

# Package: verdata (via r-universe)

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**Title** Analyze Data from the Truth Commission in Colombia

**Version** 1.0.2

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**Description** Facilitates use and analysis of data about the armed conflict in Colombia resulting from the joint project between La Jurisdicción Especial para la Paz (JEP), La Comisión para el Esclarecimiento de la Verdad, la Convivencia y la No repetición (CEV), and the Human Rights Data Analysis Group (HRDAG). The data are 100 replicates from a multiple imputation through chained equations as described in Van Buuren and Groothuis-Oudshoorn (2011) <doi:10.18637/jss.v045.i03>. With the replicates the user can examine four human rights violations that occurred in the Colombian conflict accounting for the impact of missing fields and fully missing observations.

**License** GPL-2

**URL** <https://github.com/HRDAG/verdata>

**BugReports** <https://github.com/HRDAG/verdata/issues>

**Depends** R (>= 3.5)

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combine_estimates	<i>Combine MSE estimation results for a given stratum calculated using multiple replicate files created using multiple imputation. Combination is done using the standard approach that makes use of the laws of total expectation and total variance.</i>
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---

## Description

Combine MSE estimation results for a given stratum calculated using multiple replicate files created using multiple imputation. Combination is done using the standard approach that makes use of the laws of total expectation and total variance.

## Usage

```
combine_estimates(stratum_estimates)
```

**Arguments**

stratum\_estimates

A data frame of estimates for a stratum of interest calculated using mse for all replicates being used for the analysis. The data frame should have columns N and n\_obs from the mse function and an additional column replicate indicating which replicate the estimates were calculated on.

**Value**

A data frame row with the point estimate (N\_mean) and the associated 95% uncertainty interval (lower bound is N\_025, upper bound is N\_975).

**References**

Gelman A, Carlin JB, Stern HS, Dunson DB, Vehtari A, Rubin DB (2013). *Bayesian Data Analysis*, 0 edition. Chapman and Hall/CRC. ISBN 978-0-429-11307-9. doi:10.1201/b16018.

**Examples**

```
set.seed(19481210)

library(dplyr)
library(purrr)
library(glue)

simulate_estimates <- function(stratum_data, replicate_num) {

  # simulate an imputed stratification variable to determine whether a record
  # should be considered part of the stratum for estimation
  stratification_var <- sample(c(0, 1), size = 100,
                              replace = TRUE, prob = c(0.1, 0.9))

  my_stratum <- bind_cols(my_stratum, tibble::tibble(stratification_var)) %>%
    filter(stratification_var == 1)

  results <- mse(my_stratum, "my_stratum", K = 4) %>%
    mutate(replicate = replicate_num)

  return(results)
}

in_A <- sample(c(0, 1), size = 100, replace = TRUE, prob = c(0.45, 0.65))
in_B <- sample(c(0, 1), size = 100, replace = TRUE, prob = c(0.5, 0.5))
in_C <- sample(c(0, 1), size = 100, replace = TRUE, prob = c(0.75, 0.25))

my_stratum <- tibble::tibble(in_A, in_B, in_C)

replicate_nums <- glue("R{1:20}")
```

```
estimates <- map_dfr(.x = replicate_nums,
  .f = ~simulate_estimates(stratum_data = my_stratum, replicate_num = .x))

combine_estimates(estimates)
```

---

combine\_replicates      *Combine imputed replicates according to calculate totals. Combination is done using the standard approach that makes use of the laws of total expectation and total variance.*

---

### Description

Combine imputed replicates according to calculate totals. Combination is done using the standard approach that makes use of the laws of total expectation and total variance.

### Usage

```
combine_replicates(
  violation,
  replicates_obs_data,
  replicates_data,
  strata_vars = NULL,
  conflict_filter = TRUE,
  forced_dis_filter = FALSE,
  edad_minors_filter = FALSE,
  include_props = FALSE,
  digits = 2
)
```

### Arguments

**violation**      Violation to be analyzed. Options are "homicidio", "secuestro", "reclutamiento" and "desaparicion".

**replicates\_obs\_data**      The data frame that results from applying summary\_observed.

**replicates\_data**      A data frame containing replicates data.

**strata\_vars**      Variable with all observations (without missing values).

**conflict\_filter**      Filter that indicates if the data is filtered using the "is\_conflict" rule.

**forced\_dis\_filter**      Filter that indicates if the data is filtered using the "is\_forced\_dis" rule.

**edad\_minors\_filter**      Optional filter by age (edad) < 18.

`include_props` A logical value indicating whether or not to include the proportions from the calculations before merging with `summary_observed`'s output.

