

Supplementary material for: Predicting the Change in Breast Cancer Deaths in Spain by 2019 A Bayesian Approach.

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Section 1. Assessment of prior distribution of τ parameters for the age, period and cohort effects using data from period 1990-2009.

We assumed three scenarios to select a Gamma priors for τ . We compared the posterior distribution of $\tau_\alpha | Data$, $\tau_\beta | Data$ and $\tau_\gamma | Data$ assuming the following priors (Schmid and Held 2004; Fong et al 2009):

- 1) $\tau \sim Gamma(0.5, 0.001)$
- 2) $\tau \sim Gamma(0.001, 0.001)$
- 3) $\tau \sim Gamma(1, 0.001)$

Table S1 shows the posterior distribution of τ for the age, period and cohort effects for models using AR1 in period and cohort effects. For each model, this table shows the median and the 95% credible interval (CrI) of the posterior distribution of τ . Comparing the CrIs, there were no significant differences among $\tau_\alpha | Data$ across models and scenarios. In this line, median values of $\tau_\beta | Data$ did not show large differences in the scenarios for the age-period model as well as $\tau_\gamma | Data$ did not show differences in the scenarios for the age-cohort model. When age-period-cohort model was assessed, under the prior $\tau \sim Gamma(0.001, 0.001)$ we observed a slight difference for $\tau_\beta | Data$ when compared to other priors (median value=108.936 when prior was $\tau \sim Gamma(0.001, 0.001)$ and median values of 227.368 and 214.350 when other priors were used). In all models it was observed a slightly higher median precision for $\tau_\alpha | Data$, $\tau_\beta | Data$ and $\tau_\gamma | Data$ when the prior distribution used was $\tau \sim Gamma(0.5, 0.001)$. Similar results were observed when models were using AR2 in period and cohort effects (see Table S2).

Table S1. Posterior distribution of τ for the age, period and cohort effects for models using AR1 in period and cohort effects.

Models using AR1 in period and cohort effects										
		$\tau \sim \text{Gamma}(0.5, 0.001)$			$\tau \sim \text{Gamma}(0.001, 0.001)$			$\tau \sim \text{Gamma}(1, 0.001)$		
Model	Age-Period	Credible Interval			Credible Interval			Credible Interval		
		Median	2.5%	97.5%	Median	2.5%	97.5%	Median	2.5%	97.5%
	$\tau_\alpha \mid \text{Data}$	48.132	18.907	109.400	42.274	16.173	102.363	43.503	21.777	117.339
	$\tau_\beta \mid \text{Data}$	178.544	27.619	719.377	172.163	9.781	537.356	171.778	52.149	885.941
Model	Age-Cohort	Credible Interval			Credible Interval			Credible Interval		
		Median	2.5%	97.5%	Median	2.5%	97.5%	Median	2.5%	97.5%
	$\tau_\alpha \mid \text{Data}$	46.446	17.786	106.020	41.413	15.204	98.063	41.463	20.510	113.989
	$\tau_\gamma \mid \text{Data}$	56.803	24.793	117.104	52.352	22.081	110.324	51.239	27.538	124.223
Model	Age-Period-Cohort	Credible Interval			Credible Interval			Credible Interval		
		Median	2.5%	97.5%	Median	2.5%	97.5%	Median	2.5%	97.5%
	$\tau_\alpha \mid \text{Data}$	46.871	17.870	106.607	41.853	15.340	98.759	41.787	20.900	115.241
	$\tau_\beta \mid \text{Data}$	227.362	22.548	2318.610	108.936	7.133	1133.277	214.350	52.841	3697.782
	$\tau_\gamma \mid \text{Data}$	99.436	40.252	227.135	94.129	36.927	209.317	96.317	41.177	241.532

Note: all models used AR2 in age effects.

Table S2. Posterior distribution of τ for the age, period and cohort effects for models using AR2 in period and cohort effects.

<i>Models using AR2 in period and cohort effects</i>										
		$\tau \sim \text{Gamma}(0.5, 0.001)$			$\tau \sim \text{Gamma}(0.001, 0.001)$			$\tau \sim \text{Gamma}(1, 0.001)$		
Model	<i>Age-Period</i>	Credible Interval			Credible Interval			Credible Interval		
		Median	2.5%	97.5%	Median	2.5%	97.5%	Median	2.5%	97.5%
	Age	48.716	18.796	109.267	42.422	16.160	102.138	43.924	21.652	117.330
	Period	434.715	38.455	1500.917	441.238	3.997	1434.841	429.379	110.972	2417.928
Model	<i>Age-Cohort</i>	Credible Interval			Credible Interval			Credible Interval		
		Median	2.5%	97.5%	Median	2.5%	97.5%	Median	2.5%	97.5%
	Age	49.466	19.022	112.250	44.242	16.200	103.762	44.779	21.981	120.720
	Cohort	475.679	170.972	1190.725	412.679	145.224	1081.539	437.712	199.475	1308.550
Model	<i>Age-Period-Cohort</i>	Credible Interval			Credible Interval			Credible Interval		
		Median	2.5%	97.5%	Median	2.5%	97.5%	Median	2.5%	97.5%
	Age	48.567	19.266	114.014	44.107	16.439	104.799	44.342	22.281	122.519
	Period	569.464	56.553	3232.891	516.870	7.599	2305.224	507.509	155.879	4260.667
	Cohort	477.463	176.190	1234.186	472.638	146.687	1103.321	473.271	204.869	1347.335

Note: all models used AR2 in age effects.

Section 2 Assessment of cohort effects in predictions

Baker and Bray 2005 showed that when there are strong cohort effects, Bayesian methods may be biased if data from young age groups are removed due to low mortality. Table S3 shows that predicting BC deaths for ages 64 and older using the full dataset has higher precision (lower posterior standard deviation) than using a restricted dataset excluding age groups 30-44. On the other hand, the relative error in the prediction (RE) using the full dataset is smaller than using the reduced dataset across models. Moreover, Age-Cohort models in the full dataset show the lowest posterior standard deviation of the prediction.

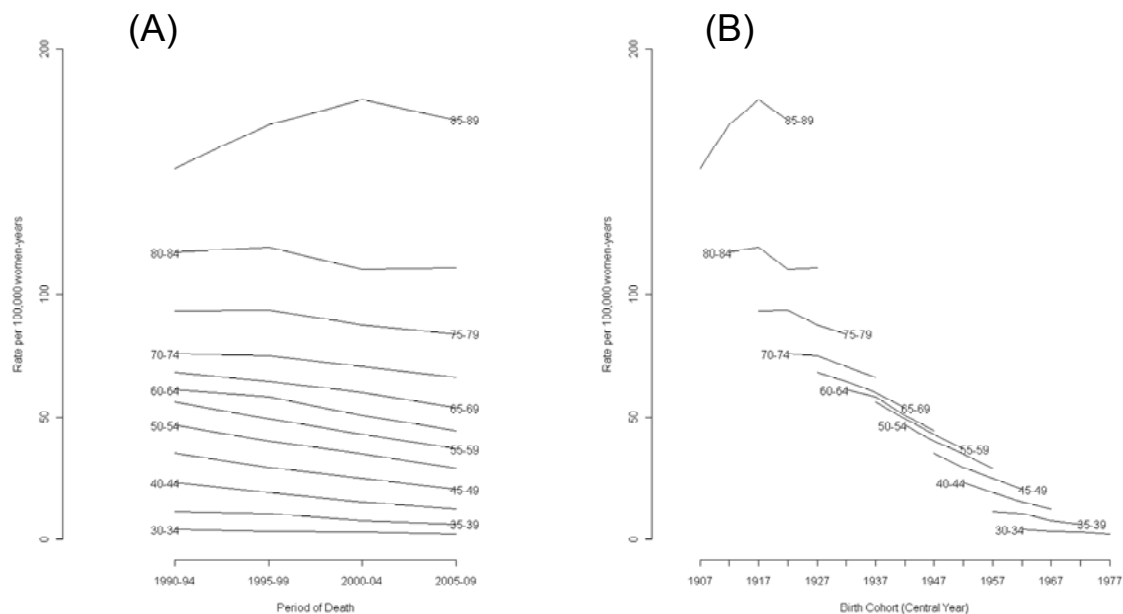
Table S3. Results of predicting breast cancer mortality in Spain during 2005-2009 for age groups 64 and older based on data from 1990-1994 using reduced and full mortality data sets.

N 2005-2009 (Observed) 19361	Full Dataset			Reduced Dataset		
	Expected			Expected		
	RE			RE		
	Median	SD	(%)	Median	SD	(%)
AP-AR1	19381	218.399	0.795	19592	231.743	1.212
AP-AR2	17736	169.525	5.391	18176	186.451	6.118
AC-AR1	19205	145.869	0.786	19599	200.464	1.208
AC-AR2	19237	146.085	0.697	18178	181.312	6.108
APC-AR1	20454	199.428	1.152	19578	201.586	5.645
APC-AR2	19107	188.201	1.312	18169	192.829	6.157

N (Observed): Observed number of breast cancer deaths in ages 64 and older in Spain during 2005-2009; **Full Dataset:** Dataset that contains data for women aged 30-90 years; **Reduced Dataset:** Age groups 30-44 were not included in the analysis. **AP:** Age-Period model; **AC:** Age-Cohort model; **APC:** Age-Period-Cohort model; **AR1:** It was made use of an autoregressive smoothing prior of order 1 for Period and Cohort parameters; **AR2:** Autoregressive smoothing prior of order 2 was used for all parameters; **DIC:** Deviance Information Criterion; **pD:** Effective number of model parameters; **Expected:** Median of the total expected number of breast cancer deaths during 2005-2009 predicted by each of the models; **SD:** Posterior Standard Deviation of the total expected number of breast cancer deaths during 2005-2009; **RE(%):** Percentage of the relative error between the total observed number of breast cancer deaths during 2005-2009 and the total predicted by each one of the models;

In this line, we have graphically represented the period and cohort effects in Figure S1. Figure S1.A shows a consistent decreasing trend of BC mortality rates through the whole period 1990-2009 in all age groups with the exception of women aged 85-89 years. In this age-group, BC mortality rates rose until year 2000 and decreased thereafter. In this line, BC mortality rates by birth cohort (Figure S1.B) show that older cohorts had higher BC mortality rates than the younger ones in each age-group considered. BC mortality rates among women aged 45-69 dramatically decreased, whereas this decreasing trend was less pronounced in women older than 69 years of age, showing a cohort effect in our data.

