2c Temporal Model: Tutorial on synthetic data

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```
library(ETAS.inlabru)
library(ggplot2)

# Increase num.threads if you have more cores on your computer
INLA::inla.setOption(num.threads = 2)
```

Introduction

This tutorial shows how to use the `ETAS.inlabru` package to generate a synthetic catalogue from a temporal ETAS model and how to fit an ETAS model on this data. We also show how to retrieve the posterior distribution of the parameters and other quantity of interest.

For a brief introduction to the ETAS model we refer to the tutorial on real earthquake data.

Generate a synthetic catalogue

The function `generate_temporal_ETAS_synthetic()` can be used to generate synthetic catalogues from a temporal ETAS model with fixed parameters spanning a given interval of time. The `generate_temporal_ETAS_synthetic()` takes as input

- `theta`: a `list` of ETAS parameters with names `mu`, `K`, `alpha`, `c`, and `p`, corresponding to the ETAS parameters.
- `beta.p`: the parameter of the magnitude distribution
- `M0`: cutoff magnitude, all the generated event will have magnitude greater than `M0`.
- `T1`: starting time of the catalogue (the unit of measure depends on the unit used to fit the model).
- `T2`: end time of the catalogue (the unit of measure depends on the unit used to fit the model).
- `Ht`: set of known events. They can also be between `T1` and `T2`, this is useful when we want to generate catalogues with imposed events. If it is `NULL` no events are imposed.

The function returns a `list` of `data.frame`, each element of the output `list` corresponds to a different generation. The `data.frame` have three columns: occurence time (`ts`), magnitude (`magnitudes`), a the generation identifier (`gen`). The generation identifier uses the following convention, -1 indicates the events in `Ht` with time between `T1` and `T2`, 0 indicates the first generation offspring of the events with `gen` equal -1, 1 indicates background events, 2 all the offspring of the events with `gen` equal 0 or 1, 3 indicates all the offspring of the events with `gen` equal 2, 4 indicates all the offspring of the events with `gen` equal 3, and so on. To obtain a unique `data.frame` containing all the simulated events it is sufficient to bind by rows all the generations.

The code below generates a synthetic catalogue of events with magnitude greater than 2.5 according to a temporal ETAS model with parameters equal to the vector `true.param`. The value of the parameters is equal to the posterior mean of the parameters obtained fitting a model on the L'Aquila seismic sequence as it is done in the tutorial on real data. Also the parameter β of the magnitude distribution comes from the same example.

```r
set.seed(111)
# set true ETAS parameters
true.param <- list(mu = 0.30106014, K = 0.13611399, alpha = 2.43945301, c = 0.07098607, p = 1.17838741)
# set magnitude distribution parameter
beta.p <- 2.353157
# set cutoff magnitude
M0 <- 2.5
# set starting time of the synthetic catalogue
T1 <- 0
# set end time of the synthetic catalogue
T2 <- 365
# generate the catalogue - it returns a list of data.frames
synth.cat.list <- generate_temporal_ETAS_synthetic(
  theta = true.param,
  beta.p = beta.p,
  M0 = M0,
  T1 = T1,
  T2 = T2,
  Ht = NULL,
  ncore = 1
)
```

The output of the function is a `list` of `data.frame`s and it is convenient to transform it in a single `data.frame` binding the rows of the `data.frames` in the list.

