# R-INLA Practical: spatial and spatio-temporal disease mapping

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## 1. Introduction

In this practical you will extend what already seen in the tutorial and estimate spatial and spatio-temporal disease mapping models. You will study salmonellosis disease in cattles in $n = 199$ swiss regions for the years 1991-2008 ($T = 18$). The data are included in the workspace `data_salmonellosis` which can be loaded in `R` via

```
load("data_salmonellosis.RData")
```

Typing

```
ls()
```

```
## [1] "data.Y"      "data.offset" "data.salm"   "map"
```

you will see several objects: `data.salm`, `data.Y`, `data.offset`, `map` (this is a `SpatialPolygonsDataFrame` object and will be used for mapping).

The main data file is `data.salm` and typing

```
str(data.salm)
```

```
## 'data.frame':    3582 obs. of  5 variables:
##  $ Y        : int  1 3 0 1 0 1 1 0 0 0 ...
##  $ offset   : num  28.4 28.4 28.4 28.4 28.4 28.4 28.4 28.4 28.4 28.4 ...
##  $ region_id: int  1 1 1 1 1 1 1 1 1 1 ...
##  $ time_id  : int  1 2 3 4 5 6 7 8 9 10 ...
##  $ BEZIRKSNR: int  0 0 0 0 0 0 0 0 0 0 ...
```

you can see that the dataset is a `data.frame` with $199 \times 18 = 3582$ rows and five columns:

- `Y`: the number of salmonellosis cases for a combination of area/year
- `offset`: the number of herds in the region
- `region_id`: the area identifier
- `time_id`: the year identifier
- `BEZIRKSNR`: another region ID which matches the one included in the `map` (which you will need for mapping).

Note that this dataset is in **long** format, i.e. each region is repeated 18 times (as there are 18 years); use `View(data.salm)` if you want to explore the data.

The workspace also contains `data.Y` and `data.offset` which are the cases and the offset in a `data.frame` format:

```
dim(data.Y)
```

```
## [1] 199  19
```

```
dim(data.offset)
```

```
## [1] 199  19
```

```
colnames(data.Y)
```

```
##  [1] "1991"      "1992"      "1993"      "1994"      "1995"
##  [6] "1996"      "1997"      "1998"      "1999"      "2000"
## [11] "2001"      "2002"      "2003"      "2004"      "2005"
## [16] "2006"      "2007"      "2008"      "BEZIRKSNR"
```

```
colnames(data.offset)
```

```
##  [1] "1991"      "1992"      "1993"      "1994"      "1995"
##  [6] "1996"      "1997"      "1998"      "1999"      "2000"
## [11] "2001"      "2002"      "2003"      "2004"      "2005"
## [16] "2006"      "2007"      "2008"      "BEZIRKSNR"
```

```
n = nrow(data.Y) #n. of areas
T = ncol(data.Y) - 1 #n. of years
```

Note that here the number of rows is given by the regions and the number of columns is given by the years (18) plus a column for the region `BEZIRKSNR` identifier.

DISCLAIMER: the code provided is one of the many ways to get the results. For advanced `R` users: feel free to ignore it and run your own code up to the INLA model.

## 2. Data preparation and exploration

Create a new `data.frame` which includes the region `BEZIRKSNR` identifier and the risk (probability) of salmonellosis given by Y/offset:

```
prob.salm = data.frame(BEZIRKSNR=data.Y$BEZIRKSNR,
                       p=data.Y[,1:T]/data.offset[,1:T]) #exclude the BEZIRKSNR col
```

Then transform the risk variables in categorical variables by using the `cut` functions and the following cutoffs: 0, 0.01, 0.5 and 1. Define a new `data.frame`:

```
prob.salm.cat = data.frame(lapply(prob.salm[,2:(T+1)],
                          function(x) (cut(x, c(0,0.01,0.5,1), include.lowest=TRUE)))
                          )
#Include area identifier in the dataframe
prob.salm.cat$BEZIRKSNR = prob.salm$BEZIRKSNR
colnames(prob.salm.cat)
```

```
##  [1] "p.1991"    "p.1992"    "p.1993"    "p.1994"    "p.1995"
##  [6] "p.1996"    "p.1997"    "p.1998"    "p.1999"    "p.2000"
## [11] "p.2001"    "p.2002"    "p.2003"    "p.2004"    "p.2005"
## [16] "p.2006"    "p.2007"    "p.2008"    "BEZIRKSNR"
```

Finally, plot the probabilities for three years (1991, 2000 and 2008):

