Image Parameters in R

par

From ?par:
Description:

'par' can be used to set or query graphical parameters. Parameters can be set by specifying them as arguments to 'par' in 'tag = value' form, or by passing them as a list of tagged values.

There are a very large number of settings in par. For the full documentation, read the par help. Common settings that would be changed are discussed here.

bg Set the background colour for the whole image. Can be set with colour names

(bg="red") or hex values (bg="#FF0000")

Set the colour that the plot is drawn with (border, tick mark labels, points, etc)

cex This changes the size of the text for the labels on a plot as a magnification factor

(default cex=1). If you wish to make them larger, set this as e.g. cex=3

cex.axis As for cex, but for tick mark labels on the axes

cex.lab ... axis title (the 'label')

cex.main ... title of plot

col.axis The colour of the axis tick mark labels col.lab ... axis titles (default col.axis="black")

col.main ... title for the plot

font The font type to use (default font=1)

1 – Normal
2 – Bold
3 – Italic
4 – Bold italic

font.axis Font for tick mark labels

font.lab ... axis title font.main ... plot title

The number of tick marks on the axes. Specified as lab=c(x,y,len) where len is

unimplemented. The defaults are c(5,5,7) - 5 tick marks per axis

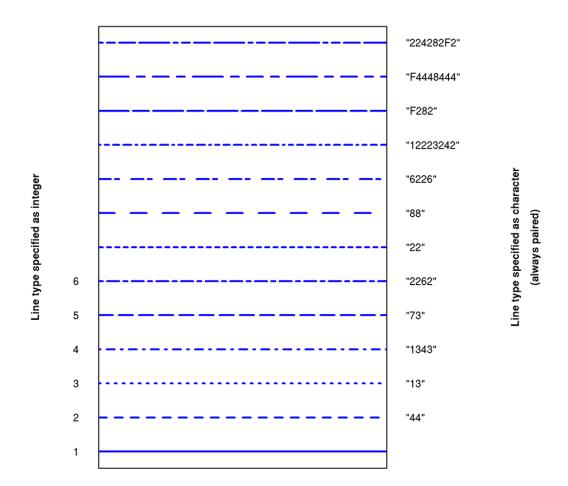
Tick mark label orientation on axes. las=0 (default) is parallel to the axis, las=2 is

perpendicular to the axis. las=1 gives horizontal labels, las=3 gives vertical labels

1ty Line type. If specified as a character, the value is the length of mark followed by

length of space, i.e. "82" would be 8 units long with a 2 unit gap. Integers 1-6 can be

used instead, as shown below



The number of (text) lines to use for the plot margins. Specified as c(bottom, left, top, mar right). Default is mar=c(5,4,4,2)The distance (in text lines) that the axis title, labels and line are displaced. Defaults to mgp mgp=c(3,1,0)The distance (in lines) around the outside of the plotting area. Good for inserting oma date/time stamps without affecting the figure itself xlab, ylab Label for *x*-axis, *y*-axis Specify ="n" to suppress plotting of axis (use axis() to add a custom axis) xaxt,yaxt Label for plot main Expand available plotting area (e.g. if legend is placed outside plot region)

xpd

Character symbol to use as point symbol. 0-25 are specified as an integer value (i.e. pch=5), while the remaining characters are specified as characters (i.e. pch="a"). Any (single) character may be used. For characters 21-25, the fill colour is specified by bg¹, i.e. bg="880000" in this case. Colours are specified by col.

Symbols for par(pch=...)

_ O	▽ 6	⊞ 12	◆ 18	▲ 24	0 0	1 1
0 1	⊠ 7	⊠ 13	• 19	▼ 25	+ +	2 2
△ 2	* 8	☑ 14	• 20	* *		9 9
+3	4 9	1 5	• 21	٠.	1.1	a a
× 4	⊕ 10	• 16	■ 22	0 0	% %	b b
♦ 5	፟ 11	▲ 17	♦ 23	0 0	# #	z z

0-25: as integers Other symbols: as characters

¹bg in this context is for the points. When as par(bg="blue"), bg is the plot background. If called as plot(bg="blue"), it is the background of the symbol (only applicable for pch=21:25)

Example

```
# Reduce dataset to single replicates of runs 1 to 5
dnase < -DNase[seq(2,80,by=2),]
# Change the ordered levels to integers
dnase$Run<-as.integer(as.character(dnase$Run))</pre>
# Define line types to use
linetype<-c("44","13","1343","73","2262")</pre>
# Define colours to use
col_list<-c("#ee3333","#3366aa","#009973","#992288","#fba300")</pre>
# Define symbols to use
pch_list<-seq(0:5)</pre>
# Set margins and allow for objects outside plot area
par(xpd=TRUE, mar=par() mar+c(0,0,0,5))
# Draw an empty plot window
                                                      # x- and y- values
# don't plot anything yet
plot(dnase$conc,dnase$density,
     type="n".
    xlab="Concentration",ylab="Density",
main="ELISA assay of DNase Activity"
                                                      # Axis titles
                                                      # Plot title
     las=1.
                                                      # Axis labels horizontal
)
# Plot each run as a separate line and create labels
legend_labels<-c()
for (ii in 1:5) {
     lines(dnase$conc[which(dnase$Run==ii)];
         dnase$conc[which(dnase$Run==ii)],
col=col_list[ii],
pch=pch_list[ii],
lty=linetype[ii],
lwd=2,type="o"
     legend_labels<-append(legend_labels,paste("Run",ii))
# Add a legend
legend("left",inset=1.05,legend_labels,col=col_list,lty=linetype,lwd=2)
```

ELISA assay of **DNase** Activity

