gaussian hyper-parameters only.
- But 2: Posteriors for functions of variables and jointly more tricky.

MCMC vs INLA, 2D example



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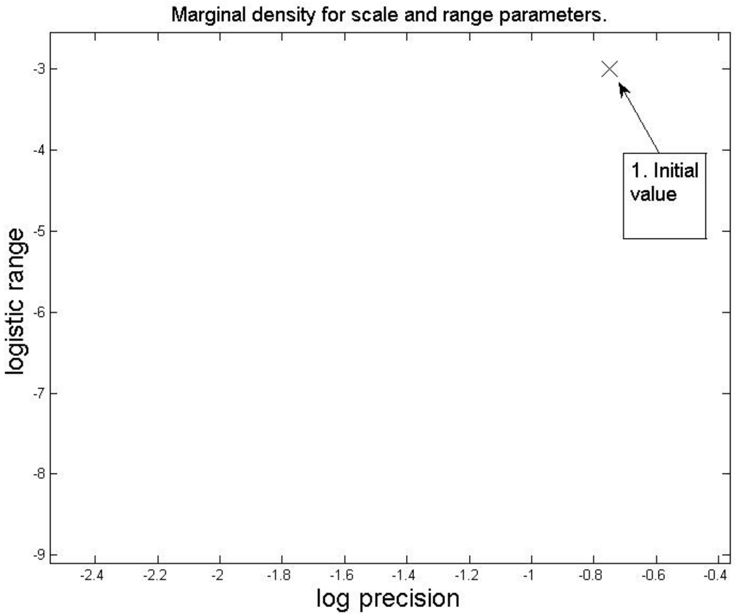

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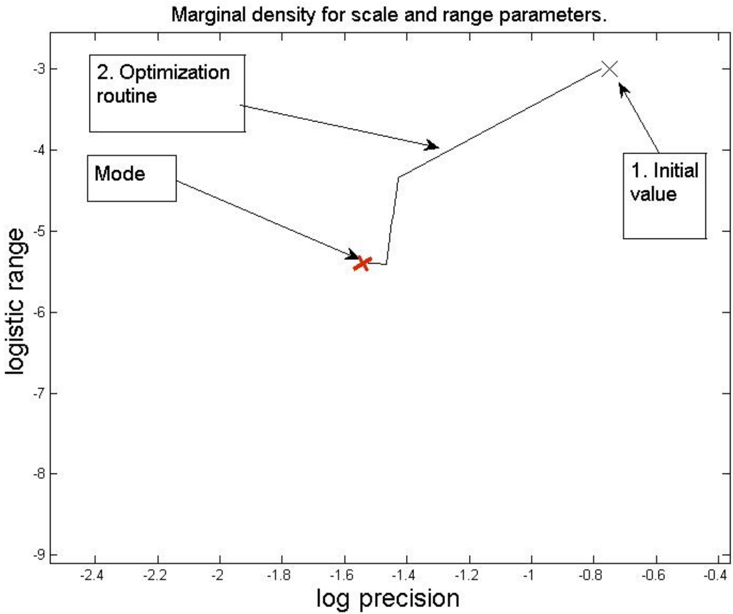

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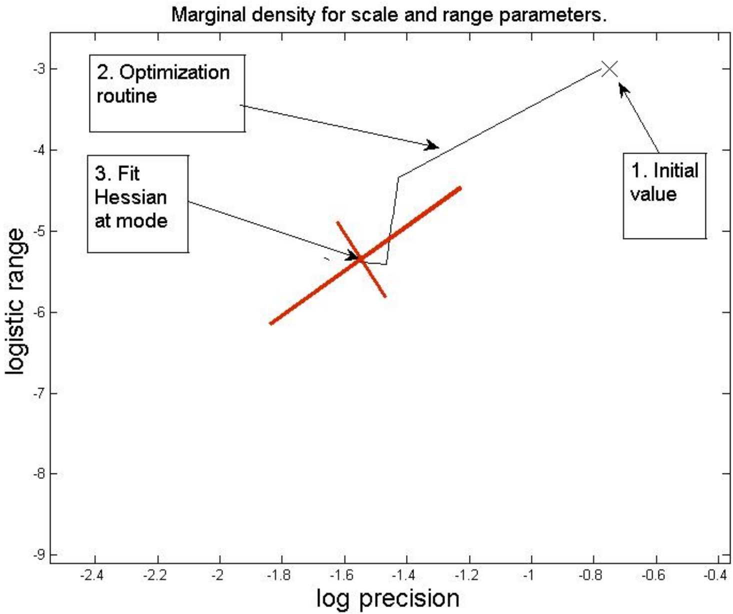

