Animal models and Integrated Nested Laplace Approximations

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Figure S1  Histogram showing phenotypic bill depth observations for house sparrows in northern Norway, indicating a Gaussian distribution.
Figure S2  Comparison of INLA and MCMC. INLA (solid line) and MCMC estimates (histogram) for different number of iterations for MCMC for the posterior marginal of $\sigma_u^2$ and $\sigma_e^2$ for the bill depth of house sparrows in northern Norway: 10000 iterations (A) $\sigma_u^2$ and (B) $\sigma_e^2$, 100000 iterations (C) $\sigma_u^2$ and (D) $\sigma_e^2$, 200000 iterations (E) $\sigma_u^2$ and (F) $\sigma_e^2$. INLA used 7 seconds and MCMC used 51 seconds, 8.4 minutes and 17 minutes, respectively.

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Figure S3  Prior sensitivity analyses for synthetic Gaussian, binary, Binomial, and Poisson case studies. Posterior mean with 95% credible interval for prior InvGamma\((a, b)\), where \(a = b \) is equal to 0.0001, 0.01, 0.5, 1 and 10, respectively (note that estimates are shifted relative to the x-axis for clarity). (A) Gaussian data for \(\sigma_u^2 = 0.31\) (open squares, solid line) and \(\sigma_u^2 = 0\) (filled squares, dashed line) for INLA, (B) binary data for \(h^2 = 0\), INLA (open squares, solid line) and MCMC (filled squares, dashed line), (C) Binomial data for \(h^2 = 0.9\) (open squares, solid line) and \(h^2 = 0.038\) (filled squares, dashed line) for INLA, (D) zero-inflated Poisson data for \(\sigma_u^2 = 0.31\) (open squares, solid line) and \(\sigma_u^2 = 0\) (filled squares, dashed line) for INLA.
Figure S4  Comparison of INLA and MCMC. INLA (solid line) and MCMC estimates (histogram) for different number of iterations for MCMC for the posterior marginal of $\sigma^2_u$ and $\sigma^2_e$ for a large synthetic pedigree and simulated dataset of $n_p = 100072$ individuals: 10000 iterations (A) $\sigma^2_u$ and (B) $\sigma^2_e$, 100000 iterations (C) $\sigma^2_u$ and (D) $\sigma^2_e$, 500000 iterations (E) $\sigma^2_u$ and (F) $\sigma^2_e$. INLA used 7.4 minutes and MCMC used 29 minutes, 3.6 hours and 17.9 hours, respectively.
Figure S5  Posterior of difference in mean breeding values for bill depth between cohorts 1993 and 2002 in house sparrows in northern Norway.
Figure S6  Histogram showing observed lifetime reproductive success (LRS) relative to the lifespan (LRS/lifespan) in house sparrows in northern Norway, indicating a zero-inflated Poisson distribution.
Table S1 Inference from INLA for synthetic Poisson data. Simulated under model $y_i | \lambda_i \sim \text{Pois}(n_i, \lambda_i)$, $\eta_i = \log(\lambda_i) = \beta_0 + u_i$, with $\beta_0 = 0$, levels of $\sigma^2_u$ ranging from 0 to 1, and missing pattern similar to the house sparrow Poisson case study. $\hat{\sigma}^2_u$ is the posterior mean additive genetic variance with standard deviations (sd), and 95% credible interval (CI).

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<th>$\sigma^2_u$</th>
<th>$\hat{\sigma}^2_u$ (sd)</th>
<th>95% CI</th>
</tr>
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<td>0.08 (0.02)</td>
<td>(0.05,0.13)</td>
</tr>
<tr>
<td>0.05</td>
<td>0.09 (0.02)</td>
<td>(0.05,0.13)</td>
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<td>(0.07,0.18)</td>
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<td>0.14 (0.03)</td>
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<td>0.2</td>
<td>0.20 (0.04)</td>
<td>(0.13,0.27)</td>
</tr>
<tr>
<td>0.3</td>
<td>0.33 (0.05)</td>
<td>(0.25,0.43)</td>
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<tr>
<td>0.4</td>
<td>0.43 (0.05)</td>
<td>(0.33,0.54)</td>
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<tr>
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<td>(0.43,0.65)</td>
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<tr>
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<td>(0.49,0.73)</td>
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<tr>
<td>0.7</td>
<td>0.68 (0.06)</td>
<td>(0.56,0.81)</td>
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<tr>
<td>0.8</td>
<td>0.84 (0.08)</td>
<td>(0.69,1.00)</td>
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<td>0.91 (0.08)</td>
<td>(0.77,1.08)</td>
</tr>
<tr>
<td>1</td>
<td>0.99 (0.09)</td>
<td>(0.83,1.17)</td>
</tr>
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</table>
File S1

Model formulations for Gaussian animal model

A Gaussian animal model can be formulated in two alternative ways, both fitting the INLA framework.

