Package: DIVINE (via r-universe)

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Type Package

Title Curated Datasets and Tools for Epidemiological Data Analysis

Version 0.1.2

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Description Curated datasets and intuitive data management functions to streamline epidemiological data workflows. It is designed to support researchers in quickly accessing clean, structured data and applying essential cleaning, summarizing, visualization, and export operations with minimal effort. Whether you're preparing a cohort for analysis or creating reports, 'DIVINE' makes the process more efficient, transparent, and reproducible.

License GPL (>= 3)

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.3

URL https://bruigtp.github.io/DIVINE/

BugReports https://github.com/bruigtp/DIVINE/issues

Suggests knitr, rmarkdown

VignetteBuilder knitr

Depends R (>= 4.1)

LazyData true

Imports dplyr, fmsb, ggplot2, gtsummary, haven, openxlsx, plotly, purrr, rlang, scales, stringr, tibble, tidyselect

Config/pak/sysreqs
cmake make libicu-dev libuv1-dev libxml2-dev libssl-dev libnode-dev libx11-dev zlib1g-dev

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Contents

`analytics` *DIVINE's table on laboratory data*

Description

Information on laboratory data of patients included in the DIVINE cohort. Data was collected at hospital admission.

Usage

```
data(analytics)
```

Format

A data frame with 5813 rows and 9 columns

record_id: Identifier of each record. This information does not match the real data.

covid_wave: A factor with levels `Wave 1`, `Wave 2`, `Wave 3`, and `Wave 5`. COVID-19 wave.

center: A factor with levels `Hospital A`, `Hospital B`, `Hospital C`, `Hospital D`, and `Hospital E`. Center of admission

analytics_available: Is there an analytic available for this patient?

total_leukocytes: Total leukocytes (mil/mm^3)

hemoglobin: Hemoglobin (g/dl)

total_lymphocytes: Total lymphocytes (mil/mm³)

d_dimer: D-dimer (μg/L)

c_reactive_protein: C-reactive protein (mg/L)

References

Pallarès, N., Tebé, C., Abelenda-Alonso, G., Rombauts, A., Oriol, I., Simonetti, A. F., Rodríguez-Molinero, A., Izquierdo, E., Díaz-Brito, V., Molist, G., Gómez Melis, G., Carratalà, J., Videla, S., & MetroSud and Divine study groups (2023). Characteristics and Outcomes by Ceiling of Care of Subjects Hospitalized with COVID-19 During Four Waves of the Pandemic in a Metropolitan Area: A Multicenter Cohort Study. Infectious diseases and therapy, 12(1), 273–289. https://doi.org/10.1007/s40121-022-00705-w

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`comorbidities` *DIVINE's table on information about comorbidities*

Description

Information about comorbidities of patients included in the DIVINE cohort. Data was collected at hospital admission.

Usage

```
data(comorbidities)
```

Format

A data frame with 5813 rows and 37 columns

record_id: Identifier of each record. This information does not match the real data.

covid_wave: A factor with levels `Wave 1`, `Wave 2`, `Wave 3`, and `Wave 5`. COVID-19 wave.

center: A factor with levels `Hospital A`, `Hospital B`, `Hospital C`, `Hospital D`, and `Hospital E`. Center of admission

sociofunctional: A factor with levels `Lives with a spouse of similar age`, `Lives with a spouse with some degree o` `Lives with a non-family caregiver`, `Lives with family. The caregiver is not their spouse`, `Lives with family without physical dependency`, `Lives alone and has no children or they are far away`, `Lives alone and has nearby children`. Sociofunctional status

frailty: A factor with levels `No`, `PCC` and `MACA`. Is the patient a chronic complex patient (PCC) or a patient with advanced chronic disease (MACA)?

barthel_score: Punctuation in the Barthel scale used to measure performance in activities of daily living

weight: Weight (kg)

height: Height (cm)

body_mass_index: Body mass index computed as $\frac{\text{weight (kg)}}{\text{height (m)}^2}$

dm: A factor with levels `No` and `Yes`. Diabetes mellitus Type 2

type_dm: A factor with levels `With target organ involvement` and `Without complications`. For patients with diabetes mellitus type 2, type of disease

chronic_lung_disease: A factor with levels `No` and `Yes`. Chronic lung disease (including COPD, asthma and obstructive sleep apnea, among others)

chronic_kidney_disease: A factor with levels `No` and `Yes`. Severe chronic kidney disease

mild_kidney_disease: A factor with levels `No` and `Yes`. Mild kidney disease

renal_therapy: A factor with levels `No` and `Yes`. Is the patient currently receiving renal replacement therapy?

heart_disease: A factor with levels `No` and `Yes`. Heart failure

coronary_disease: A factor with levels `No` and `Yes`. Coronary heart disease

myocardial_infarction: A factor with levels `No` and `Yes`. Has the patient ever had a heart attack?

hematologic_neo: A factor with levels `No` and `Yes`. Haematological neoplasia

hematologic_neo_type: A factor with levels `Leukemia`, `Lymphoma` and `Myeloma`. For patients with Haematological neoplasia, type of disease.

non_metastatic_neo: A factor with levels `No` and `Yes`. Non-Metastatic Neoplasia

metastatic_neo: A factor with levels `No` and `Yes`. Metastatic Neoplasia

stroke_tia: A factor with levels `No` and `Yes`. Has the patient ever had a stroke or a transient ischemic attack?

