Epiverse

TRACE LAC

epiCo package

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epiCo

version: 0.0.2

Authors:

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epiCo provides statistical tools for the analysis of demographic trends, spatiotemporal behavior, and outbreaks characterization of vector-borne diseases in Colombia

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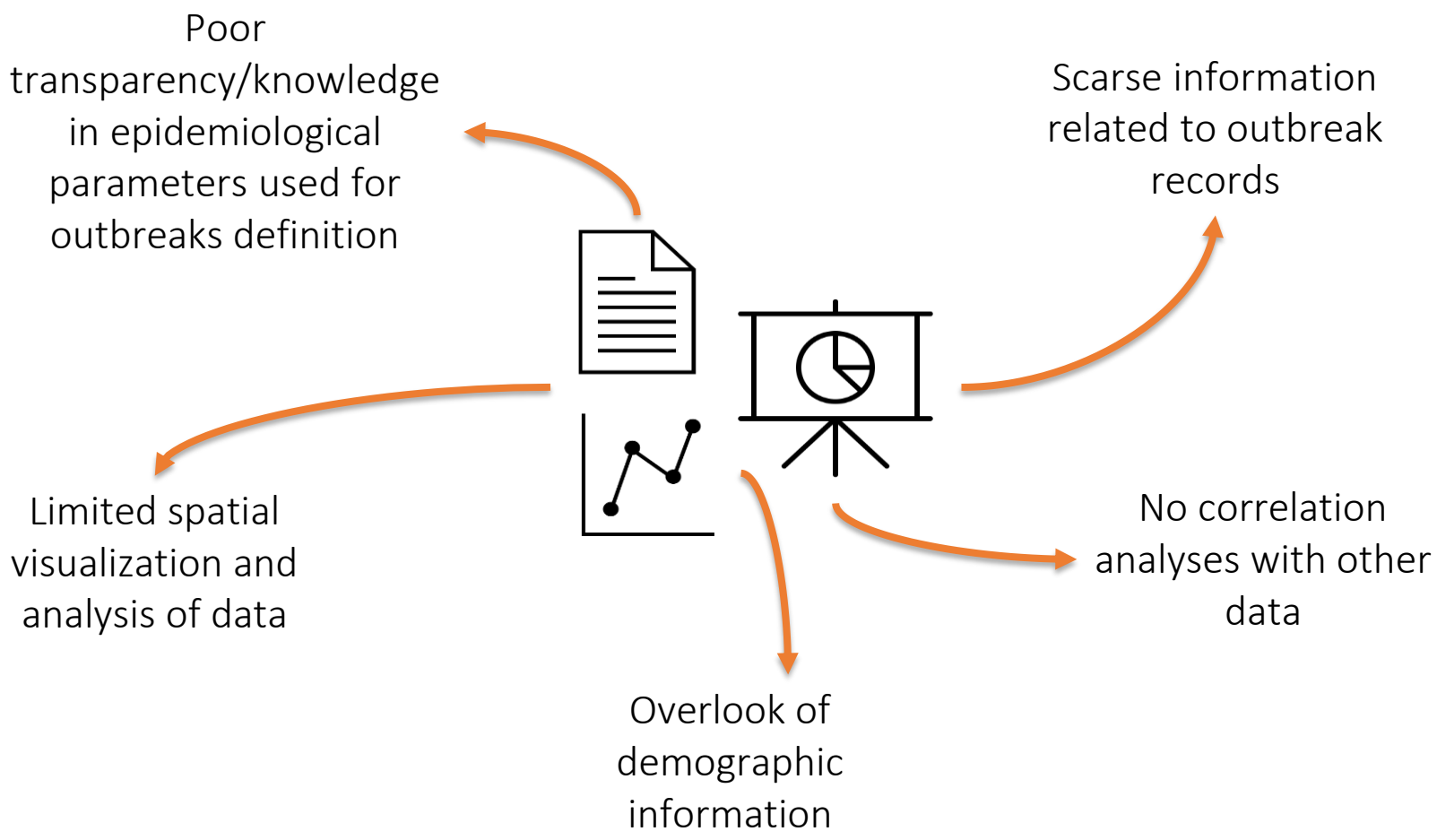
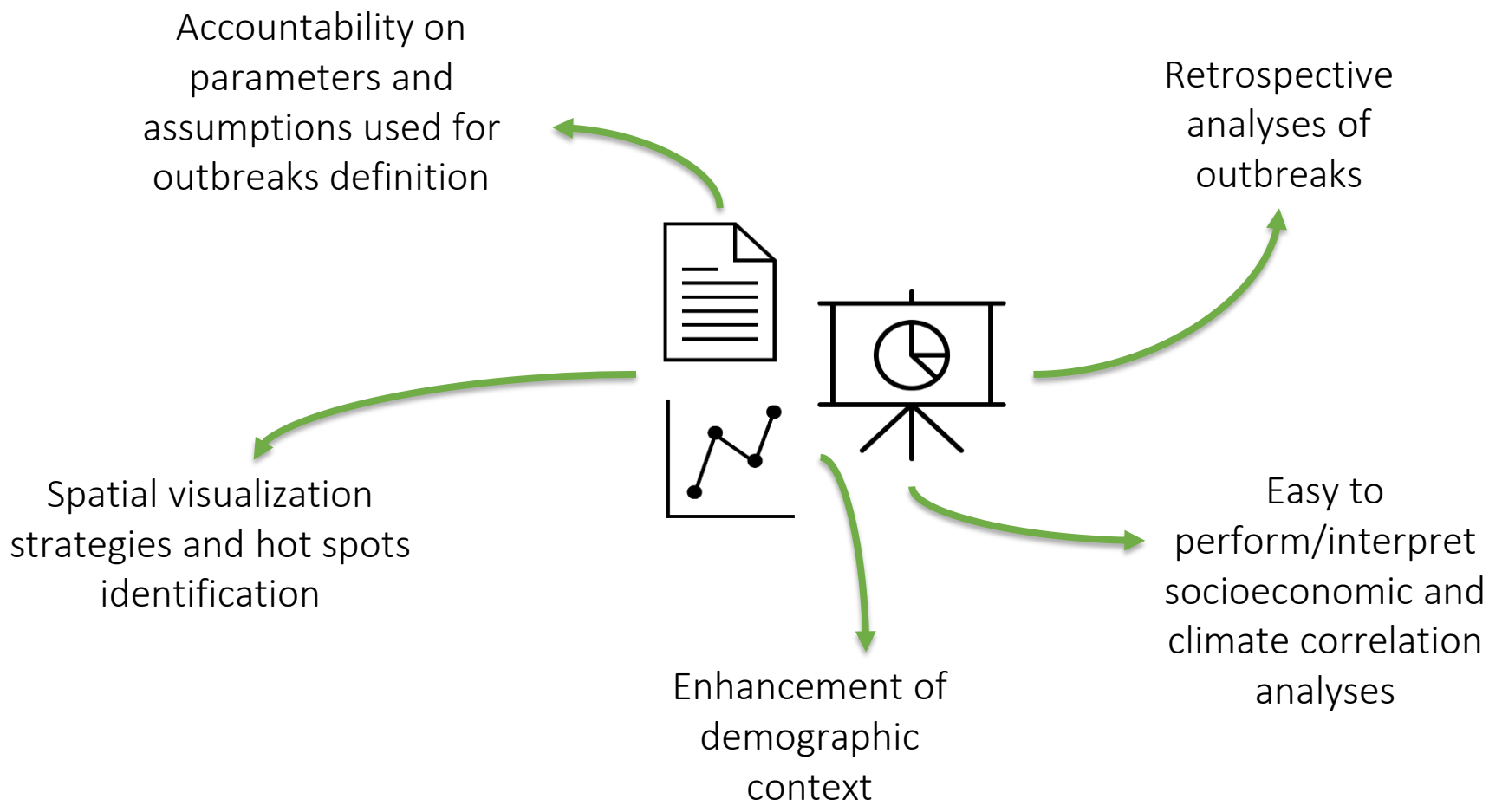
Motivation

