

A guide to robust statistical methods in neuroscience: Figure 6

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Mancini et al. (2014) report results aimed at providing a whole-body mapping of spatial acuity for pain. Here, we provide additional results based on the data from their second experiment. The sample size is $n = 10$. Briefly, spatial acuity was assessed by measuring 2-point discrimination (2PD) thresholds for both pain and touch in 11 body territories.

The data can also be downloaded here:

Mancini, Flavia (2016): ANA_mancini14_data.zip. figshare. <https://doi.org/10.6084/m9.figshare.3427766.v1>

Dependencies

```
library(ggplot2)
library(cowplot)
library(tibble)
source("../code/Rallfun-v40.txt")
source("../code/theme_gar.txt")
source("../code/xtrafun.R")
```

Make figure

get data

```
Man = read.table(file='./data/Man_try.tex',skip=1,header=T)
```

make data frame 1: marginal distributions

```
DT <- Man[,13:18] # discrimination thresholds
colnames(DT) <- c('FH', 'S', 'FA', 'H', 'B', 'T')
Participants <- seq(1,nrow(DT))
df <- as_tibble(cbind(DT,Participants))
df$Participants <- as.factor(df$Participants)
df <- tidyr::gather(df, Positions, Thresholds, -Participants) # make long format
df$Positions <- as.factor(df$Positions)
df$Positions <- keeporder(df$Positions)
dfA <- df
```

data frame of summary statistics

medians

Summarise each column using the Harrell-Davis estimate of the 50th quantile.

```
tmp <- as_tibble(DT)
df.hd <- enframe(apply(tmp, 2, hd), name="Positions", value="Thresholds")
df.hd$Positions <- as.factor(df.hd$Positions)
```

Use the median instead

```
tmp <- as_tibble(DT)
df.md <- enframe(apply(tmp, 2, median), name="Positions", value="Thresholds")
df.md$Positions <- as.factor(df.md$Positions)
```

means

```
tmp <- as_tibble(DT)
df.mn <- enframe(apply(tmp, 2, mean, trim = 0), name="Positions", value="Thresholds")
df.mn$Positions <- as.factor(df.mn$Positions)
```

parameters for plots

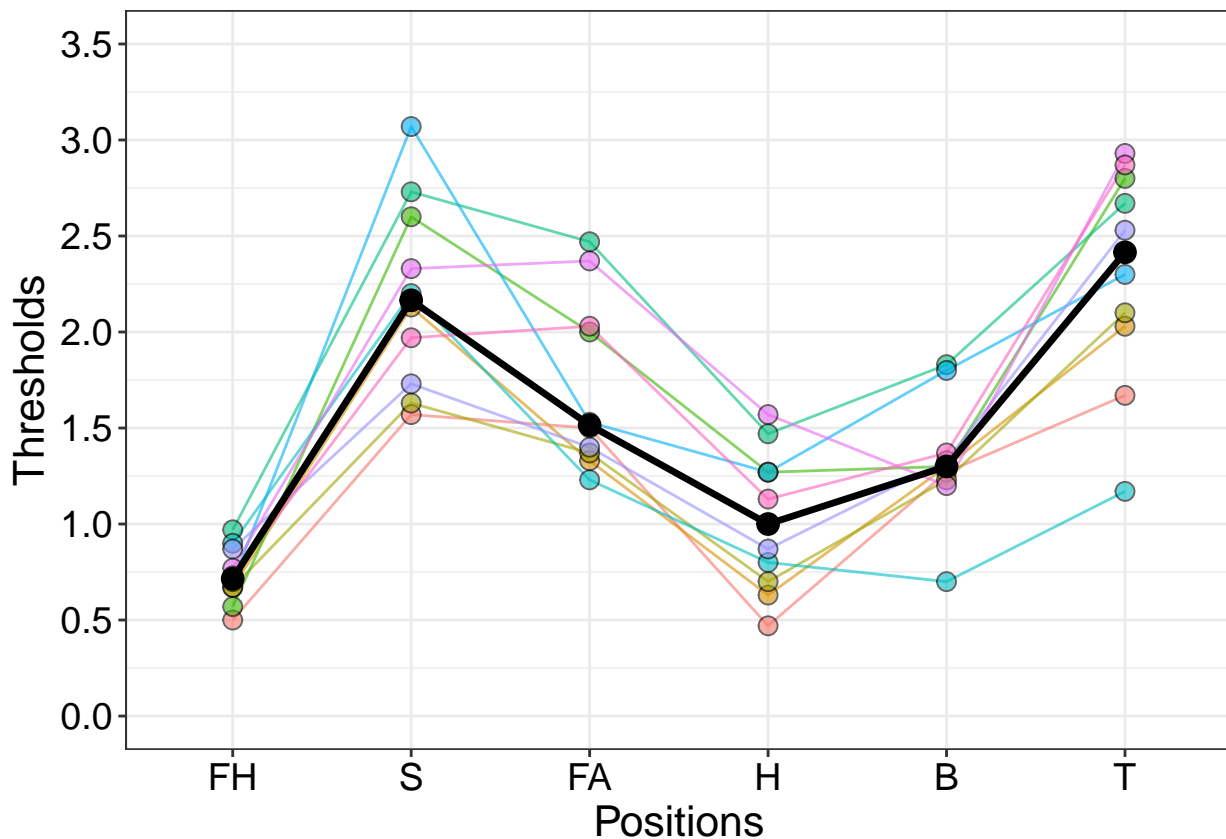
```
axis_size <- 14
axis_title_size <- 16
```

