Notes and Code for Small Area NYC Pedestrian Injury Spatiotemporal Analyses With INLA

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Contents

These notes describe the process of creating the data sets and conducting the analyses for the paper "Small-Area Spatiotemporal Analysis of Pedestrian and Bicyclist Injuries in New York City 2001-2010". In order to reproduce the analyses, you may contact the author to request access to the data files. Refer to the appendices for an introduction to the theory and application of space-time modeling in R with INLA.

1 Set Up and Data Preparation

You will need R and the following R packages.

```
> library(maptools)
> library(sp)
> library(spdep)
> library(INLA)
> library(ggplot2)
```

First, load the data file of New York City pedestrian injury counts at the census tract level spanning the years 2001 to 2010. The data consists of observed and expected counts, and was created as part of a research project evaluating a Safe Routes to School program in New York City.[1] Each row represents a census tract. [2] The first 20 columns are yearly census tract population numbers based on linear extrapolations from the 2000 to the 2010 US census. The remaining columns consist of observed and expected pedestrian injury counts for different age groups at different hours of the day. [3] There are also indicator variables for whether there was an SRTS program in the census tract.

Next, use *subset()* to extract the census tract FIPS and the columns for the observed and expected all-age, all-hour pedestrian injury crash counts. Create an indicator variable for each of the 5 boroughs from the first 5 characters in the FIPS code contained in the variable "tract". Sum the columns for observed and expected counts for an initial cross-sectional analysis. Add a small number to the total population variable to avoid division by zero.

```
> load("~/tract.injuries.RData")
> pedDat<-subset(tract.injuries, select=c(tract,
+         allAges.allHrs.2001:allAges.allHrs.2010,
+         expected.allAges.allHrs.2001:expected.allAges.allHrs.2010,
+         allAge.pop.2001:allAge.pop.2010))
> pedDat$boro<-pedDat$tract
> pedDat$boro[substr(pedDat$tract,1,5)=="36005"]<-"BX"
> pedDat$boro[substr(pedDat$tract,1,5)=="36047"]<-"BK"
```

[1] See: DiMaggio C, Li G. Effectiveness of a safe routes to school program in preventing school-aged pedestrian injury. *Pediatrics*. 2013; 131(2):290-296.

[2] The 1,929 census tracts have been restricted to those that were present in both the 2000 and 2010 US Census.

[3] There are, for example, counts for all ages during all hours, adults during school hours, and school-age children during school hours. For the sparser data, e.g. school-age during school-hours, the data were aggregated by two-year increments.

```
> pedDat$boro[substr(pedDat$tract,1,5)=="36061"]<-"NY"
> pedDat$boro[substr(pedDat$tract,1,5)=="36081"]<-"QN"
> pedDat$boro[substr(pedDat$tract,1,5)=="36085"]<-"SI"
> pedDat$allAges.allHrs.tot<-rowSums(pedDat[,2:11])
> pedDat$expected.allAges.allHrs.tot<-rowSums(pedDat[,12:21])
> pedDat$pop.tot<-rowMeans(pedDat[,22:31])+.01
> # pedDat$pop.tot<-round(rowMeans(pedDat[,22:31]))+1
```

Read in the spatial file of New York City census tracts, and plot it. (fig 1)

```
> nyc <- readShapePoly("~/nycTracts10.shp")
> plot(nyc)
```

Figure 1: All NYC census tracts present in 2000 and 2010.

Index the map file to the census tract data file to restrict to tracts with valid population data entries. This removes some census tracts assigned to objects like empty islands and costal areas by matching only to areas with valid population numbers as determined by the US Census.

```
> valid<-nyc$GEOID10 %in% pedDat$tract
> nyc<-nyc[valid,]
> plot(nyc)
```

Analyses will continue to be unstable and distorted by outlier census tracts that have very small populations. The CAR smoothing term will account for some of this instability, but it

Figure 2: NYC census tracts present in 2000 and 2010 with invalid entries removed.

is necessary to identify census tracts that are so unlike the rest of the surrounding area that they are truly outliers because they are geographies like cemeteries, beaches, and train yards that artifactually inherited some small number of population when carved up into census tract maps. Since some of these tracts had pedestrian injuries, it causes rates to explode in a way that cannot be accounted for by spatial smoothing.

Address this by identifying and exploring tracts that have more injuries than population (i.e. greater than 100% raw injury rate). I used the policy map web site to lok up the outlier census tracts.

```
> pedDat$rate<-pedDat$allAges.allHrs.tot/pedDat$pop.tot*100
> summary(pedDat$rate[!pedDat$rate>100])
> nrow(pedDat)
> length(pedDat$tract[pedDat$rate>100])
>         # 24 outliers (out of total 1929 tracts)
>
> # map and list
> outliers<-pedDat$tract[pedDat$rate>100]
> nyc.outliers<-nyc$GEOID10 %in% outliers
> nyc.out<-nyc[nyc.outliers,]
> outliers
> plot(nyc.out)
```

The following 19 tracts represent parks and cemeteries: [4] "36005002400" (Sound View Park, Bronx), "36005017100" (Claremont Park, Bronx), "36005043500" (Van Cortlandt Park, Bronx), "36047008600" (Sunset Park, Brooklyn), "36047015400" (Dyker Beach Golf Course, Brooklyn), "36047017500" (Greenwood Cemetery, Brooklyn), "36047017700" (Prospect Park, Brooklyn), "36047066600" (Floyd Bennett Field, Brooklyn), "36047085200" (Holy Cross Cemetary, Brooklyn), "36047096000" ((Conrail) Railroad Tracks, Brooklyn), "36047118000" (Cypress Hills/Mt. Hope Cemetery, Highland Park, Brooklyn), "36061014300" (Central Park, Manhattan), "36061031100" (Highbridge Park, Manhattan), "36081017100" (Sunnyside Railroad Yards, Queens), "36081022900" (Calvery Cemetery, Queens), "36081033100" (La-Guardia Airport), "36081056100" (Mt. Carmel/Mt. Lebanon/Evergreen Cemetery, Queens), "36081121100" (Kissena Park, Queens), "36081024600" (LIRR yards near York College, Queens), "36081107202" (Marsh surrounding Broad Channel, Queens), "36085015400" (Oakwood Beach, Staten Island).

Remove parks, cemeteries and rail yards from the map file.

```
> dele <- c("36005002400", "36005017100", "36005043500", "36047008600",
+ "36047015400", "36047017500", "36047017700", "36047066600",
+ "36047085200", "36047096000", "36047118000", "36061014300",
+ "36061031100", "36081022900", "36081017100", "36081033100",
+ "36081056100", "36081121100", "36081024600", "36081107202",
+ "36085015400")
> pedDat.out<-pedDat[pedDat$tract %in% dele,]
> sum(pedDat$allAges.allHrs.tot)
> sum(pedDat.out$allAges.allHrs.tot) # 1000 of 140835 injuries
> sum(pedDat.out$allAges.allHrs.tot)/sum(pedDat$allAges.allHrs.tot)*100
>      # 0.71% of all injuries
>
> pedDat<-pedDat[!pedDat$tract %in% dele,]
> # re-adjust the map object
> nrow(pedDat) # 1908 census tracts
> valid<-nyc$GEOID10 %in% pedDat$tract
> nyc<-nyc[valid,]
> plot(nyc)
```

There are three census tracts that represent highly trafficked transient/tourist areas with very small underlying populations: "36061009400" (Grand Central Area), "36061010900" (Penn Station Area), "36061011300" (Times Square, Manhattan).

These areas represent an appreciable number of pedestrian injuries and need to be addressed in a way that other than simply removing them. There area a number of possible approaches, e.g. median substitution based on Manhattan census tracts. I chose instead what seems a more informed approach based on hotel capacity in the area. There were approximately

[4] In some cases, the tract boundaries include roads, e.g. a block or two of the southern or eastbound lanes of Queens Boulevard are included in the census tact for Calvary Cemetery in Queens. The most precise way of dealing with this is to re-geocode any injury on those lanes, but this is technically unfeasible for this analysis.

82,000 hotel rooms in New York City during the mid point of the study period. Assuming these areas account for (on the conservative side) 30% or 25,000 hotel rooms, and average 2 occupants per hotel room, then we can substitute 50,000/3 = 16,000 people in each area at any given time, putting them at the high end of the population spectrum for census tracts in New York City.

```
> tourist<-c("36061009400", "36061010900","36061011300")
> pedDat$pop.tot[pedDat$tract %in% tourist]<-16000
```

Plot the NYC census tract map with deleted areas and up-populated tourist areas highlighted.

```
> plot(nyc)
> plot(nyc.out, col="green", add=TRUE)
> nyc.tour<-nyc$GEOID10 %in% tourist
> plot(nyc[nyc.tour,], col="red", add=TRUE)
```

Figure 3: NYC census tracts with deleted parks (in green) and up-populated tourist areas (red)

1.1 Create the Adjacency Matrix Graph

Create the adjacency matrix from the NYC census tract map object read into the workspace (see above) and save it to file for later use with the CAR model. This requires some close

attention to detail. Initial attempts to use an adjacency matrix created with default files and setting returned INLA warnings about disconnected subgraphs and INLA would not compute a DIC measure because isolated geographic areas with 0 neighbors returned NaN results. [5]

First, create the adjacency matrix "nb" object from the map file using *spdep::poly2nb()*. Looking at this object reveals that there are 2 regions with no links that were causing problems. The *spdep::edit.nb()* utility can be used to manually edit the nb object. It did not, though, save changes. This is recognized behavior, and online advice recommended manually editing the object using info from the *edit.nb()* session. This worked.

```
> zzz <- poly2nb(nyc)
> zzz # 3 regions no links: 452 1852 1862
> # (numbers refer to the map, not the nb list object)
> which(card(zzz)==0)
> # get ids for areas with no links indexed to nb object: 380 1625 1635
> nnb1<-edit.nb(zzz, polys=nyc) # interactive edit nb object
> nnb1 # not corrected
> # manually edit
>
> zzz[[1623]]<-as.integer(sort(c(zzz[[1623]], 1626)))
> zzz[[1626]]<-as.integer(sort(c(zzz[[1626]], 1623)))
> zzz[[1354]]<-as.integer(sort(c(zzz[[1354]], 1382)))
> zzz[[1382]]<-as.integer(sort(c(zzz[[1382]], 1354)))
> zzz[[1355]]<-as.integer(sort(c(zzz[[1355]], 1382)))
> zzz[[1382]]<-as.integer(sort(c(zzz[[1382]], 1355)))
> zzz[[1349]]<-as.integer(sort(c(zzz[[1349]], 1351)))
> zzz[[1351]]<-as.integer(sort(c(zzz[[1351]], 1349)))
> zzz[[1223]]<-as.integer(sort(c(zzz[[1223]], 1635)))
> zzz[[1635]]<-as.integer(1223)
> zzz[[1353]]<-as.integer(sort(c(zzz[[1353]], 1635)))
> zzz[[1635]]<-as.integer(sort(c(zzz[[1635]], 1353)))
> zzz[[19]]<-as.integer(sort(c(zzz[[19]], 1625)))
> zzz[[1625]]<-as.integer(19)
```

[5] The model would run with the warning "The graph for the model besag has 5 connected components!!! Model is revised accordingly." I ran the debug utility for graphs in INLA (*inla.debug.graph(nyc.adj)*) which did not return any immediate errors. There was some useful information about the issue in the help file *inla.doc("besag")*, and Havard Rue posted a helpful reply to a similar question here In summary, "connected components" refers to disconnected subgraphs (odd terminology...), and there were five such disconnected graphs in the NYC map file object. I (mistakenly) assumed these were were the 5 boros of NYC and so logical and acceptable. But, it turns out the number 5 was simply a misleading coincidence. The default setting for INLA is to "interpret this as a sum-to-zero constraint for each subgraph, instead of a sum-to-zero constraint for the union of the graphs" . You can over-ride that behavior with the option *f(..., adjust.for.con.comp = FALSE)* which I (again mistakenly) did in initial runs of these analyses thinking it was appropriate for the 5 separate but related boros of NYC. The results though did not seem make sense. Also, the problem of not being able to generate a valid overall model DIC concerned me. Addressing the issues in the adjacency matrix "nb" object as described in the text solved both these problems.

```
> zzz[[1624]]<-as.integer(sort(c(zzz[[1624]], 1625)))
> zzz[[1625]]<-as.integer(sort(c(zzz[[1625]], 1624)))
> zzz[[162]]<-as.integer(sort(c(zzz[[162]], 217)))
> zzz[[217]]<-as.integer(sort(c(zzz[[217]], 162)))
> zzz[[365]]<-as.integer(sort(c(zzz[[365]], 380)))
> zzz[[380]]<-as.integer(365)
> zzz[[380]]<-as.integer(sort(c(zzz[[380]], 602)))
> zzz[[602]]<-as.integer(sort(c(zzz[[602]], 380)))
> zzz # no unlinked regions
```

Here is a plot of the adjusted adjacency matrix.

Figure 4: NYC census tracts adjacency graph

After correcting the nb object, use *inla::nb2INLA()* to get the nb object into the correct format for INLA, and save the resulting object for later use in models. (Note, I manually moved the object "nyc.graph") into the srts inla directory I've been working from, and set up a path to it saved as an object named "nyc.adj"

```
> nb2INLA("nyc.graph", zzz)
> nyc.adj <- paste("~/srtsINLA","/nyc.graph",sep="")
> file.show(nyc.adj)
```

Here's what the file looks like:

Order the data to match the spatial dataframe, and add a sequential area ID variable for

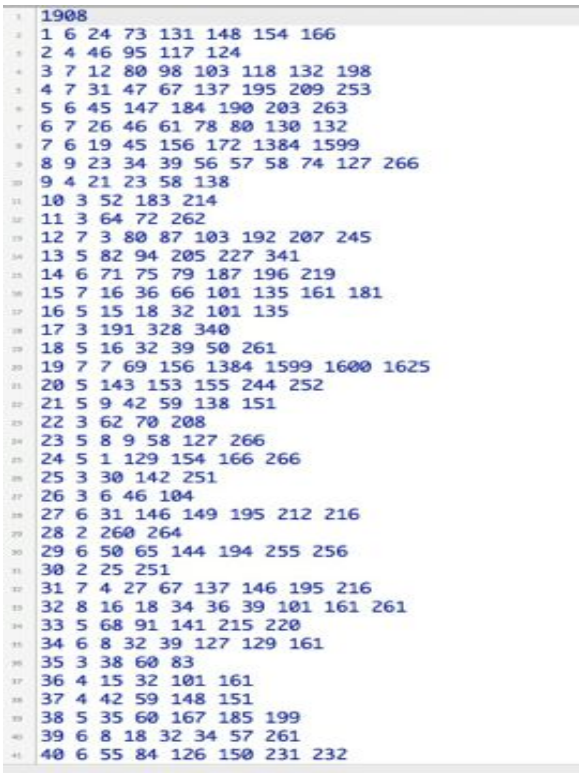


Figure 5: NYC census tracts adjacency file

the model statement.

```
> nycDat <- attr(nyc, "data")
> order <- match(nycDat$GEOID10,pedDat[,1])
> pedDat<- pedDat[order,]
> pedDat$ID.area<-seq(1,nrow(pedDat))
```

1.2 Quick Plot of Time Trend

These initial descriptive stats were taken from some of the initial analyses for the Safe Routes to School project and are not reproducible here, but simply presented for the sake of completeness.

Here is a plot for all-age pedestrian injury decline over the study period.(Figure 6) Injury rates declined 16.2% over the study period, from 23.7 per 10,000 to 16.2 per 10,000

```
> Year <- c("2001", "2002", "2003", "2004", "2005", "2006", "2007",
+ "2008", "2009", "2010")
> Count <- c(18961, 18983, 18666, 16558, 16839, 15318, 15560, 15735,
+         15214, 16226)
> Population <- seq(from=8008278, to=8175133, length.out=10)
> df1<-data.frame(c(Year, Count,as.character(Population)))
```

```
> p<-qplot(Year, Count/Population*10000, data=df1, geom="point",
+ ylab="Pedestrian Injury Rate per 10,000 Population",ylim=c(0,30))
> p<-p+geom_smooth(aes(group=1))
> p<-p+ opts(panel.background = theme_rect(colour = NA))
> print(p)
> rate<-Count/Population*10000
> (rate[1]-rate[10])/rate[1]*100
>
```

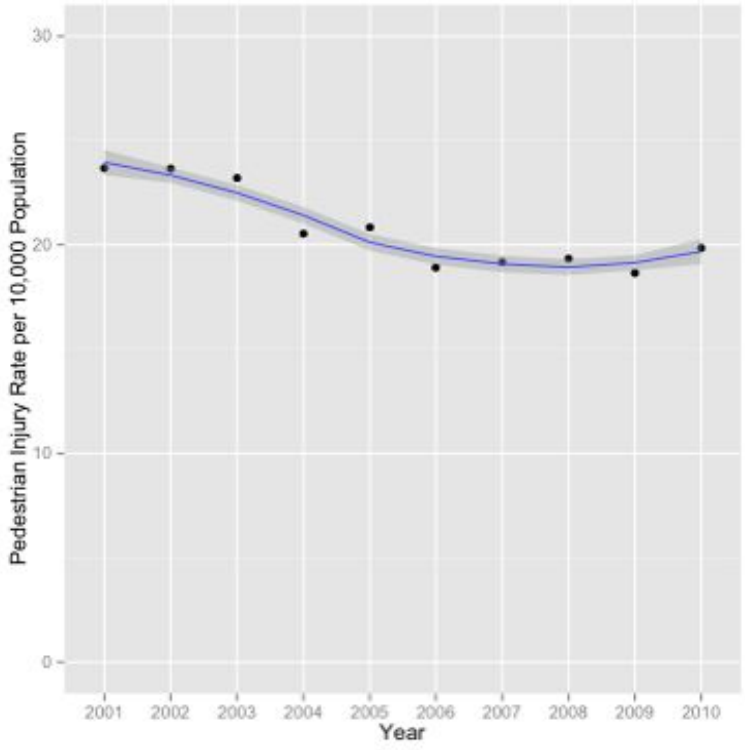


Figure 6: Number of Pedestrian Injuries, All Ages, New York City, 2001 to 2010.

2 Cross-Sectional Models

2.1 Frailty Model

As a baseline against which to measure more informative models, run a simple random effects (spatially unstructured heterogeneity) model.

$y_i = \alpha + \upsilon_i$

```
> formulaUH <- allAges.allHrs.tot~ f(ID.area, model = "iid") # specify model
> resultUH <- inla(formulaUH,family="poisson", # run inla
+ data=pedDat, control.compute=list(dic=TRUE,cpo=TRUE),E=pop.tot)
```

Review the results.

```
> summary(resultUH)
> exp(resultUH$summary.fixed)
> (exp(resultUH$summary.fixed)*10000)/10
> (((sum(pedDat$allAges.allHrs.tot))/8300000))/10*10000
```

The DIC for this baseline model is 14293.30 with 1822.78 effective parameters. The fixed effects for this model consist only of the intercept, which has a mean of -4.3627 with a sd of 0.0241 (95% CrI -4.4101, -4.3154). This exponentiates to a mean of 0.01274377, s.d. 1.024422 (95% CI 0.01215364, 0.01336109), and translates to a yearly rate of 12.7 pedestrian injuries per 10,0000 population (95% CI, 12.2, 13.4). [6] The DIC for this model was 14446.97, with 1859.61 effective number of parameters.

In this first model, we are interested in the random effect term. Those results are stored in the "region" part of "summary.random" in the named list object created from the INLA run. We can extract and examine the mean random effect term for each county. Recall, this is the random variation, on the log scale, around the mean or intercept value of the number of pedestrian injuries in a New York City census tract. A plot of the density distribution for the random effect term appears reasonably normally distributed and symmetric about zero. (Fig **??**)

To map the random effect results, we first add the random effect results to the *pedDat* dataframe and create *cuts* based on 20% quantiles to plot categories of outcomes.

```
> re1<-resultUH$summary.random$ID.area[,2]
> plot(density(re1)) # plot density random effects
> # add random effects results to dataframe
> pedDat$UH<-re1
> # create cuts
> quantile(pedDat$UH,probs = seq(0, 1, by = 0.20))
> cuts <- c(-3.7551580, -0.7665932, -0.2441329,  0.1858292,  0.7827655,
+         4.3013500)
> pedDat$UH.cut<-cut(pedDat$UH,breaks=cuts,include.lowest=TRUE)
```

To use *spplot()* to map the results, we use the census tract FIPS codes to merge the data frame to the *nycDat* data frame that was extracted from the map object and replace the

[6] This is an underestimate compared to the raw numbers. If you simply calculate the yearly rate using a recent online estimate of the NYC population you get a rate of 16.8. This is due to editing out some of the injuries in low population census tracts. Also, some of the "information" in these numbers is being shifted to the random effect term.

