Package: EpiScopeK (via r-universe)

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Type Package

Title Comprehensive Epidemiological Analysis Toolkit

Version 0.1.1

Description Provides a unified framework for epidemiological data analysis and disease surveillance. The package supports descriptive epidemiology, incidence, prevalence and mortality estimation, age standardization, trend analysis, geographic summaries, disease risk prediction, and automated analytical workflows. Designed for researchers and public health professionals, it facilitates reproducible analyses of epidemiological datasets using established statistical and predictive modeling techniques. Methods are informed by standard epidemiological references including Rothman et al. (2008, ISBN:9780781755641) and Gordis (2014, ISBN:9781455737338).

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Imports dplyr, rlang

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Contents

`epi_data` *Epidemiological Example Dataset*

Description

A simulated epidemiological dataset containing demographic and disease indicators.

Usage

```
epi_data
```

Format

A data frame with 10000 observations:

country Country

year Year

sex Sex

age_group Age Group

incidence Incidence Rate

prevalence Prevalence Rate

mortality Mortality Rate

Source

Simulated Data

`epi_pipelineK` *Automated Epidemiological Pipeline*

Description

Runs a complete epidemiological workflow.

Usage

```
epi_pipelineK(data)
```

Arguments

`data`	Data frame.

Value

List of results.

Examples

```
epi_pipelineK(epi_data)
```

`epi_summaryK` *Epidemiological Summary Statistics*

Description

Computes summary statistics for all numeric variables.

Usage

```
epi_summaryK(data)
```

Arguments

`data`	A data frame.

Value

A data frame containing mean, standard deviation, median and number of missing values.

Examples

```
epi_summaryK(epi_data)
```

`geo_epiK` *Geographic Summary of Epidemiological Data*

Description

Aggregates an indicator by region.

Usage

```
geo_epiK(data, region, indicator)
```

Arguments

`data`	Data frame.
`region`	Region variable.
`indicator`	Indicator variable.

Value

Summary table.

Examples

```
geo_epiK(epi_data, "country", "incidence")
```

`incidence_rateK` *Calculate Incidence Rate*

Description

Computes incidence rate per 100,000 population.

Usage

```
incidence_rateK(cases, population)
```

Arguments

`cases`	Number of new cases.
`population`	Population at risk.

Value

Numeric incidence rate.

Examples

```
incidence_rateK(150, 100000)
```

`mortality_rateK` *Calculate Mortality Rate*

Description

Computes mortality rate per 100,000 population.

Usage

```
mortality_rateK(deaths, population)
```

Arguments

`deaths`	Number of deaths.
`population`	Population size.

Value

Numeric mortality rate.

Examples

```
mortality_rateK(50,100000)
```

`prevalence_rateK` *Calculate Prevalence Rate*

Description

Computes prevalence per 100,000 population.

Usage

```
prevalence_rateK(existing_cases, population)
```

Arguments

`existing_cases`	Number of existing cases.
`population`	Total population.

Value

Numeric prevalence rate.

Examples

```
prevalence_rateK(500,100000)
```

`risk_predictK` *Disease Risk Prediction*

Description

Fits a logistic regression model.

Usage

```
risk_predictK(formula, data)
```

Arguments

`formula`	Model formula.
`data`	Data frame.

Value

A fitted logistic regression model.

Examples

```
df <- data.frame(
  disease = c(0,1,0,1,1,0),
  age = c(25,40,35,60,55,30),
  incidence = c(10,20,15,30,25,12)
)

risk_predictK(
  disease ~ age + incidence,
  df
)
```

`trend_epiK` *Trend Analysis for Epidemiological Data*

Description

Fits a linear trend model and visualizes temporal changes.

Usage

```
trend_epiK(data, year, outcome)
```

Arguments

`data`	Data frame.
`year`	Name of year variable.
`outcome`	Name of outcome variable.

Value

Linear model object.

Examples

```
trend_epiK(epi_data, "year", "incidence")
```

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