Package 'afdx'

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Title Diagnosis Performance Using Attributable Fraction

Version 1.1.2

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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.

License GPL (>= 3)

Encoding UTF-8

LazyData true

RoxygenNote 7.3.3

Depends R (>= 3.5.0)

Imports maxLik, dplyr, magrittr, tidyr

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

VignetteBuilder knitr

Language en-US

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NeedsCompilation no

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Repository CRAN

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afdx-package   *afdx: Diagnosis performance indicators from attributable fraction estimates.*

Description

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.

@docType package @name afdx

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See Also

Useful links:

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

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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

See: Smith T, Vounatsou P. Logistic regression and latent class models for estimating positivities in diagnostic assays with poor resolution. Communications in Statistics - Theory and Methods. 1997 Jan;26(7):1677–700.

Vounatsou P, Smith T, Smith AFM. Bayesian analysis of two-component mixture distributions applied to estimating malaria attributable fractions. Journal of the Royal Statistical Society: Series C (Applied Statistics). 1998;47(4):575–87.

Müller I, Genton B, Rare L, Kiniboro B, Kastens W, Zimmerman P, et al. Three different Plasmodium species show similar patterns of clinical tolerance of malaria infection. Malar J. 2009;8(1):158.

Plucinski MM, Rogier E, Dimbu PR, Fortes F, Halsey ES, Aidoo M, et al. Performance of Antigen Concentration Thresholds for Attributing Fever to Malaria among Outpatients in Angola. J Clin Microbiol. 2019;57(3).

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)

This corresponds to the model 3 describe 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.

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

```
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 >= 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

```
{
 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

```
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 crossectional*

Description

Simulated data with the main outcomes of a malaria crossectional, 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 crossectional*

Description

Simulated data with the main outcomes of a malaria crossectional, 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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