Package ‘directlabels’

January 16, 2021

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Version  2021.1.13

BugReports  https://github.com/tdhock/directlabels/issues
License  GPL-3
Title  Direct Labels for Multicolor Plots
Description  An extensible framework for automatically placing direct labels onto multicolor 'lattice' or 'ggplot2' plots. Label positions are described using Positioning Methods which can be re-used across several different plots. There are heuristics for examining "trellis" and "ggplot" objects and inferring an appropriate Positioning Method.

URL  https://github.com/tdhock/directlabels
LazyData  true

Suggests  MASS, knitr, markdown, inlinedocs, RColorBrewer, ggplot2 (>= 2.0), rlang, lattice, alphahull, nlme, lars, latticeExtra, dplyr, ggthemes, testthat
Imports  grid, quadprog

VignetteBuilder  knitr

NeedsCompilation  no
Repository  CRAN

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- right.points
ahull.grid

Description

Label the closest point on the alpha hull of the data.

Usage

"ahull.grid"

ahull.points

Description

Calculate the points on the ashape.

Usage

ahull.points(d, ..., 
    ahull = default.ahull(d))
angled.boxes

Arguments

d
...
ahull

Author(s)

Toby Dylan Hocking

Description

Draw a box with the label inside, at the point furthest away from the plot border and any other curve.

Usage

"angled.boxes"

angled.endpoints

Description

Useful for labeling lines that all end at the top.

Usage

"angled.endpoints"
apply.method

Apply a Positioning Method

Description

Run a Positioning Method list on a given data set. This function contains all the logic for parsing a Positioning Method and sequentially applying its elements to the input data to obtain the label positions.

Usage

apply.method(method,
    d, columns.to.check = c("x", "y", "groups", "label"), ..., 
    debug = FALSE)

Arguments

method

Direct labeling Positioning Method. Starting from the data frame of points to plot for the panel, the elements of the Positioning Method list are applied in sequence, and then each row of the resulting data frame is used to draw a direct label. The elements of a Positioning Method list can be

• a Positioning Function is any function(d,...) which takes a data.frame d with columns x,y,groups and returns another data.frame representing the positions of the desired direct labels. For a description of all the columns that are interpreted for drawing direct labels, see drawDetails.dlgrob. For example, maxvar.points is a Positioning Function that returns a data.frame with columns x,y,groups,hjust,vjust.

• a character vector of length 1 is treated as the name of an R object. For example, specifying "maxvar.points" means to look up the variable called maxvar.points and use that. Using the name of a Positioning Function is preferable to specifying the Positioning Function itself, since then the name is visible in the Positioning Method list, which is more interpretable when debugging.

• a named list element is used to add or update variables in the data.frame of direct labels to plot. For example list("first.points",cex=1.5) means take only the first points of every group and then set the cex column to 1.5.

• an element of a Positioning Method list can be another Positioning Method list, in which case the elements of the inner list are applied.

d

Data frame to which we apply the Positioning Method. The x and y columns should be in centimeters (cm), so that Positioning Methods can easily calculate the L2/Euclidean/visual distance between pairs of points.

columns.to.check

After applying each Positioning Method list element, we check for the presence of these columns, and if not found we stop with an error.
... Named arguments, passed to Positioning Functions.

**debug**
If TRUE, print each Positioning Method list element and the direct label data.frame that results from its evaluation.

**Value**
The final data frame returned after applying all of the items in the Positioning Method list, with x and y in units of cm.

**Author(s)**
Toby Dylan Hocking

---

### big.boxes

<table>
<thead>
<tr>
<th>big.boxes</th>
<th>big boxes</th>
</tr>
</thead>
</table>

**Description**
Calculate big boxes around the means of each cluster.

**Usage**

```
"big.boxes"
```

---

### bottom.pieces

<table>
<thead>
<tr>
<th>bottom.pieces</th>
<th>bottom pieces</th>
</tr>
</thead>
</table>

**Description**
Positioning Method for the bottom of a group of points.

**Usage**

```
bottom.pieces(d, ...)
```

**Arguments**

d
...

**Author(s)**
Toby Dylan Hocking
**bottom.points**  
*bottom points*

**Description**
Positioning Method for the bottom of a group of points.

**Usage**
```r
bottom.points(d, ...)
```

**Arguments**
- **d**

**Author(s)**
Toby Dylan Hocking

---

**bottom.polygons**  
*bottom polygons*

**Description**
Draw a speech polygon to the bottom point.

**Usage**
```r
"bottom.polygons"
```

---

**bumpup**  
*bumpup*

**Description**
Sequentially bump labels up, starting from the bottom, if they collide with the label underneath.

**Usage**
```r
bumpup(d, ...)
```
calc.borders

Arguments

d
...

Author(s)
Toby Dylan Hocking

calc.borders  calc borders

Description
Calculate bounding box based on newly calculated width and height.

Usage
calc.borders(d, ...)

Arguments
d  Data frame of point labels, with new widths and heights in the w and h columns.
...  ignored.

Author(s)
Toby Dylan Hocking

calc.boxes  calc boxes

Description
Calculate boxes around labels, for collision detection.

Usage
calc.boxes(d, debug = FALSE, ...)

Arguments
d
debug
d...

check.for.columns

Description
Stop if a data.frame does not have some columns.

Usage
check.for.columns(d, must.have)

Arguments
d data.frame to check.
must.have column names to check.

Author(s)
Toby Dylan Hocking

chull.grid

Description
Label the closest point on the convex hull of the data.

Usage
"chull.grid"
**Description**

Calculate the points on the convex hull.

**Usage**

```r
cull.points(d, ...)
```

**Arguments**

- `d`
- `...`

**Author(s)**

Toby Dylan Hocking

---

**Description**

Calculate the default alpha parameter for ashape based on the average size of label boxes.

**Usage**

```r
default.ahull(d, ...)
```

**Arguments**

- `d`
- `...`

**Author(s)**

Toby Dylan Hocking
Description

Look at `options()` for a user-defined default Positioning Method picker, and use that (or the hard-coded default picker), with the calling environment to figure out a good default.

Usage

```r
default.picker(f)
```

Arguments

- `f` Object class to look for (trellis or ggplot).