Figure S1. Age-specific 5-year mortality rates of breast cancer per 100,000 women-years in Spain (aggregated data) by birth cohort and period of death according to age groups 30-89 years and during the period 1990-2009.



Section 3. Assessment of age-period and age-cohort interactions in the age-period-cohort model

The Deviance Information Criterion (*DIC*), the effective number of model parameters (*pD*), and the Relative Error (RE) of the prediction were used to assess whether age-period and age-cohort interactions could improve projections. Models were fitted to breast cancer mortality data during 1990-2004 and used to predict breast cancer deaths in Spain for 2005-2009. Table S4 shows the model fit assessment using interactions in our APC models. In the AR1 scenario, differences in DIC values between the APC model without interaction and the APCs models with interactions were less than 3 units (DIC No Interaction: 11608.4; DIC Age-Period: 11607.1; DIC Age-Cohort: 11606.8; DIC Age-Period and Age-Cohort: 11606.8) and for that reason these models were considered as equivalent to the APC model without interactions. Similar conclusions can be extracted from the AR2 scenario. When assessing the RE, the APC model without interactions showed the lowest value in both scenarios (AR1 scenario RE=6.4%; AR2 scenario RE=1.2%).

Table S4. Model's selection procedure assessing interactions for the age-period-cohort model: models fitted to breast cancer mortality data during 1990-2004 and used to predict breast cancer deaths in Spain for 2005-2009.

	Interaction	DIC	<i>pD</i>	Expected (Median)	(SD)	RE (%)
AR1*	No Interaction	11608.4	74	31847	294.1	6.4
	Age-Period	11607.1	78	32181	299.6	6.5
	Age-Cohort	11606.8	79	32227	297.5	6.5
	Age-Period + Age-Cohort	11606.8	80	31978	296.5	6.6
AR2**	No Interaction	11605.5	70	29564	224.3	1.2
	Age-Period	11604.1	77	30009	225.3	1.3
	Age-Cohort	11604.0	78	30001	229.1	1.3
	Age-Period + Age-Cohort	11603.9	79	29569	227.1	1.4

Note: Interaction refer to adding an interaction term to the age-period-cohort model.

AR1*: Models Age-Period and Age-Cohort made use of an autoregressive smoothing prior of order 1 for Period and Cohort parameters; **AR2**:** Autoregressive smoothing prior of order 2 was used for all parameters; **DIC:** Deviance Information Criterion; ***pD*:** Effective number of model parameters; **Expected:** Median of the total expected number of breast cancer deaths during 2005-2009 predicted by each of the models; **SD:** Posterior Standard Deviation of the total expected number of breast cancer deaths during 2005-2009; **RE(%):** Percentage of the relative error between the total observed number of breast cancer deaths during 2005-2009 and the total predicted (expected) by each one of the models; **No Interaction:** Age-Period-Cohort model with main effects; **Age-Period:** Age-Period-Cohort model with Age-Period interaction terms; **Age-Cohort:** Age-Period-Cohort model with Age-Cohort interaction terms; **Age-Period+ Age-Cohort:** Age-Period-Cohort model with Age-Period and Age-Cohort interaction terms.

Section R Code: uses INLA library (www.r-inla.org)

1. Functions

```
#####  
##FUNCTIONS  
#####  
  
gpois<-function(x)  
{  
  rpois(1,x)  
}  
  
output.model<-function(model.tmp,n.pred=1*12*52,n.obs=2*12*52,sims=1000)  
{  
  matrix.out.pr<-matrix(0,n.pred+1,sims)  
  for (j in 1:n.pred)  
  {  
    i<-n.obs+j  
    cas.tmp<-rnorm(sims,model.tmp$summary.linear.predictor[i,1],model.tmp$summary.linear.predictor[i,2])  
    matrix.out.pr[j,<-as.numeric(lapply(exp(cas.tmp)*dades.tmp$pyr[i],FUN=gpois))  
  }  
  
  for (i in 1:sims)  
    matrix.out.pr[n.pred+1,i]<-sum(matrix.out.pr[,i])  
  
  matrix.out.pr  
}  
  
output.RE<-function(output.model,dades.obs)  
{  
  dades.obs[length(dades.obs)+1]<-sum(dades.obs)  
  output.model.tmp<-(((output.model-dades.obs)^2)^0.5)/dades.obs*100
```

```

output.model.tmp
}

risk.diff <- function(cases.init,cases.end,pop.init,pop.end,labels=c("baseline group","comparison group"))
    #cases.init and cases.end are vectors containing age-group cases for the baseline (reference) and comparison groups
    #pop.init and pop.end are vectors containing population pyramids for both groups
    #labels is a vector containing text labels for baseline and comparison groups respectively
    respectively (e.g. init and end years)
{

    adjusted.population.init <- pop.init/sum(pop.init)* 100000
    adjusted.population.end <- pop.end/sum(pop.end)* 100000
    R1 <- cases.init / pop.init * adjusted.population.init      #expected number of cases at init year for a total population of 100000
    R2 <- cases.end / pop.end * adjusted.population.end          #expected number of cases at end year for a total population of 100000
    R3 <- cases.init / pop.init * adjusted.population.end        #expected number of cases at end year for a total population of 100000 if
the risk was the same than for base3line group
    S1 <- sum(R1)
    S2 <- sum(R2)
    S3 <- sum(R3)
    table.out <- data.frame(change.in=c("Risk","Structure","Size","Net
change"),crude.rate=rep(NA,4),Perc.crude.rate=rep(NA,4),Number=rep(NA,4),Perc.Number=rep(NA,4))
    colnames(table.out) <- c("Change in","Crude rate","%", "Number","%")

    table.out[4,2] <- S2-S1
    table.out[1,2] <- S2-S3
    table.out[2,2] <- S3-S1
    table.out[,3] <- table.out[,2] / S1 * 100

    table.out[4,4] <- sum(cases.end) - sum(cases.init)
    table.out[1:2,4] <- sum(cases.init) * table.out[1:2,3] /100
    table.out[3,4] <- table.out[4,4] - table.out[1,4] - table.out[2,4]

    table.out[1:2,5] <- table.out[1:2,3]

```

```

table.out[3,5] <- table.out[3,4]/sum(cases.init) * 100
table.out[4,5] <- (sum(cases.end)-sum(cases.init))/sum(cases.init) * 100

summary.table <- data.frame(group=c(labels[1],labels[2]),cases=rep(NA,2),population=rep(NA,2),crude.rate=rep(NA,2))
summary.table[1,2] <- sum(cases.init)
summary.table[2,2] <- sum(cases.end)
summary.table[1,3] <- sum(pop.init)
summary.table[2,3] <- sum(pop.end)
summary.table$crude.rate <- summary.table$cases / summary.table$population * 100000

summary.text.1 <- paste(summary.table[1,2]," total cases observed in ",labels[1]," and ",summary.table[2,2]," in ",labels[2]," ,
representing a crude rate of ",round(summary.table[1,4])," and ",round(summary.table[2,4])," cases per 100000 persons
respectively.",collapse="",sep="")
if(table.out[1,2]>=0) risk <- "increment"
else risk <- "decrement"
if(table.out[3,4]>=0) size <- "increment"
else size <- "decrement"

summary.text.2 <- paste("The net change in terms of crude rate is ",round(table.out[4,2],2)," cases per 100000 persons
(",round(table.out[4,3],2),"%), which can be partitioned into ",round(table.out[1,2],2)," cases (",round(table.out[1,3],2),"% due to a ",risk,"
of the risk and ",round(table.out[2,2],2)," cases (",round(table.out[2,3],2),"% due to changes in the population structure.",collapse="",sep="")
summary.text.3 <- paste("The net change in terms of total number of cases is ",round(table.out[4,4],2)," cases
(",round(table.out[4,5],2),"%), which can be partitioned into ",round(table.out[1,4],2)," cases (",round(table.out[1,5],2),"% due to a ",risk,"
of the risk, ",round(table.out[2,4],2)," (",round(table.out[2,5],2),"% due to changes in the population structure and
",round(table.out[3,4],2)," cases (",round(table.out[3,5],2),"% due to an ",size," of the population size.",collapse="",sep="")

list(summary.table,table.out,c(summary.text.1,summary.text.2,summary.text.3))
}

neg.to.NA<-function(x)
{
if (x<0) x<-NA
x
}

```

2. READ DATA

```
library(INLA)

#####
##READ DATA
#####

directori<-"C:/2011 - Breast Cancer Mortality in Spain Projections 2019/"
file.input<-"Data/BCmortality 1990-2009 pr 2019.txt"
directori.out<-"Tables/"
directori.RData<-"RData 2011/"

f.input<-read.table( file=paste(directori,file.input,sep=""),header=T)
f.input<-as.data.frame(f.input)
names(f.input)<-c("cases","pyr","age","period","cohort","PR")
f.input<-as.data.frame(f.input)
f.input$cases<-as.numeric(lapply(f.input$cases,neg.to.NA))

N.AGE<-12
N.PERIOD<-6
N.COHORT<-12+6-1
N.PROV<-52
```