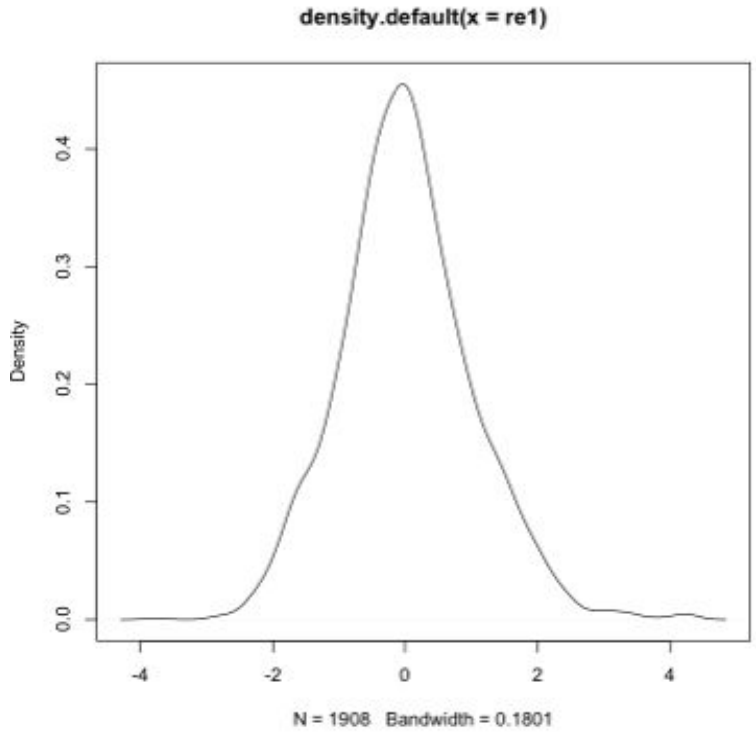


Figure 7: frailty model random effects term density

data slot of the map object with the merged datafame. It results, though, in an image that distorts the axes and makes it difficult to discern patterns. (Fig 8)

```
> #merge dataframes, save to data slot of map
> attr(nyc,"data") <- merge(nycDat,pedDat,by="tract")
> # map
> spplot(nyc, "UH.cut", col.regions= grey.colors(5),main="")
```

Instead use *ggplot2*. First use the *fortify()* method to turn the map into a data frame that can be plotted with ggplot. [7] Then merge the pedestrian injury data frame to the map data frame, and order the census tracts so they will map correctly. We then build up a map layer by layer, using *RColorBrewer* for the fill.

```
> # library(ggplot2)
> # gpclibPermit()
> nyc.df <- fortify(nyc, region=GEOID10)
> nyc.df <- merge(nyc.df, pedDat, by.x="id", by.y="tract", all=FALSE)
> nyc.df <- nyc.df[order(nyc.df$group, nyc.df$order), ]
> library(RColorBrewer)
```

[7] Fortify is (to me at least) one of the more mysterious functions, but according to Hadley Wickham, in the context of shape files and ggplot, it "melts the polygons into points, tags each point with the id value of the corresponding attribute row, and tags each point with values from the polygon from which the point was derived." Note that it is no longer necessary to enable *gpclibPermit()* to use *fortify()*

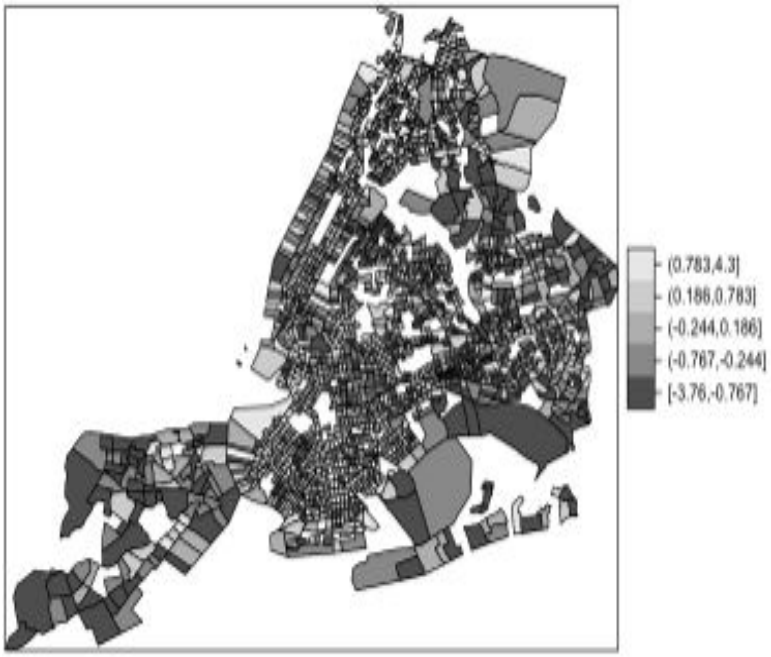
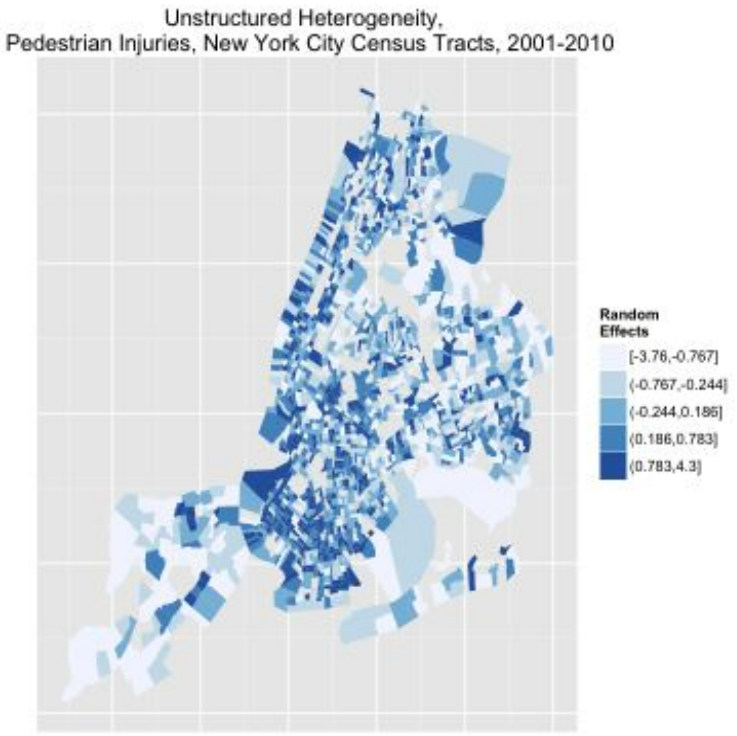


Figure 8: frailty model unstructured heterogeneity (random effects term)

```
> p1<-ggplot(nyc.df, aes(x=long, y=lat))
> p2<-p1+geom_polygon(aes(group=group, fill=UH.cut))
> p3<- p2 + scale_fill_brewer(palette="Blues", name="Random\nEffects")
> p4<- p3+ theme(axis.text.x = element_blank(), axis.text.y = element_blank(),
+ axis.ticks = element_blank()) +
+ theme(panel.background = element_rect(colour = NA)) +
+ xlab("")+ylab("")+
+ ggtitle("Unstructured Heterogeneity, \n Pedestrian Injuries,
+        New York City Census Tracts, 2001-2010")
> print(p4)
> p1<-ggplot(nyc.df[nyc.df$boro=="QN",], aes(x=long, y=lat))
> p2<-p1+geom_polygon(aes(group=group, fill=UH.cut))
> p3<- p2 + scale_fill_brewer(palette="Blues")
```

The map is not perfect. By design, it doesn't include census tracts that were not present in both the 2000 and 2010 census enumerations, or that do not have a population denominator (e.g. industrial sites, parks) so it is inherently incomplete. Census tracts themselves do not behave nicely sometimes, bleeding into adjacent areas (that large blob in south east Queens is in the area of JFK Airport). But it is better than the *spplot()* effort, and adequately illustrates the expected random pattern of the spatially unstructured heterogeneity results. (Fig 2.1)



We can index to restrict the map to a particular borough. Here, for example is Queens (Fig 2.1)

```
> p1<-ggplot(nyc.df[nyc.df$boro=="QN",], aes(x=long, y=lat))
> p2<-p1+geom_polygon(aes(group=group, fill=UH.cut))
> p2 + scale_fill_brewer(palette="Blues")+
+ ggtitle("Unstructured Heterogeneity, \n Pedestrian Injuries,
+ Queens, NY Census Tracts, 2001-2010")
```

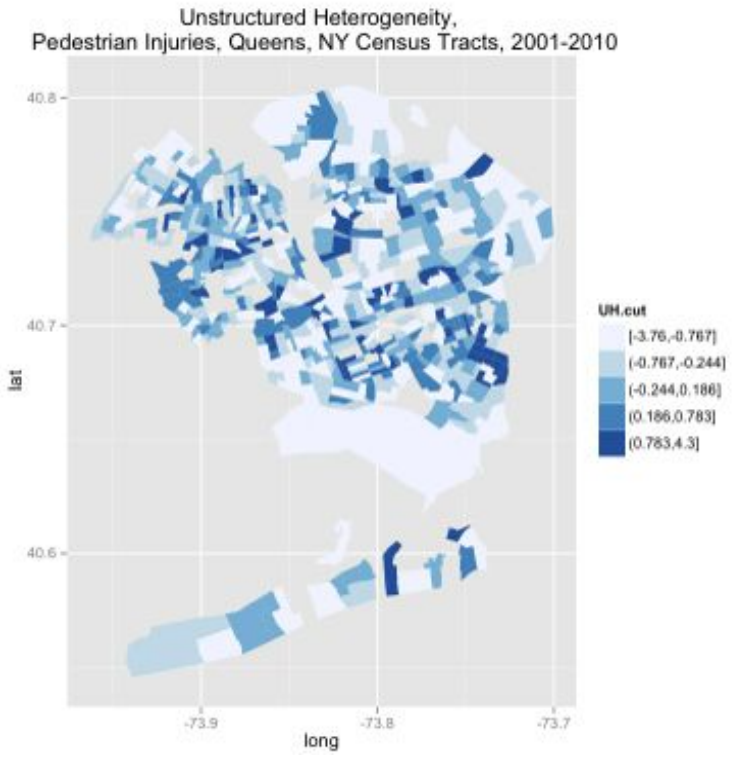
2.2 Convolution Models

The convolution models add a spatially-structured conditional autoregression term (ν) to the spatially-unstructured heterogeneity random effect term (υ) of the frailty model.

$$y_i = \alpha + \upsilon_i + \nu_i$$

Add the CAR term to the INLA model statement by specifying *f(..., model="bym")*

```
> formulaCAR <- allAges.allHrs.tot~ f(ID.area, model="bym", graph=nyc.adj)
> resultCAR <- inla(formulaCAR,family="poisson", # run inla
+ data=pedDat, control.compute=list(dic=TRUE,cpo=TRUE),E=pop.tot)
> summary(resultCAR)
> resultCAR$dic
```



The DIC on the convolution model is 14256.57 with 1761.49 effective parameters, which is an improvement on the baseline UH model. There is only one fixed effect in this model, the intercept, or average risk across all boroughs, which is 12.6 pedestrian injuries per 10,000 census tract population per year (95% CI 12.3, 12.9). The density plot of the UH term looks much like that of the simpler model. (Fig 9) The density plot for the CAR heterogeneity has a bump in the right tail that suggests a possible bimodal or multivariate distribution that might reflect differing patterns across geographic areas, with low and high risk census tracts. (Fig 10) In mapping the CAR results, we can appreciate this spatial structuring of risk, with nearby census tracts demonstrating similar risk. (Fig 2.2)

```
> (exp(resultCAR$summary.fixed))*10000/10
> re<-resultCAR$summary.random$ID.area[1:1908,2]
> plot(density(re)) # plot density random effects
> car<-resultCAR$summary.random$ID.area[1909:3816,2]
> plot(density(car)) # plot density random effects
> # add car results to dataframe
> pedDat$car<-car
> # create cuts
> quantile(pedDat$car,probs = seq(0, 1, by = 0.20))
> cuts <- c(-3.7452966, -0.6086899, -0.2123627,  0.1002341,
+         0.6466806,  3.1982722)
> pedDat$car.cut<-cut(pedDat$car,breaks=cuts,
+         include.lowest=TRUE, include.highest=TRUE)
> # library(ggplot2)
```

```
> # gpclibPermit()
> nyc.df1 <- fortify(nyc, region=GEOID10)
> nyc.df <- merge(nyc.df1, pedDat, by.x="id", by.y="tract", all=FALSE)
> nyc.df <- nyc.df[order(nyc.df$group, nyc.df$order), ]
> # library(RColorBrewer)
> p1<-ggplot(nyc.df, aes(x=long, y=lat))
> p2<-p1+geom_polygon(aes(group=group, fill=car.cut))
> p3<- p2 + scale_fill_brewer(palette="Blues", name="Spatial\nEffects")
> p4<- p3+ theme(axis.text.x = element_blank(), axis.text.y = element_blank(),
+ axis.ticks = element_blank()) +
+ theme(panel.background = element_rect(colour = NA)) +
+ xlab("")+ylab("")+
+ ggtitle("Spatially Structured (CAR) Heterogeneity, \n Pedestrian Injuries,
+ New York City Census Tracts, 2001-2010")
> print(p4)
```

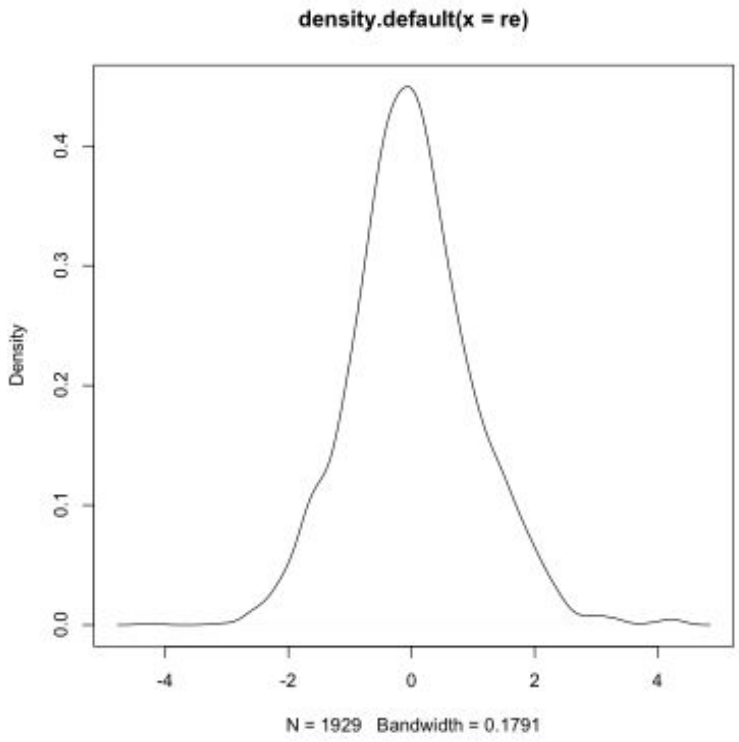


Figure 9: convolution model random effects term density

Calculate fitted values ($\theta = \alpha + \upsilon + \nu$), spatial risk ($\zeta = \upsilon + \nu$) and spatial exceedence ($\Pr[\zeta_i > 1]$).

```
> #risk (theta = alpha + upsilon + nu)
> CARfit <- resultCAR$summary.fitted.values[,1]
> #spatial risk (zeta = upsilon + nu)
> CARmarginals <- resultCAR$marginals.random$ID.area[1:1908]
```

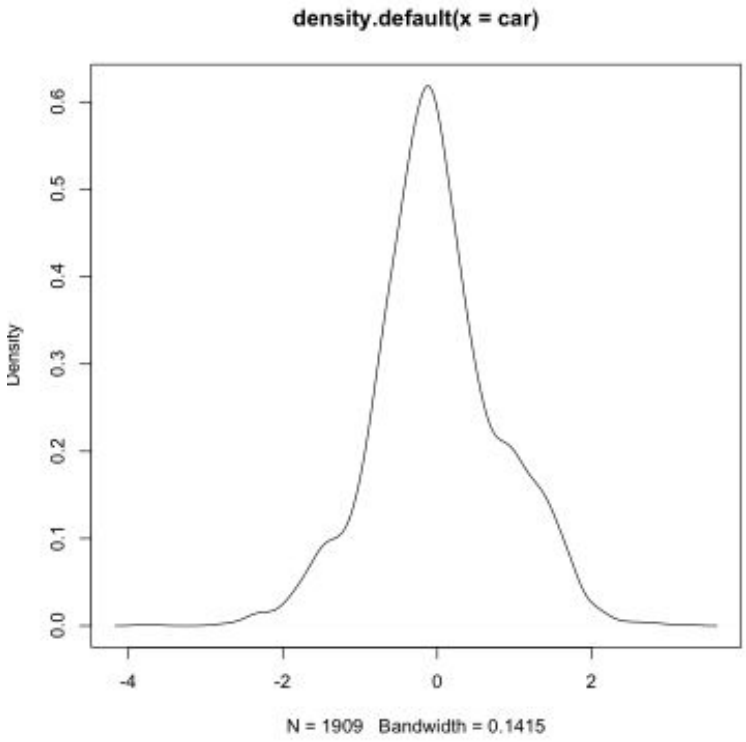
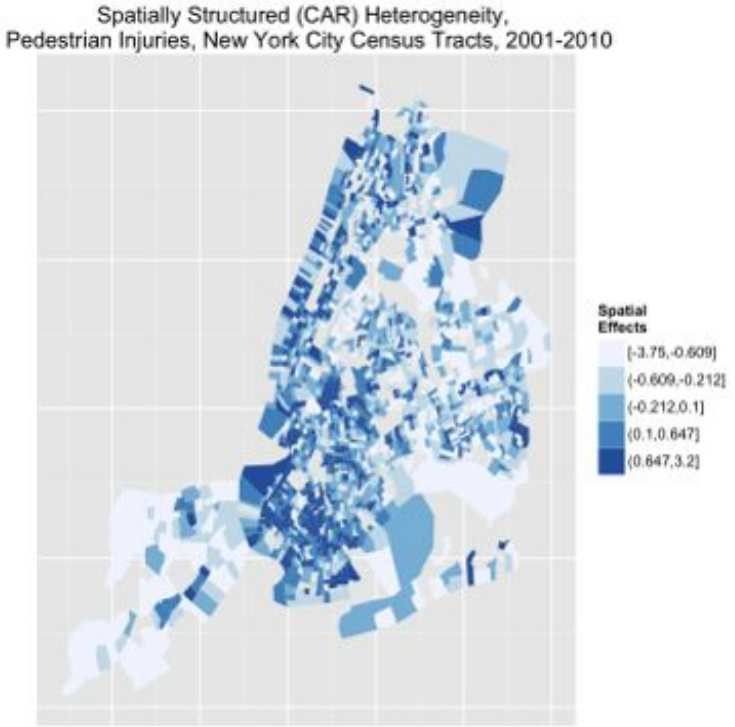


Figure 10: convolution model CAR term density

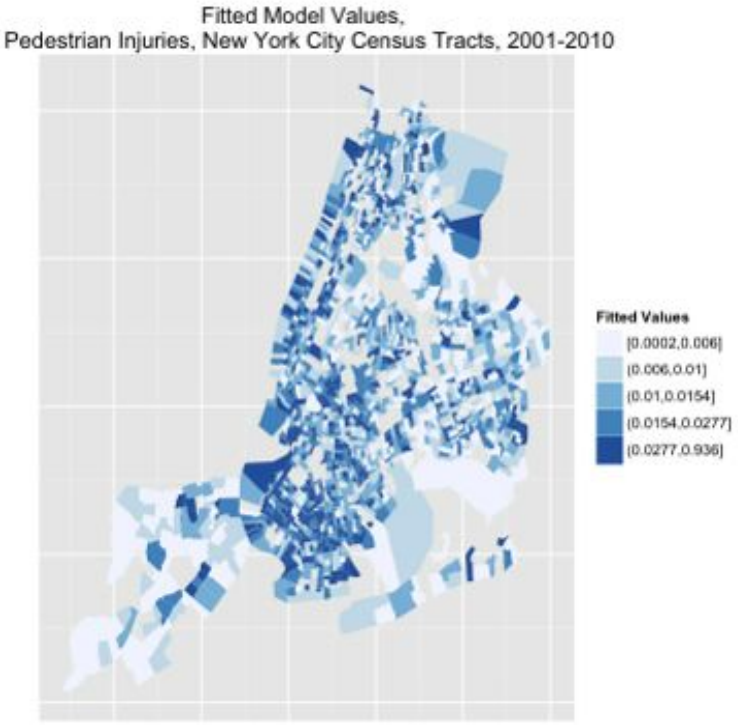


```
> CARzeta <- lapply(CARmarginals,function(x)inla.emarginal(exp,x)) # exponentiate
> # exceedence probability
> a=0
> CARexceed<-lapply(resultCAR$marginals.random$ID.area[1:1908], function(X){
+   1-inla.pmarginal(a, X)
+ })
```

Map these results.

```
> pedDat$fit<-CARfit
> quantile(pedDat$fit,probs = seq(0, 1, by = 0.20))
> cut.fit<-round(c(0.0002154018, 0.0060402579, 0.0099928608,
+         0.0154458155, 0.0276508520, 0.9359724944 ),4)
> pedDat$fit.cut<-cut(pedDat$fit,breaks=cut.fit,include.lowest=TRUE)
> summary(pedDat$fit.cut)
> pedDat$risk<-unlist(CARzeta)
> quantile(pedDat$risk, probs = seq(0, 1, by = 0.20))
> cut.risk<-round(c(0.01708582,  0.47922798,  0.79279746,
+         1.22545213,  2.19368312, 74.25152478),2)
> pedDat$risk.cut<-cut(pedDat$risk,breaks=cut.risk,include.lowest=TRUE)
> summary(pedDat$risk.cut)
> pedDat$exceed<-unlist(CARexceed)
> quantile(pedDat$exceed,probs = seq(0, 1, by = 0.20))
> cut.exceed<-c(0, .8, .99, 1)
> pedDat$exceed.cut<-cut(pedDat$exceed, breaks=cut.exceed, include.lowest=TRUE)
> summary(pedDat$exceed.cut)
> # nyc.df1 <- fortify(nyc, region=GEOID10)
> nyc.df <- merge(nyc.df1, pedDat, by.x="id", by.y="tract", all=FALSE)
> nyc.df <- nyc.df[order(nyc.df$group, nyc.df$order), ]
> p1<-ggplot(nyc.df, aes(x=long, y=lat))
> p2<-p1+geom_polygon(aes(group=group, fill=fit.cut))
> p3<- p2 + scale_fill_brewer(palette="Blues", name="Fitted Values")
> p4<- p3+ theme(axis.text.x = element_blank(), axis.text.y = element_blank(),
+ axis.ticks = element_blank()) +
+ theme(panel.background = element_rect(colour = NA)) +
+ xlab("")+ylab("")+
+ ggtitle("Fitted Model Values, \n Pedestrian Injuries,
+ New York City Census Tracts, 2001-2010")
> print(p4)
> p1<-ggplot(nyc.df, aes(x=long, y=lat))
> p2<-p1+geom_polygon(aes(group=group, fill=risk.cut))
> p3<- p2 + scale_fill_brewer(palette="Blues", name="Spatial\nRisk")
> p4<- p3+ theme(axis.text.x = element_blank(), axis.text.y = element_blank(),
+ axis.ticks = element_blank()) +
+ theme(panel.background = element_rect(colour = NA)) +
+ xlab("")+ylab("")+
```

