

# Package: vaccineff (via r-universe)

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**Title** Estimate Vaccine Effectiveness Based on Different Study Designs

**Version** 1.0.0

**Description** Provides tools for estimating vaccine effectiveness and related metrics. The 'vaccineff\_data' class manages key features for preparing, visualizing, and organizing cohort data, as well as estimating vaccine effectiveness. The results and model performance are assessed using the 'vaccineff' class.

**License** MIT + file LICENSE

**URL** <https://github.com/epiverse-trace/vaccineff>,  
<https://epiverse-trace.github.io/vaccineff/>

**BugReports** <https://github.com/epiverse-trace/vaccineff/issues>

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**Author** David Santiago Quevedo [aut]  
(<<https://orcid.org/0000-0003-1583-4262>>), Zulma M. Cucunubá  
[aut, cre] (<<https://orcid.org/0000-0002-8165-3198>>),  
International Development Research Center (IDRC) [fnd],  
Geraldine Gómez Millán [ctb]  
(<<https://orcid.org/0009-0007-8701-0568>>), Pratik Gupte [ctb]  
(<<https://orcid.org/0000-0001-5294-7819>>), Érika J Cantor [ctb]

(<<https://orcid.org/0000-0003-3320-6032>>), Santiago Loaiza [ctb] (<<https://orcid.org/0000-0002-2092-3262>>), Jaime Pavlich-Mariscal [ctb] (<<https://orcid.org/0000-0002-3892-6680>>), Hugo Gruson [ctb] (<<https://orcid.org/0000-0002-4094-1476>>), Chris Hartgerink [ctb] (<<https://orcid.org/0000-0003-1050-6809>>), Felipe Segundo Abril [ctb] (<<https://orcid.org/0000-0002-2512-4929>>), Joshua W. Lambert [ctb] (<<https://orcid.org/0000-0001-5218-3046>>), Julian Otero [ctb] (<<https://orcid.org/0009-0006-0429-7747>>), Pontificia Universidad Javeriana [cph]

**Maintainer** Zulma M. Cucunubá <[tracelacdev@gmail.com](mailto:tracelacdev@gmail.com)>

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## Contents

cohortdata . . . . .	2
estimate_vaccineff . . . . .	3
get_age_group . . . . .	4
make_vaccineff_data . . . . .	5
plot.vaccineff . . . . .	7
plot.vaccineff_data . . . . .	8
print.summary_vaccineff . . . . .	9
print.summary_vaccineff_data . . . . .	9
summary.vaccineff . . . . .	10
summary.vaccineff_data . . . . .	10

<b>Index</b>	<b>11</b>
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cohortdata	<i>Cohort data on vaccineff</i>
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## Description

Subset of data from an anonymised, real-world dataset produced as part of the early stage of the immunization program against COVID-19 in Bogota, Colombia between February 2021 and December 2021. Cohort dataset contains registers of homologous schemes for two different brands for adults aged 50 years or older. This cohort received two doses of a vaccine aimed at reducing the risk of death. All the registers were anonymised and de-identified to preserve the privacy of data. The dataset includes disaggregated information on the first and second vaccine doses (vaccine\_date1, vaccine\_date2, vaccine1, and vaccine2) for each participant and relevant demographic details (sex and age). Additionally, the dataset includes the dates of two outcomes: death associated with COVID-19 (death\_date) and death from other causes (death\_other\_causes).

## Usage

cohortdata

**Format**

cohortdata:  
**id** Anonymous ID of the individual  
**sex** Sex F/M  
**age** Age (50-100)  
**death\_date** Registered death by COVID-19  
**death\_other\_causes** Registered death by other causes  
**vaccine\_date\_1** Registered date of the first dose  
**vaccine\_date\_2** Registered date of the second dose  
**vaccine\_1** Brand of the first dose  
**vaccine\_2** Brand of the second dose

**Examples**

```
cohortdata
```

---

```
estimate_vaccineff      Estimate Vaccine Effectiveness (VE)
```

---

**Description**

This function provides methods for estimating VE. It relies on the Kaplan-Meier estimator and the Cox model for proportional hazards from the `{survival}` package. Currently, the default method is  $VE = 1 - HR$ , where HR is the Hazard Ratio calculated using the Cox model. The proportional hazards assumption is tested using the Schoenfeld test, with the p-value provided in the results. Log-log plots are also generated using the Kaplan-Meier estimator for a visual test of the proportional hazards hypothesis. The function uses column names provided in the tags `outcome_status_col`, `time_to_event_col`, and `vaccine_status_col` of the `linelist` object and status names from `make_vaccineff_data`. The return is an S3 class object with the VE (CI95%), results from the Cox model, and the Kaplan-Meier estimator. This object is compatible with `summary` and `plot` methods.