panel A: marginals

```
pA <- ggplot(dfA, aes(x=Positions, y=Thresholds)) + theme_gar +
  geom_line(size = 0.5, aes(group = Participants, colour = Participants),
    alpha = .6) +
  geom_point(aes(fill = Participants, shape = 21, size = 3,
    colour = "black", alpha = .6) +
  theme(axis.text = element_text(size = axis_size),
    axis.title = element_text(size = axis_title_size),
    legend.position = "none") +
  scale_y_continuous(limits = c(0,3.5), breaks = seq(0,3.5,0.5)) +
  xlab("Positions") +
  # superimpose medians
  geom_line(data = df.md, aes(group = 1), linewidth = 1.2) +
  geom_point(data = df.md, aes(group = 1), size = 3.5)
```

```
## Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
## i Please use `linewidth` instead.
```

```
# # superimpose means
# geom_line(data = df.mn, aes(group = 1), linewidth = 1, colour = "grey") +
# geom_point(data = df.mn, aes(group = 1), size = 2, colour = "grey")
pA
```



make data frame 2: difference distributions

```
# compute all pairwise differences
J <- ncol(DT)
n <- nrow(DT)
Jm <- J-1
d <- (J^2-J)/2
con <- matrix(0,J,d)
newnames <- vector(mode = "character", length = d)
cnames <- c('FH', 'S', 'FA', 'H', 'B', 'T')
id<-0
for (j in 1:Jm){
  jp <- j+1
  for (k in jp:J){
    id<-id+1
    con[j,id] <- 1
    con[k,id] <- 0-1
