ForestPlot

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12/20/2021

Introduction to forest plots

by Max Gordon

Code based on : https://cran.r-project.org/web/packages/forestplot/vignettes/forestplot.html

```
library(forestplot)
```

```
## Warning: package 'forestplot' was built under R version 4.1.2
```

```
## Loading required package: grid
```

```
## Loading required package: magrittr
```

```
## Loading required package: checkmate
```

```
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
# Cochrane data from the 'rmeta'-package
cochrane_from_rmeta <- structure(list(mean  = c(NA, NA, 0.578, 0.165, 0.246, 0.700, 0.348, 0.139, 1.017
                                      lower = c(NA, NA, 0.372, 0.018, 0.072, 0.333, 0.083, 0.016, 0.365
                                      upper = c(NA, NA, 0.898, 1.517, 0.833, 1.474, 1.455, 1.209, 2.831
                                .Names = c("mean", "lower", "upper"),
                                row.names = c(NA, -11L),
                                class = "data.frame")
cochrane_from_rmeta
```
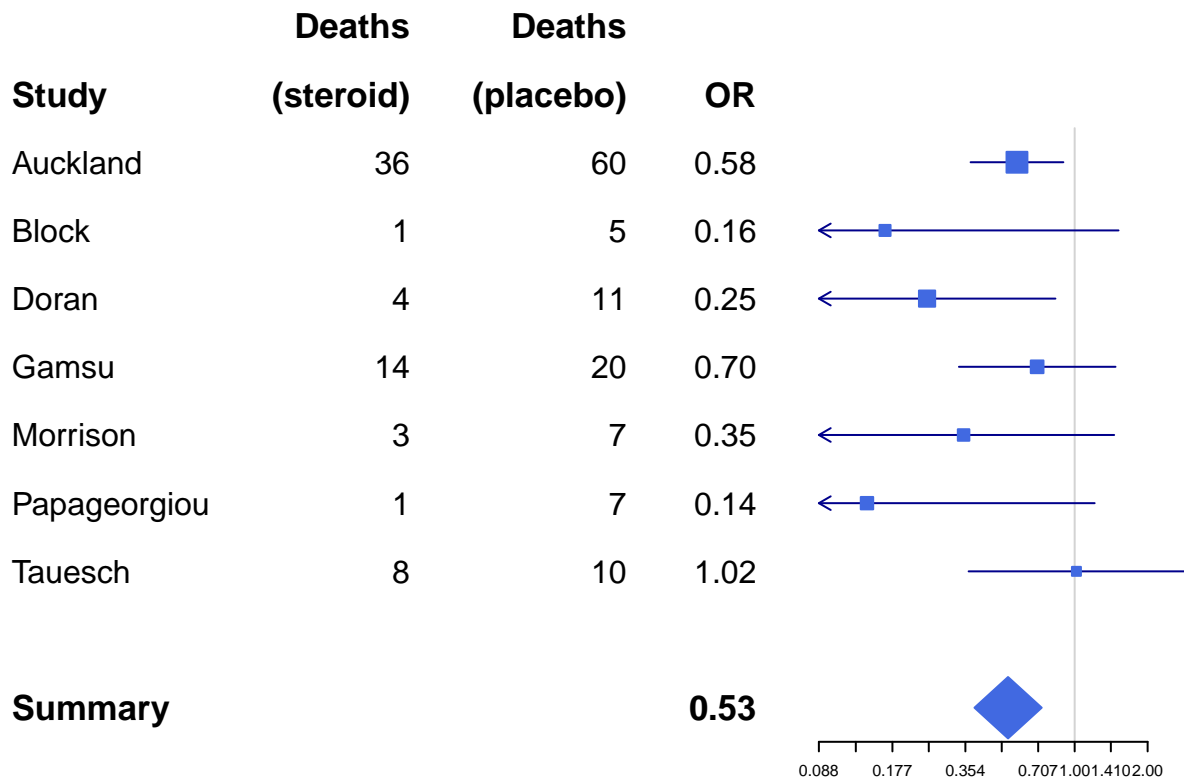
```
##     mean lower upper
## 1     NA    NA    NA
## 2     NA    NA    NA
## 3  0.578 0.372 0.898
## 4  0.165 0.018 1.517
## 5  0.246 0.072 0.833
## 6  0.700 0.333 1.474
## 7  0.348 0.083 1.455
## 8  0.139 0.016 1.209
## 9  1.017 0.365 2.831
## 10    NA    NA    NA
## 11 0.531 0.386 0.731
```

```
tabletext <- cbind(c("", "Study", "Auckland", "Block", "Doran", "Gamsu", "Morrison", "Papageorgiou", "Ta
                   c("Deaths", "(steroid)", "36", "1", "4", "14", "3", "1", "8", NA, NA),
                   c("Deaths", "(placebo)", "60", "5", "11", "20", "7", "7", "10", NA, NA),
                   c("", "OR", "0.58", "0.16", "0.25", "0.70", "0.35", "0.14", "1.02", NA, "0.53"))

tabletext
```

```
##       [,1]           [,2]        [,3]        [,4]
## [1,] ""             "Deaths"    "Deaths"    ""
## [2,] "Study"        "(steroid)" "(placebo)" "OR"
## [3,] "Auckland"     "36"        "60"        "0.58"
## [4,] "Block"        "1"         "5"         "0.16"
## [5,] "Doran"        "4"         "11"        "0.25"
## [6,] "Gamsu"        "14"        "20"        "0.70"
## [7,] "Morrison"     "3"         "7"         "0.35"
## [8,] "Papageorgiou" "1"         "7"         "0.14"
## [9,] "Tauesch"      "8"         "10"        "1.02"
## [10,] NA            NA          NA          NA
## [11,] "Summary"     NA          NA          "0.53"
```

```
cochrane_from_rmeta %>%
  forestplot(labeltext = tabletext,
             is.summary = c(rep(TRUE, 2), rep(FALSE, 8), TRUE), #Make Text Bold to highlight Summary ro
             clip = c(0.1, 9.5),  #Lower and upper limits for clipping confidence intervals to arrows
             xlog = TRUE,  #Log scale on X axis
             col = fpColors(box = "royalblue",
                            line = "darkblue",
                            summary = "royalblue"))
```

