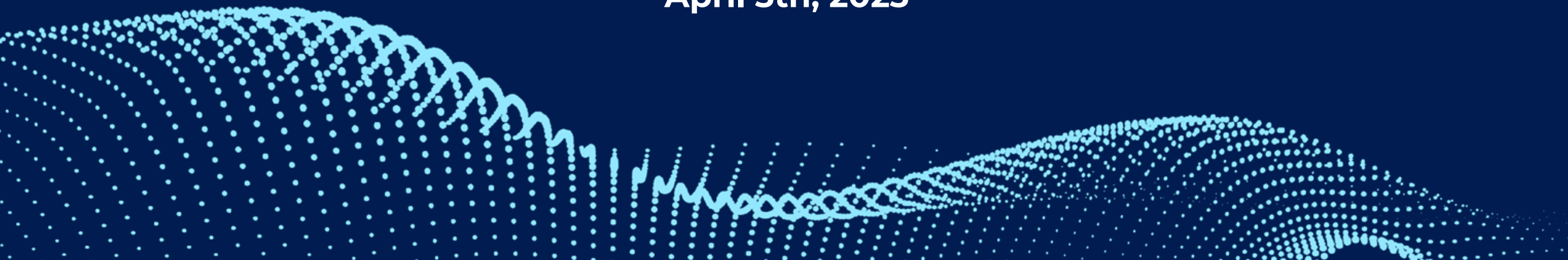
Epiverse TRACE LAC

Pontificia Universidad JAVERIANA Bogotá

sivirep 0.0.1

April 5th, 2023



sivirep

0.0.1

Authors:

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Contributors:

- Hugo Gregson
- Laura Gómez-Bermeo

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Motivation

Surveillance Systems

- Latin America has progressed in the quality of epidemiological notification and surveillance systems.

Challenges

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- Latin America has progressed in the quality of epidemiological notification and surveillance systems.

- Colombia has improved over the years the quality and openness of its system.

Challenges

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- Timeliness and quality of epidemiological analytics and reports.

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- These tasks may involve a great deal of manual labor reinforced.

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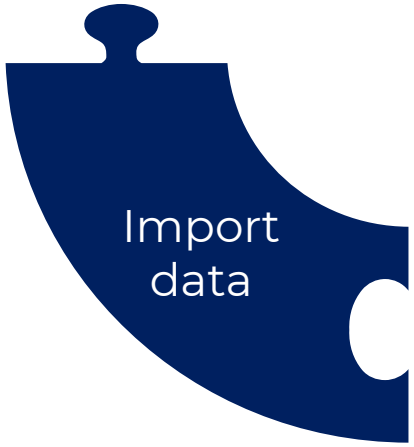
Challenges

- Timeliness and quality of epidemiological analytics and reports.
- These tasks may involve a great deal of manual labor reinforced.
- There is no standardization in epidemiological bulletins.

sivirep

A package for data wrangling and the generation of automated reports from the SIVIGILA source (Public Health Surveillance System in Colombia).

Modules



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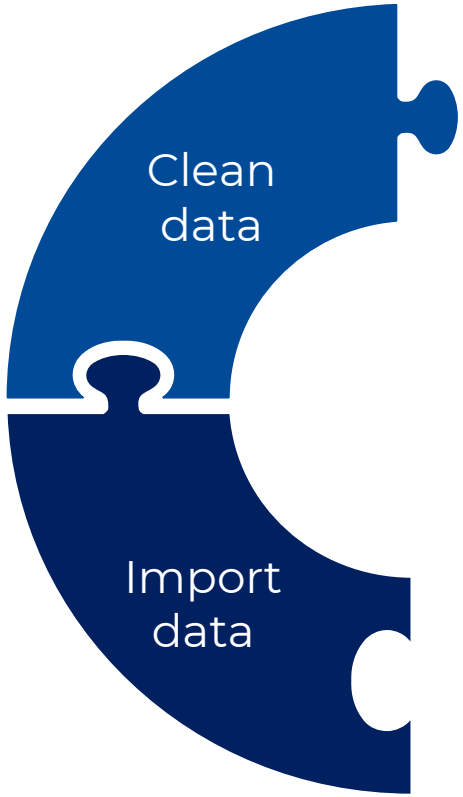
Modules