3. TABLES

```
#####
##### Table 1
#####
```

```
gen.wsp.rate<-function(dades.tmp.t,period.t=1,age.in=7,age.fin=18,ages.t=1:12)
{
#ages.tt=1:12 all age groups, 1:4 age groups 30-34,35-39,40-44,45-59
dades.tmp.tt<-dades.tmp.t[dades.tmp.t$period==period.t,c(1:3)]
wsp.tmp<-read.table("C:/Breast Cancer mortality in Spain/wsp.txt",header=F)
wsp.tmp<-wsp.tmp[age.in:age.fin,2]
dades.tmp.tt<-as.data.frame(aggregate(dades.tmp.tt,list(dades.tmp.tt$age),sum)[,1:3])
dades.tmp.tt<-dades.tmp.tt[ages.t,]
dades.tmp.tt$wsp<-wsp.tmp/sum(wsp.tmp)
dades.tmp.tt$rate<-dades.tmp.tt$cases/dades.tmp.tt$pyr*dades.tmp.tt$wsp*100000
rate.tmp.tt<-sum(dades.tmp.tt$rate)
c(rate.tmp.tt,sum(dades.tmp.tt$cases),sum(dades.tmp.tt$pyr))
}
```

```
mat.EAPCH<-as.data.frame(matrix(0,3,9))
row.names(mat.EAPCH)<-c("All","45.64","65.100")
names(mat.EAPCH)<-c("ASR.90.94","N.90.94","PYR.90.94","ASR.05.09","N.05.09","PYR.05.09","EAPCHMedian","EAPCHCIL95","EAPCHCIU95")
```

```
model.ad.base = inla(cases ~ factor(age) + I(period-1)+f(PR,values=1:N.PROV,model="iid",param=c(0.5, 0.001))-1,
data=f.input[f.input$period<=4,],family="poisson", offset=I(log(pyr)),control.predictor=list(compute=TRUE),
control.compute=list(dic=T,mlik=T),control.results=list(return.marginals.predictor=T))
```

```
mat.EAPCH[1,1:3]<-gen.wsp.rate(dades.tmp.t=f.input,age.in=1,age.fin=12)
mat.EAPCH[1,4:6]<-gen.wsp.rate(dades.tmp.t=f.input,period.t=4,age.in=1,age.fin=12)
mat.EAPCH[1,7:9]<-round(as.numeric((exp(model.ad.base$summary.fixed[13,c(4,3,5)]-1)*100),1)
```

```
spain.ad.45.64 = inla(cases ~ factor(age) + I(period-1)+f(PR,values=1:N.PROV,model="iid",param=c(0.5, 0.001))-1,
data=f.input[((f.input$age>=4)&(f.input$age<=7)&(f.input$period<=4)),, family="poisson",
offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T),control.results=list(return.marginals.predictor=T))
summary(spain.ad.45.64)
```

```

spain.ad.45.64.Random.Effects.PR<- abs(spain.ad.45.64$summary.random$PR$mean)/spain.ad.45.64$summary.random$PR$sd>1

mat.EAPCH[2,1:3]<-gen.wsp.rate(dades.tmp.t=f.input,age.in=10,age.fin=13,ages.t=4:7)
mat.EAPCH[2,4:6]<-gen.wsp.rate(dades.tmp.t=f.input,period=4,age.in=10,age.fin=13,ages.t=4:7)
mat.EAPCH[2,7:9]<-round(as.numeric((exp(spain.ad.45.64$summary.fixed[5,c(4,3,5)]-1)*100),1)

spain.ad.65 = inla(cases ~ factor(age) + I(period-1)+f(PR,values=1:N.PROV,model="iid",param=c(0.5, 0.001))-1,
data=f.input[((f.input$age>=8)&(f.input$period<=4))], family="poisson", offset=I(log(pyr)),control.predictor=list(compute=TRUE),
control.compute=list(dic=T,mlik=T),control.results=list(return.marginals.predictor=T))
summary(spain.ad.65)
spain.ad.65.Random.Effects.PR<- abs(spain.ad.65$summary.random$PR$mean)/spain.ad.65$summary.random$PR$sd>1

mat.EAPCH[3,1:3]<-gen.wsp.rate(dades.tmp.t=f.input,age.in=14,age.fin=18,ages.t=8:12)
mat.EAPCH[3,4:6]<-gen.wsp.rate(dades.tmp.t=f.input,period=4,age.in=14,age.fin=18,ages.t=8:12)
mat.EAPCH[3,7:9]<-round(as.numeric((exp(spain.ad.65$summary.fixed[6,c(4,3,5)]-1)*100),1)

write.table(mat.EAPCH,file=paste(directori,directori.out,"Table 1.txt",sep=""))

#####
##### Table 2
#####

### DUMMY DATASET with data from 1990-2004: This dataset will be used for Model Assessment

file.obs.pr<-"Data/BCMortality 1990-2004 pr 2009.txt"

f.obs.pr<-read.table( file=paste(directori,file.obs.pr,sep=""),header=T)
f.obs.pr<-as.data.frame(f.obs.pr)
names(f.obs.pr)<-c("cases","pyr","age","period","cohort","PR")
f.obs.pr<-as.data.frame(f.obs.pr)
f.obs.pr$cases<-as.numeric(lapply(f.obs.pr$cases,neg.to.NA))

```

```

N.AGE.obs<-12
N.PERIOD.obs<-4
N.COHORT.obs<-N.AGE.obs+N.PERIOD.obs-1

dades.tmp<-f.obs.pr

cases.2005.2009<-f.input[f.input$period==4,]$cases

#####
### FIT MODELS
#####

spain.period.pr.rw1 = inla(cases ~ f(age,values=1:N.AGE.obs,model="rw2",param=c(0.5, 0.001)) +
f(period,values=1:N.PERIOD.obs,model="rw1",param=c(0.5, 0.001))+f(PR,values=1:N.PROV,model="iid",param=c(0.5, 0.001)), data=dades.tmp,
family="poisson", offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))

spain.period.pr.rw2 = inla(cases ~ f(age,values=1:N.AGE.obs,model="rw2",param=c(0.5, 0.001)) +
f(period,values=1:N.PERIOD.obs,model="rw2",param=c(0.5, 0.001))+f(PR,values=1:N.PROV,model="iid",param=c(0.5, 0.001)), data=dades.tmp,
family="poisson", offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))

spain.cohort.pr.rw1 = inla(cases ~ f(age,values=1:N.AGE.obs,model="rw2",param=c(0.5, 0.001)) +
f(cohort,values=1:N.COHORT.obs,model="rw1",param=c(0.5, 0.001))+f(PR,values=1:N.PROV,model="iid",param=c(0.5, 0.001)), data=dades.tmp,
family="poisson", offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))

spain.cohort.pr.rw2 = inla(cases ~ f(age,values=1:N.AGE.obs,model="rw2",param=c(0.5, 0.001)) +
f(cohort,values=1:N.COHORT.obs,model="rw2",param=c(0.5, 0.001))+f(PR,values=1:N.PROV,model="iid",param=c(0.5, 0.001)), data=dades.tmp,
family="poisson", offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))

spain.APC.pr.rw1 = inla(cases ~ f(age,values=1:N.AGE.obs,model="rw2",param=c(0.5, 0.001)) +
f(period,values=1:N.PERIOD.obs,model="rw1",param=c(0.5, 0.001))+f(cohort,values=1:N.COHORT.obs,model="rw1",param=c(0.5,
0.001))+f(PR,values=1:N.PROV,model="iid",param=c(0.5, 0.001)), data=dades.tmp, family="poisson",
offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))

```

```

spain.APC.pr.rw2 = inla(cases ~ f(age, values=1:N.AGE.obs, model="rw2", param=c(0.5, 0.001)) +
f(period, values=1:N.PERIOD.obs, model="rw2", param=c(0.5, 0.001)) + f(cohort, values=1:COHORT.obs, model="rw2", param=c(0.5,
0.001)) + f(PR, values=1:N.PROV, model="iid", param=c(0.5, 0.001)), data=dades.tmp, family="poisson",
offset=I(log(pyr)), control.predictor=list(compute=TRUE), control.compute=list(dic=T, mlik=T))

Table.2<-as.data.frame(matrix(0,6,7))
names(Table.2)<-c("DIC", "pD", "PR2005.2009.Median", "PR2005.2009.SD", "RE", "RE.Inf", "RE.Sup")
row.names(Table.2)<-c("AP.RW1", "AC.RW1", "APC.RW1", "AP.RW2", "AC.RW2", "APC.RW2")

C.Title<-c("A (RW2) - P (RW1) - C (RW1) ", "A (RW2) - C (RW1) ", "A (RW2) - P (RW1) ", "Age (RW2) ")
Table.2$DIC<-
round(c(spain.period.pr.rw1$dic[4], spain.cohort.pr.rw1$dic[4], spain.APC.pr.rw1$dic[4], spain.period.pr.rw2$dic[4], spain.cohort.pr.rw2$dic[4], spain
.APC.pr.rw2$dic[4]))
Table.2$pD<-
round(c(spain.period.pr.rw1$dic[3], spain.cohort.pr.rw1$dic[3], spain.APC.pr.rw1$dic[3], spain.period.pr.rw2$dic[3], spain.cohort.pr.rw2$dic[3], spain
.APC.pr.rw2$dic[3]))

output.period.pr.rw1<-output.model(spain.period.pr.rw1, n.obs=3*12*52)
Table.2$PR2005.2009.Median[1]<-median(output.period.pr.rw1[625,])
Table.2$PR2005.2009.SD[1]<-sd(output.period.pr.rw1[625,])
output.RE.period.pr.rw1<-output.RE(output.period.pr.rw1, cases.2005.2009)
Table.2[1,5:7]<-quantile(output.RE.period.pr.rw1[625,], probs=c(0.5, 0.025, 0.975))

output.cohort.pr.rw1<-output.model(spain.cohort.pr.rw1, n.obs=3*12*52)
Table.2$PR2005.2009.Median[2]<-median(output.cohort.pr.rw1[625,])
Table.2$PR2005.2009.SD[2]<-sd(output.cohort.pr.rw1[625,])
output.RE.cohort.pr.rw1<-output.RE(output.cohort.pr.rw1, cases.2005.2009)
Table.2[2,5:7]<-quantile(output.RE.cohort.pr.rw1[625,], probs=c(0.5, 0.025, 0.975))

output.APC.pr.rw1<-output.model(spain.APC.pr.rw1, n.obs=3*12*52)

