# Package ‘WrightMap’

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**Type** Package

**Title** IRT Item-Person Map with 'ConQuest' Integration

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**Description** A powerful yet simple graphical tool available in the field of psychometrics is the Wright Map (also known as item maps or item-person maps), which presents the location of both respondents and items on the same scale. Wright Maps are commonly used to present the results of dichotomous or polytomous item response models. The 'WrightMap' package provides functions to create these plots from item parameters and person estimates stored as R objects. Although the package can be used in conjunction with any software used to estimate the IRT model (e.g. 'TAM', 'mirt', 'eRm' or 'IRToys' in 'R', or 'Stata', 'Mplus', etc.), 'WrightMap' features special integration with 'ConQuest' to facilitate reading and plotting its output directly.The 'wrightMap' function creates Wright Maps based on person estimates and item parameters produced by an item response analysis. The 'CQmodel' function reads output files created using 'ConQuest' software and creates a set of data frames for easy data manipulation, bundled in a 'CQmodel' object. The 'wrightMap' function can take a 'CQmodel' object as input or it can be used to create Wright Maps directly from data frames of person and item parameters.

**Depends** R (>= 3.0.0)

**Imports** methods, RColorBrewer

**Encoding** UTF-8

**NeedsCompilation** no

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**Repository** CRAN

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## `CCCfit` *Empirical category characteristic curve plot for the Partial Credit Model*

### Description

The `CCCfit` function is intended for contrasting a Rasch model's expected category characteristic curve against the empirical data from observed responses. The `CCCfit` function displays the expected probability associated with all response categories and plots the observed response proportions for all non-zero response categories.

### Usage

```
CCCfit(itemNumber, observedResponses, personEstimates,
    itemParameters, xlim = c(-4, 4), method = "Quantile", NQtiles = 10)
```

### Arguments

| | |
|---|---|
| `itemNumber` | The position of the item in the test. This position is used to select the column of observed responses and the item difficulty among the item parameters. |
| `observedResponses` | Data frame or matrix with observed responses. The data frame or matrix should be of size N * I, where N is the number of respondents and I is the number of items in the model. |
| `personEstimates` | A vector of length N containing the model based person estimates or predictions. |
| `itemParameters` | A data frame or matrix with I rows (one for each item) and M columns, where M is equal to the maximum number of item scores minus 1. This matrix contains the model based estimates for the step parameters (deltas), where column 1 contains the parameter associated with the step between category 0 versus category 1, column 2 the step parameters of category 1 versus category 2, and so on. |

| | |
|---|---|
| `xlim` | Vector with two values indicating the minimum and maximum values to be used when plotting the item characteristic curve. |
| `method` | Selects the `Quantile` method to group the respondents (see 'Details'). |
| `NQtiles` | This value controls how many grouping will be used: 4 groups cases groups respondents by quartiles, 5 by quintiles, 10 by deciles, etc. |

## Details

The function uses the step difficulty parameters to generate the model based curve. The observed responses are then grouped using the `Quantile` method in order to contrast the model predicted response probability with the observed proportion (this is the only method implemented so far). By default the function uses deciles to generate the respondent groups.

## Author(s)

David Torres Irribarra

## See Also

`ICCfit`

## Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==>  Define data, use random,
##--or do  help(data=index)  for the standard data sets.

## The function is currently defined as
function (itemNumber, observedResponses, personEstimates, itemParameters,
    xlim = c(-4, 4), method = "Quantile", NQtiles = 10)
{
    curve.cols <- paste(RColorBrewer::brewer.pal(n = 8, name = "Dark2"),
        "40", sep = "")
    points.cols <- RColorBrewer::brewer.pal(n = 8, name = "Dark2")
    deltas <- itemParameters[itemNumber, ]
    deltas <- deltas[!is.na(deltas)]
    maxCat <- length(deltas)
    probCCC <- function(theta, deltas) {
        original.length <- length(deltas) + 1
        deltas <- deltas[!is.na(deltas)]
        deltas <- c(0, deltas)
        lN <- length(deltas)
        M <- matrix(rep(NA, lN), ncol = lN)
        CM <- matrix(rep(NA, lN), ncol = lN)
        M[, 1] <- 0
        CM[, 1] <- 1
        for (k in 2:lN) {
            M[, k] <- M[, (k - 1)] + theta - deltas[k]
            CM[, k] <- CM[, (k - 1)] + exp(M[, k])
        }
        output <- exp(M)/CM[, k]
```

```
        length(output) <- original.length
        output
    }
    categoryProbs <- sapply(seq(xlim[1], xlim[2], length = 100),
        probCCC, deltas = deltas)
    plot(seq(xlim[1], xlim[2], length = 100), categoryProbs[1,
        ], type = "n", axes = FALSE, xlab = "Proficiency", ylab = "Proportion",
        ylim = c(0, 1))
    axis(2, las = 1)
    axis(1)
    lines(seq(xlim[1], xlim[2], length = 100), categoryProbs[1,
        ], type = "l", lwd = 3, lty = 1, col = "grey80")
    nCats <- length(deltas) + 1
    for (i in 2:nCats) {
        lines(seq(xlim[1], xlim[2], length = 100), categoryProbs[i,
            ], lwd = 3, col = curve.cols[i - 1])
    }
    if (method == "Quantile") {
        agg.data <- list()
        size.data <- list()
        for (i in 1:maxCat) {
            recodedResponses <- observedResponses == i
            cutPoints <- quantile(personEstimates, seq(0, 1,
                length = NQtiles + 1))
            agg.data[[i]] <- aggregate(recodedResponses, by = list(cut(personEstimates,
                cutPoints)), FUN = mean, na.rm = TRUE)
            breakMeans <- aggregate(personEstimates, by = list(cut(personEstimates,
                cutPoints)), FUN = mean, na.rm = TRUE)
            agg.data[[i]][, 1] <- breakMeans[, 2]
            agg.data[[i]][, -1][agg.data[[i]][, -1] == 1] <- 0.999
            agg.data[[i]][, -1][agg.data[[i]][, -1] == 0] <- 0.001
            size.data[[i]] <- aggregate(is.na(recodedResponses),
                by = list(cut(personEstimates, cutPoints)), FUN = length)
            size.data[[i]][, 1] <- breakMeans[, 2]
            points(agg.data[[i]][, 1], agg.data[[i]][, itemNumber +
                1], type = "b", pch = i, cex = 0.75, col = points.cols[i],
                lwd = 2)
        }
    }
    legend("right", horiz = FALSE, legend = paste("Cat", seq(1:maxCat)),
        col = points.cols[1:maxCat], pch = 1:maxCat, cex = 0.8,
        bty = "n")
    title(paste("Item", itemNumber))
  }
```

---

## `CQmodel` *ConQuest Output Processing*

---

## Description

The CQmodel function reads ConQuest item parameter and person parameter output files and converts them into a list of data frames for more convenient data processing.

## Usage