```r
synth.cat.df <- do.call(rbind, synth.cat.list)
head(synth.cat.df)
#>           ts magnitudes gen
#> 1 135.204031   2.661688   1
#> 2 187.947198   2.632073   1
#> 3 137.847074   3.073890   1
#> 4 152.693124   2.653628   1
#> 5   3.890113   2.686633   1
#> 6 194.287763   3.035756   1
```

The synthetic catalogue is composed by a total of 288 events of which 112 are background events and 176 are aftershocks. We can easily retrieve this numbers looking at the `gen` column of the data.

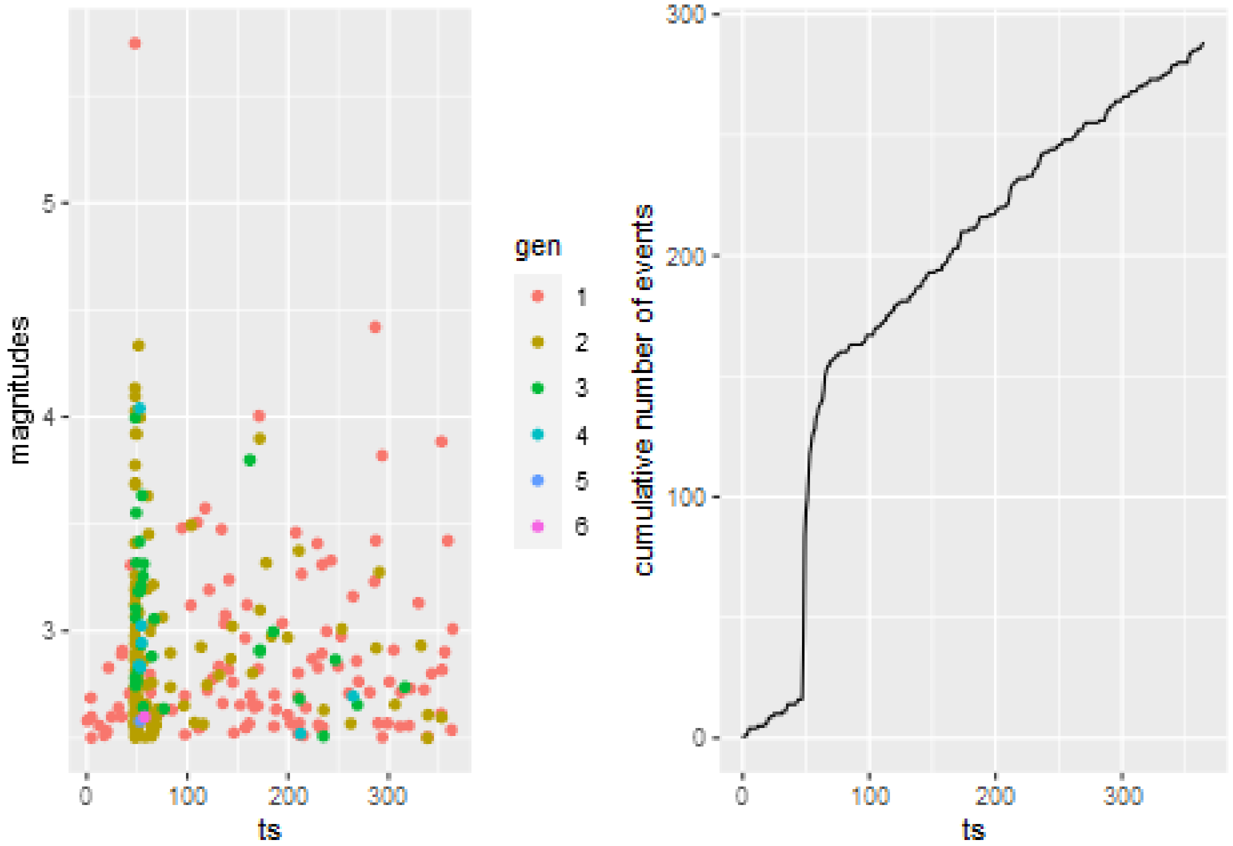
```r
c(N = nrow(synth.cat.df), N.bkg = sum(synth.cat.df$gen == 1), N.after = sum(synth.cat.df$gen > 1))
#>       N   N.bkg N.after
#>     288     112     176
```

The code below is to plot the occurrence time of the events against their magnitude with color indicating the generation of each event and the time evolution cumulative number of events. The `multiplot` function provided by the `inlabru` R-package can be used to combine the plots.

```r
pl1 <- ggplot(synth.cat.df, aes(ts, magnitudes, color = as.factor(gen))) +
  geom_point() +
  labs(color = "gen")

t.breaks <- T1:T2
N.cumsum <- vapply(t.breaks, \(x) sum(synth.cat.df$ts < x), 0)
df.to.cumsum.plot <- data.frame(ts = t.breaks, N.cum = N.cumsum)
pl2 <- ggplot(df.to.cumsum.plot, aes(ts, N.cum)) +
  geom_line() +
  ylab("cumulative number of events")
```

```r
inlabru::multiplot(pl1, pl2, cols = 2)
```



Prepare data for model fitting

In order to fit a model on the synthetic catalogue we need to

1. set parameters priors
2. set initial value of the parameters
3. set `inlabru` options
4. prepare the data for model fitting

To set the priors we need to create a list of copula transformation (or simply link) functions. This is because our method works with an internal representation of the parameters in which each parameter has a Gaussian distribution. We need the function to transform the parameters in the original ETAS scale and to set a prior for them. The `ETAS.inlabru` package offers four different functions corresponding to four different prior distributions. The functions are `gamma_t`, `unif_t`, `exp_t`, `loggaus_t` which corresponds to a Gamma distribution, a Uniform distribution, an Exponential distribution and a Log-Gaussian distribution. We also provide the inverse of this functions to retrieve the value of the parameters in the internal scale given a value in the ETAS scale. These are `inv_gamma_t`, `inv_unif_t`, `exp_t`, and `inv_loggaus_t`.

For this example we are going to consider the following priors for the parameters

$$
\begin{aligned}
\mu &\sim \Gamma(0.3, 0.6) \\
K &\sim \text{Unif}(0, 10) \\
\alpha &\sim \text{Unif}(0, 10) \\
c &\sim \text{Unif}(0, 10) \\
p &\sim \text{Unif}(1, 10)
\end{aligned}
$$

To `list` of link functions corresponding to the above priors is