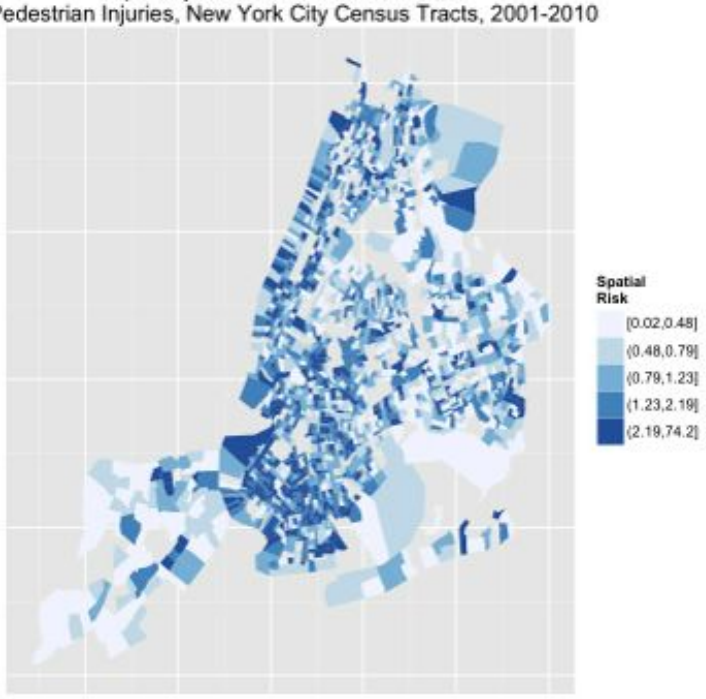
```
+ ggtitle("Spatially Structured Risk Estimates, \n Pedestrian Injuries,
+ New York City Census Tracts, 2001-2010")
> print(p4)
> p1<-ggplot(nyc.df, aes(x=long, y=lat))
> p2<-p1+geom_polygon(aes(group=group, fill=exceed.cut))
> p3<- p2 + scale_fill_brewer(palette="Blues", name="Exceedence")
> p4<- p3+ theme(axis.text.x = element_blank(), axis.text.y = element_blank(),
+ axis.ticks = element_blank()) +
+ theme(panel.background = element_rect(colour = NA)) +
+ xlab("")+ylab("")+
+ ggtitle("Probability Exceedence, \n Pedestrian Injuries,
+ New York City Census Tracts, 2001-2010")
> print(p4)
```



Increase the risk threshold to look at the probability of exceeding a relative risk of 2 (Fig 2.2)

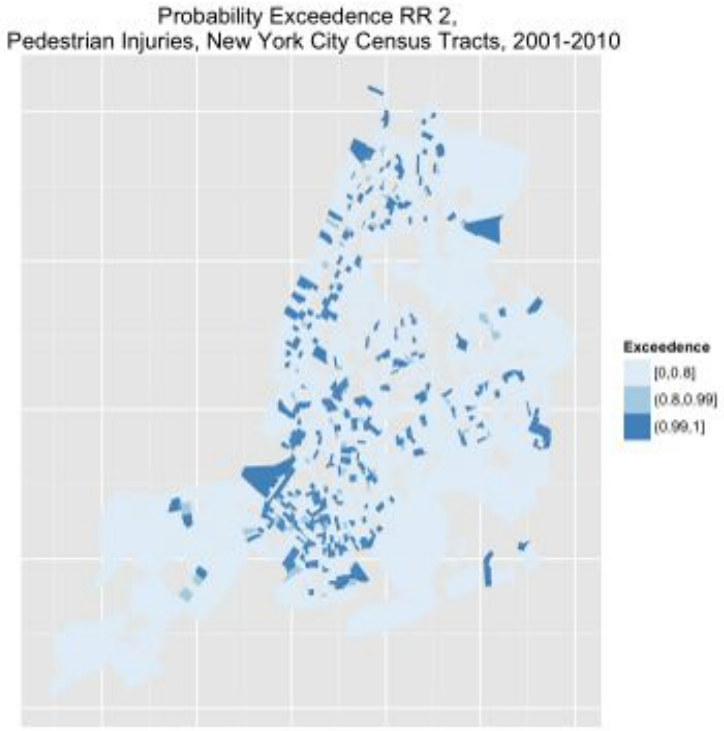
```
> a=0.6931472 # on unexponentiated scale, log(2)
> CARexceed2<-lapply(resultCAR$marginals.random$ID.area[1:1908], function(X){
+   1-inla.pmarginal(a, X)
+ })
> pedDat$exceed2<-unlist(CARexceed2)
> quantile(pedDat$exceed2,probs = seq(0, 1, by = 0.20))
> cut.exceed2<-c(0, .8, .99, 1)
> pedDat$exceed2.cut<-cut(pedDat$exceed2, breaks=cut.exceed2, include.lowest=TRUE)
```

Spatially Structured Risk Estimates,
Pedestrian Injuries, New York City Census Tracts, 2001-2010



Probability Exceedence,
Pedestrian Injuries, New York City Census Tracts, 2001-2010

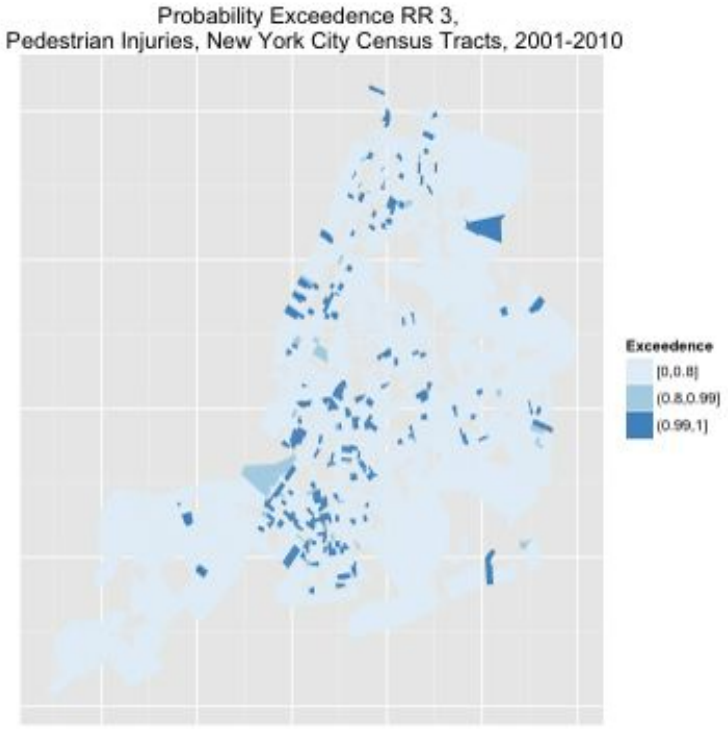
```
> summary(pedDat$exceed2.cut)
> # nyc.df1 <- fortify(nyc, region=GEOID10)
> nyc.df <- merge(nyc.df1, pedDat, by.x="id", by.y="tract", all=FALSE)
> nyc.df <- nyc.df[order(nyc.df$group, nyc.df$order), ]
> p1<-ggplot(nyc.df, aes(x=long, y=lat))
> p2<-p1+geom_polygon(aes(group=group, fill=exceed2.cut))
> p3<- p2 + scale_fill_brewer(palette="Blues", name="Exceedence")
> p4<- p3+ theme(axis.text.x = element_blank(), axis.text.y = element_blank(),
+ axis.ticks = element_blank()) +
+ theme(panel.background = element_rect(colour = NA)) +
+ xlab("")+ylab("")+
+ ggtitle("Probability Exceedence RR 2, \n Pedestrian Injuries,
+ New York City Census Tracts, 2001-2010")
> print(p4)
```



Or exceeding relative risks of 3... (Fig 2.2)

```
> a=1.098612 # on unexponentiated scale, log(3)
> CARexceed3<-lapply(resultCAR$marginals.random$ID.area[1:1908], function(X){
+   1-inla.pmarginal(a, X)
+ })
> pedDat$exceed3<-unlist(CARexceed3)
> quantile(pedDat$exceed3,probs = seq(0, 1, by = 0.20))
> cut.exceed3<-c(0, .8, .99, 1)
> pedDat$exceed3.cut<-cut(pedDat$exceed3, breaks=cut.exceed3, include.lowest=TRUE)
```

```
> summary(pedDat$exceed3.cut)
> # nyc.df1 <- fortify(nyc, region=GEOID10)
> nyc.df <- merge(nyc.df1, pedDat, by.x="id", by.y="tract", all=FALSE)
> nyc.df <- nyc.df[order(nyc.df$group, nyc.df$order), ]
> p1<-ggplot(nyc.df, aes(x=long, y=lat))
> p2<-p1+geom_polygon(aes(group=group, fill=exceed3.cut))
> p3<- p2 + scale_fill_brewer(palette="Blues", name="Exceedence")
> p4<- p3+ theme(axis.text.x = element_blank(), axis.text.y = element_blank(),
+ axis.ticks = element_blank()) +
+ theme(panel.background = element_rect(colour = NA)) +
+ xlab("")+ylab("")+
+ ggtitle("Probability Exceedence RR 3, \n Pedestrian Injuries,
+ New York City Census Tracts, 2001-2010")
> print(p4)
```



Calculate the proportion of variance explained by the spatially structured CAR component (ν) of ζ [8]

The calculation involves creating an empty matrix, with rows equal to number of regions, with 1000 columns into which we extract 1000 observations from the marginal distribution of the CAR term (ν), and from which we calculate the empirical variance. Then extract values

[8]NB. In conversation, Andrew Lawson cautioned against measures like this because CAR and UH are incompletely identified. Even Blangiardo, from whom this code is adapted, says the UH and CAR variances are not directly comparable. But, the result can give an indication of the relative contribution of each component of the total spatial heterogeneity.

for random effects (UH) term and calculate the proportion of total heterogeneity accounted for by the spatially structured heterogeneity. We see in the result that place accounts for for about 76.5% of the total heterogeneity.

```
> mat.marg <- matrix(NA, nrow=1908, ncol=1000)
> m<-resultCAR$marginals.random$ID.area
> for (i in 1:1908){
+   u<-m[[1908+i]]
+   s<-inla.rmarginal(1000, u)
+   mat.marg[i,]<-s}
> var.RRspatial<-mean(apply(mat.marg, 2, sd))^2
> var.RRhet<-inla.emarginal(function(x) 1/x,
+         resultCAR$marginals.hyper$"Precision for ID.area (iid component)")
> var.RRspatial/(var.RRspatial+var.RRhet)
```

2.3 Covariate Models

Add three types of covariates: social, economic, and traffic-related. the social variable is an index based on Peter Congdon's social fragmentation index [9] It combines 4 variables extracted from US census variables: the proportion of total housing units in a census tract that are not owner occupied, the proportion of vacant housing units in a census tract, the proportion of individuals in a census tract living alone, and the proportion of housing units in a census tract into which someone recently moved. Based on Census definitions, a "recent" move is defined as anytime in the previous 9 years (since the last decennial census). As per the Congdon paper, the variables are standardized, and added with equal weight. The resulting variable is normally distributed with mean zero and 95% quantiles -2.463311 and 2.205669. The economic measure is simply the census tract median household income for the past 12 months (in 2012 inflation-adjusted dollars). The traffic-related variables come from Zev Ross as part of this work with the New York City Department of Health and Mental Hygeine. They are road density (road length (KM) per square kilometer), traffic density (vehicle kilometers traveled per day per square kilometer), average speed (in miles per hour), and signal traffic density (traffic signals per square kilometer).

```
> # covariates:
> # from R US census
> # H0010001 Total Housing units
> # H0180002  Owner occupied
> # H0180019  Living alone
> # H0210001  Vacant housing units
> #
> # Downloaded from US census
```

[9] see: Peter Congdon. Suicide and Parasuicide in London: A Small-area Study. Urban Studies, Vol. 33, No. 1, 137-158, 1996 and Roman Pabayo, Beth E. Molnar, Nancy Street, and Ichiro Kawachi. The relationship between social fragmentation and sleep among adolescents living in Boston, Massachusetts. Journal of Public Health pp 1-12 J Public Health (2014) doi: 10.1093/pubmed/fdu001

```
> # HC01_VC72 Estimate; YEAR HOUSEHOLDER MOVED INTO UNIT
>               #- Moved in 2010 or later
> # HD01_VD01  Estimate; Median household income in the
>              #past 12 months (in 2012 inflation-adjusted dollars)
> #
> # from Zev Rosss files
> # rddenFULL Road Density (road length (KM) per square kilometer), all roads
> # trafDenFUL  Traffic Density (vehicle kilometers traveled
>           # per day per square kilometer), all roads
> # avgSpd        Average Speed (miles per hour)
> # sigDen        Traffic Signal Density (traffic signals per sqaure kilometer)
>
>
>
> # library(UScensus2010) # helper functions, like install.tract()
> # help(package=UScensus2010)
> # install.tract("osx") # one time only
> library(UScensus2010tract)
> data(new_york.tract10)
> # help(package=UScensus2010tract)
> # names(new_york.tract10)
>
> # extract housing variables for social fragmentation index from
>        #UScensus2010tract spatial polygon file
> housing<-attr(new_york.tract10, "data")
> # nrow(housing) # 4919 census tracts in NYS
> housing<-subset(housing, select=c(fips,H0010001,H0180002,H0180019,H0210001))
> names(housing)<-c("tract", "totHousing", "ownerHousing",
+           "aloneHousing", "vacantHousing")
> housing<-housing[housing$tract %in% pedDat$tract,]
> nrow(housing)
> # extract recent movers from downloaded US census file
> recent<-read.csv("~/housingNYStracts.csv",header=T, stringsAsFactors=F)
> recent<-subset(recent, select=c(GEO.id2, HC01_VC72))
> names(recent)<-c("tract", "recentMove")
> # merge housing and recent movers files
> housing<-merge(housing, recent, by="tract", all.x=T)
> nrow(housing)
> head(housing)
> names(housing)
> housing$recentMove<-as.numeric(housing$recentMove)
> # look at observation for missing recent move data
> housing[is.na(housing$recentMove),]
> # set missing housing data to zero
> housing$recentMove[is.na(housing$recentMove)]<-0
```

```
> # calculate proportions based on total housing units
> # avoid division by zero
> housing$owner<-housing$ownerHousing/(housing$totHousing+.1)
> housing$alone<-housing$aloneHousing/(housing$totHousing+.1)
> housing$vacant<-housing$vacantHousing/(housing$totHousing+.1)
> housing$notOwner<-1-housing$owner
> housing$recent<-housing$recentMove/(housing$totHousing+.1)
> # standardize proportions
> housing$aloneST<-
+ (housing$alone-mean(housing$alone, na.rm=T))/sd(housing$alone, na.rm=T)
> summary(housing$aloneST)
> housing$vacantST<-
+ (housing$vacant-mean(housing$vacant, na.rm=T))/sd(housing$vacant, na.rm=T)
> summary(housing$vacantST)
> housing$notOwnerST<-
+ (housing$notOwner-mean(housing$notOwner, na.rm=T))/sd(housing$notOwner, na.rm=T)
> summary(housing$notOwnerST)
> housing$recentST<-
+ (housing$recent-mean(housing$recent, na.rm=T))/sd(housing$recent, na.rm=T)
> summary(housing$recentST)
> # add standardized measures into single index
> housing$index<-housing$aloneST+housing$vacantST
>                   +housing$notOwnerST+housing$recentST
> summary(housing$index)
> # check and adjust for unstable outliers
> housing[housing$index>12,]
> # median substitute 3 unstable outliers
> housing$index[housing$index>12]<-median(housing$index)
> plot(density(housing$index))
> quantile(housing$index, probs=c(0.05,0.95))
>          # 95% of values between -2.463311 and 2.205669
>
> # add the index to the pedestrian data file
> index<-subset(housing, select=c(tract, index))
> nrow(pedDat)
> pedDat<-merge(pedDat, index, by="tract")
> # get median household income data
> inc<-read.csv("~/mhiNYStracts_with_ann.csv",header=T, stringsAsFactors=F)
> inc<-subset(inc, select=c(GEO.id2,HD01_VD01))
> names(inc)<-c("tract", "mhi")
> inc$mhi<-as.numeric(inc$mhi)
> summary(inc$mhi) # 111 NAs by coercion
> pedDat<-merge(pedDat, inc, by="tract", all.x=TRUE)
> nrow(pedDat)
> head(pedDat)
```

```
> summary(pedDat$mhi) # 26 NAs (~1.5% of 1908 NYC tracts)
> pedDat$mhi[is.na(pedDat$mhi)]<-median(pedDat$mhi, na.rm=T)
> # get roadway and speed data from Zev files
> zev<-read.csv("~/tract_varsFIN.csv",header=T, stringsAsFactors=F)
> str(zev)
> zev<-subset(zev,select=c(tract10, rddenFULL, trafDenFUL, avgSpd, sigDen))
> names(zev)<-c("tract", "roadDensity", "trafficDensity",
+               "avgSpeed", "signalDensity")
> zev$tract<-as.character(zev$tract)
> pedDat<-merge(pedDat, zev, by="tract", all.x=TRUE)
>
```

Before moving on, look at traffic-related variables. Address missing values in average speed with median substitution. Transform traffic density to standardized units. Create variable for median household income in increments of 1000 dollars, and variable for average speed in increments of 10 miles per hour. (In preliminary analyses these increments are easier to interpret in the models.) Variables were added to and saved as part of the "pedDat" data file.

```
> names(pedDat)
> summary(pedDat$avgSpeed)
> pedDat$avgSpeed[pedDat$avgSpeed==-99999]<-NA # set 37 missing values to NA
> pedDat$avgSpeed[is.na(pedDat$avgSpeed)]<-median(pedDat$avgSpeed, na.rm=T)
> summary(pedDat$trafficDensity)
> plot(density(log(pedDat$trafficDensity)))
> plot(density(log(pedDat$trafficDensity)))
> trafficDensityST<-(pedDat$trafficDensity
+                -mean(pedDat$trafficDensity))/sd(pedDat$trafficDensity)
> summary(trafficDensityST)
> plot(density(trafficDensityST))
> summary(pedDat$signalDensity)
> plot(density(pedDat$signalDensity))
> summary(pedDat$roadDensity)
> plot(density(pedDat$roadDensity))
> pedDat$mhi2<-pedDat$mhi/1000
> pedDat$avgSpeed2<-pedDat$avgSpeed/10
>
```

The first model adds the social fragmentation index to the previous convolution model. The model DIC (14257.68) is about the same as the convolution model, though with fewer effective parameters (1753.68) We see that a single unit increase in social fragmentation is associated with a IDR of 1.19 (95% CrI 1.15, 1.23). Note that the spatial risk (ζ) is now interpreted as the *residual relative risk for each area (compared to the whole of New York City) after social fragmentation is taken into account.*

```
> formulaCOV1 <- allAges.allHrs.tot~ f(ID.area, model="bym", graph=nyc.adj)+index
> resultCOV1 <- inla(formulaCOV1,family="poisson", # run inla
```

```
+ data=pedDat, control.compute=list(dic=TRUE,cpo=TRUE),E=pop.tot)
> summary(resultCOV1)
> # resultCOV1$dic
>
> exp(resultCOV1$summary.fixed)
```

We next look at a model that adds median household income for a census tract as an explanatory variable. Note that MHI is entered in units of thousands of dollars (it is otherwise difficult to see any effect for single dollar changes...) We see a marked improvement in DIC, which is now 14254.13 on 1753.55 effective parameters. This is the single best improvement on model fit seen yet. The effect of social fragmentation remains unchanged at 1.19 (95% CI 1.16, 1.23). There is essentially no effect for an increase of $1000 in median household income (IDR=0.99, 95% CI 0.99, 1.00)

```
> formulaCOV2 <- allAges.allHrs.tot~ f(ID.area, model="bym",
+             graph=nyc.adj)+index+mhi2
> resultCOV2 <- inla(formulaCOV2,family="poisson", # run inla
+ data=pedDat, control.compute=list(dic=TRUE,cpo=TRUE),E=pop.tot)
> summary(resultCOV2)
> # resultCOV2$dic
>
> exp(resultCOV2$summary.fixed)
```

Look at average speed (here in increments of 10 miles per hour). There is an improvement in DIC (14255.69, 1753.53 eff par), but average speed does not add very much explanatory power to the model. Appears that increased speed is associated with a decreased risk of pedestrian injury occurring. (IDR = 0.92, 95% CrI 0.84, 1.00)

```
> formulaCOV3 <- allAges.allHrs.tot~ f(ID.area, model="bym",
+              graph=nyc.adj)+index+mhi2+avgSpeed2
> resultCOV3 <- inla(formulaCOV3,family="poisson", # run inla
+ data=pedDat, control.compute=list(dic=TRUE,cpo=TRUE),E=pop.tot)
> summary(resultCOV3)
> # resultCOV3$dic
>
> exp(resultCOV3$summary.fixed)
```

Omit average speed, and look instead at traffic density. The traffic density variable is entered into the model in standardized units. The model had the best DIC of all the models looked at so far. (14252.44, with 1750.27 effective parameters). Traffic density is an important predictor of pedestrian injury risk (IDR = 1.14, 95% CrI 1.10, 1.18).