Author(s)

Toby Dylan Hocking

---

Description

Default method selection method for ggplot2 plots.

Usage

```r
defaultpf.ggplot(geom,
    p, L, colvar, ...)
```

Arguments

- `geom`
- `p`
- `L`
- `colvar`
- `...`

Author(s)

Toby Dylan Hocking
**defaultpf.trellis**

**Description**
If no Positioning Method specified, choose a default using this function. The idea is that this is called with all the variables in the environment of `panel.superpose.dl`, and this can be user-customizable by setting the `directlabels.defaultpf.lattice` option to a function like this.

**Usage**

```r
defaultpf.trellis(lattice.fun.name, groups, type, ...)
```

**Arguments**

- `lattice.fun.name`
- `groups`
- `type`
- `...`

**Author(s)**
Toby Dylan Hocking

---

**direct.label**

*Direct labels for color decoding*

**Description**
Add direct labels to a plot, and hide the color legend. Modern plotting packages like lattice and ggplot2 show automatic legends based on the variable specified for color, but these legends can be confusing if there are too many colors. Direct labels are a useful and clear alternative to a confusing legend in many common plots.

**Usage**

```r
direct.label(p, method = NULL, debug = FALSE)
```
Arguments

p  The "trellis" or "ggplot" object with things drawn in different colors.

method  Positioning Method, which determines the positions of the direct labels as a function of the plotted data. If NULL, we examine the plot p and try to choose an appropriate default. See apply.method for more information about Positioning Methods.

debug  Show debug output?

Value

A plot with direct labels and no color legend.

Author(s)

Toby Dylan Hocking

Examples

```r
if(require(ggplot2)){
  ## Add direct labels to a ggplot2 scatterplot, making sure that each
  ## label is close to its point cloud, and doesn't overlap points or
  ## other labels.
  scatter <- qplot(jitter(hwy),jitter(cty),data=mpg,colour=class,
                   main="Fuel efficiency depends on car size")
  print(direct.label(scatter))
}
```

```r
## direct labels for lineplots that do not overlap and do not go off
## the plot.
library(nlme)
library(lattice)
oldopt <- lattice.options(panel.error=NULL)
ratplot <-
  xyplot(weight~Time|Diet,BodyWeight,groups=Rat,type='l',layout=c(3,1))
  ## Using the default Positioning Method (maxvar.qp), the labels are
  ## placed on the side which is most spread out, so in multipanel
  ## plots they sometimes end up on different sides.
  print(direct.label(ratplot))
  ## To put them on the same side, just manually specify the
  ## Positioning Method.
  print(direct.label(ratplot,"last.qp"))

lattice.options(oldopt)
```
**direct.label.ggplot**

**Description**

Direct label a ggplot2 grouped plot.

**Usage**

```r
## S3 method for class 'ggplot'
direct.label(p,
              method = NULL, debug = FALSE)
```

**Arguments**

- `p` The ggplot object.
- `method` Method for direct labeling as described in `apply.method`.
- `debug` Show debug output?

**Value**

The ggplot object with direct labels added.

**Author(s)**

Toby Dylan Hocking

---

**direct.label.trellis**

**Description**

Add direct labels to a grouped lattice plot. This works by parsing the trellis object returned by the high level plot function, and returning it with a new panel function that will plot direct labels using the specified method.

**Usage**

```r
## S3 method for class 'trellis'
direct.label(p,
              method = NULL, debug = FALSE)
```
dl.combine

Combine output of several methods

Arguments

- `p` The lattice plot (result of a call to a high-level lattice function).
- `method` Method for direct labeling as described in `apply.method`.
- `debug` Show debug output?

Value

The lattice plot.

Author(s)

Toby Dylan Hocking

Description

Apply several Positioning methods to the original data frame.

Usage

dl.combine(...)

Arguments

... Several Positioning Methods.

Value

A Positioning Method that returns the combined data frame after applying each specified Positioning Method.

Author(s)

Toby Dylan Hocking

Examples

```r
## Simple example: label the start and endpoints
library(nlme)
library(lattice)
ratplot <- xyplot(weight~Time|Diet,BodyWeight,groups=Rat,type='l',layout=c(3,1))
both <- dl.combine("first.points","last.points")
rat.both <- direct.label(ratplot,"both")
print(rat.both)
```
## same as repeated call to direct.label:
rat.repeated <-
  direct.label(direct.label(ratplot,"last.points"),"first.points")
print(rat.repeated)

## same with ggplot2:
if(require(ggplot2)){
  rp2 <- qplot(
    Time, weight, data=BodyWeight, geom="line", facets=~Diet, colour=Rat)
  print(direct.label(direct.label(rp2,"last.points"),"first.points"))
  print(direct.label(rp2,"both"))
}

## more complex example: first here is a function for computing the
## lasso path.
mylars <- function
  ## Least angle regression algorithm for calculating lasso solutions.
  (x,  
  ## Matrix of predictor variables.
  y,  
  ## Vector of responses.
  epsilon=1e-6
  ## If correlation < epsilon, we are done.
  ){
    xscale <- scale(x) # need to work with standardized variables
    b <- rep(0,ncol(x))# coef vector starts at 0
    names(b) <- colnames(x)
    ycor <- apply(xscale,2,function(xj)sum(xj*y))
    j <- which.max(ycor) # variables in active set, starts with most correlated
    alpha.total <- 0
    out <- data.frame()
    while(1){## lar loop
      xak <- xscale[,j] # current variables
      r <- y-xscale%*%b # current residual
      ## direction of parameter evolution
      delta <- solve(t(xak)%*%xak)%*%t(xak)%*%r
      ## Current correlations (actually dot product)
      intercept <- apply(xscale,2,function(xk)sum(r*xk))
      ## current rate of change of correlations
      z <- xak%*%delta
      slope <- apply(xscale,2,function(xk)-sum(z*xk))
      ## store current values of parameters and correlation
      out <- rbind(out,data.frame(variable=colnames(x),
                                coef=b,
                                corr=abs(intercept),
                                alpha=alpha.total,
                                arclength=sum(abs(b)),
                                coef.unscaled=b/attr(xscale,"scaled:scale")))
      if(sum(abs(intercept)) < epsilon)#corr==0 so we are done
        return(transform(out,s=arclength/max(arclength)))
      ## If there are more variables we can enter into the regression,
      ## then see which one will cross the highest correlation line
## Calculation of alpha for where lines cross for each variable