```
CQmodel(p.est = NULL, show = NULL, p.type = NULL, equation = NULL)
## S3 method for class 'CQmodel'
print(x,...)
## S3 method for class 'SOE'
print(x,...)
```

## Arguments

| | |
|---|---|
| `p.est` | Conquest person parameters file (EAPs, MLEs, etc.). |
| `show` | ConQuest show file. |
| `p.type` | Type of person parameter estimate (EAP, MLE or WLE). If not specified, will try to determine from the extension of the p.est file. |
| `equation` | String giving the model equation, if the Summary of Estimation table was not included in the show file. |
| `x` | Object that determines which function to call. |
| `...` | Additional arguments. |

## Value

CQmodel returns an object of type CQmodel. Usually contains: Tables:

| | |
|---|---|
| `RMP` | A list of data frames containing the response model parameter estimates. One data frame is created for each table in the output. Each data frame contains parameter estimates, errors, and fit information. |
| `GIN` | A matrix containing the item thresholds (if included in the ConQuest output). The rows are items and the columns are steps. |
| `p.est` | A data frame containing the person parameter estimates |

Summary of estimation:

| | |
|---|---|
| `SOE` | A list of various parameters related to the estimation |

Items that may be in the SOE list include:

| | |
|---|---|
| `method` | Estimation method |
| `distribution` | Assumed population distribution |
| `constraint` | Constraint |
| `format` | Specified format of the datafile |
| `equation` | A character string containing the item model (e.g. "item+item*step") |
| `participants` | Sample size |

| | |
|---|---|
| `deviance` | Final deviance of the model |
| `parameters` | Total number of estimated parameters |
| `iterations` | Number of iterations |
| `seed` | Random number generation seed |
| `PV.nodes` | Number of nodes used when drawing PVs |
| `fit.nodes` | Number of nodes used when computing fit |
| `n.plausible.values` | Number of plausible values drawn |
| `max.iterations.no.improvement` | Maximum number of iterations without a deviance improvement |
| `max.steps` | Maximum number of Newton steps in M-step |
| `zero.perfect.value` | Value for obtaining finite MLEs for zero/perfects |
| `termination.reason` | Reason for iteration termination |
| `max.iterations` | |
| `parameter.change` | |
| `deviance.change` | |

Run details:

| | |
|---|---|
| `run.details` | A list of details of the run |

Items that may be included in the run.details list include:

| | |
|---|---|
| `date` | The date of the ConQuest run |
| `data.file` | The name of the datafile used |
| `format` | The specified format of the datafile |
| `names` | Names of items and/or dimensions |

Additional items:

| | |
|---|---|
| `deviance` | The deviance of the model |
| `equation` | A character string containing the model specification (e.g. "item+item*step") |
| `participants` | The number of participants |
| `parameters` | The number of parameters |
| `title` | The run title |
| `reg.coef` | Regression coefficients |
| `rel.coef` | Reliability coefficients |
| `variances` | |
| `nDim` | Number of dimensions |
| `dimensions` | Dimension names |
| `p.est.type` | |

## Author(s)

Rebecca Freund and David Torres Irribarra

## Examples

```
fpath <- system.file("extdata", package="WrightMap")

# Partial credit model
model1 <- CQmodel(p.est = file.path(fpath,"ex2.eap"),
show = file.path(fpath,"ex2.shw"))
model1 #Shows what tables are available

model1$SOE #Summary of estimation
model1$equation # Model specification
model1$reg.coef # Regression coefficients
model1$rel.coef # Reliability coefficients
model1$variances # Variances

names(model1$RMP) # Names of parameter tables
head(model1$RMP$item) #Item parameters
head(model1$RMP$"item*step") #Item by step parameters

# Complex model
model2 <- CQmodel(file.path(fpath,"ex4a.mle"),
file.path(fpath,"ex4a.shw"))
model2$equation # Model specification
names(model2$RMP) # Names of parameter tables
head(model2$RMP$"rater*topic*criteria*step") #An interaction table

model1$GIN #Item thresholds
model2$GIN #Item thresholds

head(model1$p.est)  ##EAPs
head(model2$p.est)  ##MLEs
```

---

# `extract.deltas` *Extract Master's Delta parameters from a TAM model.*

## Description

This function takes as its input a TAM object. It adds reads the TAM item parameters and organizes them into a matrix that can be used as input in the `CCCfit` function.

## Usage

```
extract.deltas(tamObject)
```

## Arguments

| | |
|---|---|
| `tamObject` | TAM object containing the results of a a Rasch model or Partial Credit model. |

## Details

This function organizes the item parameter results into a matrix where each row is contains the parameters associated with an item and each columns is contains the parameters associated with a specific step (score 0 vs score 1, score 1 vs score 2, etc.). The resulting matrix will have as many rows as items and as many columns as the maximum number of steps among the items.

## Value

A matrix in which each row is an item and each column is a step

## Author(s)

David Torres Irribarra

## References

Masters, G. N. (1982). A Rasch model for partial credit scoring. *Psychometrika*, 47(2), 149-174.

## See Also

`CCCfit` `make.thresholds`

## Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==>  Define data, use random,
##--or do  help(data=index)  for the standard data sets.

## The function is currently defined as
function (tamObject)
{
    delta.long <- tamObject$xsi
    n.deltas <- apply(tamObject$B, 1, max)
    delta.mat <- matrix(NA, nrow = length(n.deltas), ncol = max(n.deltas))
    matCoords.row <- rep(1:length(n.deltas), n.deltas)
    matCoords.col <- c()
    for (i in 1:length(n.deltas)) {
        for (j in 1:n.deltas[i]) {
            matCoords.col <- c(matCoords.col, j)
        }
    }
    delta.long$matCoords.row <- matCoords.row
    delta.long$matCoords.col <- matCoords.col
    for (k in 1:nrow(delta.long)) {
     delta.mat[delta.long$matCoords.row[k], delta.long$matCoords.col[k]] <- delta.long$xsi[k]
    }
    delta.mat
```

```
}
```

---

`fitgraph` *Item Fit Graphs*

---

## Description

This function creates a graphical summary of the item fit information.

## Usage

```
## Default S3 method:
fitgraph(fitEst, fitLB, fitUB, itemLabels, mainTitle = "Fit Plot",
pch = 18, fitColours = c("gray70", "gray60", "gray50", "gray40", "gray0"),
xlab = "Items", cex = 1.25, ...)
## S3 method for class 'numeric'
fitgraph(fitEst, fitLB, fitUB, itemLabels, mainTitle = "Fit Plot",
pch = 18, fitColours = c("gray70", "gray60", "gray50", "gray40", "gray0"),
xlab = "Items", cex = 1.25, ...)
## S3 method for class 'CQmodel'
fitgraph(fitEst, table = NULL, fit.type = "W", itemLabels = NULL, ...)
## S3 method for class 'character'
fitgraph(fitEst, ...)
```

## Arguments

fitgraph arguments:

| | |
|---|---|
| `fitEst` | vector of item fit estimates. Could also be a CQmodel object or name of a ConQuest show file. |
| `fitLB` | vector of lower bounds for critical intervals for each item. |
| `fitUB` | vector of upper bounds for critical intervals for each item. |
| `itemLabels` | vector of item labels. |
| `mainTitle` | string containing the title of the plot. |
| `pch` | number or vector indicating the type of symbols to be used for each item. |
| `fitColours` | Color that will be used to shade the critical inteval area. |
| `xlab` | Label of the x-axis. The default is ‘items‘. |
| `cex` | Size of the x-axis label. |
| `...` | Additional parameters. |

Argument to use when passing a CQmodel object:

| | |
|---|---|
| `table` | Name of the RMP table that for which the fit will be plotted. By default `fitgraph` will plot the first RMP table of the CQmodel object, this argument overrides this default. |

| | |
|---|---|
| `fit.type` | Type of fit estimate that will be used, it can be `W` for Weighted Fit (i.e. Infit, the default), or `U` for Unweighted Fit (i.e. Outfit). Called `type` in previous versions; use of that parameter is deprecated to avoid collision with the `type` parameter in the `link{plot}` function. |

## Author(s)

David Torres Irribarra and Rebecca Freund.

## References

Wilson, M. (2005). Constructing measures: An item response modeling approach.

## Examples

```
# Generating mock data
sampleLabels <- paste('item',1:10)

fitBounds <- (abs(rnorm(10, mean = 0, sd = .05)) * 2)
fitEst <- rnorm(10, mean = 1, sd = .1)

fitLB <- 1 - fitBounds
fitUB <- 1 + fitBounds
par("mar")
# running fitgraph
fitgraph(fitEst,fitLB,fitUB,itemLabels=sampleLabels)

#From ConQuest output:

fpath <- system.file("extdata", package="WrightMap")

fitgraph(file.path(fpath,"ex2.shw"))
```

---

# `ICCfit` *Empirical item characteristic curve plot for the Rasch Model~*

## Description

The `ICCfit` function is intended for contrasting a Rasch model's expected item characteristic curve against the empirical data from dichotomous responses. The `ICCfit` function displays a confidence interval for the model based curve and plots the confidence interval for the empirical proportions.