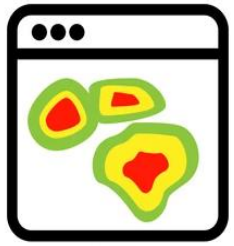

Poor transparency/knowledge in epidemiological parameters used for outbreaks definition
Scarse information related to outbreak records
Limited spatial visualization and analysis of data
No correlation analyses with other data
Overlook of demographic information

Goals

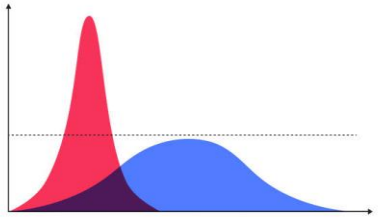

Accountability on parameters and assumptions used for outbreaks definition
Retrospective analyses of outbreaks
Spatial visualization strategies and hot spots identification
Easy to perform/interpret socioeconomic and climate correlation analyses
Enhancement of demographic context

Modules

Demographics



Spatiotemporal



Outbreaks

Decision support

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Modules

Demographics

```
library(sivirep)
library(incidence)
library(epiCo)

years_to_analyze <- c(2015:2021)
events_to_analyze <- c("DENGUE", "DENGUE GRAVE", "MORTALIDAD POR DENGUE")

data_dengue <- data.frame()

for(y in years_to_analyze) {
     for(e in events_to_analyze)  {
          temp_data_dengue <- sivirep::import_data_disease_by_year(y,e)
          data_dengue <- rbind(data_dengue, temp_data_dengue)
     }
}
```

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Modules

Demographics

```
data_dengue_ibague <- subset(data_Dengue, COD_MUN_O == 73001)

ethnicities <- data_Dengue_ibague$PER_ETN[data_Dengue_ibague$PER_ETN != 6]
describe_ethnicity(ethniclabels = ethnicities, language = "EN")

>>

Indigenous - count: 22 cases

"A person of Amerindian descent who shares feelings of  identification
with their aboriginal past, maintaining traits and values  of their
traditional culture, as well as their own forms of organization  and
social control"
```

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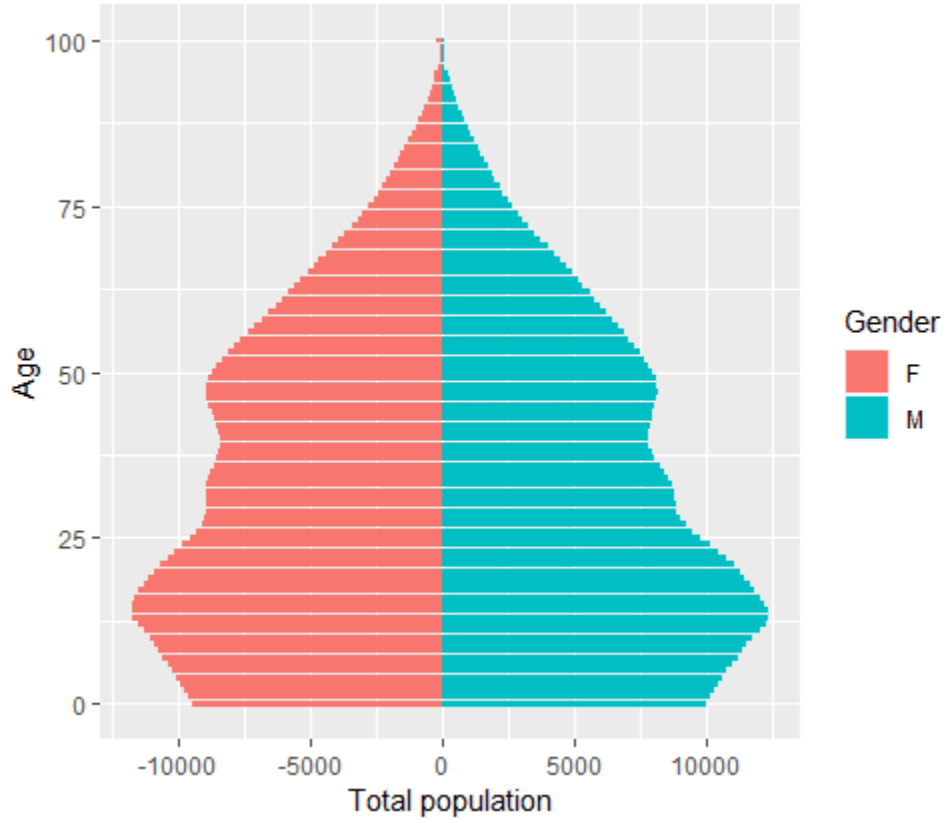
Modules