`digits` Number of decimal places to round the results to. Default value is 2.

### Value

A data frame with 5 or more columns: name of variable(s), observed the number of observations in each category for every variable, `imp_lo` the lower bound of the 95% confidence interval, `imp_hi` the upper bound of the 95% confidence interval, and `imp_mean` the point estimate of the mean value.

### Examples

```
local_dir <- system.file("extdata", "right", package = "verdata")
replicates_data <- read_replicates(local_dir, "reclutamiento", c(1, 2),
  version = "v1")
replicates_obs_data <- summary_observed("reclutamiento", replicates_data,
  strata_vars = "sexo", conflict_filter = FALSE, forced_dis_filter = FALSE,
  edad_minors_filter = FALSE, include_props = FALSE, digits = 2)
tab_combine <- combine_replicates("reclutamiento", replicates_obs_data,
  replicates_data, strata_vars = 'sexo', conflict_filter = TRUE,
  forced_dis_filter = FALSE, edad_minors_filter = FALSE, include_props = FALSE,
  digits = 2)
```

---

`confirm_files`

*Confirm files are identical to the ones published.*

---

### Description

Confirm files are identical to the ones published.

### Usage

```
confirm_files(replicates_dir, violation, replicate_nums, version)
```

### Arguments

`replicates_dir` Directory containing the replicates. The name of the files must include the violation in Spanish and lower case letters (homicidio, secuestro, reclutamiento, desaparicion).

`violation` Violation being analyzed. Options are "homicidio", "secuestro", "reclutamiento", and "desaparicion".

`replicate_nums` A numeric vector containing the replicates to be analyzed. Values in the vector should be between 1 and 100 inclusive.

`version` Version of the data being read in. Options are "v1" or "v2". "v1" is appropriate for replicating the replicating the results of the joint JEP-CEV-HRDAG project. "v2" is appropriate for conducting your new analyses of the conflict in Colombia.

**Value**

A data frame row with replicate\_num rows and two columns: replicate\_path, a string indicating the path to the replicate checked and confirmed, a boolean values indicating whether the replicate contents match the published version.

**Examples**

```
local_dir <- system.file("extdata", "right", package = "verdata")
confirm_files(local_dir, "reclutamiento", c(1, 2), version = "v1")
```

---

diccionario\_replicas *Diccionario de datos para las variables que aparecen en los archivos de las réplicas.*

---

**Description**

Diccionario de datos para las variables que aparecen en los archivos de las réplicas.

**Usage**

```
data(diccionario_replicas)
```

**Format**

Un data frame con 55 filas y 4 variables.

**nombre\_variable** nombre de la variable

**tipo** tipo de la variable: caracter, numérico, lógico

**detalle\_variable** explicación detallada de la variable

**categorias\_variable** valores posibles de la variable

**Source**

Proyecto conjunto JEP-CEV-HRDAG.

---

 diccionario\_vars\_adicional

*Variables adicionales que pueden ser útiles para analizar los datos.*


---

### Description

Variables adicionales que pueden ser útiles para analizar los datos.

### Usage

```
data(diccionario_vars_adicional)
```

### Format

Un data frame con 11 filas y 4 variables.

**nombre\_variable** nombre de la variable

**tipo** tipo de la variable: caracter, numérico, lógico

**detalle\_variable** explicación detallada de la variable

**categorias\_variable** valores posibles de la variable

### Source

Proyecto conjunto JEP-CEV-HRDAG.

---

 estimates\_exist

*Check whether stratum estimates already exist in pre-calculated files.*


---

### Description

Check whether stratum estimates already exist in pre-calculated files.

### Usage

```
estimates_exist(stratum_data_prepped, estimates_dir)
```

### Arguments

stratum\_data\_prepped

A data frame including all records in a stratum of interest. The data frame should only include the source columns prefixed with `in_` and all columns should only contain 1's and 0's.

estimates\_dir Directory containing pre-calculated estimates, if you would like to use pre-calculated results.

**Value**

A list with two entries, `estimates_exist` and `estimates_path`. `estimates_exist` is a logical value indicating whether calculations for the stratum of interest are available in the directory containing the pre-calculated estimates. If `estimates_exist` is TRUE, `estimates_path` will contain the full file path to the JSON file containing the estimates, otherwise it will be NA.