## Usage

```
ICCfit(itemNumber, observedResponses, personEstimates,
    itemParameters, xlim = c(-4, 4), method = "Quantile", NQtiles = 10)
```

## Arguments

| | |
|---|---|
| `itemNumber` | The position of the item in the test. This position is used to select the column of observed responses and the item difficulty among the item parameters. |
| `observedResponses` | Data frame or matrix with observed responses. The data frame or matrix should be of size N * I, where N is the number of respondents and I is the number of items in the model. |
| `personEstimates` | A vector of length N containing the model based person estimates or predictions. |
| `itemParameters` | A data frame or matrix of dimensions I * 2 containing the model based item difficulty estimates in the firs column and the parameter standard error in the second column. |
| `xlim` | Vector with two values indicating the minimum and maximum values to be used when plotting the item characteristic curve. |
| `method` | Selects the method used to group the respondents: `Quantile` (default), `ByPersonEstimate`, and `Histogram` (see 'Details'). |
| `NQtiles` | When using the `Quantile` method this value controls how many grouping will be used: 4 groups cases groups respondents by quartiles, 5 by quintiles, 10 by deciles, etc. |

## Details

The function uses the item difficulty parameter to generate the model based curve and the item difficulty parameter standard error to plot a confidence interval around the curve. The observed responses are then grouped using the selected method in order to contrast the model predicted response probability with the observed proportion. By default the function uses deciles to generate the respondent groups. The function allows the method `ByPersonEstimate` in order to make a different group for each observed person estimate (potentially useful when analyzing test data with large numbers with no missing data), and the `Histogram` method, which uses the Freedman-Diaconis algorithm to select the width of the bands used for grouping.

## Author(s)

David Torres Irribarra

## See Also

`CCCfit`

## Examples

```
# Simulate 1000 persons and 5 items with 2 levels (Rasch model)
set.seed(123)
simulated_data <- sim.PCM(pN = 1000, iN = 5, lN = 2)

# Extract simulated item responses and abilities
observed_responses <- simulated_data$resp - 1
person_abilities <- simulated_data$theta
```

```
item_params <- cbind(simulated_data$delta[,2],rep(0.08),5)
# Defining a 0.08 of error for the item parameters,
# this usually would be estimated.

# Plot the ICC for the first item using the Quantile method
ICCfit(itemNumber = 1,
       observedResponses = observed_responses,
       personEstimates = person_abilities,
       itemParameters = item_params,
       method = "Quantile",
       NQtiles = 10)
```

---

## `item.person.data` *Processing CQmodel objects for plotting*

### Description

The `itemData` and `personData` functions take CQmodel objects (or ConQuest output files) as inputs and return a vector or matrix. They were originally developed for use by `wrightMap`, but are separated out here to allow the outputs to be sent to other plotting functions.

### Usage

```
itemData(thresholds, ...)
## Default S3 method:
itemData(thresholds, item.type = "deltas",...)
## S3 method for class 'character'
itemData(thresholds, p.type = NULL, equation = NULL, ...)
## S3 method for class 'CQmodel'
itemData(thresholds, item.table = NULL, interactions = NULL,
step.table = NULL, item.type = "default", throld = 0.5, ...)

personData(thetas,...)
## Default S3 method:
personData(thetas,...)
## S3 method for class 'character'
personData(thetas, p.type = NULL,...)
## S3 method for class 'CQmodel'
personData(thetas,...)
```

### Arguments

itemData arguments:

| | |
|---|---|
| `thresholds` | Usually, a CQmodel object or the name of a ConQuest show file. Will also accept a matrix, but this is only really for use within other functions. In general `make.thresholds` should be used instead. |
| `item.type` | Indicates whether to use `thresholds` or `deltas`. |
| `equation` | string giving the model equation, if the Summary of Estimation table was not included in the show file. |
| `item.table` | Name of RMP table to use for the main effect of the item parameters. |
| `interactions` | Name of RMP interaction table to use in addition to `item.table`. |
| `step.table` | Name of RMP table to use in addition to `item.table`. |
| `throld` | The probability level to be used for calculating thresholds. |
| `...` | Additional parameters to pass to `make.thresholds`. |

personData arguments:

| | |
|---|---|
| `thetas` | a CQModel object or the name of the Conquest person parameters file (EAPs, MLEs, etc.) |
| `p.type` | Type of person parameter estimate (EAP, MLE or WLE). |

## Details

The itemData and personData functions are usually called by `wrightMap`. They can also be called directly.

For the itemData function, note that the `item.table`, `interactions`, and `step.table` parameters must be the exact name of specific RMP tables. You cannot specify an interactions table or a step table without also specifying an item table (although JUST an item table is fine). If your model equation is more complicated, you will have to either use a GIN table or specify in the function call which tables to use for what. A model of the form item + item * step + booklet, for example, will not run unless there is a GIN table or you have defined at least the item.table.

## Value

The itemData functions return a vector of item parameters, or a matrix in which the rows are items and the columns are steps. The personData functions return a vector of person paramenters, or a matrix in which the rows are persons and the columns are dimensions.

## Author(s)

Rebecca Freund and David Torres Irribarra

## See Also

`item.side` `person.side` `make.thresholds` `make.deltas` `wrightMap`

## Examples

```
#As a call from wrightMap:

fpath <- system.file("extdata", package="WrightMap")

model1 <- CQmodel(file.path(fpath,"ex2a.eap"), file.path(fpath,"ex2a.shw"))
# Making thresholds if there are no GIN tables (partial credit model)
wrightMap(model1, type = "thresholds")

#Complex model:

model2 <- CQmodel(file.path(fpath,"ex4a.mle"), file.path(fpath,"ex4a.shw"))
wrightMap(model2, item.table = "rater")
wrightMap(model2, item.table = "rater", interactions = "rater*topic",
  step.table = "topic")


# Plotting item results

fpath <- system.file("extdata", package="WrightMap")
model3 <- CQmodel(file.path(fpath,"ex2a.eap"), file.path(fpath,"ex2a.shw"))
m3.item <- itemData(model3)

dev.new(width=10, height=10)

#control of oma allows us to give more space to longer item names
itemModern(m3.item, label.items.srt= 90, oma = c(2,0,0,2))
itemClassic(m3.item)
itemHist(m3.item)

m3.person <- personData(model3)
personHist(m3.person)
personDens(m3.person)
```

---

# `item.side` *Wright Map Item Sides*

## Description

Draw the item side of a Wright Map in a variety of styles. Intended to be primarily called by `wrightMap`, but also available for use on their own.

## Usage

```
itemModern(thr, yRange = NULL, axis.items = "Items", show.thr.sym = TRUE
, thr.sym.cex = 0.8, thr.sym.lwd = 1, thr.sym.pch = 23
, thr.sym.col.fg = rgb(0, 0, 0, 0.3), thr.sym.col.bg = rgb(0, 0, 0, 0.3)
, show.thr.lab = TRUE, thr.lab.pos = c(2, 4), thr.lab.text = NULL
```

```
, thr.lab.col = "black", thr.lab.cex = 0.5, thr.lab.font = 2, label.items.rows = 1
, label.items.srt = 0, label.items = NULL, label.items.cex = 0.6
, label.items.ticks = TRUE, axis.logits = "Logits", show.axis.logits = "R"
, axis.logits.cex = 0.7, oma = c(0, 0, 0, 3), cutpoints = NULL
, vertLines = FALSE, vertLines.par = list(), cutpoints.par = list()
, thr.sym.par = list(), thr.lab.par = list(), label.items.par = list()
, axis.logits.par = list(), logits.text.par = list(), ...)

itemClassic(thr, yRange = NULL, axis.items = "Items", axis.logits = "Logits"
, show.axis.logits = "R", axis.logits.cex = 0.7, oma = c(0, 0, 0, 3)
, cutpoints = NULL, cutpoints.par = list(), label.items = NULL, label.steps = NULL
, label.sep = ".", thr.lab.sep = " | ", thr.lab.par = list(), axis.logits.par = list()
, logits.text.par = list(), pad.char = "_", font.family = "mono", ...)

itemHist(thr, yRange = NULL, axis.items = "Items", axis.logits = "Logits"
, show.axis.logits = "R", axis.logits.cex = 0.7, oma = c(0, 0, 0, 3)
, cutpoints = NULL, axis.logits.par = list(), logits.text.par = list()
, cutpoints.par = list(), ...)
```