Model formulation 1 (MF1): Likelihood \( y_i | \eta_i \sim \mathcal{N}(\eta_i, \sigma^2_e) \) and latent field \( \eta_i = \beta_0 + z_i^T \beta + u_i + \epsilon_i \), where the variance of \( \epsilon \) is fixed to a small value.

Model formulation 2 (MF2): Likelihood \( y_i | \eta_i \sim \mathcal{N}(\eta_i, \sigma^2_{\text{small}}) \), i.e. the variance of the likelihood is fixed to a small value, and latent field \( \eta_i = \beta_0 + z_i^T \beta + u_i + \epsilon_i \), where the variance of \( \epsilon \) is \( \sigma^2_e \). The \( \sigma^2_{\text{small}} \) can be interpreted as measurement uncertainty.

When estimating the narrow sense heritability, \( h^2 \), in the Gaussian case, we use model formulation MF2, which out of convenience is parametrized with \( (\sigma^2_u, h^2) \) instead of \( (\sigma^2_u, \sigma^2_e) \). Further, \( (\sigma^2_u, h^2) \) is given a prior such that it corresponds to the prior of \( (\sigma^2_e, \sigma^2) \), hence, the same prior under two different parametrizations.

The DIC is based on evaluating the likelihood, and is not invariant with respect to parametrization (Spiegelhalter et al. 2002). Using model formulation MF2, i.e. a fixed small variance for the likelihood does not work numerically; almost all models get the same DIC to the precision given by INLA. So if DIC needs to be calculated the animal model has to be formulated in an alternative way (in the INLA framework), where the variance of \( \epsilon \) is fixed to a small value in the latent field, i.e. using MF1. Both model formulations coincide if the same priors are used for the hyper-parameters \( (\beta, \sigma^2_e, \sigma^2_u) \), and are latent Gaussian fields with only two non-Gaussian parameters, namely \( \theta = (\sigma^2_u, \sigma^2_e) \). For MF1 \( \epsilon \) can be omitted from the model. It is included here to be consistent with MF2. Both model formulations have their numerical advantages depending on the aim of the analysis. However, we have to be cautious which model formulation we use depending on the purpose of the analysis.

To summarize, when \( u_i, \sum_{i \in C} w_i u_i, \beta \) or \( \sigma^2_u \) is of interest both MF1 and MF2 might be used. If \( \sigma^2_e \) or DIC is the aim of the analysis MF1 has to be used, while MF2 with parametrization \( (\sigma^2_e, h^2) \) has to be used if \( h^2 \) is of interest. Hence we might have to fit two (INLA) models to get all estimates of interest.
Literature Cited

To test for prior sensitivity we do a sensitivity analysis for several synthetic datasets similar to those in the Synthetic case studies section. The house sparrow pedigree with Gaussian, binary, binomial and Poisson likelihoods are used. Each dataset is analyzed with five different priors for $\sigma_u^2$ and, when relevant, $\sigma_e^2$; \textit{InvGamma}(a, b) with $a = b = \{0.0001, 0.01, 0.5, 1, 10\}$. These priors range from uninformative priors to very informative; \textit{InvGamma}(10, 10) has expected value 1.1 and a standard deviation of 0.37. The results from the sensitivity analyses are visualized in Figure S3.

(A) shows results for two synthetic Gaussian datasets, simulated under model $y_i | \mu_i, \sigma_e^2 \sim \mathcal{N}(\mu_i, \sigma_e^2)$, $\eta_i = \mu_i = \beta_0 + u_i$, with $\beta_0 = 0$ and $\sigma_u^2 + \sigma_e^2 = 1$ for $i$) $\sigma_u^2 = 0$ and $ii$) $\sigma_u^2 = 0.31$. The same missing data structure as in the house sparrow Gaussian case study is imposed giving 1025 individuals in the dataset. Inference is done with INLA. We find that with no heritability ($\sigma_u^2 = 0$) the results are very prior sensitive, while with a heritability of $h^2 = \sigma_u^2 = 0.31$ only the most informative prior changes the inference considerably.

