

# GADMTools - Graphics

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# Graphics

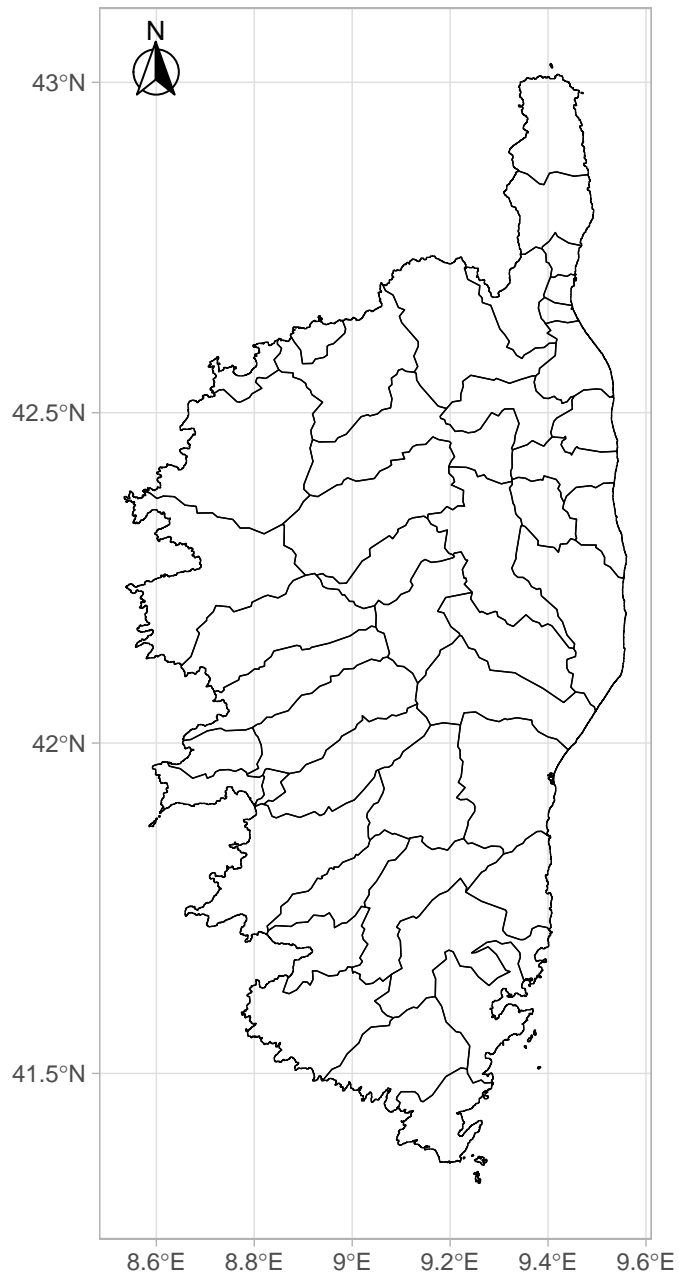
## functions

Function	Description
choropleth	Draws a choropleth on selected regions
classDots	Plots dots on a map with values between different fixed classes
dots	Plots dots on a map
dotDensity	Draws a dot-density map
isopleth	Draws an isopleth on selected regions
gadm_showNorth	Displays a north arrow on a plot
gadm_showScale	Displays a scale on a plot

## Display a north arrow on a plot

```
library(GADMTools)
data("Corsica")

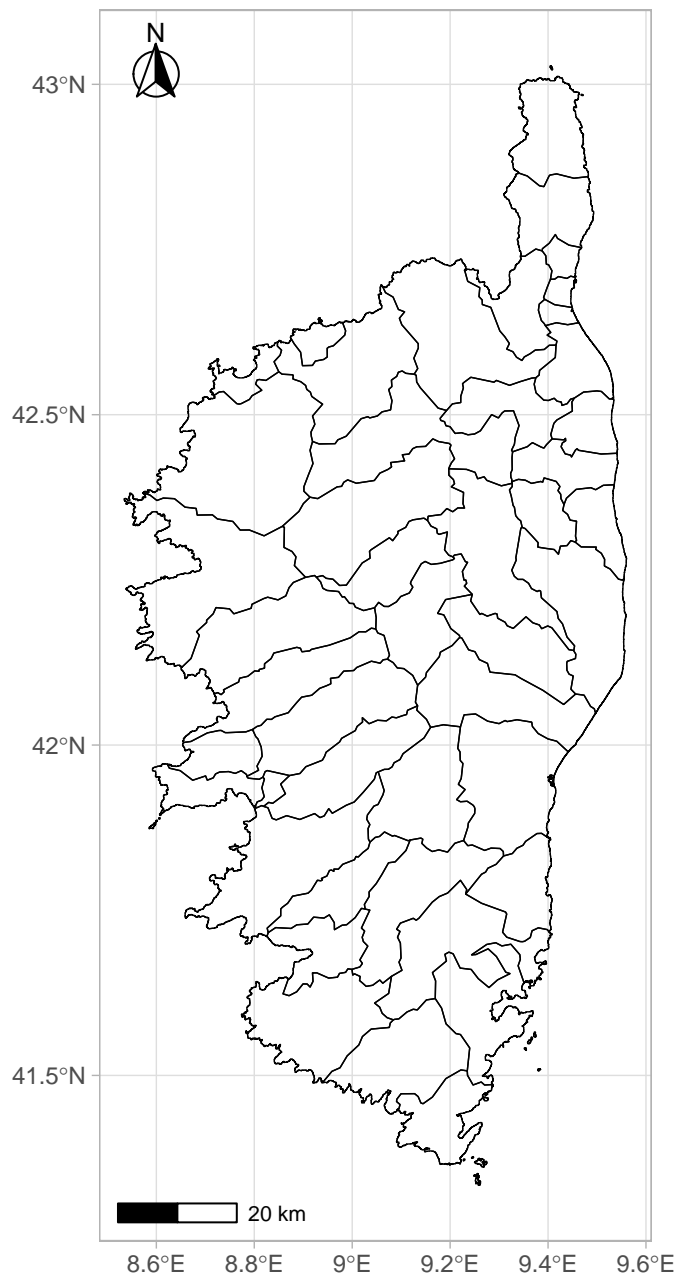
plotmap(Corsica) %>% gadm_showNorth("t1")
```