## Arguments

General arguments:

| | |
|---|---|
| `thr` | A vector or matrix of threshold parameters. If a matrix, items should be in rows and steps in columns. |
| `yRange` | A vector with 2 elements specifying the lower and upper limits of the plot's y-axis. |
| `label.items` | A vector of strings representing the item labels used in itemModern and itemClassic |
| `axis.items` | The title of the x-axis. |
| `axis.logits` | The title of the y-axis. |
| `axis.logits.cex` | The size of the logit values on the y-axis. |
| `show.axis.logits` | If set to "R" or "L", draws a logit axis on the right or left. Will also draw an axis on the right if the value is `TRUE`. If any other value, the axis is not drawn. |
| `oma` | Values to use for the `oma` parameter (see `par`). |
| `cutpoints` | Values at which to draw horizontal lines (see `cutLines`). |
| `label.items.par` | A list of parameters to further customize item labels. |
| `axis.logits.par` | A list of parameters for customizing the logit axis. |
| `logits.text.par` | A list of parameters for customizing the logit axis text. |
| `...` | Additional arguments passed to `cutLines`. |

Specific to `itemModern`:

| | |
|---|---|
| `show.thr.sym` | Logical. If `TRUE` (default), the plot will show symbols for the item thresholds. |
| `thr.sym.cex` | An integer, vector, or matrix of numerical values indicating the magnification of the threshold symbols. |
| `thr.sym.lwd` | An integer, vector, or matrix of positive numbers specifying the width of the lines used in the threshold symbols. |
| `thr.sym.pch` | An integer, vector, or matrix specifying a symbol or single character used to represent item thresholds. |
| `thr.sym.col.fg` | An integer, vector, or matrix of numerical values indicating the foreground color for the threshold symbols. |
| `thr.sym.col.bg` | An integer, vector, or matrix of numerical values indicating the background color for the threshold symbols. |
| `show.thr.lab` | Logical. If `TRUE` (default), the plot will show labels for the item thresholds. |
| `thr.lab.pos` | An integer, vector, or matrix indicating the position for displaying the threshold labels. Values 1, 2, 3, and 4 indicate below, left, above, and right, respectively. |
| `thr.lab.text` | A matrix containing the text labels for the item thresholds, where each row represents an item, and each column represents a level. |
| `thr.lab.col` | A matrix specifying the color for each threshold label. |
| `thr.lab.cex` | A numerical value indicating the magnification factor for the threshold labels. |
| `thr.lab.font` | An integer or matrix specifying the font type for the threshold labels. 1 = plain, 2 = bold, 3 = italic, 4 = bold italic. |
| `label.items.rows` | An integer specifying the number of rows used to display the item labels (default: 1). Useful when item labels overlap. |
| `label.items.srt` | Angle of rotation for item labels. Only applicable if `label.items.rows` is set to 1. |
| `label.items.cex` | A numerical value specifying the magnification factor for the item labels. |
| `label.items.ticks` | Logical. If `TRUE` (default), ticks are drawn on the x-axis for the item side. |
| `vertLines` | Logical. If `TRUE`, vertical lines are drawn to mark all symbols associated with an item. |
| `vertLines.par` | A list of parameters (e.g., `col`, `lwd`, `lty`) to control the appearance of the vertical lines. |
| `cutpoints.par` | A list of parameters (e.g., `col`, `lwd`, `lty`) to customize the cutpoint lines. |
| `thr.sym.par` | A list of parameters to further customize threshold symbols. |
| `thr.lab.par` | A list of parameters to further customize threshold labels. |

Specific to `itemClassic`:

| | |
|---|---|
| `label.steps` | A vector specifying the labels for the threshold steps. |
| `label.sep` | A string indicating the separator used between item labels and step labels. |
| `thr.lab.sep` | A string indicating the separator used between threshold labels for different items. |
| `pad.char` | A character used to pad item labels to a fixed width. |
| `font.family` | A string specifying the font family for the item labels (default: `mono`). |

## Details

These functions are designed as helper functions for `wrightMap` to draw the item side of a map. When called outside of that function, they can be used to create more customized maps. Possible uses include:

- Draw an item map on its own.
- Compare two item maps in a single figure.
- Draw a Wright Map with the item side on the left and the person side on the right.

## Note

When combining with a `person.side` function, note that those functions use `split.screen`, which are incompatible with `layout` and some other plotting functions. Ensure that all graphs on a single plot have their `yRange` explicitly specified to maintain comparable values across plots.

## Author(s)

Rebecca Freund and David Torres Irribarra

## See Also

`wrightMap`, `person.side`, `itemData`

## Examples

```
#As a call from wrightMap:

## Mock results
uni.proficiency <- rnorm(1000, mean =  -0.5, sd = 1)

items.loc <- sort(rnorm(20))
thresholds <- data.frame(
  l1 = items.loc - 0.5,
  l2 = items.loc - 0.25,
  l3 = items.loc + 0.25,
  l4 = items.loc + 0.5
)

## Setting up labels, colors, and symbols
thresholds.labels <- data.frame(
  l1 = paste('Lev', rep(1, 20), sep = ''),
  l2 = paste('Lev', rep(2, 20), sep = ''),
  l3 = paste('Lev', rep(3, 20), sep = ''),
  l4 = paste('Lev', rep(4, 20), sep = '')
)

thresholds.colors <- data.frame(
  l1 = rep('green', 20),
  l2 = rep('red', 20),
  l3 = rep('yellow', 20),
  l4 = rep('blue', 20)
```

```
)

thresholds.symbols <- data.frame(
  l1 = rep(15, 20),
  l2 = rep(16, 20),
  l3 = rep(17, 20),
  l4 = rep(18, 20)
)

wrightMap(uni.proficiency, thresholds,
  thr.lab.text = thresholds.labels,
  thr.lab.col = as.vector(as.matrix(thresholds.colors)),
  thr.sym.pch = thresholds.symbols
)

# Direct call:

## Plotting results of a unidimensional Rating Scale Model
items.loc <- sort(rnorm(20))
thresholds <- data.frame(
  l1 = items.loc - 0.5,
  l2 = items.loc - 0.25,
  l3 = items.loc + 0.25,
  l4 = items.loc + 0.5
)

itemModern(thresholds)
itemClassic(thresholds)
itemHist(thresholds)
```

---

## `make.deltas` *Calculate Master's Delta parameters.*

---

### Description

This function takes as its input a CQmodel object or the name of a ConQuest show file. It adds together the parameters as specified by the user, or if no tables are specified it reads the model equation to determine the appropriate tables to sum. This function is used by wrightMap to draw the item side of the map when a CQmodel is passed to wrightMap.

### Usage

```
make.deltas(item.params, ...)
## S3 method for class 'character'
make.deltas(item.params, ...)
## S3 method for class 'CQmodel'
make.deltas(item.params, item.table = NULL, interactions = NULL,
step.table = NULL, item.sign = NULL, inter.sign = NULL,
step.sign = NULL, ...)
```

```
## Default S3 method:
make.deltas(item.params, cross.params = 0, step.params = 0,
item.sign = 1, step.sign = 1, inter.sign = 1, ...)
```

## Arguments

| | |
|---|---|
| `item.params` | The item parameters. Can either be a vector, a CQmodel object, or a path to a ConQuest show file |
| `item.table` | If item.params is a CQmodel object or a path to a ConQuest show file, item.table is the name of the items table. Commonly "item" but can be any string representing the name of a table in the ConQuest show file. This identifies what variable will form the rows of the delta matrix. If not specified, will be the first variable mentioned in the model equation. |
| `interactions` | If item.params is a CQmodel object or a path to a ConQuest show file, item.table is the name of the table with the interactions (if present). Commonly "item*step" but can be any string containing "*" that is the name of a table in the ConQuest show file. Should be the product of the item.table variable and the step.table variable (if present). If not specified, will be the product term of the model equation. |
| `step.table` | If item.params is a CQmodel object or a path to a ConQuest show file, step.table is the name of the steps table (if present). Commonly "step" but can be any string representing the name of a table in the ConQuest show file. This identifies what variable will form the columns of the delta matrix. If not specified, will be the second variable mentioned in the model equation. |
| `item.sign` | Can be 1 or -1. Indicates whether the item parameters should be added or subtracted. |
| `inter.sign` | Can be 1 or -1. Indicates whether the interaction parameters should be added or subtracted. |
| `step.sign` | Can be 1 or -1. Indicates whether the step parameters should be added or subtracted. |
| `cross.params` | If item.params is a vector, use this parameter to pass a matrix of interaction parameters. |
| `step.params` | If item.params is a vector, use this parameter to pass a matrix of step parameters. |
| `...` | Additional parameters |

## Details

This function reshapes the tables in the ConQuest show file and adds the step parameters to the appropriate items. The vector version of this is rarely called by the user.

