

Spatial Joint Model (Spatial and Spatio-temporal Epidemiology)

```
library(dplyr)
library(rgdal)
library(spdep)
library(leaflet)
library(leafletync)
library(INLA)
library(INLAMSM)
```

Loading the dataset

```
## Load data - Ceara
load("~/Thesis/Data/dta_deng_chik.RData")
data <- data[order(data$id),]

# Read the spatial structure
setwd("~/Thesis/Data/Spatial Structure of Data/ce_municipios")
require(rgdal)
Output.Areas <- readOGR(".", "CE_Municipios_2019")
# par(mar = c(0.5, 0.5, 0.5, 0.5)); plot(Output.Areas)

# Adjacency Matrix
W.nb <- poly2nb(Output.Areas, row.names = 1:length(Output.Areas))
W.sp <- as(nb2mat(W.nb, style = "B"), "Matrix")
```

Joint Model

```
# Model originally presented by Gomez-Rubio et al (2019)

# Create intercept
data$intercept <- as.factor(data$disease)

# Create dummy indices for space
data$s.dummy <- NA

# Create spacial indices for specific effects
data$s.1 <- NA
data$s.1[data$disease == "Dengue"] <- as.numeric(as.factor(data$id_area[data$disease == "Dengue"]))

data$s.2 <- NA
data$s.2[data$disease == "Chikungunya"] <- as.numeric(as.factor(data$id_area[data$disease ==
                                                                    "Chikungunya"]))

# Indices for spatial disease-specific effects
data$id_area1 <- data$s.1; data$id_area2 <- data$s.2

# Spatial and temporal weights have been assigned a log-Normal prior with zero mean and
# precision 1/5.9 (similarly as in Downing et al., 2008)
prior.beta.s <- list(prior = "normal", param = c(0, 1 / 5.9), fixed = FALSE, initial = 0.01)

# Flat prior on sigma: Ugarte et al. (2018):
prior.prec <- list(prior = "expression: logdens = -log_precision / 2; return(logdens)", initial = 0)
```

```

inla.scale <- FALSE

formula <- observed ~ -1 + temperature + rurality + intercept +
  f(id_area1, model = "besag", scale.model = inla.scale, graph = W.sp,
    hyper = list(prec = prior.prec)) +
  f(id_area2, model = "besag", scale.model = inla.scale, graph = W.sp,
    hyper = list(prec = prior.prec)) +
  f(s.dummy, model = "besag", scale.model = inla.scale, graph = W.sp,
    hyper = list(prec = prior.prec)) +
  f(s.1, copy = "s.dummy", range = c(0, Inf), hyper = list(beta = prior.beta.s)) +
  f(s.2, copy = "s.dummy", range = c(0, Inf), hyper = list(beta = prior.beta.s))

out_fit <- inla(formula, data = data, E = expected, family = "poisson",
  verbose = FALSE, control.predictor = list(compute=TRUE),
  control.compute=list(dic = TRUE, waic = TRUE, config = TRUE))

out_fit <- inla.rerun(out_fit)
summary(out_fit)

##
## Call:
## c("inla.core(formula = formula, family = family, contrasts = contrasts,
## ", " data = data, quantiles = quantiles, E = E, offset = offset, ", "
## scale = scale, weights = weights, Ntrials = Ntrials, strata = strata,
## ", " lp.scale = lp.scale, link.covariates = link.covariates, verbose =
## verbose, ", " lincomb = lincomb, selection = selection, control.compute
## = control.compute, ", " control.predictor = control.predictor,
## control.family = control.family, ", " control.inla = control.inla,
## control.fixed = control.fixed, ", " control.mode = control.mode,
## control.expert = control.expert, ", " control.hazard = control.hazard,
## control.lincomb = control.lincomb, ", " control.update =
## control.update, control.lp.scale = control.lp.scale, ", "
## control.pardiso = control.pardiso, only.hyperparam = only.hyperparam,
## ", " inla.call = inla.call, inla.arg = inla.arg, num.threads =
## num.threads, ", " blas.num.threads = blas.num.threads, keep = keep,
## working.directory = working.directory, ", " silent = silent, inla.mode
## = inla.mode, safe = FALSE, debug = debug, ", " .parent.frame =
## .parent.frame)")
## Time used:
## Pre = 0.83, Running = 0.721, Post = 0.272, Total = 1.82
## Fixed effects:
##          mean      sd 0.025quant 0.5quant 0.975quant      mode kld
## temperature      0.562 0.215      0.139      0.562      0.984      0.562  0
## rurality        -1.348 0.461     -2.254     -1.347     -0.444     -1.347  0
## interceptChikungunya -15.165 5.356    -25.668    -15.168     -4.645    -15.174  0
## interceptDengue    -13.984 5.355    -24.487    -13.987     -3.464    -13.993  0
##
## Random effects:
##      Name      Model
## id_area1 Besags ICAR model
## id_area2 Besags ICAR model
## s.dummy Besags ICAR model
## s.1 Copy
## s.2 Copy
##
## Model hyperparameters:
##          mean      sd 0.025quant 0.5quant 0.975quant      mode
## Precision for id_area1 0.423 0.045      0.332      0.422      0.512 0.427
## Precision for id_area2 0.522 0.224      0.240      0.479      1.137 0.387

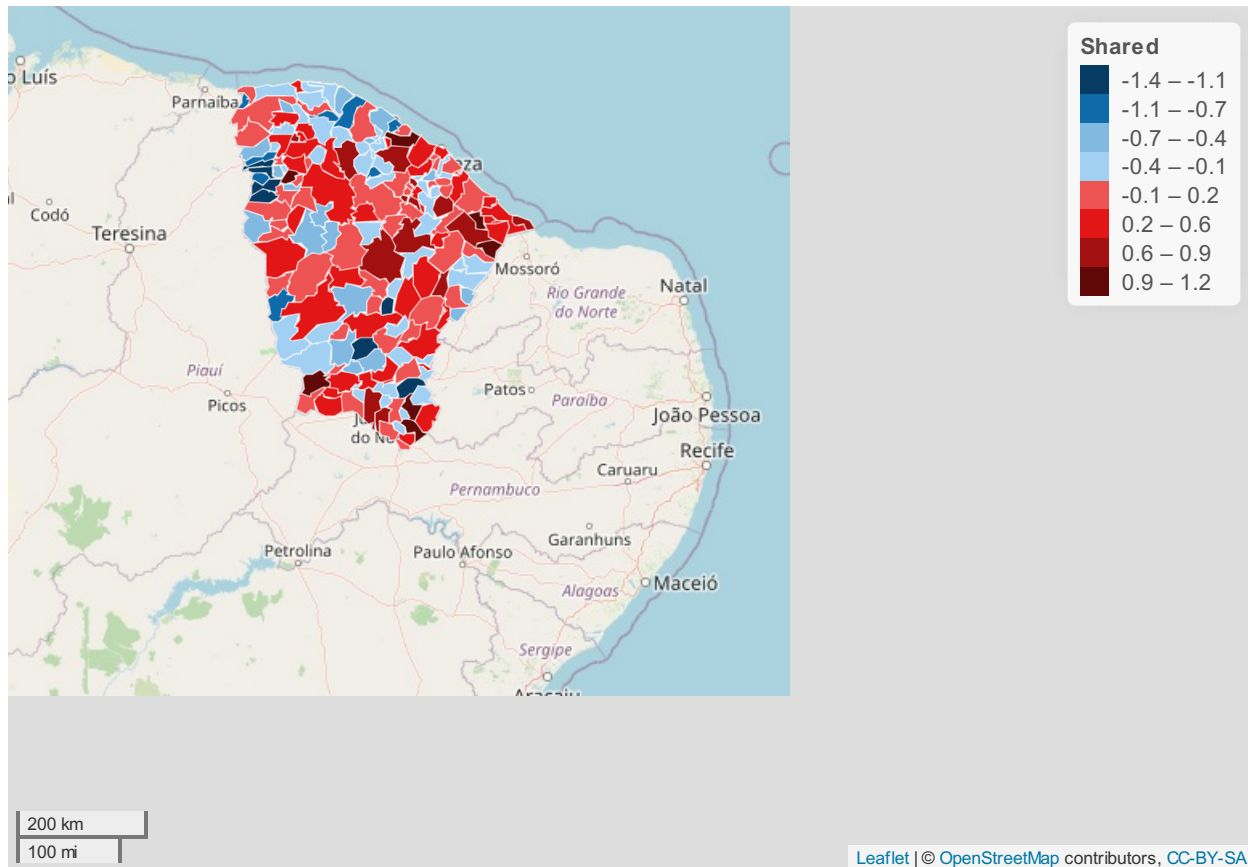
```

```
## Precision for s.dummy 0.700 0.239      0.311      0.666      1.258 0.627
## Beta for s.1          0.906 0.167      0.584      0.892      1.249 0.902
## Beta for s.2          2.075 0.518      1.213      2.019      3.262 1.922
##
## Deviance Information Criterion (DIC) .....: 3345.30
## Deviance Information Criterion (DIC, saturated) ....: 739.63
## Effective number of parameters .....: 362.46
##
## Watanabe-Akaike information criterion (WAIC) ...: 3266.25
## Effective number of parameters .....: 201.07
##
## Marginal log-Likelihood: -2895.68
## is computed
## Posterior summaries for the linear predictor and the fitted values are computed
## (Posterior marginals needs also 'control.compute=list(return.marginals.predictor=TRUE)')
```

