Package ‘BayesianReasoning’

June 21, 2021

Type Package
Title Plot Positive and Negative Predictive Values for Medical Tests
Version 0.3.3
Date 2021-06-16
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Depends R (>= 3.5.0)
Imports dplyr, reshape2, ggplot2, tidyr, magrittr, tibble, ggforce
License CC0
RoxygenNote 7.1.1
URL https://github.com/gorkang/BayesianReasoning
BugReports https://github.com/gorkang/BayesianReasoning/issues
Encoding UTF-8
Suggests testthat, knitr, rmarkdown, covr, patchwork
VignetteBuilder knitr
NeedsCompilation no
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Repository CRAN
Date/Publication 2021-06-21 11:20:06 UTC

R topics documented:

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```
Description

Create a PPV matrix helper function

Usage

```r
.createPPVmatrix(
  Min_Prevalence = 1,
  Max_Prevalence = 1000,
  Sensitivity = 100,
  Min_FP = 0,
  Max_FP = 10,
  steps_matrix = 100)
```

Arguments

- `Min_Prevalence`: [x] out of [y] prevalence of disease
- `Max_Prevalence`: x out of [y] prevalence of disease
- `Sensitivity`: Sensitivity of test
- `Min_FP`: Minimum False Positive ratio
- `Max_FP`: Maximum False Positive ratio
- `steps_matrix`: How big the matrix should be (probably better to leave as it is: 100)

Value

A DF called PPV
Description

Get PPV or NPV for the overlay

Usage

```r
.get_point_ppv_npv(
  PPV_melted,
  PPV_NPV = "PPV",
  Sensitivity,
  overlay_prevalence_1,
  overlay_prevalence_2,
  overlay_labels,
  overlay_position_FP,
  overlay_position_FN,
  point_Prevalence,
  prevalence_label,
  x_axis_label,
  y_axis_label,
  decimals_x,
  decimals_y
)
```

Arguments

- `PPV_melted`: DF out of `.createPPVmatrix()`
- `PPV_NPV`: Should calculate PPV or NPV?
- `Sensitivity`: Sensitivity of the test
- `overlay_prevalence_1`: [x] out of y prevalence of disease
- `overlay_prevalence_2`: x out of [y] prevalence of disease
- `overlay_labels`
- `overlay_position_FP`
- `overlay_position_FN`
- `point_Prevalence`
- `prevalence_label`
- `x_axis_label`
- `y_axis_label`
- `decimals_x`
- `decimals_y`
Description

The number of decimal places in the x and y axis label depends on how wide the range is.

Usage

```
.number_decimals_plot_axis(
    PPV_NPV = "PPV",
    Min_FP = 0,
    Max_FP,
    Min_FN,
    Max_FN,
    Min_Prevalence,
    Max_Prevalence
)
```

Arguments

- **PPV_NPV**
- **Min_FP**
- **Max_FP**
- **Min_FN**
- **Max_FN**
- **Min_Prevalence** [x] out of y prevalence of disease
- **Max_Prevalence** x out of [y] prevalence of disease
Description

Function to create the main heatmap plot

Usage

.plot_creation(
    PPV_melted,
    Min_Prevalence,
    Sensitivity,
    PPV_NPV = "PPV",
    Min_FP = 0,
    Max_FP,
    steps_matrix = 100,
    decimals_x,
    decimals_y,
    label_title = "",
    label_subtitle = "",
    label_caption = "",
    prevalence_label = "",
    legend_label = "",
    x_axis_label,
    y_axis_label
)

Arguments

PPV_melted .
Min_Prevalence .
Sensitivity .
PPV_NPV .
Min_FP .
Max_FP .
steps_matrix .
decimals_x .
decimals_y .
label_title .
label_subtitle .
label_caption .
prevalence_label .
Description

Add area overlay to PPV_heatmap plot

Usage

.plot.overlay_area(PPV_melted, uncertainty_prevalence = "low", Min_Prevalence, Max_Prevalence, Sensitivity, Min_FP = 0, Max_FP, overlay_labels = "", PPV_NPV = "PPV", overlay_prevalence_1, overlay_prevalence_2, overlay_position_FP, overlay_position_FN, decimals_x, decimals_y, prevalence_label, legend_label, label_title, label_subtitle, x_axis_label, y_axis_label)