## Value

A matrix in which each row is an item and each column is a step

## Author(s)

Rebecca Freund & David Torres Irribarra

## See Also

`make.thresholds` `CQmodel` `wrightMap`

## Examples

```
fpath <- system.file("extdata", package="WrightMap")

# Partial credit model
model1 <- CQmodel(file.path(fpath,"ex2a.eap"), file.path(fpath,"ex2a.shw"))
make.deltas(model1)

# Rating scale model
model2 <- CQmodel(file.path(fpath,"ex2b.eap"), file.path(fpath,"ex2b-2.shw"))
make.deltas(model2)

# Raters, criteria, topics
model3 <- CQmodel(file.path(fpath,"ex4a.mle"), file.path(fpath,"ex4a.shw"))
make.deltas(model3, item.table = "rater")
make.deltas(model3, item.table = "rater", interactions = "rater*topic", step.table = "topic")
```

---

# `make.thresholds` *Calculate Thurstonian thresholds.*

## Description

This function accepts a matrix of delta parameters and converts them to thresholds (using a threshold of .5). It can also take as input a CQmodel object or a filename of a ConQuest show file.

## Usage

```
make.thresholds(item.params, ...)
## S3 method for class 'character'
make.thresholds(item.params, design.matrix = "normal",...)
## S3 method for class 'CQmodel'
make.thresholds(item.params,item.table = NULL, interactions = NULL
,step.table = NULL, design.matrix = "normal", throld = 0.5, alpha = 1,...)
## Default S3 method:
make.thresholds(item.params, design.matrix = "normal"
, make.from = "deltas", theta.interval = c(-10, 10), throld = 0.5, alpha = 1
, c.params = 0,...)
## S3 method for class 'matrix'
make.thresholds(item.params, design.matrix = "normal"
, make.from = "deltas", theta.interval = c(-10, 10), throld = 0.5
, alpha = 1, c.params = 0,...)
```

## Arguments

| | |
|---|---|
| `item.params` | The item parameters. Can either be a matrix, a CQmodel object, or a path to a ConQuest show file |
| `design.matrix` | Can be "normal" or "ConQuest". Note that for a CQmodel object or ConQuest file, should be normal, NOT ConQuest. |
| `make.from` | Specifies whether the item.params matrix contains threshold or delta parameters. |
| `item.table` | If item.params is a CQmodel object or a path to a ConQuest show file, item.table is the name of the items table. Commonly "item" but can be any string representing the name of a table in the ConQuest show file. This identifies what variable will form the rows of the thresholds matrix. If not specified, will be the first variable mentioned in the model equation. |
| `interactions` | If item.params is a CQmodel object or a path to a ConQuest show file, item.table is the name of the table with the interactions (if present). Commonly "item*step" but can be any string containing "*" that is the name of a table in the ConQuest show file. Should be the product of the item.table variable and the step.table variable (if present). If not specified, will be the product term of the model equation. |
| `step.table` | If item.params is a CQmodel object or a path to a ConQuest show file, step.table is the name of the steps table (if present). Commonly "step" but can be any string representing the name of a table in the ConQuest show file. This identifies what variable will form the columns of the thresholds matrix. If not specified, will be the second variable mentioned in the model equation. |
| `theta.interval` | If item.params is a matrix, theta.interval specifies over what interval to search for the parameters. |
| `throld` | The probability level to use for calculating the thresholds. |
| `alpha` | A vector or single value for the slope parameter or parameters. |
| `c.params` | A vector or single value for the guessing parameter or parameters. |
| `...` | Additional parameters. |

## Value

A matrix of threshold parameters.

## Author(s)

Daniel Coulter Furr, Rebecca Freund, & David Torres Irribarra

## See Also

`make.deltas` `itemData` `CQmodel` `wrightMap`

## Examples

```
fpath <- system.file("extdata", package="WrightMap")

# Partial credit model
```

```
model1 <- CQmodel(file.path(fpath,"ex2a.eap"), file.path(fpath,"ex2a.shw"))
deltas <- make.deltas(model1)
make.thresholds(deltas)
make.thresholds(model1)
```

---

## `person.side` *Wright Map person sides*

### Description

Draw the person side of a Wright Map in a variety of styles. Intended to be primarily called by `wrightMap`, but also available for use on their own.

### Usage

```
personHist(thetas, yRange = NULL, breaks = "FD", dim.lab.cex = 0.6, dim.lab.side = 3
  , dim.lab.adj = 0.5, dim.names = NULL, dim.color = "white", person.points = NULL
  , person.range = NULL, p.point.col = "gray45", p.range.col = "gray75"
  , axis.persons = "Respondents", show.axis.persons = FALSE
  , axis.persons.par = list(), oma = c(0, 5, 0, 5), axis.logits = "Logits"
  , show.axis.logits = TRUE,...)

personDens(thetas, yRange = NULL, dim.lab.cex = 0.6, dim.lab.side = 3, dim.lab.adj = 0.5
  ,dim.names = NULL,dim.color = "black",person.points = NULL, person.range = NULL
  , p.point.col = "black", p.range.col = "gray70", oma = c(0, 5, 0, 5)
  , axis.logits = "Logits", show.axis.logits = TRUE
  , axis.persons = "Respondents",...)
```

### Arguments

| | |
|---|---|
| `thetas` | vector or matrix of person parameters. If a matrix, persons should be the rows and dimensions the columns. |
| `yRange` | vector with 2 elements specifying the lower and upper limits of the plot's y-axis. |
| `dim.lab.cex` | An integer specifying the amount the dimension labels should be magnified relative to the default. |
| `dim.lab.side` | An integer specifying which side to plot the dimension names. Values of 1, 2, 3 (default), and 4, respectively, indicate positions below, to the left of, above, and to the right of the person distributions. |
| `dim.lab.adj` | A numerical value adjusting the position of the dimension names. |
| `dim.names` | A string or a vector of strings containing the names of each dimension. |
| `dim.color` | A numerical value or vector indicating the colors to be used for representing each dimension. |
| `person.points` | A vector of individual values to highlight. |

| | |
|---|---|
| `person.range` | A pair of values, an even-length vector, or a matrix with two rows. Values indicate the start and endpoints of ranges to highlight. If a matrix, the first row should be lower bounds and the second row upper bounds of the ranges. If a vector, the values should alternate: (lower1, upper1, lower2, upper2, ...). |
| `p.point.col` | A string or vector of strings indicating the color to use for the highlighted points. |
| `p.range.col` | A string or vector of strings indicating the color to use for the highlighted ranges. |
| `axis.persons` | The title of the y-axis on the left side. |
| `show.axis.persons` | Logical indicating whether to show the persons axis on the left side. Default is `FALSE`. |
| `axis.persons.par` | A list of parameters to customize the appearance of the persons axis. This can include options such as `cex.axis`, `las`, and others as supported by the `axis` function. |
| `oma` | Values to use for the `oma` parameter (see `par`). |
| `show.axis.logits` | Logical indicating whether to show the logit axis. |
| `axis.logits` | The title of the y-axis on the right side. |
| `...` | Additional arguments passed to other methods (e.g., `cutLines`). |

For `personHist`:

| | |
|---|---|
| `breaks` | A parameter passed to the `hist` function to define the binning of the histogram. |

## Details

These functions are designed as helper functions for `wrightMap` and `ppPlot` to draw the person side of a map. When called outside of those functions, they can be used to create more customized maps. Possible uses include:

- Drawing a person map on its own
- Comparing two person maps in a single figure
- Drawing a Wright Map with the item side on the left and the person side on the right

The `personHist` style, the default, draws the person distribution as a histogram. The `personDens` style draws a density plot.

