inla v2

data

```r
dat <- readRDS('C:/Users/sympl/Documents/UMass/msthesis/Data/2014data.rds')

#dd<- readRDS('C:/Users/sympl/Documents/UMass/msthesis/Data/regiondata.rds')

ge.shp<-readOGR("C:/Users/sympl/Documents/UMass/msthesis/GPS/GHGE71FL/GHGE71FL.shp")
```

```
## OGR data source with driver: ESRI Shapefile
## Source: "C:\Users\sympl\Documents\UMass\msthesis\GPS\GHGE71FL\GHGE71FL.shp", layer: "GHGE71FL"
## with 427 features
## It has 20 fields
```

```r
bound<-readOGR("C:/Users/sympl/Documents/UMass/msthesis/GPS/sdr_subnational_boundaries_2021-03-05/shps/s
```

```
## OGR data source with driver: ESRI Shapefile
## Source: "C:\Users\sympl\Documents\UMass\msthesis\GPS\sdr_subnational_boundaries_2021-03-05\shps\sdr_s
## with 10 features
## It has 27 fields
```

```r
# district boundary
dist<-readOGR("C:/Users/sympl/Documents/UMass/msthesis/GPS/Ghana_District_CORRECT/Ghana_districts_corre
```

```
## Warning in OGRSpatialRef(dsn, layer, morphFromESRI = morphFromESRI, dumpSRS
## = dumpSRS, : Discarded ellps War Office in Proj4 definition: +proj=tmerc
## +lat_0=4.66666666666667 +lon_0=-1 +k=0.99975 +x_0=274319.739163358 +y_0=0
## +a=6378300 +rf=296 +to_meter=0.304799710181509 +no_defs

## Warning in OGRSpatialRef(dsn, layer, morphFromESRI = morphFromESRI,
## dumpSRS = dumpSRS, : Discarded datum Accra in Proj4 definition: +proj=tmerc
## +lat_0=4.66666666666667 +lon_0=-1 +k=0.99975 +x_0=274319.739163358 +y_0=0
## +a=6378300 +rf=296 +to_meter=0.304799710181509 +no_defs

## Warning in showSRID(wkt2, "PROJ"): Discarded ellps War Office in Proj4
## definition: +proj=tmerc +lat_0=4.66666666666667 +lon_0=-1 +k=0.99975
## +x_0=274319.739163358 +y_0=0 +a=6378300 +rf=296 +to_meter=0.304799710181509
## +no_defs +type=crs

## Warning in showSRID(wkt2, "PROJ"): Discarded datum Accra in Proj4 definition

## OGR data source with driver: ESRI Shapefile
## Source: "C:\Users\sympl\Documents\UMass\msthesis\GPS\Ghana_District_CORRECT\Ghana_districts_correct.s
## with 110 features
## It has 18 fields
```

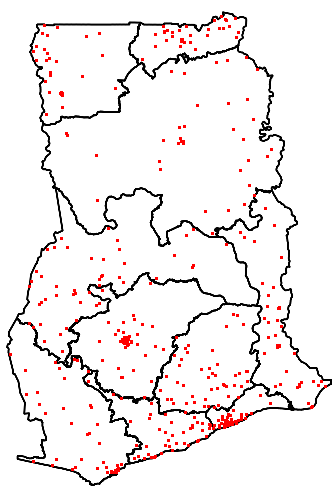
```
dist2<- readOGR("C:/Users/sympl/Documents/UMass/msthesis/GPS/gadm36_GHA_shp/gadm36_GHA_2.shp")
```

```
## OGR data source with driver: ESRI Shapefile
## Source: "C:\Users\sympl\Documents\UMass\msthesis\GPS\gadm36_GHA_shp\gadm36_GHA_2.shp", layer: "gadm3
## with 137 features
## It has 13 fields
```

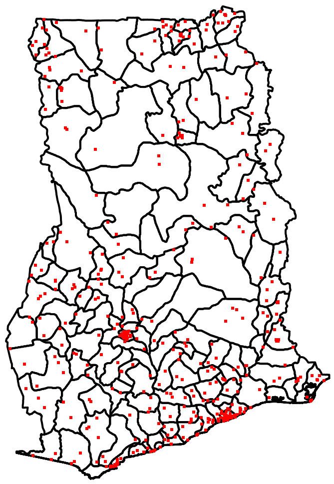
```
dist3<- readOGR("C:/Users/sympl/Documents/UMass/msthesis/GPS/Ghana_Dist_DHS_Join/GPS_Points_Districts.s
```

```
## OGR data source with driver: ESRI Shapefile
## Source: "C:\Users\sympl\Documents\UMass\msthesis\GPS\Ghana_Dist_DHS_Join\GPS_Points_Districts.shp", l
## with 427 features
## It has 41 fields
## Integer64 fields read as strings:  OBJECTID Join_Count TARGET_FID Index Household
```

```
plot(bound)
points(ge.shp, pch=".", col="red")
```



```
plot(dist2) #from LA
points(ge.shp, pch=".", col="red")
```