peripheral_vasculopathy: A factor with levels `No` and `Yes`. Peripheral artery disease

dementia: A factor with levels `No` and `Yes`. Dementia

mild_liver_disease: A factor with levels `No` and `Yes`. Mild liver disease

severe_liver_disease: A factor with levels `No` and `Yes`. Severe liver disease

connective_tissue_disease: A factor with levels `No` and `Yes`. Connective tissue disease

peptic_ulcer: A factor with levels `No` and `Yes`. Peptic ulcer

hemiplegia: A factor with levels `No` and `Yes`. Hemiplegia

hiv: A factor with levels `No` and `Yes`. Human immunodeficiency virus

charlson_index: Value of the Charlson Comorbidity Index. This index predicts the ten-year mortality for a patient given the information of their comorbid conditions

hypertension: A factor with levels `No` and `Yes`. Hypertension

dyslipidemia: A factor with levels `No` and `Yes`. Dyslipidemia

depression: A factor with levels `No` and `Yes`. Depression

ceiling: A factor with levels `Oxygen mask` (non-rebreather oxygen mask), `HFNC or NIMV` (high-flow nasal cannula or non-invasive mechanical ventilation) and `IMV and ICU admission` (invasive mechanical ventilation and acces to intensive care unit). Therapeutic ceiling of care assigned to the patient

ceiling_dico: A factor with the dichotomization of the variable ceiling in two levels `No` (`IMV and ICU admission`) and `Yes` (`Oxygen mask` and `HFNC or NIMV`)

References

Pallarès, N., Tebé, C., Abelenda-Alonso, G., Rombauts, A., Oriol, I., Simonetti, A. F., Rodríguez-Molinero, A., Izquierdo, E., Díaz-Brito, V., Molist, G., Gómez Melis, G., Carratalà, J., Videla, S., & MetroSud and Divine study groups (2023). Characteristics and Outcomes by Ceiling of Care of Subjects Hospitalized with COVID-19 During Four Waves of the Pandemic in a Metropolitan Area: A Multicenter Cohort Study. Infectious diseases and therapy, 12(1), 273–289. https://doi.org/10.1007/s40121-022-00705-w

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`complications` *DIVINE's table on complications data*

Description

Information on complications data of patients included in the DIVINE cohort. Data was collected during hospitalization.

Usage

```
data(complications)
```

Format

A data frame with 5813 rows and 9 columns

record_id: Identifier of each record. This information does not match the real data.

covid_wave: A factor with levels `Wave 1`, `Wave 2`, `Wave 3`, and `Wave 5`. COVID-19 wave.

center: A factor with levels `Hospital A`, `Hospital B`, `Hospital C`, `Hospital D`, and `Hospital E`. Center of admission

comp: A factor with levels `No` and `Yes`. Did the patient experiment a complication while hospitalised?

kidney_failure: A factor with levels `No` and `Yes`. Did the patient experiment kidney failure during hospital admission?

mental_status_change: A factor with levels `No` and `Yes`. Did the patient experiment a change in its mental status during hospital admission?

nosocomial_infection: A factor with levels `No` and `Yes`. Did the patient experiment a nosocomial infection during hospital admission?

comp_cardiac: A factor with levels `No` and `Yes`. Did the patient experiment a cardiac complication during hospital admission? Cardiac complications included heart failure and acute coronary event.

comp_respiratory: A factor with levels `No` and `Yes`. Did the patient experiment a respiratory complication during hospital admission? Respiratory complications included acute respiratory failure, venous thromboembolism, and pneumonia.

References

Pallarès, N., Tebé, C., Abelenda-Alonso, G., Rombauts, A., Oriol, I., Simonetti, A. F., Rodríguez-Molinero, A., Izquierdo, E., Díaz-Brito, V., Molist, G., Gómez Melis, G., Carratalà, J., Videla, S., & MetroSud and Divine study groups (2023). Characteristics and Outcomes by Ceiling of Care of Subjects Hospitalized with COVID-19 During Four Waves of the Pandemic in a Metropolitan Area: A Multicenter Cohort Study. Infectious diseases and therapy, 12(1), 273–289. https://doi.org/10.1007/s40121-022-00705-w

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`concomitant_medication` *DIVINE's table on treatments previous to hospital admission*

Description

Information on previous treatments for patients included in the DIVINE cohort. Data was collected at hospital admission.

Usage

```
data(concomitant_medication)
```

Format

A data frame with 5813 rows and 11 columns

record_id: Identifier of each record. This information does not match the real data.

covid_wave: A factor with levels `Wave 1`, `Wave 2`, `Wave 3`, and `Wave 5`. COVID-19 wave.

center: A factor with levels `Hospital A`, `Hospital B`, `Hospital C`, `Hospital D`, and `Hospital E`. Center of admission

statins_pre: A factor with levels `No` and `Yes`. Previous treatment with statins

cortis_pre: A factor with levels `No` and `Yes`. Previous treatment with corticosteroids

acei_pre: A factor with levels `No` and `Yes`. Previous treatment with angiotensin-converting enzyme (ACE) inhibitors

ara2_pre: A factor with levels `No` and `Yes`. Previous treatment with angiotensin II receptor antagonists (ARA-II)

cortis_systemic_pre: A factor with levels `No` and `Yes`. Routine treatment with systemic corticosteroids

cortis_inhaled_pre: A factor with levels `No` and `Yes`. Routine treatment with inhaled corticosteroids

anticoagulants_pre: A factor with levels `No` and `Yes`. Previous treatment with anticoagulants

immunosuppre_pre: A factor with levels `No` and `Yes`. Previous treatment with immunosuppressants

References

Pallarès, N., Tebé, C., Abelenda-Alonso, G., Rombauts, A., Oriol, I., Simonetti, A. F., Rodríguez-Molinero, A., Izquierdo, E., Díaz-Brito, V., Molist, G., Gómez Melis, G., Carratalà, J., Videla, S., & MetroSud and Divine study groups (2023). Characteristics and Outcomes by Ceiling of Care of Subjects Hospitalized with COVID-19 During Four Waves of the Pandemic in a Metropolitan Area: A Multicenter Cohort Study. Infectious diseases and therapy, 12(1), 273–289. https://doi.org/10.1007/s40121-022-00705-w

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`data_overview` *Data Overview Function*

Description

This function provides a comprehensive overview of a data frame, including its dimensions, variable types, missing values count and a preview of the first few rows.