```r
# set copula transformations list
link.f <- list(
  mu = \(x) gamma_t(x, 0.3, 0.6),
  K = \(x) unif_t(x, 0, 10),
  alpha = \(x) unif_t(x, 0, 10),
  c_ = \(x) unif_t(x, 0, 10),
  p = \(x) unif_t(x, 1, 10)
)
```

The initial value of the parameters for the `inlabru` algorithm must be specified in the internal scale of the parameters. For this reason, it is useful to create a `list` of inverse link functions so that we can specify the initial value of the parameters in the ETAS scale and easily retrieve the corresponding value of the parameters in the internal scale. This can be done as shown below

```r
# set inverse copula transformations list
inv.link.f <- list(
  mu = \(x) inv_gamma_t(x, 0.3, 0.6),
  K = \(x) inv_unif_t(x, 0, 10),
  alpha = \(x) inv_unif_t(x, 0, 10),
  c_ = \(x) inv_unif_t(x, 0, 10),
  p = \(x) inv_unif_t(x, 1, 10)
)
```

The initial value of the parameters have to be specified as a `list` with names `th.mu`, `th.K`, `th.alpha`, `th.c`, and `th.p`, where, for example, `th.mu` corresponds to the initial value of parameter μ in the internal scale. The initial value of the parameters is important to ensure that the algorithm will be able to converge. Indeed, if we start the algorithm from values of the parameters causing numerical problems, we may prevent the algorithm to converge. In our experience, setting the initial values such that each parameter is not *too close* (e.g. $< 10^{-5}$) or *too far* (e.g. $> 10^2$) is a safe choice. The code below uses the following initial values of the parameters $\mu_{\text{init}} = 0.5, K_{\text{init}} = 0.1, \alpha_{\text{init}} = 1, c_{\text{init}} = 0.1, p_{\text{init}} = 1.1$

```r
# set up list of initial values
th.init <- list(
  th.mu = inv.link.f$mu(0.5),
  th.K = inv.link.f$K(0.1),
  th.alpha = inv.link.f$alpha(1),
  th.c = inv.link.f$c_(0.1),
  th.p = inv.link.f$p(1.1)
)
```

Also the `inlabru` options have to be provided in a `list`, the main elements of the `list` are:

- `bru_verbose`: number indicating the type of visual output. Set it to 0 for no output.
- `bru_max_iter`: maximum number of iterations. If we do not set `max_step` the `inlabru` algorithm stops when the stopping criterion is met. However, setting `max_step` to values smaller than 1 forces the algorithm to run for exactly `bru_max_iter` iterations.

- bru_method: for what is relevant here, the only thing that we may need to set is the max_step argument. If the algorithm does not converge without fixing a max_step then we suggest to try to fix it to some value below 1, in our experience 0.5 or 0.2 works well. In the example below the line setting bru_method is commented.
- bru_initial: list of initial values created before.

```
# set up list of bru options
bru.opt.list <- list(
  bru_verbose = 3, # type of visual output
  bru_max_iter = 70, # maximum number of iterations
  # bru_method = list(max_step = 0.5),
  bru_initial = th.init
) # parameters initial values
```

Lastly, we need to prepare the data from the model fitting. The data must be provided as a data.frame with at least 3 columns with names ts corresponding to the occurrence time of the events, magnitudes corresponding to the magnitude, and idx.p with an event identifier. The events in the data.frame must be sorted with respect to the occurrence time. The synthetic catalogue we have generated at the beginning already has the columns ts and magnitudes, but it is sorted by generation and not time. The code below sort the rows of the data.frame and adds the event identifier

```
# sort catalogue by occurrence time
synth.cat.df <- synth.cat.df[order(synth.cat.df$ts), ]
# add event identifier
synth.cat.df$idx.p <- seq_len(nrow(synth.cat.df))
```

Model Fitting

The function Temporal.ETAS fit the ETAS model and returns a bru object as output. The required inputs are:

- total.data: data.frame containing the observed events. It have to be in the format described in the previous Section.
- M0: cutoff magnitude. All the events in total.data must have magnitude greater or equal to this number.
- T1: starting time of the time interval on which we want to fit the model.
- T2: end time of the time interval on which we want to fit the model.
- link.functions: list of copula transformation functions in the format described in previous sections.
- coef.t., delta.t., N.max.: parameters of the temporal binning. The binning strategy is described in Appendix B of the paper Approximation of Bayesian Hawkes process with inlabru. The parameters corresponds to coef.t.$= \delta$, delta.t.$= \Delta$, and N.max.$= n_{\max}$.
- bru.opt: list of inlabru options as described in the previous Section.