nb

```
library(spdep)
```

```
## Loading required package: spData
```

```
## Loading required package: sf
```

```
## Linking to GEOS 3.8.0, GDAL 3.0.4, PROJ 6.3.1
```

```
nb <- poly2nb(bound, row.names = bound@data$REGCODE) #for calculating neighbors

nb2INLA("map.adj", nb)
g <- inla.read.graph(filename = "map.adj")

##define stuctured and unstructured spatial re vectors
bound$re_u <- 1:nrow(bound@data)
bound$re_v <- 1:nrow(bound@data)

trial<-dat
trial$region<- as.numeric(trial$region)
trial<-trial %>% right_join(bound@data, by= c("region"="REGCODE"))
```

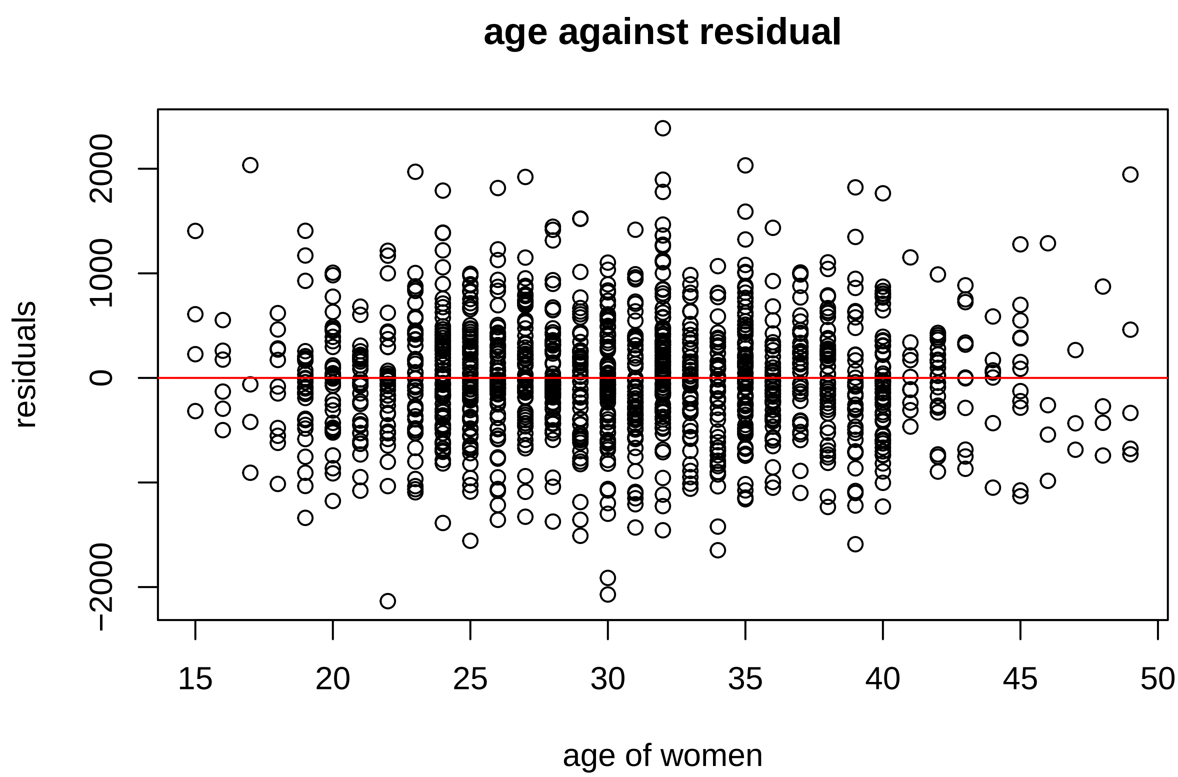
fitting iid random effect

```r
##formula
formula <- c_weight ~ fuel_bin+gender+education+ w_age+ marital_s+wealth+bmi+residence + f(re_v, model =

# inla
res <- inla(formula, family = "gaussian", data = trial,  control.predictor = list(compute = TRUE))

summary(res)
```