d2$alpha <-(d0$intercept-d2$intercept)/(d2$slope-d0$slope)
dsub <- d2[(d2$variable%in%colnames(x)[j])&d2$alpha>epsilon,]
dsub <- subd[which.min(subd$alpha),]
nextvar <- subd$variable
alpha <- if(nrow(subd))subd$alpha else 1
## If one of the coefficients would hit 0 at a smaller alpha
## value, take it out of the regression and continue.
hit0 <- xor(b[j]>0,delta>0)&b[j]!=0
alpha0 <- -b[j][hit0]/delta[hit0]
takeout <- length(alpha0)&&min(alpha0) < alpha
if(takeout){
  i <- which.min(alpha0)
  alpha <- alpha0[i]
}
b[j] <- b[j]+alpha*delta ## evolve parameters
alpha.total <- alpha.total+alpha
## add or remove a variable from the active set
j <- if(takeout)j[j!=which(names(i)==colnames(x))]else c(j,which(nextvar==colnames(x)))

## Calculate lasso path, plot labels at two points: (1) where the
## variable enters the path, and (2) at the end of the path.
if(require(lars)){
data(diabetes,envir=environment())
dres <- with(diabetes,mylars(x,y))
P <- xyplot(coef~arclength,dres,groups=variable,type="l")
mylasso <- dl.combine("lasso.labels", "last_qp")
plot(direct.label(P,"mylasso"))
}

---

### dl.env

**dl env**

#### Description

This environment holds an integer id that will be incremented to get a unique id for each `dlgrob`.

#### Usage

"dl.env"
### `dl.jitter`

**Description**

Jitter the label positions.

**Usage**

```r
dl.jitter(d, ...)
```

**Arguments**

- `d`
- `...`

**Author(s)**

Toby Dylan Hocking

---

### `dl.move`

**Manually move a direct label**

**Description**

Sometimes there is 1 label that is placed oddly by another Positioning Function. This function can be used to manually place that label in a good spot.

**Usage**

```r
dl.move(group, x, y,
        ..., )
```

**Arguments**

- `group` Group to change.
- `x` Horizontal position of the new label.
- `y` Vertical position of the new label. If missing(`y`) and !missing(`x`) then we will calculate a new `y` value using linear interpolation.
- `...` Variables to change for the specified `group`

**Value**

A Positioning Function that moves a label into a good spot.
Author(s)

Toby Dylan Hocking

Examples

```r
if(require(ggplot2)){
  library(lattice)
  scatter <- xyplot(jitter(cty)-jitter(hwy),mpg,groups=class,aspect=1)
  dlcompare(list(scatter),
           list("extreme.grid",
                '+dl.move'=list(extreme.grid,dl.move("suv",15,15)))
  p <- qplot(log10(gamma),rate,data=svmtrain,group=data,colour=data,
             geom="line",facets=replicate~nu)
  adjust.kif <- dl.move("KIF11",-0.9,hjust=1,vjust=1)
  dlcompare(list(p+xlim(-8,7)),
            list("last.points",
                 '+dl.move'=list(last.points,adjust.kif)))
}
```

dl.summarize

dl summarize

Description

summarize which preserves important columns for direct labels.

Usage

dl.summarize(OLD, ...)

Arguments

OLD data frame

...  

Author(s)

Toby Dylan Hocking
dl.trans

Direct label data transform

Description

Make a function that transforms the data. This is for conveniently making a function that calls transform on the data frame, with the arguments provided. See examples.

Usage

dl.trans(...)

Arguments

... Arguments to pass to transform.

Value

A Positioning Function.

Author(s)

Toby Dylan Hocking

Examples

```r
complicated <- list(dl.trans(x=x+10),
                    gapply.fun(d[-2,]),
                    rot=c(30,180))

library(lattice)
direct.label(dotplot(VADeaths,type="o"),complicated,TRUE)
```

dlcompare

Direct label comparison plot

Description

Compare several plots and/or label placement methods. This creates a custom grid graphics display based on lattice and/or ggplot2 output. Plots will be on the columns and positioning methods will be on the rows.

Usage

dlcompare(plots, pos.funs,
          rects = TRUE, row.items = "plots",
          debug = FALSE)
Arguments

plots List of ggplot2 or lattice plots. List names will be used to annotate the plot.
pos.funs List of label placement methods to apply to each plot. List names, or function names if specified as character strings, will be used to annotate the plot.
rects Draw rectangles around each plot, creating a grid?
row.items If "plots" then put plots on the rows and method on the columns. Otherwise, do the opposite.
debug Show debug output?

Author(s)

Toby Dylan Hocking

Examples

library(lattice)
oldopt <- lattice.options(panel.error=NULL)

## Compare two plots of the same data using lattice and ggplot2.
deaths.by.sex <- list(male=mdeaths, female=fdeaths)
deaths.list <- list()
for(sex in names(deaths.by.sex)){
    deaths.ts <- deaths.by.sex[[sex]]
deaths.list[[sex]] <-
data.frame(year=as.numeric(time(deaths.ts)),
    sex,
    deaths=as.integer(deaths.ts))
}
deaths <- do.call(rbind, deaths.list)
death.plot.list <-
    list(lattice=xyplot(deaths~year,deaths,groups=sex,type="l"))
if(require(ggplot2)){
death.plot.list$ggplot2 <-
    qplot(year,deaths,data=deaths,colour=sex,geom="line")
}

if(names(dev.cur())!="postscript"){
## to avoid error on pkg check.
## Use some exotic labeling options with different rotation, font face, family, and alpha transparency.
exotic <- list("last.points",
    rot=c(0,180),
    fontsize=c(10,20),
    fontface=c("bold","italic"),
    fontfamily=c("mono","serif"),
    alpha=c(0.25,1))
dlcompare(death.plot.list, list(exotic))
}

lattice.options(oldopt)
## Compare a legend with direct labels on the same plot.

```r
library(nlme)
if(require(ggplot2)){
    ggrat <- qplot(Time, weight, data=BodyWeight,
                   colour=Rat, geom="line", facets=-Diet)
    pfuns <- list("legend", "direct labels"="last.qp")
    dcompare(list(ggrat), pfuns, rects=FALSE, row.items="posfuns")
}
```

---

**dlhoc**

### Make directlabels documentation

**Description**

Positioning Methods for direct labels are supposed to work with only certain plot types. Each Positioning Method is defined in R/file.R and plot examples are found in tests/doc/file/*.R so that we can automatically assemble a database of example plots from the code.