```

```

Table.2$PR2005.2009.Median[3]<-median(output.APC.pr.rw1[625,])
Table.2$PR2005.2009.SD[3]<-sd(output.APC.pr.rw1[625,])
output.RE.APC.pr.rw1<-output.RE(output.APC.pr.rw1,cases.2005.2009)
Table.2[3,5:7]<-quantile(output.RE.APC.pr.rw1[625,],probs=c(0.5,0.025,0.975))

output.period.pr.rw2<-output.model(spain.period.pr.rw2,n.obs=3*12*52)
Table.2$PR2005.2009.Median[4]<-median(output.period.pr.rw2[625,])
Table.2$PR2005.2009.SD[4]<-sd(output.period.pr.rw2[625,])
output.RE.period.pr.rw2<-output.RE(output.period.pr.rw2,cases.2005.2009)
Table.2[4,5:7]<-quantile(output.RE.period.pr.rw2[625,],probs=c(0.5,0.025,0.975))

output.cohort.pr.rw2<-output.model(spain.cohort.pr.rw2,n.obs=3*12*52)
Table.2$PR2005.2009.Median[5]<-median(output.cohort.pr.rw2[625,])
Table.2$PR2005.2009.SD[5]<-sd(output.cohort.pr.rw2[625,])
output.RE.cohort.pr.rw2<-output.RE(output.cohort.pr.rw2,cases.2005.2009)
Table.2[5,5:7]<-quantile(output.RE.cohort.pr.rw2[625,],probs=c(0.5,0.025,0.975))

output.APC.pr.rw2<-output.model(spain.APC.pr.rw2,n.obs=3*12*52)
Table.2$PR2005.2009.Median[6]<-median(output.APC.pr.rw2[625,])
Table.2$PR2005.2009.SD[6]<-sd(output.APC.pr.rw2[625,])
output.RE.APC.pr.rw2<-output.RE(output.APC.pr.rw2,cases.2005.2009)
Table.2[6,5:7]<-quantile(output.RE.APC.pr.rw2[625,],probs=c(0.5,0.025,0.975))

write.table(Table.2,file=paste(directori,directori.out,"Table 2.txt",sep=""))

#####
##### PROJECTIONS 2010-2019
#####

```

```

spain.period.pr.rw1 = inla(cases ~ f(age,values=1:N.AGE,model="rw2",param=c(0.5, 0.001)) + f(period,values=1:N.PERIOD,model="rw1",param=c(0.5,
0.001))+f(PR,values=1:N.PROV,model="iid",param=c(0.5, 0.001)), data=dades.tmp, family="poisson",
offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))

spain.period.pr.rw2 = inla(cases ~ f(age,values=1:N.AGE,model="rw2",param=c(0.5, 0.001)) + f(period,values=1:N.PERIOD,model="rw2",param=c(0.5,
0.001))+f(PR,values=1:N.PROV,model="iid",param=c(0.5, 0.001)), data=dades.tmp, family="poisson",
offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))

spain.cohort.pr.rw1 = inla(cases ~ f(age,values=1:N.AGE,model="rw2",param=c(0.5, 0.001)) + f(cohort,values=1:N.COHORT,model="rw1",param=c(0.5,
0.001))+f(PR,values=1:N.PROV,model="iid",param=c(0.5, 0.001)), data=dades.tmp, family="poisson",
offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))

spain.cohort.pr.rw2 = inla(cases ~ f(age,values=1:N.AGE,model="rw2",param=c(0.5, 0.001)) + f(cohort,values=1:N.COHORT,model="rw2",param=c(0.5,
0.001))+f(PR,values=1:N.PROV,model="iid",param=c(0.5, 0.001)), data=dades.tmp, family="poisson",
offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))

spain.APC.pr.rw1 = inla(cases ~ f(age,values=1:N.AGE,model="rw2",param=c(0.5, 0.001)) + f(period,values=1:N.PERIOD,model="rw1",param=c(0.5,
0.001))+f(cohort,values=1:N.COHORT,model="rw1",param=c(0.5, 0.001))+f(PR,values=1:N.PROV,model="iid",param=c(0.5, 0.001)), data=dades.tmp,
family="poisson", offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))

spain.APC.pr.rw2 = inla(cases ~ f(age,values=1:N.AGE,model="rw2",param=c(0.5, 0.001)) + f(period,values=1:N.PERIOD,model="rw2",param=c(0.5,
0.001))+f(cohort,values=1:N.COHORT,model="rw2",param=c(0.5, 0.001))+f(PR,values=1:N.PROV,model="iid",param=c(0.5, 0.001)), data=dades.tmp,
family="poisson", offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))

output.period.pr.rw1<-output.model(spain.period.pr.rw1,n.obs=4*12*52)
quantile(output.period.pr.rw1[625,],probs=c(0.025,0.5,0.975))
sd(output.period.pr.rw1[625,])

output.period.pr.rw1<-output.model(spain.period.pr.rw1,n.obs=5*12*52)
quantile(output.period.pr.rw1[625,],probs=c(0.025,0.5,0.975))
sd(output.period.pr.rw1[625,])

```

```
output.cohort.pr.rw1<-output.model(spain.cohort.pr.rw1,n.obs=4*12*52)
quantile(output.cohort.pr.rw1[625,],probs=c(0.025,0.5,0.975))
sd(output.cohort.pr.rw1[625,])
```

```
output.cohort.pr.rw1<-output.model(spain.cohort.pr.rw1,n.obs=5*12*52)
quantile(output.cohort.pr.rw1[625,],probs=c(0.025,0.5,0.975))
sd(output.cohort.pr.rw1[625,])
```

```
output.APC.pr.rw1<-output.model(spain.APC.pr.rw1,n.obs=5*12*52)
quantile(output.APC.pr.rw1[625,],probs=c(0.025,0.5,0.975))
sd(output.APC.pr.rw1[625,])
```

```
output.APC.pr.rw1<-output.model(spain.APC.pr.rw1,n.obs=5*12*52)
quantile(output.APC.pr.rw1[625,],probs=c(0.025,0.5,0.975))
sd(output.APC.pr.rw1[625,])
```

```
output.period.pr.rw2<-output.model(spain.period.pr.rw2,n.obs=4*12*52)
quantile(output.period.pr.rw2[625,],probs=c(0.025,0.5,0.975))
sd(output.period.pr.rw2[625,])
```

```
output.period.pr.rw2<-output.model(spain.period.pr.rw2,n.obs=5*12*52)
quantile(output.period.pr.rw2[625,],probs=c(0.025,0.5,0.975))
sd(output.period.pr.rw2[625,])
```

```
output.cohort.pr.rw2<-output.model(spain.cohort.pr.rw2,n.obs=4*12*52)
quantile(output.cohort.pr.rw2[625,],probs=c(0.025,0.5,0.975))
sd(output.cohort.pr.rw2[625,])
```

```
output.cohort.pr.rw2<-output.model(spain.cohort.pr.rw2,n.obs=5*12*52)
quantile(output.cohort.pr.rw2[625,],probs=c(0.025,0.5,0.975))
sd(output.cohort.pr.rw2[625,])
```

```
output.APC.pr.rw2<-output.model(spain.APC.pr.rw2,n.obs=4*12*52)
quantile(output.APC.pr.rw2[625,],probs=c(0.025,0.5,0.975))
sd(output.APC.pr.rw2[625,])
```

```

output.APC.pr.rw2<-output.model(spain.APC.pr.rw2,n.obs=5*12*52)
quantile(output.APC.pr.rw2[625,],probs=c(0.025,0.5,0.975))
sd(output.APC.pr.rw2[625,])

#####
#####  Table 3  #####
#####

idx.out<-f.input[f.input$period==6,c(3,6)]
idx.out[,3]<-1:length(idx.out[,1])
names(idx.out)<-c("age","PR","idx")
idx.45.64<-idx.out[((idx.out$age>=4)&(idx.out$age<=7)),]$idx
idx.65<-idx.out[((idx.out$age>=8)),]$idx

stat.age.groups<-function(output.sim,idx.out.tmp)
{
  output.sim<-output.sim[idx.out.tmp,]
  vec.sim<-apply(output.sim,2,sum)
  print(quantile(vec.sim,probs=c(0.025,0.5,0.975)))
  print(sd(vec.sim))
  as.numeric(quantile(vec.sim,probs=c(0.5,0.025,0.975)))
}

stat.agreg.age.groups<-function(output.sim,N.AGE.GROUPS=12,idx.out.tmp)
{
  n.sims<-dim(output.sim)[2]
  mat.age.ag<-matrix(0,N.AGE.GROUPS,n.sims)
  for (i in 1:N.AGE.GROUPS)
  {
    idx.out.tmp.t<-idx.out.tmp[idx.out.tmp$age==i,]
    output.sim.t<-output.sim[idx.out.tmp.t$idx,]
    mat.age.ag[i,]<-apply(output.sim.t,2,sum)
  }
  mat.age.ag

```

```

}

stat.agreg.age.groups.py<-function(py.tmp,N.AGE.GROUPS=12,idx.out.tmp)
{
vect.age.ag<-rep(0,N.AGE.GROUPS)
for (i in 1:N.AGE.GROUPS)
{
idx.out.tmp.t<-idx.out.tmp[idx.out.tmp$age==i,]
vect.age.ag[i]<-sum(py.tmp[idx.out.tmp.t$idx])
}
vect.age.ag
}

stat.mat.risk.dif<-function(mat.risk.dif.t,name.t="Risk",alpha.t=0.05)
{
mat.risk.dif.q<-matrix(0,dim(mat.risk.dif.t)[1],3)
for (i in 1:dim(mat.risk.dif.t)[1])
{
mat.risk.dif.q[i,]<-as.numeric(quantile(mat.risk.dif.t[i,],probs=c(0.5,alpha.t/2,1-alpha.t/2)))
}
mat.risk.dif.q<-as.data.frame(mat.risk.dif.q)
names(mat.risk.dif.q)<-c(paste(name.t,"q","0.5",sep=""),paste(name.t,"q",alpha.t/2,sep=""),paste(name.t,"q",1-alpha.t/2,sep=""))
mat.risk.dif.q
}

mat.out.proj.2015<-matrix(0,6,9)

## Period.pr.rw1
mat.out.proj.2015[1,1:3]<-stat.age.groups(output.period.pr.rw1,idx.45.64)
mat.out.proj.2015[1,4:6]<-stat.age.groups(output.period.pr.rw1,idx.65)
mat.out.proj.2015[1,7:9]<-stat.age.groups(output.period.pr.rw1,1:624)

## Cohort.pr.rw1

