Package ‘afdx’

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Title  Diagnosis Performance Using Attributable Fraction
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URL  https://github.com/johnaponte/afdx

Description  Estimate diagnosis performance (Sensitivity, Specificity, Positive predictive value, Negative predicted value) of a diagnostic test where can not measure the golden standard but can estimate it using the attributable fraction.

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Suggests  knitr, rmarkdown, ggplot2, DescTools, kableExtra, coda, rjags, ggmcmc, spelling, testthat (>= 3.0.0)

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The afdx package provides functions to estimate the attributable fraction using logit exponential model or bayesian latent class model.

The logit exponential model

The logitexp function estimated the logit exponential function fitting a maximum likelihood model. The senspec() function estimate the sensitivity, specificity, positive predicted value and negative predicted values for the specified cut-off points.

The bayesian latent class model

The get_latent_model() provides an rjags model template to estimate the attributable fraction and the sensitivity, specificity, positive predicted value and negative predicted value of the latent class model.

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See Also

Useful links:

- https://github.com/johnaponte/afdx
get_latent_model  

Template for the bayesian latent class model

Description

This function returns a template that can be use as model in an rjags model it requires two vectors with the number of subjects in the symptoms, like fever in the case of malaria (n) and the number of non-symptomatic (m) in each of the categories of results of the diagnostic test. The first category is reserved for the negatives by the diagnostic test (in the malaria case those with asexual density 0) and the rest categories each one with higher values than the previous category.

Usage

get_latent_model()

Details


Value

a string value

Examples

{
  get_latent_model()
}
logitexp

Exponential logit model for two variables

Description

Fit a logit model of v.density on v.fever v.density with a exponential coefficient for the v.density

Usage

logitexp(v.fever, v.density)

Arguments

v.fever numeric vector of 0/1 indicating fever or equivalent  
v.density numeric vector of values >= 0 indicating the density

Details

logit(v.fever) ~ beta * (v. density ^ tau)


Value

S3 object of class afmodel with 4 components: data, model, coefficients and the estimated attributable fraction.

See Also

senspec

Examples

{
  # Get the sample data
  head(malaria_df1)
  fit <- logitexp(malaria_df1$fever, malaria_df1$density)
  fit
  senspec(fit, c(1,100,500,1000,2000,4000,8000,16000, 32000,54000,100000))
}
**make_cutoffs**

Cut-off points for densities and fever

**Description**

Generate the cutoffs at every change of density in the fever, but first category is for density 0, and last category if possible have no subjects with no fever.

**Usage**

```r
make_cutoffs(v.fever, v.density, add1 = TRUE)
```

**Arguments**

- `v.fever`: numeric vector of 0/1 indicating fever or equivalent
- `v.density`: numeric vector of values $\geq 0$ indicating the density
- `add1`: a logical value to indicate the category started with 1 is included

**Value**

a vector with the cutoff points

**Examples**

```r
{  
  make_cutoffs(malaria_df1$fever, malaria_df1$density, add1 = TRUE)
}
```

**make_n_cutoffs**

Make a defined number of categories having similar number of positives in each category

**Description**

Generate the categories in a way that each category have at least the `mintot` number of observation. It generate all possible categories were there is change and then collapse to have minimum number of observations in each category.

**Usage**

```r
make_n_cutoffs(v.fever, v.density, mintot, add1 = TRUE)
```
Arguments

- `v.fever` numeric vector of 0/1 indicating fever or equivalent
- `v.density` numeric vector of values >= 0 indicating the density
- `mintot` minimum number of observations per category
- `add1` a logical value to indicate the category started with 1 is included

Value

a vector with the cutoff points

Examples

```
{  
  make_n_cutoffs(malaria_df1$fever, malaria_df1$density, mintot=50)  
}
```

---

`malaria_df1` Synthetic data simulating a malaria crosssectional

Description

Simulated data with the main outcomes of a malaria crosssectional, fever and parasite density

Usage

`malaria_df1`

Format

a dataset with two variables

- `fever` 1 if fever or history of fever, 0 otherwise
- `density` asexual Plasmodium parasite density, in parasites per ul
**malaria_df2**

_Synthetic data simulating a malaria crosssectional_

**Description**

Simulated data with the main outcomes of a malaria crosssectional, fever and parasite density

**Usage**

malaria_df2

**Format**

A dataset with two variables

- **fever** 1 if fever or history of fever, 0 otherwise
- **density** asexual Plasmodium parasite density, in parasites per ul

---

**senspec**

_S3 methods to estimate diagnosis performance of an afmodel_

**Description**

Estimate sensitivity, specificity, positive predicted value and negative predicted value negative predictive value from an afmodel. The estimated "true" negative and "true" positive are estimated using the estimated overall attributable fraction and the predictive positive value associated with each cut-off point as described by Smith, T., Schellenberg, J.A., Hayes, R., 1994. Attributable fraction estimates and case definitions for malaria in endemic areas. Stat Med 13, 2345–2358.

**Usage**

senspec(object, ...)

## Default S3 method:
senspec(object, ...)

## S3 method for class 'afmodel'
senspec(object, cutoff, ...)

**Arguments**

- **object** with the data to calculate the sensitivity and specificity
- **...** other parameters for the implementing functions
- **cutoff** vector of cut-off points to make the estimations
Value

a matrix with the columns sensitivity and specificity, ppv (positive predicted value) and npv (negative predicted value)

No return value. Raise an error.

a matrix with the columns sensitivity and specificity, ppv (positive predicted value) and npv (negative predicted value)

See Also

logitexp

Examples

{
  # Get the sample data
  head(malaria_df1)
  fit <- logitexp(malaria_df1$fever, malaria_df1$density)
  fit
  senspec(fit, c(1,100,500,1000,2000,4000,8000,16000, 32000,54000,100000))
}
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