Study	Deaths (steroid)	Deaths (placebo)	OR
Auckland	36	60	0.58
Block	1	5	0.16
Doran	4	11	0.25
Gamsu	14	20	0.70
Morrison	3	7	0.35
Papageorgiou	1	7	0.14
Tauesch	8	10	1.02
Summary			**0.53**

```
# Cochrane data from the 'rmeta'-package
base_data <- tibble(mean  = c(0.578, 0.165, 0.246, 0.700, 0.348, 0.139, 1.017),
                    lower = c(0.372, 0.018, 0.072, 0.333, 0.083, 0.016, 0.365),
                    upper = c(0.898, 1.517, 0.833, 1.474, 1.455, 1.209, 2.831),
                    study = c("Auckland", "Block", "Doran", "Gamsu", "Morrison", "Papageorgiou", "Tauesc
                    deaths_steroid = c("36", "1", "4", "14", "3", "1", "8"),
                    deaths_placebo = c("60", "5", "11", "20", "7", "7", "10"),
                    OR = c("0.58", "0.16", "0.25", "0.70", "0.35", "0.14", "1.02"))

summary <- tibble(mean  = 0.531,
                  lower = 0.386,
                  upper = 0.731,
                  study = "Summary",
                  OR = "0.53",
                  summary = TRUE)

header <- tibble(study = c("", "Study"),
                 deaths_steroid = c("Deaths", "(steroid)"),
                 deaths_placebo = c("Deaths", "(placebo)"),
                 OR = c("", "OR"),
                 summary = TRUE)

empty_row <- tibble(mean = NA_real_)

cochrane_output_df <- bind_rows(header,
                                base_data,
```

```
                              empty_row,
                              summary)

cochrane_output_df
```

```
## # A tibble: 11 x 8
##     study          deaths_steroid deaths_placebo OR     summary   mean  lower  upper
##     <chr>          <chr>          <chr>          <chr> <lgl>     <dbl>  <dbl>  <dbl>
##  1 ""             Deaths         Deaths         ""     TRUE     NA     NA     NA
##  2 "Study"        (steroid)      (placebo)      "OR"   TRUE     NA     NA     NA
##  3 "Auckland"     36             60             "0.5~ NA        0.578  0.372  0.898
##  4 "Block"        1              5              "0.1~ NA        0.165  0.018  1.52
##  5 "Doran"        4              11             "0.2~ NA        0.246  0.072  0.833
##  6 "Gamsu"        14             20             "0.7~ NA        0.7    0.333  1.47
##  7 "Morrison"     3              7              "0.3~ NA        0.348  0.083  1.46
##  8 "Papageorgi~   1              7              "0.1~ NA        0.139  0.016  1.21
##  9 "Tauesch"      8              10             "1.0~ NA        1.02   0.365  2.83
## 10  <NA>          <NA>           <NA>            <NA> NA        NA     NA     NA
## 11 "Summary"      <NA>           <NA>           "0.5~ TRUE      0.531  0.386  0.731
```
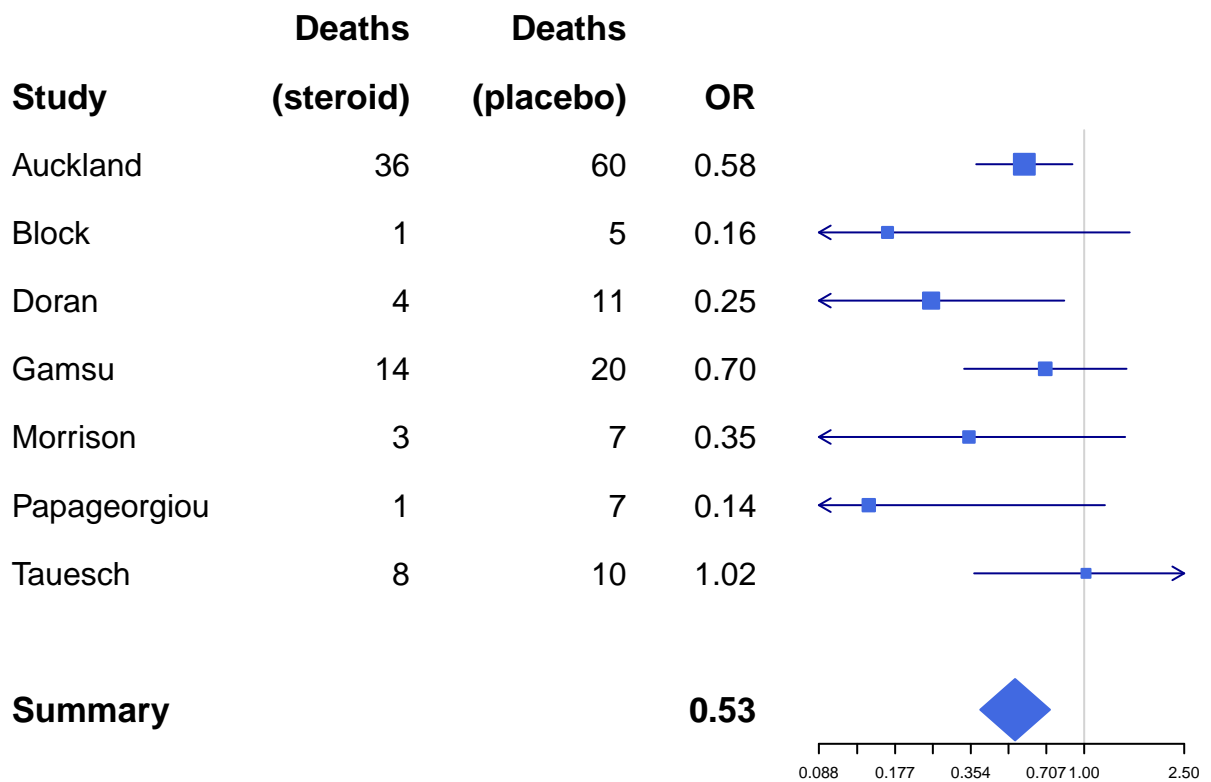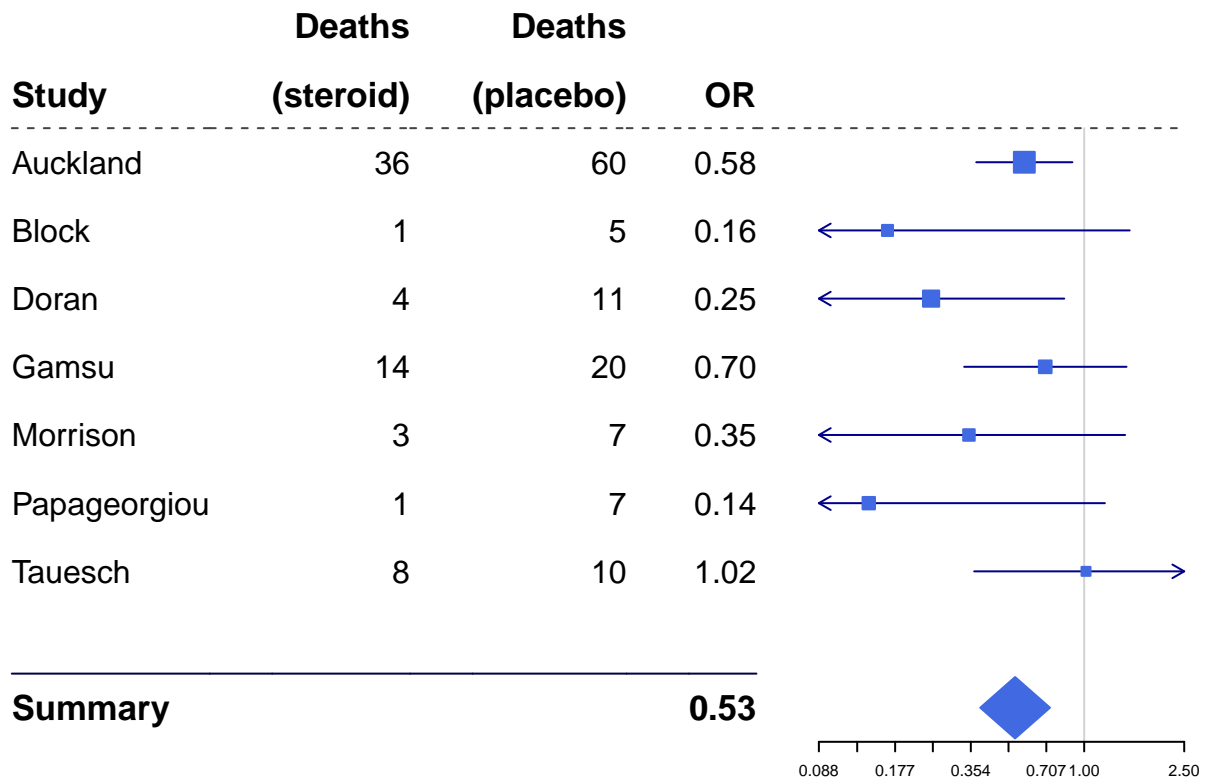
```
cochrane_output_df %>%
  forestplot(labeltext = c(study, deaths_steroid, deaths_placebo, OR),
             is.summary = summary,
             clip = c(0.1, 2.5),
             xlog = TRUE,
             col = fpColors(box = "royalblue",
                           line = "darkblue",
                           summary = "royalblue"))
```

