violinpoint package example (version 0.3.0)

Scott Sherrill-Mix, Erik Clarke

Abstract

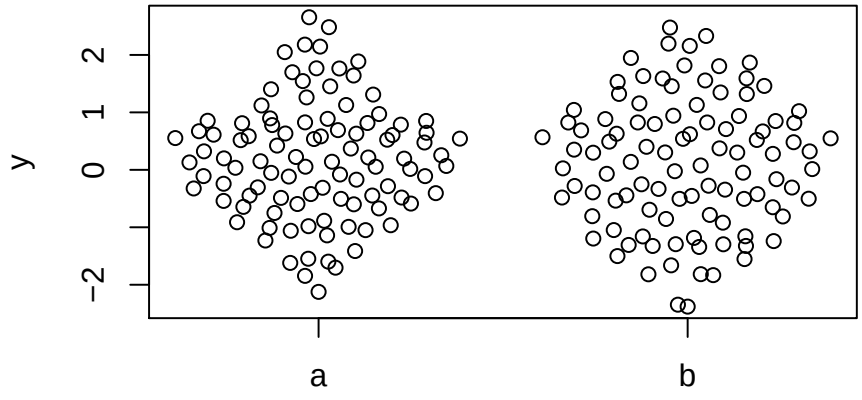
This is a collection of examples of usage for the **violinpoint** package.

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

1. The basics

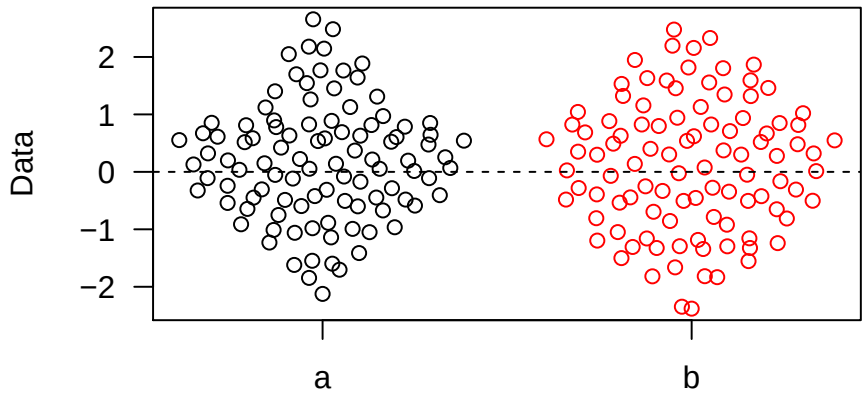
This is the simplest example of using the `vpPlot` function to generate violin scatter plots:

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



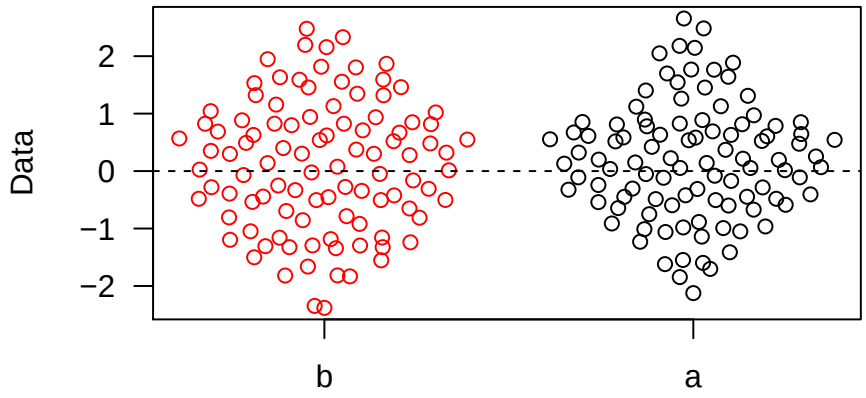
`vpPlot` is just a wrapper around `plot` so standard graphical options can be used and the plot can be annotated with R plotting functions:

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



Factors can be used to generate custom group orderings:

```
>   labs2<-factor(labs,levels=c('b','a'))
>   vpPlot(labs2,dat,las=1,ylab='Data',col=rep(1:2,n))
>   abline(h=0,lty=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] -0.18939799  0.10386912  0.28854689  0.01104941

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

[1] 0.810602 2.103869 1.288547 2.011049

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

[1] 0.810602 2.103869 1.288547 2.011049

>         all(xPos==xPos2)

[1] TRUE
```