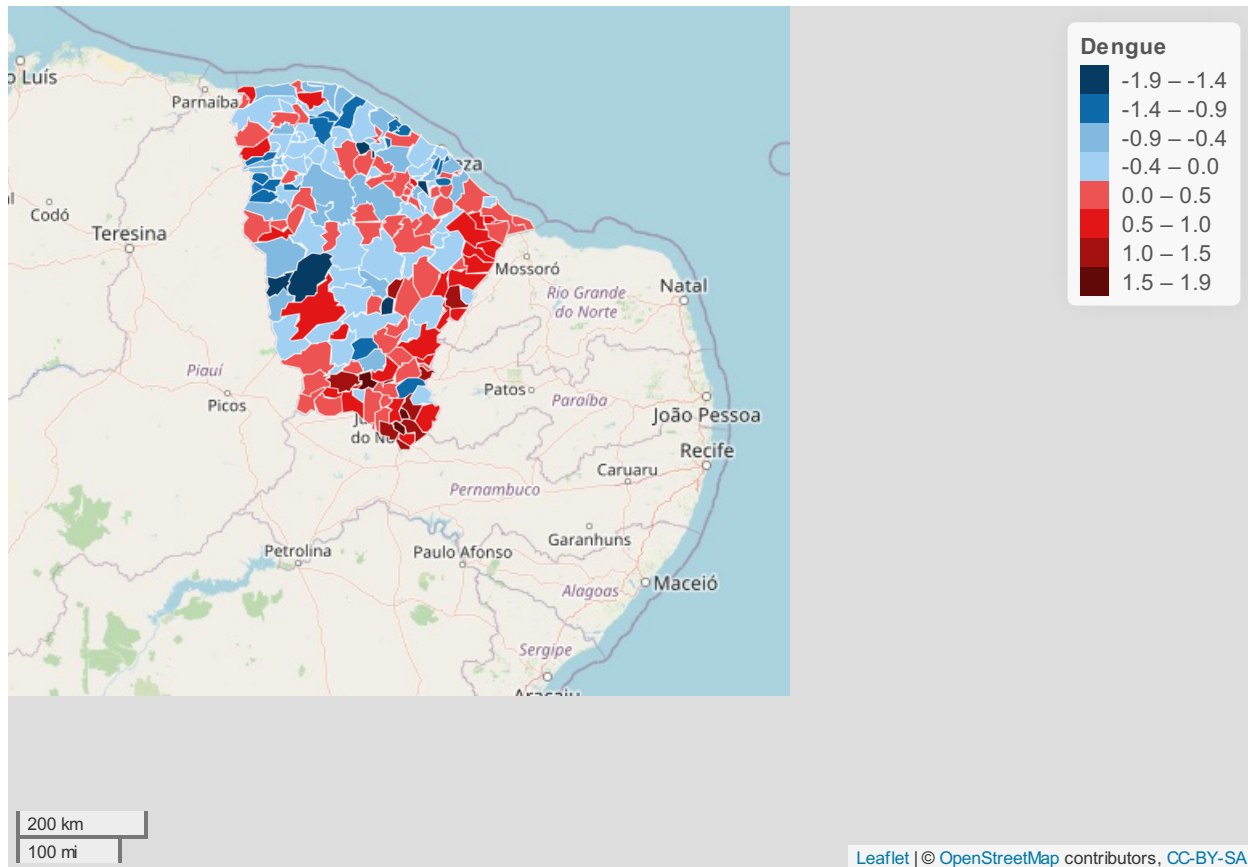
Spatial Effect

```
mycolors <- c("#063c63", "#0f6aaa", "#82b9e0", "#a2d0f2", "#ed5353", "#e21616",
              "#a21010", "#610909")

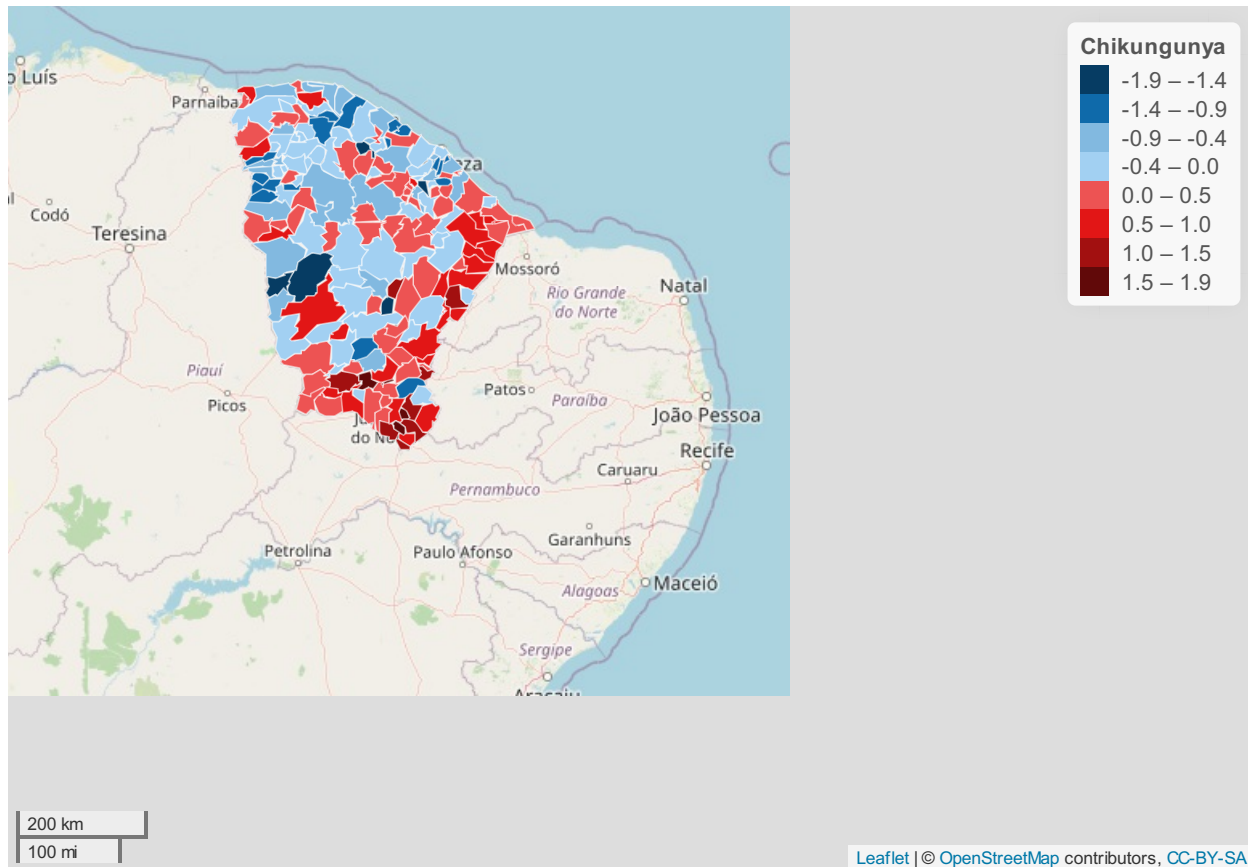
# Shared
Output.Areas@data$shared <- out_fit$summary.random$s.dummy[, "mean"]
colours <- colorBin(palette = mycolors, domain = Output.Areas@data$shared,
                   bins = seq(min(Output.Areas@data$shared), max(Output.Areas@data$shared), len=9))
map_shared <- leaflet(data=Output.Areas, options = leafletOptions(zoomControl = FALSE)) %>%
  addTiles() %>%
  addPolygons(fillColor = ~colours(shared), color="white", weight=1,
              fillOpacity = 1) %>% addLegend(pal = colours, labFormat = labelFormat(digits = 1),
              values = Output.Areas@data$shared,
              opacity = 1, title="Shared") %>%
  addScaleBar(position="bottomleft")
map_shared
```