Arguments

PPV_melted .
uncertainty_prevalence

Min_Prevalence [x] out of y prevalence of disease
Max_Prevalence x out of [y] prevalence of disease
Sensitivity .
.plot_overlay_line

Min_FP
Max_FP
overlay_labels
PPV_NPV
overlay_prevalence_1
   [x] out of y prevalence of disease for the overlay
overlay_prevalence_2
   x out of [y] prevalence of disease for the overlay
overlay_position_FP

overlay_position_FN

decimals_x

decimals_y
prevalence_label

legend_label
label_title
label_subtitle
x_axis_label
y_axis_label

Description

Add line overlay to PPV_heatmap plot

Usage

.plot_overlay_line(
   PPV_melted,
   uncertainty_prevalence = "low",
   PPV_NPV,
   Min_Prevalence,
   Max_Prevalence,
   Max_FP,
   Sensitivity,
   overlay_prevalence_1,
   overlay_prevalence_2,
   overlay_position_FP,
   overlay_position_FN,
`.plot_overlay_line`

```r
overlay_labels,
label_title,
label_subtitle,
legend_label,
decimals_x,
decimals_y,
prevalence_label,
x_axis_label,
y_axis_label
)
```

**Arguments**

- `PPV_melted` `DF`
- `uncertainty_prevalence`  
  - How big the uncertainty area should be: ["low" or "high"]
- `PPV_NPV` .
- `Min_Prevalence` `[x] out of [y] prevalence of disease`
- `Max_Prevalence` `[x] out of [y] prevalence of disease`
- `Max_FP` .
- `Sensitivity` .
- `overlay_prevalence_1`  
  - vector with [x] out of y prevalence of disease
- `overlay_prevalence_2`  
  - vector with x out of [y] prevalence of disease
- `overlay_position_FP` .
- `overlay_position_FN` .
- `overlay_labels` vector with labels for each overlay point
- `label_title` .
- `label_subtitle` .
- `legend_label` .
- `decimals_x` .
- `decimals_y` .
- `prevalence_label` .
- `x_axis_label` .
- `y_axis_label` .

Description
Supports showing plot labels in Spanish (sp) or English (default)

Usage
.translate_labels(Language, Sensitivity, Max_FP, PPV_NPV = "PPV")

Arguments
Language Can be Spanish "sp" or English (default)
Sensitivity
Max_FP
PPV_NPV

Value
A list with labels

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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Max_FP</td>
<td>False positive rate (1-Specificity) [0-100].</td>
</tr>
<tr>
<td>Sensitivity</td>
<td>Sensitivity of the test [0-100].</td>
</tr>
<tr>
<td>prevalence_screening_group</td>
<td>Prevalence of the screening group, 1 out of x [1-Inf].</td>
</tr>
<tr>
<td>prevalence_diagnostic_group</td>
<td>Prevalence of the diagnostic group, 1 out of x [1-Inf].</td>
</tr>
<tr>
<td>labels_prevalence</td>
<td>Labels to use for both groups.</td>
</tr>
<tr>
<td>folder</td>
<td>Where to save the plot (the filename would be automatically created using the plot parameters)</td>
</tr>
</tbody>
</table>
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. With 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."))

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 = 95,
    Min_FP = 0,
    Max_FP = 10,
    overlay = "no",
    overlay_labels = "",
    overlay_position_FP = 1,
    overlay_position_FN = 1,
    overlay_prevalence_1 = 1,
    overlay_prevalence_2 = 100,
    uncertainty_prevalence = "high",
    label_title = "",
    label_subtitle = "",
    Language = "en",
    folder = "",
    PPV_NPV = "PPV",
    DEBUG = 0
)
Arguments

Min_Prevalence  x in the "x out of y" prevalence (y-axis): [1-Inf]
Max_Prevalence  y in the "x out of y" prevalence (y-axis): [1-Inf]
Sensitivity     Sensitivity of the test: [0-100]
Min_FP         Minimum False Positives ratio to show in plot (x-axis): [1-100]
Max_FP         Maximum False Positives ratio to show in plot (x-axis): [1-100]
overlay        Show overlay: [TRUE, FALSE]
overlay_labels Labels for each point in the overlay. For example: c("80", "70", "60", "50", "40", "30", "20 y.o.")
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]
DEBUG            Shows debug warnings [0/1]

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,
            Max_FP = 2,
            Language = "en")
```
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