The `person.points`, `person.range`, `p.point.col`, and `p.range.col` parameters can highlight specific values or ranges, either when called directly or via `ppPlot`.

## Author(s)

Rebecca Freund and David Torres Irribarra

## See Also

`item.side` `personData` `wrightMap` `ppPlot`

### Examples

```
# Creating a Wright Map with item side on the left

multi.proficiency <- data.frame(
  d1 = rnorm(1000, mean =  -0.5, sd = 1),
  d2 = rnorm(1000, mean =   0.0, sd = 1),
  d3 = rnorm(1000, mean =  +0.5, sd = 1))


items.loc <- sort( rnorm( 20))
thresholds <- data.frame(
  l1 = items.loc - 0.5 ,
  l2 = items.loc - 0.25,
  l3 = items.loc + 0.25,
  l4 = items.loc + 0.5)

  # split.screen: Set up a split screen with the left side 80 percent of the screen
  # yRange = c(-3,4): Set the yRange to be the same for both sides
  # axis.logits.side = "L": Move the item logit axis to the left
  # oma = c(0,0,0,2): Adjust the spacing between the graphs
  # mtext("Wright Map", side = 3, font = 2, line = 1): add a title
  # screen(2): Start drawing on the second screen

  split.screen(figs = matrix(c(0,.8,0,1,.8,1,0,1),ncol = 4, byrow = TRUE))
  itemModern(thresholds, yRange = c(-3,4), show.axis.logits = "L", oma = c(0,0,0,2))
  mtext("Wright Map", side = 3, font = 2, line = 1)
  screen(2)
  personHist(multi.proficiency, axis.persons = "", yRange = c(-3,4)
    , axis.logits = "Persons", show.axis.logits = FALSE)

  ## Creating a multidimensional Wright Map with each dimension separate

  ## Mock results

  d1 = rnorm(1000, mean =  -0.5, sd = 1)
  d2 = rnorm(1000, mean =   0.0, sd = 1)

  dim1.diff <- rnorm(5)
  dim2.diff <- rnorm(5)

  split.screen(figs = matrix(c(0,.1,0,1, .12,.6,0,1, .5,.6,0,1, .5,1,0,1)
    ,ncol = 4,byrow = TRUE))

  personDens(d1, yRange = c(-3,3), show.axis.logits = FALSE, axis.logits = "")
  screen(2)
  itemModern(dim1.diff, yRange = c(-3,3), show.axis.logits = FALSE)
  mtext("Wright Map", side = 3, font = 2, line = 1)
  screen(3)
  personDens(d2, yRange = c(-3,3), show.axis.logits = FALSE
    , axis.logits = "", axis.persons = "", dim.names = "Dim2")
  screen(4)
  itemModern(dim2.diff, yRange = c(-3,3), show.axis.logits = FALSE
```

```
        , label.items = paste("Item", 6:10))
```

---

## plotCI *Plotting confidence intervals and DIF*

### Description

The `plotCI` function is intended for graphing confidence intervals. The `difplot` function is a wrapper for `plotCI` specifcally intended for examining Differential Item Functioning from ConQuest output.

### Usage

```
plotCI(ests, errors, labels = "", zeroline = TRUE, incol = "gray", outcol = "blue"
, main.title = "Statistical Significance Plot", axes = FALSE, xlab = "", pch = 16, ...)
## Default S3 method:
difplot(data, grouptype = NULL, group = NULL, item.names = NULL
, ylim = c(-1, 1), ylab = NULL, ...)
## S3 method for class 'CQmodel'
difplot(data, table.name = NULL, grouptype = NULL
, group = NULL, ...)
## S3 method for class 'character'
difplot(data, equation, ...)
```

### Arguments

`plotCI` parameters:

| | |
|---|---|
| `ests` | vector of point estimates. |
| `errors` | vector of standard errors. |
| `labels` | vector of labels for the items. |
| `zeroline` | logical indicating whether to draw a line at zero. |
| `incol` | color of intervals containing zero. |
| `outcol` | color of intervals not containing zero. |
| `main.title` | title of the plot. |
| `axes, xlab, pch` | parameters passed to `plot`. |

`difplot` parameters:

| | |
|---|---|
| `data` | A `CQmodel` object or the name of a ConQuest show file. Can also be a table of parameters taken from ConQuest output. |
| `table.name` | The RMP table to use for parameters. Should be an interactions table. |
| `grouptype` | The name of the demographic variable (e.g. “gender”). |
| `group` | The name of the group to test for DIF (e.g. “male”). |

| | |
|---|---|
| `item.names` | vector of item names. |
| `equation` | string specifying the model equation, if the Summary of Estimation table was not included in the show file. |
| `ylim`, `ylab` | more parameters passed to `plot`. |
| `...` | additional parameters to pass to `plot`. |

## Details

The `plotCI` function takes point estimates and standard errors as inputs and plots 95 percent confidence intervals in relation to a zero-line. By default, it colors the intervals gray if they include zero, and blue if they do not. The `difplot` function is a wrapper for `plotCI` specifcally intended for examining Differential Item Functioning from ConQuest output and expects tables formatted exactly like ConQuest output to work correctly. For plotting DIF from other statistical packages, it is recommended to use `plotCI` directly.

## Author(s)

David Torres Irribarra and Rebecca Freund

## Examples

```
#Plotting confidence intervals

ests <- rnorm(10,sd = .5)
errors <- runif(10,min = .1,max = .5)
plotCI(ests,errors,ylim = c(-3,3))

#DIF plot:

fpath <- system.file("extdata", package="WrightMap")

# equation must be specified because there is no summary of estimation
# table in this example
difplot(file.path(fpath,"ex6a.shw"), equation = "item-gender+item*gender")
```

---

# `ppPlot` *Person probability plots*

## Description

Plots a Wright Map for a single person (similar to a kidmap). On the person side, highlights their estimated ability and a range of one standard error. On the item side, draws lines representing item difficulties at which they are expected to have a 20%, 40%, 50%, 60%, and 80% chance of success.

## Usage

```
ppPlot(thetas, thresholds, est, SE, main.title = "Person Probability Plot"
, cut.left = 0, cut.right = .94, cut.lab.adj = c(1,.5),...)

cutLines(cutpoints = NULL,cut.left = 0, cut.right = 1, cut.lab.text = NULL
, cut.lab.adj = c(0,1),...)
```

## Arguments

| | |
|---|---|
| `thetas` | a vector, matrix or data frame of person parameter estimates. Can also be a character string specifying a ConQuest output file of person parameter estimates, or a CQmodel object. Will be sent to the function `personData`. |
| `thresholds` | matrix or data frame of item parameter estimates. Can also be a character string specifying a ConQuest show file. Will be sent to the function `itemData`. |
| `est` | estimated ability of the person |
| `SE` | standard error of the estimate |
| `main.title` | title of the Person Probability Plot. |
| `cut.left` | value between 0 and 1 describing where to place the lefthand side of the cutpoints, as a fraction of the item plot. |
| `cut.right` | value between 0 and 1 describing where to place the righthand side of the cutpoints, as a fraction of the item plot. |
| `cut.lab.adj` | similar to the `adj` parameter in `text`, describes where to place the text for the cutpoints as a pair of values between 0 and 1 in terms of left-right and up-down alignment. Left-right alignment is 0 for the left side of the item plot and 1 for the right side, while up-down alignment is 0 for below the line and 1 for above the line. |
| `cutpoints` | argument to `cutLines` when called through `wrightMap` or one of the `item.side` functions. Specifies locations of cutlines. When `cutLines` is called through `ppPlot`, the cutpoints are calculated rather than specified. |
| `cut.lab.text` | argument to `cutLines` when called through `wrightMap` or one of the `item.side` functions. Specifies text to appear for each cut line. When `cutLines` is called through `ppPlot`, the text is always the percent chance of success given the estimated ability level and difficulty location. |
| `...` | additional arguments to pass to `wrightMap` or its associated functions. |

## Details

The `ppPlot` function is a wrapper for `wrightMap` that is specifically designed for person probability plots, and as such has access to all the parameters of wrightMap and its associated functions. It uses the `person.points`, `person.range`, `p.point.col`, and `p.range.col` parameters on the `person.side` function to draw a range of one standard error around the estimated ability level. On the item side, it calculates at what item difficulty the respondent is expected to have a 20%, 40%, 50%, 60%, and 80% chance of success and then uses the `cutLines` function to illustrate these cutpoints. The cutLines function should not be called on its own and may be hidden in future versions. It is included here to show the available parameters, which can be included in a call to `wrightMap` or any of the `item.side` functions.