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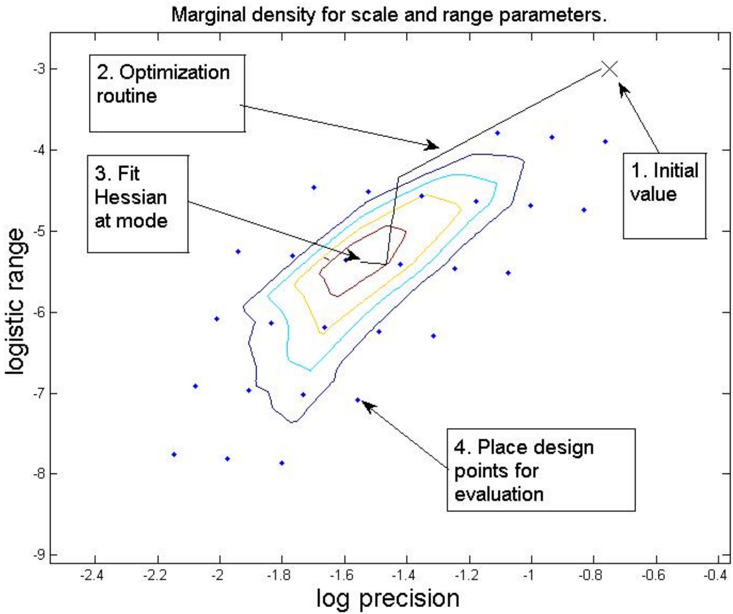

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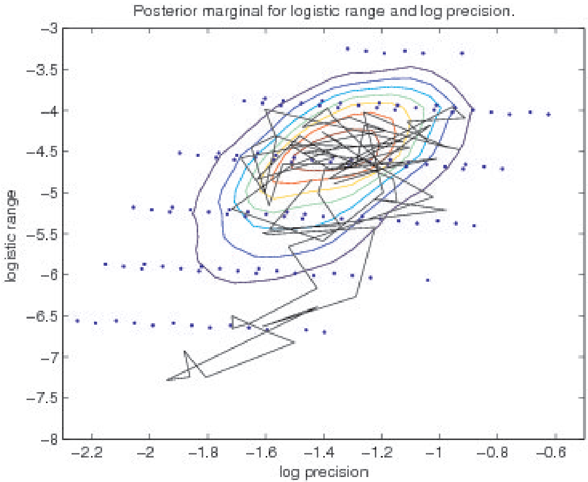

Latent Gaussian Markov Random Field Models

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Hierarchical model:

1. Data: $y \sim \pi(y|x, \theta)$,
2. Latent field: $x \sim \pi(x|\theta)$
3. Hyper-parameters: $\theta \sim \pi(\theta)$

Latent Gaussian Markov Random Field Models

Hierarchical model:

1. Data: $y \sim \pi(y|x,\theta)$, y
2. Latent field: $x \sim \pi(x|\theta)$ Breeding values a
3. Hyper-parameters: $\theta \sim \pi(\theta)$ additive genetic variance σ_a^2 and τ

Breeding model:

$y = a + E$

Latent Gaussian Markov Random Field Models

Hierarchical model: INLA requires

1. Data: $y \sim \pi(y|x,\theta)$, $= \prod_{i=1}^{n} \pi(y_i|x_i)$
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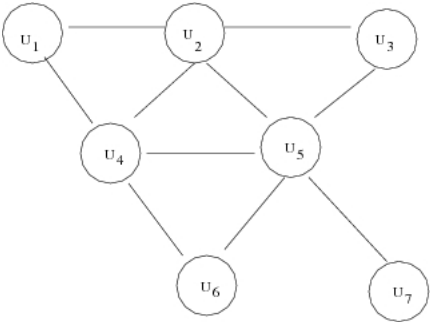
- Conditional independence structure