    newnames[id] <- paste(cnames[j], '-', cnames[k], sep = "")
  }
}
xx <- matl(DT)%*%con

# make data frame
colnames(xx) <- newnames
df <- as_tibble(xx)
df <- tidyr::gather(df, Contrasts, Differences) # make long format
df$Contrasts <- as.factor(df$Contrasts)
df$Contrasts <- keeporder(df$Contrasts)
dfB <- df

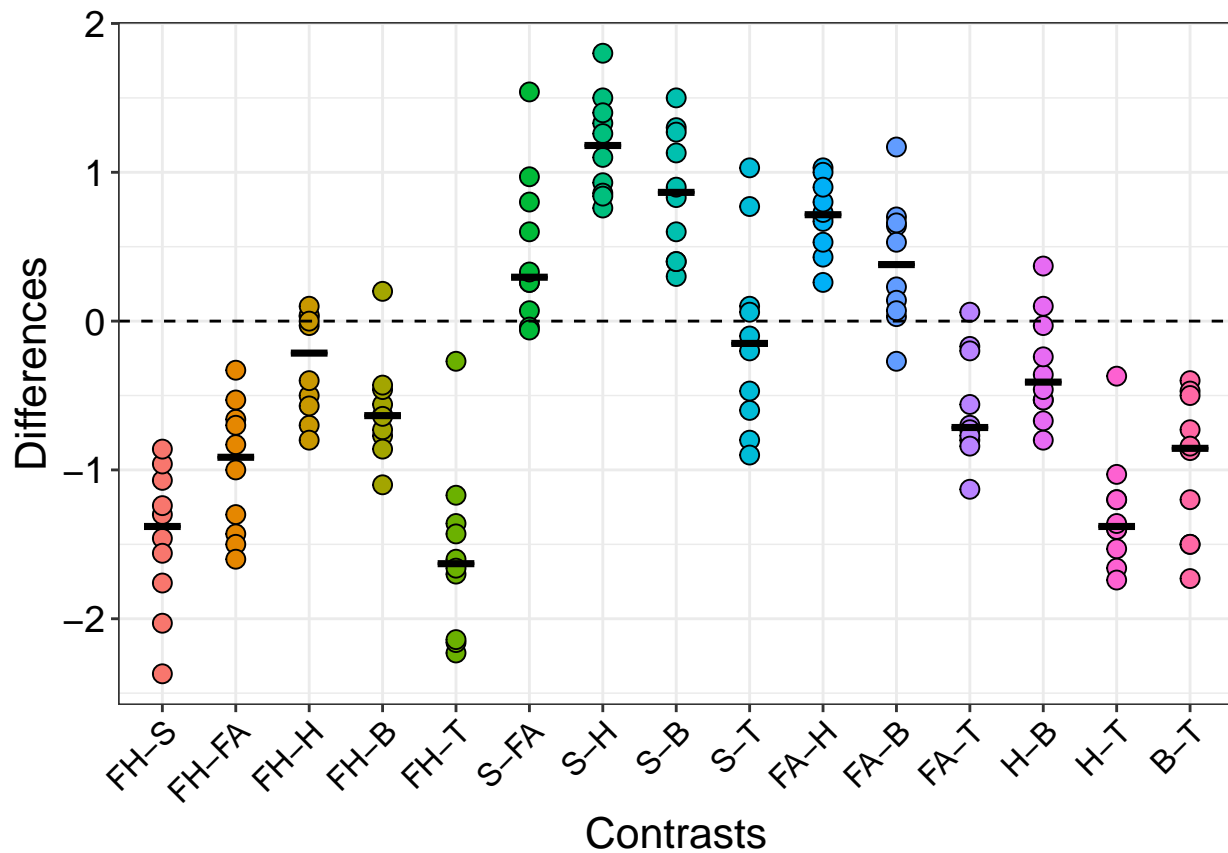
# parameters for plots
axis_title_size <- 16
```

panel B: differences

```
pB <- ggplot(dfB, aes(x=Contrasts, y=Differences,
                      colour = Contrasts, fill = Contrasts)) +
  theme_gar +
  geom_point(shape = 21, size = 3, colour = "black") +
  geom_abline(intercept = 0, slope = 0, linetype = 2) +
  theme(axis.text.y = element_text(size = 14),
        axis.text.x = element_text(angle = 45, hjust = 1, size = 12),
        axis.title = element_text(size = axis_title_size),
        legend.position = "none") +
  xlab("Contrasts") +
  # add median
  stat_summary(fun = median, fun.min = median, fun.max = median,
              geom = "crossbar",
              width = 0.5,
              colour = "black",
              size = 0.5)
```

```
# # add mean
# stat_summary(fun = mean, fun.min = mean, fun.max = mean,
#              geom = "crossbar",
#              width = 0.5,
#              colour = "grey",
#              size = 0.3)
```

