

# Package ‘symptomcheckR’

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**Type** Package

**Title** Analyzing and Visualizing Symptom Checker Performance

**Version** 0.1.3

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**Description** Easily analyze and visualize the performance of symptom checkers. This package can be used to gain comprehensive insights into the performance of single symptom checkers or the performance of multiple symptom checkers. It can be used to easily compare these symptom checkers across several metrics to gain an understanding of their strengths and weaknesses. The metrics are developed in Kopka et al. (2023) <[doi:10.1177/20552076231194929](https://doi.org/10.1177/20552076231194929)>.

**License** GPL-3

**URL** <https://github.com/ma-kopka/symptomcheckR>

**BugReports** <https://github.com/ma-kopka/symptomcheckR/issues>

**Depends** R (>= 3.5.0)

**Imports** dplyr (>= 1.0.0), ggplot2 (>= 3.2.0), ggpubr (>= 0.6.0), tidyr (>= 1.3.0), irr (>= 0.84.1)

**Suggests** knitr, rmarkdown, testthat (>= 3.0.0)

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**RoxygenNote** 7.3.1

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**Repository** CRAN

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get_accuracy	<i>get_accuracy</i>
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### Description

Calculates the accuracy of one or multiple symptom checkers

### Usage

```
get_accuracy(data, correct, apps = NULL, CI = FALSE)
```

### Arguments

data	A dataframe
correct	A string indicating the column name storing if the symptom checker solved the case (TRUE or FALSE)
apps	A string indicating the column name storing the app names (optional)
CI	A Boolean (TRUE or FALSE) indicating whether 95% confidence intervals should be output (optional)

### Value

A data frame object containing the accuracy of the symptom checker or the accuracy of multiple symptom checkers. Use the apps argument to calculate this metric for multiple symptom checkers.

**Examples**

```
data(symptomcheckRdata)
accuracy <- get_accuracy(
  data = symptomcheckRdata,
  correct = "Correct_Triage_Advice_provided_from_app",
  apps = "App_name",
  CI = TRUE
)
```

---

```
get_accuracy_by_triage
      get_accuracy_by_triage
```

---

**Description**

Calculates the accuracy on each triage level for one or multiple symptom checkers

**Usage**

```
get_accuracy_by_triage(data, correct, triagelevel, apps = NULL, CI = FALSE)
```

**Arguments**

<code>data</code>	A dataframe
<code>correct</code>	A string indicating the column name storing if the symptom checker solved the case (TRUE or FALSE)
<code>triagelevel</code>	A string indicating the column name storing the correct triage solutions
<code>apps</code>	A string indicating the column name storing the app names (optional)
<code>CI</code>	A Boolean (TRUE or FALSE) indicating whether 95% confidence intervals should be output (optional)

**Value**

A data frame object containing the accuracy on each triage level (of one or multiple symptom checkers) or the accuracy of multiple symptom checkers. Use the `apps` argument to calculate this metric for multiple symptom checkers.

**Examples**

```
data(symptomcheckRdata)
accuracy_by_triage <- get_accuracy_by_triage(
  data = symptomcheckRdata,
  correct = "Correct_Triage_Advice_provided_from_app",
  triagelevel = "Goldstandard_solution",
  apps = "App_name",
  CI = TRUE
)
```

---

get_ccs	<i>get_ccs</i>
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---

**Description**

Calculates the Capability Comparison Score (CCS) for each symptom checker

**Usage**

```
get_ccs(data, correct, vignettes, apps)
```

**Arguments**

data	A dataframe
correct	A string indicating the column name storing if the symptom checker solved the case (TRUE or FALSE)
vignettes	A string indicating the column name storing the vignette or vignette number
apps	A string indicating the column name storing the app names

**Value**

A data frame object containing the capability comparison score for each symptom checker.

**Examples**

```
data(symptomcheckRdata)
ccs <- get_ccs(
  data = symptomcheckRdata,
  correct = "Correct_Triage_Advice_provided_from_app",
  vignettes = "Vignette_id",
  apps = "App_name"
)
```

---

get_ccs_by_triage	<i>get_ccs_by_triage</i>
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---

**Description**

Calculates the Capability Comparison Score (CCS) for each symptom checker and each triage level

**Usage**

```
get_ccs_by_triage(data, correct, vignettes, apps, triagelevel)
```

**Arguments**

data	A dataframe
correct	A string indicating the column name storing if the symptom checker solved the case (TRUE or FALSE)
vignettes	A string indicating the column name storing the vignette or vignette number
apps	A string indicating the column name storing the app names
trialelevel	A string indicating the column name storing the correct triage solutions

**Value**

A data frame object containing the capability comparison score for each symptom checker on each triage level.