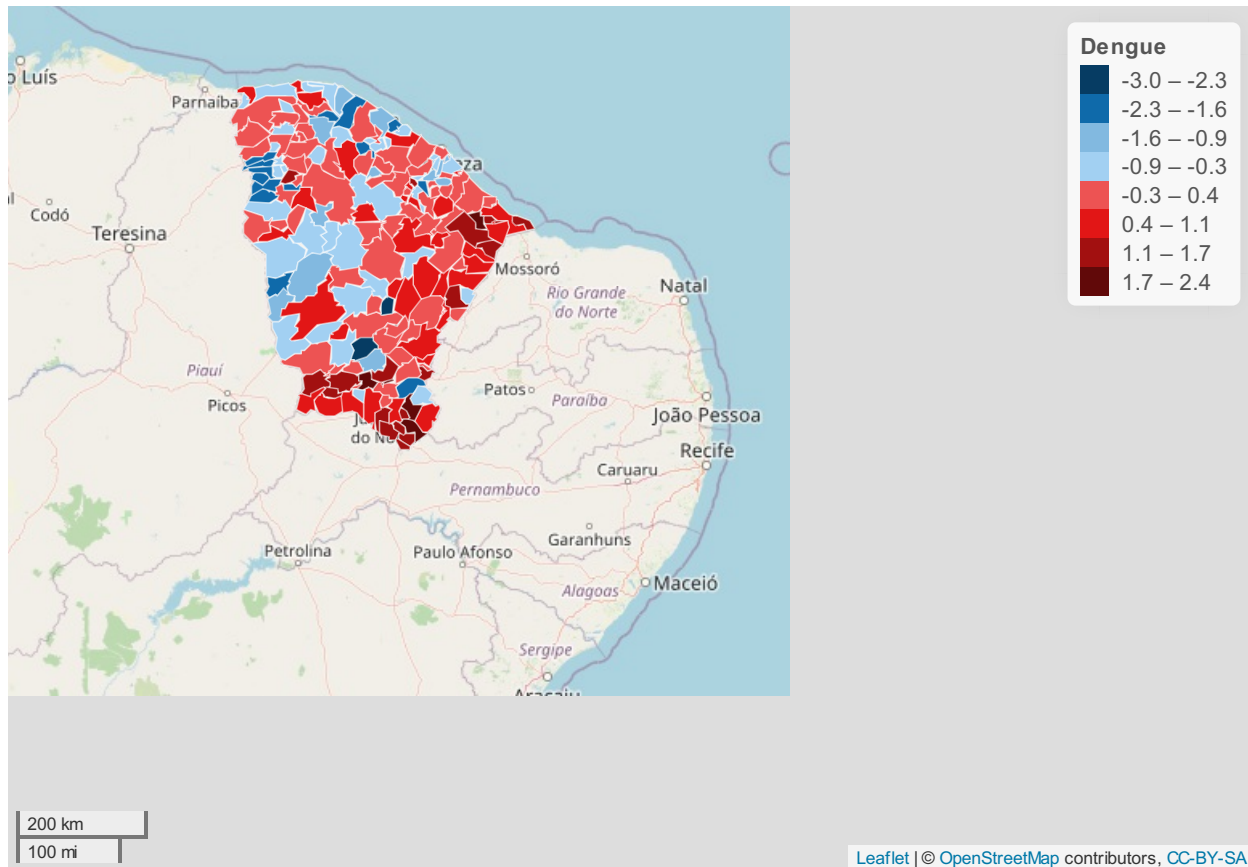
```
# Specific - dengue
Output.Areas@data$dengue <- out_fit$summary.random$id_area1[, "mean"]
colours <- colorBin(palette = mycolors, domain = Output.Areas@data$dengue,
  bins = seq(min(Output.Areas@data$dengue), max(Output.Areas@data$dengue), len=9))
map_dengue_sp <- leaflet(data=Output.Areas, options = leafletOptions(zoomControl = FALSE)) %>%
  addTiles() %>%
  addPolygons(fillColor = ~colours(dengue), color="white", weight=1,
    fillOpacity = 1) %>% addLegend(pal = colours, labFormat = labelFormat(digits = 1),
    values = Output.Areas@data$dengue,
    opacity = 1, title="Dengue") %>%
  addScaleBar(position="bottomleft")
map_dengue_sp
```



