

Grouped one dimensional data comparison (**violinpoint** version 0.3.0)

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Abstract

This is a comparison of various methods for visualizing groups of 1-dimensional data with an emphasis on the **violinpoint** package.

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

1. Methods

There are several ways to plot grouped one-dimensional data combining points and density estimation:

pseudorandom The kernel density is estimated then points are distributed uniform randomly within the density estimate for a given bin. Selection of an appropriate number of bins does not greatly affect appearance but coincidental clumpiness is common.

alternating within bins The kernel density is estimated then points are distributed within the density estimate for a given bin evenly spaced with extreme values alternating from right to left e.g. max, 3rd max, ..., 4th max, 2nd max. If maximums are placed on the outside then these plots often form consecutive “smiley” patterns. If minimums are placed on the outside then “frowny” patterns are generated. Selection of the number of bins can have large effects on appearance important.

beanplot The package **beeswarm** provides methods for generating a “beeswarm” plot where points are distributed so that no points overlap. Kernel density is not calculated although the resulting plot does provide an approximate density estimate. Selection of an appropriate number of bins affects appearance and plot and point sizes must be known in advance.

quasirandom The kernel density is estimated then points are distributed quasirandomly using the von der Corput sequence within the density estimate for a given bin. Selection of an appropriate number of bins does not greatly affect appearance and position does not depend on plotting parameters.

2. Simulated data

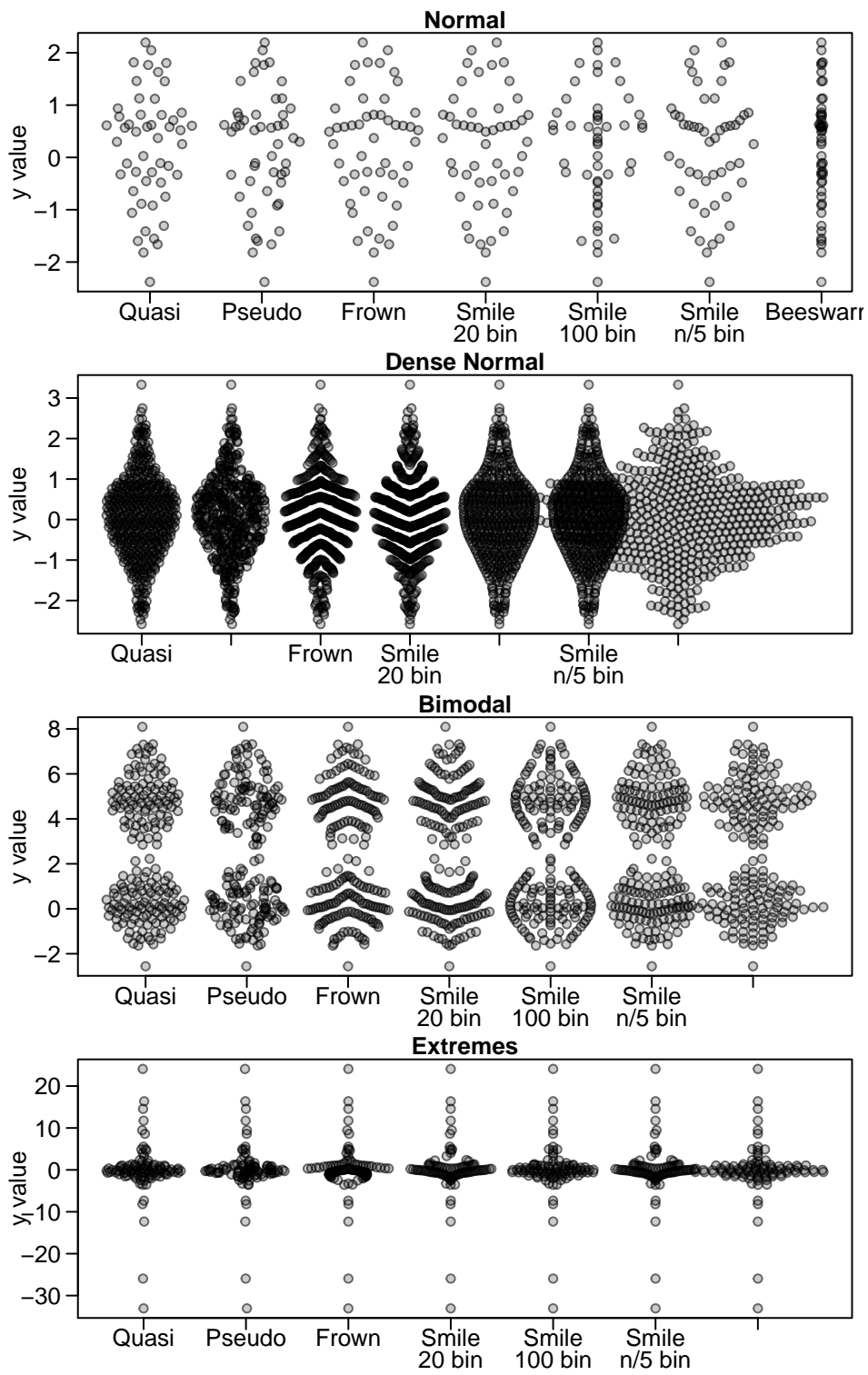
To compare between methods we’ll generate some simulated data from normal, bimodal (two