**Examples**

```
in_A <- sample(c(0, 1), size = 100, replace = TRUE, prob = c(0.45, 0.65))
in_B <- sample(c(0, 1), size = 100, replace = TRUE, prob = c(0.5, 0.5))
in_C <- sample(c(0, 1), size = 100, replace = TRUE, prob = c(0.75, 0.25))
in_D <- sample(c(0, 1), size = 100, replace = TRUE, prob = c(1, 0))

my_stratum <- tibble::tibble(in_A, in_B, in_C, in_D) %>%
  dplyr::mutate(rs = rowSums(.)) %>%
  dplyr::filter(rs >= 1) %>%
  dplyr::select(-rs)

estimates_exist(stratum_data_prepped = my_stratum, estimates_dir = "path_to_estimates")
```

---

estratificacion	<i>Datos que documentan las estratificaciones necesarias para replicar los resultados del informe metodológico del proyecto conjunto CEV-HRDAG-JEP (versión en español).</i>
-----------------	--

---

**Description**

Datos que documentan las estratificaciones necesarias para replicar los resultados del informe metodológico del proyecto conjunto CEV-HRDAG-JEP (versión en español).

**Usage**

```
data(estratificacion)
```

**Format**

Un data frame con 31 filas y 4 variables.

**violacion** el hecho de violencia al analizar

**estimacion** el tipo de análisis que utiliza la estratificación (p.ej., patrones de violencia por año, sexo, etc.)

**estratificacion** las variables utilizadas para estratificar las estimaciones

**notas** notas adicionales sobre la estratificación; NA si no hay notas

**Source**

Proyecto conjunto JEP-CEV-HRDAG.

---

filter_standard_cev	<i>Filter records to replicate results presented in the CEV methodology report.</i>
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---

**Description**

Filter records to replicate results presented in the CEV methodology report.

**Usage**

```
filter_standard_cev(replicates_data, violation, perp_change = TRUE)
```

**Arguments**

replicates_data	A data frame with data from all replicates to be filtered.
violation	Violation to be analyzed. Options are "homicidio", "secuestro", "reclutamiento", and "desaparicion".
perp_change	A logical value indicating whether victims in years after 2016 with perpetrator values (indicated by p_str) of the FARC-EP ("GUE-FARC") should be re-assigned to other guerrilla groups (p_str value "GUE-OTRO").

**Value**

A filtered data frame.

**Examples**

```
local_dir <- system.file("extdata", "right", package = "verdata")
replicates_data <- read_replicates(local_dir, "reclutamiento", c(1, 2), version = "v1")
filter_standard_cev(replicates_data, "reclutamiento", perp_change = TRUE)
```

---

get_valid_sources	<i>Determine valid sources for estimation of a stratum of interest.</i>
-------------------	---

---

**Description**

Determine valid sources for estimation of a stratum of interest.

**Usage**

```
get_valid_sources(stratum_data_prepped, min_n = 1)
```

**Arguments**

stratum_data_prepped	A data frame with all records in a stratum of interest. Columns indicating sources should be prefixed with <code>in_</code> and should be numeric with 1 indicating that an individual was documented in the source and 0 indicating that an individual was not documented in the source.
min_n	The minimum number of records that must appear in a source to be considered valid for estimation. <code>min_n</code> should never be less than or equal to 0; the default value is 1.

**Value**

A character vector containing the names of the valid sources.

**Examples**

```
set.seed(19481210)
in_A <- sample(c(0, 1), size = 100, replace = TRUE, prob = c(0.45, 0.65))
in_B <- sample(c(0, 1), size = 100, replace = TRUE, prob = c(0.5, 0.5))
in_C <- sample(c(0, 1), size = 100, replace = TRUE, prob = c(0.75, 0.25))
in_D <- sample(c(0, 1), size = 100, replace = TRUE, prob = c(1, 0))

my_stratum <- tibble::tibble(in_A, in_B, in_C, in_D)
get_valid_sources(my_stratum)
```

---

lookup_estimates	<i>lookup_estimates</i>
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---

**Description**

Look up and read in existing estimates from pre-calculated files.

**Usage**

```
lookup_estimates(stratum_data_prepped, estimates_dir)
```

**Arguments**

stratum_data_prepped	A data frame including all records in a stratum of interest. The data frame should only include the source columns prefixed with <code>in_</code> and all columns should only contain 1's and 0's.
estimates_dir	Directory containing pre-calculated estimates, if you would like to use pre-calculated results. Note, setting this option forces the model specification parameters to be identical to those used to calculate the pre-calculated estimates. Do not specify a file path if you would like to use a custom model specification.