Demographics

```
ibague_pyramid <- population_pyramid(divipola_code = 73001, year = 2021,
                                     gender = TRUE, total = FALSE, plot = TRUE)
```



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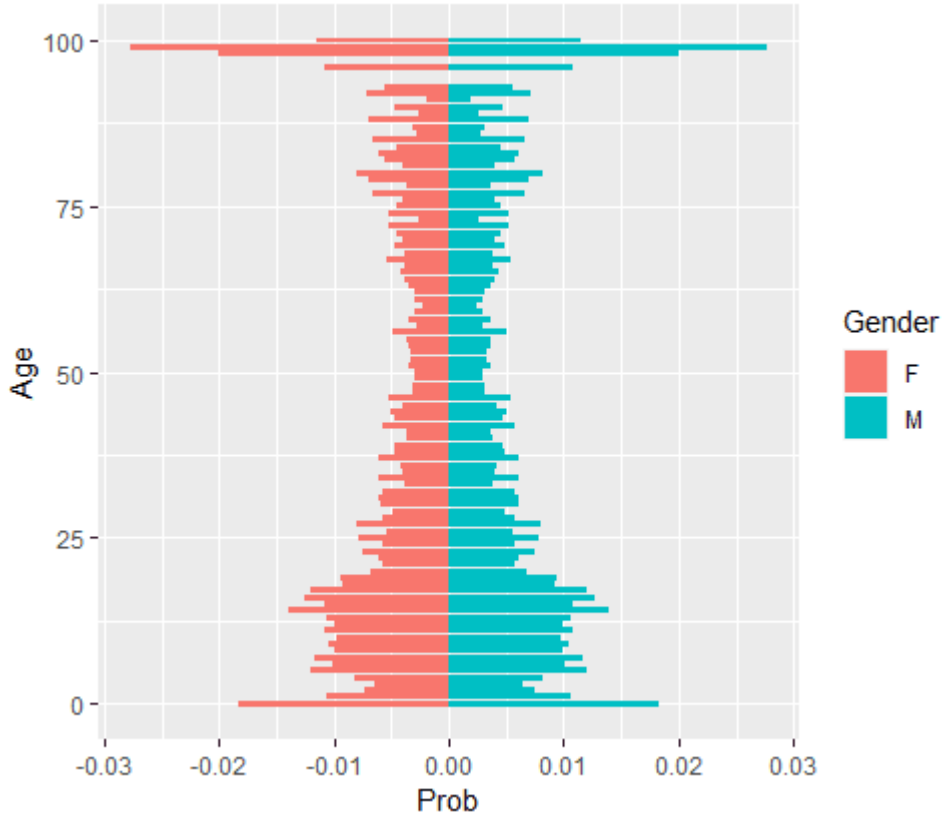
Modules