```
synth.fit <- Temporal.ETAS(
  total.data = synth.cat.df,
  M0 = M0,
  T1 = T1,
  T2 = T2,
  link.functions = link.f,
  coef.t. = 1,
  delta.t. = 0.1,
  N.max. = 5,
  bru.opt = bru.opt.list
)
#> Start creating grid...
#> Finished creating grid, time  1.175073
```

Check marginal posterior distributions

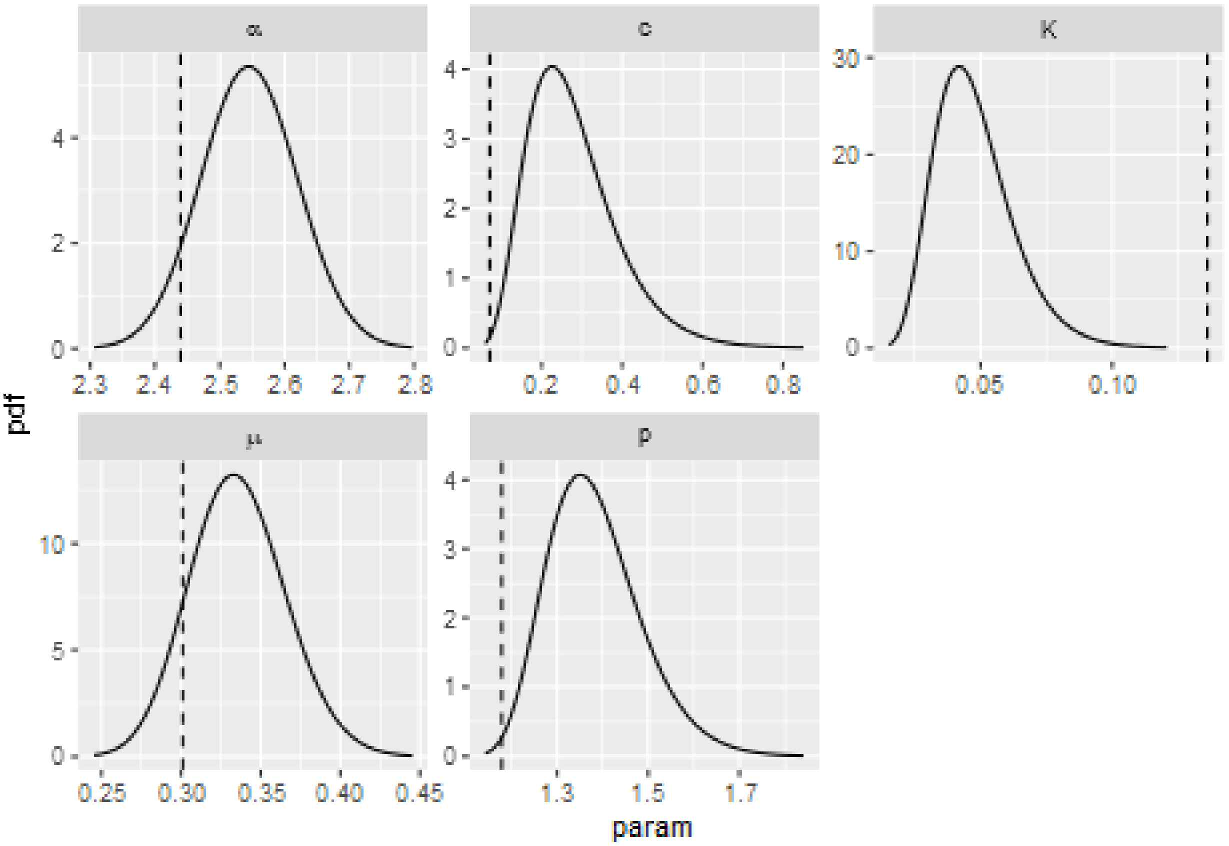
In order to retrieve the marginal posterior distributions of the parameter we need to provide a `list` containing two elements: `model.fit` which is a `bru` object containing the fitted model, and `link.functions` which is the `list` of link functions created before.

```
# create input list to explore model output
input_list <- list(
  model.fit = synth.fit,
  link.functions = link.f
)
```

Once the `list` has been created, the function `get_posterior_param` returns the marginal posterior distribution of the parameters in the ETAS scale. The function returns a `list` with two elements: `post.df` is a `data.frame` with three columns, `x` indicating the value of the parameter, `y` indicating the corresponding value of the marginal posterior distribution, and `param` which is a parameter identifier. The output `list` also contains `post.plot` which is a `ggplot` object containing the plot of the marginal posterior distributions for each parameter. The code below retrieve the marginal posterior distribution of the parameters and plot them along with the true value of the parameters represented by the vertical dashed lines.