**Value**

A data frame with one column, N, indicating the results. If the stratum was not found in the pre-calculated files, N will be NA and the data frame will have one row. If the stratum was found in the pre-calculated files, N will contain draws from the posterior distribution of the model and the data frame will contain 1,000 rows.

**Examples**

```
in_A <- sample(c(0, 1), size = 100, replace = TRUE, prob = c(0.45, 0.65))
in_B <- sample(c(0, 1), size = 100, replace = TRUE, prob = c(0.5, 0.5))
in_C <- sample(c(0, 1), size = 100, replace = TRUE, prob = c(0.75, 0.25))
in_D <- sample(c(0, 1), size = 100, replace = TRUE, prob = c(1, 0))

my_stratum <- tibble::tibble(in_A, in_B, in_C, in_D) %>%
  dplyr::mutate(rs = rowSums(.)) %>%
  dplyr::filter(rs >= 1) %>%
  dplyr::select(-rs)

lookup_estimates(stratum_data_prepped = my_stratum, estimates_dir = "path_to_estimates")
```

---

mse

*mse*


---

**Description**

Prepare data for estimation and calculate estimates using `run_lcmcr`.

**Usage**

```
mse(
  stratum_data,
  stratum_name,
  estimates_dir = NULL,
  min_n = 1,
  K = NULL,
  buffer_size = 10000,
  sampler_thinning = 1000,
  seed = 19481210,
  burnin = 10000,
  n_samples = 10000,
  posterior_thinning = 500
)
```

## Arguments

<code>stratum_data</code>	A data frame including all records in a stratum of interest. Columns indicating sources should be prefixed with <code>in_</code> and should be numeric.
<code>stratum_name</code>	An identifier for the stratum.
<code>estimates_dir</code>	File path for the folder containing pre-calculated estimates, if you would like to use pre-calculated results. Note, setting this option forces the model specification parameters to be identical to those used to calculate the pre-calculated estimates. Do not specify a file path if you would like to use a custom model specification.
<code>min_n</code>	The minimum number of records that must appear in a source to be considered valid for estimation. <code>min_n</code> should never be less than or equal to 0; the default value is 1.
<code>K</code>	The maximum number of latent classes to fit. By default the function will calculate <code>K</code> as the minimum value of 2 raised to the number of valid sources - 1 or 15.
<code>buffer_size</code>	Size of the tracing buffer. Default value is 10,000.
<code>sampler_thinning</code>	Thinning interval for the tracing buffer. Default value is 1,000.
<code>seed</code>	Integer seed for the internal random number generator. Default value is 19481210.
<code>burnin</code>	Number of burn in iterations. Default value is 10,000.
<code>n_samples</code>	Number of samples to be generated. Samples are taken one every <code>posterior_thinning</code> iterations of the sampler. Default value is 10,000. The final number of samples from the posterior is <code>n_samples</code> divided by 1,000.
<code>posterior_thinning</code>	Thinning interval for the sampler. Default value is 500.

## Value

A data frame with five columns. `validated` is a logical value indicating whether the stratum is estimable, `N` is the draws from the posterior distribution (NA if the stratum is not estimable), `valid_sources` is a string indicating which sources were used in the estimation, `n_obs` is the number of observations on valid lists in the stratum of interest (NA if the stratum is not estimable), and `stratum_name` is a stratum identifier. If the stratum is estimable the return will consist of `n_samples` divided by 1,000 rows.

## Examples

```
set.seed(19481210)
in_A <- sample(c(0, 1), size = 100, replace = TRUE, prob = c(0.45, 0.65))
in_B <- sample(c(0, 1), size = 100, replace = TRUE, prob = c(0.5, 0.5))
in_C <- sample(c(0, 1), size = 100, replace = TRUE, prob = c(0.75, 0.25))
in_D <- sample(c(0, 1), size = 100, replace = TRUE, prob = c(1, 0))

my_stratum <- tibble::tibble(in_A, in_B, in_C, in_D)
mse(stratum_data = my_stratum, stratum_name = "my_stratum")
```

---

proportions_imputed	<i>Calculate the proportions of each level of a variable after applying combine_replicates to completed data (includes imputed values).</i>
---------------------	---

---

### Description

Calculate the proportions of each level of a variable after applying combine\_replicates to completed data (includes imputed values).

### Usage

```
proportions_imputed(complete_data, strata_vars, digits = 2)
```

### Arguments

`complete_data` A data frame containing the output from combine\_replicates.