**Usage**

```
estimate_vaccineff(vaccineff_data, at)
```

**Arguments**

`vaccineff_data` Object of the class `vaccineff_data` with vaccineff data.  
`at` Number of days at which VE is estimated from the beginning of the follow-up period.

**Value**

Object of the class `vaccineff`: a list with results from the estimation of VE. `ve`: `data.frame` with VE(CI95%) `cox_model`: `survival` object with Cox model results `kaplan_meier`: `survival` object with Kaplan-Meier estimator

**Examples**

```

# Load example data
data("cohortdata")

# Create `vaccineff_data`
vaccineff_data <- make_vaccineff_data(data_set = cohortdata,
  outcome_date_col = "death_date",
  censoring_date_col = "death_other_causes",
  vacc_date_col = "vaccine_date_2",
  vaccinated_status = "v",
  unvaccinated_status = "u",
  immunization_delay = 15,
  end_cohort = as.Date("2021-12-31"),
  match = TRUE,
  exact = c("age", "sex"),
  nearest = NULL
)

# Estimate the Vaccine Effectiveness (VE)
ve <- estimate_vaccineff(vaccineff_data, 90)

# Print summary of VE
summary(ve)

# Generate loglog plot to check proportional hazards
plot(ve, type = "loglog")

# Generate Survival plot
plot(ve, type = "surv", percentage = FALSE, cumulative = FALSE)

```

---

get\_age\_group

*Construct age-group variable from age column*


---

**Description**

This method splits an age interval from `min_val` to `max_val` into intervals of size `step`. If the method finds ages greater or equal than `max_val` it assigns the string `">max_val"`. By default `min_val` is set to 0, however it can be assigned by convenience. If the method finds ages lower or equal than `min_val` it assigns the string `"<min_val-1"`. The function warns when `(max_val - min_val)` is not an integer multiple of `step`. In that case the last interval is truncated to the upper value closest to `max_val` for which `(closest_upper - min_val)` is multiple of `step`.

**Usage**

```
get_age_group(data_set, col_age, max_val, min_val = 0, step)
```

**Arguments**

data_set	data.frame with at least a column containing the age information
col_age	Name of the column containing the age information
max_val	Maximum value of age interval to split
min_val	Minimum value of age interval to split
step	Step used to split the age interval

**Value**

Column of type factor with the same length as the number of rows in data\_set, with levels corresponding to age bins between min\_val and max\_val. Ages above max\_val are represented as >max\_val.

**Examples**

```
# load data provided with the package
data(cohortdata)

# assign age groups as a column of the `data.frame`
cohortdata$age_group <- get_age_group(
  data_set = cohortdata,
  col_age = "age",
  max_val = 80,
  step = 10
)

# view the `data.frame` with new column
head(cohortdata)
```

---

make\_vaccineff\_data    *Construct vaccineff\_data Object*

---

**Description**

This function constructs an S3 object of the class vaccineff\_data that contains all the relevant information for the study. to estimate the effectiveness.

**Usage**

```
make_vaccineff_data(
  data_set,
  outcome_date_col,
  censoring_date_col = NULL,
  vacc_date_col,
  vacc_name_col = NULL,
  vaccinated_status = "v",
  unvaccinated_status = "u",
```

```

immunization_delay = 0,
end_cohort,
match = FALSE,
exact = NULL,
nearest = NULL,
take_first = FALSE,
t0_follow_up = NULL
)

```

### Arguments

**data\_set** data.frame with cohort information.

**outcome\_date\_col** Name of the column that contains the outcome dates.

**censoring\_date\_col** Name of the column that contains the censoring date. NULL by default.

**vacc\_date\_col** Name of the column(s) that contain the vaccine dates.

**vacc\_name\_col** Name of the column(s) that contain custom vaccine names for the vaccines (e.g. brand name, type of vaccine). If provided, must be of the same length as `vacc_date_col`.

**vaccinated\_status** Status assigned to the vaccinated population. Default is `v`.

**unvaccinated\_status** Status assigned to the unvaccinated population. Default is `u`.

**immunization\_delay** Characteristic time in days before the patient is considered immune. Default is 0.

**end\_cohort** End date of the study.

**match** TRUE: cohort matching is performed. Default is FALSE

**exact** Name(s) of column(s) for exact matching. Default is NULL.

**nearest** Named vector with name(s) of column(s) for nearest matching and caliper(s) for each variable (e.g., `nearest = c("characteristic1" = n1, "characteristic2" = n2)`, where `n1` and `n2` are the calipers). Default is NULL.

**take\_first** FALSE: takes the latest vaccine date. TRUE: takes the earliest vaccine date.

**t0\_follow\_up** Column with the initial dates of the follow-up period. This column is only used if `match = FALSE`. If not provided, the follow-up period starts at `start_cohort`. Default is NULL.

