

# Package ‘fullROC’

October 13, 2022

**Type** Package

**Title** Plot Full ROC Curves using Eyewitness Lineup Data

**Version** 0.1.0

**Description** Enable researchers to adjust identification rates using the 1/(lineup size) method, generate the full receiver operating characteristic (ROC) curves, and statistically compare the area under the curves (AUC).

References: Yueran Yang & Andrew Smith. (2020). “fullROC: An R package for generating and analyzing eyewitness-lineup ROC curves”. <doi:10.13140/RG.2.2.20415.94885/1> ,  
Andrew Smith, Yueran Yang, & Gary Wells. (2020). “Distinguishing between investigator discriminability and eyewitness discriminability: A method for creating full receiver operating characteristic curves of lineup identification performance”. Perspectives on Psychological Science, 15(3), 589-607. <doi:10.1177/1745691620902426>.

**BugReports** <https://github.com/yuerany/fullROC/issues>

**Language** en-US

**License** GPL (>= 3)

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.1.1

**Imports** stats, graphics

**NeedsCompilation** no

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**Repository** CRAN

**Date/Publication** 2021-01-13 11:50:10 UTC

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auc_boot	<i>Bootstrap AUCs</i>
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### Description

A function to simulate bootstrap samples and calculate AUC.

### Usage

```
auc_boot(
  data,
  group = NULL,
  nboot = 1000,
  byDR = FALSE,
  ca_adj = FALSE,
  lsize = 6,
  csize = 3
)
```

### Arguments

data	A data frame or matrix saving both cp and ca frequencies. cp must precede ca.
group	A vector indicating group membership. Will calculate AUCs by group.
nboot	Number of bootstrap iterations for each group. Defaults to 1,000.
byDR	Whether to order ids by diagnosticity ratios. Defaults to FALSE.
ca_adj	Whether to adjust id rates for ca lineups <i>after</i> simulating a sample from the unadjusted rates.
lsize	Size of lineup (used to adjust id rates). Defaults to 6.
csize	Number of confidence levels (used to adjust id rates). Defaults to 3.

### Value

A list with simulated AUCs.

### Examples

```
cpf <- c(100, 90, 80, 20, 10, 5)
caf <- c(6, 7, 15, 50, 75, 120)
auc_boot(cbind(cpf, caf), nboot = 100)
```

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auc\_ci *Bootstrap confidence intervals for AUC*

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### Description

A function to simulate bootstrap samples and calculate CIs for AUC and differences.

### Usage

```
auc_ci(cpf, caf, group = NULL, nboot = 1000, alpha = 0.05, ...)
```

### Arguments

cpf	A vector of cp frequencies.
caf	A vector of ca frequencies.
group	A vector indicating group membership. Will calculate AUC by group.
nboot	Number of bootstrap iterations. Defaults to 1,000.
alpha	Alpha level for the CIs. Defaults to 0.05.
...	Additional arguments in <code>auc_boot</code> . Will allow users to adjust ca id rates in each simulation.

### Value

A data frame of CIs for each group and group differences.

### References

Yueran Yang & Andrew Smith. (2020). "fullROC: An R package for generating and analyzing eyewitness-lineup ROC curves" doi: [10.13140/RG.2.2.20415.94885/1](https://doi.org/10.13140/RG.2.2.20415.94885/1)

Andrew Smith, Yueran Yang, & Gary Wells. (2020). "Distinguishing between investigator discriminability and eyewitness discriminability: A method for creating full receiver operating characteristic curves of lineup identification performance". *Perspectives on Psychological Science*, 15(3), 589-607. doi: [10.1177/1745691620902426](https://doi.org/10.1177/1745691620902426)

### Examples

```
cpf1 <- c(100, 90, 80, 20, 10, 5)
caf1 <- c(6, 7, 15, 50, 75, 120)
auc_ci(cpf1, caf1, nboot = 50)

cpf2 <- c(90, 40, 20)
caf2 <- c(10, 70, 80)
auc_ci(cpf2, caf2, nboot = 100)

## compare two groups
cpf <- c(cpf1, cpf2)
caf <- c(caf1, caf2)
```

```
group <- rep(letters[1:2], times = c(length(cpf1), length(cpf2) ) )
auc_ci(cpf, caf, group = group)
```

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id\_adj

*Simple adjustment*


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### Description

A function to adjust the id rates for ca lineups using the 1/(lineup size) method; is applicable to ordered id rates with the same confidence levels for all responses.

