Bayesian mixture model for environmental application

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Case study

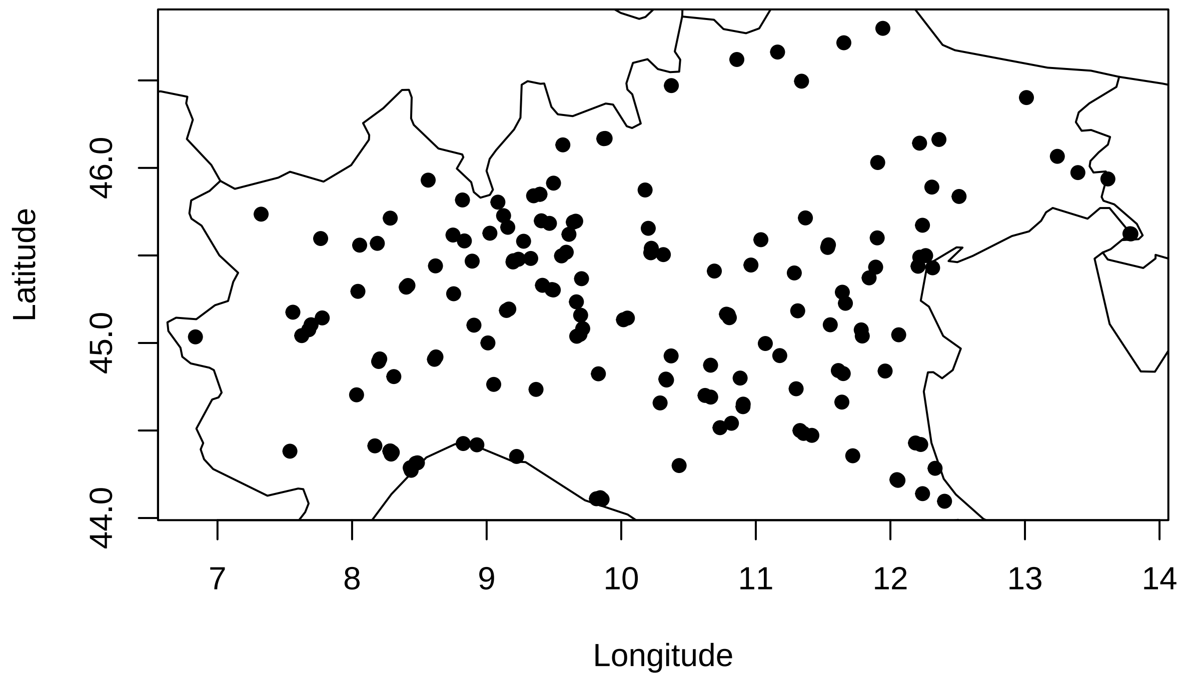
Proposed model

First we import the datasets with the time series and the stations' information, and retrieve the coordinates of the stations.

```
pollutant <- read.csv('code/data/pollutant.csv')
stationInfo <- read.csv('code/data/stationsInfo.csv')
##get latitude and longitude
latitude <- c()
longitude <- c()
region <- c()
for (i in 1:dim(pollutant)[2]) {
  site <- colnames(pollutant)[i]
  latitude <- c(latitude,stationInfo$latitude[which(stationInfo$site==site)])
  longitude <- c(longitude,stationInfo$longitude[which(stationInfo$site==site)])
  region <- c(region,stationInfo$region[which(stationInfo$site==site)])
}
```

The stations are distributed in all the Northern Italy:

```
plot(longitude,latitude,pch=19,cex=0.9,xlab='Longitude',ylab='Latitude')
map("world",add=T)
```



Then we run our code on the dataset, using the default hyperparameters $a = 1$ ecc..

```
pb=progress_bar$new(total=300)
invisible(pb$tick(0))
tseriesc.out <- tseriesclust(pollutant,maxiter=300,thinning=2,frequency = 365,
                             seasonfreq = 2,seasondelay = 80)
```