Demographics

```
ibague_age_risk <-  age_risk(age = data_Dengue_ibague$EDAD_A,
                             gender = data_Dengue_ibague$SEXO,
                             population_pyramid = ibague_pyramid)
```



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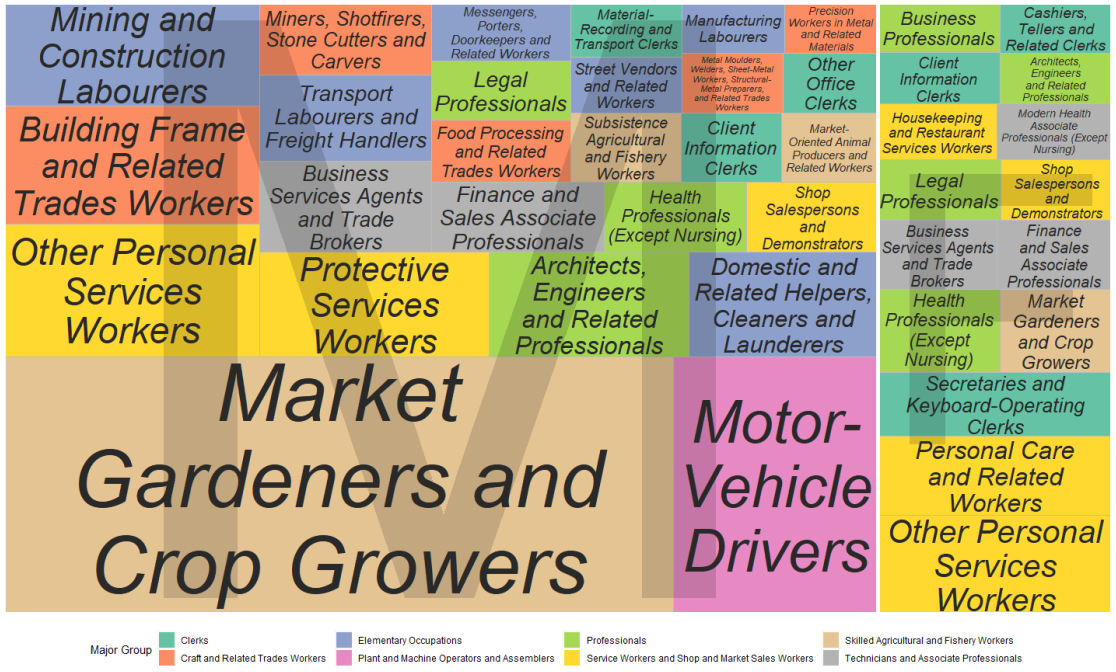
Modules

Demographics

```
ibague_occupation_dist <- occupation_dist(data_Dengue_ibague$OCUPACION)
```



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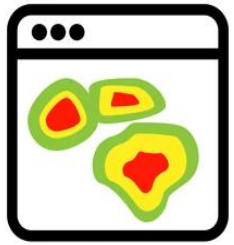
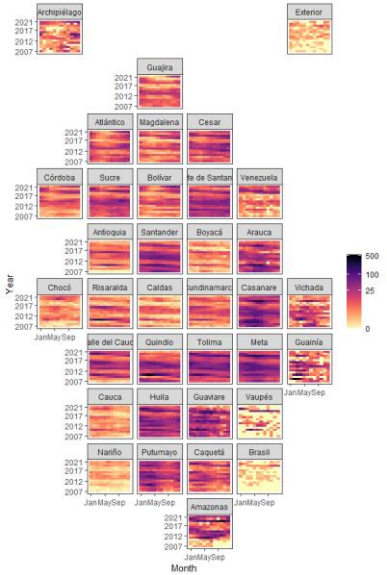
Modules



