

Package ‘AMRsurveilR’

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Title Antimicrobial Resistance Surveillance, Epidemiology and Risk Analysis

Version 0.1.0

Description Provides tools for antimicrobial resistance surveillance, epidemiological analysis, temporal trend detection, early warning detection, spatial cluster identification, and risk factor analysis. The package supports analysis of antimicrobial resistance patterns, resistance to multiple antimicrobial classes, temporal surveillance, and spatial epidemiology for applications in veterinary, medical, and One Health research. Antimicrobial resistance surveillance approaches are informed by guidelines from WHO (2023) <<https://www.who.int/publications/i/item/9789240076600>> and WOA (2024) <https://www.woah.org/fileadmin/Home/eng/Health_standards/tahc/2024/en_chapitre_antibio_harmonisation.htm>. Statistical methods include cumulative sum (CUSUM) monitoring (Page, 1954) <[doi:10.1093/biomet/41.1-2.100](https://doi.org/10.1093/biomet/41.1-2.100)>, exponentially weighted moving average (EWMA) monitoring (Roberts, 1959) <[doi:10.1080/00401706.1959.10489860](https://doi.org/10.1080/00401706.1959.10489860)>, Local Moran's I spatial analysis (Anselin, 1995) <[doi:10.1111/j.1538-4632.1995.tb00338.x](https://doi.org/10.1111/j.1538-4632.1995.tb00338.x)>, and multidrug- and extensively drug-resistant classification (Magiorakos et al., 2012) <[doi:10.1111/j.1469-0691.2011.03570.x](https://doi.org/10.1111/j.1469-0691.2011.03570.x)>.

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amr_alert	<i>Generate AMR surveillance alerts</i>
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Description

Combines EWMA and CUSUM surveillance signals.

Usage

```
amr_alert(x, lambda = 0.2, L = 3, h = 5)
```

Arguments

- x Numeric vector of resistance proportions.
- lambda EWMA smoothing parameter.
- L EWMA control-limit multiplier.
- h CUSUM decision interval.

Value

A data frame containing EWMA, CUSUM and combined alerts.

amr_cusum*Detect AMR changes using CUSUM*

Description

Calculates a one-sided cumulative sum for increases in resistance.

Usage

```
amr_cusum(x, target = mean(x), k = 0, h = 5)
```

Arguments

x	Numeric vector of resistance proportions.
target	Target resistance proportion.
k	Reference value.
h	Decision interval.

Value

A data frame containing the cumulative sum and alert status.

amr_ewma*Detect antimicrobial resistance changes using EWMA*

Description

Applies an exponentially weighted moving average to a time series of resistance proportions.

Usage

```
amr_ewma(x, lambda = 0.2, L = 3)
```

Arguments

x	Numeric vector of resistance proportions.
lambda	EWMA smoothing parameter.
L	Control-limit multiplier.

Value

A data frame containing the observed values, EWMA statistic, and upper/lower control limits.

Examples

```
x <- c(
  0.20, 0.21, 0.19, 0.22,
  0.23, 0.25, 0.40, 0.45
)

amr_ewma(x)
```

amr_example

Example antimicrobial resistance surveillance dataset

Description

A simulated dataset containing antimicrobial susceptibility results, sampling dates, and bacterial species for demonstrating functions in AMRsurveilR.

Usage

```
amr_example
```

Format

A data frame with 200 rows and 8 columns:

isolate_id Unique isolate identifier.
date Date of isolate collection.
organism Bacterial species.
AMP Ampicillin susceptibility result.
TET Tetracycline susceptibility result.
CIP Ciprofloxacin susceptibility result.
GEN Gentamicin susceptibility result.
CTX Cefotaxime susceptibility result.

Details

The dataset is simulated and is provided solely for examples, testing, and demonstration. Susceptibility results are coded as "R" for resistant and "S" for susceptible.

Source

Simulated data generated for the AMRsurveilR package.

amr_hotspot*Detect spatial hotspots of antimicrobial resistance*

Description

Identifies statistically significant spatial clusters of antimicrobial resistance using Local Moran's I (LISA).

Usage

```
amr_hotspot(  
  data,  
  geometry,  
  variable,  
  queen = TRUE,  
  p_value = 0.05,  
  zero.policy = TRUE  
)
```

Arguments

data	A data frame containing the AMR variable.
geometry	An sf polygon or point object with the same number of observations as data.
variable	Name of the numeric AMR variable as a character string.
queen	Logical. Should queen contiguity be used for polygon neighbours? Default is TRUE.
p_value	Significance level for hotspot classification. Default is 0.05.
zero.policy	Logical. Should observations with no neighbours be allowed? Default is TRUE.

Details

The function classifies observations into:

- High-High: high AMR surrounded by high AMR
- Low-Low: low AMR surrounded by low AMR
- High-Low: high AMR surrounded by low AMR
- Low-High: low AMR surrounded by high AMR
- Not significant

The function uses spatial neighbours generated from the supplied sf geometry and calculates Local Moran's I using `spdep::localmoran()`. The AMR variable is standardized before calculating the spatial clusters.

Value

A data frame containing the original AMR values, Local Moran's I, expected value, variance, Z-score, p-value, and cluster classification.