## Display a scale on a plot

```
library(GADMTools)
data("Corsica")

plotmap(Corsica) %>% gadm_showNorth("t1") %>% gadm_showScale("b1")
```



## Plotting dots on a map

```
# Preparing data.frame
# -----
data("Corsica")

Corse <- gadm_union(Corsica, 0)
Cantons <- listNames(Corsica, 4)
L <- length(Cantons)
Pop <- floor(runif(L, min=15200, max=23500))

longitude <- runif(6, min=8.74, max = 9.25)
latitude <- runif(6, min=41.7, max = 42.6)
Cases <- floor(runif(6, 25, 80))

Type <- rep(c("TYPE A", "TYPE B", "TYPE C"), 6, length.out = 6)
DAT <- data.frame(longitude, latitude, Cases)
```

```
# Simple dots  
#-----  
dots(Corsica, DAT, color="red", size = 3)
```

```
# Classified dots
#-----
dots(Corse, points = DAT,
      palette = "Reds",
      value="Cases")
```

```
# Typed points
#-----
DAT2 <- data.frame(longitude, latitude, Type)
dots(Corse, points = DAT2,
      color = "#ee00ee",
      strate="Type")
```



## Plotting proportionals dots

```
# Test of propDots with default parameters  
# -----  
propDots(Corse,  
  data = DAT,  
  value="Cases",  
  color = "blue")
```

```
# Test of propDots with defined breaks
# -----
propDots(Corse,
  data = DAT,
  value="Cases", breaks=c(30, 40, 50, 70, 100),
  color = "blue")
```

```
# Test of propDots with forced range of breaks
```

```
# -----
```

```
propDots(Corse, data = DAT, value="Cases",  
         breaks=c(0, 25, 50, 75, 100),  
         range = c(25, 100))
```

## Plotting dots with classified size

```
library(GADMTools)

classDots(Corse, DAT, color="blue", value = "Cases", steps = 4)
```

## Dot-Density

```
library(GADMTTools)
data("Corsica")

# Creates test data.frame -----
# -----
VAR_1 <- as.integer(runif(n = 43, min = 800, max = 15800))
VAR_2 <- as.integer(runif(n = 43, min = 1000, max = 15800))
VAR_3 <- as.integer(runif(n = 43, min = 1500, max = 15800))
Cantons <- listNames(Corsica, 4)
DF <- data.frame(Cantons, VAR_1, VAR_2, VAR_3, stringsAsFactors = FALSE)

dotDensity(Corsica,
            DF, adm.join="Cantons", dot.size = 0.5, cases.by.dots = 1000,
            values = c("VAR_1", "VAR_2", "VAR_3"),
            labels = c("H1N1", "H1N2", "H2N2"),
            palette = c("#ffff00", "#ffaa00", "#FF3200"))
```

## Plotting density

```
library(GADMTools)

isopleth(Corse, data = DAT, palette = "Blues")
```

## Plotting a choropleth

```
DAT <- data.frame(Cantons, Pop, stringsAsFactors = FALSE)
choropleth(Corsica, data = DAT, value = "Pop", adm.join = "Cantons",
           breaks = "sd", palette = "Greens")
```

**fast.choropleth()**

```
fast.choropleth(  
  x, data, value=NULL,  
  
  breaks = NULL, steps = 5,  
  
  adm.join=NULL, legend = NULL,  
  
  labels = NULL,  
  
  palette=NULL, title=""  
)
```

Parameter	Description
<b>x</b>	<b>Object</b> GADMWrapper
<b>data</b>	<b>data.frame</b> - data to plot
<b>value</b>	<b>String</b> - the name of the column in the data.frame we want to plot (eg: an incidence in epidemiology studies)
<b>breaks</b>	
<b>steps</b>	<b>Integer</b> - number of breaks. Default = 5. If breaks is NOT NULL this value is used internally with cut().
<b>adm.join</b>	<b>String</b> - the name in GADM spdf dataset which will be joined with a column of the data.
<b>legend</b>	<b>String</b> - legend title. Default NULL.
<b>labels</b>	<b>String vector</b> labels for the legend. Default NULL
<b>palette</b>	<b>String</b> - An RColorBrewer palette name or a String vector vector of colors. Default NULL.
<b>title</b>	<b>String</b> - Title of the plot. Default is an empty string.