```
# retrieve marginal posterior distributions
post.list <- get_posterior_param(input.list = input_list)

# create data.frame of true value of parameters
df.true.param <- data.frame(
  x = unlist(true.param),
  param = names(true.param)
)
# add to the marginal posterior distribution of the parameters the true value of the parameters.
post.list$post.plot +
  geom_vline(
    data = df.true.param,
    mapping = aes(xintercept = x), linetype = 2
  )
```



Sampling the joint posterior distribution

The function `post_sampling` generate samples from the joint posterior of ETAS parameters. The function takes in input:

- `input.list`: a list with a `model.fit` element and a `link.functions` elements as described above.
- `n.samp`: number of posterior samples.
- `max.batch`: the number of posterior samples to be generated simultaneously. If `n.samp`>`max.batch`, then, the samples are generated in parallel in batches of maximum size equal to `max.batch`. Default is 1000.
- `ncore`: number of cores to be used in parallel when `n.samp`>`max.batch`.

The function returns a `data.frame` with columns corresponding to the ETAS parameters

```
post.samp <- post_sampling(
  input.list = input_list,
  n.samp = 1000,
  max.batch = 1000,
  ncore = 1
)
head(post.samp)
#>           mu          K    alpha         c        p
#> 1 0.3279839 0.06734666 2.511810 0.2073965 1.337009
#> 2 0.3429538 0.04255420 2.525536 0.3003495 1.368902
#> 3 0.3978003 0.05008029 2.512142 0.2624318 1.382618
#> 4 0.3094680 0.06487732 2.471438 0.2268310 1.386890
#> 5 0.3804804 0.05953544 2.556805 0.1632502 1.320223
#> 6 0.3077189 0.04250790 2.538690 0.2231512 1.293125
```

The posterior samples can then be used to estimate the posterior distribution of functions of the parameters.

Triggering function and Omori law

Interesting functions of the parameters are the triggering function and the Omori law. We can estimate the posterior distribution of these functions using the samples from the joint posterior distribution of the parameters obtained in the previous section.

The functions `triggering_fun_plot` provides a plot of the quantiles of the posterior distribution of the triggering function $g(t - t_h, mh)$, namely,

$$g(t - t_h, m_h) = K \exp\{\alpha(m_h - M_0)\} \left(\frac{t - t_h}{c} + 1\right)^{-p}$$

The function takes in input

- `input.list`: the input list as defined for the functions used previously.
- `post.samp`: a `data.frame` of samples from the posterior distribution of the parameters. If it is `NULL`, then `n.samp` samples are generated from the posterior.
- `n.samp`: number of posterior samples of the parameters to be used or generated.
- `magnitude`: the magnitude of the event (m_h).
- `t.end`: the maximum value of t for the plot.
- `n.breaks`: the number of breaks in which the interval $(0, \texttt{t.end})$ is divided.

The function returns a `ggplot` object. For each sample of the parameters the triggering function between 0 and `t.end` is calculated. The black solid lines represents the 95% posterior interval of the function, the grey lines represent the triggering function calculated with the posterior samples, and the horizontal red lines represent the 95% posterior interval of the background rate μ. The function `triggering_plot_prior` does the same but using parameters sampled from the priors of the parameters.

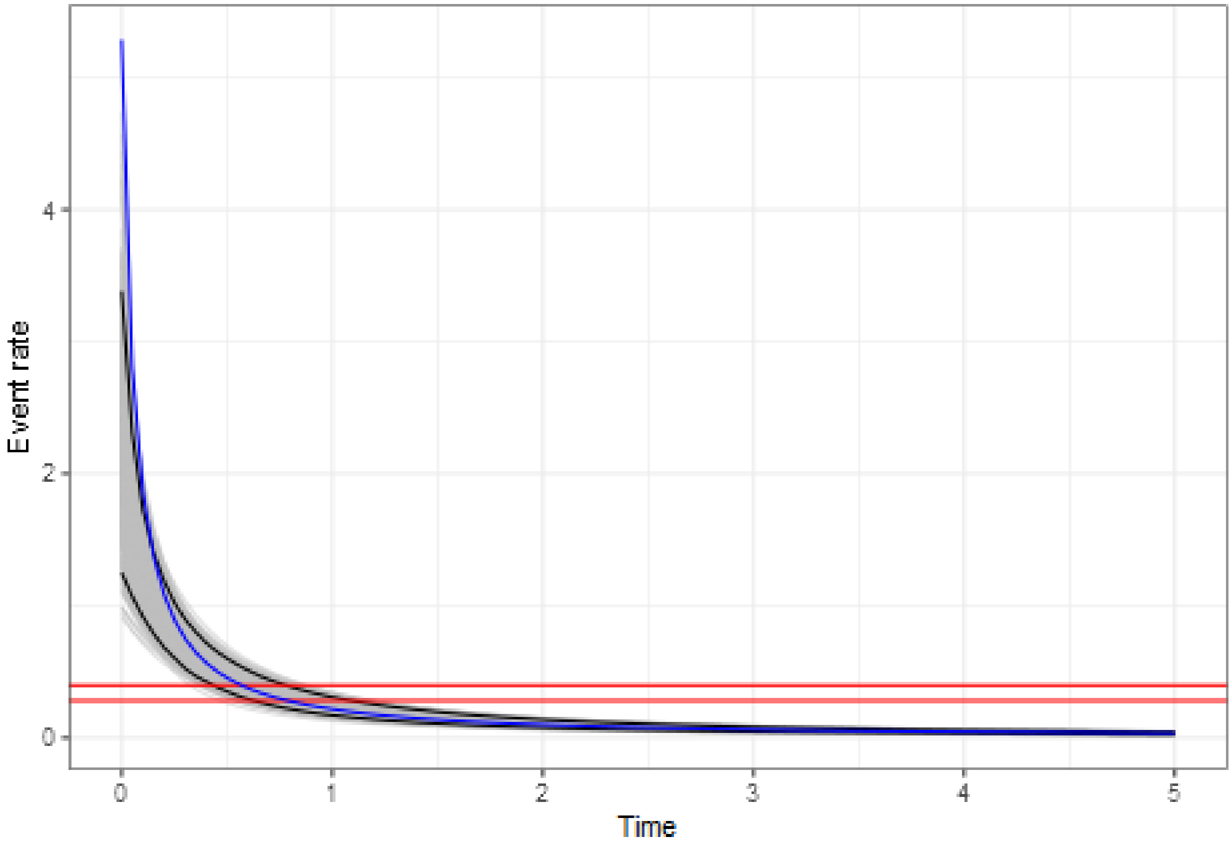
The code below creates the plot of the posterior of the triggering function and adds the triggering function calculated with the true parameter values in blue. We need to add the argument `M0` to the `input_list` to use the function `triggering_fun_plot`.