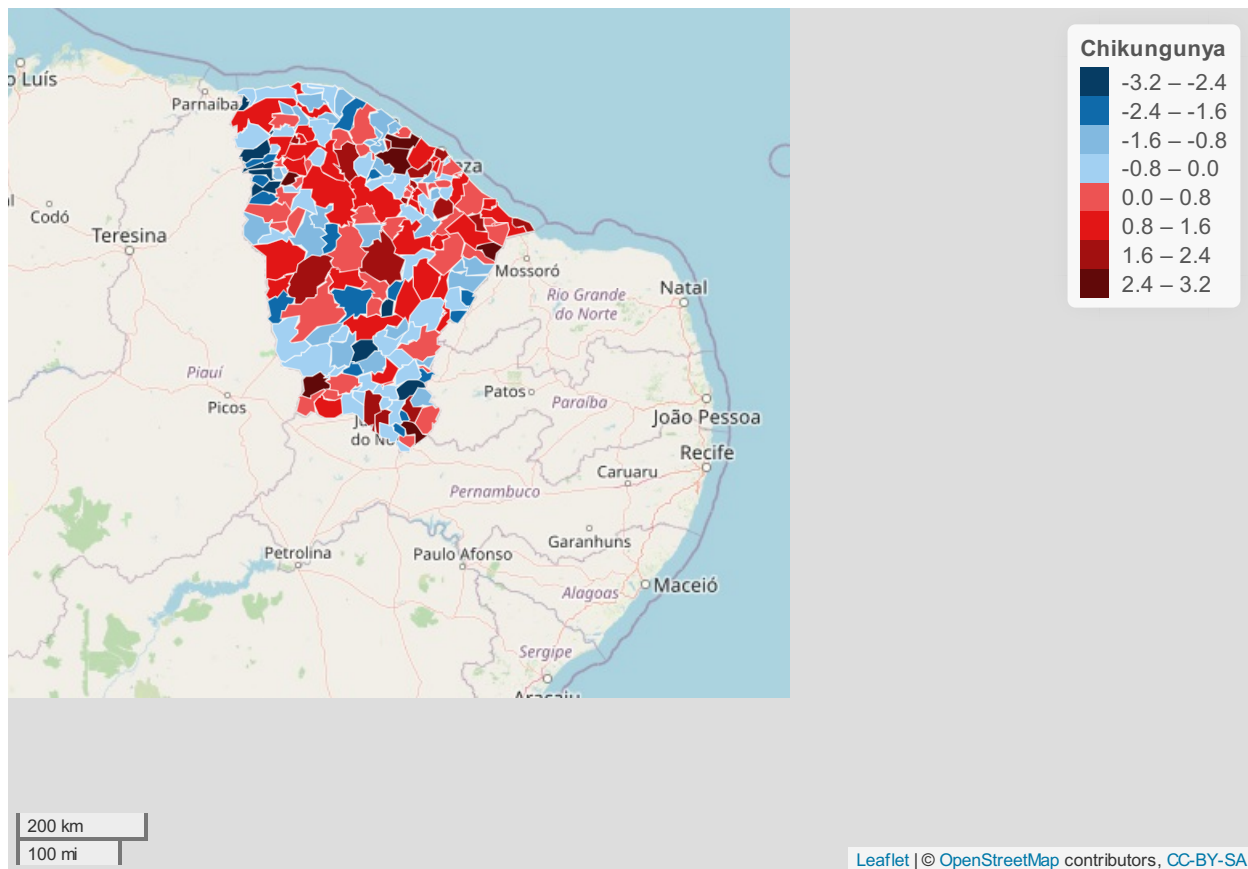
```
# Specific - chikungunya
Output.Areas@data$chiku <- out_fit$summary.random$id_area1[, "mean"]
colours <- colorBin(palette = mycolors, domain = Output.Areas@data$chiku,
                    bins = seq(min(Output.Areas@data$chiku), max(Output.Areas@data$chiku), len=9))
map_chiku_sp <- leaflet(data=Output.Areas, options = leafletOptions(zoomControl = FALSE)) %>%
  addTiles() %>%
  addPolygons(fillColor = ~colours(chiku), color="white", weight=1,
              fillOpacity = 1) %>% addLegend(pal = colours, labFormat = labelFormat(digits = 1),
              values = Output.Areas@data$chiku,
              opacity = 1, title="Chikungunya") %>%
  addScaleBar(position="bottomleft")
map_chiku_sp
```



```
# Total - dengue
Output.Areas@data$dengue_tot <- out_fit$summary.random$id_area1[, "mean"] +
                                out_fit$summary.random$s.1[, "mean"]
colours <- colorBin(palette = mycolors, domain = Output.Areas@data$dengue_tot,
                    bins = seq(min(Output.Areas@data$dengue_tot), max(Output.Areas@data$dengue_tot), len=9))
map_dengue_tot <- leaflet(data=Output.Areas, options = leafletOptions(zoomControl = FALSE)) %>%
  addTiles() %>%
  addPolygons(fillColor = ~colours(dengue_tot), color="white", weight=1,
              fillOpacity = 1) %>% addLegend(pal = colours, labFormat = labelFormat(digits = 1),
                                              values = Output.Areas@data$dengue_tot,
                                              opacity = 1, title="Dengue") %>%
  addScaleBar(position="bottomleft")
map_dengue_tot
```



```
# Total - chikungunya
Output.Areas@data$chiku_tot <- out_fit$summary.random$id_area2[, "mean"] +
  out_fit$summary.random$s.2[, "mean"]
colours <- colorBin(palette = mycolors, domain = Output.Areas@data$chiku_tot,
  bins = seq(min(Output.Areas@data$chiku_tot), max(Output.Areas@data$chiku_tot), len=9))
map_chiku_tot <- leaflet(data=Output.Areas, options = leafletOptions(zoomControl = FALSE)) %>%
  addTiles() %>%
  addPolygons(fillColor = ~colours(chiku_tot), color="white", weight=1, fillOpacity = 1) %>%
  addLegend(pal = colours, labFormat = labelFormat(digits = 1),
    values = Output.Areas@data$chiku_tot, opacity = 1, title="Chikungunya") %>%
  addScaleBar(position="bottomleft")
map_chiku_tot
```

```
# sync(map_shared, map_dengue_sp, map_chiku_sp, ncol = 3)
# sync(map_dengue_tot, map_chiku_tot, ncol = 2)
```

Relative Risk

```
mycolors <- c("#063c63", "#0f6aaa", "#82b9e0", "#a2d0f2", "#FFFFFF", "#ed5353", "#e21616",
              "#a21010", "#610909")
```

```
round(out_fit$summary.fixed, 3)
```

##	mean	sd	0.025quant	0.5quant	0.975quant	mode	kld
## temperature	0.562	0.215	0.139	0.562	0.984	0.562	0
## rurality	-1.348	0.461	-2.254	-1.347	-0.444	-1.347	0
## interceptChikungunya	-15.165	5.356	-25.668	-15.168	-4.645	-15.174	0
## interceptDengue	-13.984	5.355	-24.487	-13.987	-3.464	-13.993	0

```
# Dengue
```

```
Output.Areas@data$RR_d <- out_fit$summary.fitted.values[1:184,"mean"]
```