Examples

```
library(sf)

# Create example AMR data
amr_data <- data.frame(
  amr_prevalence = c(
    0.10, 0.20, 0.80,
    0.15, 0.75, 0.85,
    0.20, 0.70, 0.90
  )
)

# Create a 3 x 3 grid of neighbouring polygons
polygons <- lapply(0:8, function(i) {
  x <- i %% 3
  y <- i %% 3

  st_polygon(list(matrix(
    c(
      x, y,
      x + 1, y,
      x + 1, y + 1,
      x, y + 1,
      x, y
    ),
    ncol = 2,
    byrow = TRUE
  )))
})

district_sf <- st_sf(
  geometry = st_sfc(polygons)
)

hotspots <- amr_hotspot(
  data = amr_data,
  geometry = district_sf,
  variable = "amr_prevalence"
)

head(hotspots)
```

Description

Fits a binomial logistic regression model.

Usage

```
amr_logistic(data, formula)
```

Arguments

data	A data frame.
formula	A model formula.

Value

A fitted glm object.

Examples

```
dat <- data.frame(
  MDR = c(0, 1, 0, 1, 1, 0),
  antibiotic_use = c(0, 1, 0, 1, 1, 0),
  farm_size = c(10, 20, 12, 30, 25, 15)
)

amr_logistic(
  dat,
  MDR ~ antibiotic_use + farm_size
)
```

amr_mdr

Identify multidrug-resistant isolates

Description

Identifies isolates resistant to at least a specified number of antimicrobial agents.

Usage

```
amr_mdr(
  data,
  antibiotic_columns,
  isolate_id = NULL,
  resistant_value = "R",
  min_classes = 3
)
```

Arguments

<code>data</code>	A data frame.
<code>antibiotic_columns</code>	Character vector of antimicrobial columns.
<code>isolate_id</code>	Optional isolate identifier column.
<code>resistant_value</code>	Value representing resistance.
<code>min_classes</code>	Minimum number of resistant antimicrobial agents.

Value

A data frame containing the number of resistant antimicrobials and MDR classification.

Examples

```
dat <- data.frame(
  isolate = 1:3,
  AMP = c("R", "S", "R"),
  TET = c("R", "S", "S"),
  CIP = c("S", "S", "R")
)

amr_mdr(
  dat,
  c("AMP", "TET", "CIP"),
  isolate_id = "isolate"
)
```

<code>amr_prevalence</code>	<i>Calculate antimicrobial resistance prevalence</i>
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Description

Calculates the proportion of resistant isolates and its binomial confidence interval.

Usage

```
amr_prevalence(resistant, total, conf.level = 0.95, method = "exact")
```

Arguments

<code>resistant</code>	Number of resistant isolates.
<code>total</code>	Total number of isolates tested.
<code>conf.level</code>	Confidence level. Default is 0.95.
<code>method</code>	Confidence interval method passed to <code>binom.test</code> .

Value

A data frame containing resistant isolates, total isolates, prevalence, lower and upper confidence limits.

Examples

```
amr_prevalence(42, 100)
```

```
amr_resistance_profile
```

Calculate antimicrobial resistance profile

Description

Calculates resistance prevalence for multiple antimicrobial agents.

Usage

```
amr_resistance_profile(data, antibiotic_columns, resistant_value = "R")
```

Arguments

`data` A data frame.
`antibiotic_columns` Character vector containing antibiotic columns.
`resistant_value` Value representing resistance, usually "R".

Value

A data frame containing the number tested, resistant isolates, and resistance percentage for each antimicrobial.

Examples

```
data <- data.frame(  
  AMP = c("R", "S", "R", "S"),  
  TET = c("S", "R", "R", "S")  
)  
  
amr_resistance_profile(  
  data,  
  c("AMP", "TET")  
)
```

amr_trend	<i>Calculate temporal antimicrobial resistance trends</i>
-----------	---

Description

Aggregates antimicrobial resistance observations by a specified time period and calculates the proportion of resistant isolates.

Usage

```
amr_trend(data, date, outcome, resistant_value = "R", period = "month")
```

Arguments

data	A data frame.
date	Column containing dates.
outcome	Column containing antimicrobial susceptibility results.
resistant_value	Value representing resistance. Default is "R".
period	Aggregation period. One of "month", "quarter", or "year".

Value

A data frame containing the time period, number tested, number resistant, and resistance percentage.

Examples

```
data(amr_example)

trend <- amr_trend(
  data = amr_example,
  date = date,
  outcome = AMP
)

head(trend)
```

amr_xdr	<i>Identify extensively drug-resistant isolates</i>
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Description

A simple threshold-based implementation. The definition should be adapted to the organism and antimicrobial-class framework used in the study.

Usage

```
amr_xdr(data, antibiotic_columns, resistant_value = "R", min_resistant = 5)
```

Arguments

data	A data frame.
antibiotic_columns	Character vector of antimicrobial columns.
resistant_value	Value representing resistance.
min_resistant	Minimum number of resistant agents.

Value

A data frame with resistant counts and XDR classification.

plot_amr_trend	<i>Plot antimicrobial resistance trend</i>
----------------	--

Description

Produces a temporal antimicrobial resistance trend plot.

Usage

```
plot_amr_trend(x, title = "Antimicrobial Resistance Trend")
```

Arguments

x	A data frame returned by <code>amr_trend()</code> .
title	Plot title.

Value

A ggplot object.

Examples

```
data(amr_example)

trend <- amr_trend(
  data = amr_example,
  date = date,
  outcome = AMP
)

plot_amr_trend(trend)
```

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