### Value

An S3 object of class `vaccineff_data` with all the information and characteristics of the study. `data.frames` are converted into an object of class `linelist` to easily handle with the data.

## Examples

```
# Load example data
data("cohortdata")

# Create `vaccineff_data`
vaccineff_data <- make_vaccineff_data(data_set = cohortdata,
  outcome_date_col = "death_date",
  censoring_date_col = "death_other_causes",
  vacc_date_col = "vaccine_date_2",
  vaccinated_status = "v",
  unvaccinated_status = "u",
  immunization_delay = 15,
  end_cohort = as.Date("2021-12-31"),
  match = TRUE,
  exact = c("age", "sex"),
  nearest = NULL
)

# Print summary of data
summary(vaccineff_data)

# Plot vaccine coverage
plot(vaccineff_data)
```

---

plot.vaccineff

*Function for Extracting Vaccine Effectiveness Plot*

---

## Description

This function creates plots from an object of class `vaccineff`. It returns a Log-Log plot when `type = "loglog"`, or a Survival curve when `type = "surv"`. Survival plots can be shown as cumulative incidence (`cumulative = TRUE`), and using percentages (`percentage = TRUE`).

## Usage

```
## S3 method for class 'vaccineff'
plot(
  x,
  type = c("loglog", "surv"),
  cumulative = FALSE,
  percentage = FALSE,
  ...
)
```

## Arguments

`x` Object of class `vaccineff`.

type	Type of plot. Options are loglog and surv.
cumulative	If TRUE, the survival curve is shown as cumulative incidence.
percentage	If TRUE, results are shown on a percentage scale.
...	Additional arguments passed to other functions.

**Value**

Plot extracted from vaccineff.

---

plot.vaccineff\_data    *Function for Extracting Vaccineff Data Plot*

---

**Description**

This function returns a plot of the vaccine coverage or the cumulative coverage (if cumulative = TRUE). The return is a 2-axis ggplot2 element with the number of vaccines per date on the left axis and the coverage per date on the right axis. When a matching routine is performed, the left axis also accounts for the doses of the matched cohort.

**Usage**

```
## S3 method for class 'vaccineff_data'
plot(x, date_interval = NULL, cumulative = FALSE, ...)
```

**Arguments**

x	Object of class vaccineff_data.
date_interval	If NULL, the function calculates the coverage interval
cumulative	If TRUE, returns the cumulative number of doses over the time window.
...	Additional arguments passed to other functions.

**Value**

Plot extracted from vaccineff.



---

```
print.summary_vaccineff
```

*Print summary of VE Results*

---

### **Description**

Print summary of vaccineff object.

### **Usage**

```
## S3 method for class 'summary_vaccineff'  
print(x, ...)
```

### **Arguments**

x                    Object of the class `summary.vaccineff`.  
...                  Additional arguments passed to other functions.

### **Value**

None

---

```
print.summary_vaccineff_data
```

*Print Summary of Vaccineff Data*

---

### **Description**

Summarizes the results of `make_vaccineff_data`.

### **Usage**

```
## S3 method for class 'summary_vaccineff_data'  
print(x, ...)
```

### **Arguments**

x                    Object of the class `summary.vaccineff_data`.  
...                  Additional arguments passed to other functions.

### **Value**

None

---

summary.vaccineff      *Summarize VE Results*

---

**Description**

Summarizes the results of vaccineff.

**Usage**

```
## S3 method for class 'vaccineff'  
summary(object, ...)
```

**Arguments**

object            Object of the class vaccineff.  
...                Additional arguments passed to other functions.

**Value**

Summary of the results from estimate\_vaccineff.

---

summary.vaccineff\_data  
                          *Summarize Vaccineff Data*

---

**Description**

Summarizes the results of make\_vaccineff\_data.

**Usage**

```
## S3 method for class 'vaccineff_data'  
summary(object, warnings_log = FALSE, ...)
```

**Arguments**

object            Object of the class vaccineff\_data.  
warnings\_log      If TRUE, prints the warnings log.  
...                Additional arguments passed to other functions.

**Value**

Summary of the results from vaccineff data

# Index

## \* datasets

- cohortdata, [2](#)
- cohortdata, [2](#)
- estimate\_vaccineeff, [3](#)
- get\_age\_group, [4](#)
- make\_vaccineeff\_data, [5](#)
- plot.vaccineeff, [7](#)
- plot.vaccineeff\_data, [8](#)
- print.summary\_vaccineeff, [9](#)
- print.summary\_vaccineeff\_data, [9](#)
- summary.vaccineeff, [10](#)
- summary.vaccineeff\_data, [10](#)