Spatiotemporal

```
colombia_incidence <- incidence::incidence(data_Dengue$FEC_NOT,
                                           interval = "1 week",
                                           groups = data_Dengue$COD_MUN_O)

colombia_incidence_rate <- epiCo::incidence_rate(
                                        incidence_object = colombia_incidence,
                                        level = 0, scale = 1e+05)
```



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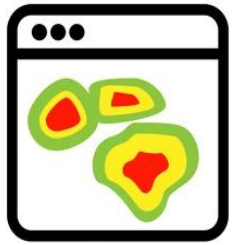
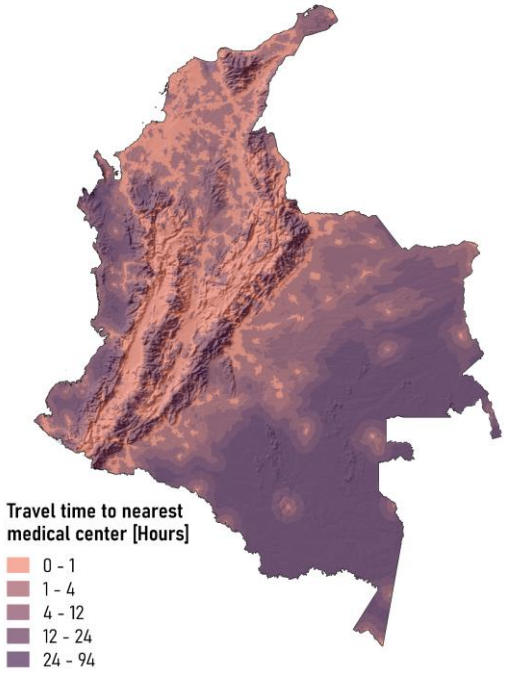
Modules



Spatiotemporal

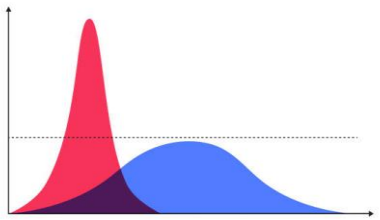
```
morans_index(colombia_incidence_rate, threshold = 2, plot = TRUE)
```



Travel time parameter i.e. neighborhoods are not defined solemnly on distances but in real travel connectivity