`strata_vars` A vector of column names identifying the variables to be used for stratification.

`digits` Number of decimal places to round the results to. Default value is 2.

### Value

A data frame that contains the proportions after applying combine\_replicates.

### Examples

```
local_dir <- system.file("extdata", "right", package = "verdata")
replicates_data <- read_replicates(replicates_dir = local_dir,
violation = "reclutamiento", replicate_nums = c(1, 2), version = "v1",
crash = TRUE)
replicates_obs_data <- summary_observed("reclutamiento", replicates_data,
strata_vars = "sexo", conflict_filter = FALSE, forced_dis_filter = FALSE,
edad_minors_filter = FALSE, include_props = FALSE)
tab_combine <- combine_replicates("reclutamiento", replicates_obs_data,
replicates_data, strata_vars = 'sexo', conflict_filter = TRUE,
forced_dis_filter = FALSE, edad_minors_filter = FALSE, include_props = FALSE)
prop_data_complete <- proportions_imputed(tab_combine, strata_vars = "sexo",
digits = 2)
```

---

proportions_observed	<i>Calculate the proportions of each level of a variable after applying summary_observed to observed values.</i>
----------------------	--

---

### Description

Calculate the proportions of each level of a variable after applying summary\_observed to observed values.

### Usage

```
proportions_observed(obs_data, strata_vars, digits = 2)
```

### Arguments

obs_data	A data frame containing the output from summary_observed.
strata_vars	A vector of column names identifying the variables to be used for stratification.
digits	Number of decimal places to round the results to. Default is 2.

### Value

A data frame that contains the proportions after applying summary\_observed.

### Examples

```
local_dir <- system.file("extdata", "right", package = "verdata")
replicates_data <- read_replicates(local_dir, "reclutamiento", c(1, 2), version = "v1")
tab_observed <- summary_observed("reclutamiento", replicates_data,
  strata_vars = "sexo", conflict_filter = TRUE, forced_dis_filter = FALSE,
  edad_minors_filter = TRUE, include_props = TRUE)
prop_data <- proportions_observed(tab_observed, strata_vars = "sexo",
  digits = 2)
```

---

read_replicates	<i>Read replicates in a directory and verify they are identical to the ones published.</i>
-----------------	--

---

### Description

Read replicates in a directory and verify they are identical to the ones published.

**Usage**

```
read_replicates(
  replicates_dir,
  violation,
  replicate_nums,
  version,
  crash = TRUE
)
```

**Arguments**

`replicates_dir` A path to the directory containing the replicates. Then file name of each replicate must contain at least the name of the violation in Spanish and lower case letters (homicidio, secuestro, reclutamiento, desaparicion), and the replicate number preceded by "R", (e.g., "R1" for replicate 1).

`violation` A string indicating the violation being analyzed. Options are "homicidio", "secuestro", "reclutamiento", and "desaparicion".

`replicate_nums` A numeric vector containing the replicates to be analyzed. Values in the vector should be between 1 and 100 inclusive.

`version` Version of the data being read in. Options are "v1" or "v2". "v1" is appropriate for replicating the replicating the results of the joint JEP-CEV-HRDAG project. "v2" is appropriate for conducting your new analyses of the conflict in Colombia.

`crash` A parameter to define whether the function should crash if the content of the file is not identical to the one published. If `crash = TRUE` (default), it will return error and not read the data, if `crash = FALSE`, the function will return a warning but still read the data.

**Value**

A data frame with the data from all indicated replicates.

**Examples**

```
local_dir <- system.file("extdata", "right", package = "verdata")
read_replicates(local_dir, "reclutamiento", 1, 2, version = "v1")
```

---

run_lcmcr	<i>Calculate multiple systems estimation estimates using the Bayesian Non-Parametric Latent-Class Capture-Recapture model developed by Daniel Manrique-Vallier (2016).</i>
-----------	--

---

**Description**

Calculate multiple systems estimation estimates using the Bayesian Non-Parametric Latent-Class Capture-Recapture model developed by Daniel Manrique-Vallier (2016).