Usage

```
data_overview(data, preview_rows = 6)
```

Arguments

`data`	A data frame. The dataset for which you want an overview.
`preview_rows`	Integer. The number of rows to display in the preview. Default is 6.

Details

The function is useful for quickly inspecting the structure of a data frame and identifying any missing values or general characteristics of the data. It also allows users to customize how many rows they want to preview from the dataset.

Value

A list containing the following components:

`dimensions`	A vector of two elements: the number of rows and columns in the data.
`variable_types`	A named vector with the class of each variable (column) in the data.
`missing_values`	A named vector with the count of missing values (NA) for each variable.
`preview`	A data frame showing the first `preview_rows` rows of the dataset.

Examples

```
# Example usage with a simple data frame
data <- data.frame(
  Age = c(25, 30, NA, 22, 35),
  Height = c(175, 160, 180, NA, 165),
  Gender = c("Male", "Female", "Female", "Male", "Male")
)
overview <- data_overview(data, preview_rows = 4)
print(overview)

# Example usage with the default preview size (6 rows)
overview_default <- data_overview(data)
print(overview_default)
```

`demographic` *DIVINE's demographic table*

Description

Demographic data of patients included in the DIVINE cohort. Data was collected at hospital admission.

Usage

```
data(demographic)
```

Format

A data frame with 5813 rows and 8 columns

record_id: Identifier of each record. This information does not match the real data.

covid_wave: A factor with levels `Wave 1`, `Wave 2`, `Wave 3`, and `Wave 5`. COVID-19 wave.

center: A factor with levels `Hospital A`, `Hospital B`, `Hospital C`, `Hospital D`, and `Hospital E`. Center of admission

sex: A factor with levels `Male` and `Female`. Sex at birth

age: Age at hospital admission

smoker: A factor with levels `Ex-smoker`, `No` and `Yes`. Smoking status

alcohol: A factor with levels `No` and `Yes`. Consumption of alcohol

residence_center: A factor with levels `No` and `Yes`. Is the patient currently living in a long-term facility?

References

Pallarès, N., Tebé, C., Abelenda-Alonso, G., Rombauts, A., Oriol, I., Simonetti, A. F., Rodríguez-Molinero, A., Izquierdo, E., Díaz-Brito, V., Molist, G., Gómez Melis, G., Carratalà, J., Videla, S., & MetroSud and Divine study groups (2023). Characteristics and Outcomes by Ceiling of Care of Subjects Hospitalized with COVID-19 During Four Waves of the Pandemic in a Metropolitan Area: A Multicenter Cohort Study. Infectious diseases and therapy, 12(1), 273–289. https://doi.org/10.1007/s40121-022-00705-w

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`end_followup` *DIVINE's table on closure data*

Description

Information on closure data of patients included in the DIVINE cohort. Data was collected at the end of hospitalization.

Usage

`data(end_followup)`

Format

A data frame with 5813 rows and 8 columns

record_id: Identifier of each record. This information does not match the real data.

covid_wave: A factor with levels `Wave 1`, `Wave 2`, `Wave 3`, and `Wave 5`. COVID-19 wave.

center: A factor with levels `Hospital A`, `Hospital B`, `Hospital C`, `Hospital D`, and `Hospital E`. Center of admission

clinical_stability_days: Days from hospital admission to clinical stability

exitus_days: Days from hospital admission to exitus

discharge_days: Days from hospital admission to discharge

discharge: A factor with levels `No` and `Yes`. Was the patient discharge from the hospital?

exitus: A factor with levels `No` and `Yes`. Did the patient die during hospital admission?

References

Pallarès, N., Tebé, C., Abelenda-Alonso, G., Rombauts, A., Oriol, I., Simonetti, A. F., Rodríguez-Molinero, A., Izquierdo, E., Díaz-Brito, V., Molist, G., Gómez Melis, G., Carratalà, J., Videla, S., & MetroSud and Divine study groups (2023). Characteristics and Outcomes by Ceiling of Care of Subjects Hospitalized with COVID-19 During Four Waves of the Pandemic in a Metropolitan Area: A Multicenter Cohort Study. Infectious diseases and therapy, 12(1), 273–289. https://doi.org/10.1007/s40121-022-00705-w

`export_data` *Export Data to Various Formats*

Description

Export a dataframe or tibble to multiple file formats. If `format` is NULL (default), the format will be inferred from the file extension of `path`. If `format` is provided and the extension in `path` does not match, the function will update the path to use the extension that corresponds to `format` and warn the user.

Usage

```
export_data(data = NULL, path = NULL, format = NULL)
```

Arguments

`data`	A dataframe or tibble to export.
`path`	A character string specifying the file path for the exported file.
`format`	Optional character string specifying the export format. Supported formats: "xlsx", "csv", "rds", "txt", "sav", "dta", "sas7bdat" (alias "xpt"). If NULL (default), the function infers the format from the `path` extension.

