spaMM:
an R package to fit generalized, linear and mixed models allowing for complex covariance structures

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General features of spaMM

- First developed (Rousset & Ferdy, *Ecography*, 2014) to fit spatial Mixed Models.
- **Polyvalent**: now allows other advanced modeling (e.g. residual dispersion models; multivariate-response models; genetic correlation matrices; basic AR1 temporal model; non-gaussian random effects; COMPoisson, Zero-Truncated Poisson and ZT-negative-binomial families; Earth distance for spatial models...).
- **Simple to use**: consistent syntax across models (LMs, GLMs, LMMs, GLMMs...).
- **Robust & fast**: robust convergence for small data sets, fast fits for large data sets.

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Methods in a nutshell:

- Laplace approximation for ML and REML (plus obscure but useful variants of penalized quasi likelihood – PQL)
- Distinct efficient matrix computations depending on sparsity of correlation matrix or random effects: sparse as in classical nested random effects, (2) dense as in spatial geostatistical, and (3) sparse inverse as in spatial autoregressive (or Markov random field) models.

A few simple examples

Model	Example of syntax in spaMM & alternatives
LM	`spaMM::fitme(y ~ X1, data = wafers)`
	`stats::lm(y ~ X1, data = wafers)`
GLM	`spaMM::fitme(y ~ X1, family = Gamma("log"), data = wafers)`
	`stats::glm(y ~ X1, family = Gamma("log"), data = wafers)`
LMM	`spaMM::fitme(y ~ X1 + (X2|batch), data = wafers)`
	`lme4::lmer(y ~ X1 + (X2|batch), data = wafers)`
GLMM	`spaMM::fitme(y ~ X1 + (X2|batch), family = Gamma("log"), data = wafers)`
	`lme4::glmer(y ~ X1 + (X2|batch), family = Gamma("log"), data = wafers)`

→ same syntax as in `stats` and `lme4` but using a single function: `fitme()`.

A few more advanced examples

Model	Example of syntax in spaMM & alternatives

"Animal"[1]	`data("DT_gryphon", package = "sommer")`
	`spaMM::fitme(BWT ~ 1 + corrMatrix(1|ID), corrMatrix = A_gryphon,`
	`data = DT_gryphon, method = "REML")`

	`prior_list <- list(G = list(G1 = list(V = matrix(p.var/2), n = 1)),`
	`R = list(V = matrix(p.var/2), n = 1))`
	`MCMCglmm::MCMCglmm(BWT ~ 1, random = ~ animal, pedigree = P_gryphon,`
	`data = Data, prior = prior_list)`

Residual-dispersion	`spaMM::fitme(y ~ 1, family = Gamma(log), resid.model = ~ X3 + I(X3^2),` `data = wafers)`
	`glmmTMB::glmmTMB(y ~ 1, family = Gamma(log), dispformula = ~ X3 + I(X3^2),` `data = wafers)`
Matérn	`spaMM::fitme(cbind(npos, ntot - npos) ~ maxNDVI1 + Matern(1|longitude + latitude),` `data = Loaloa, family = binomial())`

	`Loaloa$loc <- glmmTMB::numFactor(scale(Loaloa$latitude), scale(Loaloa$longitude))`
	`Loaloa$ID <- factor(rep(1, nrow(Loaloa)))`
	`glmmTMB::glmmTMB(cbind(npos, ntot - npos) ~ maxNDVI1 + mat(loc + 0|ID),`
	`data = Loaloa, family = binomial())`

→ same syntax from simple linear models to relatively complex models.