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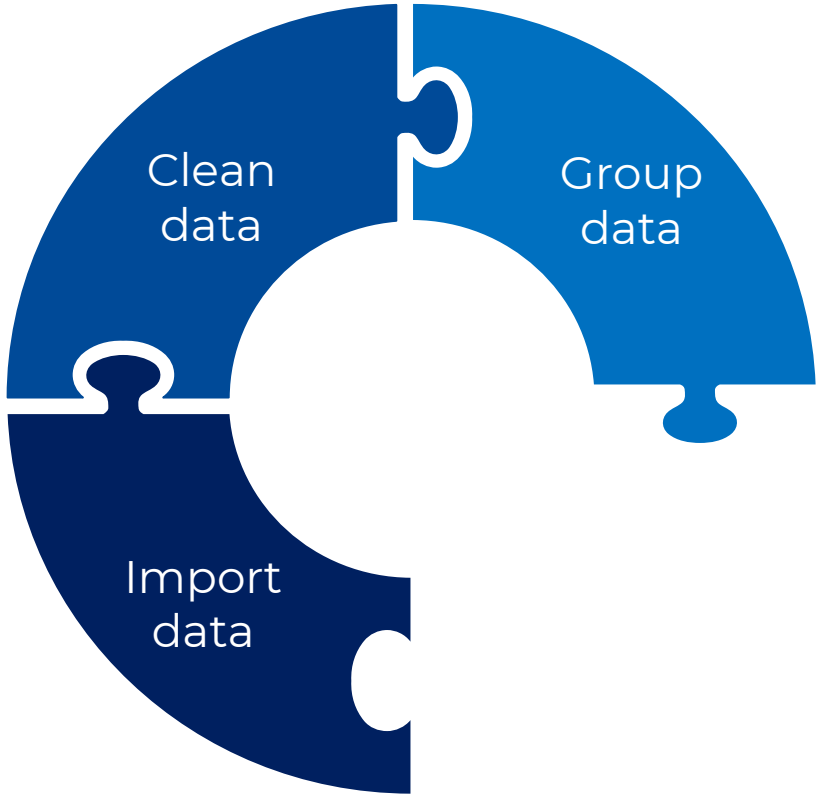
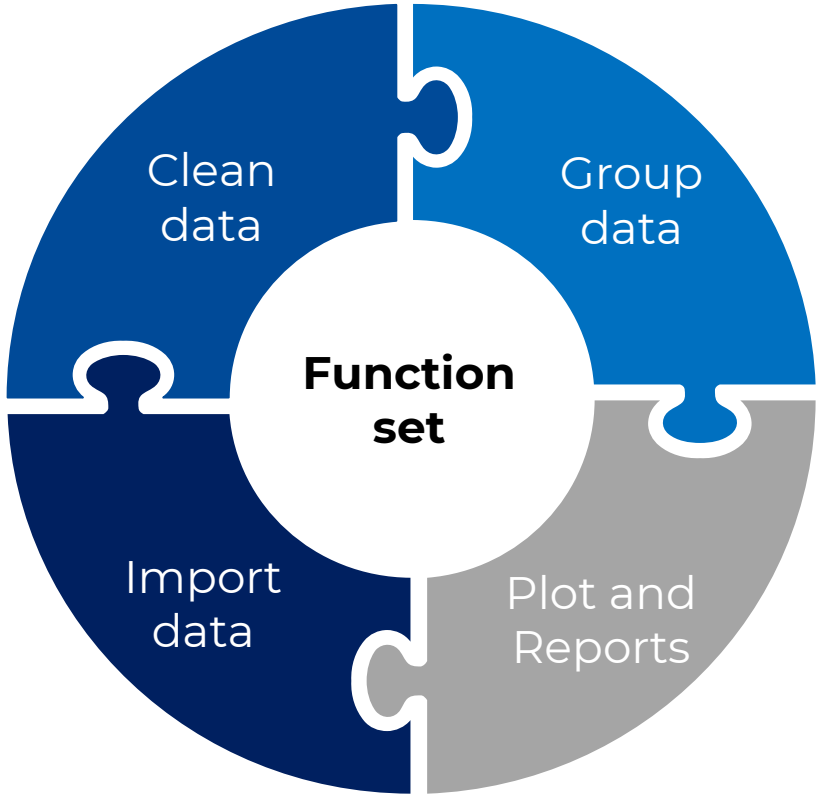
Modules