This is, I think, the model I will go with for the spatial-temporal analyses.

```
> formulaCOV4 <- allAges.allHrs.tot~ f(ID.area, model="bym",
+            graph=nyc.adj)+index+mhi2+trafficDensityST
> resultCOV4 <- inla(formulaCOV4,family="poisson", # run inla
+ data=pedDat, control.compute=list(dic=TRUE,cpo=TRUE),E=pop.tot)
```

```
> summary(resultCOV4)
> # resultCOV3$dic
>
> exp(resultCOV4$summary.fixed)
```

Putting average speed back into the model with social fragmentation, median household income and traffic density does not improve the DIC and predictive accuracy (DIC=14257.48, Eff Param = 1748.24), but the exponentiated coefficients more clearly illustrate the relative effects of each of the variables:

```
                      mean       sd 0.025quant  0.975quant
(Intercept)      0.02609339 1.122834 0.02078013  0.03274672
index            1.18796549 1.015812 1.15192887  1.22509942
mhi2             0.99704061 1.000958 0.99516755  0.99891441
trafficDensityST 1.19540308 1.021069 1.14744872  1.24531625
avgSpeed2        0.77184253 1.048879 0.70285195  0.84765271
```

```
> formulaCOV5 <- allAges.allHrs.tot~ f(ID.area, model="bym",
+               graph=nyc.adj)+index+mhi2+trafficDensityST+avgSpeed2
> resultCOV5 <- inla(formulaCOV5,family="poisson", # run inla
+ data=pedDat, control.compute=list(dic=TRUE,cpo=TRUE),E=pop.tot)
> summary(resultCOV5)
> exp(resultCOV5$summary.fixed)
```

Holding all the other covariates to zero (which doesn't make a lot of predictive sense, but does illustrate causal associations) for every one unit increase in the social deprivation index there is a 19% increase in pedestrian injury risk (95% CrI 1.16, 1.23), for every one standardized unit increase in traffic density, there is a 20% increase in pedestrian injury risk (95% CrI 1.15, 1.25), and for every 10 mile per hour increase in average traffic speed in a census tract, there is a 33% *decrease* in pedestrian injury risk (95% CrI 0.70, 0.85). Median household income has a small effect, with a 1% decrease in injury risk for every $1,000 increase in median household income (95% CrI 1.00, 0.99).

The decreased injury risk associated with increased average speed makes sense if you think in terms exposure (higher speeds means fewer cars) and pedestrian behavior (pedestrian may be less likely to venture out into traffic if cars are going very quickly). Again, note that the spatial risk (ζ) is now interpreted as the *residual relative risk for each area (compared to the whole of New York City) after social fragmentation, economics, average speed and traffic density are taken into account.*

For completeness sake, look at signal density and road density. Adding signal density to the model decreases DIC (14261.03), but is associated with a slight *increase* in pedestrian injury risk (IDR = 1.01, 95% CrI 1.00, 1.01) which is likely due to its association with road density.

```
> formulaCOV6 <- allAges.allHrs.tot~ f(ID.area, model="bym",
+                graph=nyc.adj)+index+mhi2+signalDensity
> resultCOV6 <- inla(formulaCOV6,family="poisson", # run inla
```

```
+ data=pedDat, control.compute=list(dic=TRUE,cpo=TRUE),E=pop.tot)
> summary(resultCOV6)
> exp(resultCOV6$summary.fixed)
```

The results for road density look a lot like traffic signal density (as, I suppose, they should)

```
> formulaCOV7 <- allAges.allHrs.tot~ f(ID.area, model="bym",
+                graph=nyc.adj)+index+mhi2+roadDensity
> resultCOV7 <- inla(formulaCOV6,family="poisson", # run inla
+ data=pedDat, control.compute=list(dic=TRUE,cpo=TRUE),E=pop.tot)
> summary(resultCOV7)
> exp(resultCOV7$summary.fixed)
>
```

Compare the best Poisson model so far to a zero-inflated Poisson model [10] See that there is a worse DIC

```
> formulaCOVzip <- allAges.allHrs.tot~ f(ID.area, model="bym",
+            graph=nyc.adj)+index+mhi2+trafficDensityST+avgSpeed2
> pedDat<-pedDat[,-50] # getting inla error message about NA
>                       #in the car.cut variable, so drop it for now
>
> resultCOVzip <- inla(formulaCOVzip,family="zeroinflatedpoisson0", # run inla
+ data=pedDat, control.compute=list(dic=TRUE,cpo=TRUE),
+ control.predictor=list(compute=TRUE),E=pop.tot)
> summary(resultCOVzip) # DIC 14345.12, eff par 1742.35
> exp(resultCOVzip$summary.fixed) # no change at all in sd
```

2.4 Exploring the Final Covariate Model

The final or "winning" covariate model based on DIC and informativeness of variables is the convolution model with both unstructured (random effect) and structured (conditional autoregression) spatial terms, and explanatory covariates for social fragmentation (Congdon index), economics (in $1,000 increments of median household income), average speed (in 10 mile per hour increments), and traffic density (in standardized units).

```
> formulaCOV5 <- allAges.allHrs.tot~ f(ID.area, model="bym",
+          graph=nyc.adj)+index+mhi2+trafficDensityST+avgSpeed2
> resultCOV5 <- inla(formulaCOV5,family="poisson", # run inla
+ data=pedDat, control.compute=list(dic=TRUE,cpo=TRUE),
+           control.predictor=list(compute=TRUE),E=pop.tot)
```

[10] Note, would normally also look at a negative binomial or a zero-inflated negative binomial. Negative binomial models include an extra parameter to account for overdispersion, but the frailty model specification already accounts for overdispersion. One can still fit an negative binomial model in INLA if interested in characterizing the over dispersion.

```
> summary(resultCOV5)
> exp(resultCOV5$summary.fixed)
```

	mean	sd	0.025quant	0.975quant
(Intercept)	0.02609339	1.122834	0.02078013	0.03274672
index	1.18796549	1.015812	1.15192887	1.22509942
mhi2	0.99704061	1.000958	0.99516755	0.99891441
trafficDensityST	1.19540308	1.021069	1.14744872	1.24531625
avgSpeed2	0.77184253	1.048879	0.70285195	0.84765271

As a recap, holding all the other covariates to zero, for every one unit increase in the social deprivations index there is a 19% increase in pedestrian injury risk (95% CrI 1.16, 1.23), for every one standardized unit increase in traffic density, there is a 20% increase in pedestrian injury risk (95% CrI 1.15, 1.25), and for every 10 mile per hour increase in average traffic speed in a census tract, there is a 33% *decrease* in pedestrian injury risk (95% CrI 0.70, 0.85). Median household income has a very small effect of a 1% decrease in injury risk for every $1,000 increase in median household income (95% CrI 1.00, 0.99). Again, the DIC for this model was 14257.48 with 1748.24 effective parameters.

Now explore and map the spatial risk in the model. Again, note that the spatial risk (ζ) is interpreted as the *residual relative risk for each area (compared to the whole of New York City) after social fragmentation, economics, average speed and traffic density are taken into account.* The random effect term is as specified and expected normally distributed (Fig **??**) and spatially random (Fig) Plotting the CAR term results displays more spatial structure. (Fig 2.4)

```
> # UH results
> re<-resultCOV5$summary.random$ID.area[1:1908,2]
> plot(density(re)) # plot density random effects
> # add re term to dataframe
> pedDat$re<-re
> # create cuts
> quantile(pedDat$re,probs = seq(0, 1, by = 0.20))
> re.cuts <- c(-3.7807038, -0.6539410, -0.1932530,
+         0.1476478,  0.6881801,  4.4672516)
> pedDat$re.cut<-cut(pedDat$re,breaks=re.cuts,
+         include.lowest=TRUE, include.highest=TRUE)
> # map re term
> nyc.df1 <- fortify(nyc, region=GEOID10)
> nyc.df <- merge(nyc.df1, pedDat, by.x="id", by.y="tract",
+ all=FALSE)
> nyc.df <- nyc.df[order(nyc.df$group, nyc.df$order), ]
> p1<-ggplot(nyc.df, aes(x=long, y=lat))
> p2<-p1+geom_polygon(aes(group=group, fill=re.cut))
> p3<- p2 + scale_fill_brewer(palette="Blues",
+ name="Unstructured\nSpatial Effects")
```

```
> p4<- p3+ theme(axis.text.x = element_blank(), axis.text.y = element_blank(),
+ axis.ticks = element_blank()) +
+ theme(panel.background = element_rect(colour = NA)) +
+ xlab("")+ylab("")+
+ ggtitle("Spatially Unstructured (Random) Heterogeneity, \n Pedestrian
+ Injuries, New York City Census Tracts, 2001-2010")
> print(p4)
> # CAR results
> car<-resultCOV5$summary.random$ID.area[1909:3816,2]
> plot(density(car)) # plot density random effects
> # add car results to dataframe
> pedDat$car<-car
> # create cuts
> quantile(pedDat$car,probs = seq(0, 1, by = 0.20))
> car.cuts <- c(-3.23283927, -0.44094906, -0.16440648,
+         0.09486667,  0.46995525, 2.69746658)
> pedDat$car.cut<-cut(pedDat$car,breaks=car.cuts,
+         include.lowest=TRUE, include.highest=TRUE)
> # library(ggplot2)
> # gpclibPermit()
> # nyc.df1 <- fortify(nyc, region=GEOID10)
> nyc.df <- merge(nyc.df1, pedDat, by.x="id",
+             by.y="tract", all=FALSE)
> nyc.df <- nyc.df[order(nyc.df$group, nyc.df$order), ]
> # library(RColorBrewer)
> p1<-ggplot(nyc.df, aes(x=long, y=lat))
> p2<-p1+geom_polygon(aes(group=group, fill=car.cut))
> p3<- p2 + scale_fill_brewer(palette="Blues",
+ name="Spatial\nEffects")
> p4<- p3+ theme(axis.text.x = element_blank(),
+ axis.text.y = element_blank(),
+ axis.ticks = element_blank()) +
+ theme(panel.background = element_rect(colour = NA)) +
+ xlab("")+ylab("")+
+ ggtitle("Spatially Structured (CAR) Heterogeneity, \n Pedestrian
+ Injuries, New York City Census Tracts, 2001-2010")
> print(p4)
```

We next, calculate and map the fitted values ($\theta = \alpha + \upsilon + \nu$) (Fig 2.4), spatial risk ($\zeta = \upsilon + \nu$) (Fig 2.4) and spatial exceedance for a relative risk of 1 ($\Pr[\zeta_i > 1]$) (Fig 2.4).

```
> #risk (theta = alpha + upsilon + nu)
> COVfit <- resultCOV5$summary.fitted.values[,1]
> #spatial risk (zeta = upsilon + nu)
> COVmarginals <- resultCOV5$marginals.random$ID.area[1:1908]
> COVzeta <- lapply(COVmarginals,function(x)inla.emarginal(exp,x)) # exponentiate
```

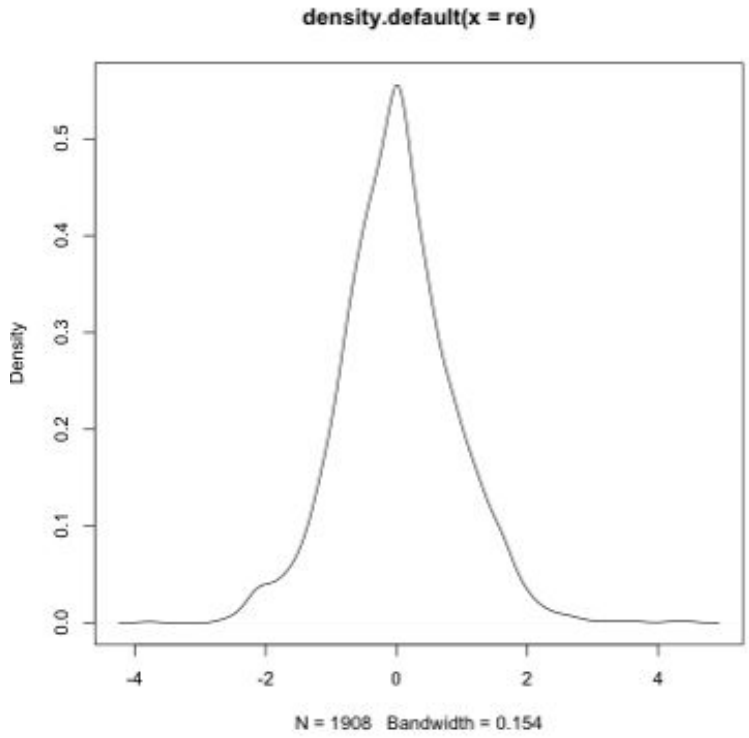
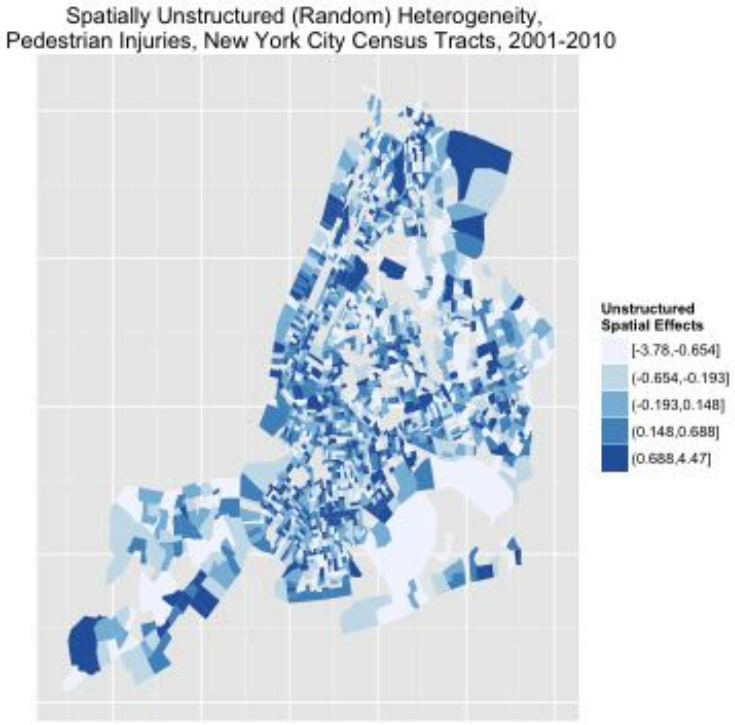
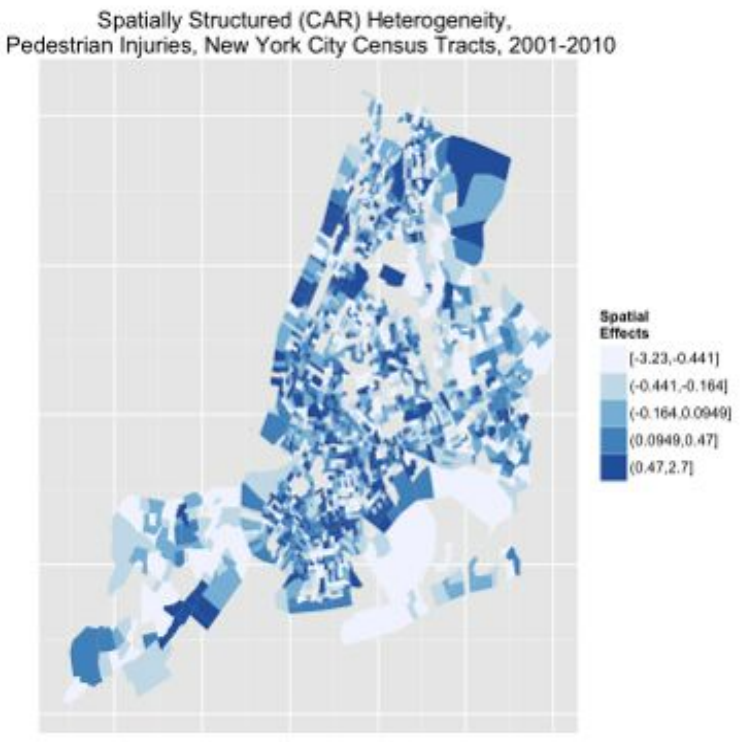


Figure 11: Density Plot Unstructured Spatial Heterogeneity






```
> # exceedence probability (RR > 1)
> a=0
> COVexceed<-lapply(resultCOV5$marginals.random$ID.area[1:1908], function(X){
+   1-inla.pmarginal(a, X)
+ })
```

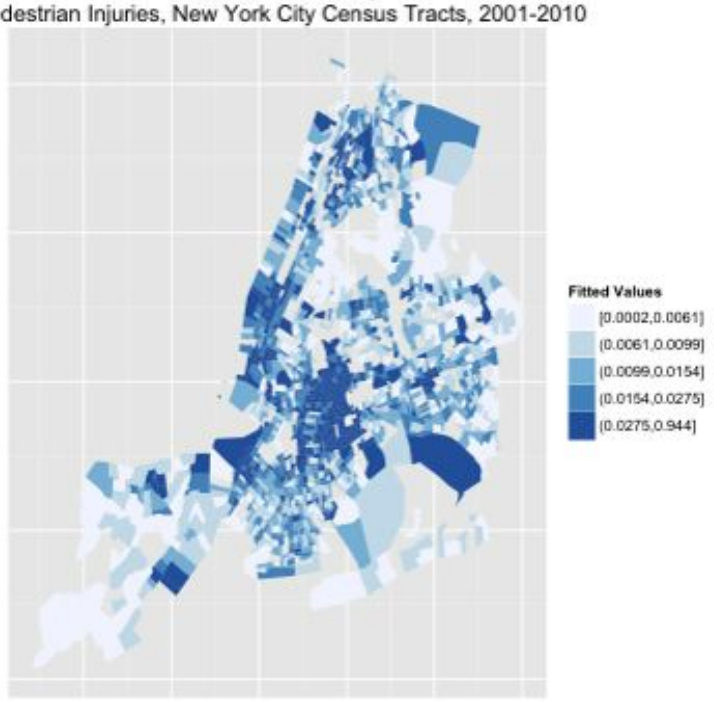
Map these results.

```
> pedDat$fit<-COVfit
> quantile(pedDat$fit,probs = seq(0, 1, by = 0.20))
> cut.fit<-round(c(0.0002386368, 0.0060769212, 0.0099230836,
+                  0.0154344092, 0.0275053642, 0.9440013730),4)
> pedDat$fit.cut<-cut(pedDat$fit,breaks=cut.fit,
+                     include.lowest=TRUE)
> summary(pedDat$fit.cut)
> pedDat$risk<-unlist(COVzeta)
> quantile(pedDat$risk, probs = seq(0, 1, by = 0.20))
> cut.risk<-round(c(0.02642057,  0.53239957,  0.84189629,
+                   1.18365006,  2.00949877, 87.96635625),2)
> pedDat$risk.cut<-cut(pedDat$risk,breaks=cut.risk,
+                   include.lowest=TRUE)
> summary(pedDat$risk.cut)
> pedDat$exceed<-unlist(COVexceed)
> quantile(pedDat$exceed,probs = seq(0, 1, by = 0.20))
```

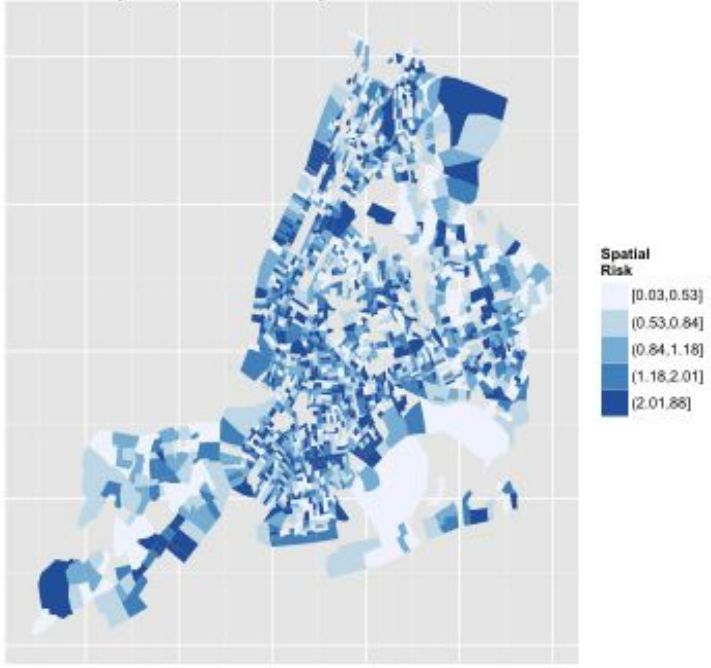
```
> cut.exceed<-c(0, .8, .99, 1)
> pedDat$exceed.cut<-cut(pedDat$exceed, breaks=cut.exceed,
+                  include.lowest=TRUE)
> summary(pedDat$exceed.cut)
> # nyc.df1 <- fortify(nyc, region=GEOID10)
> nyc.df <- merge(nyc.df1, pedDat, by.x="id",
+          by.y="tract", all=FALSE)
> nyc.df <- nyc.df[order(nyc.df$group, nyc.df$order), ]
> p1<-ggplot(nyc.df, aes(x=long, y=lat))
> p2<-p1+geom_polygon(aes(group=group, fill=fit.cut))
> p3<- p2 + scale_fill_brewer(palette="Blues",
+         name="Fitted Values")
> p4<- p3+ theme(axis.text.x = element_blank(),
+          axis.text.y = element_blank(),
+ axis.ticks = element_blank()) +
+ theme(panel.background = element_rect(colour = NA)) +
+ xlab("")+ylab("")+
+ ggtitle("Fitted Model Values, \n Pedestrian Injuries,
+           New York City Census Tracts, 2001-2010")
> print(p4)
> p1<-ggplot(nyc.df, aes(x=long, y=lat))
> p2<-p1+geom_polygon(aes(group=group, fill=risk.cut))
> p3<- p2 + scale_fill_brewer(palette="Blues", name="Spatial\nRisk")
> p4<- p3+ theme(axis.text.x = element_blank(),
+         axis.text.y = element_blank(),
+ axis.ticks = element_blank()) +
+ theme(panel.background = element_rect(colour = NA)) +
+ xlab("")+ylab("")+
+ ggtitle("Spatially Structured Risk Estimates, \n Pedestrian
+          Injuries, New York City Census Tracts, 2001-2010")
> print(p4)
> p1<-ggplot(nyc.df, aes(x=long, y=lat))
> p2<-p1+geom_polygon(aes(group=group, fill=exceed.cut))
> p3<- p2 + scale_fill_brewer(palette="Blues", name="Exceedence")
> p4<- p3+ theme(axis.text.x = element_blank(),
+            axis.text.y = element_blank(),
+ axis.ticks = element_blank()) +
+ theme(panel.background = element_rect(colour = NA)) +
+ xlab("")+ylab("")+
+ ggtitle("Probability Exceedence RR > 1, \n Pedestrian Injuries,
+              New York City Census Tracts, 2001-2010")
> print(p4)
```

