

Package ‘BayesianReasoning’

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Type Package

Title Plot Positive and Negative Predictive Values for Medical Tests

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Description Functions to plot and help understand positive and negative predictive values (PPV and NPV), and their relationship with sensitivity, specificity, and prevalence. See Akobeng, A.K. (2007) <[doi:10.1111/j.1651-2227.2006.00180.x](https://doi.org/10.1111/j.1651-2227.2006.00180.x)> for a theoretical overview of the technical concepts and Navarrete et al. (2015) for a practical explanation about the importance of their understanding <[doi:10.3389/fpsyg.2015.01327](https://doi.org/10.3389/fpsyg.2015.01327)>.

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URL <https://github.com/gorkang/BayesianReasoning>

BugReports <https://github.com/gorkang/BayesianReasoning/issues>

Depends R (>= 3.5.0)

Imports dplyr, ggforce, ggplot2, magrittr, reshape2, stats, tibble, tidy, utils

Suggests curl, httr, knitr, patchwork, purrr, rmarkdown, testthat

VignetteBuilder knitr

Encoding UTF-8

RoxygenNote 7.1.2

NeedsCompilation no

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min_possible_prevalence

Show minimum possible prevalence given the test characteristics

Description

Given a FP and a desired PPV, what is the Minimum Prevalence of a Condition

Usage

```
min_possible_prevalence(Sensitivity = 95, FP_test = 1, min_PPV_desired = 90)
```

Arguments

Sensitivity	Sensitivity of the test: [0-100]
FP_test	False positive rate (1-Specificity): [0-100]
min_PPV_desired	Which PPV is what you consider the minimum to trust a positive result in the test: [0-100]

Value

A description showing the minimum necessary prevalence.

Examples

```
# Example 1
min_possible_prevalence(Sensitivity = 99.9, FP_test = .1, min_PPV_desired = 70)
"To reach a PPV of 70 when using a test with 99.9 % Sensitivity and 0.1 % False Positive Rate,
you need a prevalence of at least 1 out of 429"

# Example 2
min_possible_prevalence(100, 0.1, 98)
"To reach a PPV of 98 when using a test with 100 % Sensitivity and 0.1 % False Positive Rate,
you need a prevalence of at least 1 out of 21"
```

`PPV_diagnostic_vs_screening`*Plot PPV values for a diagnostic and a screening group*

Description

Plot PPV associated to different levels of FP and a specific Sensitivity, for two different Prevalence groups.

Usage

```
PPV_diagnostic_vs_screening(  
  max_FP = 10,  
  Sensitivity = 100,  
  prevalence_screening_group = 100,  
  prevalence_diagnostic_group = 2,  
  labels_prevalence = c("Screening", "Diagnostic"),  
  folder = ""  
)
```

Arguments

<code>max_FP</code>	False positive rate (1-Specificity) [0-100].
<code>Sensitivity</code>	Sensitivity of the test [0-100].
<code>prevalence_screening_group</code>	Prevalence of the screening group, 1 out of x [1-Inf].
<code>prevalence_diagnostic_group</code>	Prevalence of the diagnostic group, 1 out of x [1-Inf].
<code>labels_prevalence</code>	Labels to use for both groups.
<code>folder</code>	Where to save the plot (the filename would be automatically created using the plot parameters)

Value

Shows a plot or, if given a folder argument, saves a .png version of the plot

Examples

```
# Example 1  
PPV_diagnostic_vs_screening(max_FP = 10, Sensitivity = 100,  
  prevalence_screening_group = 1500,  
  prevalence_diagnostic_group = 3)  
  
# Example 2. QWith custom labels  
PPV_diagnostic_vs_screening(max_FP = 10, Sensitivity = 100,
```

```
prevalence_screening_group = 1667,
prevalence_diagnostic_group = 44,
labels_prevalence = c("20 y.o.", "50 y.o."))
```

 PPV_heatmap

Plot PPV and NPV heatmaps

Description

Plot heatmaps showing the PPV for a given Sensitivity and a range of Prevalences and False Positive values or NPV values for a given Specificity and a range of Prevalences and True Positive values

Usage

```
PPV_heatmap(
  min_Prevalence = 1,
  max_Prevalence = 1000,
  Sensitivity = NULL,
  Specificity = NULL,
  limits_Sensitivity = NULL,
  limits_Specificity = NULL,
  one_out_of = FALSE,
  overlay = "no",
  overlay_labels = "",
  overlay_extra_info = FALSE,
  overlay_position_FP = NULL,
  overlay_position_FN = NULL,
  overlay_prevalence_1 = NULL,
  overlay_prevalence_2 = NULL,
  uncertainty_prevalence = "high",
  label_title = "",
  label_subtitle = "",
  Language = "en",
  folder = "",
  PPV_NPV = "PPV",
  steps_matrix = 100,
  DEBUG = FALSE,
  ...
)
```

Arguments

min_Prevalence	[x] out of y prevalence of disease: [1-Inf]
max_Prevalence	x out of [y] prevalence of disease: [1-Inf]
Sensitivity	Sensitivity of test: [0-100]
Specificity	Specificity of test: [0-100]

limits_Sensitivity	c(min Sensitivity, max Sensitivity)
limits_Specificity	c(min Specificity, max Specificity)
one_out_of	Show y scale as 1 out of x [TRUE, FALSE] FALSE by default
overlay	Type of overlay: ["line", "area"]
overlay_labels	Labels for each point in the overlay. For example: c("80", "70", "60", "50", "40", "30", "20 y.o.")
overlay_extra_info	show extra info in overlay? [TRUE/FALSE]
overlay_position_FP	FP value (position in the x-axis) for each point in the overlay. For example: c(7, 8, 9, 12, 14, 14)
overlay_position_FN	FN value (position in the x-axis) for each point in the overlay. For example: c(7, 8, 9, 12, 14, 14)
overlay_prevalence_1	Prevalence value (position in the y-axis) for each point in the overlay. For example: c(1, 1, 1, 2, 1, 1)
overlay_prevalence_2	Prevalence value (position in the y-axis) for each point in the overlay. For example: c(26, 29, 44, 69, 227, 1667)
uncertainty_prevalence	How much certainty we have about the prevalence ["high"/"low"]
label_title	Title for the plot
label_subtitle	Subtitle for the plot
Language	Language for the plot labels: ["sp", "en"]
folder	Where to save the plot (the filename would be automatically created using the plot parameters)
PPV_NPV	Should show PPV or NPV ["PPV", "NPV"]
steps_matrix	width of PPV/NPV matrix. 100 by default
DEBUG	Shows debug warnings [TRUE/FALSE]
...	Other parameters. Now used to pass dpi, height and width in the Show and Save plot section

Value

Shows a plot or, if given a folder argument, saves a .png version of the plot

Examples

```
PPV_heatmap(min_Prevalence = 1,
max_Prevalence = 1000,
Sensitivity = 100,
Specificity = 98,
Language = "en")
```

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