Modules



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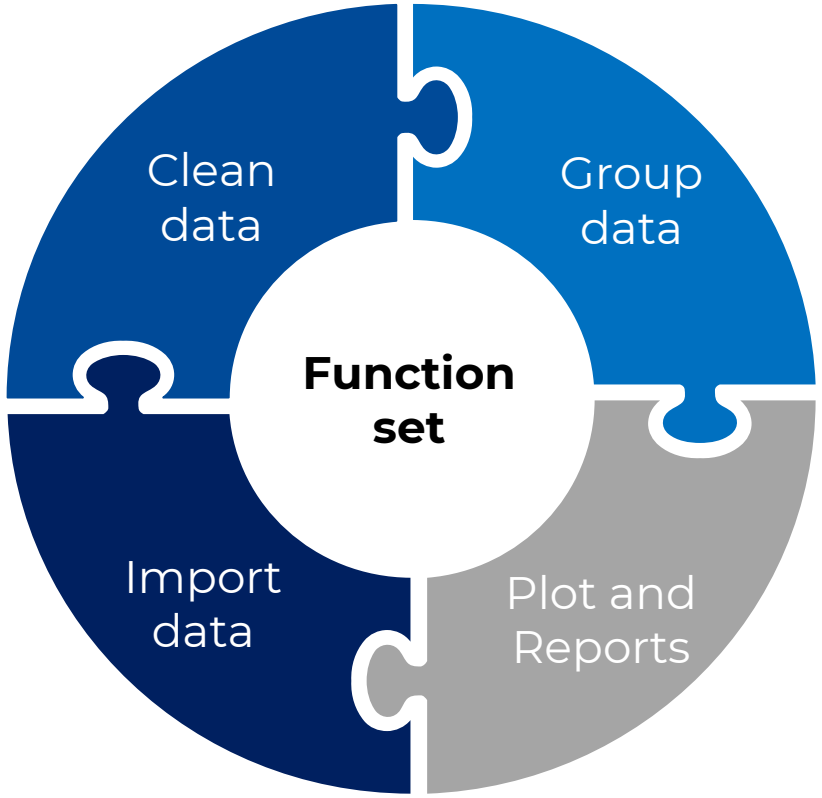
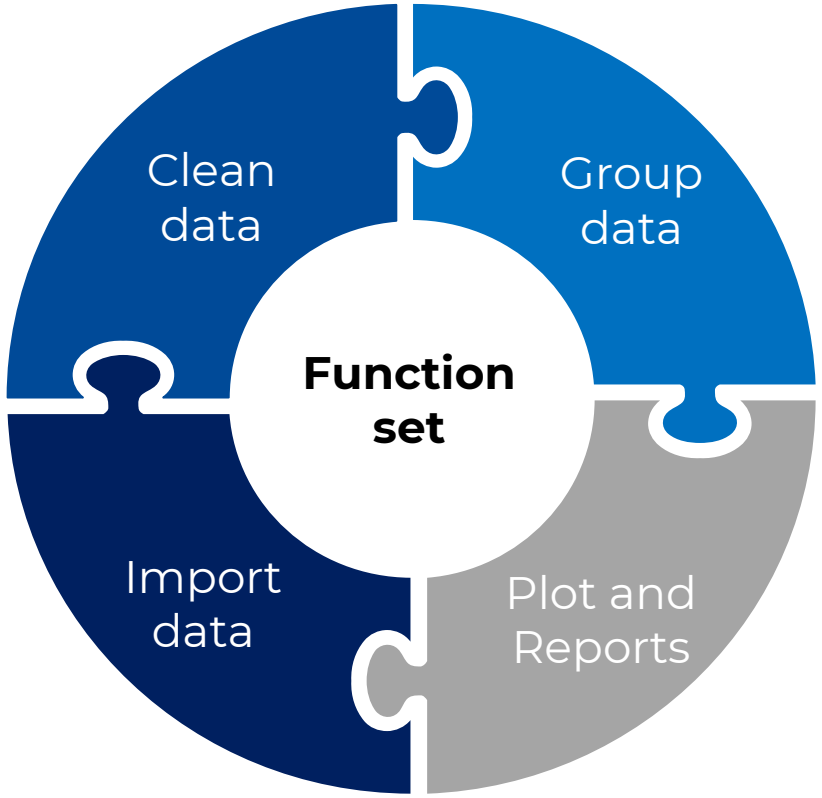
Modules