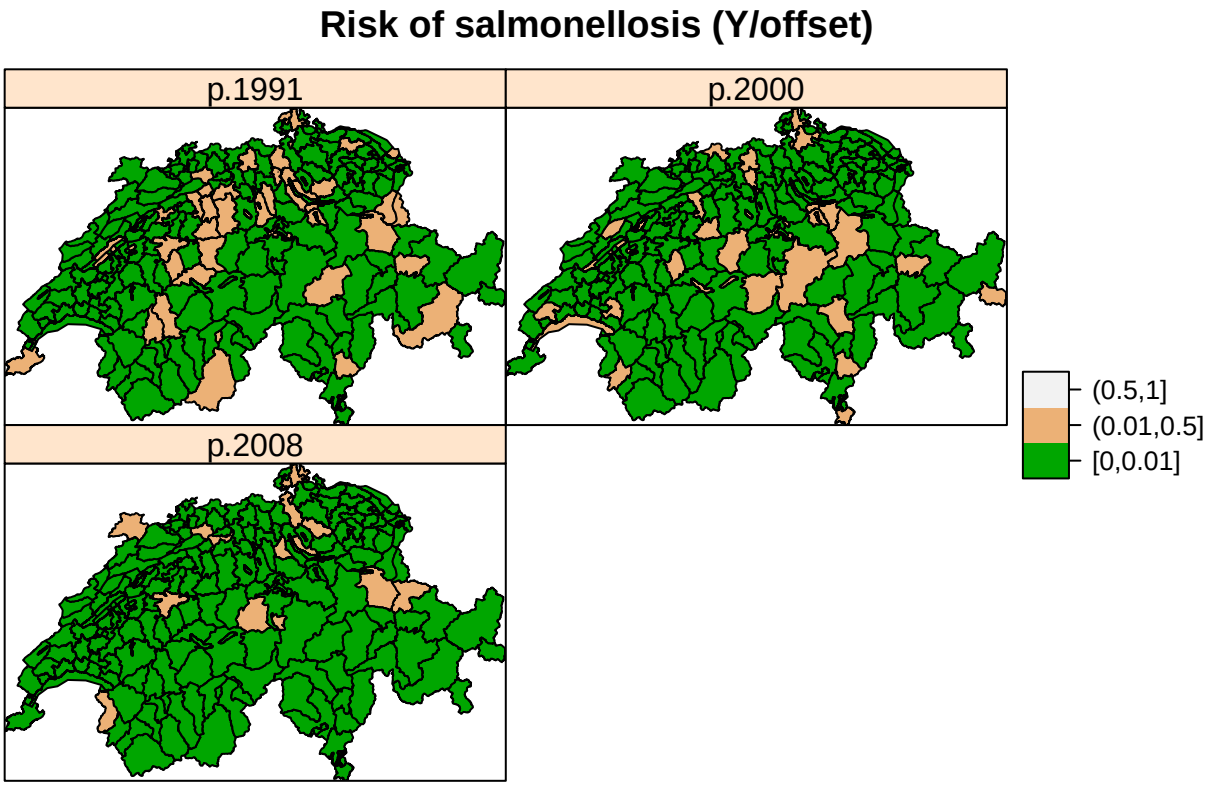
```
#Merge prob.salm and the Switzerland shapefile
map.swiss = map
map.swiss@data = merge(map.swiss@data,
                       prob.salm.cat, by="BEZIRKSNR")
```

```
## Loading required package: sp
```

```r
head(map.swiss@data)
```

```
##   BEZIRKSNR Cnt_BEZIRK     p.1991     p.1992     p.1993     p.1994
## 1         0          3 (0.01,0.5] (0.01,0.5]   [0,0.01] (0.01,0.5]
## 2       100          2   [0,0.01]   [0,0.01]   [0,0.01] (0.01,0.5]
## 3       101         14   [0,0.01]   [0,0.01] (0.01,0.5]   [0,0.01]
## 4       102         24   [0,0.01]   [0,0.01]   [0,0.01]   [0,0.01]
## 5       103         23   [0,0.01]   [0,0.01] (0.01,0.5]   [0,0.01]
## 6       104         22 (0.01,0.5] (0.01,0.5] (0.01,0.5] (0.01,0.5]
##       p.1995     p.1996     p.1997   p.1998     p.1999     p.2000   p.2001
## 1   [0,0.01] (0.01,0.5] (0.01,0.5] [0,0.01]   [0,0.01]   [0,0.01] [0,0.01]
## 2   [0,0.01]   [0,0.01]   [0,0.01] [0,0.01] (0.01,0.5]   [0,0.01] [0,0.01]
## 3   [0,0.01] (0.01,0.5]   [0,0.01] [0,0.01]   [0,0.01]   [0,0.01] [0,0.01]
## 4 (0.01,0.5]   [0,0.01]   [0,0.01] [0,0.01]   [0,0.01] (0.01,0.5] [0,0.01]
## 5 (0.01,0.5]   [0,0.01]   [0,0.01] [0,0.01] (0.01,0.5]   [0,0.01] [0,0.01]
## 6 (0.01,0.5] (0.01,0.5] (0.01,0.5] [0,0.01]   [0,0.01]   [0,0.01] [0,0.01]
##       p.2002     p.2003   p.2004     p.2005     p.2006     p.2007
## 1   [0,0.01]   [0,0.01] [0,0.01]   [0,0.01]   [0,0.01]   [0,0.01]
## 2 (0.01,0.5]   [0,0.01] [0,0.01]   [0,0.01]   [0,0.01]   [0,0.01]
## 3   [0,0.01]   [0,0.01] [0,0.01]   [0,0.01]   [0,0.01] (0.01,0.5]
## 4   [0,0.01]   [0,0.01] [0,0.01] (0.01,0.5]   [0,0.01]   [0,0.01]
## 5   [0,0.01] (0.01,0.5] [0,0.01]   [0,0.01] (0.01,0.5] (0.01,0.5]
## 6   [0,0.01]   [0,0.01] [0,0.01]   [0,0.01]   [0,0.01]   [0,0.01]
##       p.2008
## 1   [0,0.01]
## 2   [0,0.01]
## 3 (0.01,0.5]
## 4   [0,0.01]
## 5 (0.01,0.5]
## 6   [0,0.01]
```

```r
spplot(map.swiss,
       c("p.1991","p.2000","p.2008"),
       col.regions= terrain.colors(3),
       as.table=TRUE,
       main = "Risk of salmonellosis (Y/offset)")
```




## 3. Purely spatial disease mapping model

Now, focussing on year 1991, specify a BYM model as the one described in slide 40 of the lecture and Section 4 of the tutorial.