**Usage**

```
run_lcmcr(
  stratum_data_prepped,
  stratum_name,
  min_n = 1,
  K,
  buffer_size,
  sampler_thinning,
  seed,
  burnin,
  n_samples,
  posterior_thinning
)
```

**Arguments**

stratum_data_prepped	A data frame with all records in the stratum of interest documented by sources considered valid for estimation (i.e., there should be no rows with all 0's). Columns indicating sources should be prefixed with <code>in_</code> and should be numeric with 1 indicating that an individual was documented in the source and 0 indicating that an individual was not documented in the source.
stratum_name	An identifier for the stratum.
min_n	The minimum number of records that must appear in a source to be considered valid for estimation. <code>min_n</code> should never be less than or equal to 0; the default value is 1.
K	The maximum number of latent classes to fit.
buffer_size	Size of the tracing buffer.
sampler_thinning	Thinning interval for the tracing buffer.
seed	Integer seed for the internal random number generator.
burnin	Number of burn in iterations.
n_samples	Number of samples to be generated. Samples are taken one every <code>posterior_thinning</code> iterations of the sampler. Final number of samples from the posterior is <code>n_samples</code> divided by 1,000.
posterior_thinning	Thinning interval for the sampler.

**Value**

A data frame with four columns and `n_samples` divided by 1,000 rows. `N` is the draws from the posterior distribution, `valid_sources` is a string indicating which sources were used in the estimation, `n_obs` is the number of observations in the stratum of interest, and `stratum_name` is the stratum identifier.

## References

Manrique-Vallier D (2016). “Bayesian population size estimation using Dirichlet process mixtures.” *Biometrics*, **72**(4), 1246–1254. doi:10.1111/biom.12502.

## Examples

```
set.seed(19481210)
library(dplyr)

in_A <- sample(c(0, 1), size = 100, replace = TRUE, prob = c(0.45, 0.65))
in_B <- sample(c(0, 1), size = 100, replace = TRUE, prob = c(0.5, 0.5))
in_C <- sample(c(0, 1), size = 100, replace = TRUE, prob = c(0.75, 0.25))
in_D <- sample(c(0, 1), size = 100, replace = TRUE, prob = c(1, 0))

my_stratum <- tibble::tibble(in_A, in_B, in_C, in_D) %>%
  dplyr::mutate(rs = rowSums(.)) %>%
  dplyr::filter(rs >= 1) %>%
  dplyr::select(-rs)
run_lcmcr(stratum_data_prepped = my_stratum, stratum_name = "my_stratum",
  K = 4, buffer_size = 10000, sampler_thinning = 1000, seed = 19481210,
  burnin = 10000, n_samples = 10000, posterior_thinning = 500)
```

---

stratification	<i>Data documenting the stratifications used to replicate the results of the methodological report of the joint JEP-CEV-HRDAG project (version in English).</i>
----------------	---

---

## Description

Data documenting the stratifications used to replicate the results of the methodological report of the joint JEP-CEV-HRDAG project (version in English).

## Usage

```
data(stratification)
```

## Format

A data frame with 31 rows and 4 variables.

**violation** the human rights violation being analyzed

**estimation** the type of analysis the stratification was used for (e.g., patterns of violence by year, sex, etc.)

**stratification** the variables used to stratify the estimates

**notes** additional notes about the stratification; NA if no notes

**Source**

Joint JEP-CEV-HRDAG project.

---

summary_observed	<i>Summary statistics for observed data.</i>
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**Description**

Summary statistics for observed data.

**Usage**

```
summary_observed(
  violation,
  replicates_data,
  strata_vars = NULL,
  conflict_filter = FALSE,
  forced_dis_filter = FALSE,
  edad_minors_filter = FALSE,
  include_props = FALSE,
  digits = 2
)
```

**Arguments**

violation	Violation to be analyzed. Options are "homicidio", "secuestro", "reclutamiento", and "desaparicion".
replicates_data	Data frame containing replicate data.
strata_vars	Variable to be analyzed. Before imputation this variable may have missing values.
conflict_filter	Filter that indicates if the data is filtered by the rule "is_conflict" or not.
forced_dis_filter	Filter that indicates if the data is filter by the rule "is_forced_dis" or not.
edad_minors_filter	Optional filter by age ("edad") < 18.
include_props	A logical value indicating whether or not to include the proportions from the calculations.
digits	Number of decimal places to round the results to. Default is 2.

**Value**

A data frame with two or more columns, (1) name of variable(s) and (2) the number of observations in each of the variable's categories.

**Examples**

```
local_dir <- system.file("extdata", "right", package = "verdata")
replicates_data <- read_replicates(local_dir, "reclutamiento", c(1, 2), version = "v1")
tab_observed <- summary_observed("reclutamiento", replicates_data,
strata_vars = "sexo", conflict_filter = FALSE, forced_dis_filter = FALSE,
edad_minors_filter = FALSE, include_props = FALSE, digits = 2)
```

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