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Study	Deaths (steroid)	Deaths (placebo)	OR	
Auckland	36	60	0.58	
Block	1	5	0.16	
Doran	4	11	0.25	
Gamsu	14	20	0.70	
Morrison	3	7	0.35	
Papageorgiou	1	7	0.14	
Tauesch	8	10	1.02	
Summary			**0.53**	


```
cochrane_output_df %>%
  forestplot(labeltext = c(study, deaths_steroid, deaths_placebo, OR),
             is.summary = summary,
             clip = c(0.1, 2.5),
             hrzl_lines = list("3" = gpar(lty = 2),
                               "11" = gpar(lwd = 1, columns = 1:4, col = "#000044")),
             xlog = TRUE,
             col = fpColors(box = "royalblue",
                            line = "darkblue",
                            summary = "royalblue",
                            hrz_lines = "#444444"))
```
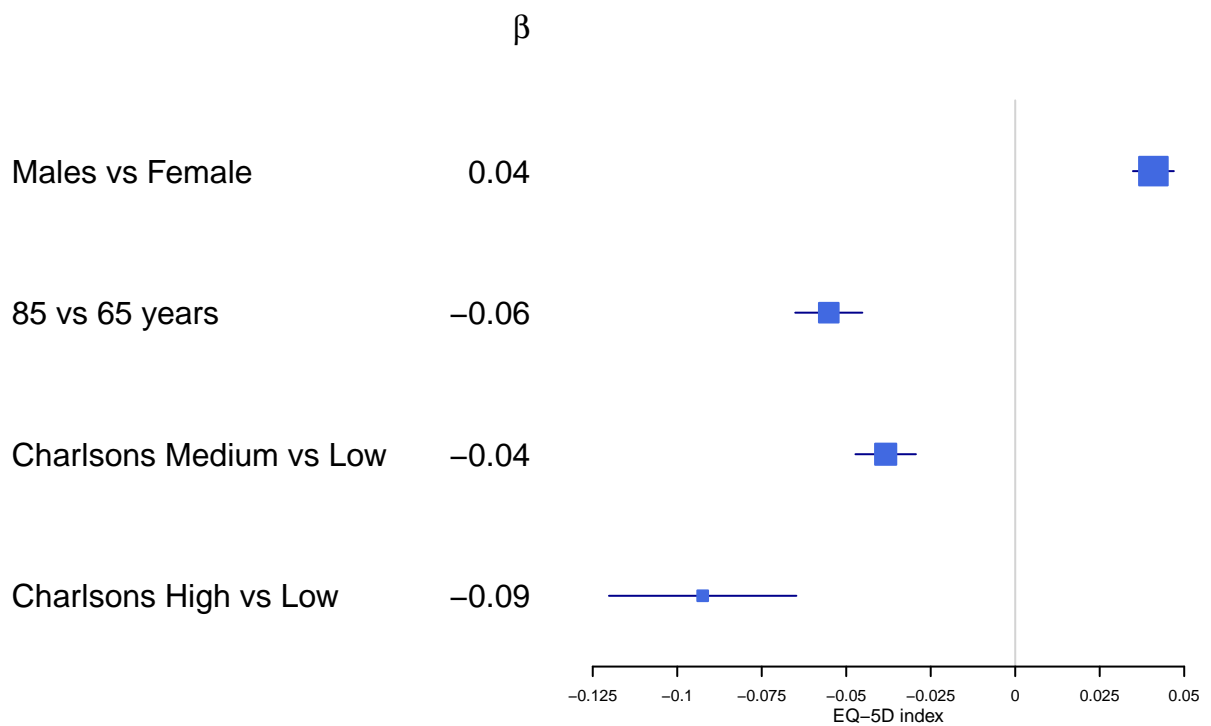
Study	Deaths (steroid)	Deaths (placebo)	OR	
Auckland	36	60	0.58	
Block	1	5	0.16	
Doran	4	11	0.25	
Gamsu	14	20	0.70	
Morrison	3	7	0.35	
Papageorgiou	1	7	0.14	
Tauesch	8	10	1.02	
Summary			**0.53**	

Using Expression

```
data(dfHRQoL)
dfHRQoL <- dfHRQoL %>% mutate(est = sprintf("%.2f", mean), .after = labeltext)

clrs <- fpColors(box = "royalblue",line = "darkblue", summary = "royalblue")
tabletext <- list(c(NA, dfHRQoL %>% filter(group == "Sweden") %>% pull(labeltext)),
                  append(list(expression(beta)),
                  dfHRQoL %>% filter(group == "Sweden") %>% pull(est)))

dfHRQoL %>%
  filter(group == "Sweden") %>%
  bind_rows(tibble(mean = NA_real_), .) %>%
  forestplot(labeltext = tabletext,
             col = clrs,                    #Set the colors for all the elements.
             xlab = "EQ-5D index")
```