The adjacency matrix in the inla format is already available through the object `switzerland.graph` saved in your directory (note that for this case study it is not possible to create the adjacency matrix from the `map.swiss` object - as shown in the tutorial - because there is a problem in the geographic structure of the polygons).

```
swiss.adj.path = "switzerland.graph"
```

Then define the `formula` and run INLA (use a logGamma(1,0.1) prior for both the precisions):

```
library(INLA)
```

```
## Warning: package 'INLA' was built under R version 3.6.1
```

```
## Loading required package: Matrix
```

```
## Loading required package: parallel
```

```
## This is INLA_19.07.21 built 2019-07-21 14:38:44 UTC.
## See www.r-inla.org/contact-us for how to get help.
## To enable PARDISO sparse library; see inla.pardiso()
```

```
formula = Y ~ 1 + f(region_id,
                    model="bym",
                    graph=swiss.adj.path,
                    hyper=list(prec.unstruct=list(prior="loggamma",param=c(1,0.1)),
                               prec.spatial=list(prior="loggamma",param=c(1,0.1))))
```

```
output1 = inla(formula,
               family = "poisson",
               data = data.salm[data.salm$time_id==1,], #select just the data of the first year
               offset = log(offset),
               control.compute=list(dic=TRUE))
summary(output1)
```

```
##
## Call:
##    c("inla(formula = formula, family = \"poisson\", data =
##    data.salm[data.salm$time_id == ", " 1, ], offset = log(offset),
##    control.compute = list(dic = TRUE))" )
## Time used:
##     Pre = 2.1, Running = 1.75, Post = 0.11, Total = 3.96
## Fixed effects:
##             mean    sd 0.025quant 0.5quant 0.975quant   mode   kld
## (Intercept) -4.7 0.215     -5.159   -4.686     -4.322 -4.657 0.001
##
## Random effects:
##   Name     Model
##     region_id BYM model
##
## Model hyperparameters:
##                                           mean    sd 0.025quant 0.5quant
## Precision for region_id (iid component)     1.89  1.10      0.652     1.60
## Precision for region_id (spatial component) 9.37 10.40      0.634     6.23
##                                           0.975quant mode
## Precision for region_id (iid component)         4.78 1.21
## Precision for region_id (spatial component)    36.95 1.72
##
## Expected number of effective parameters(stdev): 33.62(10.72)
## Number of equivalent replicates : 5.92
##
## Deviance Information Criterion (DIC) ...............: 272.29
## Deviance Information Criterion (DIC, saturated) ....: 168.82
## Effective number of parameters .....................: 33.18
##
## Marginal log-Likelihood:  -106.46
## Posterior marginals for the linear predictor and
##  the fitted values are computed
```

Now you want to map the spatial random effects. To do this you first bring back $z_i = u_i + v_i$ to the natural scale (from the logarithmic one), compute the posterior mean of $z_i$ and create the corresponding categorical variable:

```
names(output1$marginals.random)
```

```
## [1] "region_id"
```

```
length(output1$marginals.random$region_id)
```

```
## [1] 398
```

```
#Remember that the first n rows include information on z=u+v

#Go back to the natural scale
```

```
exp.z = unlist(lapply(output1$marginals.random$region_id[1:n],
                      function(x) inla.emarginal(exp,x)))
range(exp.z)
```

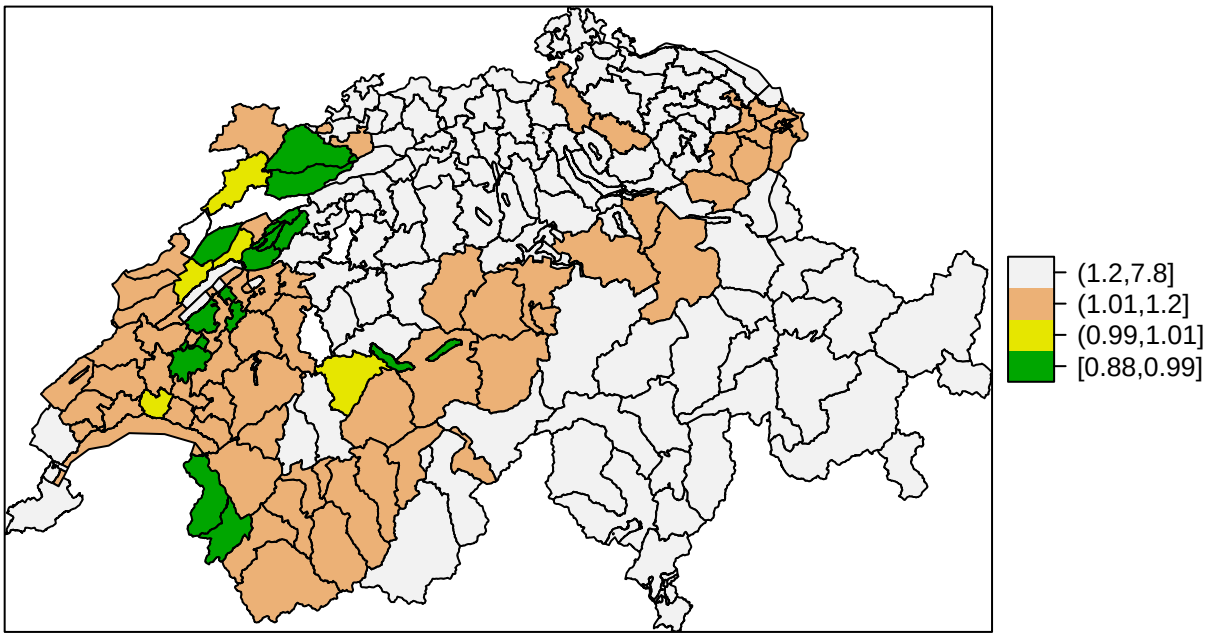
```
## [1] 0.7994591 7.7020734
```

```
#Create a new dataframe
data.exp.z = data.frame(BEZIRKSNR=data.Y$BEZIRKSNR,
                                exp.z=exp.z)
#Add also the categorical variable
data.exp.z$exp.z.cat = cut(data.exp.z$exp.z,
                               c(0.88,0.99,1.01,1.2,7.8),
                               include.lowest=T)
head(data.exp.z)
```

```
##         BEZIRKSNR    exp.z  exp.z.cat
## index.1         0 2.013811  (1.2,7.8]
## index.2       100 1.286420  (1.2,7.8]
## index.3       101 1.417807  (1.2,7.8]
## index.4       102 1.265014  (1.2,7.8]
## index.5       103 1.162092 (1.01,1.2]
## index.6       104 7.702073  (1.2,7.8]
```