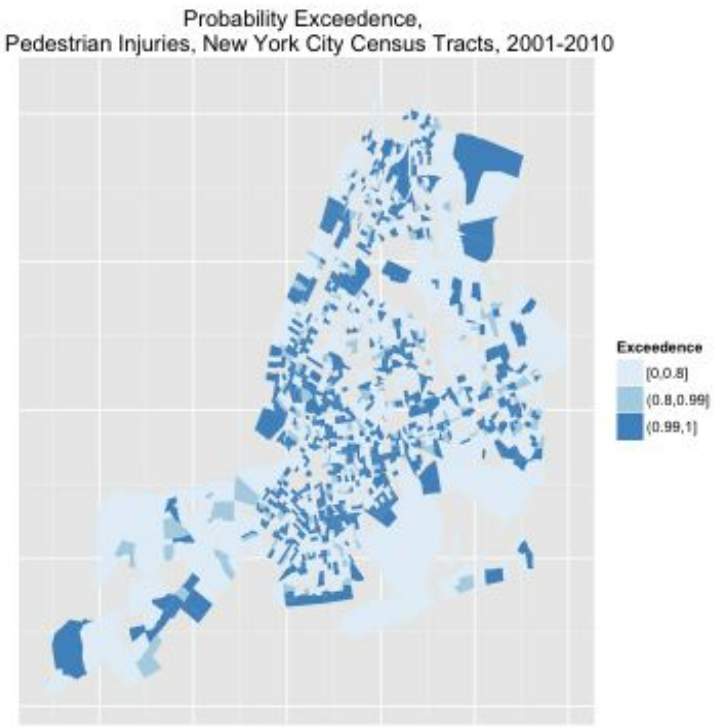
We increase the risk threshold and look at the probability of exceeding a relative risk of 2 (Fig 2.4)

Fitted Model Values,
Pedestrian Injuries, New York City Census Tracts, 2001-2010



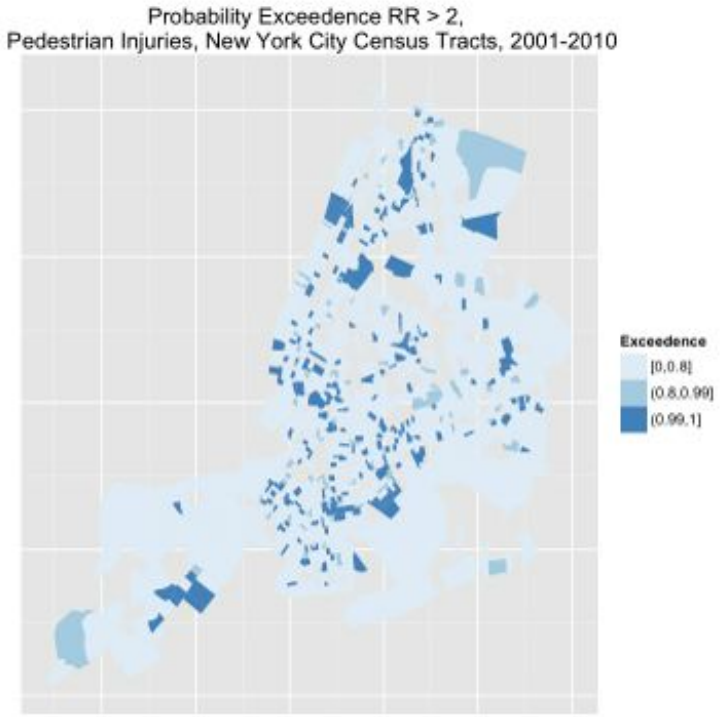
Spatially Structured Risk Estimates,
Pedestrian Injuries, New York City Census Tracts, 2001-2010






```
> a=0.6931472 # on unexponentiated scale, log(2)
> COVexceed2<-lapply(resultCOV5$marginals.random$ID.area[1:1908],
+              function(X){
+   1-inla.pmarginal(a, X)
+ })
> pedDat$exceed2<-unlist(COVexceed2)
> quantile(pedDat$exceed2,probs = seq(0, 1, by = 0.20))
> cut.exceed2<-c(0, .8, .99, 1)
> pedDat$exceed2.cut<-cut(pedDat$exceed2,
+                      breaks=cut.exceed2, include.lowest=TRUE)
> summary(pedDat$exceed2.cut)
> # nyc.df1 <- fortify(nyc, region=GEOID10)
> nyc.df <- merge(nyc.df1, pedDat, by.x="id", by.y="tract", all=FALSE)
> nyc.df <- nyc.df[order(nyc.df$group, nyc.df$order), ]
> p1<-ggplot(nyc.df, aes(x=long, y=lat))
> p2<-p1+geom_polygon(aes(group=group, fill=exceed2.cut))
> p3<- p2 + scale_fill_brewer(palette="Blues",
+         name="Exceedence")
> p4<- p3+ theme(axis.text.x = element_blank(),
+          axis.text.y = element_blank(),
+ axis.ticks = element_blank()) +
+ theme(panel.background = element_rect(colour = NA)) +
+ xlab("")+ylab("")+
```

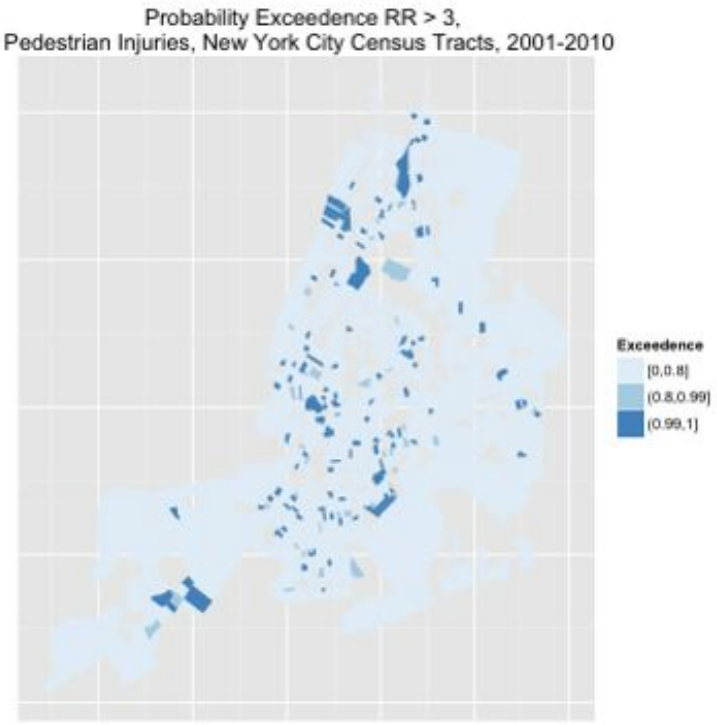
```
+ ggtitle("Probability Exceedence RR > 2, \n Pedestrian
+                 Injuries, New York City Census Tracts, 2001-2010")
> print(p4)
```



Or exceedng relative risks of 3... (Fig 2.4)

```
> a=1.098612 # on unexponentiated scale, log(3)
> COVexceed3<-lapply(resultCOV5$marginals.random$ID.area[1:1908],
+                    function(X){
+   1-inla.pmarginal(a, X)
+ })
> pedDat$exceed3<-unlist(COVexceed3)
> quantile(pedDat$exceed3,probs = seq(0, 1, by = 0.20))
> cut.exceed3<-c(0, .8, .99, 1)
> pedDat$exceed3.cut<-cut(pedDat$exceed3, breaks=cut.exceed3,
+                     include.lowest=TRUE)
> summary(pedDat$exceed3.cut)
> # nyc.df1 <- fortify(nyc, region=GEOID10)
> nyc.df <- merge(nyc.df1, pedDat, by.x="id", by.y="tract",
+            all=FALSE)
> nyc.df <- nyc.df[order(nyc.df$group, nyc.df$order), ]
> p1<-ggplot(nyc.df, aes(x=long, y=lat))
> p2<-p1+geom_polygon(aes(group=group, fill=exceed3.cut))
> p3<- p2 + scale_fill_brewer(palette="Blues", name="Exceedence")
> p4<- p3+ theme(axis.text.x = element_blank(),
```

```
+                axis.text.y = element_blank(),
+ axis.ticks = element_blank()) +
+ theme(panel.background = element_rect(colour = NA)) +
+ xlab("")+ylab("")+
+ ggtitle("Probability Exceedence RR > 3, \n Pedestrian Injuries,
+                New York City Census Tracts, 2001-2010")
> print(p4)
```



Lastly, calculate proportion of variance explained by spatially structured component (CAR). Crete an empty matrix, with rows equal to number of regions, with 1000 columns into which we extract 1000 observations from the marginal distribution of the CAR term (ν), from which we calculate the empirical variance. Then extract values for random effects (UH) term and calculate the proportion of total heterogeneity accounted for by the spatially structured heterogeneity. See that structured spatial heterogeneity or place accounts for for about 70% of the total spatial heterogeneity.

```
> mat.marg <- matrix(NA, nrow=1908, ncol=1000)
> m<-resultCOV5$marginals.random$ID.area
> for (i in 1:1908){
+   u<-m[[1908+i]]
+   s<-inla.rmarginal(1000, u)
+   mat.marg[i,]<-s}
> var.RRspatial<-mean(apply(mat.marg, 2, sd))^2
> var.RRhet<-inla.emarginal(function(x) 1/x,
```

```
+                              resultCOV5$marginals.hyper$"Precision for ID.area (iid com
> var.RRspatial/(var.RRspatial+var.RRhet)
```

3 Space-Time Interaction Models

Prepare the data for space-time interaction modeling. Begin by subsetting the pedestrian data set, then converting it from "wide" to "long" format. There are a total of 19080 (1908 census tracts x 10 years) rows of observations. The covariate data now loop over 10 (1 for each year of data) iterations of the census tract identifying variables (idvar="tract"), the yearly injury counts and population figures increment over the 10 years of repeated census tracts.

```
> # subset the pedestrian injury data set
> drops<-c("expected.allAges.allHrs.2001","expected.allAges.allHrs.2002",
+ "expected.allAges.allHrs.2003","expected.allAges.allHrs.2004",
+ "expected.allAges.allHrs.2005","expected.allAges.allHrs.2006",
+ "expected.allAges.allHrs.2007","expected.allAges.allHrs.2008",
+ "expected.allAges.allHrs.2009", "expected.allAges.allHrs.2010",
+ "allAges.allHrs.tot", "expected.allAges.allHrs.tot", "pop.tot",
+ "rate", "mhi", "raodDensity", "trafficDensity", "avgSpeed",
+ "signalDensity")
> pedDat2<-pedDat[,!(names(pedDat)%in% drops)]
> # reshape wide to long
> pedDatL<-reshape(pedDat2,direction="long",idvar="tract",
+ varying=list(c("allAges.allHrs.2001", "allAges.allHrs.2002",
+ "allAges.allHrs.2003", "allAges.allHrs.2004", "allAges.allHrs.2005",
+ "allAges.allHrs.2006", "allAges.allHrs.2007", "allAges.allHrs.2008",
+ "allAges.allHrs.2009", "allAges.allHrs.2010"),c("allAge.pop.2001",
+ "allAge.pop.2002", "allAge.pop.2003", "allAge.pop.2004",
+ "allAge.pop.2005", "allAge.pop.2006", "allAge.pop.2007",
+ "allAge.pop.2008", "allAge.pop.2009", "allAge.pop.2010")),
+ v.names=c("inj", "pop"),times=c(2001, 2002, 2003, 2004, 2005,
+         2006, 2007, 2008, 2009, 2010))
> str(pedDatL)
> # check variables looped correctly
> pedDatL$ID.area[c(2,(2+1908),(2+2*1908))]
> pedDatL$mhi2[c(2,(2+1908),(2+8*1908))]
> pedDatL$trafficDensityST[c(55,(55+1908),(55+8*1908))]
> pedDatL$intx<-1:nrow(pedDatL)
```

Look at 5 possible space-time models based on the final convolution covariate model that included social fragmentation, median household income, traffic density and average speed. Compare them on DIC and informativeness.

```
> # "winning" 10-year cross-sectionalcovariate model from above
> #
> # formulaCOV5 <- allAges.allHrs.tot~ f(ID.area, model="bym",
> #   graph=nyc.adj)+index+mhi2+trafficDensityST+avgSpeed2
> # resultCOV5 <- inla(formulaCOV5,family="poisson", # run inla
> # data=pedDat, control.compute=list(dic=TRUE,cpo=TRUE),E=pop.tot)
> #
> # summary(resultCOV5)
> #
> # exp(resultCOV5$summary.fixed)
>
>
> ###  convolution + uncorrelated time (time IID)
> STform1<-inj~1+f(ID.area, model="bym", graph=nyc.adj)+
+       f(time,model="iid")+index+mhi2+trafficDensityST+avgSpeed2
> STresult1<-inla(STform1, family="poisson", data=pedDatL, E=pop,
+         control.compute=list(dic=TRUE,cpo=TRUE),control.predictor=list(compute=TRUE)
> ###  convolution + 1st order random walk correlated time (time RW1)
> STform2<-inj~1+f(ID.area, model="bym", graph=nyc.adj)+
+           f(time,model="rw1")+index+mhi2+trafficDensityST+avgSpeed2
> STresult2<-inla(STform2, family="poisson", data=pedDatL, E=pop,
+            control.compute=list(dic=TRUE,cpo=TRUE),control.predictor=list(compute=TR
> ###  convolution + 1st order random walk correlated time (time RW1)
>   #  + uncorrelated time (time IID)
> pedDatL$time2<-pedDatL$time
> STform3<-inj~1+f(ID.area, model="bym", graph=nyc.adj)+
+         f(time,model="rw1")+f(time2,model="iid")+index+mhi2+
+                         trafficDensityST+avgSpeed2
> STresult3<-inla(STform3, family="poisson", data=pedDatL,
+        E=pop, control.compute=list(dic=TRUE,cpo=TRUE),
+                    control.predictor=list(compute=TRUE))
> ###  convolution + 1st order random walk correlated time (time RW1)
>    # + space-time interaction term
> STform4<-inj~1+f(ID.area, model="bym", graph=nyc.adj)+
+       f(time,model="rw1")+f(intx,model="iid")+
+           index+mhi2+trafficDensityST+avgSpeed2
> lcs<-inla.make.lincombs(time=diag(10)) # need to create linear combinations
> # based on number of years for temporal results
>   #and feed to inla call (see http://www.r-inla.org/faq for how inla.make.lincombs i
> STresult4<-inla(STform4, family="poisson", data=pedDatL, E=pop,
+        control.compute=list(dic=TRUE,cpo=TRUE),
+            control.predictor=list(compute=TRUE), lincomb=lcs)
> ###  convolution + 1st order random walk correlated time (time RW1) +
>   #   uncorrelated time (time IID) + space-time interaction term
> STform5<-inj~1+f(ID.area, model="bym", graph=nyc.adj)+f(time,model="rw1")+
```

```
+      f(time2,model="iid")+f(intx,model="iid")+
+           index+mhi2+trafficDensityST+avgSpeed2
> lcs<-inla.make.lincombs(time=diag(10), time2=diag(10)) # need to create linear
>   #   combinations based on number of years for temporal results
>   #   and feed to inla call
> STresult5<-inla(STform5, family="poisson", data=pedDatL, E=pop,
+       control.compute=list(dic=TRUE,cpo=TRUE),
+            control.predictor=list(compute=TRUE), lincomb=lcs)
> summary(STresult1) # DIC 99772.78,  eff par 1761.78
> summary(STresult2) # DIC 99772.88,  eff par 1761.19
> summary(STresult3) # DIC 99773.26,  eff par 1760.92
> summary(STresult4) # DIC 87047.09,  eff par 8884.79
> summary(STresult5) # DIC 87061.75,  eff par 8802.30
```

Model	DIC	Effective Parameters
uncorrelated time (time IID)	99772.78	1761.78
1st order random walk correlated time (time RW1)	99772.88	1761.19
(time RW1) and (time IID)	99773.26	1760.92
(time RW1) and space-time interaction term (time intx)	87047.09	8884.79
(time RW1) and (time IID) and (time intx)	87061.75	8802.30

The "winning" model is the convolution (UH plus CAR) with covariates for social fragmentation, household income, traffic density and average speed with a first-order random walk correlated time variable and an interaction term for time and place.

```
> exp(STresult4$summary.fixed)
```

The exponentiated results for the fixed effects are:

```
> exp(STresult4$summary.fixed)
                        mean       sd  0.025quant    0.5quant  0.975quant        mode kl
(Intercept)      0.002468534 1.126014 0.001955026 0.002468672 0.003115289 0.002468975
index            1.193281605 1.016160 1.156308704 1.193279791 1.231411155 1.193277818
mhi2             0.997454295 1.000981 0.995534207 0.997454564 0.999374804 0.997455186
trafficDensityST 1.204740311 1.021540 1.155363404 1.204740265 1.256178951 1.204742386
avgSpeed2        0.757719271 1.050069 0.688452915 0.757700712 0.833993340 0.757666440
>
```

The results for the fixed effects look very much like they did for the non-temporal, 10-year cross-sectional model. Holding all the other covariates to zero, for every one unit increase in the social deprivations index there is a 19% increase in pedestrian injury risk (95% CrI 1.16, 1.23), for every one standardized unit increase in traffic density, there is a 20% increase in pedestrian injury risk (95% CrI 1.15, 1.26), and for every 10 mile per hour increase in average traffic speed in a census tract, there is a 24% *decrease* in pedestrian injury risk (95% CrI 0.69, 0.83). Median household income has a very small effect of a 1% decrease in injury risk for every $1,000 increase in median household income (95% CrI 0.99, 0.99). Again, the decreased injury for risk associated with increased average speed may make sense if you think of in terms of pedestrian behavior (pedestrian may be less likely to venture out into

traffic if cars are going very quickly), and that more cars (increased exposure) is probably inversely correlated with speed. Also note that the traffic density and speed variables include highways, bridges and tunnels. There are version of those variables that don't, and the effects may be modified.

We now explore and map the spatial risk in the model. Again, the spatial risk (ζ) is interpreted as the *residual relative risk for each area (compared to the whole of New York City) after social fragmentation, economics, average speed traffic density, and time trend are taken into account.* The random effect term is normally distributed as specified and expected (Fig 12) and spatially random (Fig 3) Plotting the CAR term results displays more spatial structure. (Fig 3)

```
> # random effect (UH) term
> re<-STresult4$summary.random$ID.area[1:1908,2]
> plot(density(re), main="Density Plot Random Effect Term")
> # map uh
> pedDat2<-pedDat
> pedDat2$re<-re
> quantile(pedDat2$re,probs = seq(0, 1, by = 0.20))
> re.cuts <- c(-3.8122793, -0.6484124, -0.1878910,
+         0.1426332,  0.6631574,  4.7990249)
> pedDat2$re.cut<-cut(pedDat2$re,breaks=re.cuts,
+         include.lowest=TRUE, include.highest=TRUE)
> # map re term
> nyc.df1 <- fortify(nyc, region=GEOID10)
> nyc.df <- merge(nyc.df1, pedDat2, by.x="id",
+          by.y="tract", all=FALSE)
> nyc.df <- nyc.df[order(nyc.df$group, nyc.df$order), ]
> p1<-ggplot(nyc.df, aes(x=long, y=lat))
> p2<-p1+geom_polygon(aes(group=group, fill=re.cut))
> p3<- p2 + scale_fill_brewer(palette="Blues",
+           name="Unstructured\nSpatial Effects")
> # edit labels on legend based on result above
> # p3<- p2 + scale_fill_brewer(palette="Blues", name="Unstructured\nSpatial Effects",
> p4<- p3+ theme(axis.text.x = element_blank(), axis.text.y = element_blank(),
+ axis.ticks = element_blank()) +
+ theme(panel.background = element_rect(colour = NA)) +
+ xlab("")+ylab("")+
+ ggtitle("Spatially Unstructured (Random) Heterogeneity, \n Pedestrian Injuries, New
> print(p4)
> # CAR results
> car<-STresult4$summary.random$ID.area[1909:3816,2]
> plot(density(car))
> # map the CAR term
> pedDat2$car<-car
> quantile(pedDat2$car,probs = seq(0, 1, by = 0.20))
```

```
> car.cuts <- c(-3.34729876, -0.45362945, -0.17017057,
+                 0.09776985,  0.48366741,  2.94768131)
> pedDat2$car.cut<-cut(pedDat2$car,breaks=car.cuts,
+               include.lowest=TRUE, include.highest=TRUE)
> # map re term
> # nyc.df1 <- fortify(nyc, region=GEOID10)
> nyc.df <- merge(nyc.df1, pedDat2, by.x="id", by.y="tract", all=FALSE)
> nyc.df <- nyc.df[order(nyc.df$group, nyc.df$order), ]
> p1<-ggplot(nyc.df, aes(x=long, y=lat))
> p2<-p1+geom_polygon(aes(group=group, fill=car.cut))
> p3<- p2 + scale_fill_brewer(palette="Blues",
+        name="Structured Spatial\nEffects")
> # edit labels on legend based on result above
> # p3<- p2 + scale_fill_brewer(palette="Blues", name="Structured Spatial\nEffects",la
> p4<- p3+ theme(axis.text.x = element_blank(), axis.text.y = element_blank(),
+ axis.ticks = element_blank()) +
+ theme(panel.background = element_rect(colour = NA)) +
+ xlab("")+ylab("")+
+ ggtitle("Spatially Structured (CAR) Heterogeneity, \n Pedestrian
+         Injuries, New York City Census Tracts, 2001-2010")
> print(p4)
>
```