β

Males vs Female	0.04
85 vs 65 years	−0.06
Charlsons Medium vs Low	−0.04
Charlsons High vs Low	−0.09

−0.125   −0.1   −0.075   −0.05   −0.025   0   0.025   0.05
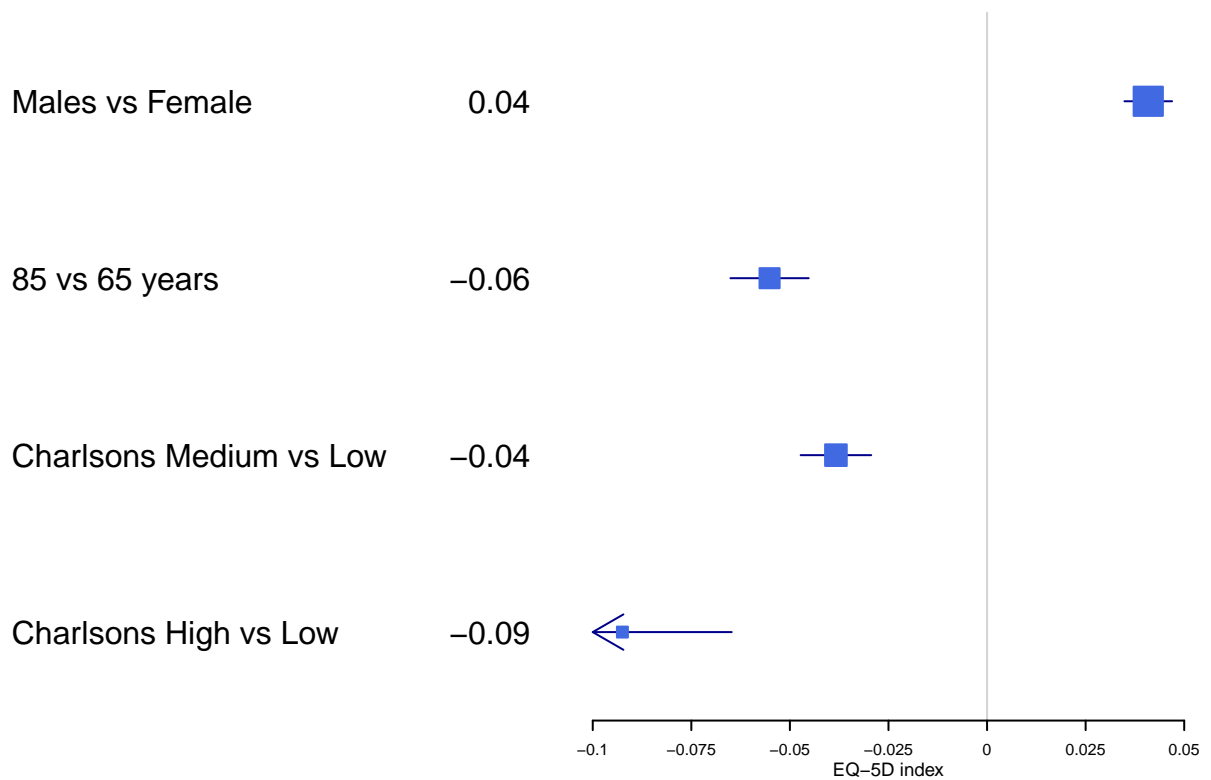
EQ−5D index

Altering Fonts

```
# You can set directly the font to desired value, the next three lines are just for handling MacOs on C
font <- "mono"
if (grepl("Ubuntu", Sys.info()["version"])) {
  font <- "HersheyGothicEnglish"
}
dfHRQoL %>%
  filter(group == "Sweden") %>%
  forestplot(labeltext = c(labeltext, est),
             txt_gp = fpTxtGp(label = gpar(fontfamily = font)),
             col = clrs,
             xlab = "EQ-5D index")
```

Males vs Female	0.04	
85 vs 65 years	−0.06	
Charlsons Medium vs Low	−0.04	
Charlsons High vs Low	−0.09	

