vipor package usage example (version 0.4.1)

Scott Sherrill-Mix, Erik Clarke

Abstract

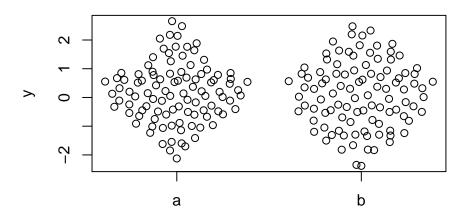
This is a collection of examples of usage for the **vipor** package.

Keywords: visualization, display, one dimensional, grouped, groups, violin, scatter, points, quasirandom, beeswarm, van der Corput.

1. The basics

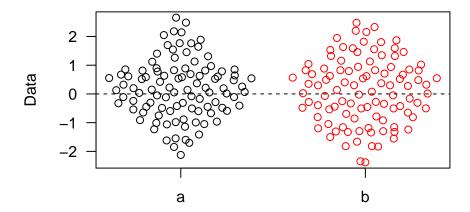
This is the simplest example of using the vpPlot function to generate violin scatter plots:

- > library(vipor)
- > set.seed(12345)
- > n<-100
- > dat<-rnorm(n*2)</pre>
- > labs<-rep(c('a','b'),n)</pre>
- > vpPlot(labs,dat)



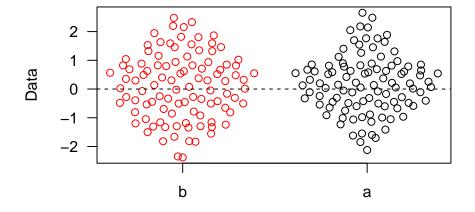
vpPlot is just a wrapper around plot so standard graphical options can be used and the plot can be annotated with R plotting functions:

- > vpPlot(labs,dat,las=1,ylab='Data',col=rep(1:2,n))
- > abline(h=0,1ty=2)



Factors can be used to generate custom group orderings:

- > labs2<-factor(labs,levels=c('b','a'))</pre>
- > vpPlot(labs2,dat,las=1,ylab='Data',col=rep(1:2,n))
- > abline(h=0,1ty=2)



For custom plotting, the offsets for a group of points can be calculated using the offsetX function. The adjusted x position of the points is also returned invisibly from vpPlot:

```
> offsets<-offsetX(dat,labs)
> head(offsets,4)

[1] -0.18939738  0.10387013  0.28854590  0.01104955

> xPos<-vpPlot(labs,dat)
> head(xPos,4)

[1] 0.8106026  2.1038701  1.2885459  2.0110496

> xPos2<-rep(1:2,n)+offsets
> head(xPos2,4)

[1] 0.8106026  2.1038701  1.2885459  2.0110496

> all(xPos==xPos2)

[1] TRUE
```

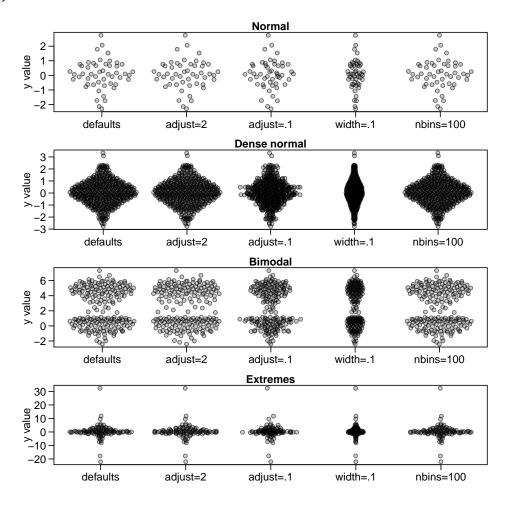
Note that offsetX returns offsets centered around 0 which will need to be added to the original x positions.

2. Options

offsetX calls stats::density to compute kernel density estimates. The tightness of the fit can be adjusted with the adjust option and the width of the offset with width. nbins to adjust the number of bins used in the kernel density is also provided but this can usually be left at its default when using quasirandom offsets:

```
dat <- list(</pre>
>
      'Normal'=rnorm(50),
      'Dense normal'= rnorm(500),
      'Bimodal'=c(rnorm(100), rnorm(100,5)),
      'Extremes'=rcauchy(100)
    )
    par(mfrow=c(4,1), mar=c(2.5,3.1, 1.2, 0.5), mgp=c(2.1,.75,0),
>
    cex.axis=1.2,cex.lab=1.2,cex.main=1.2)
    dummy<-sapply(names(dat),function(label) {</pre>
      y<-dat[[label]]
      offsets <- list(
        'defaults'=offsetX(y), # Default
        'adjust=2'=offsetX(y, adjust=2),
                                              # More smoothing
        'adjust=.1'=offsetX(y, adjust=0.1), # Tighter fit
```