### Usage

```
id_adj(rate, lsize = 6, csize = 3)
```

### Arguments

rate	ID rate vector.
lsize	Lineup size. Defaults to 6.
csize	Number of confidence levels. Defaults to 3.

### Value

Adjusted ID vector.

### Examples

```
ca_id <- c(rep(0,3), rep(c(0.1, 0.15, 0.25), 2))
id_adj(ca_id)

## change line size to 5
id_adj(ca_id, lsize = 5)

## For multiple groups
ca_id2 <- c(c(rep(0,3), rep(c(0.1, 0.15, 0.25), 2)),
           c(rep(0,3), rep(c(0.1, 0.2, 0.3), 2)) )
group <- rep(c("a", "b"), each = 9)
## Adjust id rates by groups
by(ca_id2, group, id_adj)
```

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id_adj_name	<i>Match by confidence levels</i>
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**Description**

A function to adjust the id rates for ca lineups using the  $1/(\text{lineup size})$  method; match and adjust id rates by names of confidence levels for both filler and suspect ids.

**Usage**

```
id_adj_name(rate, conf = NULL, fid, sid, lsize = 6)
```

**Arguments**

rate	ID rate vector.
conf	Confidence levels for the id rate vector. Default to be NULL.
fid	Mapping confidence levels from filler id.
sid	To-be-matched confidence levels for suspect id. Must have equal length as fid.
lsize	Lineup size. Defaults to 6.

**Value**

Adjusted ID vector.

**Examples**

```
ca_id <- c(rep(0,3), rep(c(0.1, 0.15, 0.25), 2))
names(ca_id) <- paste0(rep(c("IDS", "IDF", "REJ"), each = 3), c("high", "medium", "low"))

fid_conf <- paste0("IDF", c("high", "medium", "low"))
sid_conf <- paste0("IDS", c("high", "medium", "low"))

id_adj_name(ca_id, fid = fid_conf, sid = sid_conf)
```

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id_adj_pos	<i>Match by position</i>
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**Description**

A function to adjust the id rates for ca lineups using the  $1/(\text{lineup size})$  method; match and adjust id rates by positions of filler and suspect ids.

**Usage**

```
id_adj_pos(rate, fid, sid, lsize = 6)
```

**Arguments**

rate	ID rate vector.
fid	Mapping positions from filler id.
sid	To-be-matched positions for suspect id. Must have equal length as fid.
lsize	Lineup size. Defaults to 6.

**Value**

Adjusted ID vector.

**Examples**

```
ca_id <- c(rep(0,3), rep(c(0.1, 0.15, 0.25), 2))
id_adj_pos(ca_id, fid = 4:6, sid = 1:3, lsize = 5)
```

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response\_calculate     *A function to calculate responses from simulated memory distribution*

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**Description**

A function to calculate responses from simulated memory distribution

**Usage**

```
response_calculate(memory, criterion, id_criterion = NULL, suspect = TRUE)
```

**Arguments**

memory	A simulated data matrix with suspect (column 1) and filler memory.
criterion	A vector of judgment criterion. Must have odd number of elements if id_criterion is not specified.
id_criterion	A number to define the criterion for id or rejection. Use the middle element of criterion if not specified.
suspect	Whether there is a designated suspect. Defaults to TRUE.

**Value**

A data matrix of id responses (IDS, IDF, or REJ) and confidence levels.