Since the computational workload is not negligible and the estimated time to run is approximately 90 minutes, we decided to import the saved R.Data. The code is still replicable from the RMarkdown `Case study.Rmd`.

```
load("code/results/result_proposedmodel.RData")
```

We then used a VI loss function to find the best cluster structure using the R package `salso`. We choose the partition minimizing the posterior of the VI loss function:

$$\hat{\mathbf{c}}^* = \underset{\hat{\mathbf{c}}}{\operatorname{argmin}} \mathbb{E}\left(L_{VI}(\mathbf{c}, \hat{\mathbf{c}}) \mid \mathcal{D}\right) = \underset{\hat{\mathbf{c}}}{\operatorname{argmin}} \sum_{i=1}^{n} \log_2\left(\sum_{j=1}^{n} \mathbb{I}\left(\hat{c}_j = \hat{c}_i\right)\right) - 2\sum_{i=1}^{n} \mathbb{E}\left(\log_2\left(\sum_{j=1}^{n} \mathbb{I}\left(c_j = c_i\right)\mathbb{I}\left(\hat{c}_j = \hat{c}_i\right)\right) \mid \mathcal{D}\right),$$

where $\mathcal{D}$ represents data and $\mathbf{c}$ is the true cluster partition.

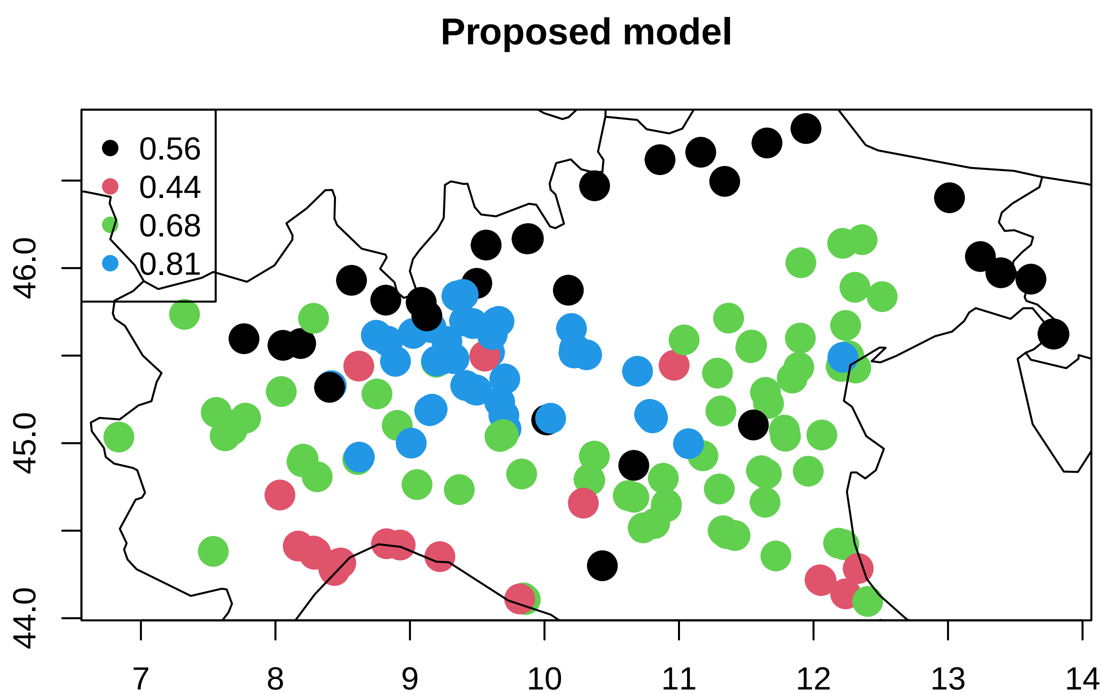
```
gnstar <- as.numeric(salso(tseriesc.out$memorygn, maxNClusters=4,
                           loss=VI(a=0.5), nRuns=50, nCores=2))
```