pB



combine panels into one figure - AB only

```
cowplot::plot_grid(pA, pB,
  labels=c("A", "B"),
  ncol = 1,
  nrow = 2,
  rel_widths = c(1, 1),
  label_size = 20,
  hjust = -0.5,
  scale=.95,
  align = "h")

# save figure
# ggsave(filename='./figures/figure6.pdf',width=10,height=10)
```

Reject at alpha level for different methods?

```
alpha.val <- 0.05
nboot <- 2000 # number of bootstrap samples
tr <- 0.2 # amount of trimming
rej.res <- matrix(data = NA, nrow = 4, ncol = d)
difs <- matrix(data = NA, nrow = 4, ncol = d)

# Means -- no correction for multiple comparisons
res <- wmcpc(Man[,13:18],tr=0) # 10 sig
rej.res[1,] <- res$test[,4] < alpha.val
difs[1,] <- res$psihat[,3]

# Means + Hochberg
rej.res[2,] <- res$test[,4] < res$test[,5]
difs[2,] <- res$psihat[,3]

# 20% trimmed means + Hochberg
set.seed(666)
res <- wmcppb(Man[,13:18], nboot=nboot, tr=tr) # 12 sig

## [1] "dif=TRUE, so analysis is done on difference scores."
## [1] " Each confidence interval has probability coverage 1-alpha."
## [1] "Also note that a sequentially rejective method is being used"

rej.res[3,] <- res$output[,3] < res$output[,4]
difs[3,] <- res$output[,2]

# Medians + Hochberg
set.seed(666)
res <- dmedpb(Man[,13:18], nboot=nboot) # 10 sig

## [1] "dif=F, so analysis is done on marginal distributions."
## [1] " Each confidence interval has probability coverage 1-alpha."
## [1] " Also note that a sequentially rejective method is being used"
## [1] "Taking bootstrap samples. Please wait."

rej.res[4,] <- res$output[,3] < res$output[,4]
difs[4,] <- res$output[,2]
```