```
# add cutoff magnitude to input_list
input_list$M0 <- M0

# generate triggering function plot
trig.plot <- triggering_fun_plot(
  input.list = input_list,
  post.samp = post.samp,
  n.samp = NULL, magnitude = 4,
  t.end = 5, n.breaks = 100
)

# set times at which calculate the true triggering function
t.breaks <- seq(1e-6, 5, length.out = 100)
# calculate the function
true.trig <- gt(unlist(true.param), t = t.breaks, th = 0, mh = 4, M0 = M0)
# store in data.frame for plotting
true.trig.df <- data.frame(ts = t.breaks, trig.fun = true.trig)
```

```
# add the true triggering function to the plot
trig.plot +
  geom_line(
    data = true.trig.df,
    mapping = aes(x = ts, y = trig.fun), color = "blue"
  )
```



The functions `omori_plot_posterior` does the same as the function `triggering_fun_plot` but considering only

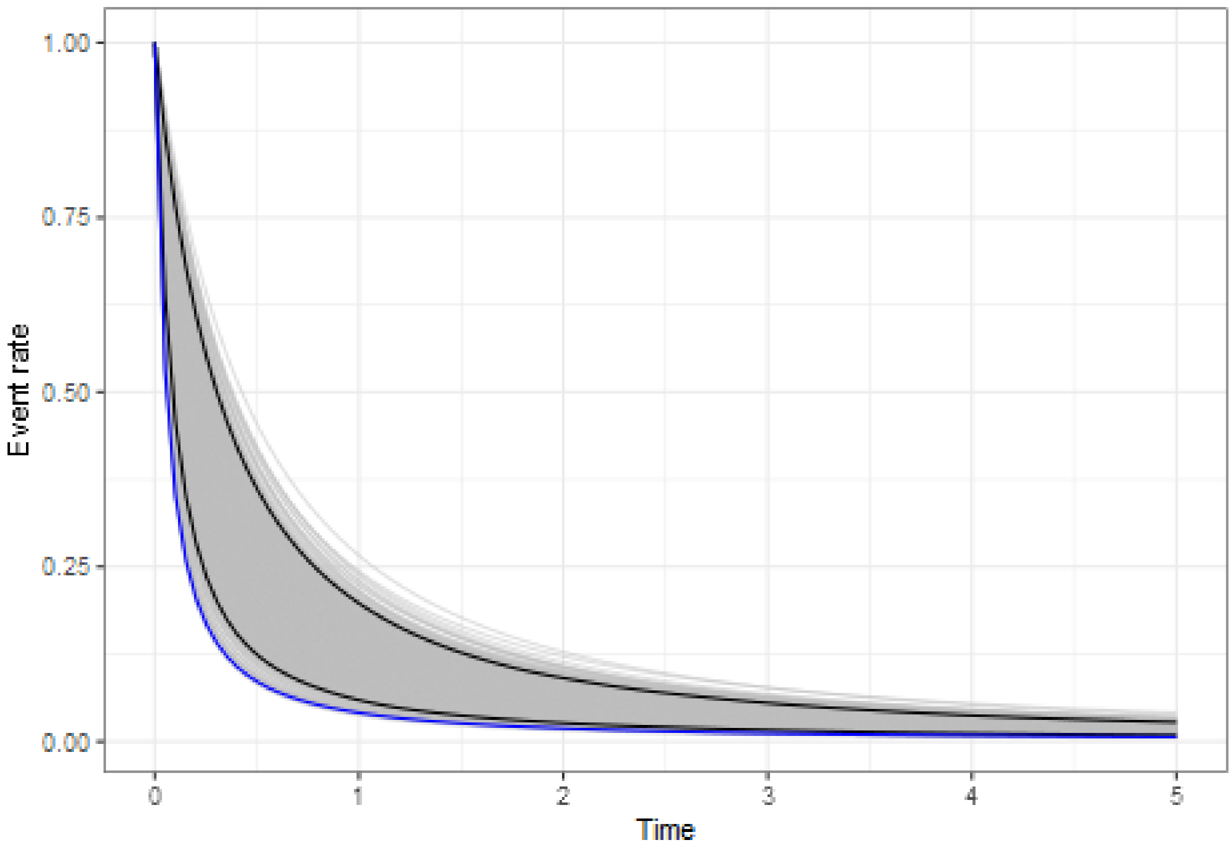
$$\left(\frac{t-t_h}{c}+1\right)^{-p}$$

instead of the whole triggering function and without the background rate.