```

```

mat.out.proj.2015[2,1:3]<-stat.age.groups(output.cohort.pr.rw1,idx.45.64)
mat.out.proj.2015[2,4:6]<-stat.age.groups(output.cohort.pr.rw1,idx.65)
mat.out.proj.2015[2,7:9]<-stat.age.groups(output.cohort.pr.rw1,1:624)

## APC.pr.rw1
mat.out.proj.2015[3,1:3]<-stat.age.groups(output.APC.pr.rw1,idx.45.64)
mat.out.proj.2015[3,4:6]<-stat.age.groups(output.APC.pr.rw1,idx.65)
mat.out.proj.2015[3,7:9]<-stat.age.groups(output.APC.pr.rw1,1:624)

## Period.pr.rw2
mat.out.proj.2015[4,1:3]<-stat.age.groups(output.period.pr.rw2,idx.45.64)
mat.out.proj.2015[4,4:6]<-stat.age.groups(output.period.pr.rw2,idx.65)
mat.out.proj.2015[4,7:9]<-stat.age.groups(output.period.pr.rw2,1:624)

## Cohort.pr.rw2
mat.out.proj.2015[5,1:3]<-stat.age.groups(output.cohort.pr.rw2,idx.45.64)
mat.out.proj.2015[5,4:6]<-stat.age.groups(output.cohort.pr.rw2,idx.65)
mat.out.proj.2015[5,7:9]<-stat.age.groups(output.cohort.pr.rw2,1:624)

## APC.pr.rw2
mat.out.proj.2015[6,1:3]<-stat.age.groups(output.APC.pr.rw2,idx.45.64)
mat.out.proj.2015[6,4:6]<-stat.age.groups(output.APC.pr.rw2,idx.65)
mat.out.proj.2015[6,7:9]<-stat.age.groups(output.APC.pr.rw2,1:624)

mat.out.proj.2015<-as.data.frame(mat.out.proj.2015)
names(mat.out.proj.2015)<-c("Med.45.64","ICI.45.64","ICS.45.64","Med.65","ICI.65","ICS.65","Med.T","ICI","ICS")

#####Table 3. Risks

list.outputs.models<-
list(output.period.pr.rw1,output.cohort.pr.rw1,output.APC.pr.rw1,output.period.pr.rw2,output.cohort.pr.rw2,output.APC.pr.rw2)
mat.risk.dif.risk<-matrix(0,6,1000)
mat.risk.dif.net<-matrix(0,6,1000)

# Dades poblacio agregada

```

```

py.target<-f.input[f.input$period==6,]$pyr
py.ref<-f.input[f.input$period==4,]$pyr
death.ref<-f.input[f.input$period==4,]$cases
pob.target<-stat.agreg.age.groups.py(py.target,N.AGE.GROUPS=12,idx.out)
pob.ref<-stat.agreg.age.groups.py(py.ref,N.AGE.GROUPS=12,idx.out)
cases.ref<-stat.agreg.age.groups.py(death.ref,N.AGE.GROUPS=12,idx.out)

for (i in 1:length(list.outputs.models))
{
mat.cases.target<-stat.agreg.age.groups(list.outputs.models[[i]],12,idx.out)
for (idx.mat in 1:dim(mat.cases.target)[2])
{
cases.target<-mat.cases.target[,idx.mat]
mat.risk.dif.risk[i,idx.mat]<-risk.diff(cases.ref,cases.target,pob.ref,pob.target)[[2]][1,5]
mat.risk.dif.net[i,idx.mat]<-sum(risk.diff(cases.ref,cases.target,pob.ref,pob.target)[[2]][4,5])
}
}

mat.proj.2015.vs.2009<-cbind(mat.out.proj.2015,stat.mat.risk.dif(mat.risk.dif.risk),stat.mat.risk.dif(mat.risk.dif.net,name.t="Net"))

write.table(mat.proj.2015.vs.2009,file=paste(directori,directori.out,"Table 3.txt",sep=""))

```

4. FIGURES

```

#####
##### FIGURE 1

```

```
#####
```

```
spain.ad.45.64.Random.Effects.PR<- abs(spain.ad.45.64$summary.random$PR$mean)/spain.ad.45.64$summary.random$PR$sd>2
spain.ad.45.64.Random.Effects.PR.WORSE<- spain.ad.45.64$summary.random$PR$mean/spain.ad.45.64$summary.random$PR$sd>2
spain.ad.45.64.Random.Effects.PR.BETTER<- spain.ad.45.64$summary.random$PR$mean/spain.ad.45.64$summary.random$PR$sd<(-2)

table(spain.ad.45.64.Random.Effects.PR)
table(spain.ad.45.64.Random.Effects.PR.WORSE)
table(spain.ad.45.64.Random.Effects.PR.BETTER)
```

```
spain.ad.65.Random.Effects.PR<- abs(spain.ad.65$summary.random$PR$mean)/spain.ad.65$summary.random$PR$sd>2
spain.ad.65.Random.Effects.PR.WORSE<- spain.ad.65$summary.random$PR$mean/spain.ad.65$summary.random$PR$sd>2
spain.ad.65.Random.Effects.PR.BETTER<- spain.ad.65$summary.random$PR$mean/spain.ad.65$summary.random$PR$sd<(-2)

table(spain.ad.65.Random.Effects.PR)
table(spain.ad.65.Random.Effects.PR.WORSE)
table(spain.ad.65.Random.Effects.PR.BETTER)
```

```
table.regions.diferent.drift<-as.data.frame(cbind(spain.ad.45.64.Random.Effects.PR,spain.ad.65.Random.Effects.PR))
names(table.regions.diferent.drift)<-c("Age.45.64","Age.65")
table.regions.diferent.drift<-table.regions.diferent.drift[c(1:34,36:37,39:50),]
```

```
ordre.r<-as.data.frame(read.table( file=paste(directori,"Ordre Mapes/Ordre Mapes.txt",sep=""),header=F))
names(ordre.r)<-c("PR","ORDRE")
### POS 99 not defined in map
```

```
ordre.r<-ordre.r[ordre.r$ORDRE!=99,]
```

```
table.regions.diferent.drift<-table.regions.diferent.drift[order(ordre.r$ORDRE),]
```

```
spain.ad.45.64.Random.Effects.PR.WORSE<-spain.ad.45.64.Random.Effects.PR.WORSE[c(1:34,36:37,39:50)]
spain.ad.45.64.Random.Effects.PR.BETTER<-spain.ad.45.64.Random.Effects.PR.BETTER[c(1:34,36:37,39:50)]
```

```

spain.ad.45.64.Random.Effects.PR.WORSE<-spain.ad.45.64.Random.Effects.PR.WORSE[order(ordre.r$ORDRE)]
spain.ad.45.64.Random.Effects.PR.BETTER<-spain.ad.45.64.Random.Effects.PR.BETTER[order(ordre.r$ORDRE)]

spain.ad.65.Random.Effects.PR.WORSE<-spain.ad.65.Random.Effects.PR.WORSE[c(1:34,36:37,39:50)]
spain.ad.65.Random.Effects.PR.BETTER<-spain.ad.65.Random.Effects.PR.BETTER[c(1:34,36:37,39:50)]
spain.ad.65.Random.Effects.PR.WORSE<-spain.ad.65.Random.Effects.PR.WORSE[order(ordre.r$ORDRE)]
spain.ad.65.Random.Effects.PR.BETTER<-spain.ad.65.Random.Effects.PR.BETTER[order(ordre.r$ORDRE)]

library(RColorBrewer)
library(maptools)

gen.mapa<-function(data.to.map,talls,cols="Greys",legend=F)
{
  nvals<-length(talls)
  cuts<-1:nvals
  cuts1<-cuts
  for (i in 1:nvals)
  #cuts1[i]<-round(quantile(data.to.map,probs=c(0,0.2,0.4,0.75,0.85,1.0))[[i]],1)
  cuts1[i]<-talls[i]
  cuts1[1]<-cuts1[1]
  cuts1[nvals]<-cuts1[nvals]
  cuts1<-cuts1
  brks <- cut((data.to.map), cuts1)
  print(brks)
  print(talls)
  plotclr <- brewer.pal(nvals,cols)
  pal <- brewer.pal(nvals, cols)
  fgs <- pal[brks]
  print(fgs)
  plot(x, fg=fgs,main="",xlab="",ylab="",axes=F)
  pp<-levels(brks)
  if (legend==T) legend(x=-8, y=36, legend=pp, fill=plotclr, cex=0.7, bty="n")
  if (legend==F) legend(x=-8, y=36, legend="", fill=plotclr, cex=0.7, bty="n")
}

```

```

read.shape<-function (filen, dbf.data = TRUE, verbose = TRUE, repair = FALSE)
{
  filen <- path.expand(filen)
  shinfo <- getinfo.shape(filen)
  if (dbf.data) {
    df <- read.dbf(filen)
    ndf <- as.integer(nrow(df))
  }
  else ndf <- as.integer(NA)
  if (shinfo[[2]] == 8) {
    if (!dbf.data)
      stop("to test for multipoint compliance, set dbf.data=TRUE")
    if (ndf != shinfo[[3]])
      stop("noncompliant multipoint shapefile")
  }
  shp.lst <- .Call("Rshapeget", as.character(filen), as.logical(repair),
    PACKAGE = "maptools")
  if (verbose) {
    print(shinfo)
  }
  n <- length(shp.lst)
  for (i in 1:n) {
    attr(shp.lst[[i]], "nVerts") <- as.integer(shp.lst[[i]]$nVerts)
    attr(shp.lst[[i]], "nParts") <- as.integer(shp.lst[[i]]$nParts)
    attr(shp.lst[[i]], "shp.type") <- as.integer(shp.lst[[i]]$shp.type)
    attr(shp.lst[[i]], "bbox") <- as.double(shp.lst[[i]]$bbox)
  }
  class(shp.lst) <- "ShapeList"
  if (dbf.data) {
    map <- list(Shapes = shp.lst, att.data = df)
    class(map) <- "Map"
    return(map)
  }
}

```

```

    else {
      return(shp.lst)
    }
  }

setwd("C:\\Map of Spain")
library(maptools)
library(RColorBrewer)
##Llegeix mapa
x<-read.shape("C:\\epi2000\\esp.shp")

par(mfrow=c(1,2))
gen.mapa(as.numeric(table.regions.diferent.drift[,1]),talls=c(-0.1,0.1,1))
gen.mapa(as.numeric(table.regions.diferent.drift[,2]),talls=c(-0.1,0.1,1))

table.regions.diferent.drift.W.B<-table.regions.diferent.drift
table.regions.diferent.drift.W.B[,1]<-0
table.regions.diferent.drift.W.B[,2]<-0

for (i in 1:length(table.regions.diferent.drift[,1]))
{
  if (spain.ad.45.64.Random.Effects.PR.WORSE[i]) table.regions.diferent.drift.W.B[i,1]<-1
  if (spain.ad.45.64.Random.Effects.PR.BETTER[i]) table.regions.diferent.drift.W.B[i,1]<- (-1)
  if (spain.ad.65.Random.Effects.PR.WORSE[i]) table.regions.diferent.drift.W.B[i,2]<-1
  if (spain.ad.65.Random.Effects.PR.BETTER[i]) table.regions.diferent.drift.W.B[i,2]<- (-1)
}

## Figure 1
par(mfrow=c(1,2))
gen.mapa(as.numeric(table.regions.diferent.drift.W.B[,1]),talls=c(-1.1,-0.01,0.99,1.1))
gen.mapa(as.numeric(table.regions.diferent.drift.W.B[,2]),talls=c(-1.1,-0.01,0.99,1.1))

#####