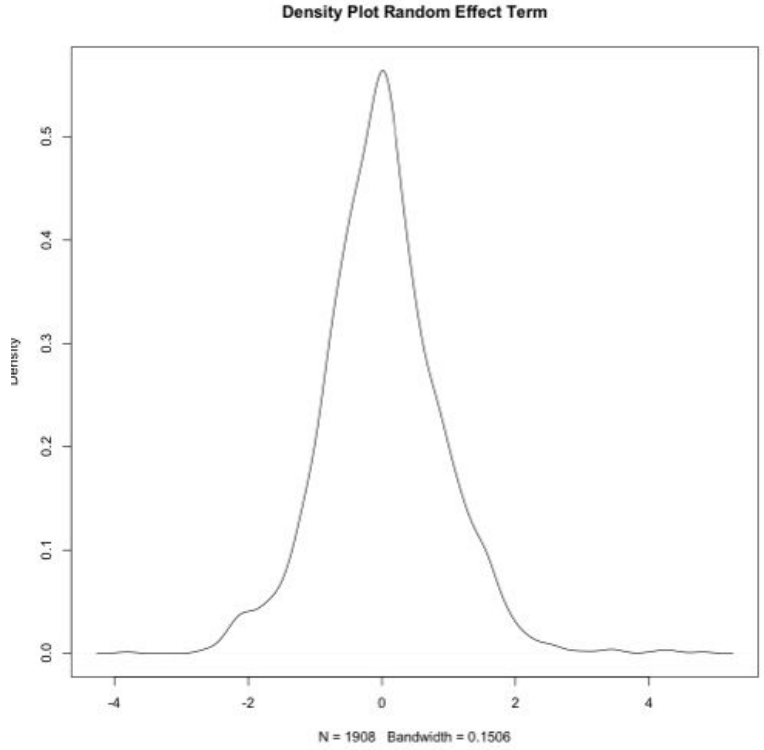
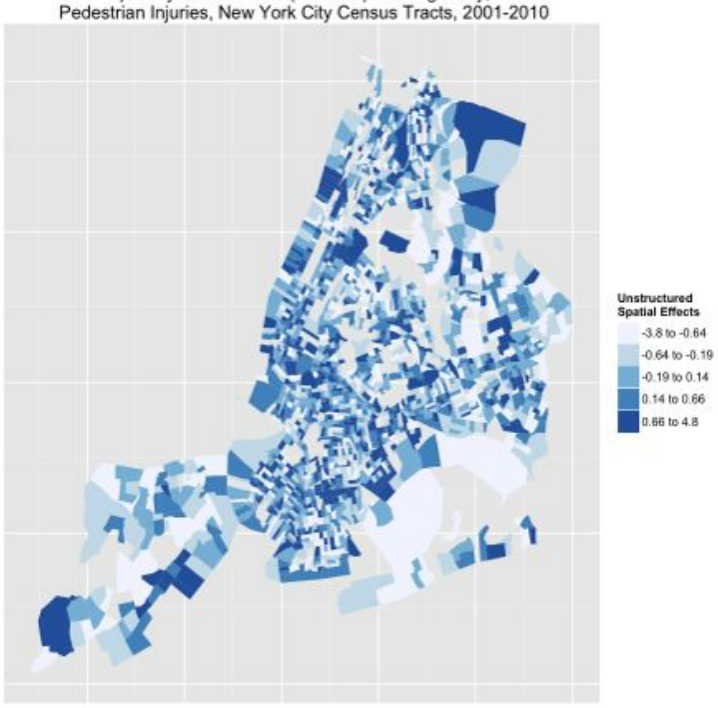
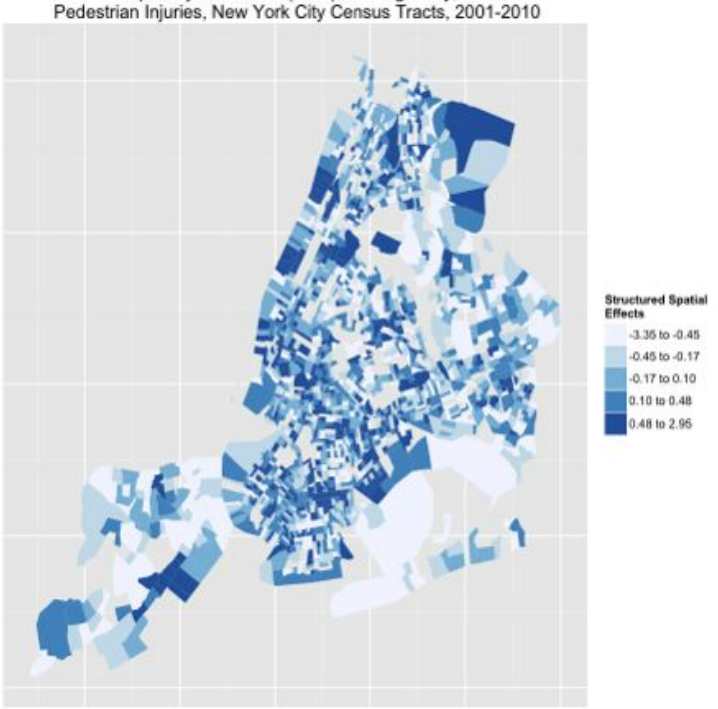


Figure 12: Density Plot Unstructured Spatial Heterogeneity

Spatially Unstructured (Random) Heterogeneity,
Pedestrian Injuries, New York City Census Tracts, 2001-2010



Spatially Structured (CAR) Heterogeneity,
Pedestrian Injuries, New York City Census Tracts, 2001-2010



The fitted values ($\theta = \alpha + \upsilon + \nu$) for the space-time model stored in summary.fitted.values loop over the 10 years of data, so are not easily calculated and are here omitted. Spatial risk ($\zeta = \upsilon + \nu$) (Fig 2.4) and spatial exceedance for a relative risk of 2 ($\Pr[\zeta_i > 1]$) (Fig 2.4) are more readily accessible.

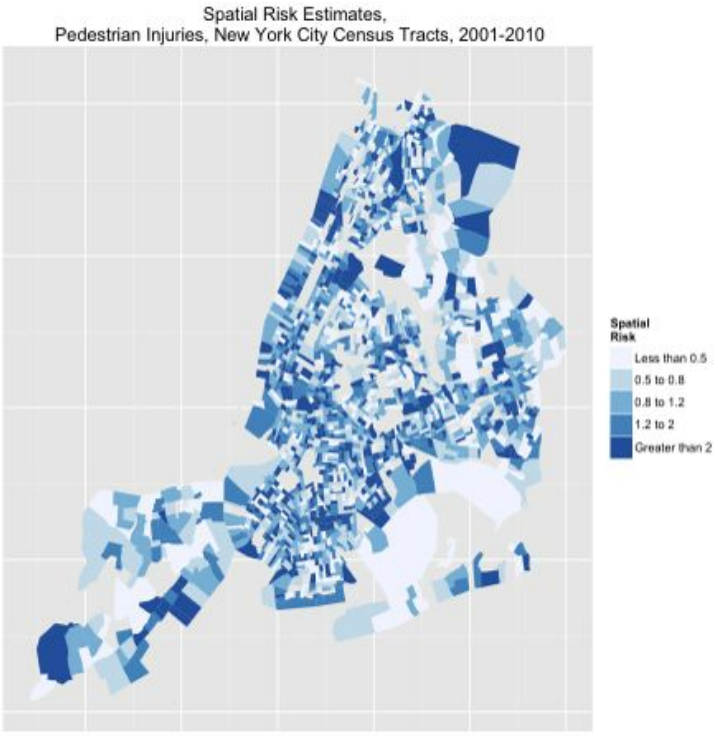
Extract the results for incidence density ratio (risk) and posterior probability exceedence for an IDR of 2.

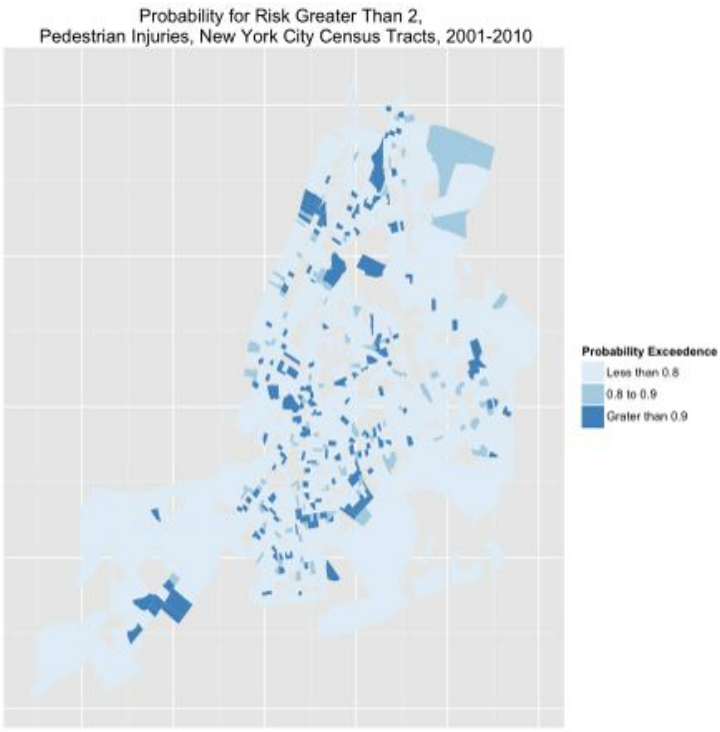
```
> #risk (theta = alpha + upsilon + nu)
> # COVfit <- STresult4$summary.fitted.values[,1]
> # str(STresult4$summary.fitted.values)
>
> #str(STresult4$marginals.random)
>
> #spatial risk (zeta = upsilon + nu)
> STmarginals <- STresult4$marginals.random$ID.area[1:1908]
> STzeta <- lapply(STmarginals,function(x)inla.emarginal(exp,x)) # exponentiate
> # exceedence probability (RR > 2)
> a=log(2)
> STexceed2<-lapply(STresult4$marginals.random$ID.area[1:1908],
+         function(X){
+   1-inla.pmarginal(a, X)
+ })
```

Categorize and map these results.

```
> pedDat2$risk<-unlist(STzeta)
> quantile(pedDat2$risk, probs = seq(0, 1, by = 0.20))
> cut.risk<-round(c(0.02599555,   0.54279971,   0.85085326,
+         1.18297656,   1.98622577, 123.71994602),2)
> pedDat2$risk.cut<-cut(pedDat2$risk,breaks=cut.risk,include.lowest=TRUE)
> summary(pedDat2$risk.cut)
> pedDat2$exceed2<-unlist(STexceed2)
> # quantile(pedDat2$exceed2,probs = seq(0, 1, by = 0.20))
> cut.exceed<-c(0, .8, .99, 1)
> pedDat2$exceed2.cut<-cut(pedDat2$exceed2, breaks=cut.exceed,
+         include.lowest=TRUE)
> summary(pedDat2$exceed2.cut)
> # nyc.df1 <- fortify(nyc, region=GEOID10)
> nyc.df <- merge(nyc.df1, pedDat2, by.x="id",
+ by.y="tract", all=FALSE)
> nyc.df <- nyc.df[order(nyc.df$group, nyc.df$order), ]
> p1<-ggplot(nyc.df, aes(x=long, y=lat))
> p2<-p1+geom_polygon(aes(group=group, fill=risk.cut))
> c("0.03,0.54", "0.54,0.85", "0.85,1.18", "1.18,1.99", "1.99,124")
> p3<- p2 + scale_fill_brewer(palette="Blues",
+             name="Spatial\nRisk")
```

```
> # edit labels on legend based on result above
> p3<- p2 + scale_fill_brewer(palette="Blues", name="Spatial\nRisk",
+        labels=c("Less than 0.5", "0.5 to 0.8", "0.8 to 1.2", "1.2 to 2",
+              "Greater than 2"))
> p4<- p3+ theme(axis.text.x = element_blank(), axis.text.y = element_blank(),
+ axis.ticks = element_blank()) +
+ theme(panel.background = element_rect(colour = NA)) +
+ xlab("")+ylab("")+
+ ggtitle("Spatial Risk Estimates, \n Pedestrian Injuries,
+ New York City Census Tracts, 2001-2010")
> print(p4)
> p1<-ggplot(nyc.df, aes(x=long, y=lat))
> p2<-p1+geom_polygon(aes(group=group, fill=exceed2.cut))
> p3<- p2 + scale_fill_brewer(palette="Blues", name="Exceedence")
> p3<- p2 + scale_fill_brewer(palette="Blues", name="Probability Exceedence",
+ labels=c("Less than 0.8","0.8 to 0.9","Grater than 0.9"))
> p4<- p3+ theme(axis.text.x = element_blank(), axis.text.y = element_blank(),
+ axis.ticks = element_blank()) +
+ theme(panel.background = element_rect(colour = NA)) +
+ xlab("")+ylab("")+
+ ggtitle("Probability for Risk Greater Than 2, \n Pedestrian Injuries,
+ New York City Census Tracts, 2001-2010")
> print(p4)
```





Calculate the proportion of variance explained by the spatially structured component (CAR) [11] See that structured spatial heterogeneity or place accounts for for about 73.2% of the total spatial heterogeneity.

```
> mat.marg <- matrix(NA, nrow=1908, ncol=1000)
> m<-STresult4$marginals.random$ID.area
> for (i in 1:1908){
+   u<-m[[1908+i]]
+   s<-inla.rmarginal(1000, u)
+   mat.marg[i,]<-s}
> var.RRspatial<-mean(apply(mat.marg, 2, sd))^2
> var.RRhet<-inla.emarginal(function(x) 1/x,
+   STresult4$marginals.hyper$"Precision for ID.area (iid component)")
> var.RRspatial/(var.RRspatial+var.RRhet)
```

Next, extract and plot the temporal effects. This is the trend over the 10-year period holding the covariates and spatial risk constant. (Fig 13)

```
> #Put the temporal effect on the natural scale
> temporal<-lapply(STresult4$marginals.lincomb.derived, function(X){
+   # marg <- inla.marginal.transform(function(x) exp(x), X)
+   #  note, inla.marginal.transform() changed to inla.tmarginal() in recent versions
```

[11] Note. Andrew Lawson cautioned against measures like this because CAR and UH are incompletely identified. Even Blangiardo, from whom this code is adapted, says the UH and CAR variances are not directly comparable, but the result can give an indication of the relative contribution of each.

```
+   marg <- inla.tmarginal(function(x) exp(x), X)
+   inla.emarginal(mean, marg)
+ })
> #Plot the citywide temporal trend
>
>
> plot(seq(1,10),seq(0.8,1.2,length=10),type="n",xlab="year",ylab="temporal trend")
> lines(unlist(temporal))
> abline(h=1,lty=2)
```

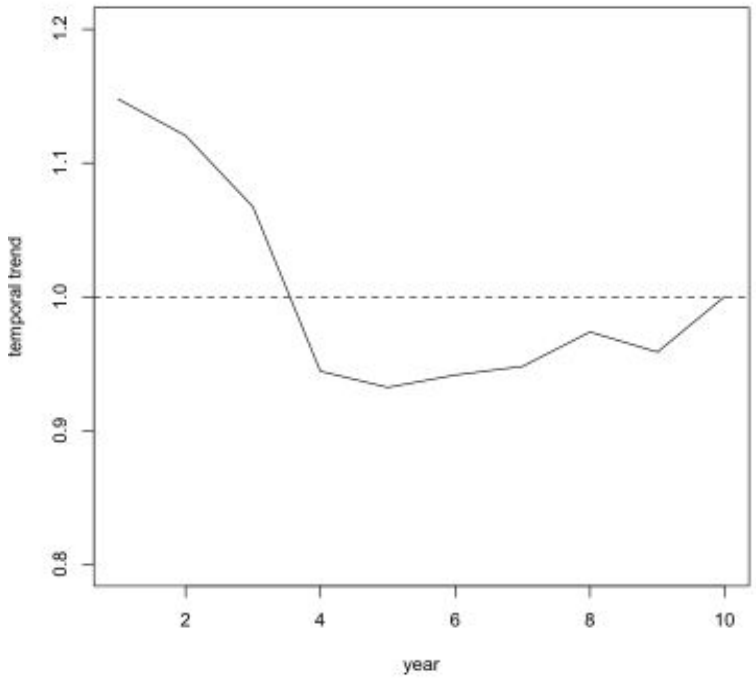


Figure 13: Temporal trend pedestrian injury risk, New York City, 2001-2010

Lastly, plot the space-time interaction for 2001, 2004, 2007 and 2010, of the posterior probability exceedance of a relative risk of 2. The space-time interaction is a random-effect term that can be viewed as a kind of residual effect after the unstructured, spatially structured and time effects are modeled. It is the additional effect beyond that which is already picked up with the other space and time terms. In this case, the areas with elevated values represent sporadic outbreaks, like short-term clusters. There do not appear to be census tracts that consistently display additional elevated risk of pedestrian injury.

```
> #Space-Time Interaction
> delta <- data.frame(delta=STresult4$summary.random$intx[,2],
+         year=pedDatL$time,ID.area=pedDatL$ID.area)
> delta.matrix <- matrix(delta[,1], 1908,10,byrow=FALSE)
> rownames(delta.matrix)<- delta[1:1908,3]
```

```
> #Space time probability > 2
>
> # note lapply() code differs subtly from that for the STresult5 marginals.random lis
> # extract third ([[3]]) list object, not fourth ([[4]])
> # STresult5 has additional year variable (time2)
>
> a=log(2)
> inlaprob.delta<-lapply(STresult4$marginals.random[[3]],
+         function(X){
+   1-inla.pmarginal(a, X)
+ })
> pp.delta<-unlist(inlaprob.delta)
> pp.cutoff.interaction <- c(0,0.6,0.8,1)
> pp.delta.matrix <- matrix(pp.delta, 1908,10,byrow=FALSE)
> nyc.dat<-attr(nyc,"data")
> pp.delta.factor <- data.frame(tract=nyc.dat$tract)
> for(i in 1:10){
+   pp.delta.factor.temp <- cut(pp.delta.matrix[,i],
+           breaks=pp.cutoff.interaction,include.lowest=TRUE)
+   pp.delta.factor <- cbind(pp.delta.factor,pp.delta.factor.temp)
+ }
> colnames(pp.delta.factor)<- c("tract","YR2001", "YR2002", "YR2003",
+ "YR2004", "YR2005", "YR2006", "YR2007", "YR2008", "YR2009", "YR2010")
> nyc.df1 <- fortify(nyc, region=GEOID10)
> nyc.df <- merge(nyc.df1, pp.delta.factor, by.x="id",
+          by.y="tract", all=FALSE)
> nyc.df <- nyc.df[order(nyc.df$group, nyc.df$order), ]
> #plot 2001
> p1<-ggplot(nyc.df, aes(x=long, y=lat))
> p1<-p1+geom_polygon(aes(group=group, fill=YR2001))
> p1<- p1 + scale_fill_brewer(palette="Blues",
+        name="Exceedence")
> p1<- p1+ theme(axis.text.x = element_blank(), axis.text.y = element_blank(),
+ axis.ticks = element_blank()) +
+ theme(panel.background = element_rect(colour = NA)) +
+ xlab("")+ylab("")+
+ ggtitle("Probability Exceedence RR > 2, \n Pedestrian Injuries,
+        New York City Census Tracts, 2001")
> print(p1)
> #plot 2004
> p4<-ggplot(nyc.df, aes(x=long, y=lat))
> p4<-p4+geom_polygon(aes(group=group, fill=YR2004))
> p4<- p4 + scale_fill_brewer(palette="Blues",
+       name="Exceedence")
> p4<- p4+ theme(axis.text.x = element_blank(), axis.text.y = element_blank(),
```

```
+ axis.ticks = element_blank()) +
+ theme(panel.background = element_rect(colour = NA)) +
+ xlab("")+ylab("")+
+ ggtitle("Probability Exceedence RR > 2, \n Pedestrian Injuries,
+       New York City Census Tracts, 2004")
> print(p4)
> #plot 2007
> p7<-ggplot(nyc.df, aes(x=long, y=lat))
> p7<-p7+geom_polygon(aes(group=group, fill=YR2007))
> p7<- p7 + scale_fill_brewer(palette="Blues",
+        name="Exceedence")
> p7<- p7+ theme(axis.text.x = element_blank(), axis.text.y = element_blank(),
+ axis.ticks = element_blank()) +
+ theme(panel.background = element_rect(colour = NA)) +
+ xlab("")+ylab("")+
+ ggtitle("Probability Exceedence RR > 2, \n Pedestrian Injuries,
+         New York City Census Tracts, 2007")
> print(p7)
> #plot 2010
> p10<-ggplot(nyc.df, aes(x=long, y=lat))
> p10<-p10+geom_polygon(aes(group=group, fill=YR2010))
> p10<- p10 + scale_fill_brewer(palette="Blues",
+          name="Exceedence")
> p10<- p10+ theme(axis.text.x = element_blank(), axis.text.y = element_blank(),
+ axis.ticks = element_blank()) +
+ theme(panel.background = element_rect(colour = NA)) +
+ xlab("")+ylab("")+
+ ggtitle("Probability Exceedence RR > 2, \n Pedestrian Injuries,
+      New York City Census Tracts, 2010")
> print(p10)
> # Multiple plot function for ggplot2,
> #   from http://www.cookbook-r.com/Graphs/Multiple_graphs_on_one_page_(ggplot2)/
> # ggplot objects can be passed in ..., or to plotlist (as a list of ggplot objects)
> # - cols:   Number of columns in layout
> # - layout: A matrix specifying the layout. If present, cols is ignored.
> #
> # If the layout is something like matrix(c(1,2,3,3), nrow=2, byrow=TRUE),
> # then plot 1 will go in the upper left, 2 will go in the upper right, and
> # 3 will go all the way across the bottom.
> #
> multiplot <- function(..., plotlist=NULL, file, cols=1, layout=NULL) {
+   require(grid)
+
+   # Make a list from the ... arguments and plotlist
+   plots <- c(list(...), plotlist)
```

```
+
+   numPlots = length(plots)
+
+   # If layout is NULL, then use cols to determine layout
+   if (is.null(layout)) {
+     # Make the panel
+     # ncol: Number of columns of plots
+     # nrow: Number of rows needed, calculated from # of cols
+     layout <- matrix(seq(1, cols * ceiling(numPlots/cols)),
+                      ncol = cols, nrow = ceiling(numPlots/cols))
+   }
+
+  if (numPlots==1) {
+     print(plots[[1]])
+
+   } else {
+     # Set up the page
+     grid.newpage()
+     pushViewport(viewport(layout =
+                  grid.layout(nrow(layout), ncol(layout))))
+
+     # Make each plot, in the correct location
+     for (i in 1:numPlots) {
+       # Get the i,j matrix positions of the regions that contain this subplot
+       matchidx <- as.data.frame(which(layout == i,
+                    arr.ind = TRUE))
+
+       print(plots[[i]], vp = viewport(layout.pos.row = matchidx$row,
+                                       layout.pos.col = matchidx$col))
+     }
+   }
+ }
> multiplot(p1, p4, p7, p10, cols=2)
```

4 Appendix: Brief Introduction to Spatiotemporal Modeling in R and INLA

This brief introduction and overview is intended to supplement the material on creating the data sets and conducting the analyses for the paper "Small-Area Spatiotemporal Analysis of Pedestrian and Bicyclist Injuries in New York City 2001-2010". It is based primarily on textbooks and workshops by Andrew Lawson of the Medical University of South Carolina, articles and analyses by Marta Blangiardo of Imperial Medical College in London and and colleagues, papers by Birgit Schroedle and Leonhard Held of the University of Zurich, and

documents by Havard Rue of the Norwegian University of Science and Technology, who is the author of INLA. If you are interested in a fuller introduction to spatial epidemiology in R (similarly stolen from folks smarter than I), please see this document.

