

Plot of a treatment comparisons network in R

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Version: 2.1**Author:** Antonis Mairgiotis**Description:** Function that plots a network of treatment comparisons.

Functions	Usage
mtm.networkplot.fun	plot of a network
Support package	
network	
Example dataset	
Dataset from clinical trials of antihypertensive drugs [W. Elliot et. al, 2007]	

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DESCRIPTION:

This R function plots a network of comparisons. Each treatment is represented by a node, and there are links between nodes that represent studies comparing pairs of treatments. The size of the link is proportional to the number of the studies and the size of the nodes could be proportional to the sample size randomized in each treatment (optional).

USAGE:

```
mtm.networkplot.fun(c1,c2,percomparison,nameoftreatments,VAR1,
graphtitle,thickness,nodetextsize,nodesize)
```

REQUIRED ARGUMENTS:

c1, c2: the first two arguments depend on the third argument (**percomparison**) and correspond to one of the following data formats.

A) If **percomparison=TRUE** then the user has to supply two vectors **t1, t2** where:

t1: the treatment in the first arm of a comparison

t2: the treatment in the second arm of a comparison

Studies with $N > 2$ arms should be included in the first format by specifying all the $\binom{N}{2}$ comparisons.

B) If **percomparison=FALSE** then the user has to supply two vectors **ID, t** where:

ID: the study ID column

t: the treatment vector

OPTIONAL ARGUMENTS:

nameoftreatments: The user can specify the names of the treatments in a vector of characters. By default the names are "treat.1", "treat.2"...

VAR: This optional argument can be used to plot the size of each node according to a treatment characteristic e.g by providing a vector with the sample size randomized in each treatment. The default is to plot the node proportional to the number of trials that include the given treatment.

thickness: To change (proportionally) the thickness of the edges, set this parameter larger (for increasing thickness) or smaller (for decreasing thickness) than the default value 10.

nodetextsize: To change (proportionally) the text size of the node label, set this parameter larger (for increasing the font) or smaller (for decreasing the font) than the default value 1.

nodesize: To change (proportionally) the size of the nodes, set this parameter larger (for increasing size) or smaller (for decreasing size) than the default value 5.

graphtitle: if the user wants to add a title, has to specify this as an argument, unless the plot will be drawn without a title.

NOTE: The plot is editable if transferred to PowerPoint or in an image processing tool.

VALUE:

The network of the interventions is plotted.

WARNING:

When large values given to the `nodetextsize` argument (e.g. larger than 4) the graph might be forced out of the margins.

EXAMPLES

If the user wants to run the A-C examples, the following dataset in appropriate `t1`, `t2` format is available:

```
t1<-c(1,1,1,1,1,1,1,1,1,1,1,7,1,1,1,1,1,1,3,2,3)
t2<- c(2,3,4,4,5,5,8,8,8,8,10,7,9,9,9,10,6,6,3,4)
```

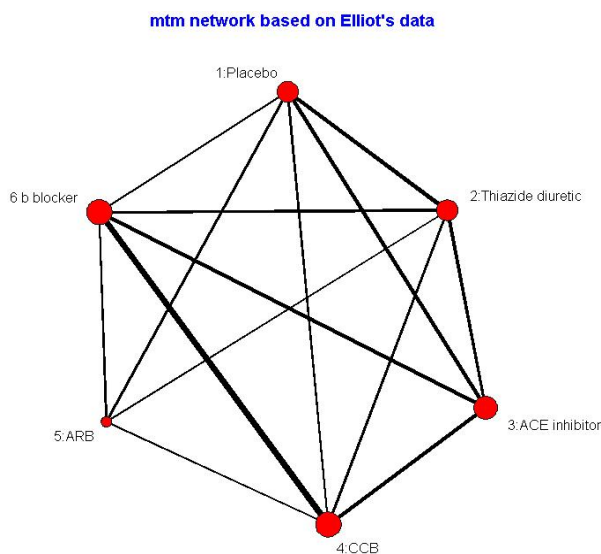
For the other examples (D-I), the following dataset (Elliot's dataset) is available:

```
ID <-c(1, 1, 1, 2, 2, 2, 3, 3, 4, 4, 5, 5, 6, 6, 7, 7, 8, 8, 9, 9, 10,
10, 11, 11, 12, 12, 13, 13, 14, 14, 15, 15, 16, 16, 16, 17, 17, 18, 18,
19, 19, 20, 20, 21, 21, 21, 22, 22)
t<-c(3, 6, 4, 3, 4, 2, 5, 2, 3, 2, 6, 4, 3, 6, 5, 1, 3, 1, 2, 1, 4, 1, 6,
2, 3, 1, 4, 2, 6, 4, 5, 6, 6, 2, 1, 6, 4, 3, 1, 5, 1, 2, 1, 3, 6, 4, 5,
4)
```

The names of the treatments are:

```
names<- ("1:Placebo", "2:Thiazidediuretic", "3:ACEinhibitor", "4:CCB",
"5:ARB", "6b blocker")
```

```
A) mtm.networkplot.fun(t1,t2,T)
B) mtm.networkplot.fun (t1,t2,T,nameoftreatments)
C) mtm.networkplot.fun (t1,t2,T,nameoftreatments,VAR1)
D) mtm.networkplot.fun (ID,t,F)
E) mtm.networkplot.fun (ID,t,F,nameoftreatments)
F) mtm.networkplot.fun (ID,t,F,nameoftreatments,VAR1)
G) mtm.networkplot.fun (ID,t,F,thickness=7)
H) mtm.networkplot.fun (ID,t,F,nodetextsize=0.7)
I) mtm.networkplot.fun (ID,t,F,nodesize=3)
J) mtm.networkplot.fun (ID,t,F,graphtitle="mtm network based on
Elliot's data")
```



REFERENCES

W. J. Elliot, P. M. Meyer, "Incident diabetes in clinical trials of antihypertensive drugs: a network meta-analysis", *Lancet* 2007; 369; 201-07