```

FIGURE 2

#####

```
data.high.dens.regions<-f.input[ ((f.input$period<=4) & (f.input$PR%in%c(29,8,34,43,45,48,19,1,2))) , ]
data.other.regions<-f.input[ ((f.input$period<=4) & (! (f.input$PR%in%c(29,8,34,43,45,48,19,1,2))) ) , ]
data.high.dens.regions.45.64<-f.input[ ((f.input$age>=4) & (f.input$age<=7) & (f.input$period<=4) & (f.input$PR%in%c(29,8,34,43,45,48,19,1,2))) , ]
data.other.regions.45.64<-f.input[ ((f.input$age>=4) & (f.input$age<=7) & (f.input$period<=4) & (! (f.input$PR%in%c(29,8,34,43,45,48,19,1,2))) ) , ]
data.high.dens.regions.65<-f.input[ ((f.input$age>=8) & (f.input$period<=4) & (f.input$PR%in%c(29,8,34,43,45,48,19,1,2))) , ]
data.other.regions.65<-f.input[ ((f.input$age>=8) & (f.input$period<=4) & (! (f.input$PR%in%c(29,8,34,43,45,48,19,1,2))) ) , ]

mat.asr.period.1990.2009<-as.data.frame(matrix(0,4,3))
names(mat.asr.period.1990.2009)<-c("Period", "High", "Other")
mat.asr.period.1990.2009$Period<-c(1992,1997,2002,2007)

for (idx.asr in 1:4)
{
mat.asr.period.1990.2009$High[idx.asr]<-gen.wsp.rate(dades.tmp.t=data.high.dens.regions,period.t=idx.asr,age.in=1,age.fin=12) [1]
mat.asr.period.1990.2009$Other[idx.asr]<-gen.wsp.rate(dades.tmp.t=data.other.regions,period.t=idx.asr,age.in=1,age.fin=12) [1]
}

mat.asr.period.1990.2009.45.64<-as.data.frame(matrix(0,4,3))
names(mat.asr.period.1990.2009.45.64)<-c("Period", "High", "Other")
mat.asr.period.1990.2009.45.64$Period<-c(1992,1997,2002,2007)

for (idx.asr in 1:4)
{
mat.asr.period.1990.2009.45.64$High[idx.asr]<-
gen.wsp.rate(dades.tmp.t=data.high.dens.regions,period.t=idx.asr,age.in=10,age.fin=13,ages.t=4:7) [1]
mat.asr.period.1990.2009.45.64$Other[idx.asr]<-gen.wsp.rate(dades.tmp.t=data.other.regions,period.t=idx.asr,age.in=10,age.fin=13,ages.t=4:7) [1]
}

mat.asr.period.1990.2009.65<-as.data.frame(matrix(0,4,3))
names(mat.asr.period.1990.2009.65)<-c("Period", "High", "Other")
```

```

mat.asr.period.1990.2009.65$Period<-c(1992,1997,2002,2007)

for (idx.asr in 1:4)
{
mat.asr.period.1990.2009.65$High[idx.asr]<-gen.wsp.rate(dades.tmp.t=data.high.dens.regions,period.t=idx.asr,age.in=14,age.fin=18,ages.t=8:12)[1]
mat.asr.period.1990.2009.65$Other[idx.asr]<-gen.wsp.rate(dades.tmp.t=data.other.regions,period.t=idx.asr,age.in=14,age.fin=18,ages.t=8:12)[1]
}

plot(mat.asr.period.1990.2009.65$Period,mat.asr.period.1990.2009.65$High,type="n",ylim=c(20,100),xlab="Time Period",ylab="ASR breast cancer
mortality rate per 100,000 women-years",xaxt="n")
axis(1, at=c(1992,1997,2002,2007),labels=c("1990-1994","1995-1999","2000-2004","2005-2009"))
lines(mat.asr.period.1990.2009.65$Period,mat.asr.period.1990.2009.65$High,lty=1)
lines(mat.asr.period.1990.2009.65$Period,mat.asr.period.1990.2009.65$Other,lty=2)
lines(mat.asr.period.1990.2009.45.64$Period,mat.asr.period.1990.2009.45.64$High,lty=1)
lines(mat.asr.period.1990.2009.45.64$Period,mat.asr.period.1990.2009.45.64$Other,lty=2)
lines(mat.asr.period.1990.2009$Period,mat.asr.period.1990.2009$High*1.1,lty=1)
lines(mat.asr.period.1990.2009$Period,mat.asr.period.1990.2009$Other*1.1,lty=2)

#### ORDER PROVINCES

### POS 99 not defined in map

ordre.r<-ordre.r[ordre.r$ORDRE!=99,]

cases.base<-f.input[f.input$period==4,]$cases
pob.base<-f.input[f.input$period==4,]$pyr
pob.pred<-f.input[f.input$period==6,]$pyr

apreg.rw1<- (round(apply(output.period.pr.rw1,1,median),0)[1:624])
apreg.rw2<- (round(apply(output.period.pr.rw2,1,median),0)[1:624])
acreg.rw1<- (round(apply(output.cohort.pr.rw1,1,median),0)[1:624])
acreg.rw2<- (round(apply(output.cohort.pr.rw2,1,median),0)[1:624])

```

```

apcreg.rw1<- (round(apply(output.APC.pr.rw1,1,median),0)[1:624])
apcreg.rw2<- (round(apply(output.APC.pr.rw2,1,median),0)[1:624])

list.models<-list(apreg.rw1,acreg.rw1,apcreg.rw1,apreg.rw2,acreg.rw2,apcreg.rw2)

matrix.cases<-matrix(0,624,9)

matrix.cases<-cbind(cases.base,pob.base,pob.pred,apreg.rw1,apreg.rw2,acreg.rw1,acreg.rw2,apcreg.rw1,apcreg.rw2)

provs.tmp<-dades.tmp$PR[1:624]

scen.by.model<-function(model.tmp=apnoreg.rw1)
{
mat.out.sp<-as.data.frame(matrix(0,52,4))
names(mat.out.sp)<-c("Risk","Struct","Size","Net")
for (i in 1:52)
{
res.risk.diff<-risk.diff(cases.base[provs.tmp==i],model.tmp[provs.tmp==i],pob.base[provs.tmp==i],pob.pred[provs.tmp==i])
mat.out.sp[i,]<-res.risk.diff[[2]][,5]
}
mat.out.sp<-mat.out.sp[c(1:34,36:37,39:50),]
mat.out.sp<-mat.out.sp[order(ordre.r$ORDRE),]
mat.out.sp
}

### 12 Models
list.rd<-list(1:length(list.models))

for (i in 1:length(list.models))
list.rd[[i]]<-scen.by.model(list.models[[i]])

#####
### FIGURE 3
#####

```

```
#####
### FIGURE 3: functions
#####

gen.agg<-function(dades.tmp.tt)
{
  as.data.frame(aggregate(dades.tmp.tt,list(dades.tmp.tt$age),sum)[,1:3])
}

#gen.agg(data.high.dens.regions[data.high.dens.regions$P==1,])

gen.risk.diff.area<-function(pop.ref,pop.targ)
{
  cases.ref<-pop.ref$cases
  cases.targ<-pop.targ$cases
  popu.ref<-pop.ref$pyr
  popu.targ<-pop.targ$pyr
  risk.diff(cases.ref,cases.targ,popu.ref,popu.targ)[[2]][1:3,5]
}

graf.risk.dif<-function(mat.data)
{
  plot(mat.data$Risk,type="n",ylim=c(-30,30),xlim=c(0,4),axes=F,xlab="",ylab="% Change in number of BC deaths (Reference Period 1990-94)")
  lines(mat.data$Risk,lty=1)
  lines(mat.data$Risk,lty=1,type="p")
  lines(mat.data$Struc,lty=2)
  lines(mat.data$Struc,lty=2,type="p")
  lines(mat.data$Size,lty=3)
  lines(mat.data$Size,lty=3,type="p")
  axis(side=1,at=c(1:3),labels=c("1995-99","2000-04","2005-09"))
  axis(side=2,at=c(-30,-20,-10,0,10,20,30),labels=c("-30","-20","-10","0","10","20","30"))
  abline(h=0)
}
```

```
#####
### FIGURE 3: Generate Figure
#####

data.high.dens.P1<-gen.agg(data.high.dens.regions[data.high.dens.regions$period==1,])
data.high.dens.P2<-gen.agg(data.high.dens.regions[data.high.dens.regions$period==2,])
data.high.dens.P3<-gen.agg(data.high.dens.regions[data.high.dens.regions$period==3,])
data.high.dens.P4<-gen.agg(data.high.dens.regions[data.high.dens.regions$period==4,])

mat.high.dens<-as.data.frame(matrix(0,3,3))
names(mat.high.dens)<-c("Risk", "Struc", "Size")

mat.high.dens[1,]<-gen.risk.diff.area(pop.ref=data.high.dens.P1,pop.targ=data.high.dens.P2)
mat.high.dens[2,]<-gen.risk.diff.area(pop.ref=data.high.dens.P1,pop.targ=data.high.dens.P3)
mat.high.dens[3,]<-gen.risk.diff.area(pop.ref=data.high.dens.P1,pop.targ=data.high.dens.P4)

mat.other.dens<-as.data.frame(matrix(0,3,3))
names(mat.other.dens)<-c("Risk", "Struc", "Size")

data.other.dens.P1<-gen.agg(data.other.regions[data.other.regions$period==1,])
data.other.dens.P2<-gen.agg(data.other.regions[data.other.regions$period==2,])
data.other.dens.P3<-gen.agg(data.other.regions[data.other.regions$period==3,])
data.other.dens.P4<-gen.agg(data.other.regions[data.other.regions$period==4,])

mat.other.dens[1,]<-gen.risk.diff.area(pop.ref=data.other.dens.P1,pop.targ=data.other.dens.P2)
mat.other.dens[2,]<-gen.risk.diff.area(pop.ref=data.other.dens.P1,pop.targ=data.other.dens.P3)
mat.other.dens[3,]<-gen.risk.diff.area(pop.ref=data.other.dens.P1,pop.targ=data.other.dens.P4)

par(mfrow=c(1,2))

graf.risk.dif(mat.high.dens)
graf.risk.dif(mat.other.dens)
```