4.1 Spatial Models

The standard Besag-York-Mollie[12] (BYM) spatial analystic model is

$$\begin{aligned} y_i &\sim Pois(\lambda_i = e_i\theta_i) \\ log(\theta_i) &= \beta_n + \upsilon_i + \nu_i \\ \upsilon &\sim nl(0, \tau_\upsilon) \\ \nu &\sim nl(\bar{\nu_\delta}, \tau_\nu/n_\delta) \end{aligned}$$

where,

(1) the y_i counts in area i, are independently identically Poisson distributed and have an expectation in area i of e_i , the expected count, times θ_i , the risk for area i :

$$y_i, iid \sim Pois(e_i\theta_i)$$

(2) a logarithmic transformation ($log(\lambda_i)$) allows a linear, additive model of regression terms (β_n), along with

(3) a spatially *unstructured* random effects component (υ_i) that is i.i.d normally distributed with mean zero ($\sim nl(0, \tau_\nu)$), and

(4) a conditional autoregressive spatially structured component ($\nu \sim nl(\bar{\nu_\delta}, \tau_\nu/n_\delta)$) In the usual formulation, each "neghborhood" consists of adjacent spatial shapes that share a common border. The mean θ_j in neighborhood j is normally distributed with its parameters defined as μ_j the average of the μ_{ij}'s in the neighborhood and σ_j equal to the σ's of the neighborhood μ_{ij}'s divided by the number (δ_j) of spatial shapes in the neighborhood. [13]

The spatially *unstructured* random effects component (υ_i) is a random effects term that captures normally-distributed or Gaussian random variation around the mean or intercept α_θ. This unstructured heterogeneity represents, essentially, "noise" that arises from the data that we can't capture with our covariates. It is important, and it contributes to the

[12] J. Besag, J. York, A. Mollie (1991). Bayesian image restoration, with two applications in spatial statistics (with discussion). Annals of the Institute of Statistical Mathematics 43(1), 1-59

[13] The spatially structured component CAR is sometimes described as a Gaussian process $\lambda \sim Nl(W, \tau_\lambda)$ where W represents the matrix of neighbors that defines the neighborhood structure, and the conditional distribution of each λ_i , given all the other λ_i is normal with μ = the average λ of it's neighbors and a precision (τ_λ). See Banerjee, 2004

risk estimate, but it is essentially random and varies normally around zero. A model that consists solely of a random effects term is sometimes referred to as a "frailty" or susceptibility model, because it can be thought of as describing the individual (or area) level susceptibility or frailty to disease given some overall or global susceptibility. It doesn't take covariates, space or geography into account. The addition of a spatially-structured term, ν to a random effect model is sometimes referred to as a convolution model.

A useful and commonly used prior distribution for θ in the setting of spatial analyses is the gamma (Γ) distribution:

$$\theta \sim \Gamma(\alpha, \beta)$$

where, $\mu = \alpha/\beta$, and $var = \alpha/\beta^2$

The Gamma distribution consists of a very flexible class of probability distributions. For example, $\Gamma(1, b)$ is exponential with $\mu = 1/b$, $\Gamma(\frac{v}{2}, \frac{1}{2})$ is chi square distributed with v degrees of freedom. Gamma distributions are constrained to be positive, which is necessary when dealing with count data, and setting the two parameters equal to each other $\alpha = \beta$ returns a null value of 1, which is useful for modeling risk estimates. Finally, the Gamma distribution is conjugate to the Poisson distribution, making our prior and our likelihood of the same family which not only allows for simplified statistics in one parameter problems, but carries with it additional advantages in terms of a valid choice of prior in more complicated analyses.

Since a basic Bayesian assumption is that any parameter in a problem has a prior distribution of its own, the α and β parameters in the gamma also have prior distributions. The usual approach is to put exponential distributions on α and β, so that: [14]

$$\begin{aligned} y_i &\sim Pois(e_i\theta_i) \\ \theta &\sim \Gamma(\alpha, \beta) \\ \alpha &\sim exp(v), \\ \beta &\sim exp(\rho) \end{aligned}$$

4.2 Space-Time Models

We are often interested in both the spatial and temporal aspects of disease data, e.g. disease location and date of diagnosis, or (perhaps more commonly) disease counts in small areas in a fixed time period. A frequently used approach to spatial disease modeling in small areas dates to work by Besag (1991) which was extended by Bernardinelli (1995) to include a linear term for space-time interaction, and by Knorr-Held (2000) to include a non-parametric spatio-temporal time trend.[15]

[14] At this point we begin to see the inherently hierarchical nature of the Bayesian approach

[15] See "A primer on disease mapping and ecological regression using INLA" by Birgit Schroedle and Leonhard Held for a nice description of the evolution of spatiotemporal disease modeling.

Space-time (ST) data can be thought of as multivariate or correlated observations of disease counts within fixed spatial and temporal units that evolve over time, with both space and time are subscripted in the analysis. One might, for example, have 10 years of monthly SMR's at the county level for a state. We could (if we wanted) look at separable models of spatial and temporal terms, or look at the interaction between space and time. For i= 1...M small areas, and $j = 1...$J time periods the disease outcome, y_{ij}, is characterized by an expected counts, e_{ij}, and a risk, $\theta)ij$. The simplest overall average for the expected counts is $e_{ij} = p_{ij} \cdot \Sigma\Sigma/\Sigma\Sigma p_{ij}$, where p_{ij} is the population of the ij^{th} unit.

A basic retrospective model assumes a Poisson distributed outcome in an infinite population with a small disease probability:

$$\begin{aligned} y_{ij} &\sim Pois(e_{ij}, \theta_{ij}) \\ log(\theta_{ij}) &= \alpha_o + S_i + T_j + ST_{ij} \end{aligned}$$

where, S = spatial term(s), T= temporal terms(s), ST = space-time interaction

In broad overview, possible random effects specifications for the temporal term include a linear time trend (β_t), a random time effect (γ_j), a random walk (γ_{1j}), a first-order autoregression (γ_{2j}), or an interaction between space and time (ψ_{ij}). Some commonly seen specification are:

$$\begin{aligned} log(\theta_{ij}) &= \alpha_0 + \upsilon_i + \nu_i + \beta_t \\ log(\theta_{ij}) &= \alpha_0 + \upsilon_i + \nu_i + \gamma_j \\ log(\theta_{ij}) &= \alpha_0 + \upsilon_i + \nu_i + \gamma_{1j} + \gamma_{2j} \\ log(\theta_{ij}) &= \alpha_0 + \upsilon_i + \nu_i + \gamma_{2j} + \psi_{ij} \\ log(\theta_{ij}) &= \alpha_0 + \upsilon_i + \nu_i + \gamma_{1j} + \gamma_{2j} + \psi_{ij} \end{aligned}$$

Which can separated into simple models vs. interaction models.

4.2.1 Simple (Separable) Models

- $log(\theta_{ij}) = \alpha_0 + \upsilon_i + \nu_i + \beta_t$
  - simple separable model, spatial components (BYM) plus *linear* time trend
- $log(\theta_{ij}) = \alpha_0 + \upsilon_i + \nu_i + \gamma_j$
  - simple trend model, spatial component + *random* time effect
  - the γ_j random time effect can be a
    - random walk: $\gamma_j \sim N(\gamma_{j-1}, \tau_\gamma^{-1})$

    - * or an AR_1 : $\gamma_j \sim N(\lambda\gamma_{j-1}, tau_\gamma^{-1})$
- $log(\theta_{ij}) = \alpha_0 + \upsilon_i + \nu_i + \gamma_{1j} + \gamma_{2j}$
    - simple model with two random time effects

4.2.2 Interaction Models

- $log(\theta_{ij}) = \alpha_0 + \upsilon_i + \nu_i + \gamma_j + \psi_{ij}$
    - interaction with single random time effect
    - Knorr-Held (2000) suggested dependent priors, but, two simple possible priors are:
        - * uncorrelated prior for interaction term: $\psi_{ij} \sim N(0, \tau_\psi)$
        - * random walk prior for interaction term: $psi_{ij} \sim N(\psi_{i,j-1}, \tau_\psi)$
- $log(\theta_{ij}) = \alpha_0 + \upsilon_i + \nu_i + \gamma_{1j} + \gamma_{2j} + \psi_{ij}$
    - interaction with two random time effects

In general, the best fitting DICs are seen with the interaction models. The space-time interaction term is essentially a random-effect added to the linear model in the way the unstructured heterogeneity term and spatially-structured conditional autoregression (CAR) heterogeneity terms are added to spatial convolution models. It can be viewed as a kind of residual effect after the unstructured, spatially structured and time effects are modeled. The interaction then is the heterogeneity you didn't "pick up" with the other terms, or (perhaps more accurately) the *additional effect* beyond that which is already picked up with the other space and time terms. In infectious disease models, space-time interaction may represent sporadic outbreaks, like short-term clusters.

4.3 About INLA

Integrated Nested Laplace Approximations (INLA) are a less computationally expensive alternative to MCMC to estimate the integral of a posterior distribution.[16] Commonly used MCMC software like BUGS and JAGS use a computational approach to sample from the posterior distribution of parameters. The INLA approach returns similarly accurate approximations to posterior marginals in significantly less time. Laplace approximations have been known for some time, but only recently developed sufficiently to be accurate enough for inclusion in statistical software and practical application. [17]

[16] Most of this material on the application of INLA to spatial epidemiology comes from Dr. Andrew Lawson's workshop and textbook on the topic.

[17] See Rue, 2009 Approximate Bayesian inference for latent Gaussian models by using integrated nested Laplace approximations

Rasmus Baath has a wonderfully succinct and clear explanation of Laplace approximations. In a nutshell, Laplace approximations "work" because most posterior distributions have the largest proportion of their probability "heaped up" in the center and "trail off" symmetrically on either side, i.e. they "look" normal. The Laplace approximation uses the mode as the mean, and calculates the derivative in the area of the mode to approximate the variance.[18] As you might expect, the closer the posterior is to Gaussian, the better the approximation. Fortunately, this is usually the case. When it is not log and logit transformations can be helpful.

Because it doesn't rely on sampling and computations, INLA returns results very quickly, often much faster than MCMC in BUGS or JAGS.[19] It is also useful for large and high dimensional datasets that can stall or freeze up up in BUGS or JAGS, for random effects models, and for complex spatial and spatiotemporal modeling. Also, INLA was written to be seamlessly integrated into R code, and this ease of use has made it an increasingly popular alternative to MCMC for Bayesian spatial modelin.

INLA documentation lags somewhat behind its popularity, but r-inla.org is very helpful website, with numerous examples and useful links, such as lists of likelihoods that can be specified in INLA. [20] Because there is no sampling in INLA, deviance is determined using the likelihood. [21]

You will need to install INLA from from source as described on the r-inla site

```
source("http://www.math.ntnu.no/inla/givemeINLA.R")
```

Once installed, INLA is accessed through an R session. A call to INLA consists of two parts: a formula statement, followed by a model fitting statement.

4.3.1 The INLA Formula Statement

A formula statement for a spatial model looks like this:

```
form1<-obs ~ 1 +f(region, model="iid")
```

where ,

- *obs* is the disease count or outcome from your dataset

[18] Recall from calculus that the derivative is the instantaneous rate of change. The Laplace approximation makes use of the inverse of the Hessian matrix for the curve to arrive at the result for the variance. The Hessian matrix is a square matrix of partial derivatives for a multivariate function that can be used to describe a local curvature.

[19] INLA is not the only game in town. See for example, Hoffman and Gelman. The no-U-turn sampler: Adaptively setting path lengths in Hamiltonian Monte Carlo. INLA, though, is currently the most mature package in terms of spatial analytic capabilities.

[20] For spatial models, you may notice many of the precisions specified as gamma distributed. This has fallen out of favor in BUGS and JAGS because of computational difficulties, but that is not an issue in INLA.

[21] Recall the deviance information criterion (DIC) is a relative measure. Smaller is better, and results can be negative. As opposed to the number of effective parameters (pD), where smaller is also better, but results can't be negative.

- *1* forces an intercept onto the model
- and, *f()* is a function to specify the spatial region, and how it should be modeled
  - In this statement, spatial region is modeled as "iid" which is Gaussian zero uncorrelated heterogeneity or a random effects term

The *f()* function is a powerful feature of INLA, and is quite flexible. It can be used to invoke most any spatial model, such as geographically weighted regressions (different explanatory associations for outcomes in different regions), or local conditional autoregression models. You can add *f()* functions to each other to build up models. So, for example, you can add a conditional autoregression to a model by adding an *f()* statement with *model = "besag"* to a "iid" uncorrelated heterogeneity *f()*, to create a convolution model. The same model can be specified in more than one way. For example, you can also specify a convolution model directly with a single *f(model="bym")* statement. The approaches differ only in how some elements of the INLA output are displayed.

4.3.2 The INLA Model Statment

An INLA model-fitting statement looks like this:

```
results1<-inla(form1, family="poisson",
data=myDat, control.compute=list(dic=T, cpo=T, graph=T),
E=exp)
```

where,

- *form1* refers to and invokes the previously defined formula
- *family=* specifies the likelihood
- *data=* specifies the data
- *control.compute* = specifies options like DIC and CPO.
  - You can request a DIC for each spatial area with *local dic*, where lighter colors indicate smaller, better fits.
  - **CPO** is the conditional predictive ordinate, a cross validation tool, that predicts an area value using all the data except that area, and compares that value to the actual value. Values range from 0 (poor) to 1 (perfect)
- and, E = specifies the offset variable (required for a Poisson likelihood)

You will need some additional tools and utilities to set up a neighborhood adjacency matrix for use with conditional autoregression models and to map results. The R tools *maptools::readShapePoly()* will read shapefiles into R, and *spdep::poly2nb()* followed by *INLA::nb2INLA()* are used to create the adjacency matrix neighbor structures for use with a CAR model. To map results, you can use *sp::spplot()* or *ggplot2* (with some tweaks...)

As an alternative for uncomplicated map and data structures, a function written by Andrew Lawson's colleague, Bo Cai, called "fillmap" can be used to create simple thematic maps. The function is available in Appendix C of Dr. Lawson's textbook on Bayesian Disease Modeling The *fillmap()* function is sourced, and can then be used with any polygon object to fill a thematic map. The basic arguments are:

```
source("~/fillmap.R")
fillmap(obj, "title", varToPlot, n.col=)
```

As a quick example of the use of *fillmap()*, first source the *fillmap()* function, read in a map file (here using *spdep::readSplus* to read a map exported from geobugs) and plot a normally simulated set of data.

```
> #source fillmap function
> source("/Users/charlie/Dropbox/charleston14/charleston14Files/BDMIfiles/BDMI\ partic
> # quick demo use of fillmap
> geobugsSC<-readSplus("/Users/charlie/Dropbox/charleston14/charleston14Files/ABDMfile
> plot(geobugsSC)
> x<-rnorm(46,1,1)
> fillmap(geobugsSC,"normal simulation",x,n.col=6)
```

4.4 Example: Poisson Model of Suicides in London Boroughs

Blangiardo, et al present an INLA tutorial using suicides counts in the 32 boroughs of London from 1989 to 1983. [22] The data consist of observed suicide counts at the borough level, the expected counts (the result of standardizing the borough rates, by applying London-wide rates to borough populations), a measure of economic deprivation, and a social fragmentation index.

The first basic model is based on a Poisson-distributed variable of counts for each borough $y_i \sim Pois(\lambda_i)$, where the rate in a borough, λ_i, is a risk, θ_i, times the expected count, E_i, for that borough, and the linear predictor for risk on the log scale, $log(\theta_i) = \alpha + \upsilon$, is a linear additive combination of the intercept or *average* city-wide risk on the log scale (α) and a term for spatially *unstructured* heterogeneity, υ.

In WinBUGS or JAGS a model with only unstructured heterogeneity looks like this:

```
model{
for (i in 1: 32){
y[i]~dpois(lambda[i])
log(lambda[i])<-log(expected[i])+log(theta[i])
log(theta[i])<-a0+u[i]
u[i]~dnorm(0,tau.u)}
```

[22] See also Marta Blangiardo, Michela Cameletti, Gianluca Baio, Havard Rue. Spatial and spatio-temporal models with R-INLA. Spatial and Spatio-temporal Epidemiology. 4 (2013): 33–49, and Congdon P. Bayesian statistical modelling. John Wiley and Sons Ltd; 2007.

```
a0~dnorm(0,tau.0)
sd0~dunif(0,100)

sdu~dunif(0,100)
tau.0<-1/(sd0*sd0)

tau.u<-1/(sdv*sdv)
}
```

We will fit this in INLA.

Load the necessary packages, download the London borough map shapefile, and read it into R.

```
> library(INLA)
> library(maptools)
> library(spdep)
> london<-readShapePoly("~/LDNSuicides.shp")
> str(london)
> plot(london)
> names(london)
> london$NAME
```

The next two chunks of code involve data manipulations. First, read in vectors of data for observed suicide counts (y), expected counts (E), economic deprivation (x1), and social fragmentation (x2). These data vectors are arranged by an alphabetically sorted list of London borough names. Sort the names of the boroughs in the London map object to match the data order and combine the data with this list of alphabetically sorted borough names into a data frame.

```
> y=c(75,145,99,168,152,173,152,169,130,117,124,119,134,90,
+     98,89,128,145,130,69,246,166,95,135,98,97,202,75,100,
+     100,153,194)
> E=c(80.7,169.8,123.2,139.5,169.1,107.2,179.8,160.4,147.5,
+     116.8,102.8,91.8,119.6,114.8,131.1,136.1,116.6,98.5,
+     88.8,79.8,144.9,134.7,98.9,118.6,130.6,96.1,127.1,97.7,
+     88.5,121.4,156.8,114)
> x1=c(0.87,-0.96,-0.84,0.13,-1.19,0.35,-0.84,-0.18,-0.39,0.74,
+      1.93,0.24,0.59,-1.15,-0.8,-0.59,-0.12,1.43,-0.04,-1.24,1,
+      0.53,-0.75,1.36,-0.93,-1.24,1.68,-1.04,2.38,0.03,-0.2,0.14)
> x2=c(-1.02,-0.33,-1.43,-0.1,-0.98,1.77,-0.73,-0.2,-0.96,-0.58,
+      0.36,1.48,0.46,-0.93,-1.62,-0.96,-0.48,0.81,2.41,-0.4,
+      0.71,-0.05,-0.33,-0.47,-0.92,0.06,0.22,-0.73,0.1,-0.59,
+      0.7,2.28)
> names<- sort(london$NAME) # sort vector of borough names
> suicideDat <- data.frame(NAME=names, y=y, E=E, x1=x1, x2=x2) # create dataframe
```

Get the data back into the same order as the map so they line up for plotting. Copy the map

to an object called "boroughs", extract the data slot from this map object to a dataframe called "boroughsDat" using the *attr()* function. Create an index called "lineUp" and use it to reorder the suicide data. Then add a sequential ID number to the suicide data set.

```
> boroughs <- london # copy map object
> boroughsDat <- attr(boroughs, "data") # extract data from map
> lineUp <- match(boroughsDat$NAME,suicideDat$NAME) # index map data to dataframe on b
> suicideDat <- suicideDat[lineUp,] # sort dataframe by index names from map
> ID<-seq(1,32) # create region ID variable for modeling
> suicideDat <- cbind(ID,suicideDat)
```

4.4.1 Uncorrelated Heterogeneity (Frailty) Model

Run the model in INLA. [23]

```
> formulaUH <- y ~ f(ID, model = "iid") # specify model
> resultUH <- inla(formulaUH,family="poisson", # run inla
+ data=suicideDat, control.compute=list(dic=TRUE,cpo=TRUE),E=E)
```

A summary of the results returns some general information about the run, along with the results for the fixed effects part of the model (α), as well as the DIC. More precise estimates of the fixed effects results are stored in the "summary.fixed" list object in the results object, *resultUH*. Exponentiate the fixed effects to see that based on these data there is on average a 4.6% suicide rate across all London boroughs, with a 95% probability interval ranging from -5.5% to 14.5%.[24]

In this first model, we are interested in the random effect term. Those results are stored in the "region" part of "summary.random" in the named list object created from the INLA run. Extract and examine the mean random effect term for each county. Recall, this is the random variation, on the log scale, around the mean or intercept value of the number of deaths due to congenital birth defects in a county. A plot of the density distribution for the random effect term appears reasonably (for such a small number of observations) normally distributed.

```
> summary(resultUH)
> exp(resultUH$summary.fixed)
> names(resultUH) # want "summary.random" for UH effects
> resultUH$summary.random # want the mean, which is 2nd column
> RE1<-resultUH$summary.random$ID[,2]
> plot(density(RE1)) # plot density random effects
```

[23] You may want to compare the speed of this run with WinBUGS or JAGS and consider the implications for data much larger than 32 observations...

[24] If this strikes you a high, it did me too. And it is. In fact, the most recent population-based rates for the high-risk middle-age male group across all London is about 0.3%. Clearly , this spatial model is most useful for relative rather than absolute differences.

Next, map the UH results. It takes a bit of care to make sure the results are matched to the correct geographic regions. The *fillmap()* function is a quick and easy approach to simple, consecutive data, but in this case the default approach returns the wrong results. Rather than adjust the results to fit *fillmap()*, I find the *attr()* function to be the most reliable tool to manipulate modeling results into the correct order and format for mapping.

