Lattice Graphs – Control of Panel of Panel & Strip Borders[1]

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Abstract

The discussion that follows will use as starting point a dotplot graph that has been enhanced to show limits around the points. Modifications will then be deomonstrated, to provide a graph that conforms to the guidelines for the journal *Eocologia*.

1 Dotplot, with Limits around the Estimates

The `segplot()` function (*latticeExtra*) gives the graph that is required. The data are:

```
> numsDF <- data.frame(
    species=rep(c("Jimajing teresaeta", "Sasquatch rutilusaeta"), c(3,3)),
    bcat=rep(c("<2 y", "5-10 y", ">20 y"), 2),
    estlog=c(0.286, 1.660, -0.616, 2.488, 3.689, 2.290),
    halfwid=rep(c(0.198, 0.464), c(3,3)))
> numsDF$bcat <- factor(numsDF$bcat, levels=c("<2 y", "5-10 y", ">20 y"))
> ## Data are on a log scale.  Transform to a scale that has
> ## estimated numbers, and limits about those estimates
> numsDF <- within(numsDF, {
        estnum=exp(estlog)
        lolim=exp(estlog-halfwid)
        hilim=exp(estlog+halfwid)
  }
  )
> ## Check the data
> print(numsDF, quote=FALSE)
```

```
                species  bcat estlog halfwid   hilim  lolim estnum
1    Jimajing teresaeta   <2 y  0.286  0.198   1.623  1.092   1.33
2    Jimajing teresaeta  5-10 y  1.660  0.198   6.411  4.315   5.26
3    Jimajing teresaeta  >20 y -0.616  0.198   0.658  0.443   0.54
4 Sasquatch rutilusaeta   <2 y  2.488  0.464  19.144  7.569  12.04
5 Sasquatch rutilusaeta  5-10 y  3.689  0.464  63.625 25.154  40.00
6 Sasquatch rutilusaeta  >20 y  2.290  0.464  15.705  6.209   9.87
```

The following uses the function `segplot()` from the *latticeExtra* package to show estimated numbers, with ranges around those numbers;

```
> library(latticeExtra)
> segplot(bcat ~ lolim+hilim | species, centers=estnum, draw.bands=FALSE,
         data=numsDF,
         scales=list(x="free"),
         cex=1.5,
         lwd=2,
         layout=c(1,2))
```

2   Modified Graph, now in an Oecologia Style

We make the following changes:

- Left justify the strip panel label.

- Use the abilities for plotting expressions to show the species names in italics.

- Omit the bounding box of the strip panel.

- Use L-shaped panel boxes.

```
> ## Setup for panel text
> specfac <- numsDF$species
> speclabs <- gsub(".", " ", levels(specfac), fixed=TRUE)
> abc <- paste(letters[1:length(speclabs)],": ", sep="")
> levlist <- lapply(1:length(speclabs), function(i)
                 substitute(id*italic(z),
                            list(id=abc[i], z=speclabs[i])))
> ## Define a strip function that displays the panel text
> stripfun <- function(which.given, which.panel,
                    factor.levels=as.expression(levlist), ...){
  panel.text(x=0, y=0.6,
             lab = as.expression(levlist[which.panel[which.given]]),
             adj=0)
  }
```

```
> ## Use the function that follows to control box type
> axis.L <-
    function(side, ..., line.col)
      {
        if (side %in% c("bottom", "left")) {
          col <- trellis.par.get("axis.text")$col
          axis.default(side, ..., line.col = col)
          if (side == "bottom")
            grid::grid.lines(y = 0)
          if (side == "left")
            grid::grid.lines(x = 0)
        }
      }

> ## hide panel and strip borders by using col = NA
> sty <- list()
> sty$axis.line$col <- NA
> sty$strip.border$col <- NA
> sty$strip.background$col <- NA
```

Now use `segplot()` to create the plot:

```
> gph <- segplot(bcat ~ lolim+hilim | species, centers=estnum,
                 draw.bands=FALSE,
                 data=numsDF, as.table=TRUE,
                 strip=stripfun, par.settings=sty, axis=axis.L,
                 scales=list(x="free"), lwd=2, cex=1.5,
                 layout=c(1,2),
                 between=list(x=0, y=0.5))
```

The argument `as.table=TRUE` causes the first panel to appear in the topmost position.
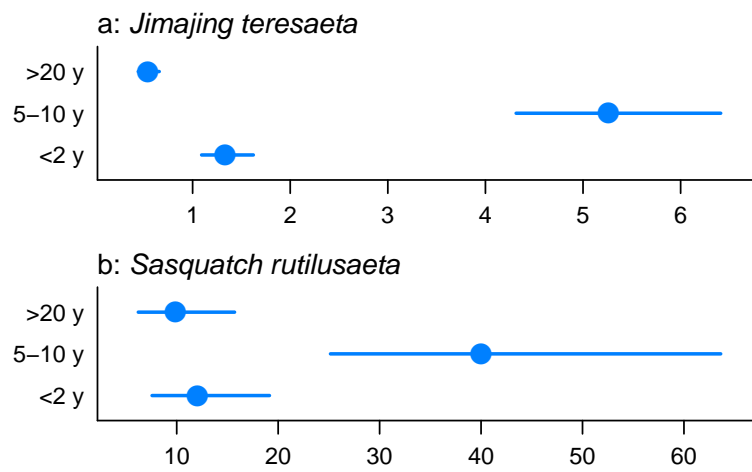Figure 1 shows the result:

Figure 1: Adaptation of a plot dervived using `segplot()`, to use the style required for the journal Oecologia.

To prepare a pdf of the right size, do:

```
> trellis.device(device, width=3.3, height=2.25, color=FALSE,
                 file="imaginaryCreatures.pdf")
> print(gph)
> dev.off()
```