EQ−5D index
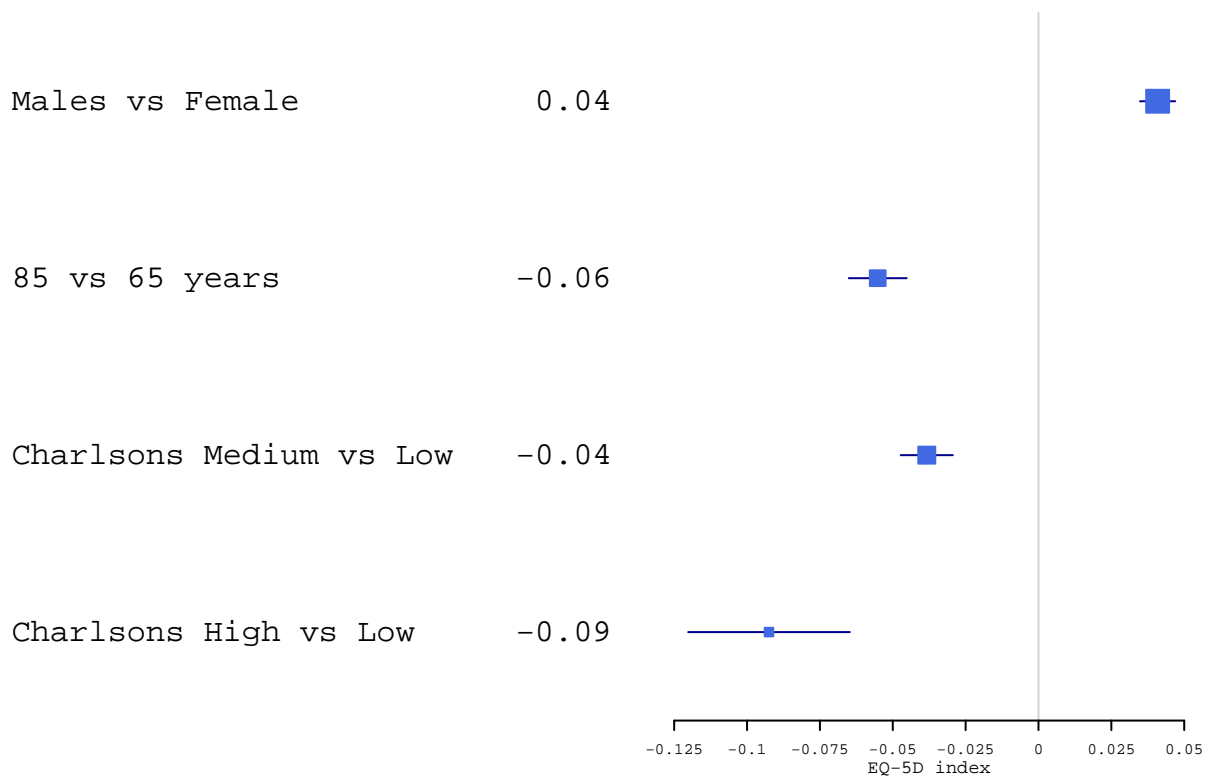
Condidence Intervals

Clipping the interval is convenient for uncertain estimates in order to retain the resolution for those of more interest. The clipping simply adds an arrow to the confidence interval, see the bottom estimate below:

```
dfHRQoL %>%
  filter(group == "Sweden") %>%
  forestplot(labeltext = c(labeltext, est),
             clip = c(-.1, Inf),   #Change here
             col = clrs,
             xlab = "EQ-5D index")
```

Males vs Female	0.04	
85 vs 65 years	−0.06	
Charlsons Medium vs Low	−0.04	
Charlsons High vs Low	−0.09	

EQ−5D index

Custom box size

```
dfHRQoL %>%
  filter(group == "Sweden") %>%
  forestplot(labeltext = c(labeltext, est),
             boxsize = 0.2,
             clip = c(-.1, Inf),
             col = clrs,
             xlab = "EQ-5D index")
```
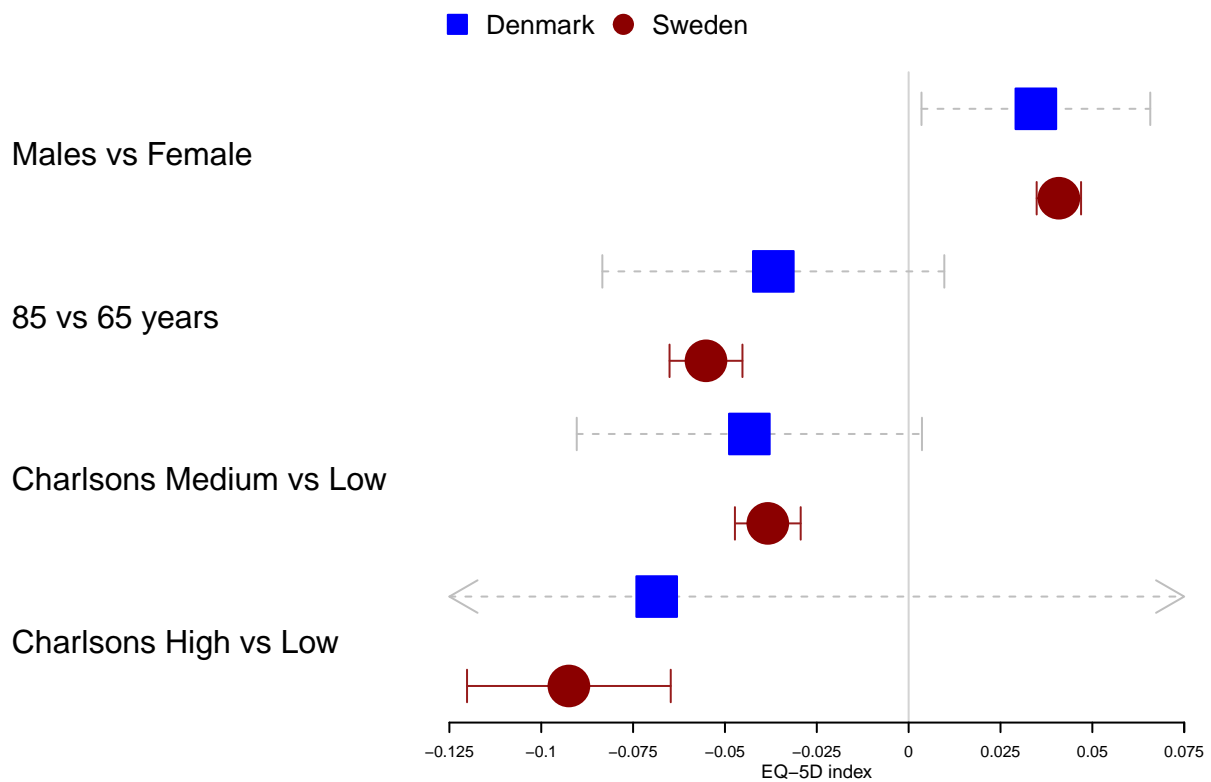
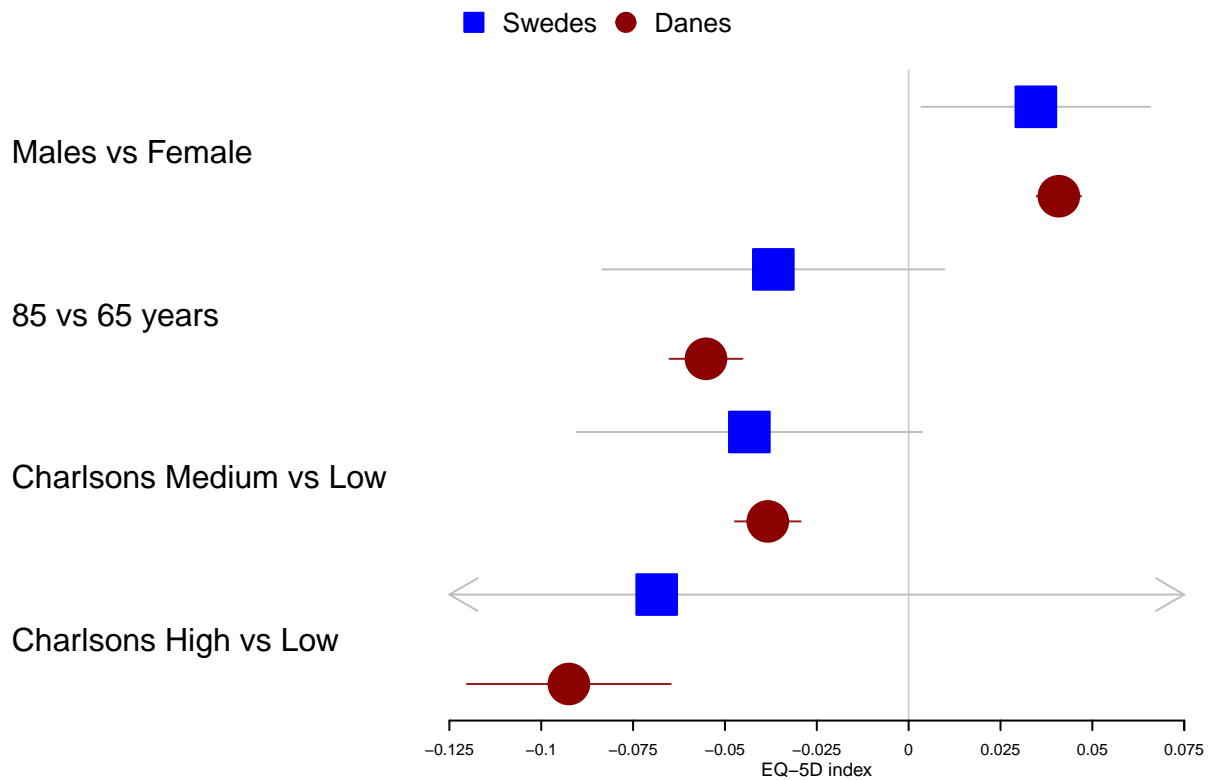| Males vs Female | 0.04 | |
85 vs 65 years	−0.06	
Charlsons Medium vs Low	−0.04	
Charlsons High vs Low	−0.09	