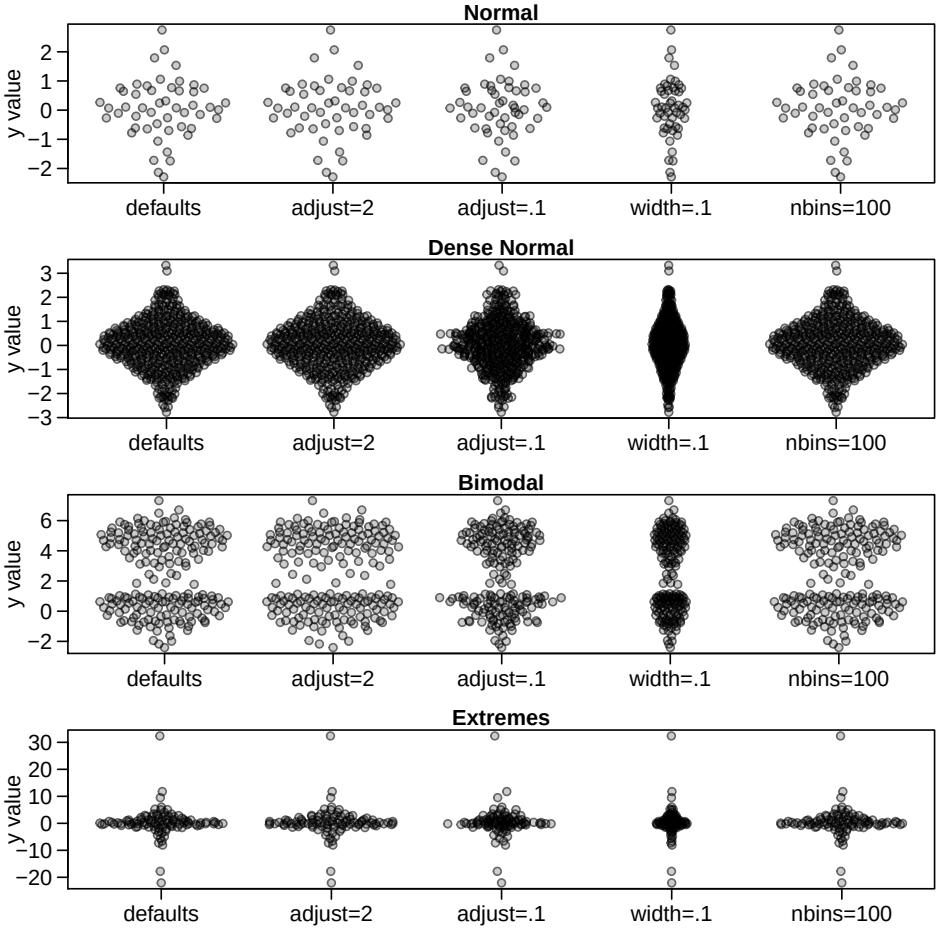
Note that `offsetX` returns offsets centered around 0 which will need to be added to the original x positions.

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(rnorm(50), rnorm(500), c(rnorm(100),
+         rnorm(100,5)), rcauchy(100))
> names(dat) <- c("Normal", "Dense Normal", "Bimodal", "Extremes")
> 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) {
+         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
+         )
```

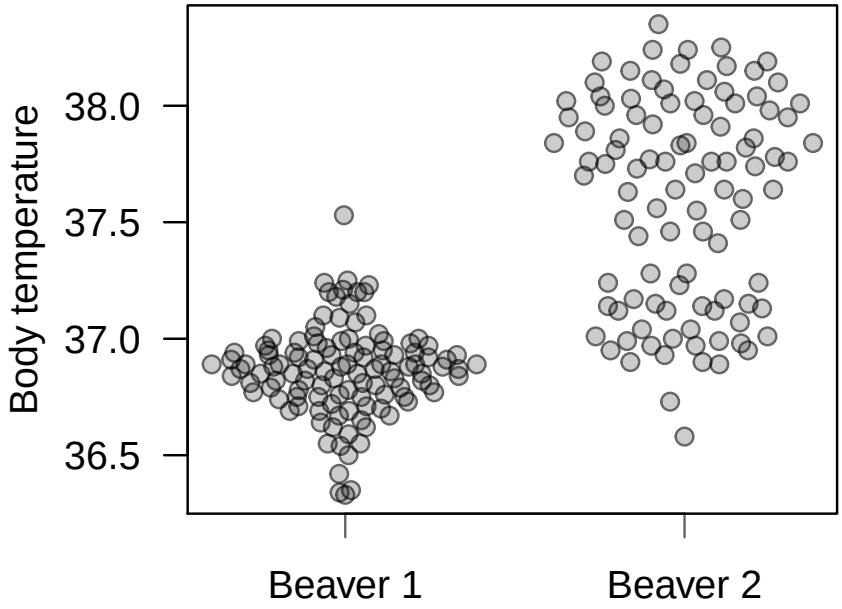
```
+         ids <- rep(1:length(offsets), each=length(y))
+         plot(unlist(offsets) + ids, rep(y, length(offsets)), ylab='y value',
+                 xlab='', xaxt='n', pch=21,
+                 col='#00000099',bg='#00000033',las=1,main=label)
+         axis(1, 1:length(offsets), names(offsets))
+ })
```



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'
+   )
```



Affiliation:

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