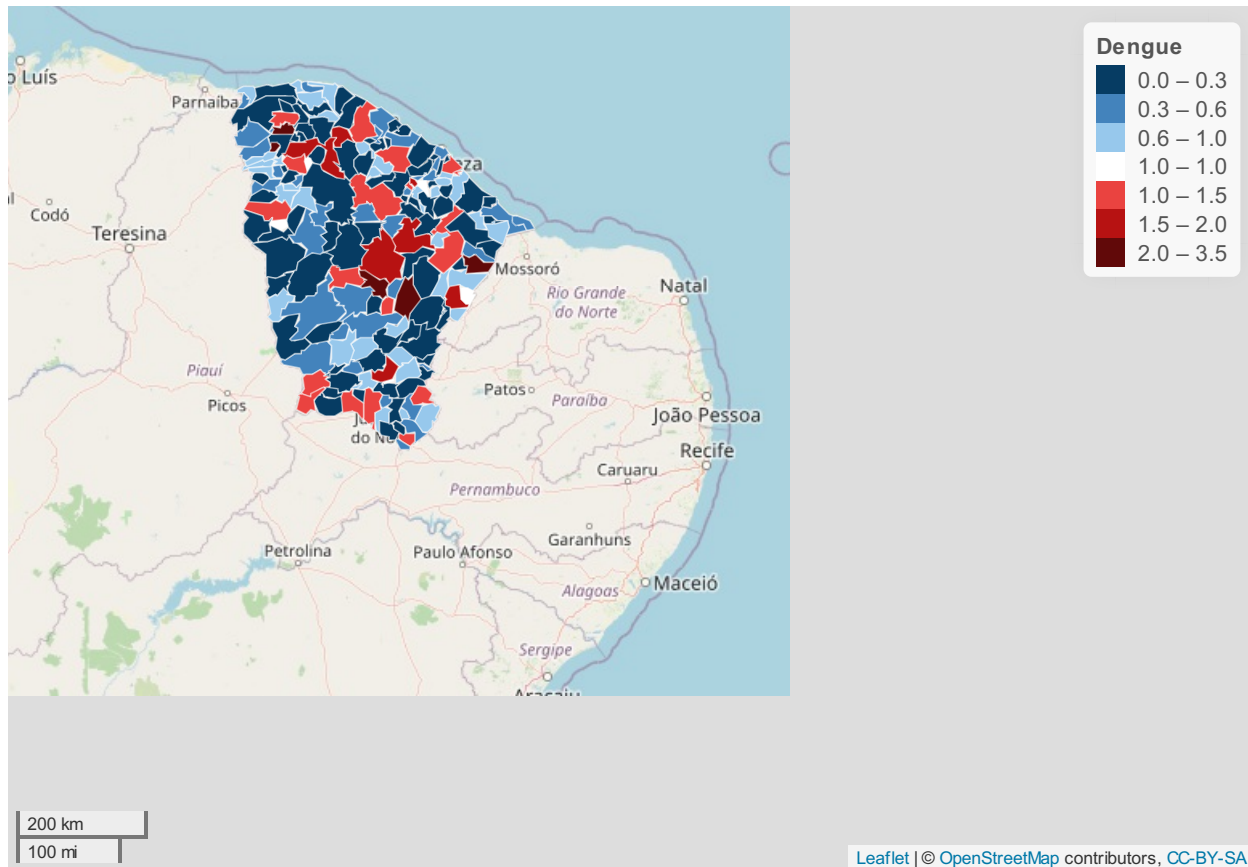
```
Output.Areas@data$LL_d <- out_fit$summary.fitted.values[1:184,"0.025quant"]
```

```
Output.Areas@data$UL_d <- out_fit$summary.fitted.values[1:184,"0.975quant"]
```

```
colours <- colorBin(palette = mycolors, domain = Output.Areas@data$RR_d,
                    bins = c(0, 0.3, 0.6, 0.975, 1.025, 1.5, 2, max(Output.Areas@data$RR_d)))
```

```
(map_RR_d2 <- leaflet(data=Output.Areas, options = leafletOptions(zoomControl = FALSE)) %>%
  addTiles() %>%
```

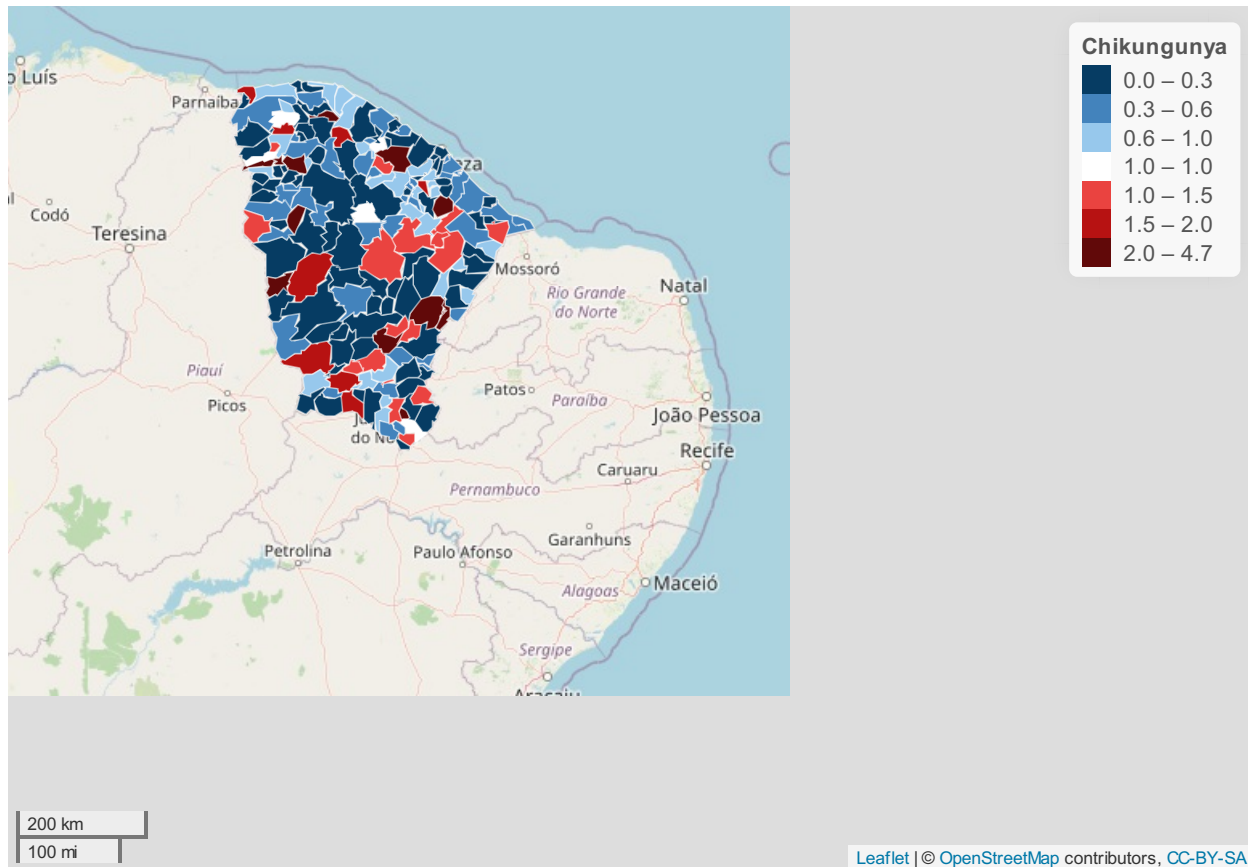
```
  addPolygons(fillColor = ~colours(RR_d), color="white", weight=1, fillOpacity = 1) %>%
  addLegend(pal = colours, values = Output.Areas@data$RR_d, opacity = 1,
    labFormat = labelFormat(digits = 1), title="Dengue") %>%
  addScaleBar(position="bottomleft"))
```

Chikungunya

```
Output.Areas@data$RR_c <- out_fit$summary.fitted.values[185:368,"mean"]
Output.Areas@data$LL_c <- out_fit$summary.fitted.values[185:368,"0.025quant"]
Output.Areas@data$UL_c <- out_fit$summary.fitted.values[185:368,"0.975quant"]

colours <- colorBin(palette = mycolors, domain = Output.Areas@data$RR_c,
  bins = c(0, 0.3, 0.6, 0.975, 1.025, 1.5, 2, max(Output.Areas@data$RR_c)))
(map_RR_c2 <- leaflet(data=Output.Areas, options = leafletOptions(zoomControl = FALSE)) %>%
  addTiles() %>%
  addPolygons(fillColor = ~colours(RR_c), color="white", weight=1, fillOpacity = 1) %>%
  addLegend(pal = colours, values = Output.Areas@data$RR_c, opacity = 1,
    labFormat = labelFormat(digits = 1), title="Chikungunya") %>%
  addScaleBar(position="bottomleft"))
```



```
#sync(map_RR_d2, map_RR_c2, ncol = 2)
```