Used by the report template

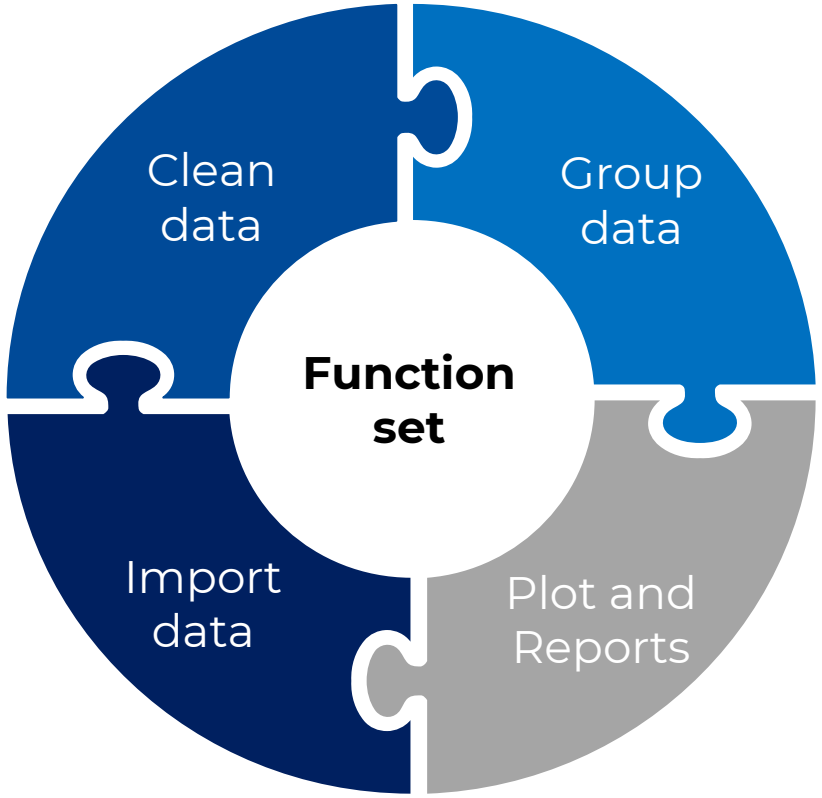
Modules



Used by the report template

Used for analytics or Customising the report

Modules



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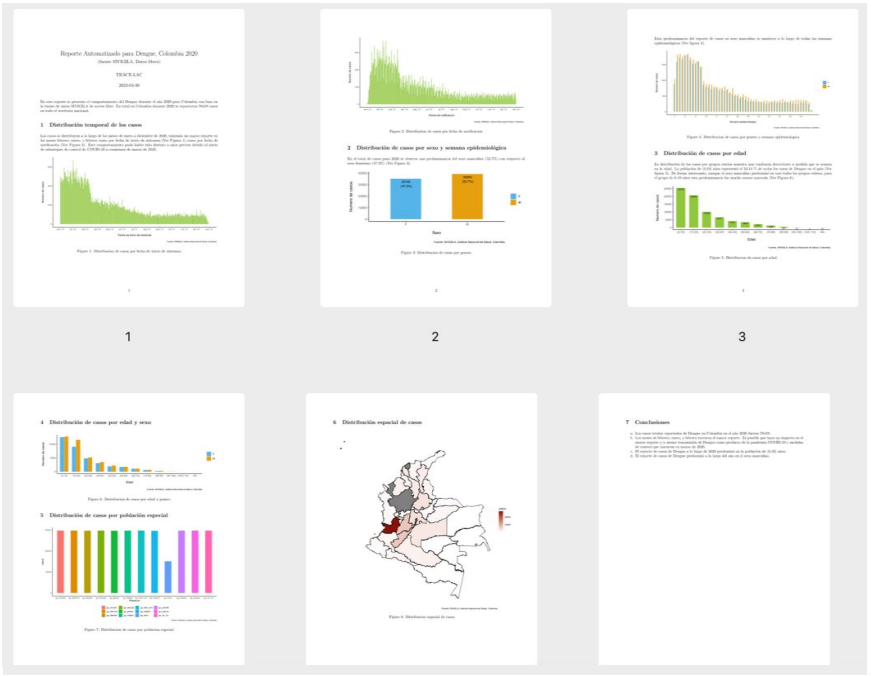
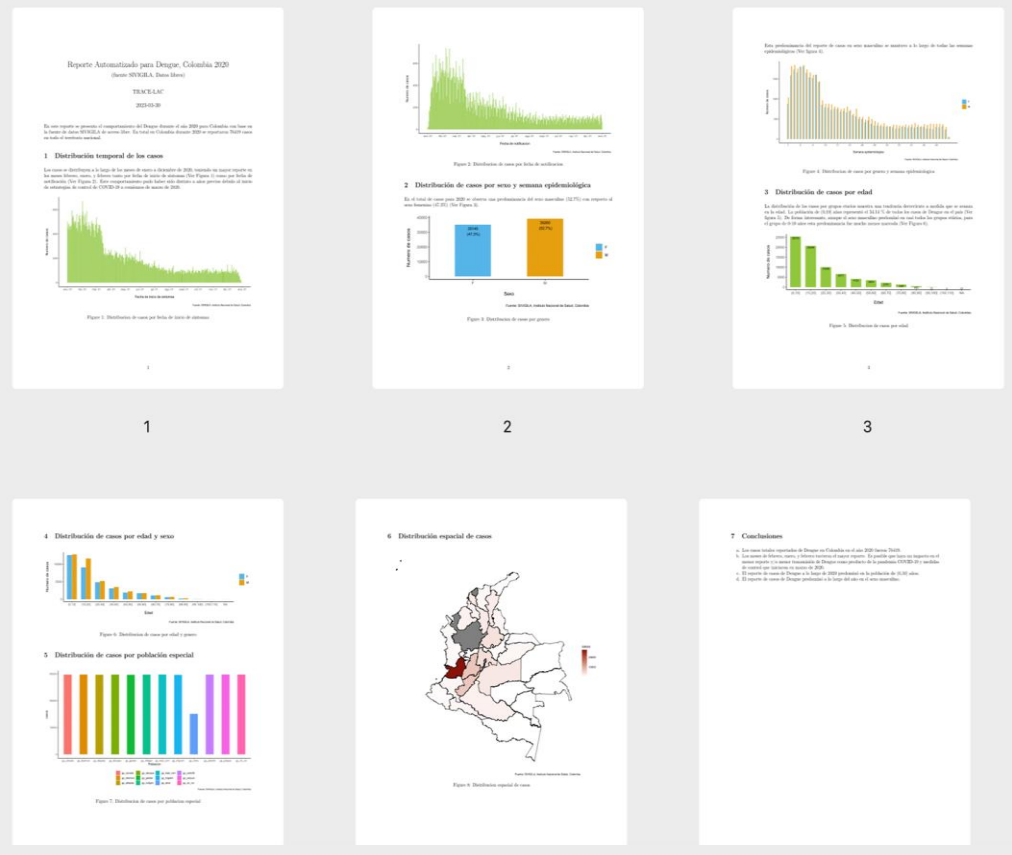