**Usage**

```r
dhoc(pkgdir = "..")
```

**Arguments**

- `pkgdir` Package directory root.

**Value**

Matrix of lists describing example plots and matching builtin Positioning Methods.

**Author(s)**

Toby Dylan Hocking

---

**dlgrob**

### dlgrrob

**Description**

Make a grid grob that will draw direct labels.

**Usage**

```r
dlgrbob(data, method,
        debug = FALSE, axes2native = identity,
        ...)
```
**draw.rects**

**Arguments**
- **data**: Data frame including points to plot in native coordinates.
- **method**: Positioning Method.
- **debug**: Axis-related positional arguments.
- **axes2native**: Axes-related positional arguments.

**Author(s)**
- Toby Dylan Hocking

**draw.polygons**

**draw polygons**

**Description**
Draw polygons around label positions.

**Usage**
```r
draw.polygons(d, ...)
```

**Arguments**
- **d**: ...

**Author(s)**
- Toby Dylan Hocking

**draw rects**

**draw.rects**

**Description**
Positioning Function that draws boxes around label positions. Need to have previously called `calc.boxes`. Does not edit the data frame.

**Usage**
```r
draw.rects(d, ...)
```
drawDetails.dlgrob

Arguments

d

...  

Author(s)

Toby Dylan Hocking

--

drawDetails.dlgrob   drawDetails dlgrob

Description

Process data points using the Positioning Method and draw the resulting direct labels. This is called for every panel with direct labels, every time the plot window is resized.

Usage

## S3 method for class 'dlgrob'
drawDetails(x,
   recording)

Arguments

x

The dlgrob list object. x$method should be a Positioning Method list and x$data should be a data.frame with the following variables:

x,y numeric horizontal and vertical positions of direct labels, in native units. These are converted to cm units before applying the Positioning Method.

groups factor that indices the different groups, and colour indicates the corresponding group colour.

hjust and vjust (optional) numeric values usually in [0,1] that control the justification of the text label relative to the x,y position.

rot (optional) numeric value in [0,360] that specifies the degrees which the text should be rotated.

cex, alpha, fontface, fontfamily (optional) passed to gpar.

Additionally, x$debug should be set to TRUE or FALSE, and x$saxestonative should be a function that converts units shown on the axes to native units of x$data[,c("x","y")].

recording

Author(s)

Toby Dylan Hocking
edges.to.outside  
(edges to outside)

Description
Given a list of edges from the convex or alpha hull, and a list of cluster centers, calculate a point near to each cluster on the outside of the hull.

Usage
edges.to.outside(edges, centers, debug = FALSE, ...)

Arguments
edges
centers
debug
...

Author(s)
Toby Dylan Hocking

empty.grid  
(empty grid)

Description
Label placement method for scatterplots that ensures labels are placed in different places. A grid is drawn over the whole plot. Each cluster is considered in sequence and assigned to the point on this grid which is closest to the point given by the input data points. Makes use of attr(d,"orig.data").

Usage
empty.grid(d, debug = FALSE, ...)

Arguments
d  Data frame of target points on the scatterplot for each label.
debug  Show debugging info on the plot?
d...  ignored.
Value

Data frame with columns `groups x y`, 1 line for each group, giving the positions on the grid closest to each cluster.

Author(s)

Toby Dylan Hocking

---

**enlarge.box**

**enlarge box**

Description

Make text bounding box larger by some amount.

Usage

enlarge.box(d, ...)

Arguments

d
...

Author(s)

Toby Dylan Hocking

---

**extract.plot**

Extract plot and definition for documentation

Description

Given an R code file, execute it, store the definition, and save the resulting plot in a variable.

Usage

extract.plot(f)

Arguments

f R code file with plot example.

Author(s)

Toby Dylan Hocking
extract.posfun  

*Extract Positioning Method for documentation*

**Description**

Use inlinedocs to extract comments and definitions from code, then for each item found add the value and its name to the list.

**Usage**

```r
extract.posfun(f)
```

**Arguments**

- `f`  
  R code file, which should contain only Positioning Methods that can be used with examples defined in the doc/ subdirectory with the same name.

**Value**

List of lists, each of which describes one Positioning Method defined in `f`.

**Author(s)**

Toby Dylan Hocking

---

**extreme.grid**

**Description**

Label each point cloud near the extremities of the plot region.

**Usage**

```
"extreme.grid"
```
**extreme.points**

Description

Label the points furthest from the middle for each group.

Usage

```r
extreme.points(d, ...)
```

Arguments

d
...

Author(s)

Toby Dylan Hocking

---

**far.from.others.borders**

Description

Find the point on each curve which maximizes the distance to the plot border or to another curve.

Usage

```r
far.from.others.borders(all.groups,
                          ..., debug = FALSE)
```

Arguments

all.groups
...
debug

Author(s)

Toby Dylan Hocking
filltemplate

**Description**

Fill in occurrences of OBJ\$item in the file template with the value in R of L\$item.

**Usage**

filltemplate(L, template)

**Arguments**

- L
- template

**Author(s)**

Toby Dylan Hocking

first.bumpup

**Description**

Label first points, bumping labels up if they collide.

**Usage**

"first.bumpup"

first.points

**Description**

Positioning Method for the first of a group of points.

**Usage**

first.points(d, ...)

first.polygons

Arguments

d
...

Author(s)

Toby Dylan Hocking

first.polygons  first polygons

Description

Draw a speech polygon to the first point.

Usage

"first.polygons"

first.qp  first qp

Description

Label first points from QP solver that ensures labels do not collide.

Usage

"first.qp"
Description
apply a Positioning Method to every group. works like ddply from plyr package, but the grouping
column is always called groups, and the Positioning Method is not necessarily a function (but can
be).