Multivariate CAR Model

Model originally presented by Palmi-Perales et al (2021)

```
data$s <- NA
data$s[data$disease == "Dengue"] <- as.numeric(as.factor(data$id_area[data$disease == "Dengue"]))
data$s[data$disease == "Chikungunya"] <- as.numeric(as.factor(data$id_area[data$disease == "Chikungunya"]))

# Number of diseases
k <- length(unique(data$disease))

alpha.min <- 0.99; alpha.max <- 1
model <- inla.MCAR.model(k = k, W = W.sp, alpha.min = alpha.min,
                        alpha.max = alpha.max)
formula <- observed ~ 0 + disease + f(s, model = model) + temperature + rurality
IMCAR <- inla(formula, data = data, E = expected, family = "poisson",
              control.compute = list(config = TRUE, dic = TRUE, waic = TRUE),
              control.predictor = list(compute = TRUE),
              control.inla(strategy = "laplace"))
IMCAR <- inla.rerun(IMCAR)
summary(IMCAR)

##
## Call:
## inla.core(formula = formula, family = family, contrasts = contrasts,
##           ", " data = data, quantiles = quantiles, E = E, offset = offset, ", "
##           scale = scale, weights = weights, Ntrials = Ntrials, strata = strata,
##           ", " lp.scale = lp.scale, link.covariates = link.covariates, verbose =
##           verbose, ", " lincomb = lincomb, selection = selection, control.compute
```

```
## = control.compute, ", " control.predictor = control.predictor,
## control.family = control.family, ", " control.inla = control.inla,
## control.fixed = control.fixed, ", " control.mode = control.mode,
## control.expert = control.expert, ", " control.hazard = control.hazard,
## control.lincomb = control.lincomb, ", " control.update =
## control.update, control.lp.scale = control.lp.scale, ", "
## control.pardiso = control.pardiso, only.hyperparam = only.hyperparam,
## ", " inla.call = inla.call, inla.arg = inla.arg, num.threads =
## num.threads, ", " blas.num.threads = blas.num.threads, keep = keep,
## working.directory = working.directory, ", " silent = silent, inla.mode
## = inla.mode, safe = FALSE, debug = debug, ", " .parent.frame =
## .parent.frame)")
## Time used:
## Pre = 0.726, Running = 3.59, Post = 0.17, Total = 4.49
## Fixed effects:
##              mean      sd 0.025quant 0.5quant 0.975quant      mode kld
## diseaseChikungunya -13.542 5.466    -24.271  -13.543    -2.807  -13.546    0
## diseaseDengue      -13.542 5.466    -24.271  -13.543    -2.807  -13.546    0
## temperature         0.540 0.216      0.115   0.540     0.963   0.540    0
## rurality            -1.356 0.465     -2.268  -1.356    -0.444  -1.355    0
##
## Random effects:
##      Name      Model
##      s RGeneric2
##
## Model hyperparameters:
##              mean      sd 0.025quant 0.5quant 0.975quant      mode
## Theta1 for s -0.429 1.452     -3.32   -0.411      2.38  -0.349
## Theta2 for s -1.263 0.107     -1.48   -1.261     -1.06  -1.256
## Theta3 for s -0.682 1.423     -3.78   -0.552      1.75  -0.050
## Theta4 for s  0.009 0.964     -1.88    0.007      1.91  -0.001
##
## Deviance Information Criterion (DIC) .....: -42122.84
## Deviance Information Criterion (DIC, saturated) ....: -43393.44
## Effective number of parameters .....: -46749.36
##
## Watanabe-Akaike information criterion (WAIC) ...: 47568.26
## Effective number of parameters .....: 16312.77
##
## Marginal log-Likelihood: -26385.79
## is computed
## Posterior summaries for the linear predictor and the fitted values are computed
## (Posterior marginals needs also 'control.compute=list(return.marginals.predictor=TRUE)')
hyper.imcar <- inla.MCAR.transform(IMCAR, k, model = "IMCAR",
                                   alpha.min = alpha.min, alpha.max = alpha.max)
```

Spatial Effect

```
mycolors <- c("#063c63", "#0f6aaa", "#82b9e0", "#a2d0f2", "#ed5353", "#e21616",
              "#a21010", "#610909")
n <- nrow(W.sp)

# Dengue

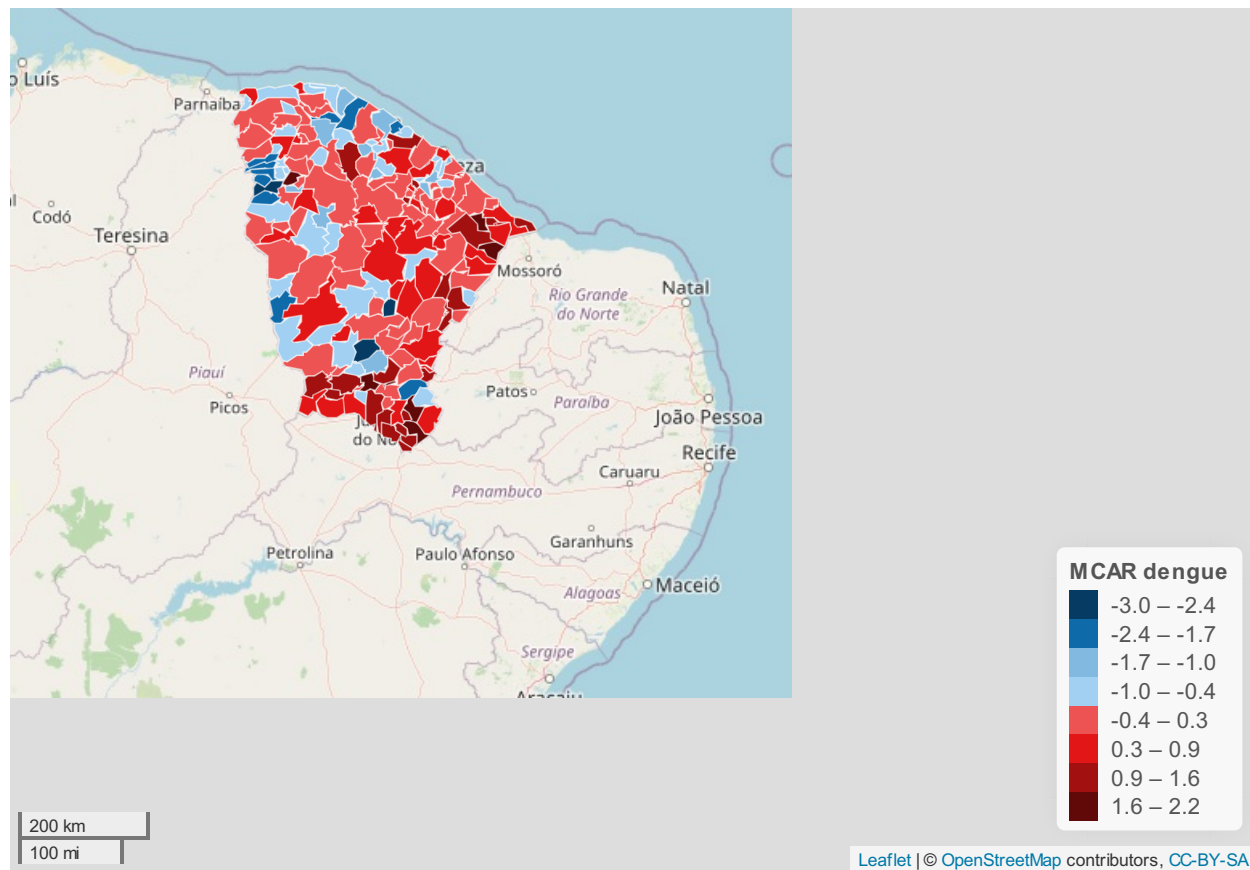
Output.Areas@data$IMCAR_dengue <- IMCAR$summary.random$s[1:n, "mean"]
colours <- colorBin(palette = mycolors, domain = Output.Areas@data$IMCAR_dengue,
                   bins = seq(min(Output.Areas@data$IMCAR_dengue), max(Output.Areas@data$IMCAR_dengue), len=
map_IMCAR_dengue_sp <- leaflet(data=Output.Areas, options = leafletOptions(zoomControl = FALSE)) %>%
```

```

addTiles() %>%
addPolygons(fillColor = ~colours(IMCAR_dengue), color="white", weight=1,
             fillOpacity = 1) %>% addLegend(pal = colours, labFormat = labelFormat(digits = 1),
             values = Output.Areas@data$IMCAR_dengue,
             opacity = 1, title="MCAR dengue",
             position = "bottomright") %>%

addScaleBar(position="bottomleft")
map_IMCAR_dengue_sp