## Example

```
MAP <- gadm_sp_loadCountries("BEL", level = 3, simplify=0.01)
DAT = read.csv2("BE_chlamydia_incidence.csv")

# Rewriting District names
# -----
DAT$district <- as.character(DAT$district)
DAT[7,1] = "Brussel"
DAT[20,1] <- "Liège"
DAT[22,1] = "Marche-en-Famenne"
DAT[27,1] = "Neufchâteau"
DAT <- rename(DAT, NAME_3 = district)

fast.choropleth(MAP, DAT,
  adm.join = "NAME_3",
  value = "rate03",
  steps = 4,
  breaks = "jenks",
  palette="Greens",
  legend = "Incidence",
  title="Chlamydia incidence by Belgian district (2003)")
```

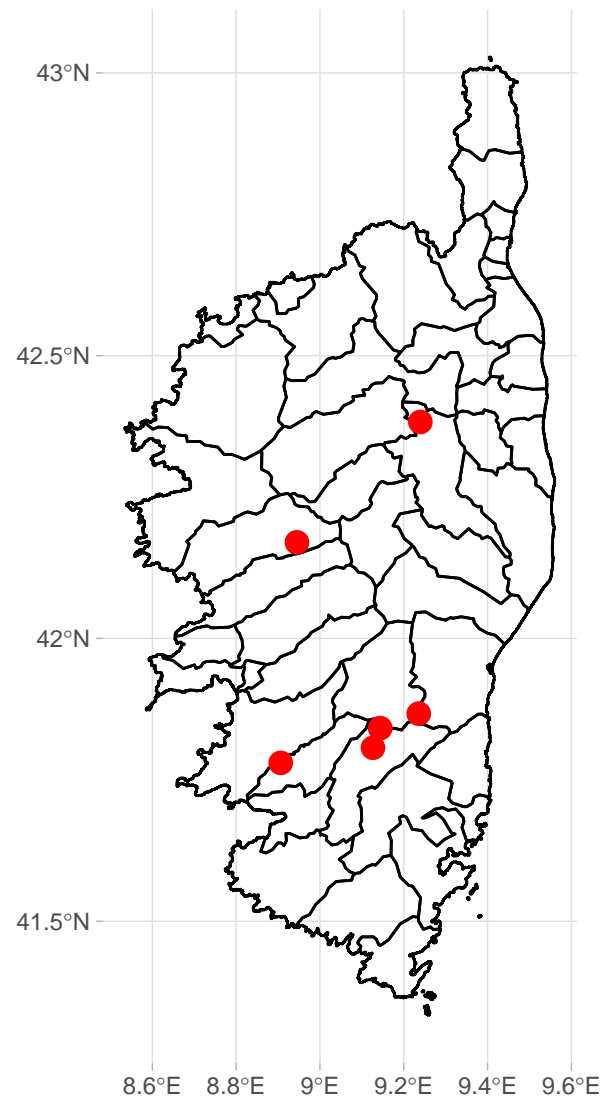


Figure 1: Simple dots

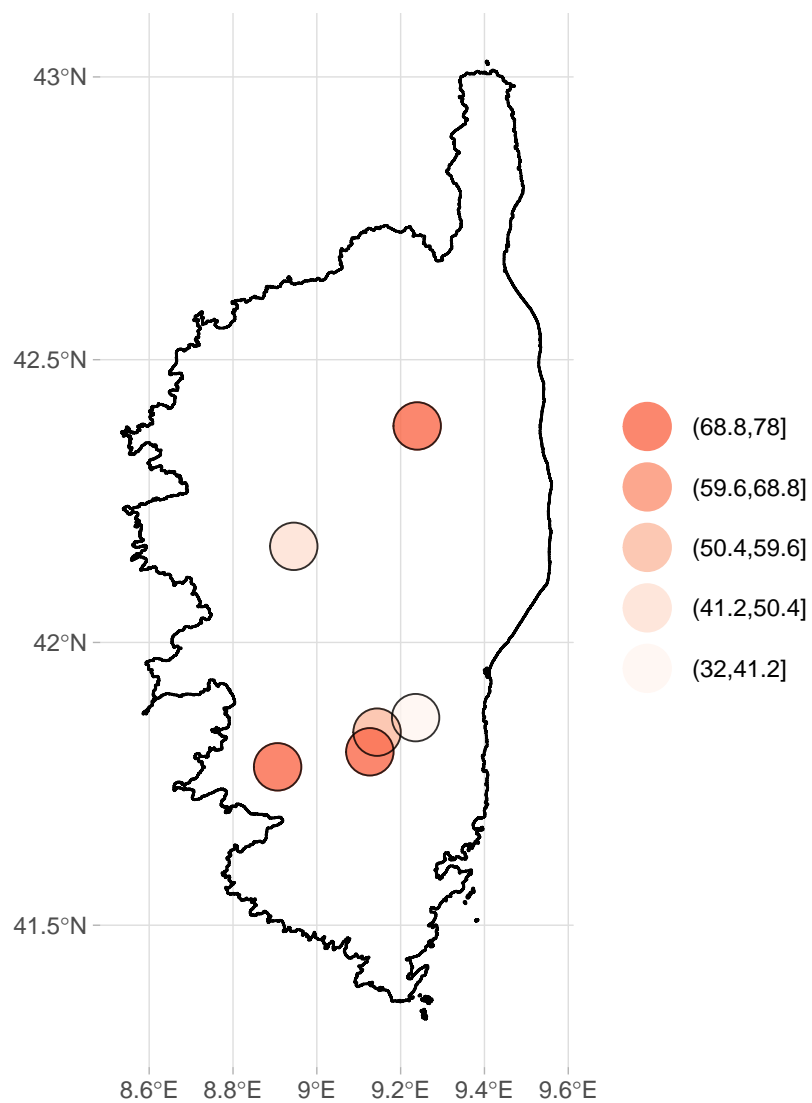