EQ–5D index
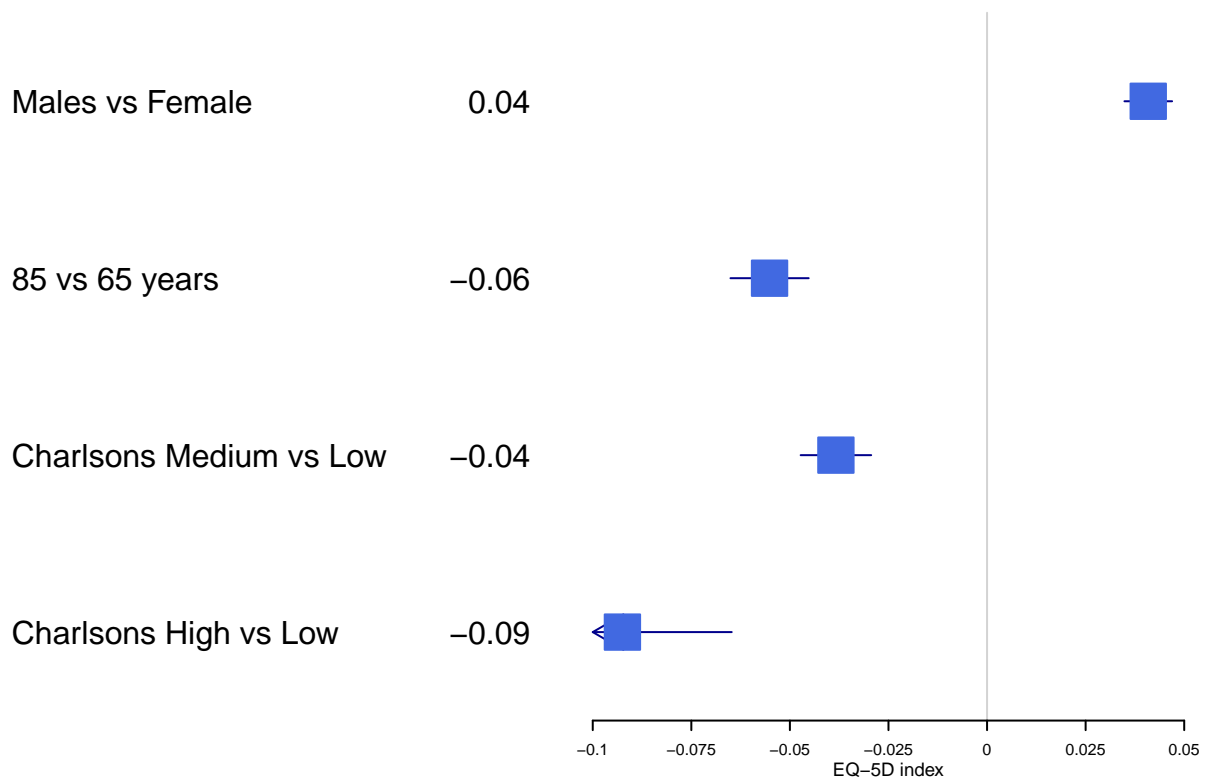
Multiple confidence bands

```
dfHRQoL %>%
  group_by(group) %>%
  forestplot(fn.ci_norm = c(fpDrawNormalCI, fpDrawCircleCI), #how the line with the box is drawn for th
             boxsize = .25, # We set the box size to better visualize the type
             line.margin = .1, # We need to add this to avoid crowding
             clip = c(-.125, 0.075),
             shapes_gp = fpShapesGp(box = c("blue", "darkred") %>% lapply(function(x) gpar(fill = x, col
                        default = gpar(vertices = TRUE)), #Sets graphical parameters (squar
             xlab = "EQ-5D index")
```
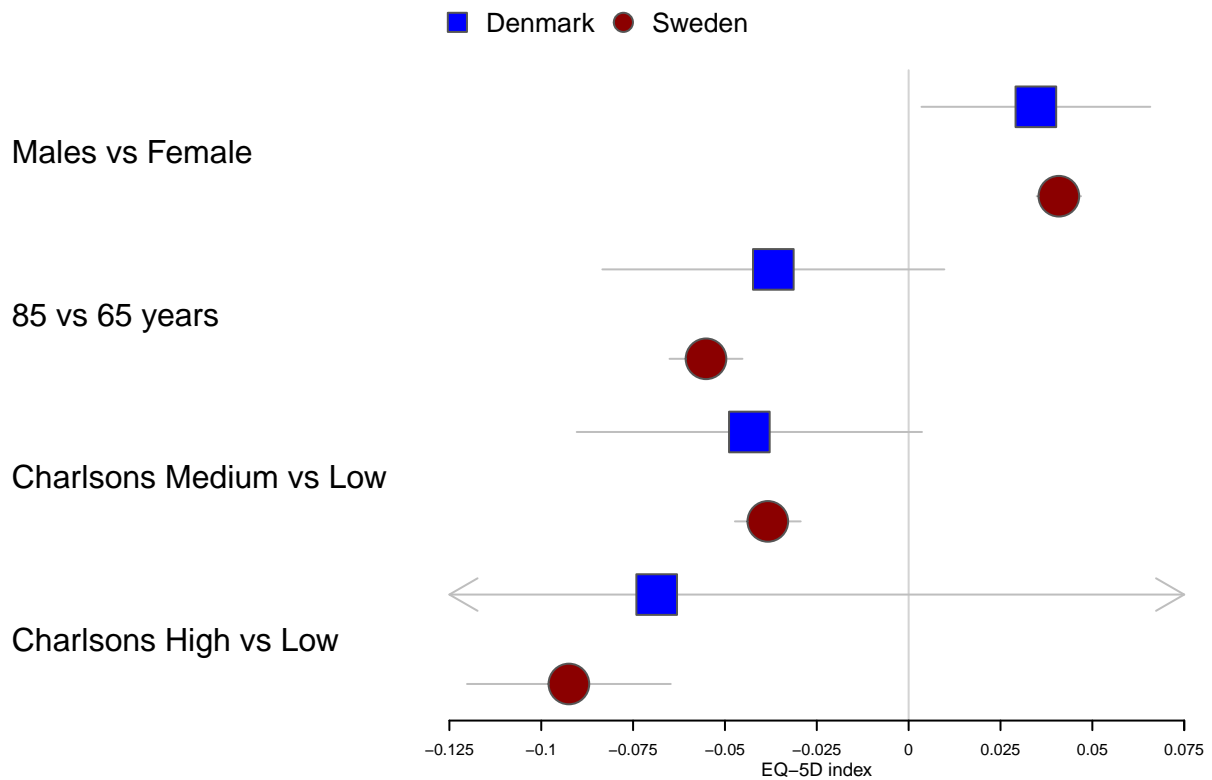
```
#c("blue", "darkred") %>% lapply(function(x) gpar(fill = x, col = "#555555"))
#Use this to visualize the list piped into the shape functions
```