Details

Supported formats and their functionality are provided via the package dependencies:

- **xlsx**: Uses `openxlsx` for Excel exports.
- **csv**: Base R functionality.
- **rds**: Base R functionality.
- **txt**: Base R functionality with tab-separated values.
- **sav**: Uses `haven` for SPSS exports.
- **dta**: Uses `haven` for Stata exports.
- **sas7bdat**: Uses `haven` for SAS exports.

Value

This function does not return a value. It writes the data to the specified file path and displays a success message upon completion.

Examples

```
## Not run:
df <- data.frame(Name = c("Alice", "Bob"), Age = c(25, 30))

# Infer format from path extension (no format argument)
export_data(df, path = "example.xlsx")
export_data(df, path = "example.csv")

# Explicit format (function will ensure path extension matches)
export_data(df, format = "csv", path = "example")        # adds .csv
export_data(df, format = "rds", path = "example.rds")

## End(Not run)
```

`icu` *DIVINE's table on icu data*

Description

Information on ICU data of patients included in the DIVINE cohort. Data was collected during hospitalization.

Usage

```
data(icu)
```

Format

A data frame with 5813 rows and 12 columns

record_id: Identifier of each record. This information does not match the real data.

covid_wave: A factor with levels `Wave 1`, `Wave 2`, `Wave 3`, and `Wave 5`. COVID-19 wave.

center: A factor with levels `Hospital A`, `Hospital B`, `Hospital C`, `Hospital D`, and `Hospital E`. Center of admission

icu: A factor with levels `No` and `Yes`. Was the patient admitted to the ICU?

icu_enter_days: Days from hospital admission to ICU admission.

icu_exit_days: Days from hospital admission to ICU discharge.

vent_mec: A factor with levels `No` and `Yes`. Did the patient received invasive mechanical ventilation?

vent_mec_start_days: Days from hospital admission to start of invasive mechanical ventilation.

vent_mec_end_days: Days from hospital admission to end of invasive mechanical ventilation.

vent_mec_no_inv: A factor with levels `No` and `Yes`. Did the patient received non-invasive mechanical ventilation?

vent_mec_no_inv_start_days: Days from hospital admission to start of non-invasive mechanical ventilation.

vent_mec_no_inv_end_days: Days from hospital admission to end of non-invasive mechanical ventilation.

sev_pneum: A factor with levels `No` and `Yes`. Indicates whether the patient presented severe pneumonia.

sev_pneum_days: Days from hospital admission to end of severe pneumonia.

References

Pallarès, N., Tebé, C., Abelenda-Alonso, G., Rombauts, A., Oriol, I., Simonetti, A. F., Rodríguez-Molinero, A., Izquierdo, E., Díaz-Brito, V., Molist, G., Gómez Melis, G., Carratalà, J., Videla, S., & MetroSud and Divine study groups (2023). Characteristics and Outcomes by Ceiling of Care of Subjects Hospitalized with COVID-19 During Four Waves of the Pandemic in a Metropolitan Area: A Multicenter Cohort Study. Infectious diseases and therapy, 12(1), 273–289. https://doi.org/10.1007/s40121-022-00705-w

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`impute_missing` *Replace Missing Values*

Description

Replace missing values (NA) in a data.frame with a specified value or method (such as mean, median, mode, constant, or custom function), applying imputation column-wise.

Usage

```
impute_missing(
  data,
  method = list(dplyr::where(is.numeric) ~ "mean", dplyr::where(is.character) ~ "mode",
    dplyr::where(is.factor) ~ "mode"),
  filter_by = NULL,
  drop_all_na = FALSE,
  verbose = TRUE
)
```

Arguments

`data`	A data frame. The dataset in which missing values should be imputed.
`method`	A list of one-sided formulas of the form `<selector> ~ <value>`. Supported `<value>` options are: • `"mean"`: replace with the column mean (numeric columns only). • `"median"`: replace with the column median (numeric columns only). • `"mode"`: replace with the most frequent value (works for numeric, character, or factor).

- A numeric constant: replace with that constant (numeric columns).
- A character constant: replace with that value (character/factor columns).
- A function: a function `function(col)` that receives the column and returns a single value to be used as replacement for NA.

The default is `list(dplyr::where(is.numeric) ~ "mean",dplyr::where(is.character) ~ "mode",dplyr::where(is.factor) ~ "mode")`.

`filter_by`	Character vector of column names. If provided, only rows that have **all** specified columns non-NA are kept (applied *before* imputation).
`drop_all_na`	Logical; if `TRUE`, rows where **all** columns are `NA` are removed *before* imputation.
`verbose`	Logical; if `TRUE` (default) print a concise final summary of what was imputed. Set to `FALSE` to suppress messages.

Details

You can remove rows that are entirely `NA` before imputation using `drop_all_na`, or filter rows based on specific variables using `filter_by`.

- The `method` argument uses **tidyselect** helpers. For example, `where(is.numeric()) ~ "median"` imputes all numeric columns by their medians.
- `"mode"` works for numeric, character and factor columns.
- When imputing factors with a character constant, the constant is added as a new level if needed.
- When passing a custom function, it should return at least one value; if multiple values are returned, only the first is used (with a warning).

Value

A tibble with missing values replaced according to the provided specifications.

Note

Caution: Single imputation methods may introduce bias or underestimate variability in your data. For more robust handling of missing data, consider multiple imputation approaches, such as those implemented in the `mice` package.