**Examples**

```
data(symptomcheckRdata)
ccs <- get_ccs_by_triage(
  data = symptomcheckRdata,
  correct = "Correct_Triage_Advice_provided_from_app",
  vignettes = "Vignette_id",
  apps = "App_name",
  trialelevel = "Goldstandard_solution"
)
```

---

get\_comprehensiveness *get\_comprehensiveness*

---

**Description**

Calculates the comprehensiveness for one or multiple symptom checkers

**Usage**

```
get_comprehensiveness(
  data,
  trialelevel_advice,
  vector_not_entered,
  apps = NULL,
  CI = FALSE
)
```

**Arguments**

<code>data</code>	A dataframe
<code>trialelevel_advice</code>	A string indicating the column name storing the recommendation of a symptom checker for a case
<code>vector_not_entered</code>	A vector indicating the values in which missing values are coded (e.g., as NA or a specified value such as -99)
<code>apps</code>	A string indicating the column name storing the app names
<code>CI</code>	A Boolean (TRUE or FALSE) indicating whether 95% confidence intervals should be output (optional)

**Value**

A list containing both a raw number and the percentage of comprehensiveness for one or multiple symptom checkers

**Examples**

```
data(symptomcheckRdata)
comprehensiveness <- get_comprehensiveness(
  data = symptomcheckRdata,
  trialelevel_advice = "Triage_advice_from_app",
  vector_not_entered = c(NA),
  apps = "App_name",
  CI = TRUE
)
```

---

```
get_inclination_to_overtriage
      get_inclination_to_overtriage
```

---

**Description**

Calculates the inclination to overtriage for one or multiple symptom checkers

**Usage**

```
get_inclination_to_overtriage(
  data,
  trialelevel_correct,
  trialelevel_advice,
  order_triagelevel,
  apps = NULL,
  CI = FALSE
)
```

**Arguments**

data	A dataframe
trialelevel_correct	A string indicating the column name storing the correct triage solutions
trialelevel_advice	A string indicating the column name storing the recommendation of a symptom checker for a case
order_trialelevel	A vector indicating the order of triage levels. The triage level with highest urgency should be the first value and the triage level with lowest urgency the last value.
apps	A string indicating the column name storing the app names (optional)
CI	A Boolean (TRUE or FALSE) indicating whether 95% confidence intervals should be output (optional)

**Value**

A list containing both a raw number and the percentage of the inclination to overtriage for one or multiple symptom checkers

**Examples**

```
data(symptomcheckRdata)
inclination_to_overtriage <- get_inclination_to_overtriage(
  data = symptomcheckRdata,
  trialelevel_correct = "Goldstandard_solution",
  trialelevel_advice = "Triage_advice_from_app",
  order_trialelevel = c("Emergency", "Non-Emergency", "Self-care"),
  apps = "App_name",
  CI = TRUE
)
```

---

get\_irr

*get\_irr*


---

**Description**

Calculates the inter-rater reliability of multiple raters using a two-way, absolute agreement, average-measures, mixed intra-class correlation

**Usage**

```
get_irr(data, ratings, order_trialelevel)
```

**Arguments**

data	A dataframe
ratings	A vector indicating the column names storing the ratings of reach rater
order_triagelevel	A vector indicating the order of triage levels. The triage level with highest urgency should be the first value and the triage level with lowest urgency the last value.

**Value**

A list containing the inter-rater reliability

**Examples**

```
## Not run:
#' irr <- get_irr(
  data = df,
  ratings = c("datarater1", "datarater2", "datarater3"),
  order_triagelevel = c("Emergency", "Non-Emergency", "Self-care"),
  )
## End(Not run)
```

---

get\_item\_difficulty    *get\_item\_difficulty*

---

**Description**

Calculates the item difficulty for each case / vignette

**Usage**

```
get_item_difficulty(data, correct, vignettes)
```

**Arguments**

data	A dataframe
correct	A string indicating the column name storing if the symptom checker solved the case (TRUE or FALSE)
vignettes	A string indicating the column name storing the vignette or vignette number

**Value**

A data frame object containing the item difficulty for each vignette



## Examples

```
data(symptomcheckRdata)
item_difficulty <- get_item_difficulty(
  data = symptomcheckRdata,
  correct = "Correct_Triage_Advice_provided_from_app",
  vignettes = "Vignette_id"
)
```

---

get\_safety\_of\_advice    *get\_safety\_of\_advice*

---

## Description

Calculates the safety of advice for one or multiple symptom checkers

## Usage

```
get_safety_of_advice(
  data,
  triagelevel_correct,
  triagelevel_advice,
  order_triagelevel,
  apps = NULL,
  CI = FALSE
)
```