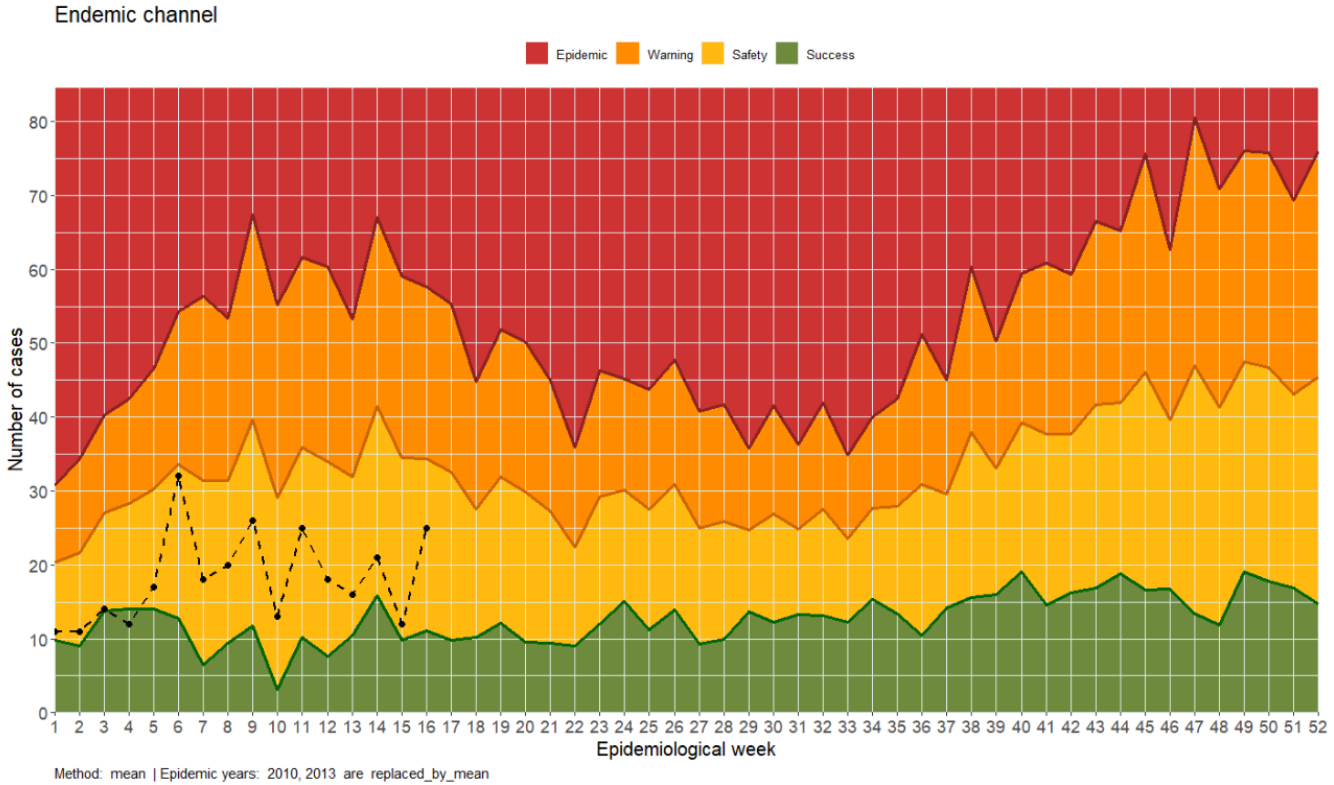
Bravo-Vega, Carlos, et al. 2023
https://doi.org/10.1371/journal.pntd.0011117

Modules



Outbreaks

```
endemic_channel(observations = obs,
                incidence_historic = colombia_incidence,
                method = mean, outlier_years = NULL)
```