Figure 2: Classified dots

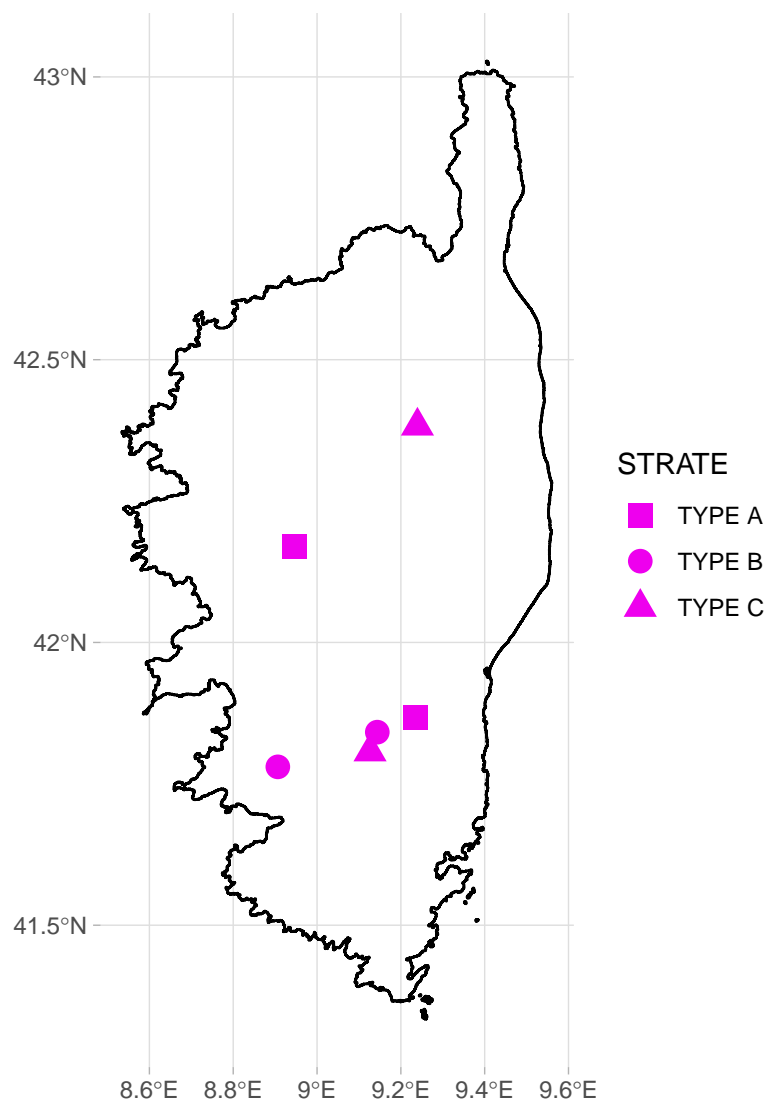


Figure 3: Typed dots

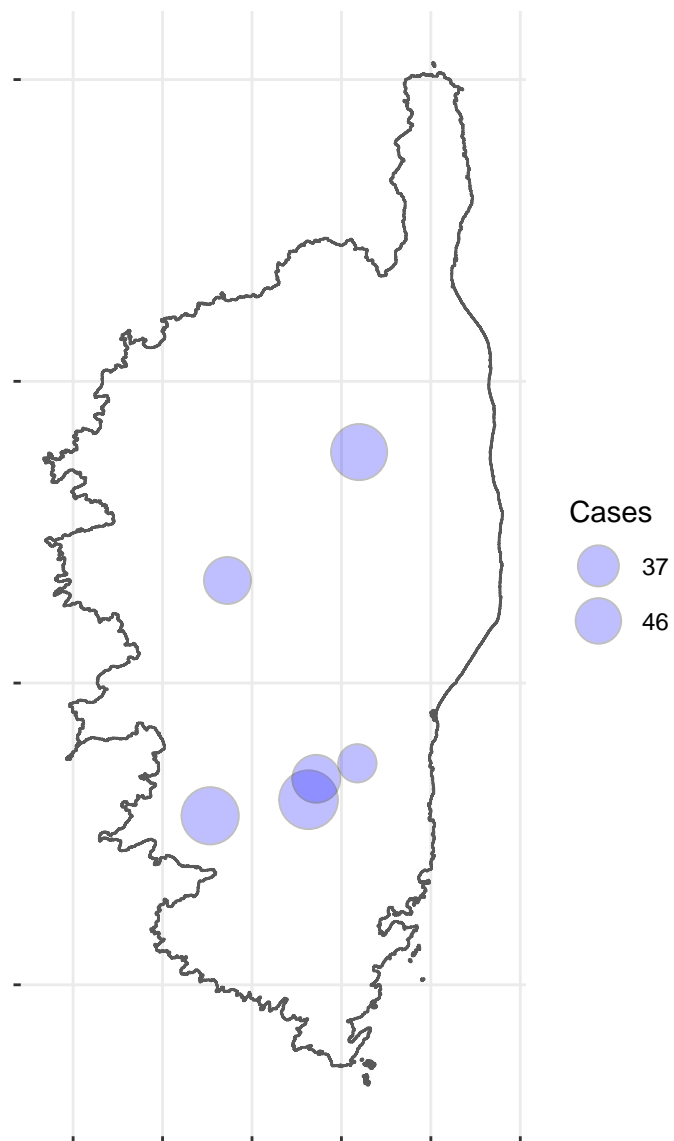


Figure 4: propDots

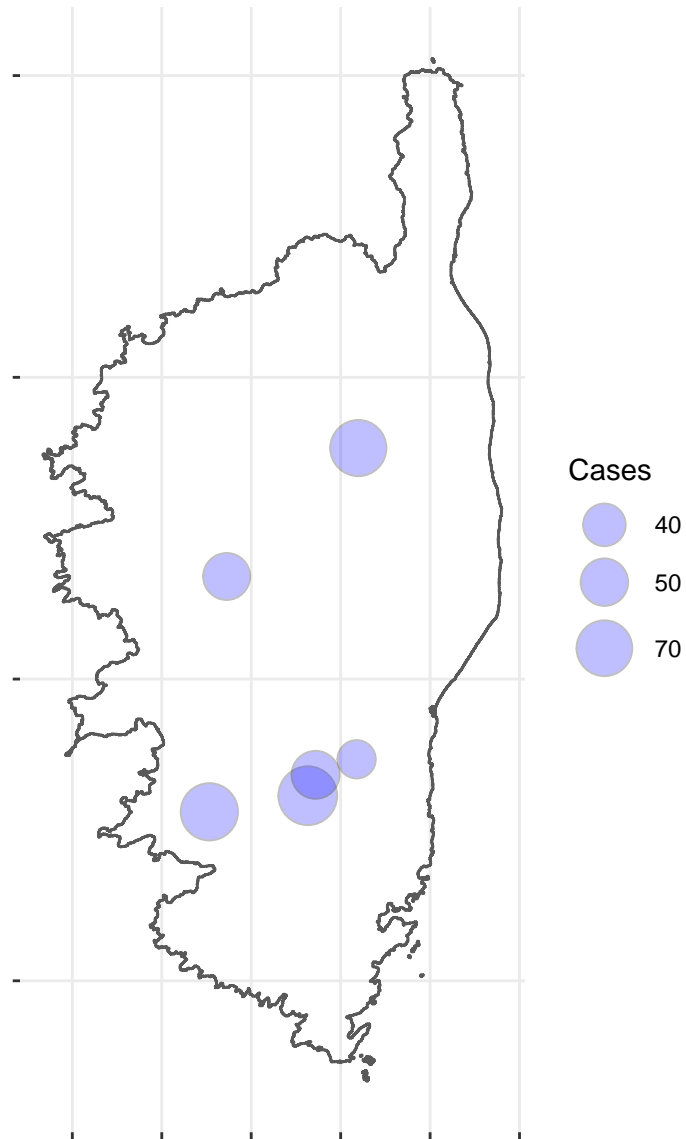