```



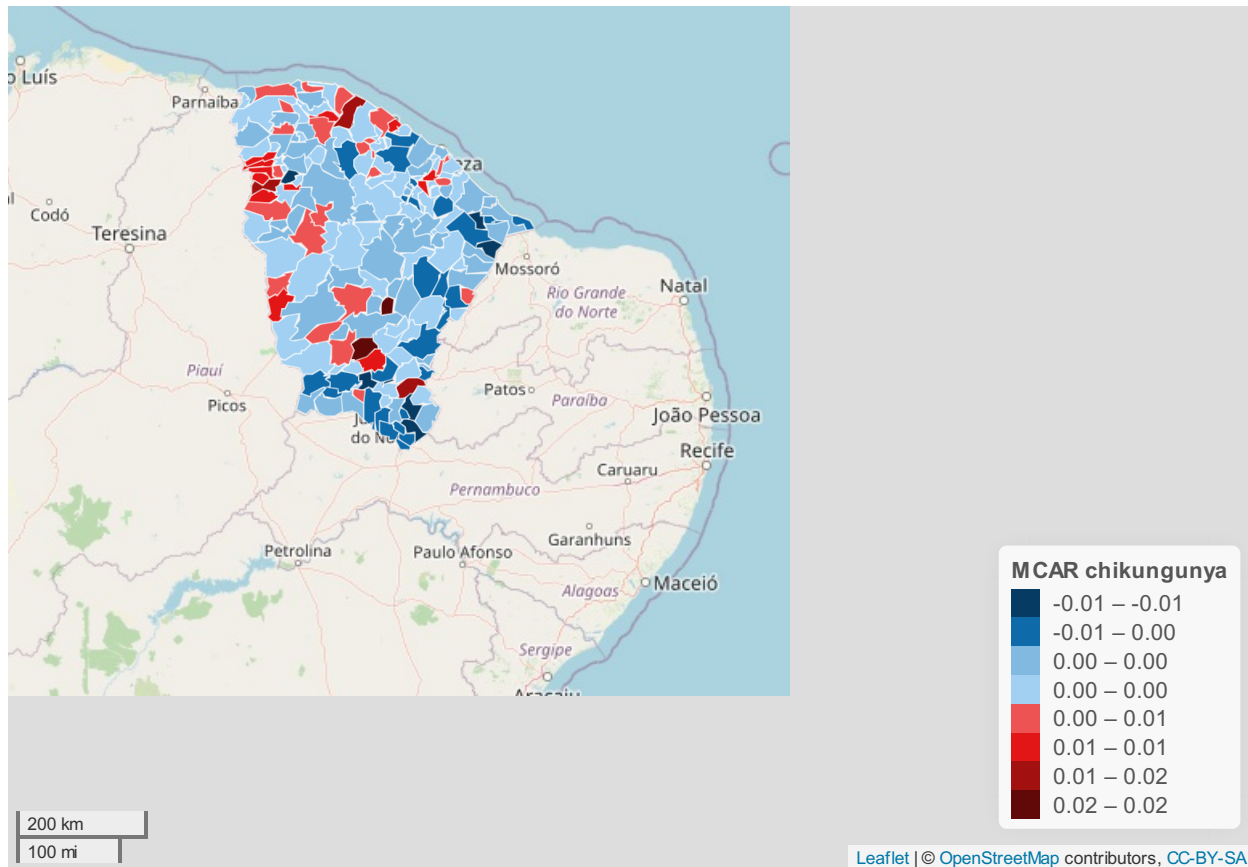
Chikungunya

```

Output.Areas@data$IMCAR_chiku <- IMCAR$summary.random$s[(n+1):(2*n), "mean"]
colours <- colorBin(palette = mycolours, domain = Output.Areas@data$IMCAR_chiku,
                    bins = seq(min(Output.Areas@data$IMCAR_chiku), max(Output.Areas@data$IMCAR_chiku), len=9))
map_IMCAR_chiku_sp <- leaflet(data=Output.Areas, options = leafletOptions(zoomControl = FALSE)) %>%
  addTiles() %>%
  addPolygons(fillColor = ~colours(IMCAR_chiku), color="white", weight=1,
             fillOpacity = 1) %>% addLegend(pal = colours, labFormat = labelFormat(digits = 2),
             values = Output.Areas@data$IMCAR_chiku,
             opacity = 1, title="MCAR chikungunya",
             position = "bottomright") %>%

  addScaleBar(position="bottomleft")
map_IMCAR_chiku_sp

