Package ‘BayesianReasoning’

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Type Package

Title Plot Positive and Negative Predictive Values for Medical Tests

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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, tidyr, utils

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

VignetteBuilder knitr

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NeedsCompilation no

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Description

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

Usage

```r
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

```r
# 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

max_FP False positive rate (1-Specificity) [0-100].
Sensitivity Sensitivity of the test [0-100].
prevalence_screening_group Prevalence of the screening group, 1 out of x [1-Inf].
prevalence_diagnostic_group Prevalence of the diagnostic group, 1 out of x [1-Inf].
labels_prevalence Labels to use for both groups.
folder 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.")

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**PPV_heatmap**

**PPV and NPV heatmaps**

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**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**

```r
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]
PPV_heatmap

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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