

# Package ‘BayesianReasoning’

July 3, 2020

**Type** Package

**Title** Plot Positive and Negative Predictive Values for Medical Tests

**Version** 0.3.2

**Date** 2020-07-03

**Maintainer** Gorka Navarrete <gorkang@gmail.com>

**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> 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>.

**LazyData** TRUE

**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

**Author** Gorka Navarrete [aut, cre] (<<https://orcid.org/0000-0001-7678-8656>>)

**Repository** CRAN

**Date/Publication** 2020-07-03 16:40:16 UTC

**R topics documented:**

<code>.createPPVmatrix</code>	2
<code>.get_point_ppv_npv</code>	3
<code>.number_decimals_plot_axis</code>	4
<code>.plot_creation</code>	5
<code>.plot_overlay_area</code>	6
<code>.plot_overlay_line</code>	7
<code>.translate_labels</code>	9
<code>min_possible_prevalence</code>	9
<code>PPV_diagnostic_vs_screening</code>	10
<code>PPV_heatmap</code>	11

<b>Index</b>	<b>13</b>
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<code>.createPPVmatrix</code>	<i>.createPPVmatrix</i>
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**Description**

Create a PPV matrix helper function

**Usage**

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

**Arguments**

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

**Value**

A DF called PPV

---

*.get\_point\_ppv\_npv*     *.get\_point\_ppv\_npv*

---

**Description**

Get PPV or NPV for the overlay

**Usage**

```
.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 .
```

---

```
.number_decimals_plot_axis  
    .number_decimals_plot_axis
```

---

### **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
```

---

*.plot\_creation*      *.plot\_creation*

---

### **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 .  
                 .

```

legend_label  .
x_axis_label  .
y_axis_label  .

```

---

```

.plot_overlay_area  .plot_overlay_area

```

---

### 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     .

```

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 .

---

*.plot\_overlay\_line*     *.plot\_overlay\_line*

---

### **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,
```





---

.translate\_labels      *.translate\_labels*

---

**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, FP\_test, min\_PPV\_desired)

**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**

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."))
```

---

 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,
  Max_Prevalence,
  Sensitivity,
  Min_FP = 0,
  Max_FP,
  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")
```

# Index

[.createPPVmatrix](#), 2  
[.get\\_point\\_ppv\\_npv](#), 3  
[.number\\_decimals\\_plot\\_axis](#), 4  
[.plot\\_creation](#), 5  
[.plot\\_overlay\\_area](#), 6  
[.plot\\_overlay\\_line](#), 7  
[.translate\\_labels](#), 9

[min\\_possible\\_prevalence](#), 9

[PPV\\_diagnostic\\_vs\\_screening](#), 10  
[PPV\\_heatmap](#), 11