- Gives non-zero structure of $\Sigma^{-1} \Rightarrow \mathcal{O}(n^3) \rightarrow \mathcal{O}(n^{1.5})$

Integrated nested Laplace approximation

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Want to find $\pi(\theta|y)$, $\pi(x_i|y)$,....

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Ideas

1. Laplace approximation
2. Numerical integration

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1. Laplace approximation

$$\pi(\theta|y) = \frac{\pi(\theta, x|y)}{\pi(x|y,\theta)} \approx \frac{\pi(\theta, x|y)}{\hat{\pi}(x|y,\theta)}$$

   where $\hat{\pi}(x|y,\theta)$ Gaussian approximation to $\pi(x|y,\theta)$

2. Numerical integration

Integrated nested Laplace approximation

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   $\pi(y_i|x_i)$ Gaussian $\Rightarrow$ $\pi(x|y,\theta)$ Gaussian

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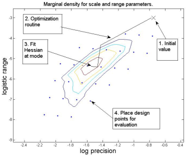

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INLA-Integrated Laplace

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- $\int\ \mathrm{d}\theta \Rightarrow$ Numerical integration

INLA and our model, Relationship matrix A

$$Y = \beta_0 + Za + Zd + w + E,$$
$$a \sim N(0, \sigma_a^2 A)$$

- $A_{ij} = 2\times$ coefficient of coancestry.
- Coefficient of coancestry: Probability that allele picked at random identical by descent.

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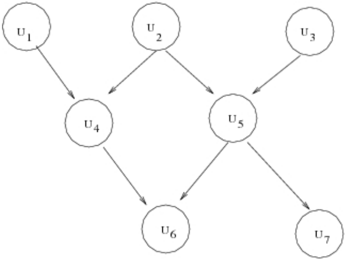
- A is nearly a full matrix.
- Pedigree = DAG (Directed Acyclic Graph)



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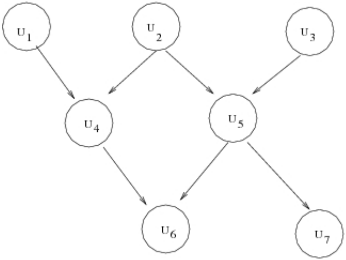

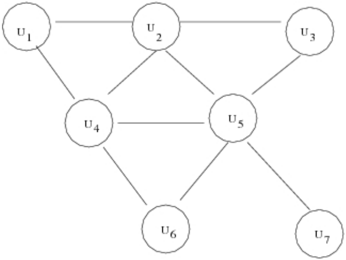

- Structure of A^{-1} from moralising the pedigree $\Rightarrow A^{-1}$ sparse.

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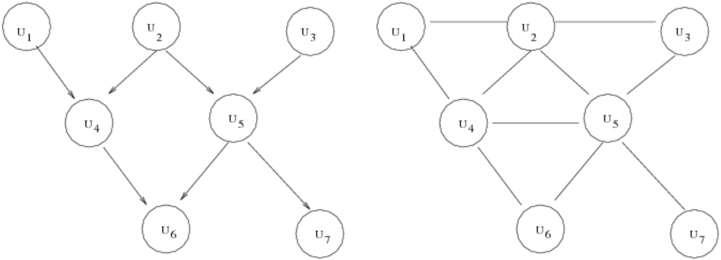

- Calculate non-zero elements of A^{-1} as in Quaas (1976).
- Steinsland & Jensen, 2010

INLA and our model, Dominance

$$Y = \beta_0 + Za + Zd + w + E,\ d \sim N(0, \sigma_d^2 D)$$

Remodel:

- $Y = \beta_0 + Za + ZWf + w + E$
- f: *parental animal effects*, pair of parents.
- $f \sim N(0, \frac{1}{4}\sigma_d^2 F)$.
- Specification of W and calculation of F^{-1}, see Hoeschele and VanRanden (1991) and Misztal(1997).