Code Section 1 Supplementary Material file

```
gen.quantile<-function(model,n.obs=1:1872)
{
as.numeric(quantile(model$cpo$cpo[n.obs],probs=c(0.5,0.025,0.975)))
}
```

```
gen.pit<-function(model,n.obs=1:1872)
{
hist(model$cpo$pit[n.obs],main="",xlab="")
}
```

```
##### MODELS
```

```
# Prior Gamma(0.5,0.001)
```

```
spain.period.pr.rw1.1 = inla(cases ~ f(age,values=1:N.AGE,model="rw2",param=c(0.5, 0.001)) + f(period,values=1:N.PERIOD,model="rw1",param=c(0.5,
0.001))+f(PR,values=1:N.PROV,model="iid",param=c(0.5, 0.001)), data=dades.tmp, family="poisson",
offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))
```

```
spain.period.pr.rw2.1 = inla(cases ~ f(age,values=1:N.AGE,model="rw2",param=c(0.5, 0.001)) + f(period,values=1:N.PERIOD,model="rw2",param=c(0.5,
0.001))+f(PR,values=1:N.PROV,model="iid",param=c(0.5, 0.001)), data=dades.tmp, family="poisson",
offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))
```

```
spain.cohort.pr.rw1.1 = inla(cases ~ f(age,values=1:N.AGE,model="rw2",param=c(0.5, 0.001)) + f(cohort,values=1:N.COHORT,model="rw1",param=c(0.5,
0.001))+f(PR,values=1:N.PROV,model="iid",param=c(0.5, 0.001)), data=dades.tmp, family="poisson",
offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))
```

```
spain.cohort.pr.rw2.1 = inla(cases ~ f(age,values=1:N.AGE,model="rw2",param=c(0.5, 0.001)) + f(cohort,values=1:N.COHORT,model="rw2",param=c(0.5, 0.001))+f(PR,values=1:N.PROV,model="iid",param=c(0.5, 0.001)), data=dades.tmp, family="poisson",
offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))
```

```
spain.APC.pr.rw1.1 = inla(cases ~ f(age,values=1:N.AGE,model="rw2",param=c(0.5, 0.001)) + f(period,values=1:N.PERIOD,model="rw1",param=c(0.5, 0.001))+f(cohort,values=1:N.COHORT,model="rw1",param=c(0.5, 0.001))+f(PR,values=1:N.PROV,model="iid",param=c(0.5, 0.001)), data=dades.tmp,
family="poisson", offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))
```

```
spain.APC.pr.rw2.1 = inla(cases ~ f(age,values=1:N.AGE,model="rw2",param=c(0.5, 0.001)) + f(period,values=1:N.PERIOD,model="rw2",param=c(0.5, 0.001))+f(cohort,values=1:N.COHORT,model="rw2",param=c(0.5, 0.001))+f(PR,values=1:N.PROV,model="iid",param=c(0.5, 0.001)), data=dades.tmp,
family="poisson", offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))
```

```
# Prior Gamma(0.001,0.001)
```

```
spain.period.pr.rw1.2 = inla(cases ~ f(age,values=1:N.AGE,model="rw2",param=c(0.001, 0.001)) +
f(period,values=1:N.PERIOD,model="rw1",param=c(0.001, 0.001))+f(PR,values=1:N.PROV,model="iid",param=c(0.001, 0.001)), data=dades.tmp,
family="poisson", offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))
```

```
spain.period.pr.rw2.2 = inla(cases ~ f(age,values=1:N.AGE,model="rw2",param=c(0.001, 0.001)) +
f(period,values=1:N.PERIOD,model="rw2",param=c(0.001, 0.001))+f(PR,values=1:N.PROV,model="iid",param=c(0.001, 0.001)), data=dades.tmp,
family="poisson", offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))
```

```
spain.cohort.pr.rw1.2 = inla(cases ~ f(age,values=1:N.AGE,model="rw2",param=c(0.001, 0.001)) +
f(cohort,values=1:N.COHORT,model="rw1",param=c(0.001, 0.001))+f(PR,values=1:N.PROV,model="iid",param=c(0.001, 0.001)), data=dades.tmp,
family="poisson", offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))
```

```
spain.cohort.pr.rw2.2 = inla(cases ~ f(age,values=1:N.AGE,model="rw2",param=c(0.001, 0.001)) +
f(cohort,values=1:N.COHORT,model="rw2",param=c(0.001, 0.001))+f(PR,values=1:N.PROV,model="iid",param=c(0.001, 0.001)), data=dades.tmp,
family="poisson", offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))
```

```

spain.APC.pr.rw1.2 = inla(cases ~ f(age,values=1:N.AGE,model="rw2",param=c(0.001, 0.001)) +
f(period,values=1:N.PERIOD,model="rw1",param=c(0.001, 0.001))+f(cohort,values=1:N.COHORT,model="rw1",param=c(0.001,
0.001))+f(PR,values=1:N.PROV,model="iid",param=c(0.001, 0.001)), data=dades.tmp, family="poisson",
offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))

spain.APC.pr.rw2.2 = inla(cases ~ f(age,values=1:N.AGE,model="rw2",param=c(0.001, 0.001)) +
f(period,values=1:N.PERIOD,model="rw2",param=c(0.001, 0.001))+f(cohort,values=1:N.COHORT,model="rw2",param=c(0.001,
0.001))+f(PR,values=1:N.PROV,model="iid",param=c(0.001, 0.001)), data=dades.tmp, family="poisson",
offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))

# Prior Gamma(1,0.001)

spain.period.pr.rw1.3 = inla(cases ~ f(age,values=1:N.AGE,model="rw2",param=c(1, 0.001)) + f(period,values=1:N.PERIOD,model="rw1",param=c(1,
0.001))+f(PR,values=1:N.PROV,model="iid",param=c(1, 0.001)), data=dades.tmp, family="poisson",
offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))

spain.period.pr.rw2.3 = inla(cases ~ f(age,values=1:N.AGE,model="rw2",param=c(1, 0.001)) + f(period,values=1:N.PERIOD,model="rw2",param=c(1,
0.001))+f(PR,values=1:N.PROV,model="iid",param=c(1, 0.001)), data=dades.tmp, family="poisson",
offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))

spain.cohort.pr.rw1.3 = inla(cases ~ f(age,values=1:N.AGE,model="rw2",param=c(1, 0.001)) + f(cohort,values=1:N.COHORT,model="rw1",param=c(1,
0.001))+f(PR,values=1:N.PROV,model="iid",param=c(1, 0.001)), data=dades.tmp, family="poisson",
offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))

spain.cohort.pr.rw2.3 = inla(cases ~ f(age,values=1:N.AGE,model="rw2",param=c(1, 0.001)) + f(cohort,values=1:N.COHORT,model="rw2",param=c(1,
0.001))+f(PR,values=1:N.PROV,model="iid",param=c(1, 0.001)), data=dades.tmp, family="poisson",
offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))

spain.APC.pr.rw1.3 = inla(cases ~ f(age,values=1:N.AGE,model="rw2",param=c(1, 0.001)) + f(period,values=1:N.PERIOD,model="rw1",param=c(1,
0.001))+f(cohort,values=1:N.COHORT,model="rw1",param=c(1, 0.001))+f(PR,values=1:N.PROV,model="iid",param=c(1, 0.001)), data=dades.tmp,
family="poisson", offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))

```

```

spain.APC.pr.rw2.3 = inla(cases ~ f(age,values=1:N.AGE,model="rw2",param=c(1, 0.001)) + f(period,values=1:N.PERIOD,model="rw2",param=c(1,
0.001))+f(cohort,values=1:N.COHORT,model="rw2",param=c(1, 0.001))+f(PR,values=1:N.PROV,model="iid",param=c(1, 0.001)), data=dades.tmp,
family="poisson", offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))

# Generate matrix of precissions

gen.mat.prec<-function(model,rows.t,cols.t)
{
#as.matrix(summary(spain.period.pr.rw1.1)[[4]][1:2,3:5])
as.matrix(summary(model)[[4]][rows.t,cols.t])[c(2,1,3)]
}

mat.pp.AP<-matrix(0,2,3*3*2)
mat.pp.AC<-matrix(0,2,3*3*2)
mat.pp.APC<-matrix(0,3,3*3*2)

mat.pp.AP[1:2,]<-
cbind(gen.mat.prec(model=spain.period.pr.rw1.1,rows.t=1:2,cols.t=3:5),gen.mat.prec(model=spain.period.pr.rw1.2,rows.t=1:2,cols.t=3:5),gen.mat.prec(model=spain.period.pr.rw1.3,rows.t=1:2,cols.t=3:5),gen.mat.prec(model=spain.period.pr.rw2.1,rows.t=1:2,cols.t=3:5),gen.mat.prec(model=spain.period.pr.rw2.2,rows.t=1:2,cols.t=3:5),gen.mat.prec(model=spain.period.pr.rw2.3,rows.t=1:2,cols.t=3:5))

mat.pp.AC[1:2,]<-
cbind(gen.mat.prec(model=spain.cohort.pr.rw1.1,rows.t=1:2,cols.t=3:5),gen.mat.prec(model=spain.cohort.pr.rw1.2,rows.t=1:2,cols.t=3:5),gen.mat.prec(model=spain.cohort.pr.rw1.3,rows.t=1:2,cols.t=3:5),gen.mat.prec(model=spain.cohort.pr.rw2.1,rows.t=1:2,cols.t=3:5),gen.mat.prec(model=spain.cohort.pr.rw2.2,rows.t=1:2,cols.t=3:5),gen.mat.prec(model=spain.cohort.pr.rw2.3,rows.t=1:2,cols.t=3:5))

mat.pp.APC[1:3,]<-
cbind(gen.mat.prec(model=spain.APC.pr.rw1.1,rows.t=1:3,cols.t=3:5),gen.mat.prec(model=spain.APC.pr.rw1.2,rows.t=1:3,cols.t=3:5),gen.mat.prec(model=spain.APC.pr.rw1.3,rows.t=1:3,cols.t=3:5),gen.mat.prec(model=spain.APC.pr.rw2.1,rows.t=1:3,cols.t=3:5),gen.mat.prec(model=spain.APC.pr.rw2.2,rows.t=1:3,cols.t=3:5),gen.mat.prec(model=spain.APC.pr.rw2.3,rows.t=1:3,cols.t=3:5))