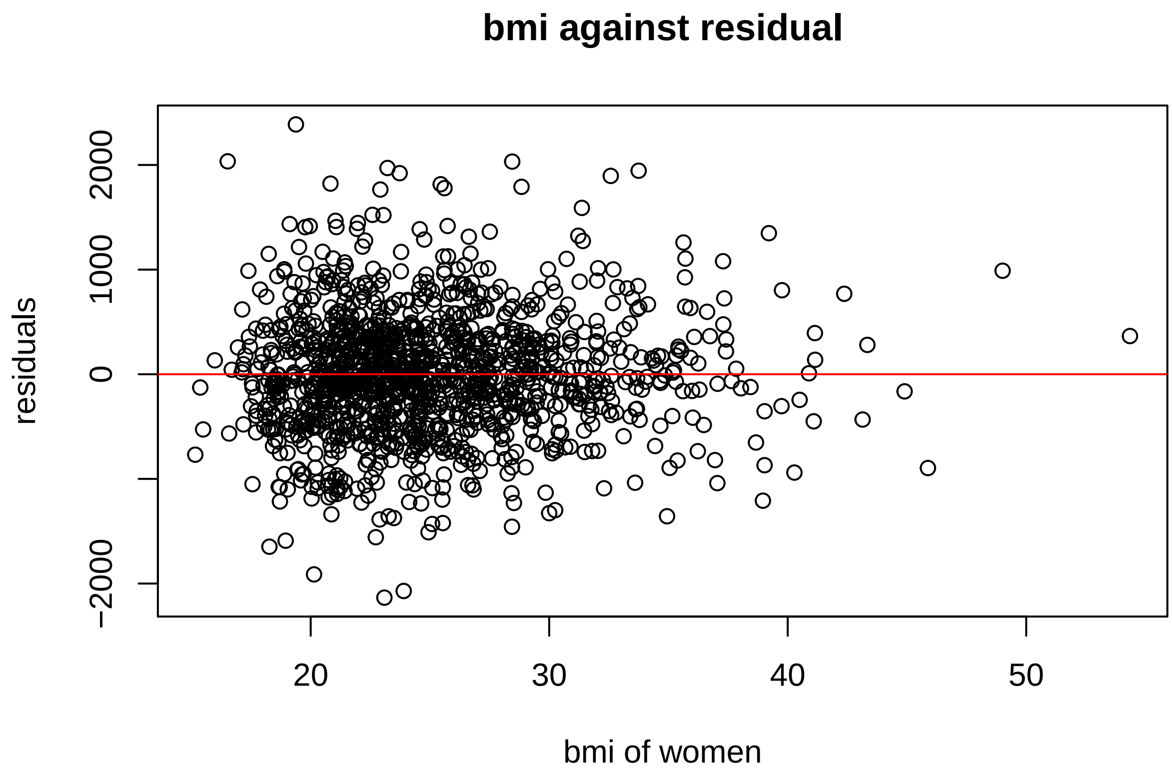
```
##
## Call:
##    "inla(formula = formula, family = \"gaussian\", data = trial,
##    control.predictor = list(compute = TRUE))"
## Time used:
##     Pre = 3.08, Running = 1.48, Post = 1.04, Total = 5.6
## Fixed effects:
##                 mean     sd 0.025quant 0.5quant 0.975quant     mode kld
## (Intercept) 2599.682 69.199   2463.822 2599.680   2735.429 2599.682   0
## fuel_bin1     -5.315 21.769    -48.054   -5.315     37.389   -5.315   0
## gender2     -103.282 17.023   -136.703 -103.283    -69.889 -103.282   0
## education1    11.251 21.314    -30.595   11.251     53.063   11.251   0
## education2    10.229 18.874    -26.827   10.228     47.253   10.229   0
## education3    -2.386 26.490    -54.394   -2.387     49.579   -2.386   0
## w_age          6.169  1.595      3.037    6.169      9.299    6.169   0
## marital_s1     0.947 21.572    -41.406    0.946     43.263    0.947   0
## wealth2       13.454 21.673    -29.098   13.453     55.971   13.454   0
## wealth3       48.840 20.685      8.229   48.840     89.418   48.840   0
## wealth4      -32.590 21.678    -75.151  -32.591      9.935  -32.590   0
## wealth5       31.310 23.696    -15.213   31.309     77.794   31.310   0
## bmi           14.521  1.980     10.633   14.521     18.405   14.521   0
## residence2    15.009 18.799    -21.901   15.008     51.887   15.009   0
##
## Random effects:
##   Name     Model
##     re_v IID model
##
## Model hyperparameters:
##                                         mean    sd 0.025quant 0.5quant
## Precision for the Gaussian observations 0.00 0.000      0.000     0.00
## Precision for re_v                      0.52 0.002      0.517     0.52
##                                         0.975quant mode
## Precision for the Gaussian observations      0.000 0.00
## Precision for re_v                           0.524 0.52
##
## Expected number of effective parameters(stdev): 8.98(0.005)
## Number of equivalent replicates : 145.81
##
## Marginal log-Likelihood:  -10650.49
## Posterior marginals for the linear predictor and
##  the fitted values are computed
```