Illustrate results

Size of disks reflects size of differences.

```
dfC <- tibble(Reject = as.factor(as.vector(rej.res)),
              Methods = as.factor(rep(c("M(nc)", "M", "TM", "MD"), d)),
              Contrasts = as.factor(rep(newnames, each = 4)),
              Differences = as.vector(abs(difs)) # use absolute differences
              )

dfC$Methods <- keeporder(dfC$Methods)
dfC$Contrasts <- keeporder(dfC$Contrasts)

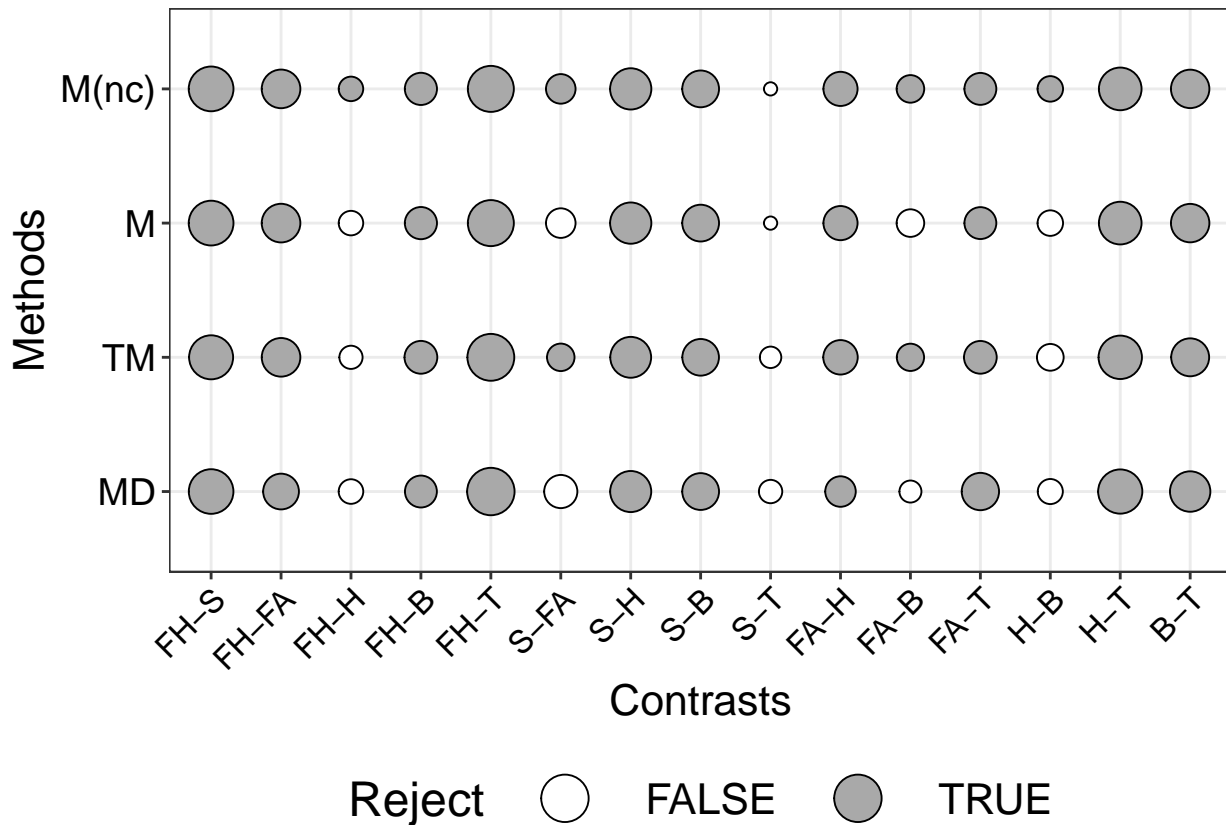
pC <- ggplot(dfC, aes(x = Contrasts, y = Methods,
```

```

    colour = Reject, fill = Reject, size = Differences)) +
  theme_gar +
  geom_point(shape = 21, colour = "black") +
  scale_fill_manual(values = c("white", "darkgrey")) +
  scale_y_discrete(limits=rev) +
  scale_size_continuous(range = c(2,8), guide = "none") +
  theme(axis.text.y = element_text(size = 14),
        axis.text.x = element_text(angle = 45, hjust = 1, size = 12),
        axis.title = element_text(size = axis_title_size),
        legend.position = "bottom") +
  guides(fill = guide_legend(override.aes = list(size = 8)))

```

pC



combine panels into one figure - ABC

```

cowplot::plot_grid(pA, pB, pC,
  labels=c("A", "B", "C"),
  ncol = 1,
  nrow = 3,
  rel_widths = c(1, 1, 1),
  rel_heights = c(1, 1, 0.6),
  label_size = 20,
  hjust = -0.5,
  scale=.95,

```

```
align = "v")

# save figure
ggsave(filename='./figures/figure6.pdf',width=10,height=15)
```

Results reported in the text

Comparing foot and thigh pain measures

T-test

```
t.test(Man$FootP-Man$thighP)

##
## One Sample t-test
##
## data: Man$FootP - Man$thighP
## t = 1.7594, df = 9, p-value = 0.1124
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
## -0.1117268 0.8937268
## sample estimates:
## mean of x
## 0.391
```