```

Code Section 2 Supplementary Material file

```
# Aggregated Data
```

```
directori<-"C:/2011 - Breast Cancer Mortality in Spain Projections 2019/"
file.input<-"Data/BCmortality 1990-2009 pr 2019.txt"
directori.out<-"Tables/"
directori.RData<-"RData 2011/"
f.input<-read.table( file=paste(directori,file.input,sep=""),header=T)
f.input<-as.data.frame(f.input)
names(f.input)<-c("cases","pyr","age","period","cohort","PR")
f.input<-as.data.frame(f.input)
f.input$cases<-as.numeric(lapply(f.input$cases,neg.to.NA))
N.AGE<-12
N.PERIOD<-6
N.COHORT<-12+6-1
N.PROV<-52
Spain.BC<-
as.data.frame((aggregate(f.input[f.input$period<=4,],list(f.input[f.input$period<=4,]$age,f.input[f.input$period<=4,]$period,f.input[f.input$period<=4,]$cohort),sum)[,1:5]))
names(Spain.BC)<-c("Age","Period","Cohort","D","Y")
Spain.BC$R<-Spain.BC$D/Spain.BC$Y*100000
par(mfrow=c(1,2))
#####
# Period effect graph
#####
Spain.BC.tmp<-Spain.BC[Spain.BC$Age==10,]
plot(Spain.BC.tmp$R,type="n",xlim=c(0,5),ylim=c(0,200),axes=F,xlab="Period of Death",ylab="Rate per 100,000 women-years")
axis(1,at=c(1:4),lab=c("1990-94","1995-99","2000-04","2005-09"))
axis(2,at=c(0,50,100,200),lab=c(0,50,100,200))

for (i.A in 1:12)
{
salt.t<-(-1)^i.A
Spain.BC.tmp<-Spain.BC[Spain.BC$Age==i.A,]
lines(Spain.BC.tmp$R,lty=1)
```

```

if (salt.t<0)
{
x.pos<-0.9
y.pos<-1
}

if (salt.t>0)
{
x.pos<-4.1
y.pos<-4
}

text(x.pos,Spain.BC.tmp$R[y.pos],paste(25+5*i.A,29+5*i.A,sep="-"))

}

```

```

gen.period<-function(x)
{
if (x==1) y<-1992.5
if (x==2) y<-1997.5
if (x==3) y<-2002.5
if (x==4) y<-2007.5
y
}

```

```

gen.age<-function(x)
{
25.5+5*x
}

```

```

Spain.BC$P<-as.numeric(lapply(Spain.BC$Period,gen.period))
Spain.BC$A<-as.numeric(lapply(Spain.BC$Age,gen.age))

```

```

Spain.BC$C<-Spain.BC$P-Spain.BC$A

#####
# Cohort Effect
#####

Spain.BC.tmp<-Spain.BC[Spain.BC$Age==10,]
plot(Spain.BC.tmp$C, Spain.BC.tmp$R,type="n",xlim=c(min(Spain.BC$C)-5,max(Spain.BC$C)+5),ylim=c(0,200),axes=F,xlab="Birth Cohort (Central
Year)",ylab="Rate per 100,000 women-years")
axis(1,at=unique(Spain.BC$C),lab=c(seq(1907,1977,5)))
axis(2,at=c(0,50,100,200),lab=c(0,50,100,200))

for (i.A in 1:12)
{
salt.t<-(-1)^i.A
Spain.BC.tmp<-Spain.BC[Spain.BC$Age==i.A,]
lines(Spain.BC.tmp$C, Spain.BC.tmp$R,lty=1)

if (salt.t<0)
{
x.pos<-min(Spain.BC.tmp$C)-2
y.pos<-1
}

if (salt.t>0)
{
x.pos<-max(Spain.BC.tmp$C)+2
y.pos<-4
}

text(x.pos,Spain.BC.tmp$R[y.pos],paste(25+5*i.A,29+5*i.A,sep="-"))

}

```

Code Section 3 Supplementary Material file

```
# Interactions
```

```
# Generate Interactions
```

```
dades.tmp.I<-dades.tmp[1:1872,]
```

```
dades.tmp.I$age.period<-dades.tmp.I$age*1000+dades.tmp.I$period
```

```
dades.tmp.I$age.period<-as.numeric(as.factor(dades.tmp.I$age.period))
```

```
dades.tmp.I$age.cohort<-dades.tmp.I$age*1000+dades.tmp.I$cohort
```

```
dades.tmp.I$age.cohort<-as.numeric(as.factor(dades.tmp.I$age.cohort))
```

```
spain.APC.pr.rw1.NO.I = inla(cases ~ f(age,values=1:N.AGE,model="rw2",param=c(0.5, 0.001)) + f(period,values=1:3,model="rw1",param=c(0.5, 0.001))+f(cohort,values=1:N.COHORT,model="rw1",param=c(0.5, 0.001))+f(PR,values=1:N.PROV,model="iid",param=c(0.5, 0.001)), data=dades.tmp.I, family="poisson", offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))
```

```
spain.APC.pr.rw1.I.AP = inla(cases ~ f(age,values=1:N.AGE,model="rw2",param=c(0.5, 0.001)) + f(period,values=1:3,model="rw1",param=c(0.5, 0.001))+f(cohort,values=1:N.COHORT,model="rw1",param=c(0.5, 0.001))+f(age.period,values=1:36,model="rw1",param=c(0.5, 0.001))+f(PR,values=1:N.PROV,model="iid",param=c(0.5, 0.001)), data=dades.tmp.I, family="poisson", offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))
```

```
spain.APC.pr.rw1.I.AC = inla(cases ~ f(age,values=1:N.AGE,model="rw2",param=c(0.5, 0.001)) + f(period,values=1:3,model="rw1",param=c(0.5, 0.001))+f(cohort,values=1:N.COHORT,model="rw1",param=c(0.5, 0.001))+f(age.cohort,values=1:36,model="rw1",param=c(0.5, 0.001))+f(PR,values=1:N.PROV,model="iid",param=c(0.5, 0.001)), data=dades.tmp.I, family="poisson", offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))
```

```
spain.APC.pr.rw1.I.AP.AC = inla(cases ~ f(age,values=1:N.AGE,model="rw2",param=c(0.5, 0.001)) + f(period,values=1:3,model="rw1",param=c(0.5, 0.001))+f(cohort,values=1:N.COHORT,model="rw1",param=c(0.5, 0.001))+f(age.period,values=1:36,model="rw1",param=c(0.5, 0.001))+f(age.cohort,values=1:36,model="rw1",param=c(0.5, 0.001))+f(PR,values=1:N.PROV,model="iid",param=c(0.5, 0.001)), data=dades.tmp.I, family="poisson", offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))
```

```
spain.APC.pr.rw2.NO.I = inla(cases ~ f(age,values=1:N.AGE,model="rw2",param=c(0.5, 0.001)) + f(period,values=1:3,model="rw1",param=c(0.5, 0.001))+f(cohort,values=1:N.COHORT,model="rw1",param=c(0.5, 0.001))+f(PR,values=1:N.PROV,model="iid",param=c(0.5, 0.001)), data=dades.tmp.I, family="poisson", offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))
```

```
spain.APC.pr.rw2.I.AP = inla(cases ~ f(age,values=1:N.AGE,model="rw2",param=c(0.5, 0.001)) + f(period,values=1:3,model="rw1",param=c(0.5, 0.001))+f(cohort,values=1:N.COHORT,model="rw1",param=c(0.5, 0.001))+f(age.period,values=1:36,model="rw2",param=c(0.5,
```

```

0.001))+f(PR,values=1:N.PROV,model="iid",param=c(0.5, 0.001)), data=dades.tmp.I, family="poisson",
offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))
spain.APC.pr.rw2.I.AC = inla(cases ~ f(age,values=1:N.AGE,model="rw2",param=c(0.5, 0.001)) + f(period,values=1:3,model="rw1",param=c(0.5,
0.001))+f(cohort,values=1:N.COHORT,model="rw1",param=c(0.5, 0.001))+f(age.cohort,values=1:36,model="rw2",param=c(0.5,
0.001))+f(PR,values=1:N.PROV,model="iid",param=c(0.5, 0.001)), data=dades.tmp.I, family="poisson",
offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))
spain.APC.pr.rw2.I.AP.AC = inla(cases ~ f(age,values=1:N.AGE,model="rw2",param=c(0.5, 0.001)) + f(period,values=1:3,model="rw1",param=c(0.5,
0.001))+f(cohort,values=1:N.COHORT,model="rw1",param=c(0.5, 0.001))+f(age.period,values=1:36,model="rw2",param=c(0.5,
0.001))+f(age.cohort,values=1:36,model="rw2",param=c(0.5, 0.001))+f(PR,values=1:N.PROV,model="iid",param=c(0.5, 0.001)), data=dades.tmp.I,
family="poisson", offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))

spain.period.pr.rw1.NO.I = inla(cases ~ f(age,values=1:N.AGE,model="rw2",param=c(0.5, 0.001)) + f(period,values=1:3,model="rw1",param=c(0.5,
0.001))+f(PR,values=1:N.PROV,model="iid",param=c(0.5, 0.001)), data=dades.tmp.I, family="poisson",
offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))
spain.period.pr.rw1.I = inla(cases ~ f(age,values=1:N.AGE,model="rw2",param=c(0.5, 0.001)) + f(period,values=1:3,model="rw1",param=c(0.5,
0.001))+f(age.period,values=1:36,model="rw2",param=c(0.5, 0.001))+f(PR,values=1:N.PROV,model="iid",param=c(0.5, 0.001)), data=dades.tmp.I,
family="poisson", offset=I(log(pyr)),control.predictor=list(compute=TRUE), control.compute=list(dic=T,mlik=T))

```