plotting residuals

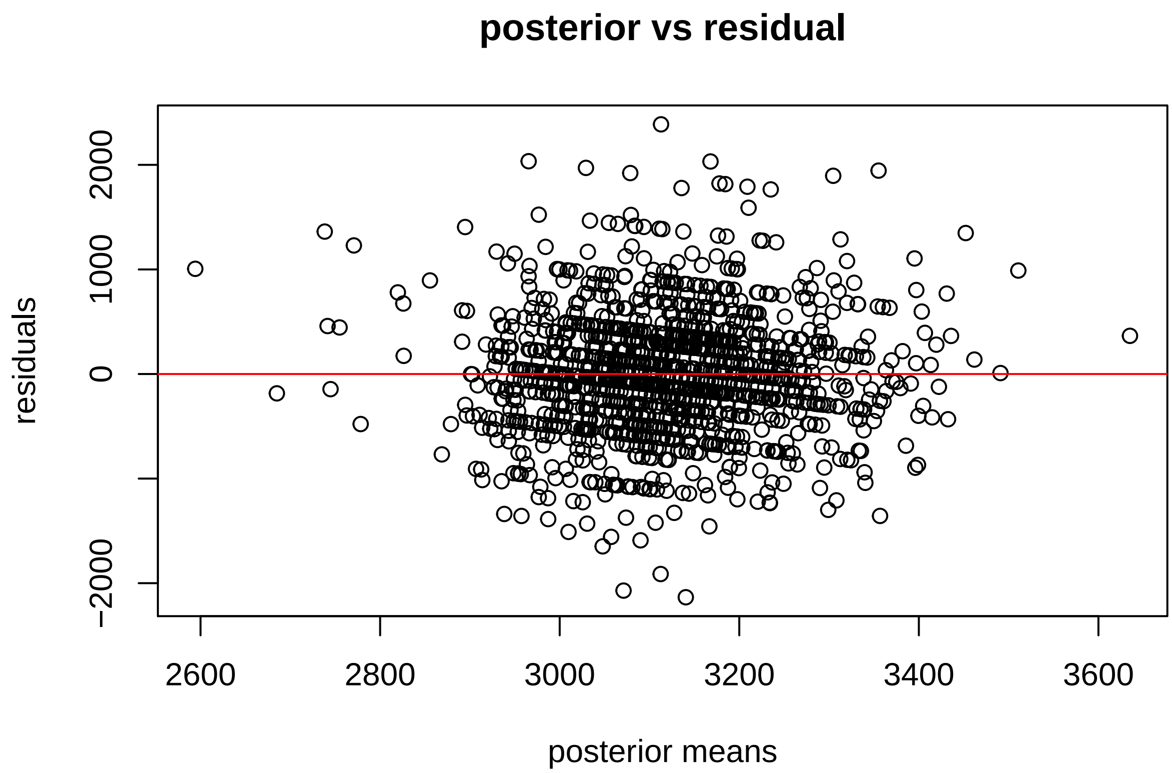
```
#age
residuals=  trial$c_weight-res$summary.fitted.values[,1]
plot(trial$w_age,residuals, main= "age against residual", xlab="age of women")
abline(h=0, col="red")
```




```
#bmi
plot(trial$bmi,residuals, main= "bmi against residual", xlab="bmi of women")
abline(h=0, col="red")
```




```
#posterior
plot(res$summary.fitted.values[,1],residuals, main= "posterior vs residual", xlab="posterior means")
abline(h=0, col="red")
```




```
#priors not sure
```

```
dd <- trial %>% group_by(region) %>%
  summarize(meanbw = mean(c_weight))
```

```
## `summarise()` ungrouping output (override with `.groups` argument)
```

```
#how to interpret
moran.test(dd$meanbw, nb2listw(nb), 10)
```

```
##
##  Moran I test under randomisation
##
## data:  dd$meanbw
## weights: nb2listw(nb)
##
## Moran I statistic standard deviate = 2.4512, p-value = 0.007119
## alternative hypothesis: greater
## sample estimates:
## Moran I statistic       Expectation          Variance
##        0.33609153       -0.11111111        0.03328468
```