INLA and our model, Spatial effects

$$Y = \beta_0 + Za + ZWf + w + E,\ w \sim N(0, \sigma_w^2 R(\phi))$$

In Finley et al (2009):

- Predictive process with Matern.
- Ornstein-Uhlenbeck process

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- Need to specify spatial dependence structure.
- Available spatial models with GMRF structure:
  - CAR-models, for discretized domains.
- Popular spatial modelling, $corr(w_i, w_j) = f(d(s_i, s_j); \phi)$.
- Matern model: $f(d) = f(d; r, \nu)$
- GMRF approximations available for Matern model on a lattice for fixed ν, Rue & Tjelmeland (2002).

INLA and our model

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3. Hyper-parameters: $\theta \sim \pi(\theta)$, only few non-Gaussian.

$$Y = \beta_0 + Za + ZWf + w + E,$$

Additive: $a \sim N(0, \sigma_a^2 A)$,

Dominance: $f \sim N(0, 0.25 \cdot \sigma_d^2 D)$

Space: $w \sim N(0, \sigma_w^2 R(r))$

Random effect: $E \sim N(0, \tau I)$

INLA and our model

Hierarchical model:

1. Data: $y \sim \pi(y|x,\theta) = \prod_{i=1}^{n} \pi(y_i|x_i)$ OK, $y \sim N(,)$, $y \sim bin(,1)$
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$$Y = \beta_0 + Za + ZWf + w + E,$$

Additive: $a \sim N(0, \sigma_a^2 A)$, $n_a = 5026$

Dominance: $f \sim N(0, 0.25 \cdot \sigma_d^2 D)$ $n_f = 250$

Space: $w \sim N(0, \sigma_w^2 R(r))$ $n_w = 8120$

Random effect: $E \sim N(0, \tau I)$ $n_e = 4970$

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Non-Gaussian hyper-parameters $(\sigma_a^2, \sigma_d^2, \tau, \sigma_w^2, r)$

Full model, hight

$$Y = \beta_0 + Za + ZWf + w + E$$

Finley et al 2009;

- w Predictive process
- $\beta \sim Unif$
- $\sigma_a^2 \sim IG(2, 40)$
- $\sigma_d^2 \sim IG(2, 40)$
- $\tau \sim IG(2, 50)$

Full model, hight

$$Y = \beta_0 + Za + ZWf + w + E$$

Finley et al 2009; Steinsland & Finley 2010

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- $\tau \sim IG(2, 50)$ $\tau^2 \sim IG(2, 50)$

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- $\beta \sim Unif$ $\beta \sim N(0, 10.000)$
- $\sigma_a^2 \sim IG(2, 40)$ $\sigma_a^2 \sim IG(2, 40)$
- $\sigma_d^2 \sim IG(2, 40)$ $0.25 \cdot \sigma_d^2 \sim IG(2, 40)$
- $\tau \sim IG(2, 50)$ $\tau^2 \sim IG(2, 50)$

Software

`www.r-inla.org`

	a	$a+d$	$a+d+w$
β	72.5 (69.7, 75.1) 70.4 (68.7,71.9)	72.3 (70.0, 74.6) 70.3 (68.8,71.8)	70.3 (66.4, 73.8) 70.9 (69.3, 72.4)
σ_a^2	31.9 (18.3, 49.6) 32.2 (22.2 46.8)	25.2 (14.1, 44.0) 28.8 (18.8,43.0)	35.6 (22.2, 59.2) 27.7 (20.2, 41.9)
σ_d^2		22.4 (11.2, 40.1) 24.7 (16.6,36.4)	18.0 (5.7, 31.4) 24.3 (18.2, 33.9)
τ^2	133.6 (121.2, 144.7) 148.4 (140.6,156.7)	116.1 (100.5, 127.8) 146.6 (138.6,155.4)	80.5 (62.8, 92.4) 127.3 (120.8 135.0)
σ_w^2			50.1 (36.8, 70.1) 42.2 (28.2, 71.5)