normal) and Cauchy distributions:

```
> library(beeswarm)
> library(violinpoint)
> set.seed(12345)
> dat <- list(rnorm(50), rnorm(500), c(rnorm(100), rnorm(100,5)), rcauchy(100))
> names(dat) <- c("Normal", "Dense Normal", "Bimodal", "Extremes")
```

Here, we plot the data using quasirandom, pseudorandom, alternating and beeswarm methods:

```
> 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(
+     'Quasi'=offsetX(y), # Default
+     'Pseudo'=offsetX(y, method='pseudorandom',nbins=100),
+     'Frown'=offsetX(y, method='frowney',nbins=20),
+     'Smile\n20 bin'=offsetX(y, method='smiley',nbins=20),
+     'Smile\n100 bin'=offsetX(y, method='smiley',nbins=100),
+     'Smile\nn/5 bin'=offsetX(y, method='smiley',nbins=round(length(y)/5)),
+     'Beeswarm'=swarmx(rep(0,length(y)),y)$x
+   )
+   ids <- rep(1:length(offsets), each=length(y))
+   plot(unlist(offsets) + ids, rep(y, length(offsets)),
+        xlab='', xaxt='n', pch=21,las=1,main=label, ylab='y value',
+        col='#00000099',bg='#00000033')
+   par(lheight=.8)
+   axis(1, 1:length(offsets), names(offsets),padj=1,mgp=c(0,-.3,0),tcl=-.5)
+ })
```

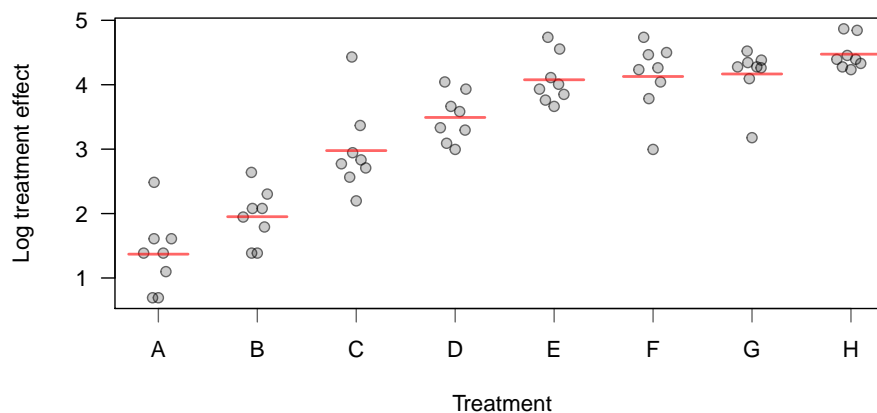


3. Real data

3.1. Suboptimal examples

An example with few data points (maybe a bit too few for optimal use of this package) using the `OrchardSprays` data from the **datasets** package:

```
> vpPlot(
+   OrchardSprays$treatment, log(OrchardSprays$decrease),
+   las=1, ylab='Log treatment effect',
+   offsetXArgs=list(width=.2),
+   pch=21, col='#00000099', bg='#00000033'
+ )
> means<-tapply(log(OrchardSprays$decrease), OrchardSprays$treatment, mean)
> segments(
+   1:length(means)-.3, means, 1:length(means)+.3, means,
+   col='#FF000099', lwd=2
+ )
> title(xlab='Treatment')
```