Usage
gapply(d, method, ..., 
groups = "groups")

Arguments
d data frame with column groups.
method Positioning Method to apply to every group separately.
... additional arguments, passed to Positioning Methods.
groups can also be useful for piece column.

Value
data frame of results after applying FUN to each group in d.

Author(s)
Toby Dylan Hocking

Description
Makes a function you can use to specify the location of each group independently.

Usage
gapply.fun(expr)

Arguments
expr Expression that takes a subset of the d data frame, with data from only a single
group, and returns the direct label position.
Value

A Positioning Function.

Author(s)

Toby Dylan Hocking

Examples

```r
complicated <- list(dl.trans(x=x+10),
               gapply.fun(d[-2,]),
               rot=c(30,180))

library(lattice)
direct.label(dotplot(VADeaths,type="o"),complicated,TRUE)
```

Description

ggproto object implementing direct labels.

Usage

```
"GeomDl"
```

Description

Geom that will plot direct labels.

Usage

```r
geom_dl(mapping = NULL,
  data = NULL, ..., 
  method = stop("must specify method= argument"),
  debug = FALSE, stat = "identity",
  position = "identity",
  inherit.aes = TRUE)
```
Arguments

mapping  
aes(label=variable_that_will_be_used_as_groups_in_Positioning_Methods).
data  
data.frame to start with for direct label computation.
method  
Positioning Method for direct label placement, passed to apply.method.
debug  
Show directlabels debugging output?
stat  
passed to layer.
position  
passed to layer.
inherit.aes  
inherit aes from global ggplot definition?

Author(s)

Toby Dylan Hocking

Examples

if(require(ggplot2)){
  vad <- as.data.frame.table(VADeaths)
  names(vad) <- c("age","demographic","deaths")
  leg <- ggplot(vad,aes(deaths,age,colour=demographic)) +
         geom_line(aes(group=demographic)) +
         xlim(8,80)
  print(direct.label(leg,list("last.points",rot=30)))
  labeled <- leg +
             geom_dl(aes(label=demographic), method=list("last.points",rot=30)) +
             scale_colour_discrete(guide="none")
  print(labeled)
  p <- ggplot(vad,aes(deaths,age)) +
       geom_line(aes(group=demographic)) +
       geom_dl(aes(label=demographic),method="top.qp")
  print(p)
  p+aes(colour=demographic)+
       scale_colour_discrete(guide="none")
  p+aes(linetype=demographic)+
       scale_linetype(guide="none")
  bwbase <- ggplot(BodyWeight,aes(Time,weight,label=Rat)) +
           geom_line(aes(group=Rat)) +
           facet_grid(.~Diet)
  bw <- bwbase+geom_dl(method="last.qp")
  print(bw)
  bw2 <- bw+geom_dl(method="first.qp")
}
get.means

## add color
colored <- bw2+aes(colour=Rat)+
  scale_colour_discrete(guide="none")
print(colored)
## or just use direct.label if you use color:
direct.label(bwbase+aes(colour=Rat),dl.combine("first_qp","last_qp"))

## iris data example
giris <- ggplot(iris,aes(Petal.Length,Sepal.Length))+
  geom_point(aes(shape=Species))
giris.labeled <- giris+
  geom_dl(aes(label=Species),method="smart.grid")+
  scale_shape_manual(values=c(setosa=1,virginica=6,versicolor=3),
                     guide="none")
##png("~/R/directlabels/www/scatter-bw-ggplot2.png",h=503,w=503)
print(giris.labeled)
##dev.off()

get.means

Description

Positioning Function for the mean of each cluster of points.

Usage

get.means(d, ...)

Arguments

  d
  ...

Author(s)

Toby Dylan Hocking
getLegendVariables  

**Description**  
get the aes which are variable in one legend.

**Usage**  
getLegendVariables(mb)

**Arguments**  
mb

**Author(s)**  
Toby Dylan Hocking

ignore.na  

**Description**  
Remove rows for which either x or y is NA

**Usage**  
ignore.na(d, ...)

**Arguments**  
d  
...

**Author(s)**  
Toby Dylan Hocking
**Description**

Calculate how many points fall in a box.

**Usage**

\[
in1box(p, box)
\]

**Arguments**

- \(p\)  
- \(box\)

**Author(s)**

Toby Dylan Hocking

---

**Description**

Calculate which points fall in a box.

**Usage**

\[
in1which(p, box)
\]

**Arguments**

- \(p\)  
  - data frame of points with columns \(x\) and \(y\) and many rows.  
- \(box\)  
  - data frame of 1 row with columns left right top bottom.

**Author(s)**

Toby Dylan Hocking
**inside**

**Description**

Calculate for each box how many points are inside.

**Usage**

`inside(boxes, points)`

**Arguments**

- `boxes`  
  Data frame of box descriptions, each row is 1 box, need columns `left` right `top` `bottom`.
- `points`  
  Data frame of points, each row is 1 point, need columns `x` `y`.

**Value**

Vector of point counts for each box.

**Author(s)**

Toby Dylan Hocking

---

**iris.l1.cluster**

*Clustering of the iris data with the l1 clusterpath*

**Description**

The l1 clustering algorithm from the clusterpath package was applied to the iris dataset and the breakpoints in the solution path are stored in this data frame.

**Usage**

`data(iris.l1.cluster)`

**Format**

A data frame with 9643 observations on the following 8 variables.

- `row` a numeric vector: row of the original iris data matrix.
- `Species` a factor with levels `setosa` `versicolor` `virginica`: Species from corresponding row.
- `alpha` a numeric vector: the value of the optimal solution.
- `lambda` a numeric vector: the regularization parameter (ie point in the path).
col a factor with levels Sepal.Length Sepal.Width Petal.Length Petal.Width: column from the original iris data.
gamma a factor with levels 0: parameter from clustering.
norm a factor with levels 1 parameter from clustering.
solver a factor with levels path algorithm used for clustering.

Source

clusterpath package

References

clusterpath article

Examples

data(iris.l1.cluster,package="directlabels")
iris.l1.cluster$y <- iris.l1.cluster$alpha
if(require(ggplot2)){
  p <- ggplot(iris.l1.cluster,aes(lambda,y,group=row,colour=Species))+
    geom_line(alpha=1/4)+
    facet_grid(col~.)
  p2 <- p+xlim(-0.0025,max(iris.l1.cluster$lambda))
  print(direct.label(p2,list(first.points,get.means)))
}

label.endpoints label endpoints

Description

Make a Positioning Method that labels a certain x value.