Examples

```
# Impute all numeric columns by their means:
impute_missing(icu)

# Impute numeric columns by median:
impute_missing(
  icu,
  method = list(where(is.numeric) ~ "median")
)

# Keep only rows where both "vent_mec_no_inv" and "vent_mec" are non-missing:
impute_missing(
```

```
  icu,
  filter_by = c("vent_mec_no_inv", "vent_mec")
)
```

`inhosp_antibiotics` *DIVINE's table on antibiotics received during hospitalization*

Description

Information on antibiotics received for patients included in the DIVINE cohort. Data was collected during hospitalization.

Usage

```
data(inhosp_antibiotics)
```

Format

A data frame with 5813 rows and 17 columns

record_id: Identifier of each record. This information does not match the real data.

covid_wave: A factor with levels `Wave 1`, `Wave 2`, `Wave 3`, and `Wave 5`. COVID-19 wave.

center: A factor with levels `Hospital A`, `Hospital B`, `Hospital C`, `Hospital D`, and `Hospital E`. Center of admission

any_antibiotic: A factor with levels `No` and `Yes`. Did the patient receive treatment with antibiotics during hospital admission?

amoxicillin: A factor with levels `No` and `Yes`. Treatment with amoxicillin

amoxicillin_clavulanic_acid: A factor with levels `No` and `Yes`. Treatment with amoxicillin and clavulanic acid

azithromycin: A factor with levels `No` and `Yes`. Treatment with azithromycin

ceftriaxone: A factor with levels `No` and `Yes`. Treatment with ceftriaxone

ciprofloxacin: A factor with levels `No` and `Yes`. Treatment with ciprofloxacin

cotrimoxazole: A factor with levels `No` and `Yes`. Treatment with cotrimoxazole

levofloxacin: A factor with levels `No` and `Yes`. Treatment with levofloxacin

linezolid: A factor with levels `No` and `Yes`. Treatment with linezolid

meropenem: A factor with levels `No` and `Yes`. Treatment with meropenem

piperacillin: A factor with levels `No` and `Yes`. Treatment with piperacillin

piperacillin_tazobactam: A factor with levels `No` and `Yes`. Treatment with piperacillin+tazobactam

teicoplanin: A factor with levels `No` and `Yes`. Treatment with teicoplanin

other_antibiotic: A factor with levels `No` and `Yes`. Treatment with another antibiotic

References

Pallarès, N., Tebé, C., Abelenda-Alonso, G., Rombauts, A., Oriol, I., Simonetti, A. F., Rodríguez-Molinero, A., Izquierdo, E., Díaz-Brito, V., Molist, G., Gómez Melis, G., Carratalà, J., Videla, S., & MetroSud and Divine study groups (2023). Characteristics and Outcomes by Ceiling of Care of Subjects Hospitalized with COVID-19 During Four Waves of the Pandemic in a Metropolitan Area: A Multicenter Cohort Study. Infectious diseases and therapy, 12(1), 273–289. https://doi.org/10.1007/s40121-022-00705-w

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`inhosp_antivirals` *DIVINE's table on antivirals received during hospitalization*

Description

Information on antivirals for patients included in the DIVINE cohort. Data was collected during hospitalization.

Usage

```
data(inhosp_antivirals)
```

Format

A data frame with 5813 rows and 10 columns

record_id: Identifier of each record. This information does not match the real data.

covid_wave: A factor with levels `Wave 1`, `Wave 2`, `Wave 3`, and `Wave 5`. COVID-19 wave.

center: A factor with levels `Hospital A`, `Hospital B`, `Hospital C`, `Hospital D`, and `Hospital E`. Center of admission

any_antiviral: A factor with levels `No` and `Yes`. Did the patient receive treatment with antivirals during hospital admission?

hydroxychloroquine: A factor with levels `No` and `Yes`. Treatment with hydroxychloroquine

interferon_b: A factor with levels `No` and `Yes`. Treatment with interferon beta

kaletra_ritonavir_lopinavir: A factor with levels `No` and `Yes`. Treatment with kaletra/ritonavir-lopinavir

remdesivir: A factor with levels `No` and `Yes`. Treatment with remdesivir

tocilizumab: A factor with levels `No` and `Yes`. Treatment with tocilizumab

other_antiviral: A factor with levels `No` and `Yes`. Treatment with another antiviral

References

Pallarès, N., Tebé, C., Abelenda-Alonso, G., Rombauts, A., Oriol, I., Simonetti, A. F., Rodríguez-Molinero, A., Izquierdo, E., Díaz-Brito, V., Molist, G., Gómez Melis, G., Carratalà, J., Videla, S., & MetroSud and Divine study groups (2023). Characteristics and Outcomes by Ceiling of Care of Subjects Hospitalized with COVID-19 During Four Waves of the Pandemic in a Metropolitan Area: A Multicenter Cohort Study. Infectious diseases and therapy, 12(1), 273–289. https://doi.org/10.1007/s40121-022-00705-w

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`inhosp_other_treatments` *DIVINE's table on other treatments received during hospitalization.*

Description

Information on other treatments for patients included in the DIVINE cohort. Data was collected during hospitalization.