Method using 20% trimmed means

```
set.seed(666)
nboot <- 2000 # number of bootstrap samples
tr <- 0.2 # amount of trimming
trimpb(Man$FootP-Man$thighP, nboot=nboot, tr=tr)

## [1] "The p-value returned by this function is based on the"
## [1] "null value specified by the argument null.value, which defaults to 0"

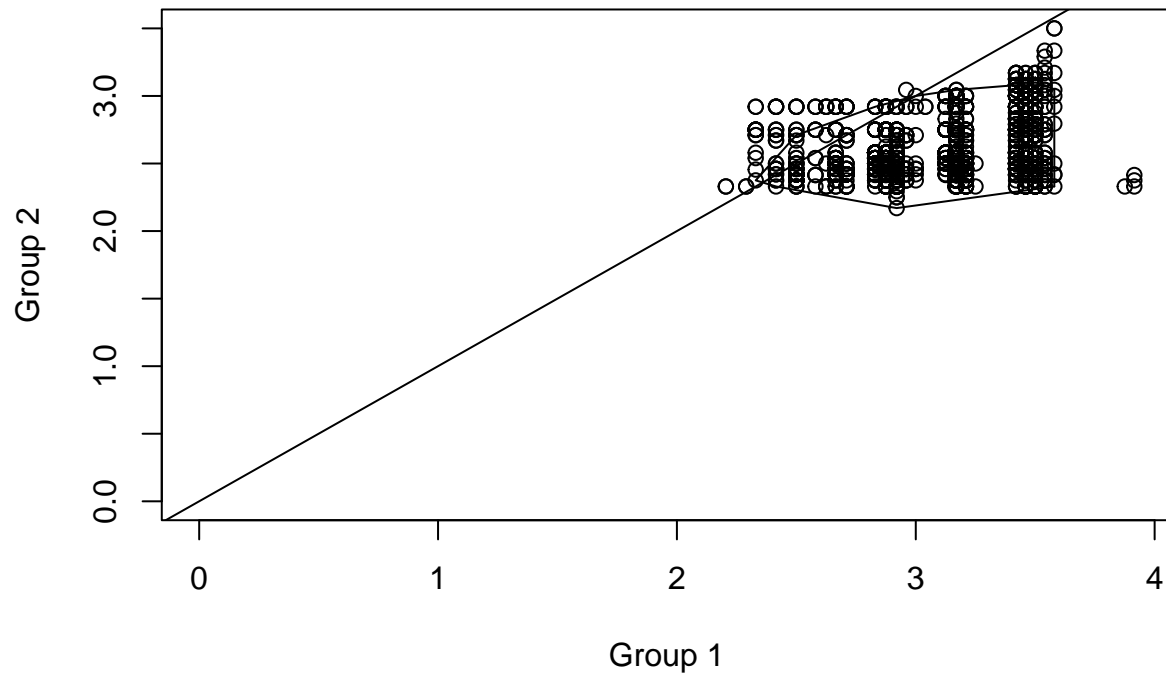
## $estimate
## [1] 0.305
##
## $ci
## [1] -0.03166667 0.79333333
##
## $p.value
## [1] 0.096
```

Method using medians

```
set.seed(666)
dmedpb(Man$FootP,Man$thighP,nboot=nboot)
```



```
## [1] "dif=F, so analysis is done on marginal distributions."
## [1] " Each confidence interval has probability coverage 1-alpha."
## [1] " Also note that a sequentially rejective method is being used"
## [1] "Taking bootstrap samples. Please wait."
```



```
## $output
##      con.num psihat p-value p.crit ci.lower ci.upper
## [1,]      1  0.63  0.111  0.05   -0.21   1.085
##
## $con
##      [,1]
## [1,]    1
## [2,]   -1
##
## $num.sig
## [1] 0
```

All pairwise comparisons

All pairwise comparisons, based on touch, were performed for the following body parts: forehead, shoulder, forearm, palm, dorsum, back and thigh. The probability of one or more Type I errors was controlled using an improvement on the Bonferroni method derived by Hochberg (1988).