Usage

label.endpoints(FUN,
    HJUST)

Arguments

FUN FUN(d$x) should return an index of which point to label. for example you can use which.min or which.max.

HJUST hjust of the labels.

Value

A Positioning Method like first.points or last.points.
**Author(s)**

Toby Dylan Hocking

---

**Description**

Make a Positioning Method that will, for every piece, select points and assign a vjust value.

**Usage**

`label.pieces(FUN, VJUST)`

**Arguments**

- **FUN**
- **VJUST**

---

**Author(s)**

Toby Dylan Hocking

---

**Description**

Label points at the zero before the first nonzero y value.

**Usage**

```
"lasso.labels"
```

---

**Description**

Label last points, bumping labels up if they collide.

**Usage**

```
"last.bumpup"
```
last.points

**Description**
Positioning Method for the last of a group of points.

**Usage**
last.points(d, ...)

**Arguments**
d
...

**Author(s)**
Toby Dylan Hocking

last.polygons

**Description**
Draw a speech polygon to the last point.

**Usage**
"last.polygons"

last.qp

**Description**
Label last points from QP solver that ensures labels do not collide.

**Usage**
"last.qp"
**lattice.translators**  
*lattice translators*

**Description**

Some lattice plot functions do some magic in the background to translate the data you give them into the data points that are plotted onscreen. We have to replicate this magic in native coordinate space before applying the Positioning Method in cm space. These functions accomplish this translation.

**Usage**

"lattice.translators"

---

**left.points**  
*left points*

**Description**

Positioning Method for the first of a group of points.

**Usage**

left.points(d, ...)

**Arguments**

- `d`
- `...`

**Author(s)**

Toby Dylan Hocking

---

**left.polygons**  
*left polygons*

**Description**

Draw a speech polygon to the first point.

**Usage**

"left.polygons"
legs2hide

Description
Extract guides to hide from a ggplot.

Usage
```r
legs2hide(p)
```

Arguments
- `p`

Value
NULL if no legends with colour or fill to hide.

Author(s)
Toby Dylan Hocking

lines2

Description
Positioning Method for 2 groups of longitudinal data. One curve is on top of the other one (on average), so we label the top one at its maximal point, and the bottom one at its minimal point. Vertical justification is chosen to minimize collisions with the other line. This may not work so well for data with high variability, but then again lineplots may not be the best for these data either.

Usage
```r
lines2(d, offset = 0.3, ...)
```

Arguments
- `d` The data.
- `offset` Offset from 0 or 1 for the vjust values.
- `...` ignored.

Author(s)
Toby Dylan Hocking
**LOPART.ROC**

*ROC curve for LOPART algorithm and competitors*

**Description**

For the LOPART paper we computed ROC curves for predictions of changepoint detection algorithms.

**Usage**

```r
data("LOPART.ROC")
```

**Format**

A named list of two data frames: points has one row per model/algorithm, roc has one row per point on the ROC curve.

**Source**

Figure/paper describing LOPART algorithm and R package, https://github.com/tdhock/LOPART-paper/blob/master/figure-cv-BIC.R

---

**LOPART100**

*Labeled Optimal Partitioning (LOPART) results*

**Description**

Results of running LOPART algorithm (for changepoint detection in partially labeled data sequence) on a simulated data set of size 100.

**Usage**

```r
data("LOPART100")
```

**Format**

Named list of data frames: signal has one row per data point, labels has one row per label, segments has one row per segment, cost has one row per feasible last changepoint for model up to t=100 data.

**Source**

Figure/paper describing LOPART algorithm and R package, https://github.com/tdhock/LOPART-paper/blob/master/figure-candidates.R
**make.tiebreaker**

**Description**

Make a tiebreaker function that can be used with `qp.labels`.

**Usage**

```r
make.tiebreaker(x.var, tiebreak.var)
```

**Arguments**

- `x.var`
- `tiebreak.var`

**Author(s)**

Toby Dylan Hocking

---

**maxvar.points**  
**maxvar points**

**Description**

Do first or last, whichever has points most spread out.

**Usage**

```r
maxvar.points(d, ...)
```

**Arguments**

- `d`
- `...`

**Author(s)**

Toby Dylan Hocking
Description

Label first or last points, whichever are more spread out, and use a QP solver to make sure the labels do not collide.

Usage

"maxvar.qp"

Description

Copied from reshape.

Usage

merge_recurse(dfs, ...)

Arguments

dfs
...

Author(s)

Toby Dylan Hocking
midrange

**Description**

Point halfway between the min and max

**Usage**

midrange(x)

**Arguments**

x

**Author(s)**

Toby Dylan Hocking

---

normal.l2.cluster

Clustering of some normal data in 2d with the l2 clusterpath

**Description**

The l2 clustering algorithm from the clusterpath package was applied to some randomly generated data in 2 dimensions, and the solutions found using the descent algorithm are stored in this data frame.

**Usage**

data(normal.l2.cluster)

**Format**

The format is: List of 2 $ pts :'data.frame': 320 obs. of 3 variables: ..$ class: Factor w/ 8 levels "1","2","3","4"...: 1 1 1 1 1 1 1 1 1 ... $ x : num [1:320] -2.73 -3.63 -2.13 -1.27 -2.98 ... $ y : num [1:320] -3.89 -3.43 -3.42 -3.17 -2.75 ... $ path:Classes 'l2', 'clusterpath' and 'data.frame': 21760 obs. of 7 variables: ..$ x : num [1:21760] -2.73 -3.63 -2.13 -1.27 -2.98 ... ..$ y : num [1:21760] -3.89 -3.43 -3.42 -3.17 -2.75 ... ..$ lambda: num [1:21760] 0 0 0 0 0 0 0 0 0 0 ... ..$ row : Factor w/ 320 levels "1","2","3","4"...: 1 2 3 4 5 6 7 8 9 10 ... ..$ gamma : Factor w/ 1 level "0.1": 1 1 1 1 1 1 1 1 1 1 ... ..$ norm : Factor w/ 1 level "2": 1 1 1 1 1 1 1 1 1 1 ... ..$ solver: Factor w/ 1 level "descent.nocheck": 1 1 1 1 1 1 1 1 1 1 ... .. attr(*, "data")= num [1:320, 1:2] -2.73 -3.63 -2.13 -1.27 -2.98 ... .. attr(*, "dimnames")=List of 2 .. ..$ : chr [1:2] "x" "y" .. ..$ : chr [1:2] "x" "y" .. attr(*, "alphacolnames")= chr [1:2] "x" "y" .. attr(*, "weight.pts")= num [1:320, 1:2] -2.73 -3.63 -2.13 -1.27 -2.98 ... .. attr(*, "dimnames")=List of 2 .. ..$ : NULL .. ..$ : NULL ..$ : chr [1:2] "x" "y"
Source