(B) shows results for synthetic binary dataset with observations for all the individuals in the pedigree. The data are simulated from a model with logit link, $\eta_i = \beta_0 + u_i$ with $\beta_0 = 0$ and no genetic component ($\sigma_u^2 = 0$). As we in Synthetic Binomial case study section experienced problems using INLA in the binary case, the inference is done with both INLA and MCMC. From the MCMC results we find that the inference is prior sensitive, and also that the systematic errors for INLA are prior sensitive.

(C) shows results for two synthetic binomial datasets. In both datasets the number of trials $n_i$ is as in the house sparrow breeding season success dataset, and also the missing patterns coincide with this. A logit link is used and $\eta_i = \beta_0 + u_i$ with $\beta_0 = 0$. We have a case with high heritability; $i$) $h^2 = 0.9$ and one with low $ii$) $h^2 = 0.038$ (or $\sigma_u^2 = 0.13$ as estimated from the breeding season success dataset). Analyses are done using INLA. We find that neither case is very prior sensitive.

(D) shows results for two synthetic zero-inflated Poisson datasets. They are simulated under model $y_i | \lambda_i \sim \text{Pois}(n_i, \lambda_i), \eta_i = \log(\lambda_i) = \beta_0 + u_i$ with $\beta_0 = 0$, with missing pattern as in the house sparrow Poisson case study, and with no heritability ($h^2 = \sigma_u^2 = 0$) and moderate heritability ($\sigma_u^2 = 0.31$). Inference is done with INLA. The results are very prior sensitive for the dataset without heritability, while only the most informative prior gives any considerable difference for the dataset simulated with...
\sigma_u^2 = 0.31.
R code for synthetic data using the R package AnimalINLA

R code for simulating data with same dependency as the real pedigree, where the sparse structure matrix Cmatrix is obtained from $A^{-1}$ calculated in the R package AnimalINLA (www.r-inla.org/related-projects/animalinla).

We simulated data with different values of $\sigma^2_u = \text{var}.u$ and $\sigma^2_e = \text{var}.e$ with the function simulate.breeding.values:

Simulation code for breeding value:

```r
##need the package "spam"
install.packages("spam")

inla.complete.Cmatrix <- function(C)
{
 idx = (C$i != C$j)
 return (list(i=c(C$i, C$j[idx]), j=c(C$j, C$i[idx]),
 values=c(C$values, C$values[idx])))
}
simulate.breeding.values <- function(Cmatrix, varu, nsamples = 1)
{
 library(spam)
 prec = 1/varu
 Comp = inla.complete.Cmatrix(Cmatrix)
 S = spam(x = list(i = Comp$i, j = Comp$s, values =
 Comp$values))
 Q = prec * S
 breeding = rmvnorm.prec(nsamples, mu=rep(0, nrow(Q)), Q)
 breeding = as.vector(breeding)

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"13SI"
```r
## define the sparse-matrix from the relationship matrix
## computed in compute.Ainverse(), used in simulate.breeding.values()
Cmatrix = list(i = xx$Ainverse[,1], j = xx$Ainverse[,2], values = xx$Ainverse[,3])

Synthetic Gaussian case study

library(AnimalINLA)
data(sparrowpedigree)

## Run AnimalINLA
xx = compute.Ainverse(sparrowpedigree)

## number of individuals in the pedigree
Nbird = dim(sparrowpedigree)[1]

## choose the values of the hyperparameters
var.u = 0.6
var.e = 0.4

## simulate the breeding values and the environmental effect
breeding = simulate.breeding.values(Cmatrix, var.u)
env = rnorm(Nbird, mean = 0, sd = sqrt(var.e))

## compute the trait
trait = breeding + env

## make the data frame
data = data.frame(y = trait, u = 1:Nbird)
```

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## Run AnimalINLA

```r
gauss = animal.inla(response = y, genetic = c("u"),
                    Ainverse = sparseMatrix(i = xx$Ainverse[,1],
                                            j = xx$Ainverse[,2], x = xx$Ainverse[,3]),
                    data = data, type.data = "gaussian",
                    dic = TRUE, sigma.e = TRUE)
```

## Hyperparameters

```r
gauss$summary.hyperparam
```

### Synthetic Binomial case study

```r
library(AnimalINLA)
data(sparrowpedigree)
```

```r
## need the package "boot"
install.packages("boot")
library(boot)
```

```r
## numbers of individuals in the pedigree
Nbird = dim(pedigree)[1]
```

```r
## set the value for the hyperparameter, where beta0 is the intercept
var.u = 0.3
beta0 = 1
```