Means

```
wmcpc(Man[,13:18],tr=0) # 10 sig
```

```
## $n
## [1] 10
##
## $test
```

```
##      Group Group      test      p.value      p.crit      se
## [1,]      1      2 -9.589432 5.066785e-06 0.003846154 0.15235521
## [2,]      1      3 -7.010090 6.254719e-05 0.005000000 0.14093970
## [3,]      1      4 -2.586528 2.938032e-02 0.025000000 0.10941308
## [4,]      1      5 -5.520758 3.701213e-04 0.007142857 0.10831846
## [5,]      1      6 -8.541909 1.306340e-05 0.004545455 0.18403381
## [6,]      2      3  2.940082 1.648454e-02 0.010000000 0.16087987
## [7,]      2      4 11.025676 1.578584e-06 0.003333333 0.10684152
## [8,]      2      5  6.371728 1.295117e-04 0.006250000 0.13544207
## [9,]      2      6 -0.553076 5.936812e-01 0.050000000 0.20069573
## [10,]     3      4  9.052608 8.140314e-06 0.004166667 0.07787811
## [11,]     3      5  2.911204 1.727735e-02 0.012500000 0.13396517
## [12,]     3      6 -5.028673 7.106492e-04 0.008333333 0.11613402
## [13,]     4      5 -2.722258 2.352072e-02 0.016666667 0.11571277
## [14,]     4      6 -10.500208 2.380129e-06 0.003571429 0.12275948
## [15,]     5      6 -6.418584 1.225689e-04 0.005555556 0.15174687
##
## $psihat
##      Group Group psihat  ci.lower  ci.upper
## [1,]      1      2 -1.461 -2.0634459 -0.8585541
## [2,]      1      3 -0.988 -1.5453064 -0.4306936
## [3,]      1      4 -0.283 -0.7156433  0.1496433
## [4,]      1      5 -0.598 -1.0263149 -0.1696851
## [5,]      1      6 -1.572 -2.2997100 -0.8442900
## [6,]      2      3  0.473 -0.1631542  1.1091542
## [7,]      2      4  1.178  0.7555252  1.6004748
## [8,]      2      5  0.863  0.3274324  1.3985676
## [9,]      2      6 -0.111 -0.9045949  0.6825949
## [10,]     3      4  0.705  0.3970529  1.0129471
## [11,]     3      5  0.390 -0.1397276  0.9197276
## [12,]     3      6 -0.584 -1.0432193 -0.1247807
## [13,]     4      5 -0.315 -0.7725536  0.1425536
## [14,]     4      6 -1.289 -1.7744178 -0.8035822
## [15,]     5      6 -0.974 -1.5740403 -0.3739597
##
## $con
##      [,1]
## [1,]      0
##
## $num.sig
## [1] 10
```

Medians

```
set.seed(666)
dmedpb(Man[,13:18], nboot=nboot) # 10 sig

## [1] "dif=F, so analysis is done on marginal distributions."
## [1] " Each confidence interval has probability coverage 1-alpha."
## [1] " Also note that a sequentially rejective method is being used"
## [1] "Taking bootstrap samples. Please wait."

## $output
```

```
##          con.num psihat p-value      p.crit ci.lower ci.upper
## [1,]          1 -1.450  0.0000 0.008333333 -1.915  -1.010
## [2,]          2 -0.800  0.0000 0.007142857 -1.380  -0.530
## [3,]          3 -0.285  0.1145 0.025000000 -0.600   0.035
## [4,]          4 -0.585  0.0000 0.006250000 -0.750  -0.430
## [5,]          5 -1.700  0.0000 0.005555556 -2.100  -1.180
## [6,]          6  0.650  0.0320 0.010000000  0.065   0.935
## [7,]          7  1.165  0.0000 0.005000000  0.840   1.415
## [8,]          8  0.865  0.0000 0.004545455  0.415   1.285
## [9,]          9 -0.250  0.4110 0.050000000 -0.730   0.300
## [10,]         10  0.515  0.0000 0.004166667  0.260   0.885
## [11,]         11  0.215  0.0390 0.012500000  0.050   0.785
## [12,]         12 -0.900  0.0000 0.003846154 -1.130  -0.415
## [13,]         13 -0.300  0.0735 0.016666667 -0.600   0.020
## [14,]         14 -1.415  0.0000 0.003571429 -1.660  -1.030
## [15,]         15 -1.115  0.0000 0.003333333 -1.500  -0.615
##
## $con
##      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13] [,14]
## [1,]      1      1      1      1      1      0      0      0      0      0      0      0      0      0
## [2,]     -1      0      0      0      0      1      1      1      1      0      0      0      0      0
## [3,]      0     -1      0      0      0     -1      0      0      0      1      1      1      0      0
## [4,]      0      0     -1      0      0      0     -1      0      0     -1      0      0      1      1
## [5,]      0      0      0     -1      0      0      0     -1      0      0     -1      0     -1      0
## [6,]      0      0      0      0     -1      0      0      0     -1      0      0     -1      0     -1
##      [,15]
## [1,]       0
## [2,]       0
## [3,]       0
## [4,]       0
## [5,]       1
## [6,]      -1
##
## $num.sig
## [1] 10
```