```



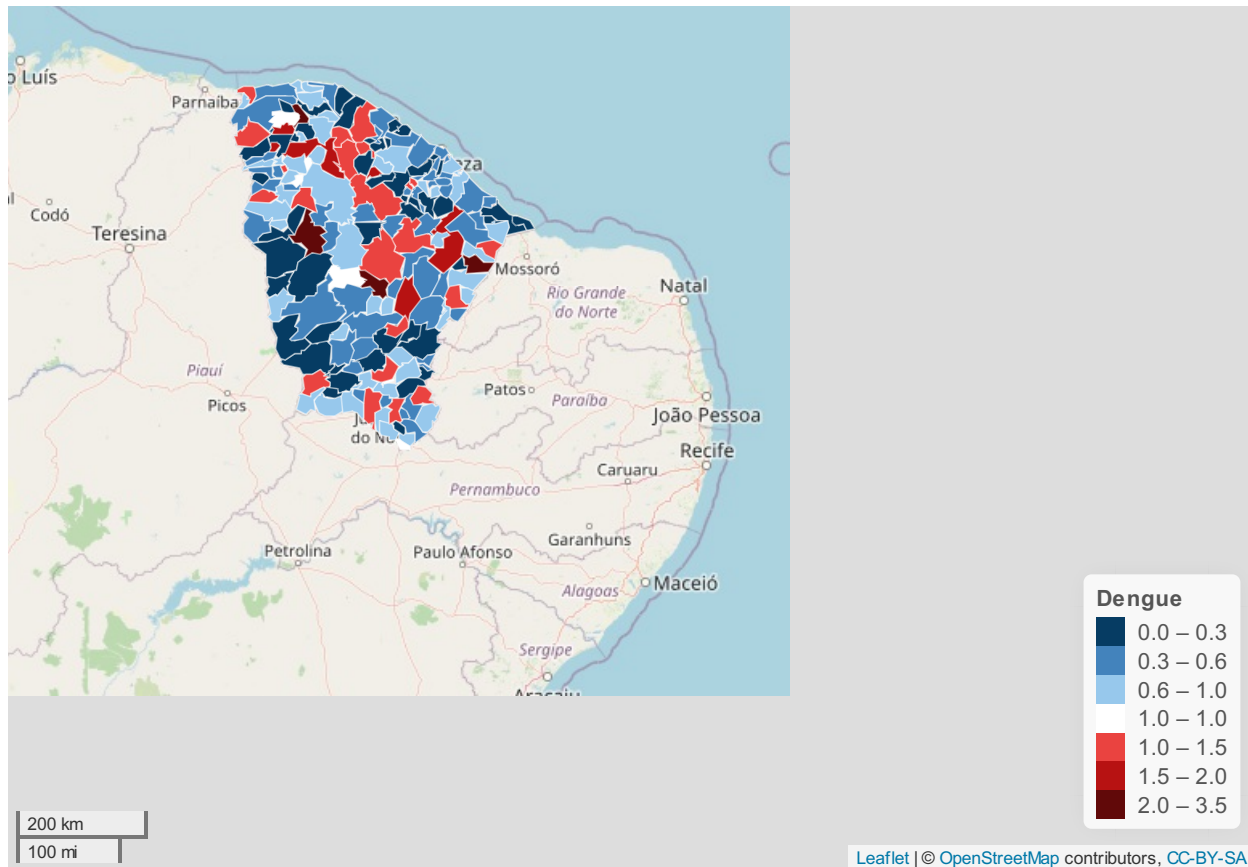
Relative Risk

```
mycolors <- c("#063c63", "#0f6aaa", "#82b9e0", "#a2d0f2", "#FFFFFF", "#ed5353", "#e21616",
              "#a21010", "#610909")

# Dengue

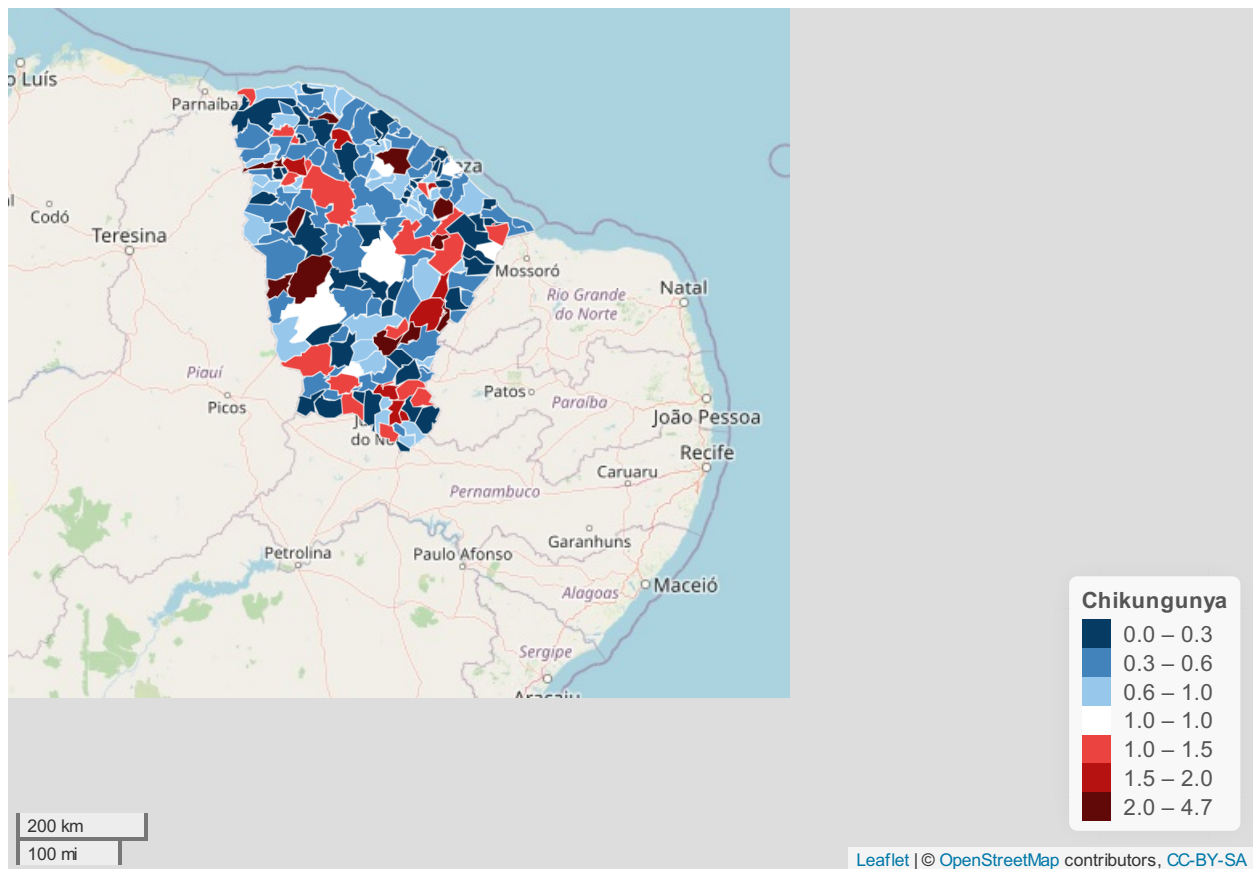
Output.Areas@data$IMCAR_dengue <- IMCAR$summary.fitted[1:n, "mean"]
colours <- colorBin(palette = mycolors, domain = Output.Areas@data$RR_d,
                    bins = c(0, 0.3, 0.6, 0.975, 1.025, 1.5, 2,
                             max(Output.Areas@data$RR_d)))

map_IMCAR_dengue <- leaflet(data=Output.Areas, options = leafletOptions(zoomControl = FALSE)) %>%
  addTiles() %>%
  addPolygons(fillColor = ~colours(IMCAR_dengue), color="white", weight=1,
              fillOpacity = 1) %>%
  addLegend(pal = colours, values = Output.Areas@data$IMCAR_dengue, opacity = 1,
            labFormat = labelFormat(digits = 1), title = "Dengue",
            position = "bottomright") %>%
  addScaleBar(position="bottomleft")
map_IMCAR_dengue
```



Chikungunya

```
Output.Areas@data$IMCAR_chiku <- IMCAR$summary.fitted[(n+1):(2*n), "mean"]
colours <- colorBin(palette = mycolors, domain = Output.Areas@data$RR_c,
  bins = c(0, 0.3, 0.6, 0.975, 1.025, 1.5, 2,
    max(Output.Areas@data$RR_c)))
map_IMCAR_chiku <- leaflet(data=Output.Areas, options = leafletOptions(zoomControl = FALSE)) %>%
  addTiles() %>%
  addPolygons(fillColor = ~colours(IMCAR_chiku), color="white", weight=1,
    fillOpacity = 1) %>%
  addLegend(pal = colours, values = Output.Areas@data$IMCAR_chiku, opacity = 1,
    labFormat = labelFormat(digits = 1), title = "Chikungunya",
    position = "bottomright") %>%
  addScaleBar(position="bottomleft")
map_IMCAR_chiku
```

```
#sync(map_RR_d2, map_RR_c2, ncol = 2)
```