We computed the mean value of ρ in each cluster:

```r
#compute mean rho
d <- dim(tseriesc.out$rhosample)[1]
rho <- tseriesc.out$rhosample[d,]
rho_m <- c()
for (i in 1:4) {
  rho_m <- c(rho_m, round(mean(rho[which(gnstar==i)]),2) )
}
```

and plotted the cluster obtained on the map:

```r
plot(longitude,latitude,pch=19,cex=2,main = "Proposed model", xlab="", ylab="",col=gnstar)
legend('topleft',legend=rho_m,col=1:4,pch=19)
map("world",add=T)
```



We can see that the four clusters obtained can be divided into 4 distinct natural regions.

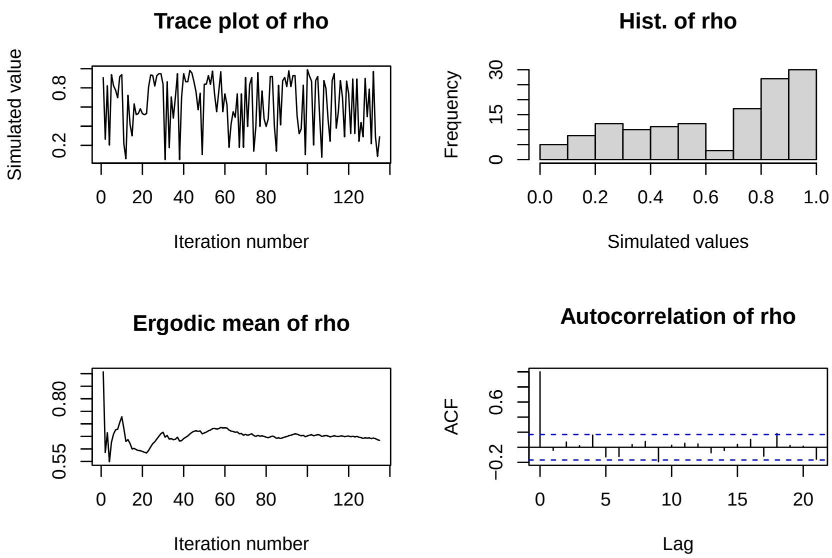
The Milan area has the highest persistence cluster, and the cities of the Padan Pianury are home to another significant cluster. The other two clusters, with less persistence, are in the Genoa or marine cities zone and in the stations of the Alps.

In fact, a search of the literature revealed studies analysing PM10 concentration that confirmed that the persistence is often higher in the proximity of urban areas and dry zones while it is lower in greener areas and more breezy regions.

We confronted the obtained values of ρ in the clusters with the distribution of the ρ estimated with the function `arima`.

and plot of the ergodic mean of the station x:

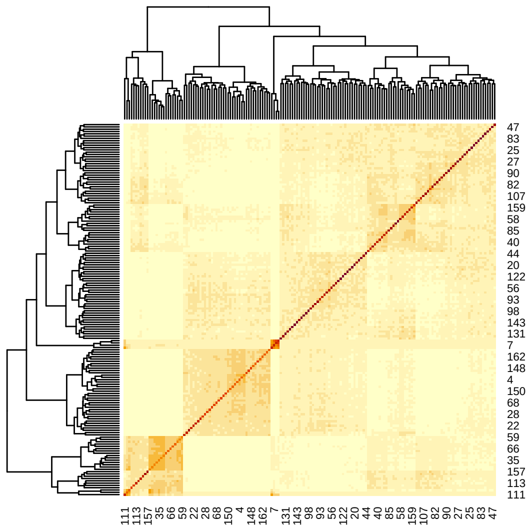
```
station <- 2
rhosample <- tseriesc.out$rhosample[,station]
n <- length(rhosample)
par(mfrow=c(2,2))
plot(rhosample,type = "l",main = "Trace plot of rho",
     xlab = "Iteration number",ylab = "Simulated value")
hist(rhosample,main = "Hist. of rho",xlab = "Simulated values")
plot(1:n,cumsum(rhosample)/1:n,type = "l",
     main = "Ergodic mean of rho",xlab = "Iteration number",ylab = "")
acf(rhosample, main='Autocorrelation of rho')
```



we see that concerges to ... as expected.