Usage

```
data(inhosp_other_treatments)
```

Format

A data frame with 5813 rows and 6 columns

record_id: Identifier of each record. This information does not match the real data.

covid_wave: A factor with levels `Wave 1`, `Wave 2`, `Wave 3`, and `Wave 5`. COVID-19 wave.

center: A factor with levels `Hospital A`, `Hospital B`, `Hospital C`, `Hospital D`, and `Hospital E`. Center of admission

corticosteroids: A factor with levels `No` and `Yes`. Treatment with corticosteroids

lmwh: A factor with levels `No` and `Yes`. Treatment with low-molecular-weight heparin (LMWH)

oral_anticoagulants: A factor with levels `No` and `Yes`. Treatment with oral anticoagulants

References

Pallarès, N., Tebé, C., Abelenda-Alonso, G., Rombauts, A., Oriol, I., Simonetti, A. F., Rodríguez-Molinero, A., Izquierdo, E., Díaz-Brito, V., Molist, G., Gómez Melis, G., Carratalà, J., Videla, S., & MetroSud and Divine study groups (2023). Characteristics and Outcomes by Ceiling of Care of Subjects Hospitalized with COVID-19 During Four Waves of the Pandemic in a Metropolitan Area: A Multicenter Cohort Study. Infectious diseases and therapy, 12(1), 273–289. https://doi.org/10.1007/s40121-022-00705-w

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`multi_join` *Multi-Dataset Join Utility*

Description

This function performs a sequential join of multiple datasets by a specified key column.

Usage

```
multi_join(
  datasets,
  key = c("record_id", "covid_wave", "center"),
  join_type = "left"
)
```

Arguments

`datasets`	A list of data frames to be joined.
`key`	A character string representing the key column to join by. Defaults to "record_id".
`join_type`	A character string specifying the type of join. Options are "left", "right", "inner", or "full".

Value

A single data frame containing the joined datasets.

Examples

```
multi_join(
  list(analytics, comorbidities),
  join_type = "left"
)

multi_join(
  list(analytics, comorbidities),
  key = c("record_id", "covid_wave", "center"),
  join_type = "left"
)
```

`multi_plot` *multi_plot: Flexible Static or Interactive Plotting of Variables*

Description

Generate a variety of plots—histogram, density, boxplot, barplot, violin, scatter, heatmap, or spider (radar)—either as static ggplot2 objects or interactive Plotly widgets.

Usage

```
multi_plot(
  data,
  x = NULL,
  y = NULL,
  plot_type = NULL,
```

```
  interactive = FALSE,
  fill_color = "steelblue",
  color = "black",
  bin_width = NULL,
  group = NULL,
  facet = NULL,
  radar = NULL,
  radar_color = "steelblue",
  radar_labels = NULL,
  radar_cex = 1,
  radar_ref_lev = "Yes",
  title = NULL,
  x_lab = NULL,
  y_lab = NULL,
  legend_position = "right",
  axis_text_angle = 0,
  axis_text_size = 12,
  title_size = 14,
  theme_custom = ggplot2::theme_minimal()
)
```

Arguments

`data`	A data frame or tibble containing your data.
`x`	Character; name of the variable for x-axis (required for all plot types except spider).
`y`	Character; name of the variable for y-axis (required for boxplot, violin, scatter, and heatmap).
`plot_type`	Character; one of `"histogram"`, `"density"`, `"boxplot"`, `"barplot"`, `"violin"`, `"scatter"`, `"heatmap"`, or `"spider"`.
`interactive`	Logical; if `TRUE`, returns a Plotly interactive plot (not available for spider/radar charts). Default: `FALSE`.
`fill_color`	Character; fill color for non-grouped geoms (default `"steelblue"`).
`color`	Character; outline/line color (default `"black"`).
`bin_width`	Numeric; bin width for histograms. If `NULL`, computed automatically.
`group`	Character; name of grouping variable (optional).
`facet`	Character; name of variable to facet by (optional).
`radar`	Character vector; names of exactly 5 variables for spider plot (only for `"spider"`).
`radar_color`	Character or vector; border/fill color for spider chart (only for `"spider"`).
`radar_labels`	Character or vector; names of the variables for spider chart (only for `"spider"`).
`radar_cex`	Numeric; font size for variable labels in the spider chart (only for `"spider"`).
`radar_ref_lev`	Character; reference level for factors included in the spider chart (only for `"spider"`).
`title`	Character; plot title (optional).
`x_lab`	Character; x-axis label (defaults to `x`).

`y_lab`	Character; y-axis label (defaults to `y` or `"Count"`).
`legend_position`	Character; one of `"right"`, `"left"`, `"top"`, `"bottom"`, `"none"` (default `"right"`).
`axis_text_angle`	Numeric; rotation angle (degrees) for x-axis tick labels (default `0`).
`axis_text_size`	Numeric; size of axis text in pts (default `12`).
`title_size`	Numeric; size of plot title text in pts (default `14`).
`theme_custom`	A ggplot2 theme object (default `theme_minimal()`).

Details

- **Histogram:** requires `x`; uses `geom_histogram()`. Use for continuous numeric variables only.
- **Density:** requires `x`; uses `geom_density()`. It should be numeric.
- **Boxplot/Violin:** require both `x` and `y`; automatically groups by `x` or by `group` if provided, with dynamic dodge width.
- **Barplot:** requires `x`; counts occurrences. Use for categorical variables only.
- **Scatter:** requires both `x` and `y`; uses `geom_point()`. Both variables must be numeric.
- **Heatmap:** requires both `x` and `y`. Both variables must be categorical.
- **Spider:** requires `radar` (vector of variables); uses `fmsb::radarchart()`, static only.

Value

A `ggplot` object (if `interactive = FALSE` or `plot_type = "spider"`) or a `plotly` object (if `interactive = TRUE`).