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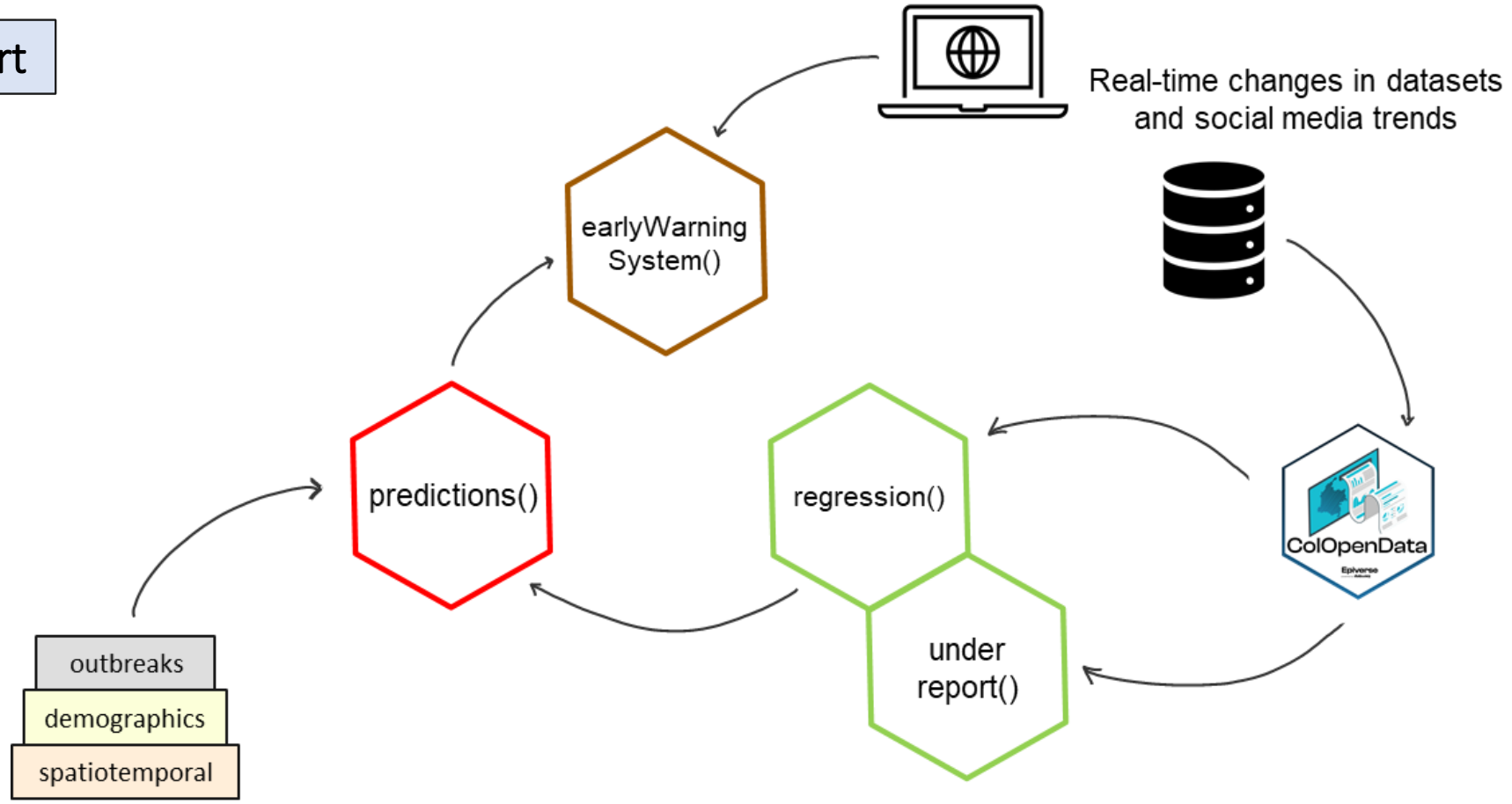
Modules

decision support



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Repository

```
remotes::install_github("epiverse-trace/epiCo")
```

- demographics and spatiotemporal modules have an stable version on GitHub
- Our repository is open to suggestions and features requests
- First user testings are taking place in April and May

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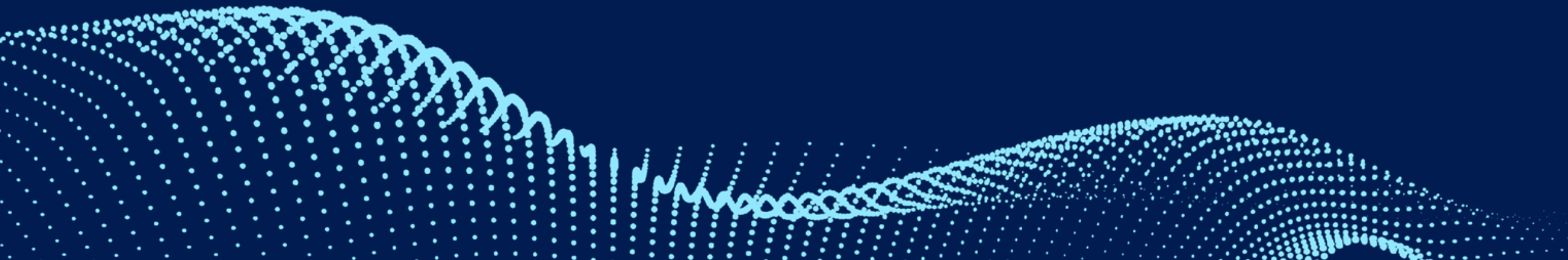
Thanks!

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