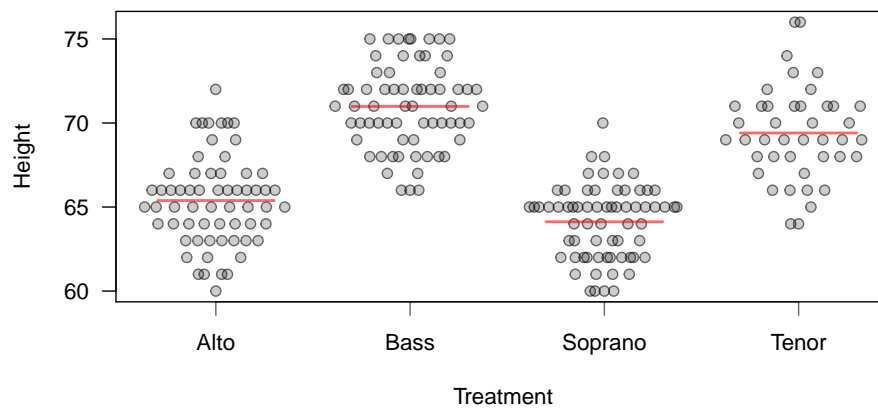
Data with discrete bins are plotted adequately but might be better suited example with few data points using the `singer` data from the **lattice** package:

```
> data('singer', package='lattice')
> part<-sub(' [0-9]+$',' ', singer$voice)
> vpPlot(
+   part, singer$height,
+   las=1, ylab='Height',
+   pch=21, col='#00000099', bg='#00000033'
+ )
> means<-tapply(singer$height, part, mean)
```

```

> segments(
+   1:length(means)-.3,means,1:length(means)+.3,means,
+   col='#FF000099',lwd=2
+ )
> title(xlab='Treatment')

```

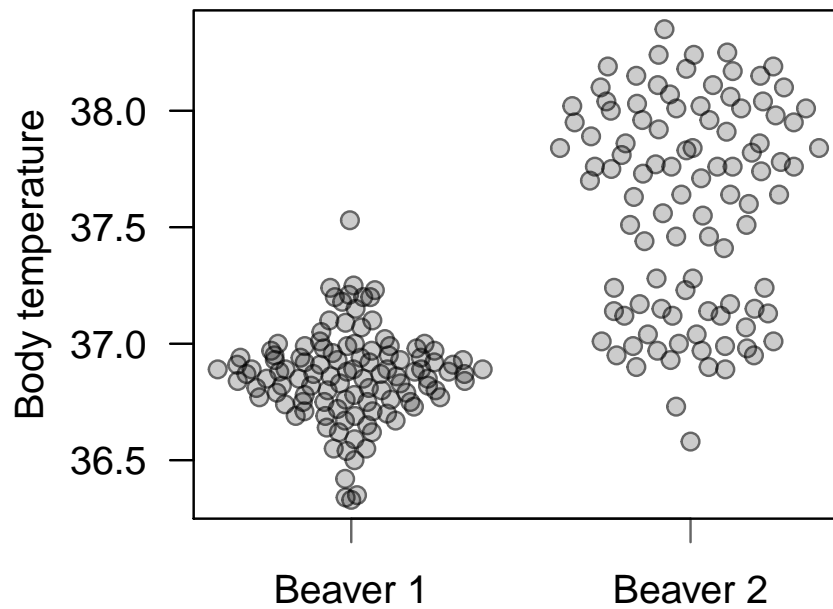


An example with using the beaver1 and beaver2 data from R:

```

> 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'
+ )

```



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