[1] mixed-effect model with breeding value as a random effect

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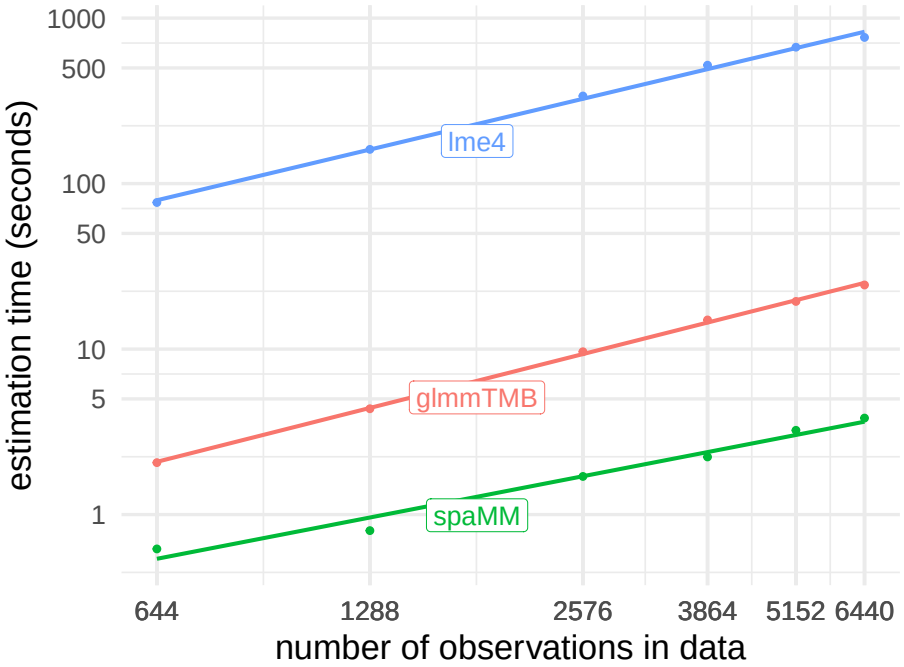
- However, proven performance (controlled error rates...) was the first objective. The few spatial procedures available a few years ago were poor in this respect (see simulation study in Rousset & Ferdy 2014).
- "Performance" also means low non-convergence rates (e.g., for binary GLMMs; but also more robust than stats::glm() for GLMs).
- Thereafter, faster procedures have been implemented without sacrificing such performance criteria.
- Still mostly R code, hence easy to extend; C++ code only for a few selected operations (and Matrix package for sparse Cholesky factorization).
- Thus, not always the fastest possible implementation; but exhibits a reasonable combination of speed, robustness and evolvability of software.

