

Package ‘ZooRisk’

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Type Package

Title Quantitative Assessment of Zoonotic Disease Risk

Version 1.0.0

Description Provides quantitative tools for assessing zoonotic disease risk across animal, human, environmental, and transmission interfaces. The package supports exposure and transmission risk estimation, spillover risk assessment, risk scoring, cross-species comparison, transmission-network analysis, Monte Carlo uncertainty simulation, and sensitivity analysis. The One Health framework underlying these assessments is described by World Health Organization, Food and Agriculture Organization of the United Nations, United Nations Environment Programme, and World Organisation for Animal Health (2022) <[doi:10.4060/cc2289en](https://doi.org/10.4060/cc2289en)>.

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URL <https://github.com/vinodhpm/ZooRisk>

BugReports <https://github.com/vinodhpm/ZooRisk/issues>

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Contents

cross_species	2
exposure_risk	3
host_risk	3
monte_carlo_risk	4
network_centrality	4
network_risk	5
onehealth_summary	5
plot_network	6
plot_risk	6
plot_risk_matrix	7
print.zoorisk	7
risk_contribution	8
risk_matrix	8
risk_rank	9
risk_score	9
risk_simulate	10
sensitivity_risk	11
spillover_risk	11
summary.zoorisk	12
transmission_network	12
transmission_risk	13
zoonotic_risk	13

Index	15
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cross_species	<i>Compare risk across host species</i>
---------------	---

Description

Compare risk across host species

Usage

cross_species(species, risk)

Arguments

- | | |
|---------|--------------------------------------|
| species | Character species names. |
| risk | Numeric risk values between 0 and 1. |

Value

A ranked data frame.

exposure_risk	<i>Exposure risk</i>
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Description

Exposure risk

Usage

exposure_risk(prevalence, exposure)

Arguments

- prevalence Probability or prevalence of pathogen occurrence.
- exposure Probability of exposure.

Value

Numeric exposure-associated risk.

host_risk	<i>Calculate host-specific risk</i>
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Description

Calculate host-specific risk

Usage

host_risk(prevalence, exposure)

Arguments

- prevalence Prevalence.
- exposure Exposure probability.

Value

Numeric host risk.

monte_carlo_risk	<i>Summarize Monte Carlo risk</i>
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Description

Summarizes the distribution of zoonotic risk obtained from `risk_simulate()`.

Usage

```
monte_carlo_risk(x, probs = c(0.025, 0.5, 0.975))
```

Arguments

<code>x</code>	A data frame returned by <code>risk_simulate()</code> .
<code>probs</code>	Probability levels used to calculate the lower and upper quantiles.

Value

A data frame containing the mean, median, lower, and upper risk estimates.

Examples

```
sim <- risk_simulate(
  prevalence = c(0.1, 0.3),
  exposure = c(0.2, 0.6),
  transmission = c(0.3, 0.8),
  n_sim = 100
)
monte_carlo_risk(sim)
```

network_centrality	<i>Calculate transmission network centrality</i>
--------------------	--

Description

Calculates node-level centrality measures for a transmission network. When the optional **igraph** package is available, degree, betweenness, and closeness centrality are calculated. Otherwise, degree is calculated from the network structure and the other measures are returned as NA.

Usage

```
network_centrality(x)
```

Arguments

<code>x</code>	A transmission network created by <code>transmission_network()</code> .
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Value

A data frame containing node-level network centrality measures.

network_risk	<i>Summarize transmission network connectivity</i>
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Description

Calculates node-level connectivity in a transmission network using in-degree, out-degree, and total degree. Higher total degree indicates greater network connectivity and does not itself represent epidemiological risk or probability of transmission.

Usage

```
network_risk(x)
```

Arguments

x A transmission network created by [transmission_network\(\)](#).

Value

A data frame containing the node identifier, out-degree, in-degree, and total degree, ordered by decreasing total degree.

onehealth_summary	<i>Summarize One Health risk components</i>
-------------------	---

Description

Summarize One Health risk components

Usage

```
onehealth_summary(animal, human, environment)
```

Arguments

animal, human, environment
 Numeric risk components between 0 and 1.

Value

A data frame.

plot_network	<i>Plot a transmission network</i>
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Description

Plots a transmission network using **igraph** when available. Otherwise, a base R degree plot is produced.

Usage

```
plot_network(x, ...)
```

Arguments

x	A transmission network created by transmission_network() .
...	Graphical arguments passed to the plotting method.

Value

Invisibly returns x.

plot_risk	<i>Plot a zoonotic risk score</i>
-----------	-----------------------------------

Description

Plot a zoonotic risk score

Usage

```
plot_risk(x, ...)
```

Arguments

x	Numeric risk score or <code>zoorisk</code> object.
...	Graphical arguments.

Value

Invisibly returns x.

plot_risk_matrix	<i>Plot a two-dimensional risk matrix</i>
------------------	---

Description

Plot a two-dimensional risk matrix

Usage

```
plot_risk_matrix(x, y = NULL, ...)
```

Arguments

x	Numeric risk values.
y	Optional second risk dimension.
...	Graphical arguments.

Value

Invisibly returns x.

print.zoorisk	<i>Print a ZooRisk result</i>
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Description

Prints a quantitative zoonotic risk result, including the overall multiplicative risk estimate and its component probabilities.

Usage

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

Arguments

x	A zoorisk object.
...	Ignored.

Value

Invisibly returns the original zoorisk object of class zoorisk. The object contains the overall risk estimate, component probabilities, and the model specification.

risk_contribution	<i>Calculate component contributions</i>
-------------------	--

Description

Calculate component contributions

Usage

```
risk_contribution(probabilities, weights = NULL)
```

Arguments

probabilities	Numeric component probabilities.
weights	Optional weights.