Automated report



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Import data

Import data

Check the available diseases and years:

```
list_available_diseases_years()
```

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list_available_diseases_years()
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enfermedad	aa
ACCIDENTE OFIDICO	2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021
AGRESIONES POR ANIMALES POTENCIALMENTE TRANSMISORES DE RABIA	2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021
ANOMALIAS CONGENITAS	2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021
BAJO PESO AL NACER	2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021

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68 diseases available

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Import data

Importing SIVIGILA data:

```
disease_data <-  import_linelist_disease_year(year = 2020,
                                              disease_name = "dengue")
```

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```
disease_data <-  import_linelist_disease_year(year = 2020,
                                              disease_name = "dengue")
```

disease_data

Filter | Cols: « < 1 - 50 > »

	CONSECUTIVE	COD_EVE	FEC_NOT	SEMANA	ANO	COD_PRE	COD_SUB	EDAD	UNI_MED	NACIONALID	NOM_NACIONALIDAD	SEXO
1	7212061	210	2020-04-02	14	2020	7604104065	1	13	1	170	COLOMBIA	F
2	7212037	210	2020-04-06	14	2020	2736100902	1	35	1	170	COLOMBIA	F
3	7212059	210	2020-01-22	4	2020	4129800357	1	29	1	170	COLOMBIA	F
4	7212047	210	2020-09-28	39	2020	5022300873	1	6	2	170	COLOMBIA	F
5	7213565	210	2020-09-14	37	2020	2548885069	80	4	1	170	COLOMBIA	M
6	7212063	210	2020-05-14	20	2020	7321700924	1	31	1	170	COLOMBIA	F

Clean data

Cleansing SIVIGILA data:

```
clean_disease_data <- cleansing_sivigila_data(disease_data,
                                              year = 2020)
```

Clean data

Cleansing SIVIGILA data:

```
clean_disease_data <- cleansing_sivigila_data(disease_data,
                                              year = 2020)
```

clean_disease_data

Filter | Cols: « < 1 - 50 > »

	cod_eve	fec_not	semana	ano	cod_pre	cod_sub	edad	uni_med	nacionalid
1	210	2020-04-02	14	2020	7604104065	1	13.000	1	170
2	210	2020-04-06	14	2020	2736100902	1	35.000	1	170
3	210	2020-01-22	4	2020	4129800357	1	29.000	1	170
4	210	2020-09-28	39	2020	5022300873	1	0.042	2	170
5	210	2020-09-14	37	2020	2548885069	80	4.000	1	170
6	210	2020-05-14	20	2020	7321700924	1	31.000	1	170

Group data

Variable grouping functions

Standart

```
group_varible_name(disease_data, percentage)
```

Group data

Variable grouping functions

Standart

```
group_varible_name(disease_data, percentage)
```

```
group_sex(disease_data = clean_disease_data, percentage = TRUE)
```

```
group_age(disease_data = clean_disease_data, age_interval = 10)
```

```
group_dept(disease_data = clean_disease_data, percentage = TRUE)
```

```
group_onset_symptoms(disease_data = clean_disease_data, type = "day")
```

Customisable analytics or reports

Variable grouping functions

```
group_age(disease_data = clean_disease_data, age_interval = 10)
```

Customisable analytics or reports

Variable grouping functions

```
group_age(disease_data = clean_disease_data, age_interval = 10)
```

cases_age

Filter

	edad	casos
1	(0,10]	25379
2	(10,20]	20699
3	(20,30]	10038
4	(30,40]	6577
5	(40,50]	4125
6	(50,60]	3454
7	(60,70]	2191
8	(70,80]	1287
9	(80,90]	493
10	(90,100]	72
11	(100,110]	3

Plot and building reports

Plot functions by variable and cases

Plot and building reports

Plot functions by variable of distribution cases

Standart