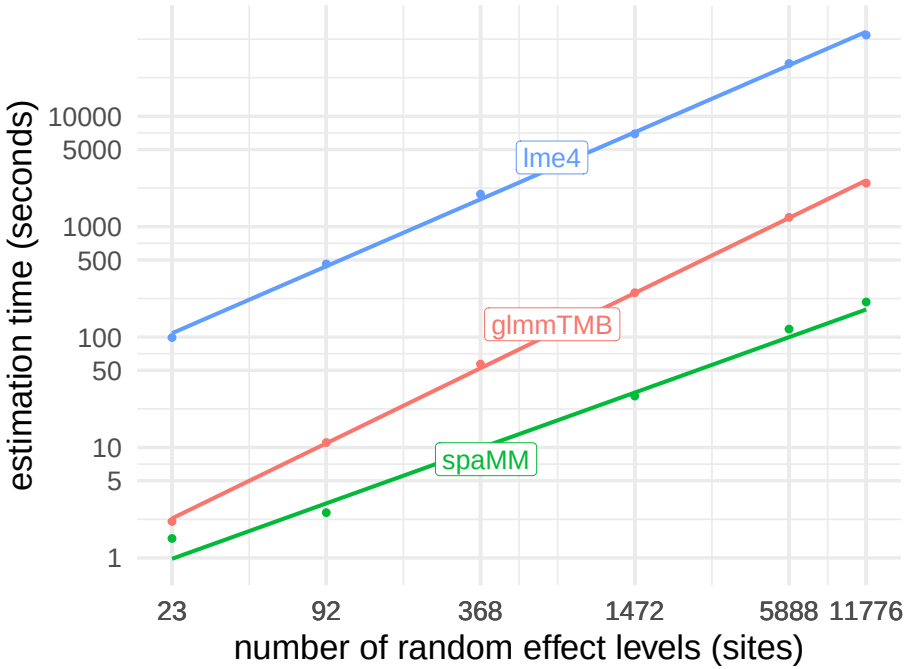
Comparisons with other packages

- Comparisons with lme4::glmer (non-spatial), INLA (spatial) and glmmTMB (both)
- Not only speed, but also expected fit results, may differ:
  - They are expected to give slightly different results for non-canonical link (e.g., Gamma(log)) because Laplace approximations slightly differ;
  - glmmTMB and spaMM should give equivalent results for GLMM with canonical link (binomial(logit), poisson(log), Gamma(inverse));
  - glmer results more often differ, even when glmmTMB and spaMM agree together.
- To limit cherry-picking, the following comparisons are based on examples used to showcase speed of glmmTMB and INLA.
- These examples are all favorable to spaMM, but don't take this too seriously (glmmTMB has some interesting features).
- Additional comparisons in the Gentle Introduction to spaMM: `https://gitlab.mbb.univ-montp2.fr/francois/spamm-ref/-/blob/master/vignettePlus/spaMMintro.pdf`

Speed: non-spatial models

Example from Brooks et al. *R Journal* (2017) Figures 1 and 2, which considers a GLMM with negative-binomial family with log link [the fitme call is **fitme**(count spp * mined + (1|grp), x, family=**negbin**())].





Note the log scale for y-axis is the plots

Comparisons for spatial models: design

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  spaMM can fit random effects with the MRF correlation model defined by some INLA functions, There are some subtleties in using these INLA functions:
  - a cutoff parameter controlling the quality of the approximation (two values are considered in next computations);
  - an alpha that corresponds to a fixed value of a smoothness parameter $\nu = 1$ of the Matérn model (alpha=2 in next computations, corresponding to $\nu = 1$)

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- Comparisons use an example provided to demonstrate INLA's efficiency (https://stat.ethz.ch/pipermail/r-sig-mixed-models/2020q3/028837.html); either the full data set of 29507 observations; or random subsets of 200, 500, 1000, 5000 and 10000 observations.

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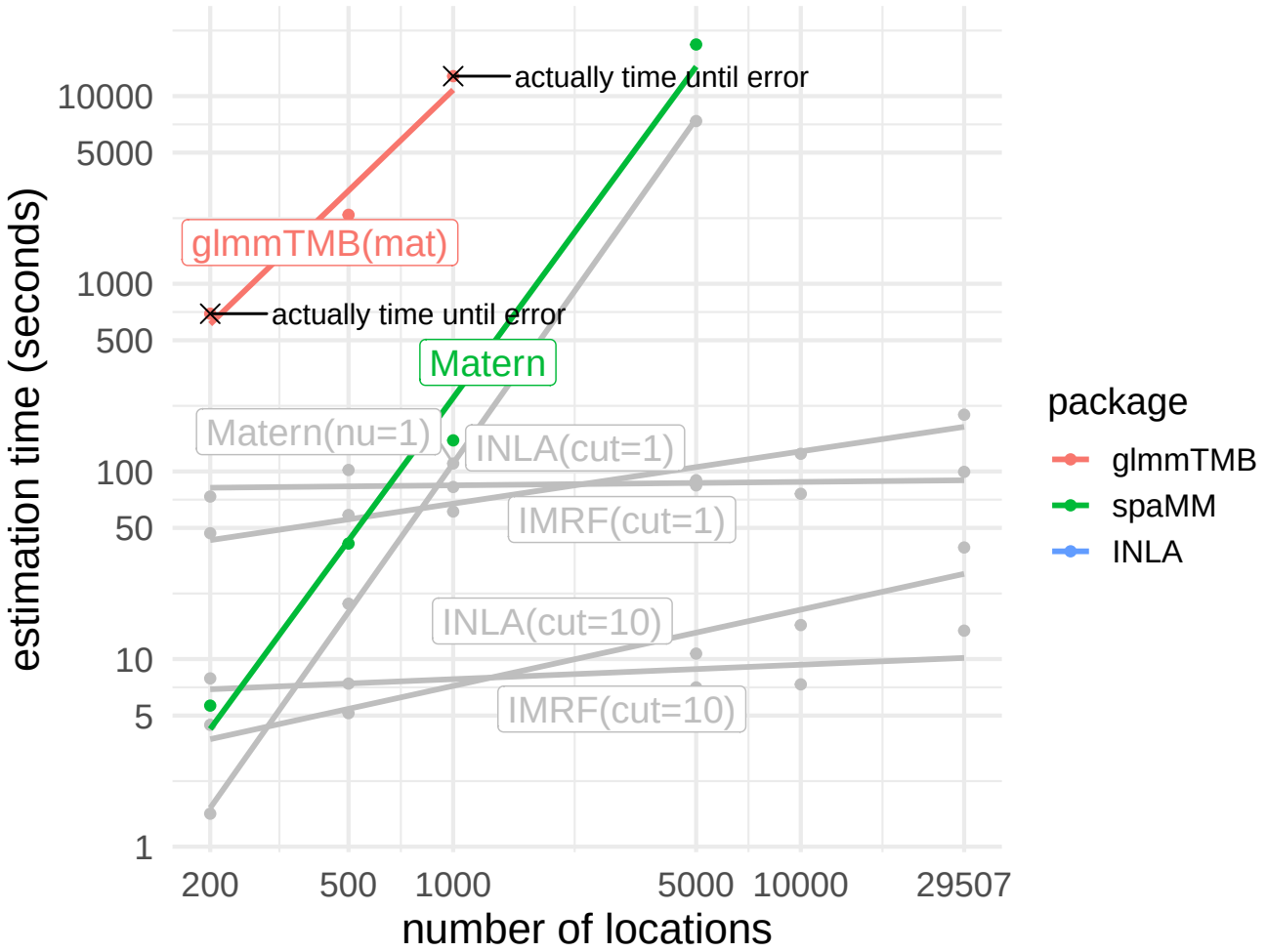
- Simple syntax for all models and for fixing parameters:

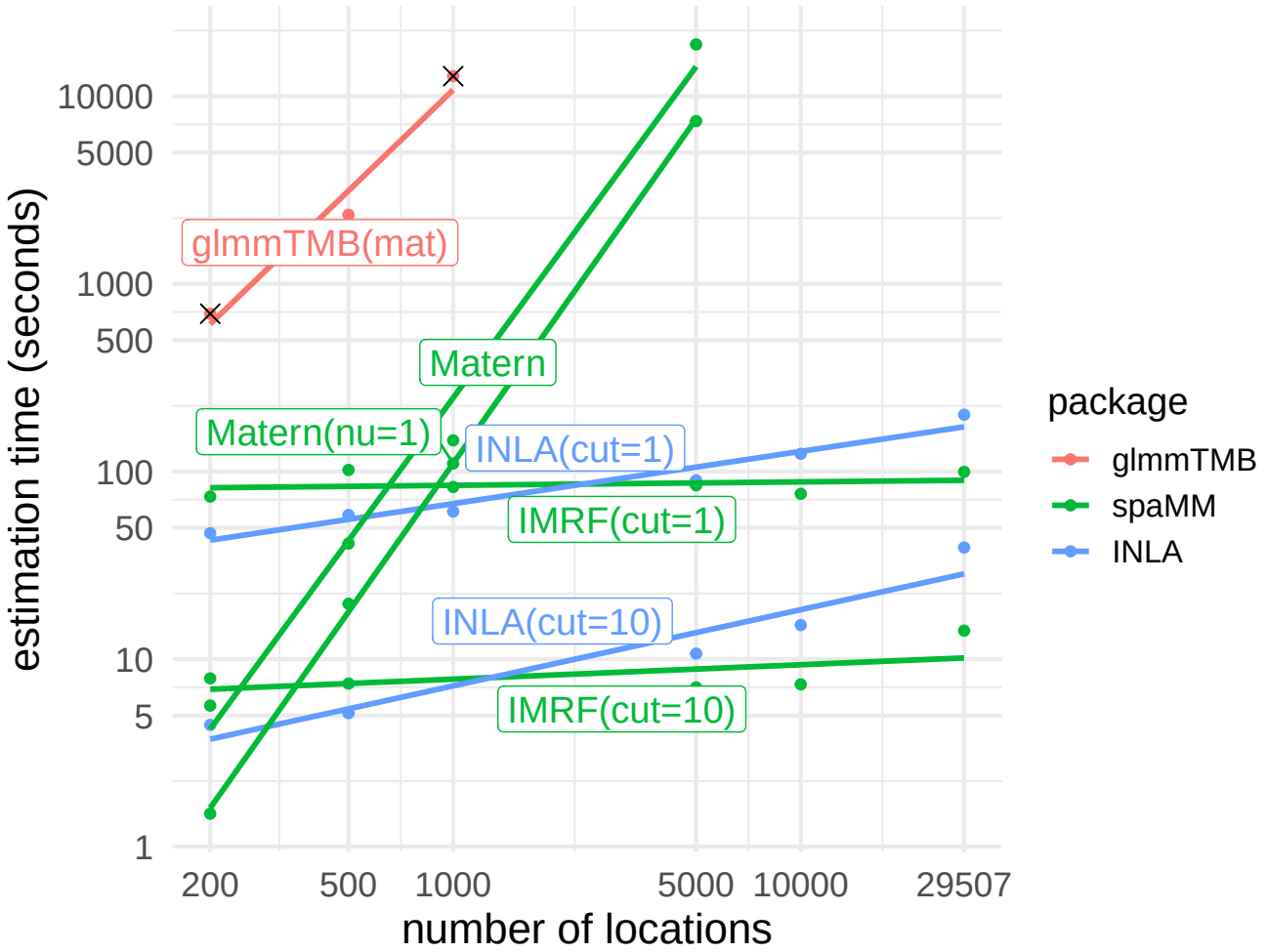
```
fitme(response ~1 + loc_x + loc_y + IMRF(1|loc_x+loc_y, model=pcmat),
      data=v, family=Gamma(log))
# where 'pcmat' correlation model provided by INLA::inla.spde2.pcmatern().
fitme(response ~1 + loc_x + loc_y + Matern(1|loc_x+loc_y),
      data=v, family=Gamma(log))
fitme(response ~1 + loc_x + loc_y + Matern(1|loc_x+loc_y),
      data=v, family=Gamma(log), fixed=list(nu=1))
```