Choosing line type

```
dfHRQoL %>%
  group_by(group) %>%
  forestplot(fn.ci_norm = c(fpDrawNormalCI, fpDrawCircleCI),#how the line with the box is drawn for the
             boxsize = .25, # We set the box size to better visualize the type
             line.margin = .1, # We need to add this to avoid crowding
             clip = c(-.125, 0.075),
             lty.ci = c(2, 1), #line type for the confidence bands,
             col = fpColors(box = c("blue", "darkred")),
             xlab = "EQ-5D index",
             ci.vertices=TRUE) #Add vertices
```

Legend: ■ Swedes ● Danes

Categories (top to bottom): Males vs Female, 85 vs 65 years, Charlsons Medium vs Low, Charlsons High vs Low

X-axis: EQ–5D index, with ticks at −0.125, −0.1, −0.075, −0.05, −0.025, 0, 0.025, 0.05, 0.075

Ticks on Axis
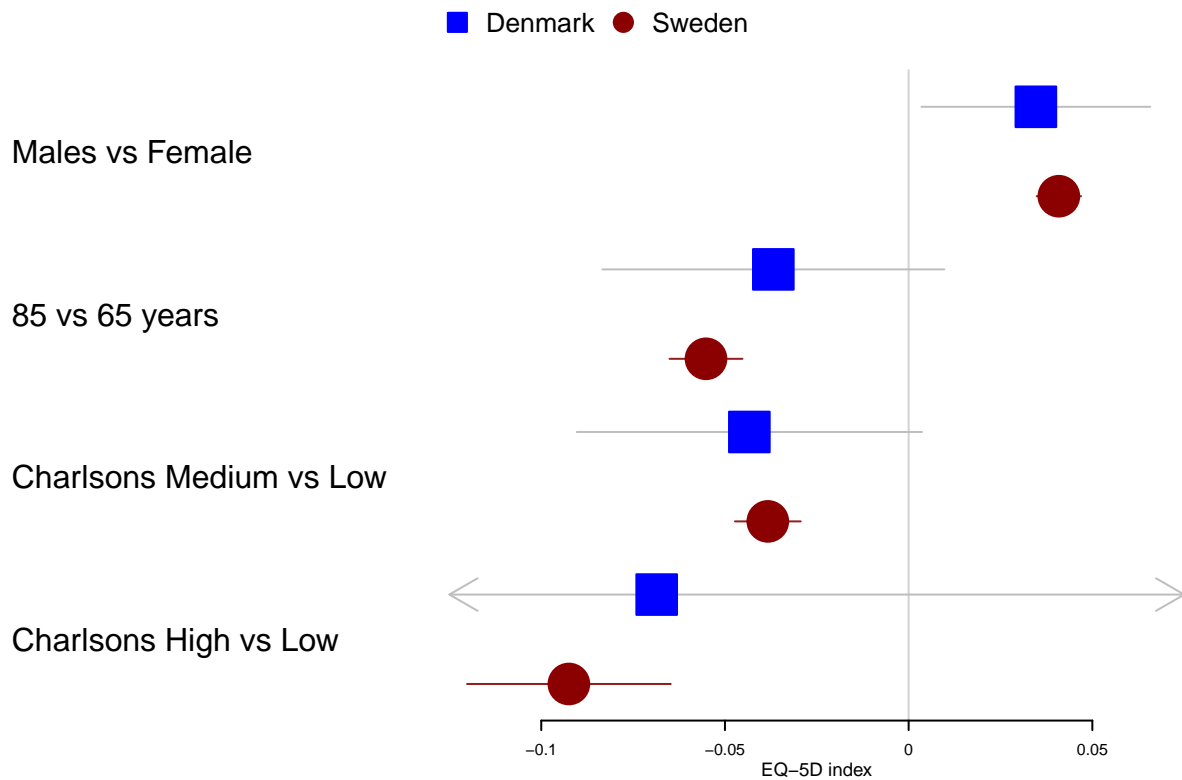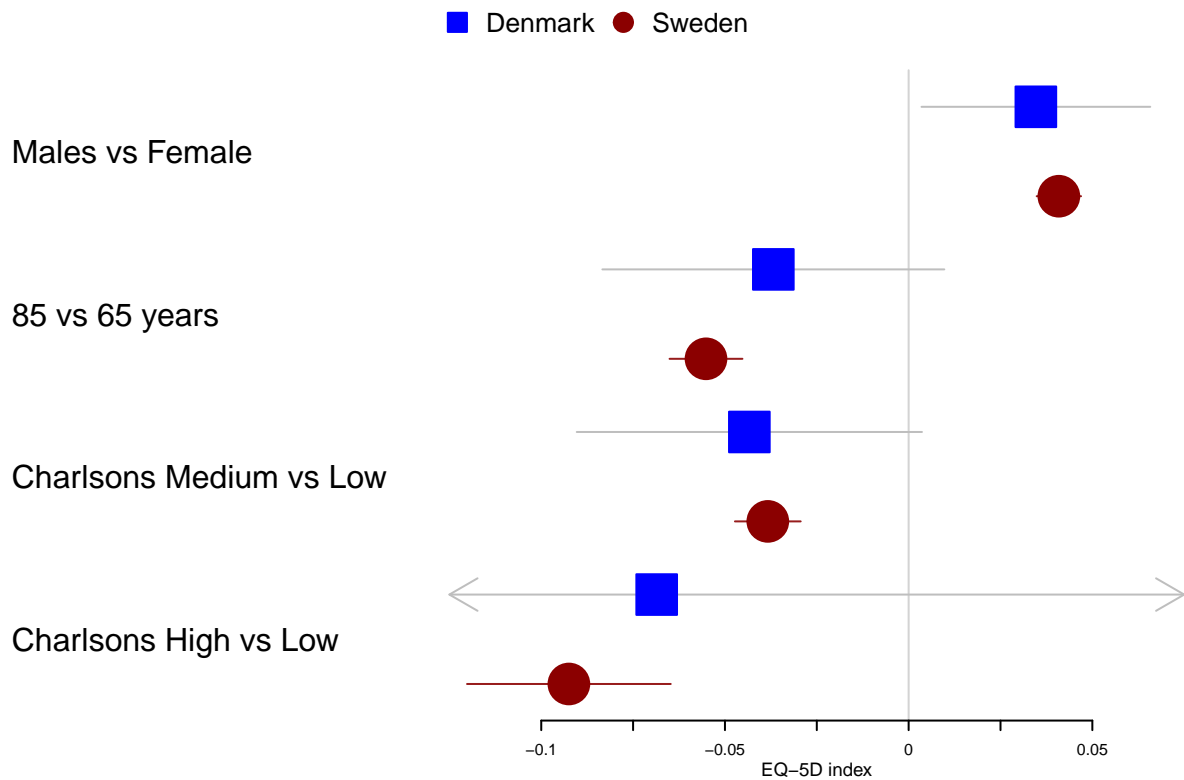
```
dfHRQoL %>%
  group_by(group) %>%
  forestplot(fn.ci_norm = c(fpDrawNormalCI, fpDrawCircleCI),
             boxsize = .25, # We set the box size to better visualize the type
             line.margin = .1, # We need to add this to avoid crowding
             clip = c(-.125, 0.075),
             col = fpColors(box = c("blue", "darkred")),
             xticks = c(-.1, -0.05, 0, .05),
             xlab = "EQ-5D index")
```