```
plot_varible(data_grouped)
```

Plot and building reports

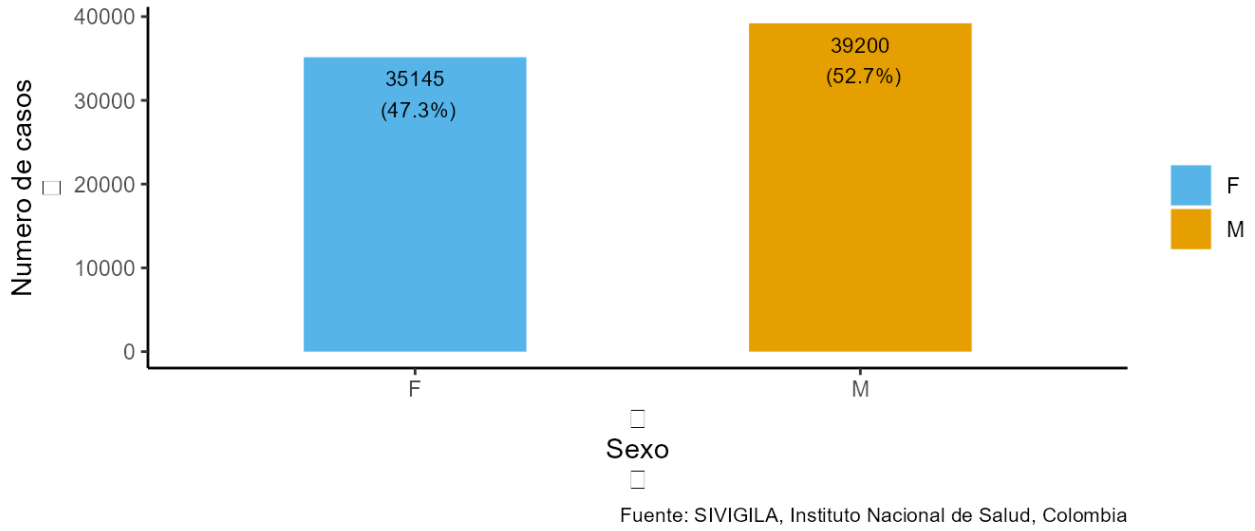
Plot functions by variable and cases

```
plot_sex(data_grouped = cases_sex)
```

Plot and building reports

Plot functions by variable and cases

```
plot_sex(data_grouped = cases_sex)
```



Fuente: SIVIGILA, Instituto Nacional de Salud, Colombia

Plot and building reports

Plot functions by variable and cases