Speed: Matérn models



spaMM is efficient, but (as is well known) computation times increase sharply with number of locations

Speed: MRF approximation of Matérn(smoothness=1)



MRF approximation is fast for large number of locations (known) and spaMM is efficient in fitting it.

Conclusions

- Polyvalent, simple to use, robust and fast;
- any model parameter can be fixed;
- Has functions for parametric bootstrap, prediction variances, marginal of conditional AIC...

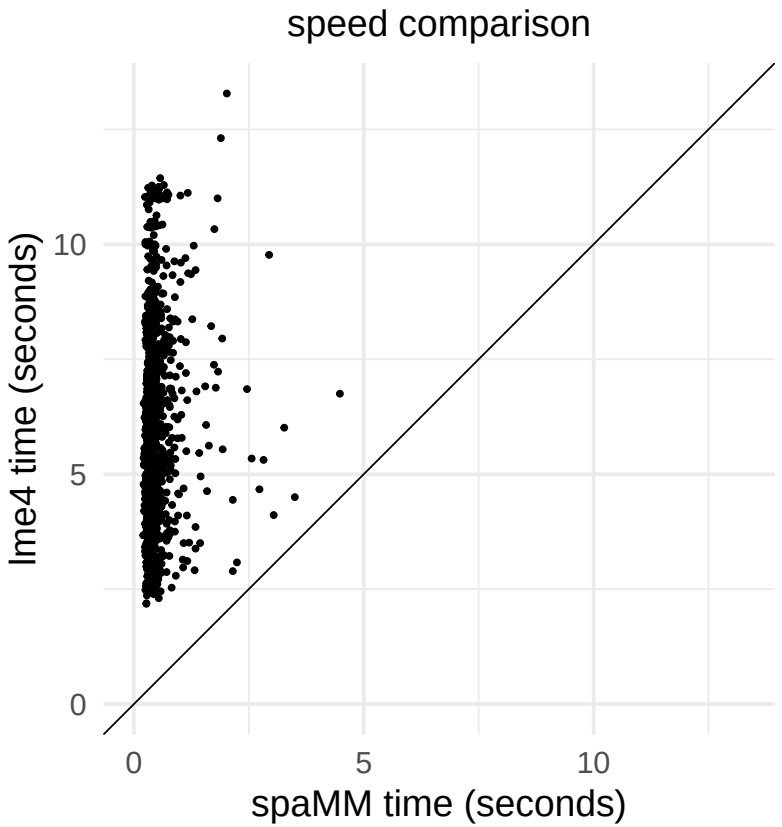
Planned developments:

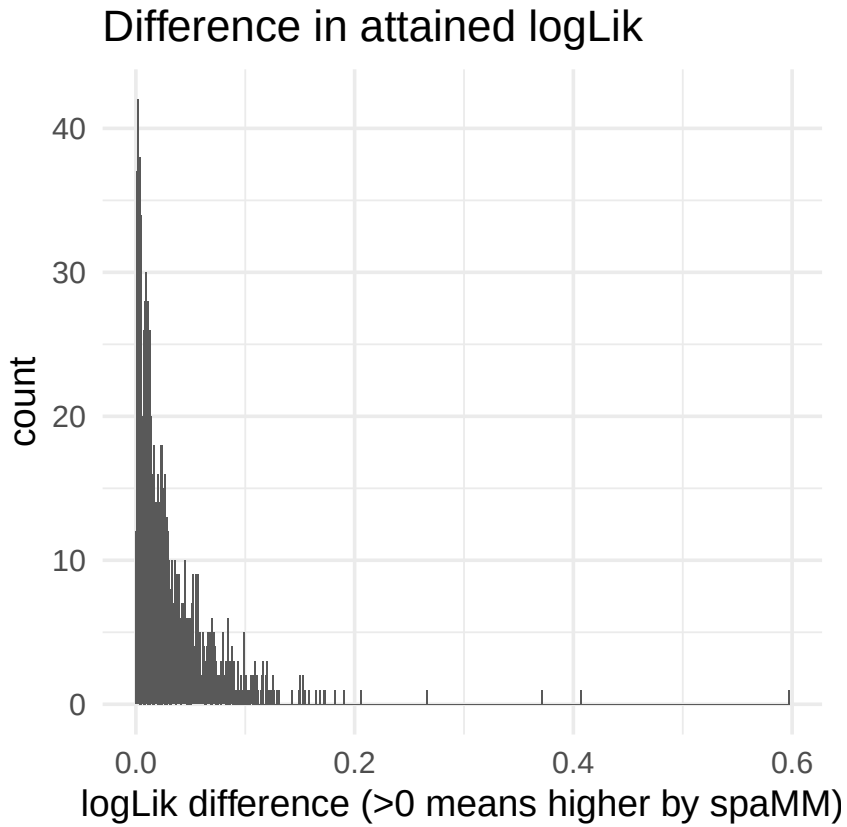
- Add parametric correlation structures for multivariate response (e.g. quantitative genetics);
- add or improve interfaces with other packages (e.g., broom.mixed, future);
- further additions potentially driven by collaborations

Comparison on non-spatial binary GLMMs

- binary GLMM, with 9 fixed-effect terms + nested random effect;
- unpublished data set of 585 observations, initially (2017) considered because fits did not converge on some bootstrap replicates;
- Assess performance on 1000 simulated bootstrap samples from the fitted model.