clusterpath package

References

clusterpath article

Examples

data(normal.l2.cluster)
if(require(ggplot2)){
  p <- ggplot(normal.l2.cluster$path,aes(x,y))+
  geom_path(aes(group=row),colour="grey")+
  geom_point(aes(size=lambda),colour="grey")+
  geom_point(aes(colour=class),data=normal.l2.cluster$pts)+
  coord_equal()
  print(direct.label(p))
}

odd_timings

<table>
<thead>
<tr>
<th>odd_timings</th>
<th>Odd timings</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Description

These timings data made strange output labels with the "right.polygons" method.

Usage

data("odd_timings")

Format

A data frame with 116 observations on the following 4 variables. Plot median.seconds versus N.col using a different line for each fun and a different panel for each captures.

- N.col  a numeric vector
- fun  a character vector
- captures  a numeric vector
- median.seconds  a numeric vector

Source

https://github.com/tdhock/nc-article
**only.unique.vals**

---

**Description**

Create a 1-row data.frame consisting of only the columns for which there is only 1 unique value.

**Usage**

`only.unique.vals(d, ...)`

**Arguments**

- `d`
- `...`

**Author(s)**

Toby Dylan Hocking

---

**outside.ahull**

---

**Description**

Calculate closest point on the alpha hull with size of the boxes, and put it outside that point.

**Usage**

`outside.ahull(d, ...)`

**Arguments**

- `d`
- `...`

**Author(s)**

Toby Dylan Hocking
outside.chull  
outside chull

Description

Calculate closest point on the convex hull and put it outside that point. Assume \( d \) is the center for each point cloud and then use orig.data to calculate hull.

Usage

outside.chull(d, ...)

Arguments

d
...

Author(s)

Toby Dylan Hocking

panel.superpose.dl  
panel superpose dl

Description

Call panel.superpose for the data points and then for the direct labels. This is a proper lattice panel function that behaves much like panel.superpose.

Usage

panel.superpose.dl(x,
                      y = NULL, subscripts,
                      groups, panel.groups,
                      method = NULL, .panel.superpose = lattice::panel.superpose,
                      type = "p", debug = FALSE,
                      ...)

Arguments

x  Vector of x values.
y  Vector of y values.
subscripts  Subscripts of x,y.groups.
groups  Vector of group ids.
panel.superpose.dl

panel.groups  To be parsed for default labeling method, and passed to panel.superpose.
method  Positioning Method for direct labeling. NULL indicates to choose a Positioning Method based on the panel.groups function.
.panel.superpose  The panel function to use for drawing data points.
type  Plot type, used for default method dispatch.
debug  passed to dlgrob.
...  passed to real panel function, and to translator.

Author(s)
Toby Dylan Hocking

Examples

loci <- data.frame(ppp=c(rbeta(800,10,10),rbeta(100,0.15,1),rbeta(100,1,0.15)),
type=factor(c(rep("NEU",800),rep("POS",100),rep("BAL",100))))
## 3 equivalent ways to make the same plot:
library(lattice)
print(direct.label( ## most user-friendly
densityplot(~ppp,loci,groups=type,n=500)
))
print(direct.label( ## exactly the same as above but with specific panel fns
densityplot(~ppp,loci,groups=type,n=500,
panel=lattice::panel.superpose,
panel.groups="panel.densityplot")
))
## using panel.superpose.dl as the panel function automatically adds
## direct labels
print(densityplot(~ppp,loci,groups=type,n=500,
panel=panel.superpose.dl,panel.groups="panel.densityplot"))

## Exploring custom panel and panel.groups functions
library(nlme)
## Say we want to use a simple linear model to explain rat body weight:
fit <- lm(weight~Time+Diet+Rat,BodyWeight)
bw <- BodyWeight
bw$.fitted <- predict(fit,BodyWeight)
## lots of examples to come, all with these arguments:
ratxy <- function(...){
  xyplot(weight~Time|Diet,bw,groups=Rat,type="l",layout=c(3,1),...)
}
## No custom panel functions:
##regular <- ratxy(par.settings=simpleTheme(col=c("red","black")))
regular <- ratxy()
print(regular) ## normal lattice plot
print(direct.label(regular)) ## with direct labels

## The direct label panel function panel.superpose.dl can be used to
## display direct labels as well:
print(ratxy(panel=panel.superpose.dl,panel.groups="panel.xyplot"))
print(ratxy(panel=function(...)  
    panel.superpose.dl(panel.groups="panel.xyplot",...)))