Value

Data frame of normalized contributions.

risk_matrix	<i>Classify risk into qualitative categories</i>
-------------	--

Description

Classify risk into qualitative categories

Usage

```
risk_matrix(x, breaks = c(0, 0.25, 0.5, 0.75, 1))
```

Arguments

x	Numeric risk scores between 0 and 1.
breaks	Five increasing cut points from 0 to 1.

Value

A factor of risk categories.

risk_rank	<i>Rank zoonotic risks</i>
-----------	----------------------------

Description

Rank zoonotic risks

Usage

```
risk_rank(x, decreasing = TRUE)
```

Arguments

x	Numeric risk scores.
decreasing	Sort from highest to lowest when TRUE.

Value

Integer ranks.

risk_score	<i>Calculate a weighted zoonotic risk score</i>
------------	---

Description

Calculate a weighted zoonotic risk score

Usage

```
risk_score(probabilities, weights = NULL)
```

Arguments

probabilities	Numeric probabilities between 0 and 1.
weights	Optional non-negative weights.

Value

A numeric risk score between 0 and 1.

risk_simulate	<i>Simulate zoonotic risk under uncertainty</i>
---------------	---

Description

Generates random combinations of zoonotic risk components within user-specified bounds and calculates the resulting risk.

Usage

```
risk_simulate(
  prevalence,
  exposure,
  transmission,
  susceptibility = c(1, 1),
  n_sim = 10000,
  seed = NULL
)
```

Arguments

prevalence	Numeric vector of length two giving the lower and upper bounds for prevalence.
exposure	Numeric vector of length two giving the lower and upper bounds for exposure.
transmission	Numeric vector of length two giving the lower and upper bounds for transmission.
susceptibility	Numeric vector of length two giving the lower and upper bounds for susceptibility.
n_sim	Number of simulations.
seed	Optional random seed.

Value

A data frame containing simulated prevalence, exposure, transmission, susceptibility, and zoonotic risk values.

Examples

```
set.seed(123)
sim <- risk_simulate(
  prevalence = c(0.1, 0.3),
  exposure = c(0.2, 0.6),
  transmission = c(0.3, 0.8),
  susceptibility = c(0.5, 1),
  n_sim = 100
)
head(sim)
```

sensitivity_risk	<i>One-at-a-time sensitivity analysis</i>
------------------	---

Description

Evaluates the effect of fractional changes to each risk component while holding the other components at their baseline values.

Usage

```
sensitivity_risk(base, changes = c(-0.2, 0.2))
```

Arguments

base	Named numeric vector of baseline risk components. Values must be between 0 and 1.
changes	Numeric vector of fractional changes applied to each component individually.

Value

A data frame containing the component and simulated risk values for each specified change. The baseline risk is returned as the `baseline_risk` attribute.

Examples

```
base <- c(
  prevalence = 0.2,
  exposure = 0.5,
  transmission = 0.6,
  susceptibility = 0.8
)

sensitivity_risk(base)
```

spillover_risk	<i>Spillover risk</i>
----------------	-----------------------

Description

Spillover risk

Usage

```
spillover_risk(prevalence, exposure, transmission, susceptibility = 1)
```

Arguments

- prevalence Probability or prevalence in the reservoir.
- exposure Probability of relevant exposure.
- transmission Probability of transmission given exposure.
- susceptibility Probability of infection given transmission.

Value

Numeric spillover risk.

summary.zoorisk	<i>Summarize a ZooRisk result</i>
-----------------	-----------------------------------

Description

Summarize a ZooRisk result

Usage

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

Arguments

- object A zoorisk object.
- ... Ignored.

Value

A data frame.

transmission_network	<i>Construct a transmission network</i>
----------------------	---

Description

Constructs an edge-list representation of a transmission network.

Usage

```
transmission_network(from, to, directed = TRUE)
```

Arguments

from	Source node identifiers.
to	Destination node identifiers.
directed	Logical; whether edges are directed.

Value

An edge-list data frame of class `zoorisk_network`.

transmission_risk	<i>Transmission risk</i>
-------------------	--------------------------

Description

Transmission risk

Usage

```
transmission_risk(exposure, transmission)
```

Arguments

exposure	Probability of exposure.
transmission	Probability of transmission given exposure.

Value

Numeric transmission-associated risk.

zoonotic_risk	<i>Quantitative zoonotic disease risk</i>
---------------	---

Description

Calculates a transparent multiplicative risk estimate.

Usage

```
zoonotic_risk(prevalence, exposure, transmission, susceptibility)
```

Arguments

prevalence	Probability or prevalence of pathogen occurrence.
exposure	Probability of relevant exposure.
transmission	Probability of transmission given exposure.
susceptibility	Probability of infection given transmission.

Value

An object of class `zoorisk`.

Index

`cross_species`, [2](#)
`exposure_risk`, [3](#)
`host_risk`, [3](#)
`monte_carlo_risk`, [4](#)
`network_centrality`, [4](#)
`network_risk`, [5](#)
`onehealth_summary`, [5](#)
`plot_network`, [6](#)
`plot_risk`, [6](#)
`plot_risk_matrix`, [7](#)
`print.zoorisk`, [7](#)
`risk_contribution`, [8](#)
`risk_matrix`, [8](#)
`risk_rank`, [9](#)
`risk_score`, [9](#)
`risk_simulate`, [10](#)
`risk_simulate()`, [4](#)
`sensitivity_risk`, [11](#)
`spillover_risk`, [11](#)
`summary.zoorisk`, [12](#)
`transmission_network`, [12](#)
`transmission_network()`, [4–6](#)
`transmission_risk`, [13](#)
`zoonotic_risk`, [13](#)