Binary GLMM: comparison with lme4

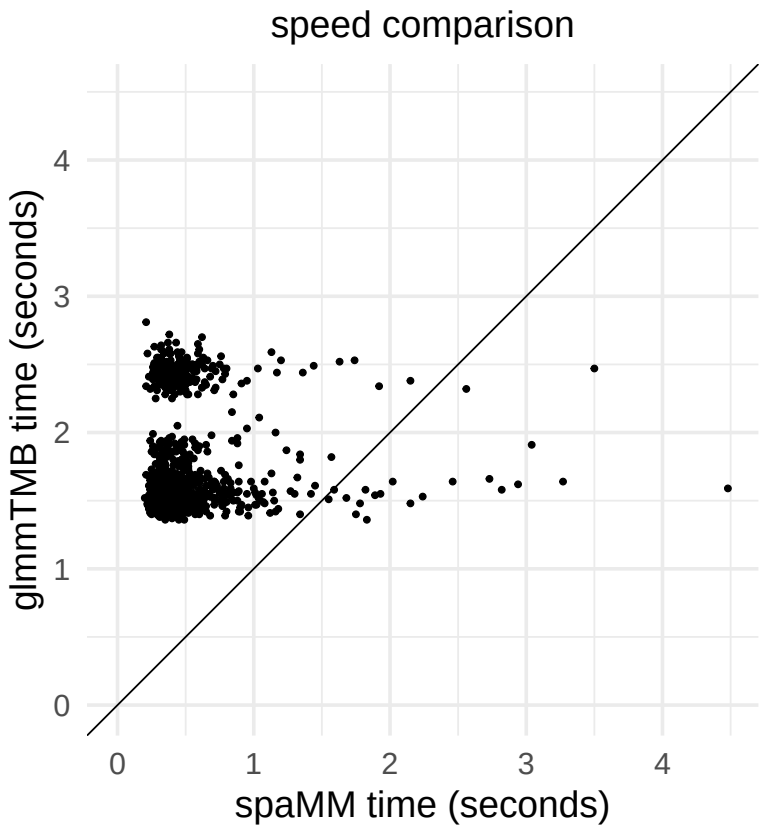


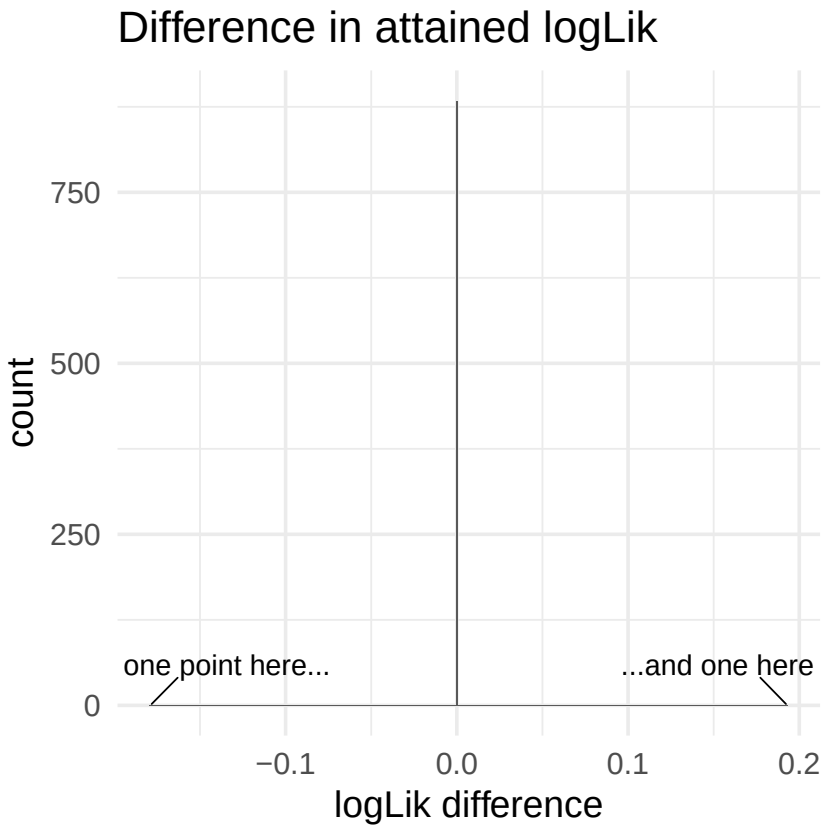


Binary GLMM: comparison with glmmTMB

Same 1000 simulated data sets: glmmTMB fails to fit 111 of them:

```
## Warning:  Removed 111 rows containing non-finite values (stat_bin).
```





```
  INLA::inla.upgrade()
```

```
## This is INLA_21.02.23 built 2021-05-08 00:36:08 UTC.
##  - See www.r-inla.org/contact-us for how to get help.
##  - Save 379.7Mb of storage running 'inla.prune()'
```

```
##
##  *** You already have the latest version.
```

```
  packageVersion("glmmTMB")
```

```
## [1] '1.1.1'
```

```
  packageDate("glmmTMB")
```

```
## [1] "2021-06-23"
```

```
  packageVersion("lme4")
```

```
## [1] '1.1.27.1'
```

```
  packageDate("lme4")
```

```
## [1] "2021-06-21"
```

```
  packageVersion("spaMM")
```

```
## [1] '3.8.9'
```