Examples

```
multi_plot(icu,
  x = "icu_enter_days",
  y = "vent_mec_start_days",
  plot_type = "scatter",
  color = "darkred",
  title = "ICU exit vs MV days"
)

multi_plot(
  comorbidities,
  radar = c("hypertension", "dyslipidemia", "depression", "mild_kidney_disease", "dm"),
  radar_color = "steelblue",
  radar_ref_lev = "Yes",
  plot_type = "spider"
)
```

`scores` *DIVINE's table on severity scores at hospital admission*

Description

Information on severity scores at hospital admission for patients included in the DIVINE cohort. Data was collected at hospital admission.

Usage

```
data(scores)
```

Format

A data frame with 5813 rows and 10 columns

record_id: Identifier of each record. This information does not match the real data.

covid_wave: A factor with levels `Wave 1`, `Wave 2`, `Wave 3`, and `Wave 5`. COVID-19 wave.

center: A factor with levels `Hospital A`, `Hospital B`, `Hospital C`, `Hospital D`, and `Hospital E`. Center of admission

psi: Pneumonia severity index (PSI) at hospital admission

group_psi: A factor with levels `1`, `2`, `3`, and `4`. PSI group

curb65: CURB65 score at hospital admission

group_curb65: A factor with levels `1`, `2`, and `3`. CURB65 group

mulbsta: MULBSTA score at hospital admission

group_mulbsta: A factor with levels `Low-risk` and `High-risk`. MULBSTA group

rox_index: ROX index at hospital admission

References

Pallarès, N., Tebé, C., Abelenda-Alonso, G., Rombauts, A., Oriol, I., Simonetti, A. F., Rodríguez-Molinero, A., Izquierdo, E., Díaz-Brito, V., Molist, G., Gómez Melis, G., Carratalà, J., Videla, S., & MetroSud and Divine study groups (2023). Characteristics and Outcomes by Ceiling of Care of Subjects Hospitalized with COVID-19 During Four Waves of the Pandemic in a Metropolitan Area: A Multicenter Cohort Study. Infectious diseases and therapy, 12(1), 273–289. https://doi.org/10.1007/s40121-022-00705-w

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`stats_table` *Create Summary Table*

Description

This function generates a summary table using the `gtsummary` package. It allows customization of the reported statistics for continuous variables and categorical variables. Users can optionally include p-values for group comparisons and manage the reporting of missing values.

Usage

```
stats_table(
  data,
  vars = NULL,
  var_labels = NULL,
  by = NULL,
  statistic_type = "mean_sd",
  pvalue = FALSE,
  test_method = NULL,
  include_na = TRUE
)
```

Arguments

`data`	A data frame containing the dataset.
`vars`	A character vector of variable names to include in the summary. If NULL (default), all variables are included.
`var_labels`	A list of labels to replace variable names in the table.
`by`	A character string specifying a grouping variable. If NULL (default), no grouping is applied.
`statistic_type`	A character string specifying the type of statistic to report **for continuous variables**. Options are: • "mean_sd": Mean (SD) for continuous variables. • "median_iqr": Median (Q1; Q3) for continuous variables. • "both": Both Mean (SD) and Median (Q1; Q3).
`pvalue`	A logical value indicating whether to include p-values in the summary. Defaults to FALSE.
`test_method`	Optional. Only used if `pvalue = TRUE`. A list specifying custom statistical tests for each variable. If NULL, `gtsummary` will choose default tests based on variable type.
`include_na`	A logical value indicating whether to include rows with missing values in the output. Defaults to TRUE.

Value

A gtsummary table object.

Examples

```
# Mean ± SD summary
stats_table(
  vital_signs,
  vars = c("temperature", "saturation"),
  by = "supporto2",
  statistic_type = "mean_sd"
)

# Both mean ± SD and median [Q1; Q3]
stats_table(
 vital_signs,
 statistic_type = "both",
 include_na = FALSE
)

# Add p-value with default tests
stats_table(
 vital_signs,
 vars = c("temperature", "saturation"),
 by = "supporto2",
 pvalue = TRUE
)

# Add p-value and define method
stats_table(
 vital_signs,
 vars = c("temperature", "saturation"),
 by = "supporto2",
 pvalue = TRUE,
 test_method = list(temperature ~ "t.test")
)
```

`symptoms` *DIVINE's symptoms table*

Description

Information on COVID-19 associated symptoms of patients included in the DIVINE cohort. Data was collected at hospital admission.

Usage

```
data(symptoms)
```

Format

A data frame with 5813 rows and 24 columns

record_id: Identifier of each record. This information does not match the real data.

covid_wave: A factor with levels `Wave 1`, `Wave 2`, `Wave 3`, and `Wave 5`. COVID-19 wave.