Finally, we plotted the similarity matrix of the cluster obtained:

```
simm <- comp.psm(tseriesc.out$memorygn)
heatmap(as.matrix(simm))
```



We can indeed denote from the dendrogram the formation of the 4 clusters.

Starting model

Using the same dataset its reproducible also the clustering using the starting model.

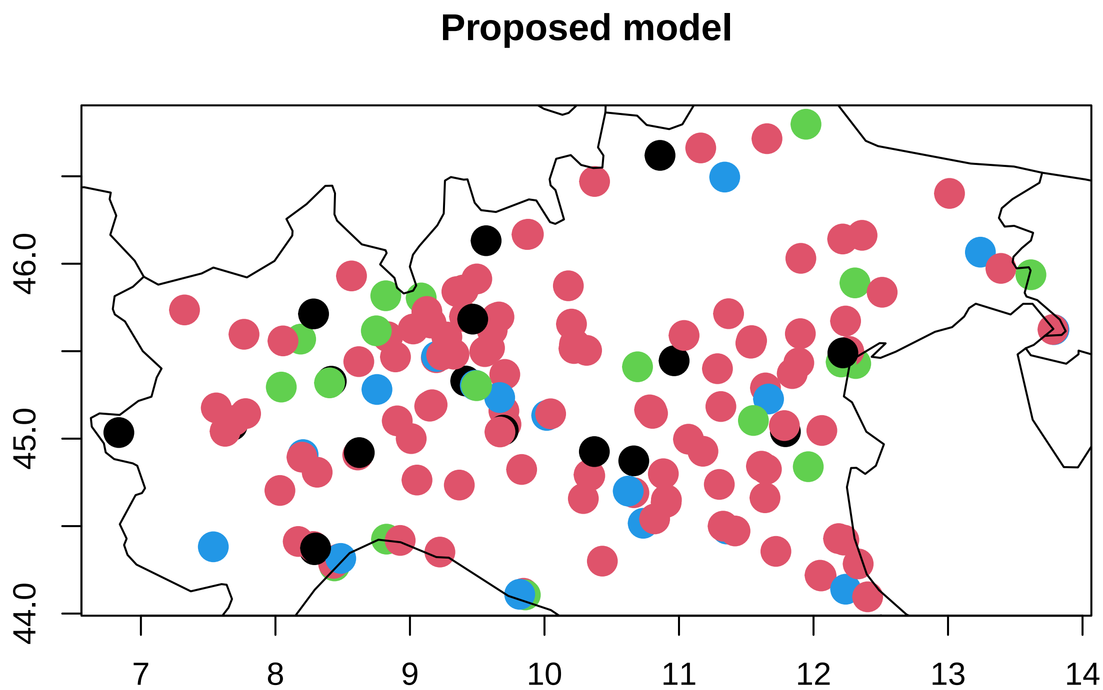
```
tseriesc.out <- tseriesclust_first(pollutant,maxiter=300,
                    thinning=2,frequency = 365, seasonfreq = 2,seasondelay = 80)
```

Same as before we load the results, but all the code is reproducible in the file `Case study.Rmd`.

```
load("code/results/result_firstmodel.RData")
```

```
gnstar_f <- as.numeric(salso(tseriesc.out.first$memorygn, maxNClusters=4,
                             loss=VI(a=0.5), nRuns=50, nCores=2))
```

```
plot(longitude,latitude,pch=19,cex=2,main = "Proposed model", xlab="", ylab="",col=gnstar_f)
map("world",add=T)
```



We could have expected a poor outcome because there isn't much of a difference in level or trend between the stations, as can be seen in the matplot of the PM10 concentration in Northern Italy in the data exploration section.