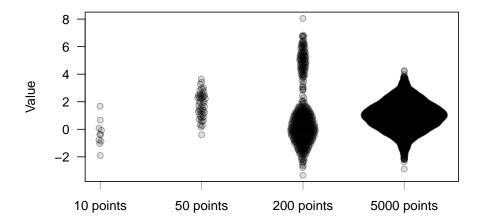
```
+ 'width=.1'=offsetX(y, width=0.1),  # Less wide
+ 'nbins=100'=offsetX(y, nbins=100)  # Less bins
+ )
+ ids <- rep(1:length(offsets), each=length(y))
+ plot(unlist(offsets) + ids, rep(y, length(offsets)), ylab='y value',
+ xlab='', xaxt='n', pch=21,
+ col='#00000099',bg='#00000033',las=1,main=label)
+ axis(1, 1:length(offsets), names(offsets))
+ })</pre>
```



The varwidth argument scales the width of a group by the square root of the number of observations in that group (as in the function boxplot). Arguments to offsetX can be passed into vpPlot as a list through the offsetXArgs argument.

```
> dat <- list(
+ '10 points'=rnorm(10),
+ '50 points'=rnorm(50,2),
+ '200 points'=c(rnorm(400), rnorm(100,5)),
+ '5000 points'= rnorm(5000,1)
+ )</pre>
```

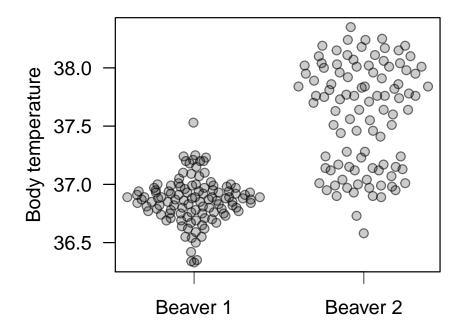
```
> labs<-rep(names(dat),sapply(dat,length))
> labs<-factor(labs,levels=unique(labs))
> vpPlot( labs,unlist(dat),offsetXArgs=list(varwidth=TRUE),
+ las=1,ylab='Value',col='#00000066',bg='#00000022',pch=21)
```



3. Real data

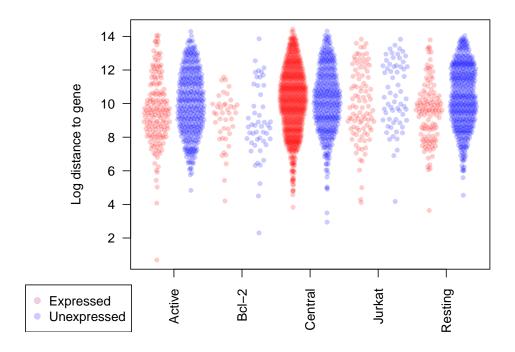
An example using the beaver1 and beaver2 data from the datasets package:

```
> y<-c(beaver1$temp,beaver2$temp)
> x<-rep(
+ c('Beaver 1','Beaver 2'),
+ c(nrow(beaver1),nrow(beaver2))
+ )
> vpPlot(x,y,las=1, ylab='Body temperature',
+ pch=21, col='#00000099',bg='#00000033')
```



An example using the integrations data from this package:

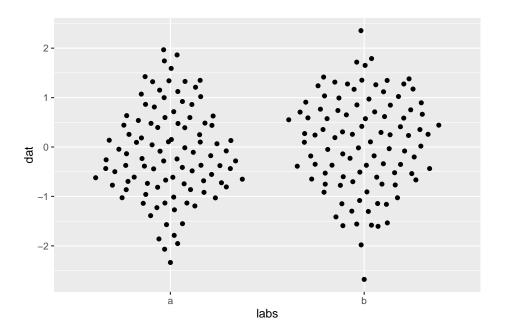
```
> ints<-integrations[integrations$nearestGene>0,]
> y<-log(ints$nearestGene)
> x<-as.factor(paste(ints$study,ints$latent))
> activeCols<-c('Expressed'='#FF000033','Unexpressed'='#0000FF33')
> cols<-activeCols[ints$latent]
> par(mar=c(4,7,.1,.1))
> vpPlot(x,y,las=2, ylab='Log distance to gene',xaxt='n',
+ pch=21, col=cols,bg=cols,cex=.7)
> uniqX<-levels(x)
> prettyX<-tapply(1:length(uniqX),sub('(Une|E)xpressed$','',uniqX),mean)
> axis(1,prettyX,names(prettyX),las=2)
> legend(grconvertX(0.01,from='ndc'),grconvertY(0.15,from='ndc'),
+ names(activeCols),pch=21,col=cols,pt.bg=activeCols,xpd=NA)
```



4. ggbeeswarm package

This package is also wrapped by the **ggbeeswarm** package so if you prefer **ggplot** then you can do something like:

- > library(ggbeeswarm)
- > n<-100
- > dat<-rnorm(n*2)</pre>
- > labs<-rep(c('a','b'),n)
- > ggplot(mapping=aes(labs,dat))+geom_quasirandom()



Affiliation:

Github: http://github.com/sherrillmix/vipor