### Author(s)

David Torres Irribarra and Rebecca Freund

### See Also

`wrightMap`

### Examples

```
fpath <- system.file("extdata", package="WrightMap")
model1 <- CQmodel(p.est = file.path(fpath,"ex2.eap"), show = file.path(fpath,"ex2.shw"))

#Person histogram, modern item
ppPlot(model1,est = 0, SE = 1)

#Person density, classic item
ppPlot(model1,est = 0, SE = 1, person.side = personDens,item.side = itemClassic)
```

---

## `sim.PCM` *Simulate Item Responses for Partial Credit and Rasch Models with Varying Levels*

---

### Description

Simulate polytomous item responses based on item difficulty thresholds (`delta`) and person abilities (`theta`) for the Partial Credit Model (PCM) and the Rasch Model as a special case. The function allows items to have varying numbers of levels, making it useful for generating data in contexts such as item response theory (IRT) models for polytomous items (e.g., Likert scales).

### Usage

```
sim.PCM(pN, iN, lN, itemLevels = NULL, delta = NULL, delta.l = NULL, theta = NULL)
```

### Arguments

| | |
|---|---|
| `pN` | `integer`. The number of people (respondents) to simulate. |
| `iN` | `integer`. The number of items in the test or survey. |
| `lN` | `integer`. The default number of levels (categories) for each polytomous item. Must be greater than or equal to 2. This is used if `itemLevels` is not provided. |
| `itemLevels` | `integer vector`. An optional vector specifying the number of levels for each item. If provided, the length must equal `iN`. If not provided, all items are assumed to have `lN` levels. |
| `delta` | `matrix`. An optional matrix of item thresholds with dimensions `iN` by the maximum number of levels in `itemLevels`. If not provided, the function will generate thresholds internally. The first column must contain zeros or the function will automatically prepend a column of zeros. If provided as a vector, it will be converted into a single-column matrix. |

| | |
|---|---|
| `delta.l` | `numeric` `vector`. An optional vector of common level thresholds (with length `lN - 1`). This vector represents the difficulty of each level. If not provided, the function will generate it. |
| `theta` | `numeric` `vector`. An optional vector of person abilities. If not provided, abilities will be drawn from a standard normal distribution (mean = 0, sd = 1). |

## Details

This function generates polytomous item responses using a logistic IRT model. It first creates or uses given person abilities (`theta`) and item thresholds (`delta`). Responses are simulated by computing the probability of a person responding in each category of an item based on their ability and the item's threshold. The function allows for items to have different numbers of response categories through the `itemLevels` argument.

## Value

A list with the following components:

| | |
|---|---|
| `pN` | The number of people (respondents). |
| `iN` | The number of items. |
| `lN` | The default number of levels (categories) for the polytomous items. |
| `itemLevels` | A vector specifying the number of levels for each item. |
| `M` | A list of `iN` matrices containing logits (differences between person ability and item threshold) for each person and item. |
| `CM` | A list of `iN` matrices containing cumulative probabilities for each person and item. |
| `U` | A `pN` by `iN` matrix of uniform random values used to generate the responses. |
| `theta` | A numeric vector of person abilities. |
| `delta.l` | (Optional) A vector of common level thresholds if it was generated internally. |
| `delta.il` | (Optional) A matrix of item-specific deviations for thresholds if `delta.l` was generated internally. |
| `delta` | A matrix of item thresholds. |
| `resp` | A `pN` by `iN` matrix of simulated responses. Each entry corresponds to the level chosen by the person for the respective item. |

## Author(s)

David Torres Irribarra

## See Also

`runif`, `rnorm`

## Examples

```
# Simulate 100 respondents, 5 items, and 3 levels (e.g., Likert scale with 3 options)
simulated_data <- sim.PCM(pN = 100, iN = 5, lN = 3)

# Simulate with custom item thresholds
custom_delta <- matrix(c(-0.5, -1, -2, 1, 0.5, 1), nrow = 3)
simulated_data_custom <- sim.PCM(pN = 50, iN = 3, lN = 3, delta = custom_delta)

# Simulate with custom person abilities
custom_theta <- rnorm(100, mean = 0, sd = 1.5)
simulated_data_theta <- sim.PCM(pN = 100, iN = 5, lN = 3, theta = custom_theta)

# Rasch model simulation (dichotomous items)
# 50 persons with abilities ranging from -3 to 3
rasch_theta <- seq(-3, 3, length.out = 50)
rasch_delta <- matrix(c(0,1.5,0,-1,0,0.5,0,-0.5,0,1,0,-1.5,0,2,0,-2,0,0.8,0,-0.8)
                      , ncol = 2, byrow = TRUE)
simulated_rasch <- sim.PCM(pN = 50, iN = 10, lN = 2, delta = rasch_delta, theta = rasch_theta)

# Simulation with items having different numbers of levels
# 4 items with 5 levels, 3 items with dichotomous responses, and 3 items with 3 levels
# Simulate with a total of 10 items and varying levels
simulated_mixed_levels <- sim.PCM(pN = 50, iN = 10, lN = 5,
                                  itemLevels = c(5, 5, 5, 5, 2, 2, 2, 3, 3, 3))
```

---

# `WrightMap` *Wright Map: IRT Item-Person Map*

## Description

This package allows the easy generation of ‘Wright Maps’ (named after Ben Wright), also known as item-person maps to display unidimensional and multidimensional assessment results. These maps represent simultaneously the proficiency distribution of respondents and the item difficulty parameters as estimated by a model of the Rasch Family. The package contains several other functions for graphing common IRT statistics.

Additionally, the package contains the `CQmodel` function, which reads output files created using ConQuest software and creates a set of data frames for easy data manipulation, bundled in a CQmodel object. The wrightMap function can take a CQmodel object as input or it can be used to create Wright Maps directly from data frames of person and item parameters.

## Details

| | |
|---|---|
| Package: | WrightMap |
| Type: | Package |
| Version: | 1.0 |
| Date: | 2014-03-02 |
| License: | BSD_3_clause \| LICENSE |

The wrightMap function relies on two main inputs: (a) `thetas`: a vector or matrix of respondent proficiences, and (b) `thresholds`: a vector or matrix of item thresholds. In the simplest case, say for a unidimensional Rasch model, `thetas` can be a vector of person proficiencies and `thresholds` a vector of item difficulties.

To plot multiple dimensions of person proficiency, simply provide them as a matrix were the results for each dimension is stored in a different column, such that for a 3-dimensional model with 1,000 persons, `theta` is a matrix of 1000 rows and 3 columns.

To plot polytomous items, the thresholds for each level must be passed to the functions through the `thresholds` matrix, where each row represents an item and each column represents a level. For instance, if the results of a Rating Scale model with 5 response categories and 10 items is being plotted, the `thresholds` matrix will have 10 rows and 4 columns ( column one represents the thresholds between the 1 and 2 response category, column 2 the threshold between categories 2 and 3, etc.).

Alternatively, wrightMap can read directly the `.shw` and `.eap/.mle/.wle` output files from a Conquest analysis, and will automatically generate the `thetas` and `thresholds` matrices.