- Using object to define ticks and grids

```
xticks <- seq(from = -.1, to = .05, by = 0.025)
xtlab <- rep(c(TRUE, FALSE), length.out = length(xticks))
attr(xticks, "labels") <- xtlab

dfHRQoL %>%
  group_by(group) %>%
  forestplot(fn.ci_norm = c(fpDrawNormalCI, fpDrawCircleCI),
             boxsize = .25, # We set the box size to better visualize the type
             line.margin = .1, # We need to add this to avoid crowding
             clip = c(-.125, 0.075),
             col = fpColors(box = c("blue", "darkred")),
             xticks = xticks,
             xlab = "EQ-5D index")
```

Adding Grids

```
dfHRQoL %>%
  group_by(group) %>%
  forestplot(fn.ci_norm = c(fpDrawNormalCI, fpDrawCircleCI),
             boxsize = .25, # We set the box size to better visualize the type
             line.margin = .1, # We need to add this to avoid crowding
             clip = c(-.125, 0.075),
             col = fpColors(box = c("blue", "darkred")),
             grid = TRUE,
             xticks = c(-.1, -0.05, 0, .05),
             zero = 0,
             xlab = "EQ-5D index")
```
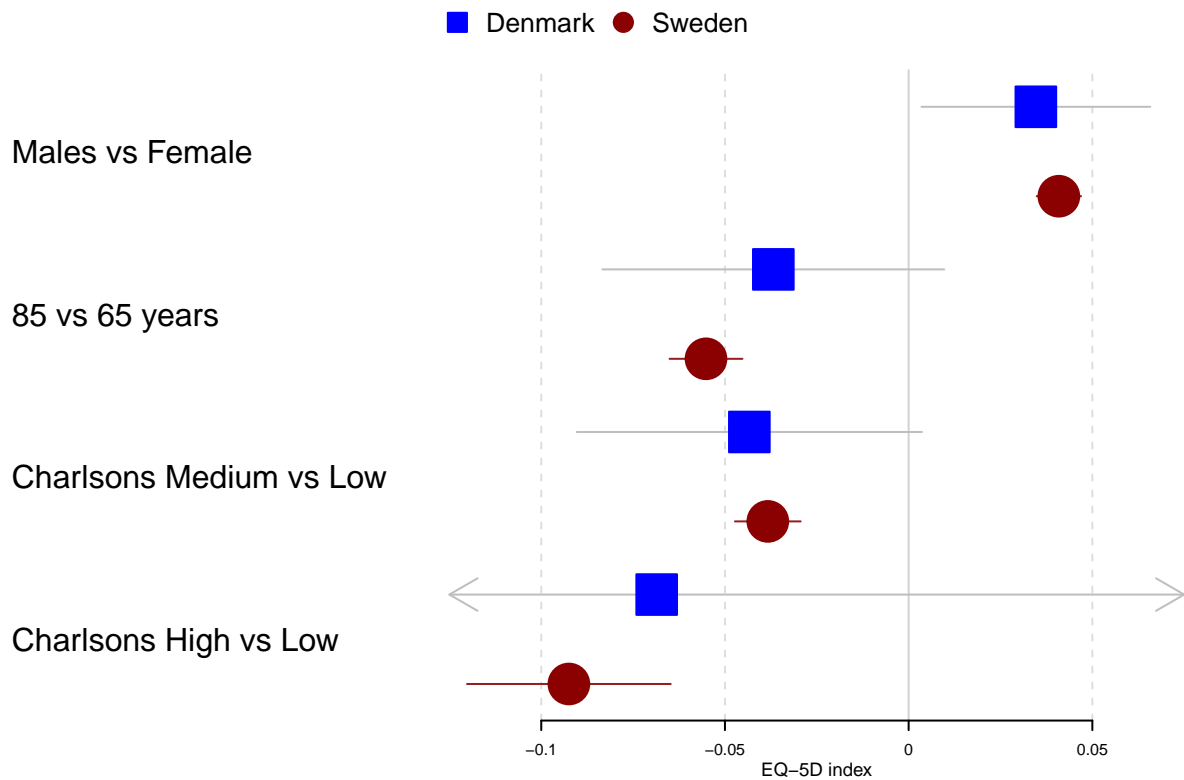
```
dfHRQoL %>%
  group_by(group) %>%
  forestplot(fn.ci_norm = c(fpDrawNormalCI, fpDrawCircleCI),
             boxsize = .25, # We set the box size to better visualize the type
             line.margin = .1, # We need to add this to avoid crowding
             clip = c(-.125, 0.075),
             col = fpColors(box = c("blue", "darkred")),
             grid = structure(c(-.1, -.05, .05),
                              gp = gpar(lty = 3, col = "#CCCCFF")),
             xlab = "EQ-5D index")
```