```r
## set the number of trials
Ntrials = sample(1:9, 3574, replace = T)
```

```r
## simulate breeding values
```
breeding = simulate.breeding.values(Cmatrix, var.u)
eta = beta0 + breeding
p = inv.logit(eta)

## simulate the trait
trait = rbinom(Nbird, Ntrials, p)
data = data.frame(y = trait, u = 1:Nbird,
                   Ntrial = Ntrials)

##Run AnimalINLA
xx=compute.Ainverse(sparrowpedigree)
bin=animal.inla(response=y, genetic=c("u"),
                 Ntrials = Ntrial,
                 Ainverse =sparseMatrix(i=xx$Ainverse[,1],
                            j=xx$Ainverse[,2],x=xx$Ainverse[,3]),
                 data=data,type.data="binomial",
                 dic=TRUE)

##hyperparameteres
bin$summary.hyperparam

**Synthetic Poisson case study**

library(AnimalINLA)
data(sparrowpedigree)

##number of individuals in the pedigree
Nbird = dim(sparrowpedigree)[1]
## choose the values of the hyperparameters
var.u = 0.7
beta0 = 1

## Run AnimalINLA
breeding = simulate.breeding.values(Cmatrix, var.u)

## compute the trait
eta = beta0 + breeding
lambda = exp(eta)
trait = rpois(Nbird, lambda)

## make the data frame
data = data.frame(y=trait, u=1:Nbird, n=rep(1, Nbird))

## Run AnimalINLA
xx = compute.Ainverse(sparrowpedigree)

pois = animal.inla(response = "y", genetic = c("u"),
                    Ainverse = sparseMatrix(i = xx$Ainverse[,1],
                                             j = xx$Ainverse[,2],
                                             x = xx$Ainverse[,3]),
                    E = n, data = data, type.data = "poisson", dic = TRUE)

## hyperparameters
pois$summary.hyperparam
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**R code for random effects in INLA**

Including individual as a independent random effect in the latent field is implemented the same way in INLA for all case studies in house sparrow population (Gaussian, binomial and Poisson). Note that in the Gaussian case study we have repeated measurements, i.e. possible several observation for each individual random effect, while in the binomial and Poisson cases there are only one observation for each individual. For the simulated datasets in AnimalINLA (only one measurement for each individual):

```r
library(AnimalINLA)
library(INLA)
library(Matrix)

data(sparrowpedigree)
xx = compute.Ainverse(sparrowpedigree)
Ainv = xx$Ainverse
map = xx$map
Cmatrix = sparseMatrix(i=Ainv[,1],j=Ainv[,2],x=Ainv[,3])

**Gaussian case study:**

data(sparrowGaussian)
Ndata = dim(sparrowGaussian)[1]

## Mapping the same index number for "Individual" as in Ainv
## The IndexA column is the index in the A inverse matrix
sparrowGaussian$IndexA = rep(0,Ndata)
for(i in 1:Ndata)
    sparrowGaussian$IndexA[i] = which(map[,1]==sparrowGaussian$Individual[i])