Then merge the new dataframe `data.exp.z.c` with the data from the shapefile and finally plot the categorical variable:

```
map.swiss@data =  merge(map.swiss@data,
                        data.exp.z,
                        by="BEZIRKSNR")
spplot(obj=map.swiss,
       zcol="exp.z.cat",
       col.regions=terrain.colors(4),
       as.table=TRUE)
```




It is also possible to compute the probability $p(z_i > 1 \mid \mathbf{y})$ (or equivalently $p(u_i + v_i > 0 \mid \mathbf{y})$) using the

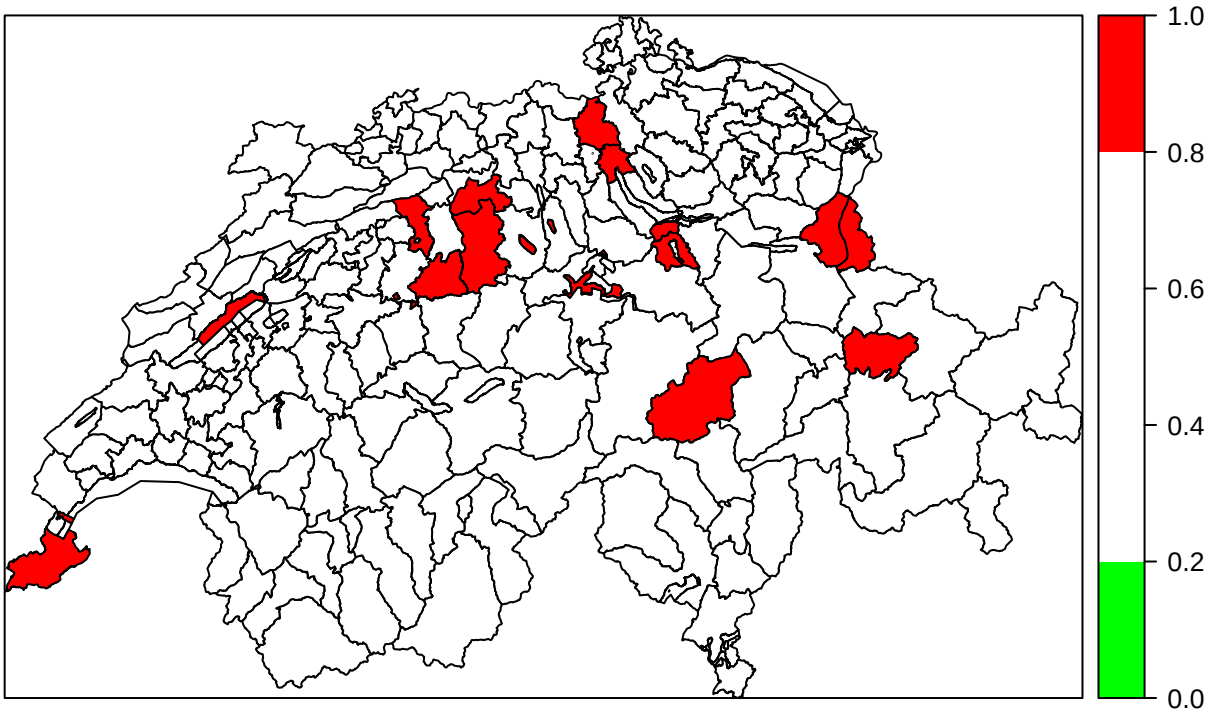
built-in function `inla.pmarginal`:

```
#Compute the probabilities
threshold = 0
prob.z = unlist(lapply(output1$marginals.random$region_id[1:n],
                       function(x) 1-inla.pmarginal(threshold,x)))
#Create a new dataframe
data.prob.z = data.frame(BEZIRKSNR=data.Y$BEZIRKSNR,
                         prob.z=prob.z)
head(data.prob.z)
```

```
##         BEZIRKSNR    prob.z
## index.1         0 0.7280462
## index.2       100 0.5146102
## index.3       101 0.5531924
## index.4       102 0.4903488
## index.5       103 0.4688590
## index.6       104 0.9933805
```

Then you merge the new dataframe `data.prob.z.cat1` with the data from the shapefile and finally plot the categorical variable with the probabilities:

```
prob.cutoff = c(0,0.2,0.8,1)
map.swiss@data =  merge(map.swiss@data,
                        data.prob.z,
                        by="BEZIRKSNR")
spplot(obj=map.swiss,
       zcol="prob.z",
       col.regions=c("green","white","red"),
       at=prob.cutoff,
       as.table=TRUE,
       main="BYM model - exp(z)")
```




Note the same purely spatial model could be estimated indipendently for all the available years.