Figure 5: propDots with provided breaks

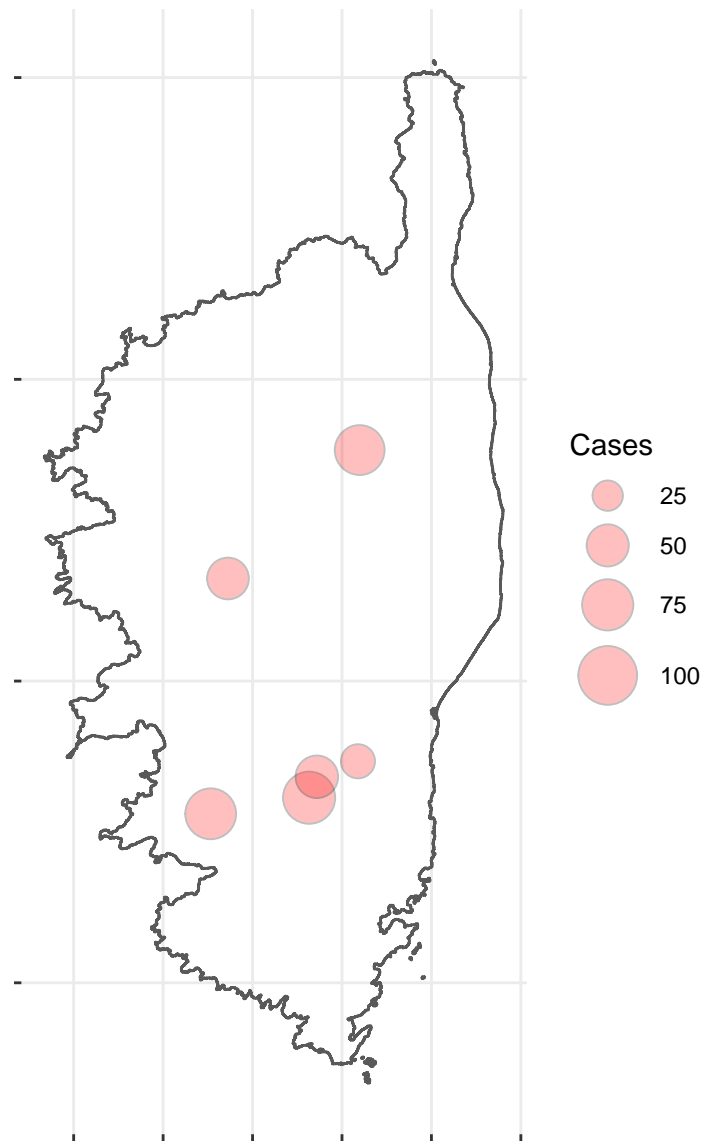


Figure 6: propDots

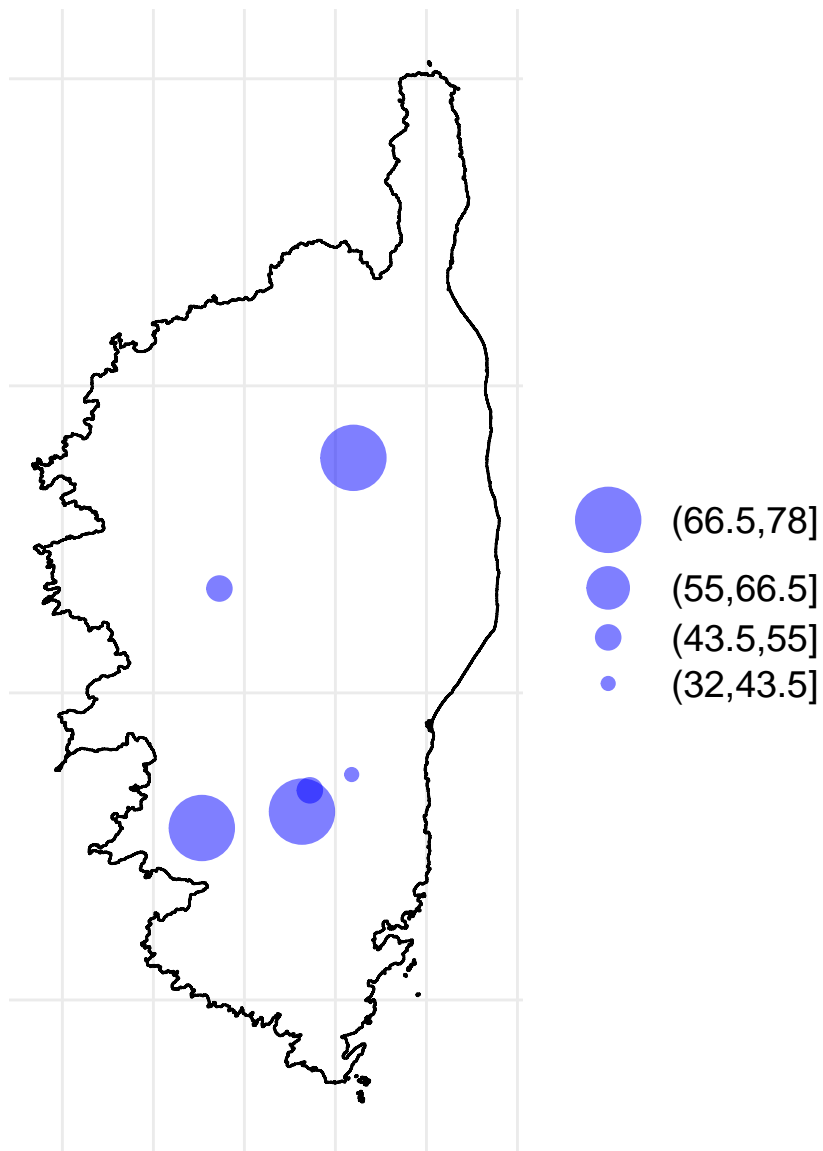


Figure 7: classDots



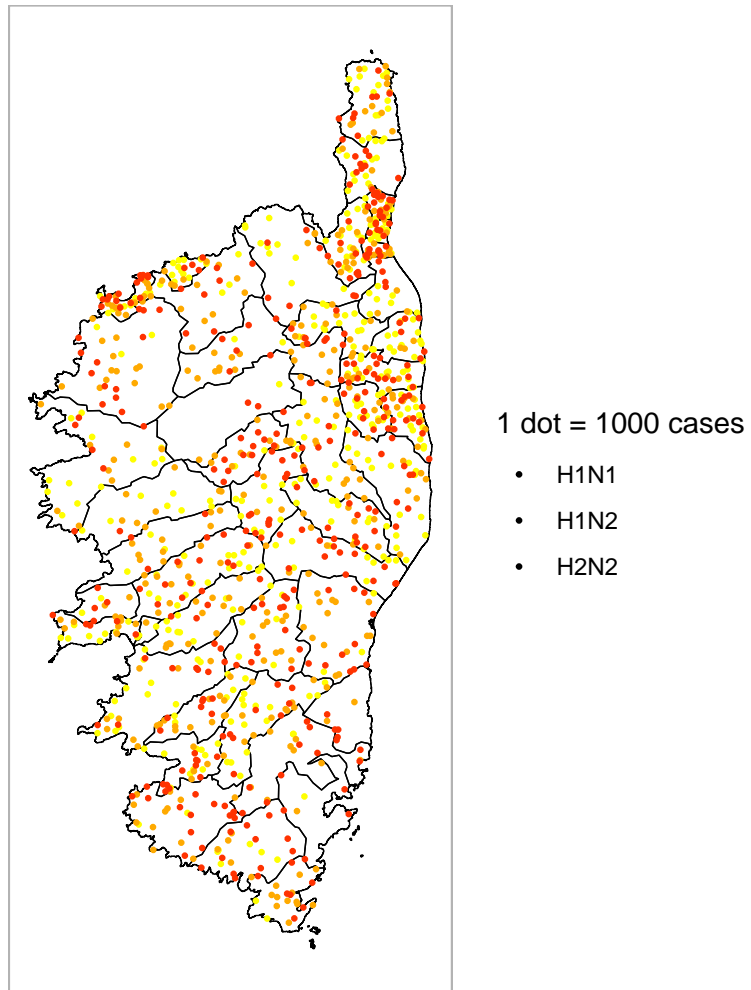


Figure 8: Dot-Density