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response_simu	<i>Simulate witness responses</i>
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### Description

A function to simulate both CP and CA responses

### Usage

```
response_simu(  
  guilt_diff,  
  inno_diff = 0,  
  n_sim = 1000,  
  size = 6,  
  inno_suspect = FALSE,  
  criterion,  
  id_criterion = NULL  
)
```

### Arguments

guilt_diff	Mean difference between guilty suspect and filler distributions.
inno_diff	Mean difference between innocent suspect and filler distributions. Defaults to 0.
n_sim	Number of simulations per condition. Defaults to 1,000.
size	Number of lineup members. Defaults to 6.
inno_suspect	Whether there is a designated innocent suspect. Defaults to FALSE.
criterion	A vector of response criteria. Must have odd number of elements if id_criterion is not specified.
id_criterion	A number to define the criterion for id or rejection. Use the middle element of criterion if not specified.

### Value

A data frame including both CP and CA ID responses and confidence levels.

### Examples

```
## Set up response criteria  
rc1 <- seq(-1, 3, length.out = 5)  
  
## no designated innocent suspect  
response_simu(guilt_diff = 2, criterion = rc1)  
  
## with a designated innocent suspect  
response_simu(guilt_diff = 2, inno_diff = 0.2, inno_suspect = TRUE, criterion = rc1)  
  
## define a criterion for id/rejection instead of using the middle criterion  
response_simu(guilt_diff = 2, criterion = 0:3, id_criterion = 1)
```

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roc_auc	<i>A function to calculate AUC using non-cumulative response rates.</i>
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**Description**

A function to calculate AUC using non-cumulative response rates.

**Usage**

```
roc_auc(cpr, car, group = NULL, byDR = FALSE)
```

**Arguments**

cpr	A vector of cp id rates.
car	A vector of ca id rates.
group	A vector indicating group membership. If specified, will calculate AUC by group.
byDR	Whether to order ids by diagnosticity ratios. Defaults to FALSE.

**Value**

Area under the curve.

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roc_plot	<i>A function to plot ROC curves.</i>
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**Description**

A function to plot ROC curves.

**Usage**

```
roc_plot(cp, ca, group = NULL, byDR = FALSE, grayscale = FALSE, ...)
```

**Arguments**

cp	A vector of cp id rates or frequencies.
ca	A vector of ca id rates or frequencies.
group	Grouping variable to indicate group membership. Will create an ROC curve and calculate AUC for each group.
byDR	Whether to order ids by diagnosticity ratios. Defaults to FALSE.
grayscale	Whether to produce the plot in grayscale. Defaults to FALSE.
...	Additional plotting parameters. For example, users can change x-axis and y-axis labels using xlab and ylab.



**Value**

Plot ROC curves and calculate AUCs as side effects.

**References**

Yueran Yang & Andrew Smith. (2020). "fullROC: An R package for generating and analyzing eyewitness-lineup ROC curves" doi: [10.13140/RG.2.2.20415.94885/1](https://doi.org/10.13140/RG.2.2.20415.94885/1)

Andrew Smith, Yueran Yang, & Gary Wells. (2020). "Distinguishing between investigator discriminability and eyewitness discriminability: A method for creating full receiver operating characteristic curves of lineup identification performance". *Perspectives on Psychological Science*, 15(3), 589-607. doi: [10.1177/1745691620902426](https://doi.org/10.1177/1745691620902426)

**Examples**

```
cpf1 <- c(100, 90, 80, 20, 10, 5)
caf1 <- c(6, 7, 15, 50, 75, 120)
roc_plot(cpf1, caf1)

cpf2 <- c(90, 40, 20)
caf2 <- c(10, 70, 80)
roc_plot(cpf2, caf2)

## plot two ROC curves
cpf <- c(cpf1, cpf2)
caf <- c(caf1, caf2)
group <- rep(letters[1:2], times = c(length(cpf1), length(cpf2)) )
roc_plot(cpf, caf, group = group)
```

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