## 4. Spatio-temporal disease mapping

Now specify a spatio-temporal dynamic model for the salmonellosis data. The model you want to use is the following (see page 65 of the lecture slides):

$$
\begin{aligned}
y_{it} &\sim \text{Poisson}(\phi_{it} E_{it}) \\
\log(\phi_{it}) &= \beta_0 + u_i + v_i + \lambda_t + \gamma_t \\
v_i &\sim \text{Normal}(0, \sigma_v^2) \\
\mathbf{u} &\sim \text{ICAR}(\mathbf{W}, \sigma_u^2) \\
\gamma_t &\sim \text{Normal}(0, \sigma_\gamma^2) \\
\lambda_t &\sim \text{RW1}(\sigma_\lambda^2)
\end{aligned}
$$

The model includes, besides the BYM components, two temporal effects (unstructured (`model=iid`) and structured (`model=rw1`)). A logGamma(1,0.1) prior is specified for the four precisions.

To estimate this model you have to create a new temporal identifier as you need to define two time specific components in the model and INLA does not allow to assign more than one `f()` to any identifier:

```
data.salm$time_id2 = data.salm$time_id
formula.ST1 = Y ~  1+ f(region_id,
                        model="bym",
                        graph=swiss.adj.path,
                        hyper=list(prec.unstruct=list(prior="loggamma",param=c(1,0.1)),
                               prec.spatial=list(prior="loggamma",param=c(1,0.1)))) +
```

```
                        f(time_id, model="iid",
                          hyper=list(prec=list(prior="loggamma",param=c(1,0.1)))) +
                        f(time_id2, model="rw1",
                          hyper=list(prec=list(prior="loggamma",param=c(1,0.1))))
```

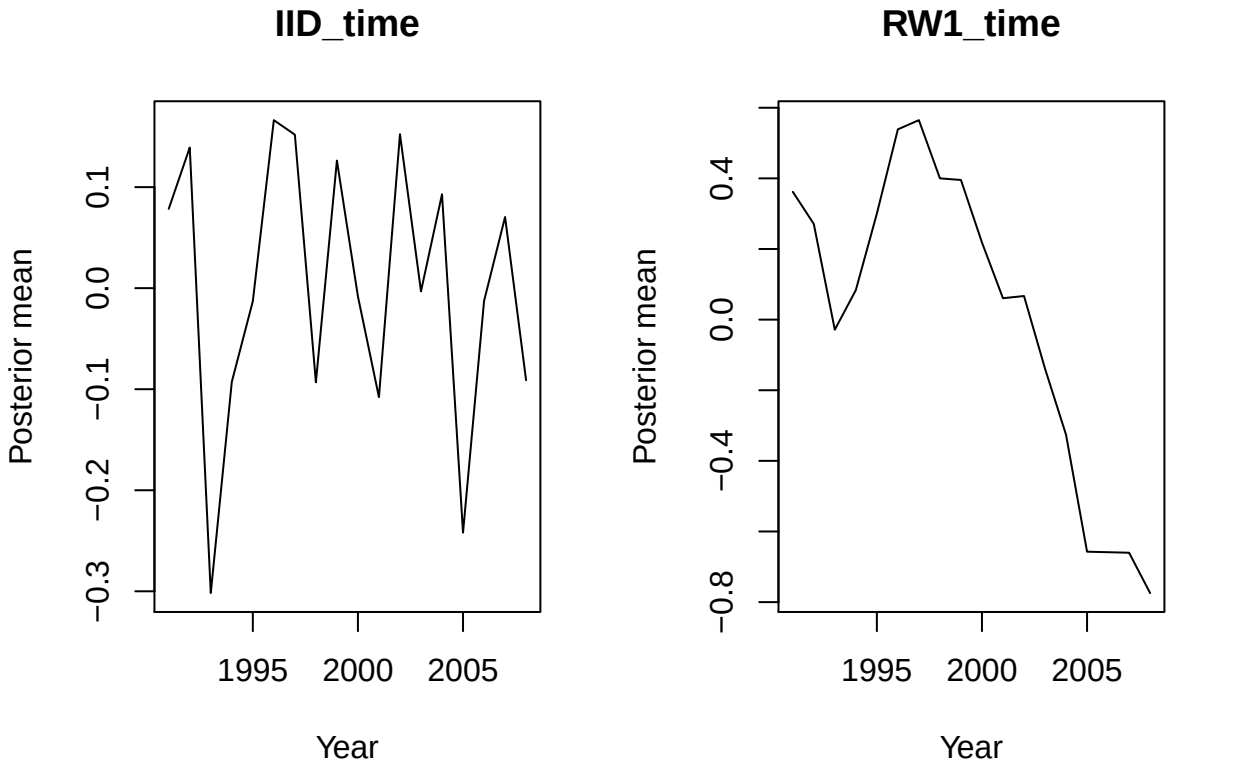
Then run the model

```
output2 = inla(formula.ST1,
               family="poisson",
               data=data.salm,
               offset=log(offset),
               control.compute=list(dic=TRUE))
summary(output2)
```

```
##
## Call:
##    c("inla(formula = formula.ST1, family = \"poisson\", data =
##    data.salm, ", " offset = log(offset), control.compute = list(dic =
##    TRUE))" )
## Time used:
##     Pre = 2.77, Running = 15.6, Post = 0.232, Total = 18.6
## Fixed effects:
##               mean    sd 0.025quant 0.5quant 0.975quant   mode kld
## (Intercept) -5.404 0.119     -5.644   -5.402     -5.177 -5.397   0
##
## Random effects:
##   Name     Model
##     region_id BYM model
##    time_id IID model
##    time_id2 RW1 model
##
## Model hyperparameters:
##                                             mean     sd 0.025quant
## Precision for region_id (iid component)     1.02  0.205      0.674
## Precision for region_id (spatial component)  4.58  4.620      0.788
## Precision for time_id                       19.80 11.533      5.699
## Precision for time_id2                      15.13  8.828      4.453
##                                             0.5quant 0.975quant  mode
## Precision for region_id (iid component)        0.998       1.48  0.96
## Precision for region_id (spatial component)    3.209      16.64  1.80
## Precision for time_id                         17.180      49.35 12.76
## Precision for time_id2                        13.081      37.92  9.76
##
## Expected number of effective parameters(stdev): 145.74(4.51)
## Number of equivalent replicates : 24.58
##
## Deviance Information Criterion (DIC) ...............: 3672.45
## Deviance Information Criterion (DIC, saturated) ....: 2390.67
## Effective number of parameters .....................: 142.23
##
## Marginal log-Likelihood:  -1889.31
## Posterior marginals for the linear predictor and
##  the fitted values are computed
```