## Arguments

data	A dataframe
triagelevel_correct	A string indicating the column name storing the correct triage solutions
triagelevel_advice	A string indicating the column name storing the recommendation of a symptom checker for a case
order_triagelevel	A vector indicating the order of triage levels. The triage level with highest urgency should be the first value and the triage level with lowest urgency the last value.
apps	A string indicating the column name storing the app names (optional)
CI	A Boolean (TRUE or FALSE) indicating whether 95% confidence intervals should be output (optional)

## Value

A list containing both a raw number and the percentage of safe advice for one or multiple symptom checkers

## Examples

```
data(symptomcheckRdata)
safety_of_advice <- get_safety_of_advice(
  data = symptomcheckRdata,
  triagelevel_correct = "Goldstandard_solution",
  triagelevel_advice = "Triage_advice_from_app",
  order_triagelevel = c("Emergency", "Non-Emergency", "Self-care"),
  apps = "App_name",
  CI = TRUE
)
```

---

plot_accuracy	<i>plot_accuracy</i>
---------------	----------------------

---

## Description

Plots the accuracy for one or multiple symptom checkers

## Usage

```
plot_accuracy(input)
```

## Arguments

input            A dataframe containing the output of get\_accuracy()

## Value

A ggplot object visualizing the accuracy for either one or multiple symptom checkers

## Examples

```
data(symptomcheckRdata)
accuracy <- get_accuracy(
  data = symptomcheckRdata,
  correct = "Correct_Triage_Advice_provided_from_app",
  apps = "App_name"
)
accuracy_plot <- plot_accuracy(accuracy)
```

---

plot\_accuracy\_by\_triage  
*plot\_accuracy\_by\_triage*

---

**Description**

Plots the accuracy on each triage level for one or multiple symptom checkers

**Usage**

```
plot_accuracy_by_triage(input)
```

**Arguments**

input                    A dataframe containing the output of get\_accuracy\_by\_triage()

**Value**

A ggplot object visualizing the accuracy on each triage level for either one or multiple symptom checkers

**Examples**

```
data(symptomcheckRdata)
accuracy_by_triage <- get_accuracy_by_triage(
  data = symptomcheckRdata,
  correct = "Correct_Triage_Advice_provided_from_app",
  triagelevel = "Goldstandard_solution",
  apps = "App_name"
)
accuracy_triage_plot <- plot_accuracy_by_triage(accuracy_by_triage)
```

---

plot\_ccs                    *plot\_ccs*

---

**Description**

Plots the Capability Comparison Score (CCS) for multiple symptom checkers

**Usage**

```
plot_ccs(input)
```

**Arguments**

input                    A dataframe containing the output of get\_ccs()

**Value**

A ggplot object visualizing the CCS for multiple symptom checkers

**Examples**

```
data(symptomcheckRdata)
ccs <- get_ccs(
  data = symptomcheckRdata,
  correct = "Correct_Triage_Advice_provided_from_app",
  vignettes = "Vignette_id",
  apps = "App_name"
)
ccs_plot <- plot_ccs(ccs)
```

---

plot\_comprehensiveness

*plot\_comprehensiveness*

---

**Description**

Plots the comprehensiveness for one or multiple symptom checkers

**Usage**

```
plot_comprehensiveness(input)
```

**Arguments**

input                    A dataframe containing the output of get\_comprehensiveness()

**Value**

A ggplot object visualizing the comprehensiveness for either one or multiple symptom checkers

**Examples**

```
data(symptomcheckRdata)
comprehensiveness <- get_comprehensiveness(
  data = symptomcheckRdata,
  triagelevel_advice = "Triage_advice_from_app",
  vector_not_entered = c(NA),
  apps = "App_name"
)
comprehensiveness_plot <- plot_comprehensiveness(comprehensiveness)
```

---

```
plot_inclination_to_overtriage  
  plot_inclination_to_overtriage
```

---

**Description**

Plots the inclination to overtriage for one or multiple symptom checkers

**Usage**

```
plot_inclination_to_overtriage(input)
```

**Arguments**

input            A dataframe containing the output of get\_inclination\_to\_overtriage()

**Value**

A ggplot object visualizing the inclination to overtriage for either one or multiple symptom checkers

**Examples**

```
data(symptomcheckRdata)  
inclination_to_overtriage <- get_inclination_to_overtriage(  
  data = symptomcheckRdata,  
  triagelevel_correct = "Goldstandard_solution",  
  triagelevel_advice = "Triage_advice_from_app",  
  order_triagelevel = c("Emergency", "Non-Emergency", "Self-care"),  
  apps = "App_name"  
)  
overtriage_plot <- plot_inclination_to_overtriage(inclination_to_overtriage)
```