```
omori.plot <- omori_plot_posterior(input.list = input_list, post.samp = post.samp, n.samp = NULL, t.end

true.omori <- omori(theta = unlist(true.param), t = t.breaks, ti = 0)
true.omori.df <- data.frame(ts = t.breaks, omori.fun = true.omori)

omori.plot +
  geom_line(
    data = true.omori.df,
    mapping = aes(x = ts, y = omori.fun), color = "blue"
  )
```



Comparison between different fitted models

It is interesting to fit the model on multiple synthetic catalogues and compare the parameters posterior distributions obtained with different catalogues. In this section, we are going to generate a second synthetic catalogue, fit the model, and compare the posterior distributions with the ones obtained before. For the second catalogue we impose a large event with magnitude 6 happening in the midpoint of the time interval.

The first step is to set the `data.frame` of known events and generate a second synthetic catalogue

```
# set up data.frame of imposed events
Ht.imposed <- data.frame(
  ts = mean(c(T1, T2)),
  magnitudes = 6
)
# generate second catalogue
set.seed(1)
synth.cat.list.2 <- generate_temporal_ETAS_synthetic(
  theta = true.param,
  beta.p = beta.p,
  M0 = M0,
  T1 = T1,
  T2 = T2,
  Ht = Ht.imposed,
  ncore = 1
)
# transform it in a data.frame
```

```
synth.cat.df.2 <- do.call(rbind, synth.cat.list.2)
```

Counting the number of background events and aftershocks in this case is slightly different from before. In fact, we count the imposed event as a background event, and the aftershocks need to include also the event with `gen = 0` which are the ones induced by the imposed event which in this case are 192.

```
sum(synth.cat.df.2$gen == 0)
#> [1] 192
```

Below the comparison between the number of events in the two catalogues. Notice that the background events are roughly the same which is expected given that the time interval is the same.

```
rbind(
  first = c(
    N = nrow(synth.cat.df),
    N.bkg = sum(synth.cat.df$gen == 1),
    N.after = sum(synth.cat.df$gen > 1)
  ),
  second = c(
    N = nrow(synth.cat.df.2),
    N.bkg = sum(synth.cat.df.2$gen == 1 | synth.cat.df.2$gen == -1),
    N.after = sum(synth.cat.df.2$gen > 1 | synth.cat.df.2$gen == 0)
  )
)
#>           N N.bkg N.after
#> first  288   112     176
#> second 408   104     304
```

Then, we just need to set up the `data.frame` for model fitting. For all the other inputs we can use the ones created for the first model fit.

```
synth.cat.df.2 <- synth.cat.df.2[order(synth.cat.df.2$ts), ]
synth.cat.df.2$idx.p <- seq_len(nrow(synth.cat.df.2))

synth.fit.2 <- Temporal.ETAS(
  total.data = synth.cat.df.2,
  M0 = M0,
  T1 = T1,
  T2 = T2,
  link.functions = link.f,
  coef.t. = 1,
  delta.t. = 0.1,
  N.max. = 5,
  bru.opt = bru.opt.list
)
#> Start creating grid...
#> Finished creating grid, time  0.881247
```

Now, to extract the marginal posterior distributions, we need to create the `input_list` of the second model fit.