It is possible to plot the posterior mean of the two temporal effects:

```r
par(mfrow=c(1,2))
plot(1991:2008,
     output2$summary.random$time_id$mean,
     type="l", main="IID_time",ylab="Posterior mean",xlab="Year")
plot(1991:2008,
     output2$summary.random$time_id2$mean,
     type="l", main="RW1_time",ylab="Posterior mean",xlab="Year")
```




```r
par(mfrow=c(1,1))
```

It would be also possible to compute the **sum** of the two temporal effect as the total temporal trend $\gamma_t + \lambda_t$. To do this you need to use `inla.make.lincombs` function (see for example Section 7.1.1 of the INLA book) to create a linear combination of two random effects.

As done in the previous Section 2., it is also possible to plot for this model the residual spatial random effects ($z_i = u_i + v_i$).

## 5. Spatio-temporal disease mapping with space-time interaction

You will now run a spatio-temporal model with a type I interaction (see page 66 of the lecture slides).

$$
\begin{aligned}
y_{it} &\sim \text{Poisson}(\phi_{it} E_{it}) \\
\log(\phi_{it}) &= \beta_0 + u_i + v_i + \lambda_t + \gamma_t + \delta_{it} \\
v_i &\sim \text{Normal}(0, \sigma_v^2) \\
\mathbf{u} &\sim \text{ICAR}(\mathbf{W}, \sigma_u^2) \\
\gamma_t &\sim \text{Normal}(0, \sigma_\gamma^2) \\
\lambda_t &\sim \text{RW1}(\sigma_\lambda^2) \\
\delta_{it} &\sim N(0, \sigma_\delta^2)
\end{aligned}
$$

A logGamma(1,0.1) prior is specified for the five precisions. To run this model you need to specify another identifier for the interaction, going from 1 to the total number of rows in `data.salm`:

```
#ID
region_time_id = seq(1,nrow(data.salm))

#Formula
formula.intI = Y ~  1+ f(region_id,
                         model="bym",
                         graph=swiss.adj.path,
                         hyper=list(prec.unstruct=list(prior="loggamma",param=c(1,0.1)),
                                prec.spatial=list(prior="loggamma",param=c(1,0.1)))) +
                         f(time_id, model="iid",
                           hyper=list(prec=list(prior="loggamma",param=c(1,0.1)))) +
                         f(time_id2, model="rw1",
                           hyper=list(prec=list(prior="loggamma",param=c(1,0.1)))) +
                         f(region_time_id, model="iid",
                           hyper=list(prec=list(prior="loggamma",param=c(1,0.1))))
#Run INLA
output3 = inla(formula.intI,
               family="poisson",
               data=data.salm,
               offset=log(offset),
               control.compute=list(dic=TRUE))
summary(output3)
```

```
##
## Call:
##    c("inla(formula = formula.intI, family = \"poisson\", data =
##    data.salm, ", " offset = log(offset), control.compute = list(dic =
##    TRUE))" )
## Time used:
##     Pre = 2.87, Running = 60.8, Post = 0.609, Total = 64.2
## Fixed effects:
##               mean    sd 0.025quant 0.5quant 0.975quant   mode kld
## (Intercept) -5.674 0.125     -5.927   -5.672     -5.434 -5.668   0
##
## Random effects:
##   Name     Model
##     region_id BYM model
##    time_id IID model
##    time_id2 RW1 model
##    region_time_id IID model
```

```
##
## Model hyperparameters:
##                                                mean    sd 0.025quant
## Precision for region_id (iid component)        1.13  0.25      0.727
## Precision for region_id (spatial component)    3.73  3.36      0.708
## Precision for time_id                         20.22 12.11      5.932
## Precision for time_id2                        17.42 10.03      4.992
## Precision for region_time_id                   1.62  0.24      1.216
##                                               0.5quant 0.975quant  mode
## Precision for region_id (iid component)           1.10       1.70  1.05
## Precision for region_id (spatial component)       2.75      12.57  1.62
## Precision for time_id                            17.31      51.64 12.79
## Precision for time_id2                           15.19      43.07 11.32
## Precision for region_time_id                      1.60       2.16  1.55
##
## Expected number of effective parameters(stdev): 495.12(35.32)
## Number of equivalent replicates : 7.24
##
## Deviance Information Criterion (DIC) ...............: 3387.19
## Deviance Information Criterion (DIC, saturated) ....: 2105.41
## Effective number of parameters .....................: 434.22
##
## Marginal log-Likelihood:  -1831.36
## Posterior marginals for the linear predictor and
##  the fitted values are computed
```