Time

MCMC

24 hours

INLA

- $\pi(\theta|y)$: $\sim$ 5 minutes
- $\pi(w|y)$: 1 hour

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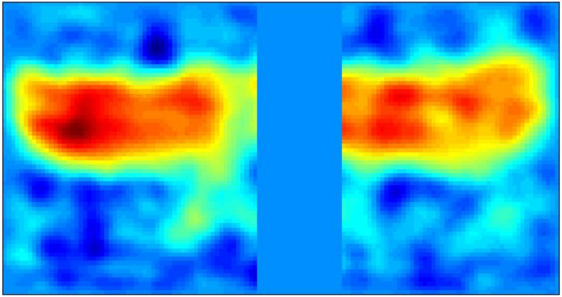

Results, branch angle

- Genetic effects
  - Additive, a
  - Dominant, d
- Spatial structure, w

For one tree:

$$y_1 = bin(p_i, 1)$$

$$p_i = logit(\eta)$$

$$\eta_i = \beta_0 + a_i + d_i + w(s_i)$$

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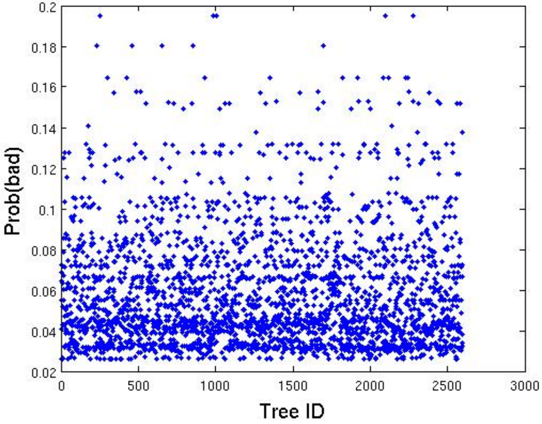
Model	DIC	Comp. time (sec)
β_0	1165	1
$\beta_0 + a$	1073	6
$\beta_0 + a + d$	1092	11
$\beta_0 + a + w$	1162	660

Posterior mean $P(bad)$



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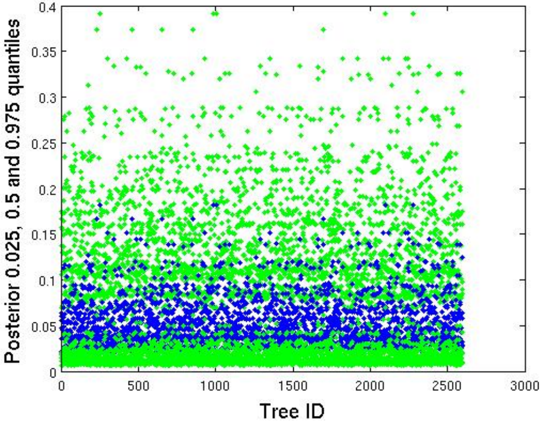

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Heritability

$$h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_d^2 + \tau}$$

MCMC: Calculate for each iteration.
INLA: Coarse or tricks.

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- 24 hours or 1 hour?
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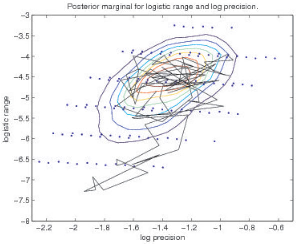

Relevent work in progress

- Animal INLA, R-package, also for non-Gaussian traits. (Holand, Steinsland, Martino & Jensen)
- Sex-linked inheritance (Larsen & Steinsland)
- Missing-not-at-random (Larsen & Steinsland)
- Predictive process and INLA (Eidsvik, Finley, Banerjee & Rue)

Further work

Missing at random, because of genes, or because of location?

Summary

Use Bayesian models that include both genetic and spatial dependences.

Inference:

- MCMC: flexible, but slow.
- INLA: less flexible, but fast(er).

Conclusion: For this kind of models INLA can take us very fare.

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Thank you!