```
plot_age(data_grouped = cases_age)
```

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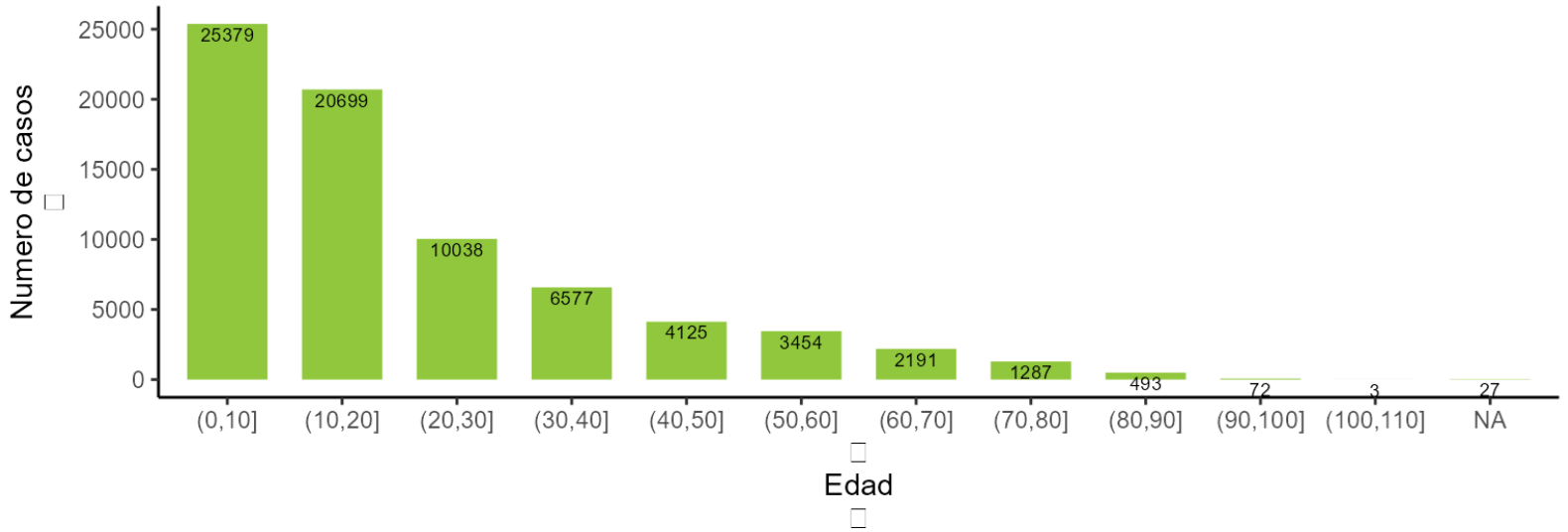

Fuente: SIVIGILA, Instituto Nacional de Salud, Colombia

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Plot and building reports

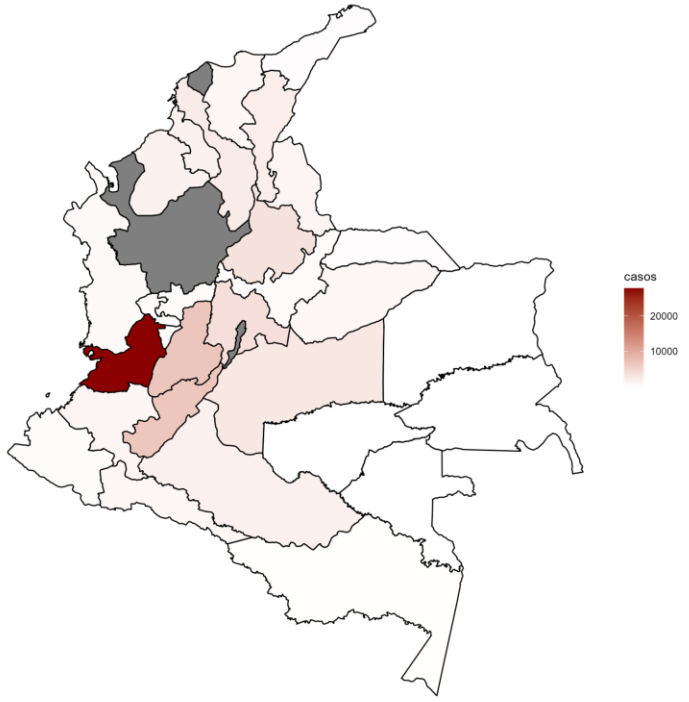
Plot functions by variable and cases

```
plot_dept_map(data_grouped = spatial_dept_dist)
```

Plot and building reports

Plot functions by variable and cases

```
plot_dept_map(data_grouped = spatial_dept_dist)
```



Plot and building reports

Plot functions by variable and cases