## Author(s)

David Torres Irribarra and Rebecca Freund

Maintainer: David Torres Irribarra <dti@berkeley.edu> and Rebecca Freund <rlfreund@berkeley.edu>

## References

Andrich, D. (1978). A rating formulation for ordered response categories. *Psychometrika*, *43*(4), 561–573. Masters, G. N. (1982). A Rasch model for partial credit scoring. *Psychometrika*, *47*(2), 149–174. Wilson, M. (2005). Constructing measures: An item response modeling approach. Wright, B. D., & Stone, M. H. (1979). *Best test design.* Chicago: Mesa Press.

## Examples

```
# Plotting results of a unidimensional Rasch Model

## Mock results
uni.proficiency <- rnorm(1000, mean =  -0.5, sd = 1)
difficulties  <- sort( rnorm( 20))

## Default map
wrightMap( uni.proficiency, difficulties)

## Density version
wrightMap( uni.proficiency, difficulties, person.side = personDens)

# Plotting results of a multidimensional Rasch Model

## Mock results
multi.proficiency <- data.frame(
d1 = rnorm(1000, mean =  -0.5, sd = 1),
```

```
d2 = rnorm(1000, mean =   0.0, sd = 1),
d3 = rnorm(1000, mean =  +0.5, sd = 1))

difficulties  <- sort( rnorm( 20))

dev.new(width=10, height=10)
wrightMap( multi.proficiency, difficulties)

# Plotting results of a unidimensional Rating Scale Model

## Mock results
uni.proficiency <- rnorm(1000, mean =  -0.5, sd = 1)

items.loc <- sort( rnorm( 20))
thresholds <- data.frame(
l1 = items.loc - 0.5,
l2 = items.loc - 0.25,
l3 = items.loc + 0.25,
l4 = items.loc + 0.5)

dev.new(width=10, height=10)
wrightMap( uni.proficiency, thresholds)

## Setting up labels, colors and symbols

thresholds.labels <- data.frame(
l1 = paste('Lev',rep(1,20),sep = ''),
l2 = paste('Lev',rep(2,20),sep = ''),
l3 = paste('Lev',rep(3,20),sep = ''),
l4 = paste('Lev',rep(4,20),sep = ''))

thresholds.colors <- data.frame(
l1 = rep(  'green',20),
l2 = rep(    'red',20),
l3 = rep( 'yellow',20),
l4 = rep(   'blue',20))

thresholds.symbols <- data.frame(
l1 = rep( 15,20),
l2 = rep( 16,20),
l3 = rep( 17,20),
l4 = rep( 18,20))

dev.new(width=10, height=10)
wrightMap( uni.proficiency, thresholds
, thr.lab.text = thresholds.labels
, thr.lab.col = as.vector(as.matrix(thresholds.colors))
, thr.sym.pch = thresholds.symbols
)
```

---

## `wrightMap` *wrightMap: item-person maps*

---

### Description

This function allows the easy generation of ‘Wright Maps’ (named after Ben Wright), also known as item-person maps. They are used to to display unidimensional and multidimensional assessment results. These maps represent simultaneously the proficiency distribution of respondents and the item difficulty parameters as estimated by a model of the Rasch family.

### Usage

```
wrightMap(thetas, thresholds = NULL, item.side = itemModern, person.side = personHist
,  main.title = "Wright Map", min.logit.pad = 0.25, max.logit.pad = 0.25, min.l = NULL
, max.l = NULL, item.prop = 0.8, return.thresholds = TRUE, new.quartz = FALSE
, use.hist = NULL,...)
## S3 method for class 'CQmodel'
plot(x, ...)
```

### Arguments

The parameters documented here do not include many of the options included in the Wright Map family of functions. For graphical parameters, see `item.side` and `person.side`. For data handling, see `item.person.data` and `CQmodel`.

wrightMap parameters:

| | |
|---|---|
| `thetas` | a vector, matrix or data frame of person parameter estimates. Can also be a character string specifying a ConQuest output file of person parameter estimates, or a CQmodel object. Will be sent to the function `personData`. |
| `thresholds` | matrix or data frame of item parameter estimates. Can also be a character string specifying a ConQuest show file. Will be sent to the function `itemData`. |
| `item.side` | function to use to draw the item side of the map. Currently included options are itemModern (default), itemClassic (for ConQuest-style Wright Maps) and itemHist. See `item.side` for details. |
| `person.side` | function to use to draw the person side of the map. Currently included options are personHist (default), to draw the person distribution as a histogram, and personDens, which draws a density plot. See `person.side` for details. |
| `main.title` | title of the Wright Map. |
| `min.logit.pad` | numeric value indicating how much of the lower end of the logit scale should be included in the plot. |
| `max.logit.pad` | numeric value indicating how much of the upper end of the logit scale should be included in the plot. |
| `min.l` | numeric value for fixing the lower end of the logit scale. It overrides the automatic detection of the range and the `min.logit.pad` correction. |

| | |
|---|---|
| `max.l` | numeric value for fixing the upper end of the logit scale. It overrides the automatic detection of the range and the `max.logit.pad` correction. |
| `item.prop` | numeric value greater than 0 and smaller than 1 indicating the proportion of the plot to be allocated to the item part of the Wright Map. |
| `return.thresholds` | logical. Determines whether the to return or not the numeric values used to position the parameters on the item side of the Wright Map. Enabled by default. |
| `new.quartz` | logical. Determines whether the wrightMap will be created on a new graphical device or if it will reuse one already open. By default is set to `FALSE` to avoid creating new devices. |
| `use.hist` | deprecated. Use the `person.side` parameter instead |
| `...` | Additional arguments to pass to `personData`, `itemData`, `person.side`, or `item.side` |

wrightMap can also be called by passing a CQmodel object to plot:

| | |
|---|---|
| `x` | CQmodel object to pass to plot |

## Author(s)

David Torres Irribarra and Rebecca Freund

## References

Wilson, M. (2005). Constructing measures: An item response modeling approach. Wright, B. D., & Stone, M. H. (1979). *Best test design.* Chicago: Mesa Press.

## See Also

`person.side` `item.side` `personData` `itemData`

## Examples

```
# Plotting results of a unidimensional Rasch Model

## Mock results
  uni.proficiency <- rnorm(1000, mean =  -0.5, sd = 1)
  difficulties  <- sort( rnorm( 20))

## Default map
wrightMap( uni.proficiency, difficulties)

## Density version
wrightMap( uni.proficiency, difficulties, person.side = personDens)


# Plotting results of a multidimensional Rasch Model

## Mock results
  multi.proficiency <- data.frame(
    d1 = rnorm(1000, mean =  -0.5, sd = 1),
```

```
    d2 = rnorm(1000, mean =   0.0, sd = 1),
    d3 = rnorm(1000, mean =  +0.5, sd = 1))

  difficulties  <- sort( rnorm( 20))

dev.new(width=10, height=10)
wrightMap( multi.proficiency, difficulties)

# Plotting results of a unidimensional Rating Scale Model

## Mock results
  uni.proficiency <- rnorm(1000, mean =  -0.5, sd = 1)

  items.loc <- sort( rnorm( 20))
  thresholds <- data.frame(
    l1 = items.loc - 0.5 ,
    l2 = items.loc - 0.25,
    l3 = items.loc + 0.25,
    l4 = items.loc + 0.5)

wrightMap( uni.proficiency, thresholds)



    ####ConQuest integration###

   fpath <- system.file("extdata", package="WrightMap")

   #Partial credit model:

model1 <- CQmodel(p.est = file.path(fpath,"ex2.eap"), show = file.path(fpath,"ex2.shw"))
wrightMap(model1)

# Rating scale model:
model2 <- CQmodel(file.path(fpath,"ex2b.eap"), file.path(fpath,"ex2b-2.shw"))
wrightMap(model2, label.items.row = 2)

  # Complex model
model3 <- CQmodel(file.path(fpath,"ex4a.mle"), file.path(fpath,"ex4a.shw"))
wrightMap(model3, min.logit.pad = -29, person.side = personDens)


  ### Skip CQmodel
wrightMap(file.path(fpath,"ex2a.eap"), file.path(fpath,"ex2a.shw"),
  label.items.row = 3)
```

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