First, add the random effect results to the *suicideDat* dataframe and create *cuts* to plot categories of outcomes. Then use the unique names to merge the data frame to the *boroughsDat* data frame that was extracted from the map object and replace the *data* slot of the map object with the merged datafame.

```
> source("/Users/charlie/Dropbox/charleston14/charleston14Files/ABDMfiles/participant_
> fillmap(london, "UH effect", RE1*100, n.col=6) # map
> # add random effects results to dataframe
> suicideDat$UH<-RE1
> #categorize the random effects results
> summary(suicideDat$UH)
> cuts <- c(-0.396100, -0.184800, -0.035180,  0.131400,  0.450200)
> suicideDat$UH.cut<-cut(suicideDat$UH,breaks=cuts,include.lowest=TRUE)
> #merge suicide and map dataframes and save into data slot of map
> attr(london,"data") <- merge(boroughsDat,suicideDat,by="NAME")
> # map
> spplot(london, "UH.cut", col.regions=gray(3.5:0.5/4),main="")
>
>
```

Looking at the uncorrelated heterogeneity is useful from a purely spatial perspective, but as epidemiologists we will invariably be most interested in extracting and characterizing the risk estimates from the INLA results. The result list object "summary.fitted.values" is the exponentiated risk $\theta_i = \alpha_i + \upsilon_i$. A more nuanced result is the exponentiated υ_i output which is the risk represented by the uncorrelated heterogeneity, which can be interpreted as the normally distributed geographic risk. This is obtained by applying the INLA function *inla.emarginal()* on the marginal results for the random effect. [25] In a convolution model with a CAR term, this process will return the spatially correlated or structured risk, $\zeta = \upsilon_i + \nu_i$.

Exceedance probabilities for an area are the posterior probabilities that the spatial risk is greater than 1 ($Pr[\zeta_i > 1|y]$). They are obtained by applying the INLA function *inla.pmarginal()* to the marginals for the random effect. [26]

The exceedance probability of spatial risk $\upsilon + \nu$ greater than 1 is more readily accessible from the model results on the un-exponentiated scale, so we set the threshold to 0 ("a=0").

[25] For this simple frailty or random effects model of uncorrelated hetergeneity, if you exponentiate the random effects result from the previous section you should get the same result as that from *inla.marginal()* ($exp(RE1)$ vs. $unlist(UHzeta)$). And you do. Basically. There are some slight differences. I am not sure why.

[26] Exceedance probabilities have been proposed as a Bayesian approach to hotspot identification. They can be very useful, though they can be sensitive to model specification. See this commentary

To obtain exceedance of a greater threshold, change that value, e.g. risk of 2 on the un-exponentiated scale is 0.6931472.[27]

```
> #risk (theta = alpha + upsilon)
> UHrisk <- resultUH$summary.fitted.values[,1]
> UHrisk
> #spatial risk (zeta = upsilon only)
> UHmarginals <- resultUH$marginals.random$ID[1:32] # extract UH term (1 to number of
> UHzeta <- lapply(UHmarginals,function(x)inla.emarginal(exp,x)) # exponentiate
> # exceedence probability
> a=0
> UHexceedence<-lapply(resultUH$marginals.random$ID[1:32], function(X){
+   1-inla.pmarginal(a, X)
+ })
```

Add these results to the dataframe, categorize, save the dataframe to the map data slot and map.

```
> spatResults <- data.frame(NAME=suicideDat$NAME, risk=UHrisk,    geoRisk=unlist(UHzet
+                                exceed=unlist(UHexceedence))
> RR.cut<-c(0.6, 0.9, 1.0, 1.1,  1.8)
> geoRisk.cut<- c(0.6, 0.9, 1.0, 1.1,  1.8)
> exceed.cut<- c(0,0.2,0.5,0.8,1)
> spatResults$risk.cut<-cut(spatResults$risk,breaks=RR.cut,include.lowest=TRUE)
> spatResults$geoRisk.cut<-cut(spatResults$geoRisk,breaks=geoRisk.cut,include.lowest=T
> spatResults$exceed.cut<-cut(spatResults$exceed,breaks=exceed.cut,include.lowest=TRUE
> attr(london,"data")<-merge(boroughsDat,spatResults,by="NAME")
> spplot(london, c("risk.cut","geoRisk.cut"), col.regions=gray(3.5:0.5/4),main="")
> spplot(london, c("exceed.cut"), col.regions=gray(3.5:0.5/4),main="")
```

We see that the patterns are fairly similar across all three outcomes.

4.4.2 Conditional Autoregression (Convolution) Model with Covariates

As mentioned above, there are two ways to specify a convolution model in INLA. You can add a CAR term to a random effect component:[28]

```
f(region, model = "iid") + f(region2,model="besag",graph="adj_matrix.txt")
```

or, you can specify a convolution model with a single *f()* function:[29]

[27] There is a function unrelated to INLA that automates exceedance probability calculations. It is called *excProb*, is available in the "geostatsp" package, and requires the package "pracma". To use it, extract the list of two-column matrices with columns named x and y containing the posterior distributions of random effects, as produced by INLA (e.g. inlaMargs<-resultCAR$marginals.random$ID.area[1:1000]) and set the threshold to what you want, e.g. excProb(inlaMargs, threshold=2)

[28] "besag" refers to Julian Besag, who developed the CAR model of spatially correlated heterogeneity in 1974.

[29] "bym" refers to Besag, York and Mollie. To whom this model formulation is attributed.

```
f(region,model="bym",graph="adj_matrix.txt")
```

The only difference in the results is how the output is structured and hence extracted for evaluation and display. In the formulation with two *f()* statements, there is a separate summary result for each part of the model, one stored in summary.random$region the other in summary.random$region2. (We need to create a second, identical geographic indexing variable called region2.) In the single *f(model="bym")* statement formulation, the results for each component of the model are concatenated in a single summary.random$region result, with the UH terms listed first, followed by the CAR terms. We extract the terms we want by indexing. In either case we must provide an adjacency matrix, which we create by first using the *spdep:::poly2nb* tool to create the matrix, and then the *INLA:nb2INLA* tool to format the matrix for INLA.

```
> temp <- poly2nb(london)
> nb2INLA("LDN.graph", temp)
> LDN.adj <- paste(getwd(),"/LDN.graph",sep="")
```

In this example we'll run a convolution model and include the covariates for economic deprivation and social fragmentation. The model is

$$y_i = \alpha + \beta_1 x_{1i} + \beta_2 x_{2i} + \upsilon_i + \nu_i$$

Run the model with a single *f(model="bym")* statement.

```
> formulaCONVcov <- y ~ 1+ f(ID, model="bym", graph=LDN.adj) + x1 + x2
> resultCONVcov <- inla(formulaCONVcov,family="poisson",
+ data=suicideDat, control.compute=list(dic=TRUE,cpo=TRUE),E=E)
```

Review the results. Looking at the fixed effects, the intercept, or average risk across all boroughs, is about 6%. The exponentiated risks for economic deprivation and social fragmentation are interpreted as incidence density ratios or risks. For each 1 unit increase in economic deprivation, there is an approximate 9.5% risk in suicide. Each 1 unit increase in social deprivation is associated with an approximate 19.7% increase in suicide risk.

```
> summary(resultCONVcov) #DIC 259 vs 270 for UH alone
> exp(resultCONVcov$summary.fixed) # mean 6%, econ 9.5%, social 19.7%
> names(resultCONVcov) # "summary.random" stores UH and CAR effects
> resultCONVcov$summary.random # want the mean, which is 2nd column
> re2<-resultCONVcov$summary.random$ID[1:32,2]# random effects
> plot(density(re2)) # plot density random effects
> car1<-resultCONVcov$summary.random$ID[33:64,2] # correlated spatial (car)
> plot(density(car1))
```

Calculate overall risk ($\theta = \alpha + \upsilon + \nu$), spatial risk ($\zeta = \upsilon + \nu$) and spatial exceedance ($\Pr[\zeta_i > 1]$). Note that the spatial risk (ζ) is now interpreted as the *residual relative risk for each area (compared to the whole of London) after economic deprivation and social fragmentation are taken into account.*

```
> #risk (theta = alpha + upsilon + nu)
> CONVcovrisk <- resultCONVcov$summary.fitted.values[,1]
> CONVcovrisk
> #spatial risk (zeta = upsilon + nu)
> CONVcovmarginals <- resultCONVcov$marginals.random$ID[1:32]
> CONVcovzeta <- lapply(CONVcovmarginals,function(x)inla.emarginal(exp,x)) # exponenti
> # exceedence probability
> a=0
> CONVcovexceedence<-lapply(resultCONVcov$marginals.random$ID[1:32], function(X){
+   1-inla.pmarginal(a, X)
+ })
>
```

Mapping these results demonstrates the spatial character of suicide risk more clearly than with the simple UH model.

```
> spatResults2 <- data.frame(NAME=suicideDat$NAME, risk=CONVcovrisk,    geoRisk=unlist
+                                exceed=unlist(CONVcovexceedence))
> RR.cut<-c(0.6, 0.9, 1.0, 1.1,  1.8)
> geoRisk.cut<- c(0.6, 0.9, 1.0, 1.1,  1.8)
> exceed.cut<- c(0,0.2,0.5,0.8,1)
> spatResults2$risk.cut<-cut(spatResults2$risk,breaks=RR.cut,include.lowest=TRUE)
> spatResults2$geoRisk.cut<-cut(spatResults2$geoRisk,breaks=geoRisk.cut,include.lowest
> spatResults2$exceed.cut<-cut(spatResults2$exceed,breaks=exceed.cut,include.lowest=TR
> attr(london,"data")<-merge(boroughsDat,spatResults2,by="NAME")
> spplot(london, c("risk.cut","geoRisk.cut"), col.regions=gray(3.5:0.5/4),main="")
> spplot(london, c("exceed.cut"), col.regions=gray(3.5:0.5/4),main="")
>
```

From these results, you can calculate the proportion of variance explained by spatially structured (CAR) component [30] The process involves creating an empty matrix with rows equal to the number of regions, and 1000 columns into which we extract 1000 observations from the marginal distribution of the CAR term (ν), which is used to calculate the empirical variance. Similarly, values are extracted for the random effects (UH) term and the variance calculated. Finally, sum the two variances, and calculate the proportion of total heterogeneity accounted for by the spatially structured heterogeneity. In this case, spatially structured variance accounts for about 74% of the total variance.

[30]Note. Andrew Lawson cautions against measures like this because CAR and UH are incompletely identified. Even Blangiardo, from whom this code is adapted, says the UH and CAR variances are not directly comparable, though the result can give an indication of the relative contribution of each.

```
> mat.marg <- matrix(NA, nrow=32, ncol=1000)
> m<-resultCONVcov$marginals.random$ID
> for (i in 1:32){
+   u<-m[[32+i]]
+   s<-inla.rmarginal(1000, u)
+   mat.marg[i,]<-s}
> var.RRspatial<-mean(apply(mat.marg, 2, sd))^2
> var.RRhet<-inla.emarginal(function(x) 1/x,
+                           resultCONVcov$marginals.hyper$"Precision for ID (iid compo
> var.RRspatial/(var.RRspatial+var.RRhet)
```

4.5 Example: Logit Model of Cumbria Foot and Mouth Disease

INLA can be used for other model specifications. Here we look at counts of foot and mouth disease in 138 Cumbrian parishes in northwest England in 2001. The data are disease counts and an estimate of the population over a single time period. We will use the following model:

$$
\begin{aligned}
y_i &\sim bin(n_i, p_i) \\
logit(p_i) &= \alpha_0 + v_i \\
\alpha_0 &\sim N(0, \tau_0^{-1}) \\
v_i &\sim N(0, \tau_v^{-1})
\end{aligned}
$$

In the following code, we set up the data as a list object, read in a map file and use *fillmap()* to quickly map the crude rates. We then set up and run a binomial model in INLA.

```
> # set up FMD data
>
> FMDframe<-list(n=138,
+ count=c(1,0,1,0,2,3,1,0,1,0,3,2,0,3,1,6,1,10,2,1,8,4,4,1,1,
+ 3,9,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
+ 0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,
+ 0,0,0,1,1,1,0,0,0,0,0,0,2,0,0,2,0,0,0,0,0,0,0,0,0,0,0,0,0,
+ 0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,4,0,0),pop=c( 26,19,28,42,55,30,45,20,35,73,
> FMDmap<-readSplus("~/FMD_splusMAP.txt")
> plot(FMDmap)
> ### map of crude rates with fillmap
>
> rate<-FMDframe$count/FMDframe$pop
> fillmap(FMDmap,"crude rate map",rate,n.col=6)
> # set up area indicators for map (NB need to be indexed to map units...)
> ind<-seq(1:138)
> # set up and call inla
```

```
> formula1<-count~1+f(ind,model="iid")
> res1<-inla(formula1,family="binomial",data=FMDframe,Ntrials=FMDframe$pop,
+ control.compute=list(dic=TRUE))
>
```

Assess the results by first looking first at a summary, then at the UH or unstructured spatial random effects and then at a map of residuals. The unstructured random effect term picks up some spatial structure since it is the only spatial term on the right side of the equation. Map a measure of the local DIC, as well as the probability of infection based on the linear predictor results in the logistic formula:

$$\frac{e^{\beta_0+\beta_1 x1 \ldots \beta_i xi}}{1+e^{\beta_0+\beta_1 x1 \ldots \beta_i xi}}$$

```
> summary(res1)
> # look at uncorrelated heterogeneity
> UH<-res1$summary.random$ind[,2]
> fillmap(FMDmap,"posterior mean UH component",UH,n.col=4)
> # calculate and map residuals
> fit<-res1$summary.fitted.values$mean
> resid<-FMDframe$count-fit
> fillmap(FMDmap,"estimated crude residuals",resid,n.col=4)
> # map local dic
> LOCdic<-res1$dic$local.dic
> fillmap(FMDmap,"local DIC",LOCdic,n.col=5)
> # calculate and map risk estimates
> # grab the linear predictors, then calculate inverse logit to
> # get probability vector
> linPred<-res1$summary.linear.predictor$mean
> prob<-exp(linPred)/(1+exp(linPred))
> fillmap(FMDmap,"posterior mean infection probability",prob,n.col=4)
>
```

4.6 Space-Time Models With INLA

4.6.1 Example: Spatiotemporal Model of Respiratory Cancer in Ohio Counties

As an example of spatiotemporal modeling in INLA we look at respiratory cancer in Ohio counties. 21 years of data are available. We will analyze 10 years of data, from 1979 ti 1988.

The first task is setting up the data. The data are in a list object called *ohioDat* and consist of observed (y) and expected (e) respiratory cancers over 10 years for 88 counties in Ohio. The variable m stores the number of counties (88); the variable T is the number of years (10), the variable t is the sequence of years from 1 to 10.

Next manipulate the data object to get it from the "wide" format into the "long" format of one space-time observation per row required for analysis in INLA. [31]

```
> load("/Users/charlie/Dropbox/srtsAnalysis/srtsNotes/srtsINLA/ohioDat.RData")
> # convert data to long form
> yL<-rep(0,880)
> eL<-rep(0,880)
> T <- 10
> for (i in 1:88){
+ for (j in 1:10){
+ k<-j+T*(i-1)
+ yL[k]<-ohioDat$y[i,j]
+ eL[k]<-ohioDat$e[i,j]
+ }}
>  # set up variables for year (simple trend 1-10 repeated), region, then copy repeat
>  # (for use in second f() function), then set up space-time interaction term (ind2)
>  # (incrementing over each observation)
> year<-rep(1:10,len=880)
> region<-rep(1:88,each=10)
> region2<-region
> ind2<-rep(1:880) # this is the space-time interaction term
> # inla requires a data frame
> ohioDatL<-data.frame(year,region,yL,eL,region2,ind2)
```

The next step is to read in the map file and create the adjacency matrix.[32]

```
> library(maptools)
> polyOHIO<-readSplus("~/Ohio_splusMAP.txt")
> plot(polyOHIO)
> source("~/fillmap.R")
> x<-rnorm(88,1,1)
> fillmap(polyOHIO, "Ohio Cancer", x, 6)
> library(spdep)
> library(INLA)
> adjpoly<-poly2nb(polyOHIO)
> nb2INLA("OHIO_map",adjpoly)
> # OHIO.adj <- paste(getwd(),"OHIO.adj",sep="")
```

In the following code we run and save a number of potential models. These models are various combinations of unstructured heterogeneity or spatial random effect (UH), spatially structured heterogeneity (SH) or CAR models, linear time trend (just adding the sequential time variable), unstructured time (iid distributed time variable), autoregressive time (random walk) and space time interactions. We compare them on DIC.

[31] There are a number of ways to do this, e.g with *base::reshape* or *reshape2::melt*. Here we use an approach described by Dr. Lawson.

[32] Note that though I am not doing it here, a good place to start any time-space analysis is to simply look at a series of maps for each year...

```
> #### spatial only UH, poisson likelihood
> formula1<-yL~1+f(region,model="iid")
> result1<-inla(formula1,family="poisson",data=ohioDatL,
+ E=eL,control.compute=list(dic=TRUE,cpo=TRUE))
> summary(result1)
> result1$dic$dic # 6823
> # random effect (UH)
> result1$summary.random$region[,2]
> #risk (theta = alpha + upsilon) value for each space-time observation
> result1$summary.fitted.values[,1]
> #exponentiated fixed effect
> exp(result1$summary.fixed) # avg -3%
> #### add  random effect (UH) and correlated spatial (CH or CAR), i.e. convolution mo
> formula2<-yL~1+f(region,model="iid")+f(region2,model="besag",graph="OHIO_map")
> result2<-inla(formula2,family="poisson",data=ohioDatL,
+ E=eL,control.compute=list(dic=TRUE,cpo=TRUE))
> result2$dic$dic # 6824 (no improvement)
> ### spatial (u and v) + time trend (simply add year as covariate)
> formula3<-yL~1+f(region,model="iid")+f(region2,model="besag",graph="OHIO_map")+year
> result3<-inla(formula3,family="poisson",data=ohioDatL,
+ E=eL,control.compute=list(dic=TRUE,cpo=TRUE))
> result3$dic$dic # 6777 (improved over UH only)
> exp(result3$summary.fixed) # avg 3.7% (intercept) ~1.3% decrease each year
> result1$summary.fitted.values[,1]
> result3$summary.random$region[,2] # UH result
> result3$summary.random$region2[,2] # CAR result
> ###  uncorrelated (UH or random effect) + correlated (CH or CAR) spatial + uncorrela
> formula4<-yL~1+f(region,model="iid")+f(region2,model="besag",graph="OHIO_map")+f(yea
> result4<-inla(formula4,family="poisson",data=ohioDatL,
+ E=eL,control.compute=list(dic=TRUE,cpo=TRUE))
> result4$dic$dic # 6598 (random effect time better than linear time)
> ### uncorrelated (UH or random effect) + correlated (CH or CAR) spatial + random wal
> formula5<-yL~1+f(region,model="iid")+f(region2,model="besag",graph="OHIO_map")+f(yea
> result5<-inla(formula5,family="poisson",data=ohioDatL,
+ E=eL,control.compute=list(dic=TRUE,cpo=TRUE))
> result5$dic$dic # 6598 (correlated time same as random effect time)
> result5$summary.random$region[,2] # UH
> result5$summary.random$region2[,2] # CAR
> result5$summary.random$year[,2] # time effect
> ###  uncorrelated (UH or random effect) + correlated (CH or CAR) spatial + random wa
> year2<-year # need second time variable for model
> formula6<-yL~1+f(region,model="iid")+f(region2,model="besag",graph="OHIO_map")+f(yea
> result6<-inla(formula6,family="poisson",data=ohioDatL,
+ E=eL,control.compute=list(dic=TRUE,cpo=TRUE))
> result6$dic$dic # 6598  (having random plus correlated time effects same as having o
```

```
> ### now adding an interaction term to the UH random effect model with random walk ti
> formula7<-yL~1+f(region,model="iid")+f(year,model="rw1")+f(ind2,model="iid")
> result7<-inla(formula7,family="poisson",data=ohioDatL,
+ E=eL,control.compute=list(dic=TRUE,cpo=TRUE))
> result7$dic$dic # 6033 (adding interaction meaningfully improves the model)
> ###  convolution model with interaction term:  UH +CH + year RW1 + INT IID
> formula8<-yL~1+f(region,model="iid")+f(region2,model="besag",graph="OHIO_map")+f(yea
> result8<-inla(formula8,family="poisson",data=ohioDatL,
+ E=eL,control.compute=list(dic=TRUE,cpo=TRUE))
> result8$dic$dic # 6033 (no improvement over previous random effect)
```

Model 7 appears to have the best combination of DIC and parsimony. This model consisted of a spatial random effect or unstructured heterogeneity term, an autoregressive temporal term and a space-time interaction term.

Explore some results. Save the spatial random effect, autoregressive temporal term and the interaction results to objects. Map the unstructured heterogeneity term and plot it's density. It appears random and centered around zero. Then plot the temporal heterogeneity terms by year. There appears to be an overall negative trend with the final year perhaps something of an outlier. A plot omitting year 10 with a line for the simple linear regression of temporal heterogeneity on time perhaps illustrates the trend more clearly.

Finally, set up a matrix of 88 rows counties and 10 columns for time and populate it with the interaction effect results. Plot the first two years of results.

As noted above, the space-time interaction is a random-effect term can be viewed as a kind of residual effect after the unstructured, spatially structured and time effects are modeled. It is the additional effect beyond that which is already picked up with the other space and time terms. In this case, the areas with elevated values represent sporadic outbreaks, like short-term clusters, in years one and two.

```
>  UH<-result7$summary.random$region[,2]
> yearR<-result7$summary.random$year[,2]
> STint<-result7$summary.random$ind2[,2]
> fillmap(polyOHIO,"UH",UH*100,n.col=6)
> plot(density(UH))
> time<-seq(1:10)
> plot(time,yearR)
> lines(time,yearR)
> yearR[-10]
> plot(time[-10],yearR[-10])
> abline(lm(yearR[-10]~time[-10]))
> STest<-matrix(0,nrow=88,ncol=10)
> for(k in 1:880){
+ i=ceiling(k/10)
+ j=k-10*(i-1)
+ STest[i,j]<-STint[k]}
```

```
> ST1<-STest[,1]
> ST2<-STest[,2]
> fillmap(polyOHIO,"ST interaction yr 1",ST1,n.col=6)
> x11()
> fillmap(polyOHIO,"ST interaction yr 2",ST2,n.col=6)
```