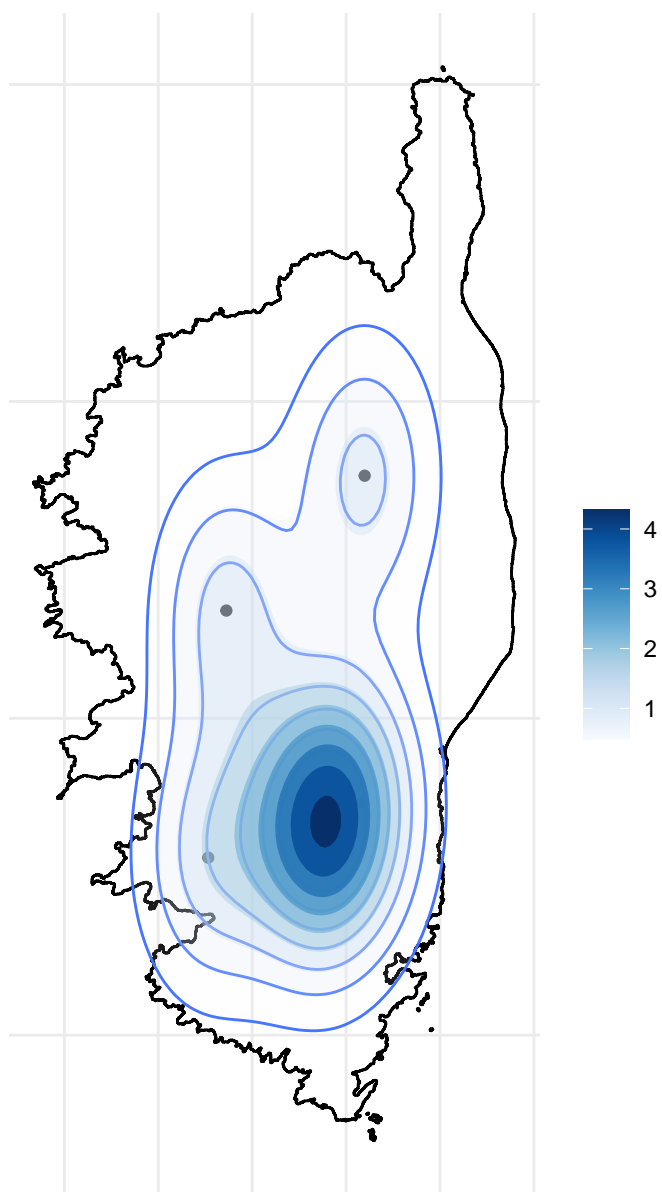


Figure 9: Isopleth

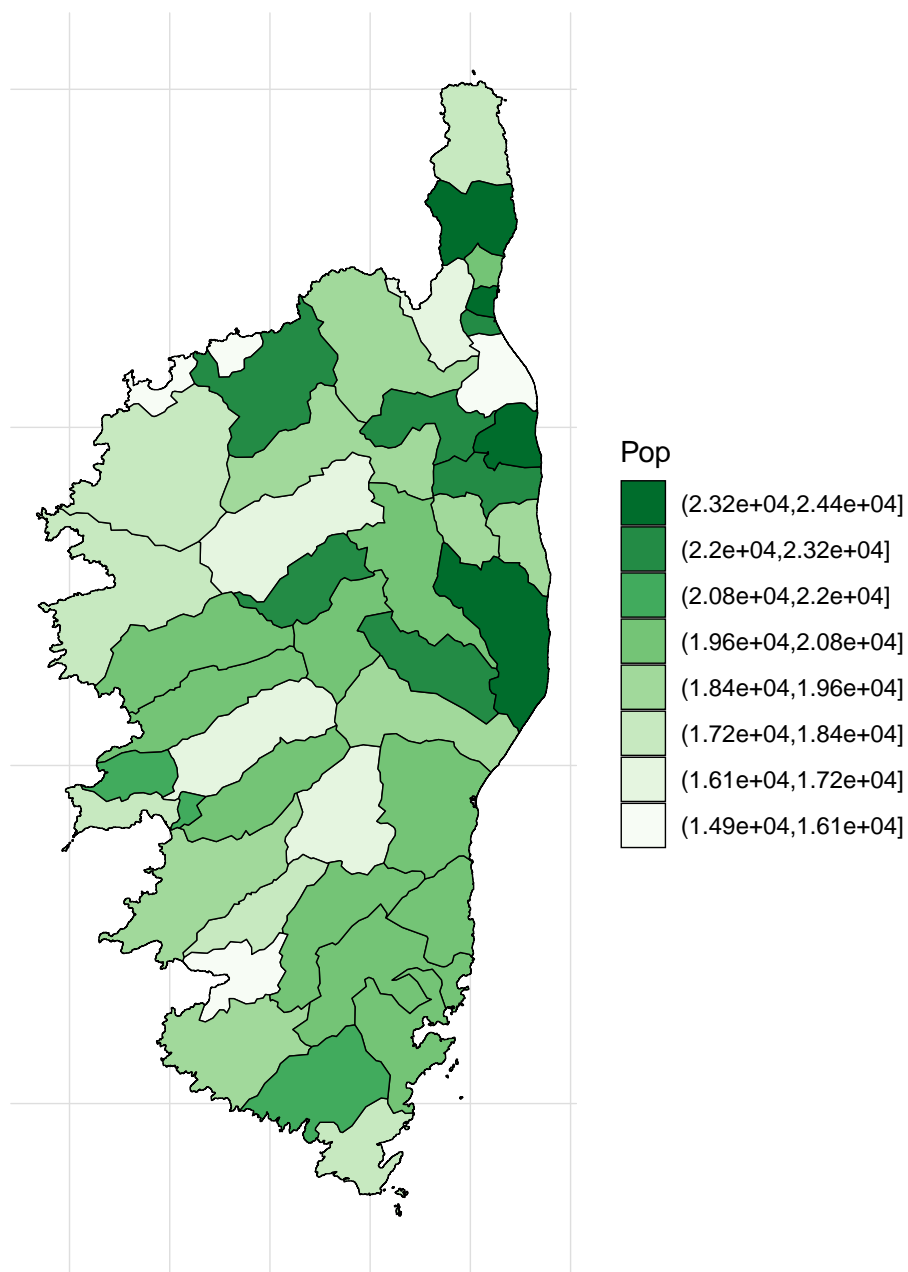


Figure 10: Choropleth

### Chlamydia incidence by Belgian district (2003)



Figure 11: drawing a fast.choropleth