```
input_list.2 <- list(
  model.fit = synth.fit.2,
  link.functions = link.f
)
```

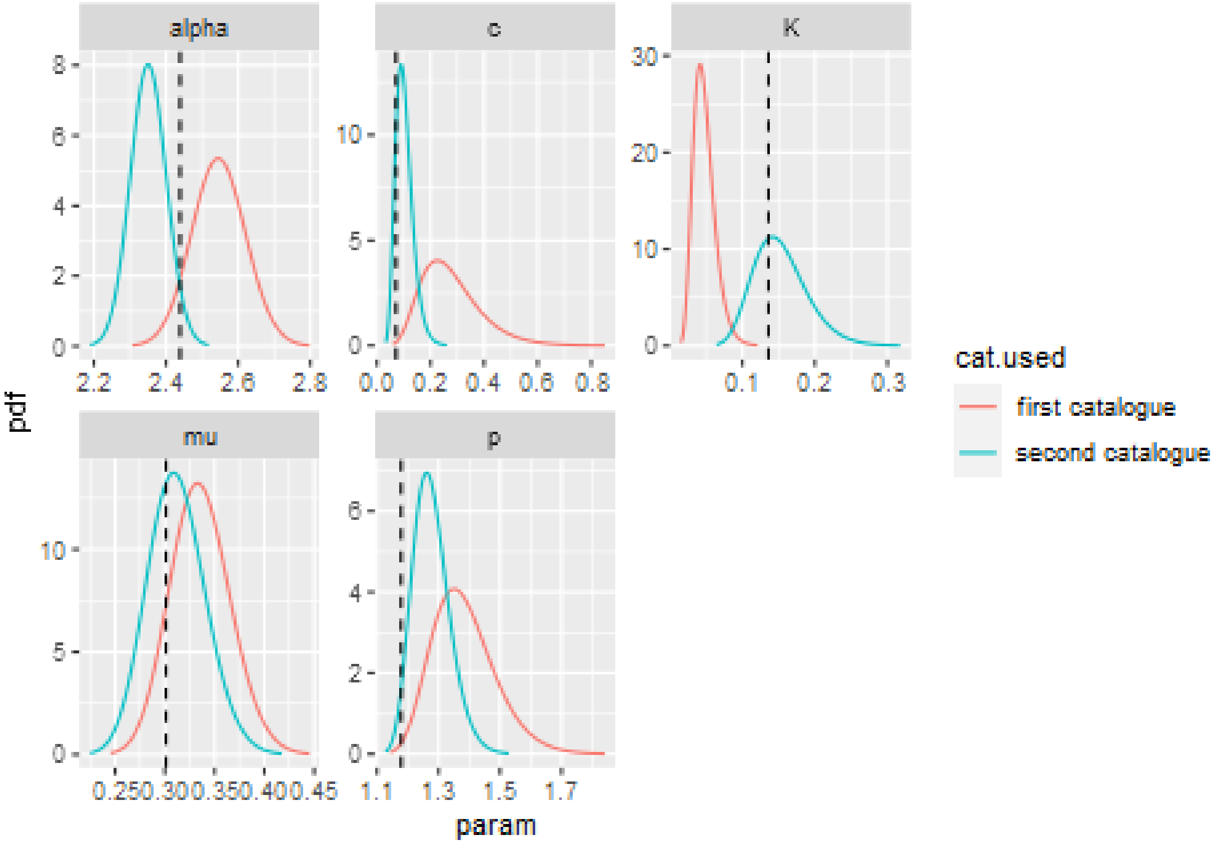
Now, we can retrieve the marginal posterior distributions provided by the model fitted on the second catalogue and compare them with the ones obtained before.

```
# retrieve marginal posterior distributions
post.list.2 <- get_posterior_param(input.list = input_list.2)

# set model identifier
post.list$post.df$cat.used <- "first catalogue"
post.list.2$post.df$cat.used <- "second catalogue"

# bind marginal posterior data.frames
bind.post.df <- rbind(post.list$post.df, post.list.2$post.df)

# plot them
ggplot(bind.post.df, aes(x = x, y = y, color = cat.used)) +
  geom_line() +
  facet_wrap(facets = ~param, scales = "free") +
  xlab("param") +
  ylab("pdf") +
  geom_vline(
    data = df.true.param,
    mapping = aes(xintercept = x), linetype = 2
  )
```



The process shown here can be extended to multiple (> 2) input catalogues in order to study if the parameters are identifiable. Also, using characteristics of the input catalogue as catalogue identifier we can study the change in the posterior distribution as the characteristic of the input catalogue changes. An interesting example is the number of events in the catalogue, and studying how the marginal posterior distributions change as we increase or decrease the number of events.