Trimmed means

```
set.seed(666)
wmcppb(Man[,13:18], nboot=nboot, tr=tr) # 12 sig

## [1] "dif=TRUE, so analysis is done on difference scores."
## [1] " Each confidence interval has probability coverage 1-alpha."
## [1] "Also note that a sequentially rejective method is being used"

## $output
##          con.num      psihat p.value      p.crit      ci.lower      ci.upper
## [1,]          1 -1.3983333  0.000 0.008333333 -1.81166667 -1.10833333
## [2,]          2 -0.9866667  0.000 0.007142857 -1.35333333 -0.65166667
## [3,]          3 -0.2450000  0.096 0.025000000 -0.55666667  0.01500000
## [4,]          4 -0.6316667  0.000 0.006250000 -0.78666667 -0.41166667
## [5,]          5 -1.6483333  0.000 0.005555556 -1.99000000 -1.21833333
## [6,]          6  0.3866667  0.002 0.010000000  0.11000000  0.79000000
```

```
## [7,]      7  1.1466667  0.000 0.005000000  0.91666667  1.40500000
## [8,]      8  0.8550000  0.000 0.004545455  0.51666667  1.19500000
## [9,]      9 -0.2016667  0.437 0.050000000 -0.56166667  0.36166667
## [10,]     10  0.7216667  0.000 0.004166667  0.53833333  0.87500000
## [11,]     11  0.3783333  0.007 0.012500000  0.09833333  0.66333333
## [12,]     12 -0.6266667  0.000 0.003846154 -0.81166667 -0.32833333
## [13,]     13 -0.3583333  0.024 0.016666667 -0.56500000 -0.05666667
## [14,]     14 -1.3483333  0.000 0.003571429 -1.52333333 -1.06166667
## [15,]     15 -0.9400000  0.000 0.003333333 -1.35000000 -0.59500000
##
## $con
##      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13] [,14]
## [1,]      1      1      1      1      1      0      0      0      0      0      0      0      0      0
## [2,]     -1      0      0      0      0      1      1      1      1      0      0      0      0      0
## [3,]      0     -1      0      0      0     -1      0      0      0      1      1      1      0      0
## [4,]      0      0     -1      0      0      0     -1      0      0     -1      0      0      1      1
## [5,]      0      0      0     -1      0      0      0     -1      0      0     -1      0     -1      0
## [6,]      0      0      0      0     -1      0      0      0     -1      0      0     -1      0     -1
##      [,15]
## [1,]      0
## [2,]      0
## [3,]      0
## [4,]      0
## [5,]      1
## [6,]     -1
##
## $num.sig
## [1] 12
```

Sign test

```
signmcp(Man[,13:18], method='SD')
```