---

```
plot_performance_multiple  
  plot_performance_multiple
```

---

**Description**

Plots the all performance metrics for all symptom checkers in dataframe

**Usage**

```
plot_performance_multiple(
  data,
  triagelevel_correct,
  triagelevel_advice,
  order_triagelevel,
  vector_not_entered,
  vignettes,
  apps
)
```

**Arguments**

<code>data</code>	A dataframe
<code>triagelevel_correct</code>	A string indicating the column name storing the correct triage solutions
<code>triagelevel_advice</code>	A string indicating the column name storing the recommendation of a symptom checker for a case
<code>order_triagelevel</code>	A vector indicating the order of triage levels. The triage level with highest urgency should be the first value and the triage level with lowest urgency the last value.
<code>vector_not_entered</code>	A vector indicating the values in which missing values are coded (e.g., as NA or a specified value such as -99)
<code>vignettes</code>	A string indicating the column name storing the vignette or vignette number
<code>apps</code>	A string indicating the column name storing the app names

**Value**

A ggplot object visualizing all performance metrics for all symptom checkers in dataframe

**Examples**

```
data(symptomcheckRdata)
performance_plot <- plot_performance_multiple(
  data = symptomcheckRdata,
  triagelevel_correct = "Goldstandard_solution",
  triagelevel_advice = "Triage_advice_from_app",
  order_triagelevel = c("Emergency", "Non-Emergency", "Self-care"),
  vector_not_entered = c(NA),
  vignettes = "Vignette_id",
  apps = "App_name"
)
```

---

```
plot_performance_single  
  plot_performance_single
```

---

**Description**

Plots all performance metrics for one symptom checker

**Usage**

```
plot_performance_single(  
  data,  
  triagelevel_correct,  
  triagelevel_advice,  
  order_triagelevel,  
  vector_not_entered  
)
```

**Arguments**

data	A dataframe
triagelevel_correct	A string indicating the column name storing the correct triage solutions
triagelevel_advice	A string indicating the column name storing the recommendation of a symptom checker for a case
order_triagelevel	A vector indicating the order of triage levels. The triage level with highest urgency should be the first value and the triage level with lowest urgency the last value.
vector_not_entered	A vector indicating the values in which missing values are coded (e.g., as NA or a specified value such as -99)

**Value**

A ggplot object visualizing all performance metrics for one symptom checker

**Examples**

```
data(symptomcheckRdata)  
performance_plot <- plot_performance_single(  
  data = symptomcheckRdata,  
  triagelevel_correct = "Goldstandard_solution",  
  triagelevel_advice = "Triage_advice_from_app",  
  order_triagelevel = c("Emergency", "Non-Emergency", "Self-care"),  
  vector_not_entered = c(NA)  
)
```

plot\_safety\_of\_advice *plot\_safety\_of\_advice*

---

**Description**

Plots the safety of advice for one or multiple symptom checkers

**Usage**

```
plot_safety_of_advice(input)
```

**Arguments**

input                    A dataframe containing the output of get\_safety\_of\_advice()

**Value**

A ggplot object visualizing the safety of advice for either one or multiple symptom checkers

**Examples**

```
data(symptomcheckRdata)
safety_of_advice <- get_safety_of_advice(
  data = symptomcheckRdata,
  triagelevel_correct = "Goldstandard_solution",
  triagelevel_advice = "Triage_advice_from_app",
  order_triagelevel = c("Emergency", "Non-Emergency", "Self-care"),
  apps = "App_name"
)
safety_plot <- plot_safety_of_advice(safety_of_advice)
```

---

symptomcheckRdata            *Data on the performance of different symptom checkers*

---

**Description**

Dataset generated by Schmieding et al. that tested different symptom checkers with 45 vignettes in 2020. It includes the solution to the case vignettes and the advice each symptom checker gave.

**Usage**

```
data(symptomcheckRdata)
```



### **Format**

An object of class "data.frame"

**App\_name** The name of the app used in this evaluation)

**Vignette\_id** An identifier referencing the number of each vignette (same numbers indicate the same vignettes)

**Triage\_advice\_from\_app** The triage advice the app recommended for this case (Emergency, Non-Emergency or Self-care)

**Goldstandard\_solution** The goldstandard solution for this vignette

**Correct\_Triage\_Advice\_provided\_from\_app** A Boolean whether the app provided the correct advice)

### **References**

This data set was created by Schmieding et al.: <https://doi.org/10.5281/zenodo.6054092>

### **Examples**

```
data(symptomcheckRdata)
head(symptomcheckRdata)
```

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