#Including an extra column for individual effect
sparrowGaussian$IndexA.2=sparrowGaussian$IndexA
```

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formula = y ~ f(IndexA,model="generic0", Cmatrix=Cmatrix, 
   constr=TRUE,param = c(0.5, 0.5)) +
   f(IndexA.2,model="iid",param = c(1,0.001),
   constr=TRUE)

in formula is the trait, i.e bill depth in the case study. IndexA and IndexA.2 is the individuals in the 
data (these have to be given different names) where IndexA is the additive genetic effect and IndexA.2 is 
the individual random effect.

the likelihood is implemented in the inla call:

model = inla(formula=formula, family="gaussian",
   data=sparrowGaussian,
   control.family=list(hyper = list(theta =
   list(param = c(0.5, 0.5), fixed = FALSE))),
   only.hyperparam =FALSE,control.compute=list(dic=T))

summary(model)
#Example finding the posterior marginal distribution and mean (95% CI)
#for additive genetic variance and individual random variance
sigma.IndexA = inla.marginal.transform(function(x) 1/x,
   model$marginals.hyperpar$"Precision for IndexA")
 e.IndexA=inla.expectation(function(x) x, sigma.IndexA)
 ci.IndexA=inla.qmarginal(c(0.025, 0.975), sigma.IndexA)

#and posterior marginal distribution and mean (95% CI)
#for individual random variance
sigma.IndexA.2 = inla.marginal.transform(function(x) 1/x,
   model$marginals.hyperpar$"Precision for IndexA.2")
 e.IndexA.2=inla.expectation(function(x) x, sigma.IndexA.2)
 ci.IndexA.2=inla.qmarginal(c(0.025, 0.975), sigma.IndexA.2)

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Binomial case study:

data(sparrowBinomial)

Ndata = dim(sparrowBinomial)[1]

## Mapping the same index number for "Individual" as in Ainv
## The IndexA column is the index in the A inverse matrix
sparrowBinomial$IndexA = rep(0,Ndata)
for(i in 1:Ndata)
    sparrowBinomial$IndexA[i] = which(map[,1]==sparrowBinomial$Individual[i])

#Including an extra column for individual effect
sparrowBinomial$IndexA.2 = sparrowBinomial$IndexA

formula = y ~ f(IndexA,model="generic0", Cmatrix=Cmatrix,
    constr=TRUE,param = c(0.5, 0.5)) +
    f(IndexA.2,model="iid",param = c(1,0.001),
    constr=TRUE)

    y in formula is the trait, i.e number of years individuals produced at least one recruit in the case study, IndexA and IndexA.2 is the individuals in the data (these have to be given different names) where
    IndexA is the additive genetic effect and IndexA.2 is the individual random effect.

    The likelihood is implemented in the inla call;

    model = inla(formula=formula , family="binomial", data=sparrowBinomial, Ntrial=Ntrial,
    only.hyperparam = FALSE,control.compute=list(dic=T))
\textit{Ntrial} is the number of trials, i.e the number of breeding seasons individuals were alive during the study period.

\begin{verbatim}
summary(model)
#Example finding the posterior marginal distribution and mean (95% CI) for
#additive genetic variance and individual random variance
sigma.IndexA = inla.marginal.transform(function(x) 1/x,
    model$marginals.hyperpar$"Precision for IndexA")
e.IndexA=inla.expectation(function(x) x, sigma.IndexA)
ci.IndexA=inla.qmarginal(c(0.025, 0.975), sigma.IndexA)

#and posterior marginal distribution and mean (95% CI)
#for individual random variance
sigma.IndexA.2 = inla.marginal.transform(function(x) 1/x,
    model$marginals.hyperpar$"Precision for IndexA.2")
e.IndexA.2=inla.expectation(function(x) x, sigma.IndexA.2)
ci.IndexA.2=inla.qmarginal(c(0.025, 0.975), sigma.IndexA.2)
\end{verbatim}

\textbf{Poisson case study:}

\begin{verbatim}
data(sparrowPoisson)

Ndata = dim(sparrowPoisson)[1]

## Mapping the same index number for "Individual" as in Ainv
## The IndexA column is the index in the A inverse matrix
sparrowPoisson$IndexA = rep(0,Ndata)
for(i in 1:Ndata)
    sparrowPoisson$IndexA[i] = which(map[,1]==sparrowPoisson$Individual[i])

#Including an extra column for individual effect
\end{verbatim}

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sparrowPoisson$IndexA.2=sparrowPoisson$IndexA

formula = y ~ f(IndexA,model="generic0", Cmatrix=Cmatrix, constr=TRUE,param = c(0.5, 0.5)) + f(IndexA.2,model="iid",param = c(1,0.001), constr=TRUE)

*y in formula* is the trait, i.e. total number of recruits individuals produced in the study period in the case study. *IndexA* and *IndexA.2* is the individuals in the data (these have to be given different names) where *IndexA* is the additive genetic effect and *IndexA.2* is the individual random effect.

The likelihood is implemented in the inla call;

```r
model = inla(formula=formula,
               family="zeroinflatedpoisson1",
               data=sparrowPoisson,
               E=n,
               only.hyperparam = FALSE,
               control.compute=list(dic=TRUE))
```

*E* is the exposure, i.e. the number of breeding seasons individuals were alive during the study period in the case study.

```r
summary(model)
#Example finding the posterior marginal distribution and mean (95% CI)
#for additive genetic variance and individual random variance
sigma.IndexA = inla.marginal.transform(function(x) 1/x, model$marginals.hyperpar$"Precision for IndexA")
e.IndexA=inla.expectation(function(x) x, sigma.IndexA)
ci.IndexA=inla.qmarginal(c(0.025, 0.975), sigma.IndexA)
```

#and posterior marginal distribution and mean (95% CI)
# for individual random variance

\[
\text{sigma.IndexA.2} = \text{inla.marginal.transform}(\text{function}(x) \ 1/x, \\
\quad \text{model}$\text{marginals.hyperpar$"Precision for IndexA.2"})
\]

\[
\text{e.IndexA.2} = \text{inla.expectation}(\text{function}(x) \ x, \ \text{sigma.IndexA.2})
\]

\[
\text{ci.IndexA.2} = \text{inla.qmarginal}(\text{c}(0.025, 0.975), \ \text{sigma.IndexA.2})
\]