```
plot_onset_symptoms(data_grouped = cases_onset_symptoms_by_day,
                    break_tick_date = "months")
```

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plot_onset_symptoms(data_grouped = cases_onset_symptoms_by_day,
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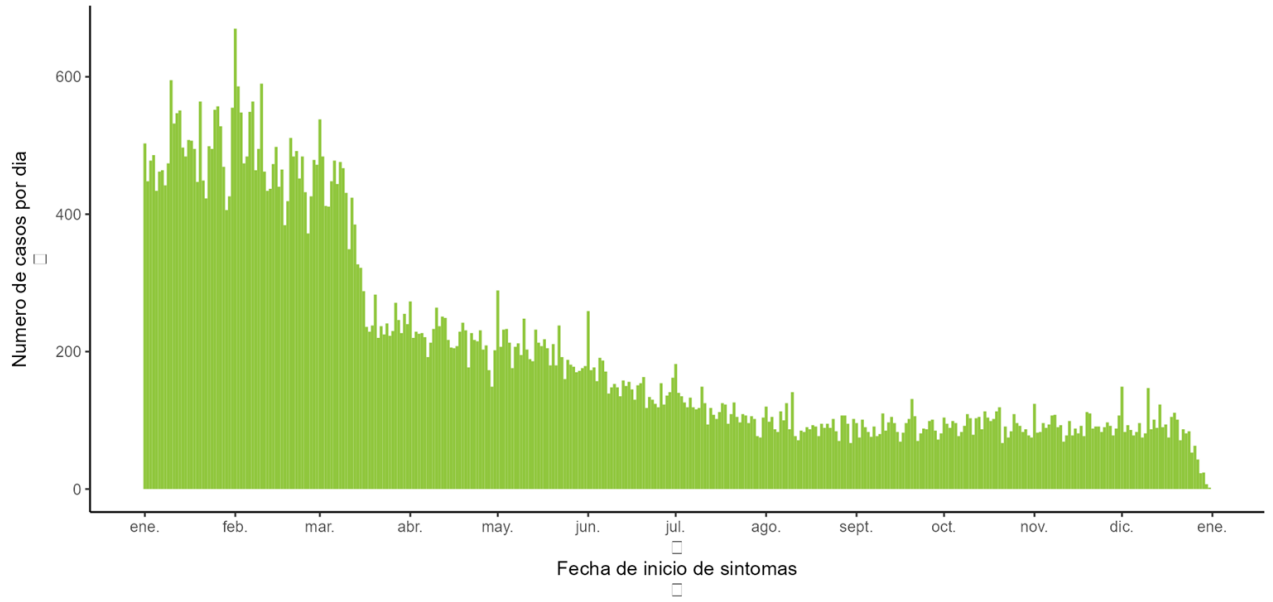

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Specialised functions by variable

User friendly

Easy to understand

Easy to use

Reduce the knowledge requirement in R

Result of last year user test

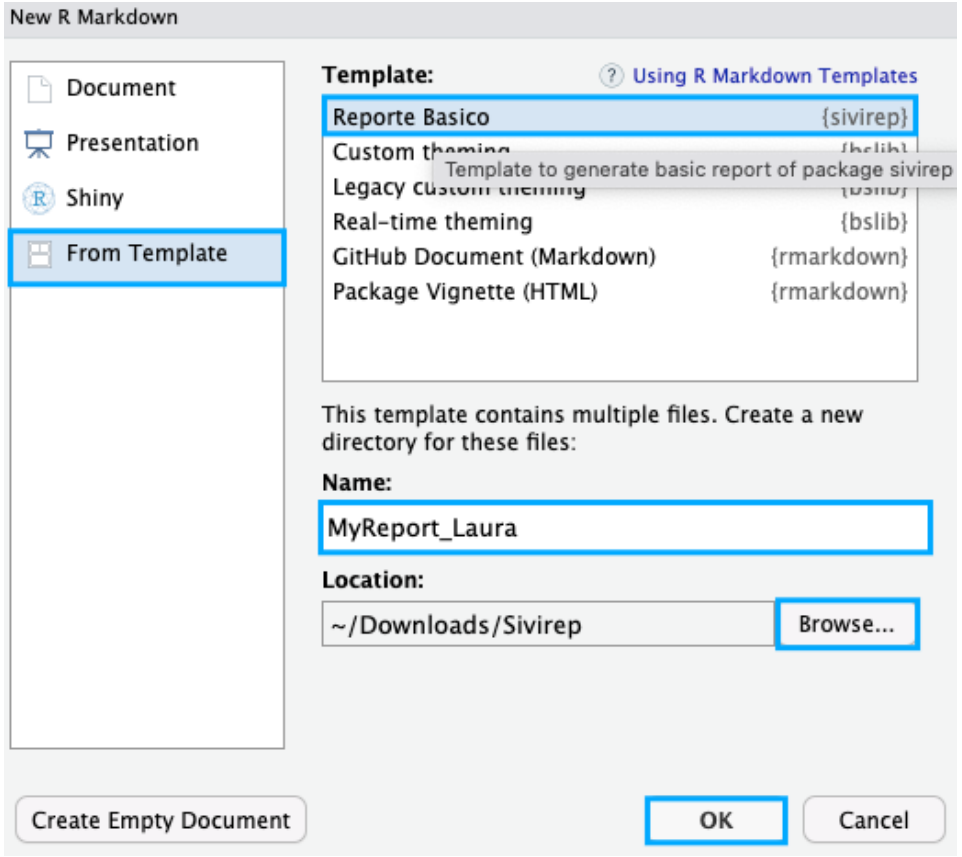
Automated reporting

Report template:

```
Reporte Básico {sivirep}
```

Input parameters:

- Disease
- Year



sivirep - dev-feature-sections-bsreport - RStudio

File Edit Code View Plots Session Build Debug Profile Tools Help

Go to file/function | Addins | sivirep — TRACE

Console | Terminal | Render | Background Jobs

R 4.2.1 · ~/TRACE/sivirep/

>

Environment | History | Connections | Build | Git | Tutorial

Import Dataset | 60 MiB | List

R | Global Environment

Environment is empty

Files | Plots | Packages | Help | Viewer | Presentation

New Folder | New Blank File | Delete | Rename | More

Home > TRACE > demo

Name | Size | Modified

..

Applicability

Users

- Public health professionals
- Field epidemiologist users of SIVIGILA source at local levels
- Health secretaries

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Applicability

sivirep can help with:

- Reducing time for report generation
- Reducing errors and manual labor
- Facilitating access to information for decision makers and citizens
- Standardization of epidemiological reports

Contribute in sivirep:

Contributions are welcome via pull requests, taking into account the code of conduct.

GitHub: https://github.com/epiverse-trace/sivirep/

Website: epiverse-trace.github.io/sivirep/

Get in touch:

Email: geralidine.gomez@javeriana.edu.co

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Thanks!