center: A factor with levels `Hospital A`, `Hospital B`, `Hospital C`, `Hospital D`, and `Hospital E`. Center of admission

symptoms_days: Days from symptoms onset to hospitalization

rhinorrhea: A factor with levels `No` and `Yes`. Rhinorrhea

anosmia: A factor with levels `No` and `Yes`. Anosmia

ageusia: A factor with levels `No` and `Yes`. Ageusia

arthromyalgia: A factor with levels `No` and `Yes`. Arthromyalgia

odynophagia: A factor with levels `No` and `Yes`. Odynophagia

fever: A factor with levels `No` and `Yes`. Fever

cough: A factor with levels `No` and `Yes`. Cough

dyspnea: A factor with levels `No` and `Yes`. Dyspnoea

expectoration: A factor with levels `No` and `Yes`. Expectoration

diarrhea: A factor with levels `No` and `Yes`. Diarrhea

vomit: A factor with levels `No` and `Yes`. Vomiting

nausea: A factor with levels `No` and `Yes`. Nausea

asthenia: A factor with levels `No` and `Yes`. Asthenia

anorexia: A factor with levels `No` and `Yes`. Anorexia

cephal: A factor with levels `No` and `Yes`. Headache

chest_pain: A factor with levels `No` and `Yes`. Chest pain

abdominal_pain: A factor with levels `No` and `Yes`. Abdominal pain

confusional_syndrome: A factor with levels `No` and `Yes`. Confusional syndrome

shock_admission: A factor with levels `No` and `Yes`. Shock on admission

bacterial_infection: A factor with levels `No` and `Yes`. Bacterial infection

References

Pallarès, N., Tebé, C., Abelenda-Alonso, G., Rombauts, A., Oriol, I., Simonetti, A. F., Rodríguez-Molinero, A., Izquierdo, E., Díaz-Brito, V., Molist, G., Gómez Melis, G., Carratalà, J., Videla, S., & MetroSud and Divine study groups (2023). Characteristics and Outcomes by Ceiling of Care of Subjects Hospitalized with COVID-19 During Four Waves of the Pandemic in a Metropolitan Area: A Multicenter Cohort Study. Infectious diseases and therapy, 12(1), 273–289. https://doi.org/10.1007/s40121-022-00705-w

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`vaccine` *DIVINE's vaccine table*

Description

Information on COVID-19 vaccines of patients included in the DIVINE cohort. Data was collected at hospital admission and it is available for waves 3 and 5 (patients were not yet vaccinated in waves 1 and 2).

Usage

```
data(vaccine)
```

Format

A data frame with 5813 rows and 6 columns

record_id: Identifier of each record. This information does not match the real data.

covid_wave: A factor with levels `Wave 1`, `Wave 2`, `Wave 3`, and `Wave 5`. COVID-19 wave.

center: A factor with levels `Hospital A`, `Hospital B`, `Hospital C`, `Hospital D`, and `Hospital E`. Center of admission

vaccine: A factor with levels `No`, `Yes` and `Not applicable` (for patients included in waves before vaccination started). Is the patient vaccinated for COVID-19?

complete_vaccine: A factor with levels `No`, `Partial`, `Complete` and `Not applicable` (for patients included in waves before vaccination started). Is the patient partially vaccinated (one dose of two-dose vaccines), completely vaccinated (one dose for one-dose vaccines or two doses for two-dose vaccines) or not vaccinated at all?

immune_vaccine: A factor with levels `No immunity`, `Partial immunity`, `Total immunity` and `Not applicable` (for patients included in waves before vaccination started). Defines the level of immunity of the patient: not vaccinated (`No immunity`), vaccinated with only one dose for two-dose vaccines (`Partial immunity`), vaccinated with two doses but less than 7 days have passed since the second dose (`Partial immunity`) or vaccinated with all the doses and more than 7 days have passed since the second dose (`Total immunity`)

References

Pallarès, N., Tebé, C., Abelenda-Alonso, G., Rombauts, A., Oriol, I., Simonetti, A. F., Rodríguez-Molinero, A., Izquierdo, E., Díaz-Brito, V., Molist, G., Gómez Melis, G., Carratalà, J., Videla, S., & MetroSud and Divine study groups (2023). Characteristics and Outcomes by Ceiling of Care of Subjects Hospitalized with COVID-19 During Four Waves of the Pandemic in a Metropolitan Area: A Multicenter Cohort Study. Infectious diseases and therapy, 12(1), 273–289. https://doi.org/10.1007/s40121-022-00705-w

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`vital_signs` *DIVINE's table on vital signs*

Description

Information on vital signs of patients included in the DIVINE cohort. Data was collected at hospital admission.

Usage

```
data(vital_signs)
```

Format

A data frame with 5813 rows and 13 columns

record_id: Identifier of each record. This information does not match the real data.

covid_wave: A factor with levels `Wave 1`, `Wave 2`, `Wave 3`, and `Wave 5`. COVID-19 wave.

center: A factor with levels `Hospital A`, `Hospital B`, `Hospital C`, `Hospital D`, and `Hospital E`. Center of admission

temperature: Human body temperature (ºC)

fio2_contributed: Fraction of inspired oxygen (%)

syst_blood_press: Systolic blood pressure (mmHg)

diast_blood_press: Diastolic blood pressure (mmHg)

saturation: Oxygen saturation (%)

cardiac_freq: Heart rate (bpm)

supporto2: A factor with levels `No` and `Yes`. Oxygen Support

normal_radio: A factor with levels `No` and `Yes`. Normal X-ray

pleural_effusion: A factor with levels `No` and `Yes`. Pleural effusion

saturation_fio2: Oxygen Saturation to FiO2 Ratio

References

Pallarès, N., Tebé, C., Abelenda-Alonso, G., Rombauts, A., Oriol, I., Simonetti, A. F., Rodríguez-Molinero, A., Izquierdo, E., Díaz-Brito, V., Molist, G., Gómez Melis, G., Carratalà, J., Videla, S., & MetroSud and Divine study groups (2023). Characteristics and Outcomes by Ceiling of Care of Subjects Hospitalized with COVID-19 During Four Waves of the Pandemic in a Metropolitan Area: A Multicenter Cohort Study. Infectious diseases and therapy, 12(1), 273–289. https://doi.org/10.1007/s40121-022-00705-w

Index