It is possible to map the **posterior mean** of the interaction $\delta_{it}$ where $i = 1, \ldots, n$ and $t = 1, \ldots, T$:

```
#Extract the posterior mean (log scale) and create a new data frame
delta.intI = data.frame(delta=output3$summary.random$region_time_id$mean,
                        year=data.salm$time_id,
                        ID.area=data.salm$region_id)
dim(delta.intI)
```

```
## [1] 3582    3
```

```
head(delta.intI)
```

```
##         delta year ID.area
## 1  0.31852263    1       1
## 2  1.16193664    2       1
## 3 -0.09983847    3       1
## 4  0.41458621    4       1
## 5 -0.15261009    5       1
## 6  0.29121551    6       1
```

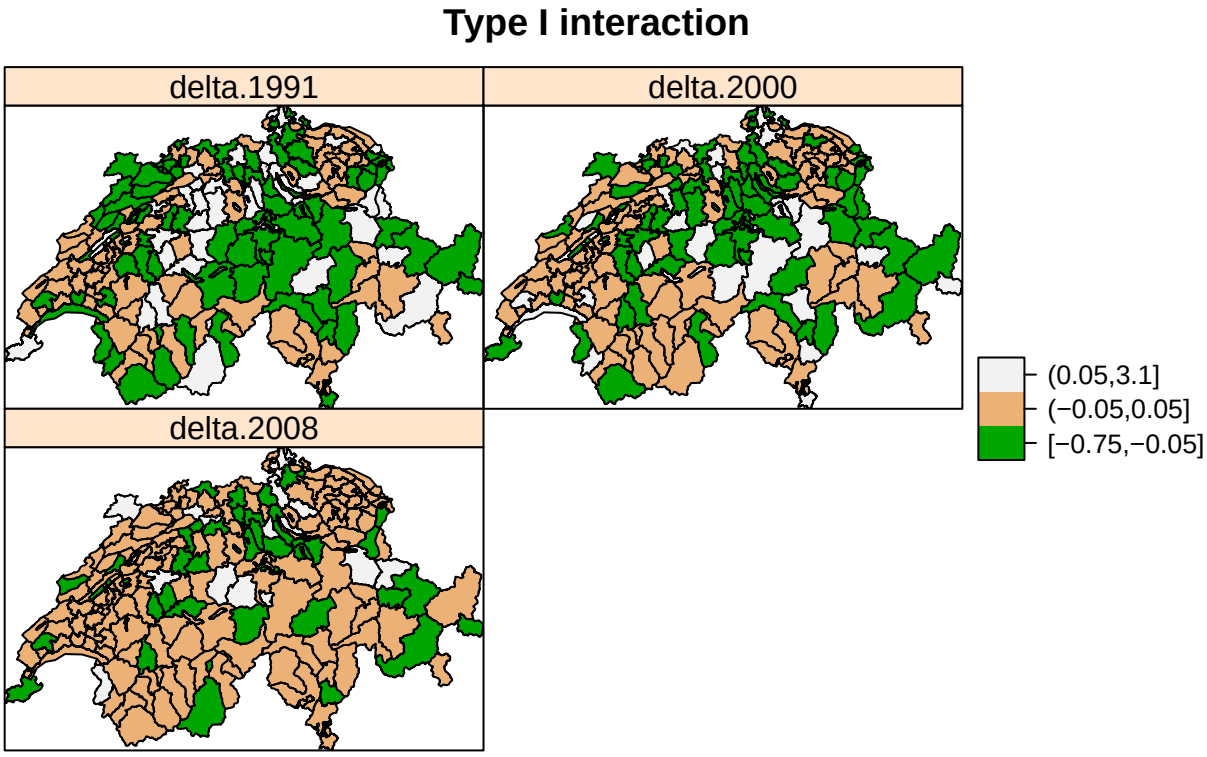
```
#Transform into categories
delta.intI$delta.cat = cut(delta.intI$delta,
                           c(-0.75,-0.05,0.05,3.1),
                           include.lowest=T)

#Reshape the dataframe so that the dimension is 199 (n) X 18 (T)
delta.intI.wide = reshape(delta.intI,direction="wide",
                          timevar = "year",
                          idvar = "ID.area",
                          drop = "delta")
dim(delta.intI.wide)
```

```
## [1] 199  19
```

```
#Remove the first column with the station ID
delta.intI.wide = delta.intI.wide[,-1]
#Change the column names
colnames(delta.intI.wide) = paste("delta.",seq(1991,2008),sep="")
#Add the BEZIRKSNR identifier
delta.intI.wide$BEZIRKSNR = data.Y$BEZIRKSNR
```

For mapping it is necessary to merge the shapefile datatable with the new dataframe `delta.intI.wide`:

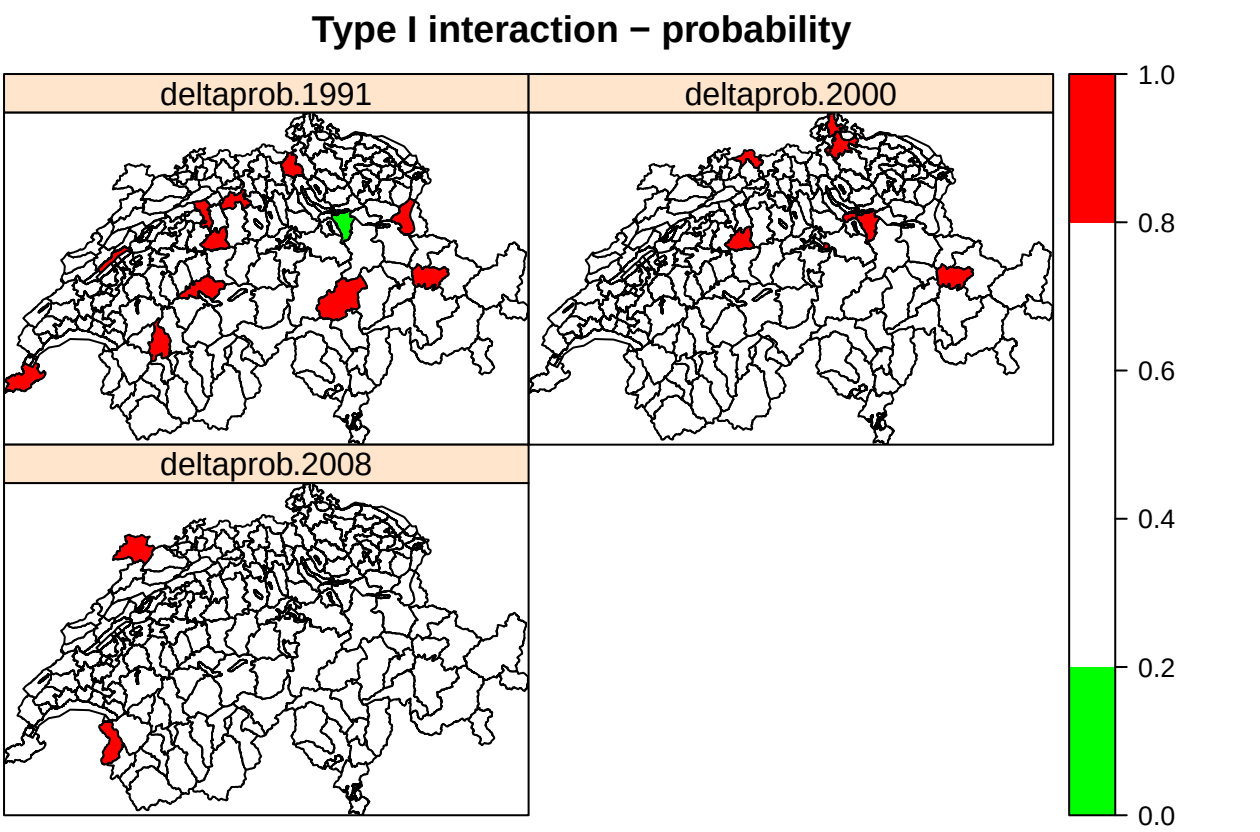
```
map.swiss@data = merge(map.swiss@data,
                       delta.intI.wide,
                       by="BEZIRKSNR")
spplot(obj=map.swiss,
       zcol=c("delta.1991","delta.2000","delta.2008"),
       col.regions= terrain.colors(3),
       main="Type I interaction",
       as.table=TRUE)
```




The same approach could be adopted to map for each available year the posterior probability that $\delta$ exceeds the threshold 0:

```
#Extract the probability
prob.delta.vec = unlist(lapply(output3$marginals.random$region_time_id,
                       function(x){1 - inla.pmarginal(threshold, x)}))

#Create a new dataframe
prob.delta.intI = data.frame(prob.delta=prob.delta.vec,
                       year=data.salm$time_id,
                       ID.area=data.salm$region_id)
```

```
#Reshape the dataframe so that the dimension is 199 (n) X 18 (T)
prob.delta.intI.wide = reshape(prob.delta.intI,direction="wide",
                           timevar = "year",
                           idvar = "ID.area")

#Remove the first column with the station ID
prob.delta.intI.wide = prob.delta.intI.wide[,-1]
#Change the column names
colnames(prob.delta.intI.wide) = paste("deltaprob.",seq(1991,2008),sep="")
#Add the BEZIRKSNR identifier
prob.delta.intI.wide$BEZIRKSNR = data.Y$BEZIRKSNR

#Merge before mapping
map.swiss@data = merge(map.swiss@data, prob.delta.intI.wide, by="BEZIRKSNR")
spplot(obj=map.swiss,
       zcol=c("deltaprob.1991","deltaprob.2000","deltaprob.2008"),
       col.regions=c("green","white", "red"),
       at=prob.cutoff,
       main="Type I interaction - probability",
       as.table=TRUE)
```




Finally we compare the dic of the two spatio-temporal models (output2: spatio-temporal model with bym + 2 temporal effects, output3: spatio-temporal model with bym and space-time type I interaction)

```
output2$dic$dic
```

```
## [1] 3672.448
```

```
output3$dic$dic
```

```
## [1] 3387.19
```

It seems that the model with the interaction is preferable.