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"`)
`fg`	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
`lab`	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
`las`	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

`lty`	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

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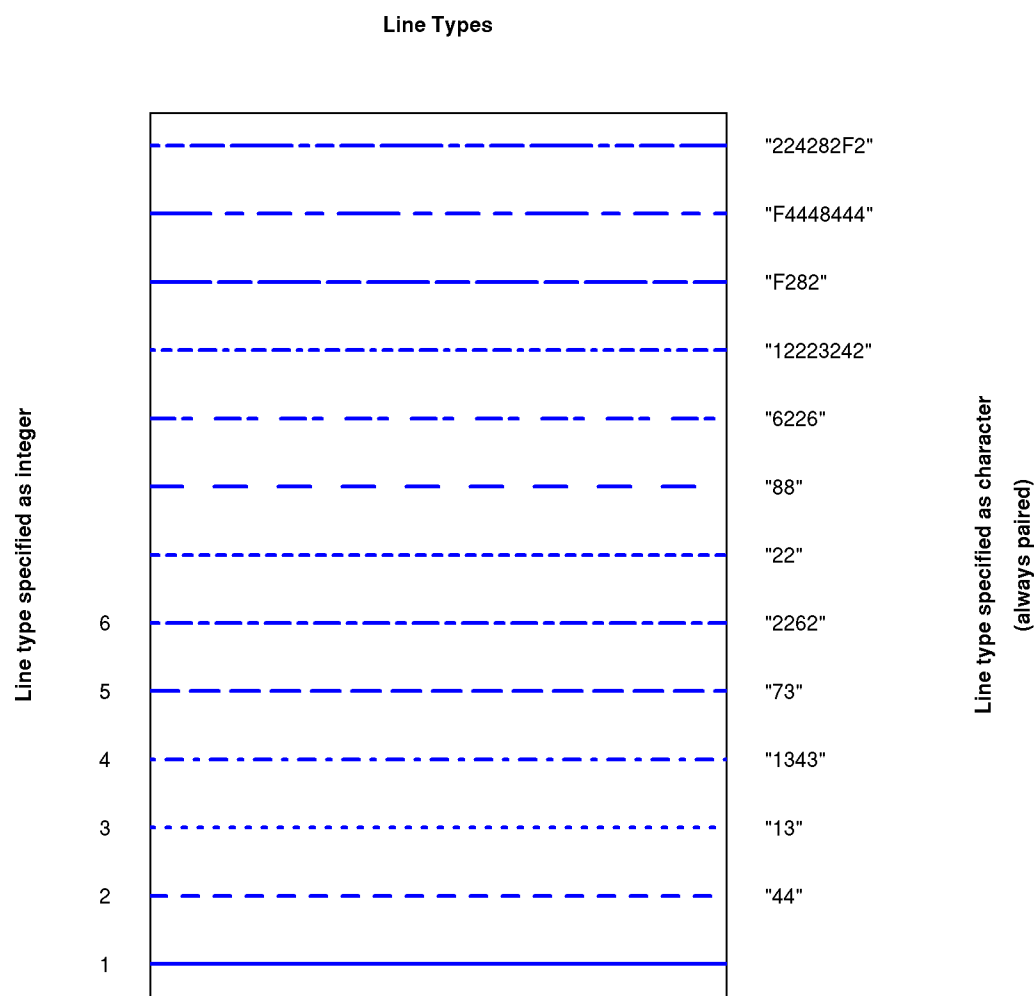
`mar`	The number of (text) lines to use for the plot margins. Specified as c(bottom, left, top, right). Default is `mar=c(5,4,4,2)`
`mgp`	The distance (in text lines) that the axis title, labels and line are displaced. Defaults to `mgp=c(3,1,0)`
`oma`	The distance (in lines) around the outside of the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

pch   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 bg[1], i.e. bg="880000" in this case. Colours are specified by col.

Symbols for par(pch=...)

□ 0	▽ 6	⊞ 12	◆ 18	▲ 24	0 0	1 1
○ 1	⊠ 7	⊗ 13	● 19	▼ 25	+ +	2 2
△ 2	✳ 8	▽ 14	● 20	* *	- -	9 9
+ 3	⊕ 9	■ 15	● 21	. .	| |	a a
× 4	⊕ 10	● 16	■ 22	o o	% %	b b
◇ 5	✖ 11	▲ 17	◆ 23	○ O	# #	z z

0-25: as integers   Other symbols: as characters

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

ELISA assay of DNase Activity