## Not very user-friendly, since default label placement is  
## impossible, but these should work:  
print(ratxy(panel=panel.superpose.dl,panel.groups=panel.xyplot,  
    method=first.points))  
print(ratxy(panel=function(...)  
    panel.superpose.dl(panel.groups=panel.xyplot,...),  
    method=first.points))

## Custom panel.groups functions:  
## This panel.groups function will display the model fits:  
panel.model <- function(x,subscripts,col.line,...){  
    panel.xyplot(x=x,subscripts=subscripts,col.line=col.line,...)  
    llines(x,bw[subscripts,".fitted"],col=col.line,lty=2)  
}
pg <- ratxy(panel=lattice::panel.superpose,panel.groups=panel.model)  
print(pg)  
## If you use panel.superpose.dl with a custom panel.groups function,  
## you need to manually specify the Positioning Method, since the  
## name of panel.groups is used to infer a default:  
print(direct.label(pg,method="first.qp"))  
print(ratxy(panel=panel.superpose.dl,panel.groups="panel.model",  
    method="first.qp"))

## Custom panel function that draws a box around values:  
panel.line1 <- function(ps=lattice::panel.superpose){  
    function(y,...){  
        panel.abline(h=range(y))  
        ps(y=y,...)  
    }  
}
custom <- ratxy(panel=panel.line1())  
print(custom)  
print(direct.label(custom))  
## Alternate method, producing the same results, but using  
## panel.superpose.dl in the panel function. This is useful for direct  
## label plots where you use several datasets.  
print(ratxy(panel=panel.line1(panel.superpose.dl),panel.groups="panel.xyplot"))

## Lattice plot with custom panel and panel.groups functions:  
both <- ratxy(panel=panel.line1(),panel.groups="panel.model")  
print(both)  
print(direct.label(both,method="first.qp"))  
print(ratxy(panel=panel.line1(panel.superpose.dl),  
    panel.groups=panel.model,method="first.qp"))

pkgFun
Description

https://github.com/tdhock/directlabels/issues/2 CRAN won’t complain about this version of :::

Usage

pkgFun(fun, pkg = "ggplot2")

Arguments

fun
pkg

top.bottom.left.right
offset.cm
padding.cm
custom.colors

Author(s)

Toby Dylan Hocking
Description

When adding direct labels to a grouped plot, label placement can be specified using a Positioning Method (or a list of them), of the form function(d,...), where d is a data frame of the points to plot, with columns x y groups. The job of the Positioning Method(s) is to return the position of each direct label you want to plot as a data frame, with 1 row for each label. Thus normally a Positioning Method will return 1 row for each group. Several built-in Positioning Methods are discussed below, but you can also create your own, either from scratch or by using dl.indep and dl.trans.

Author(s)

Toby Dylan Hocking <toby.hocking@inria.fr>

Examples

## Not run:
### contourplot Positioning Methods
for(p in list({
  ## Example from help(contourplot)
  require(stats)
  require(lattice)
  attach(environmental)
  ozo.m <- loess((ozone^(1/3)) ~ wind * temperature * radiation,
             parametric = c("radiation", "wind"), span = 1, degree = 2)
  w.marginal <- seq(min(wind), max(wind), length.out = 50)
  t.marginal <- seq(min(temperature), max(temperature), length.out = 50)
  r.marginal <- seq(min(radiation), max(radiation), length.out = 4)
  wtr.marginal <- cbind(w=marginal, temperature=t.marginal, radiation=r.marginal)
  grid <- expand.grid(wtr.marginal)
  grid[, "fit"] <- predict(ozo.m, grid)
  detach(environmental)
  library(ggplot2)
  p <- ggplot(grid,aes(wind,temperature,z=fit)) +
      stat_contour(aes(colour=..level..)) +
      facet_wrap(~radiation)
})
## example from help(stat_contour)
library(reshape2)
volcano3d <- melt(volcano)
names(volcano3d) <- c("x", "y", "z")
library(ggplot2)
p <- ggplot(volcano3d, aes(x, y, z = z)) +
    stat_contour(aes(colour = ..level..))
}))
positioning.functions

```r
print(direct.label(p,"bottom.pieces"))
print(direct.label(p,"top.pieces"))
}

### densityplot Positioning Methods
for(p in list({
data(Chem97,package="mlmRev")
library(lattice)
p <- densityplot(~gcsescore|gender,Chem97,
groups=factor(score),layout=c(1,2),
n=500,plot.points=FALSE)
},
{library(reshape2)
iris2 <- melt(iris,id="Species")
library(lattice)
p <- densityplot(~value|variable,iris2,groups=Species,scales="free")
},
{loci <- data.frame(ppp=c(rbeta(800,10,10),rbeta(100,0.15,1),rbeta(100,1,0.15)),
type=factor(c(rep("NEU",800),rep("POS",100),rep("BAL",100))))
library(ggplot2)
p <- qplot(ppp,data=loci,colour=type,geom="density")
})
print(direct.label(p,"top.bumptwice"))
print(direct.label(p,"top.bumpup"))
print(direct.label(p,"top.points"))
}

### dotplot Positioning Methods
for(p in list({
library(lattice)
p <- dotplot(VADeaths,xlim=c(8,85),type="o")
},
{vad <- as.data.frame.table(VADeaths)
names(vad) <- c("age","demographic","deaths")
library(ggplot2)
p <- qplot(deaths,age,data=vad,group=demographic,geom="line",colour=demographic)+
xlim(8,80)
})
print(direct.label(p,"angled.endpoints"))
print(direct.label(p,"top.qp"))
}

### lineplot Positioning Methods
for(p in list({
data(BodyWeight,package="nlme")
library(lattice)
p <- xyplot(weight~Time|Diet,BodyWeight,groups=Rat,type="l",
layout=c(3,1),xlim=c(-10,75))
},
{});```
data(Chem97, package="mlmRev")
library(lattice)
p <- qqmath(~gcsescore|gender, Chem97, groups=score, 
type=c("l", "g"), f.value=ppoints(100))
}
{data(Chem97, package="mlmRev")
library(lattice)
p <- qqmath(~gcsescore, Chem97, groups=gender, 
type=c("l", "g"), f.value=ppoints(100))
}
{data(prostate, package="ElemStatLearn")
pros <- subset(prostate, select=-train, train==TRUE)
ycol <- which(names(pros)=="lpsa")
x <- as.matrix(pros[-ycol])
y <- pros[[ycol]]
library(lars)
fit <- lars(x,y, type="lasso")
beta <- scale(coef(fit), FALSE, 1/fit$normx)
arclength <- rowSums(abs(beta))
library(reshape2)
path <- data.frame(melt(beta), arclength)
names(path)[1:3] <- c("step", "variable", "standardized.coef")
library(ggplot2)
p <- ggplot(path, aes(arclength, standardized.coef, colour=variable)) + 
  geom_line(aes(group=variable)) + 
  ggtitle("LASSO path for prostate cancer data calculated using the LARS") + 
  xlim(0, 20)
}
{data(projectionSeconds, package="directlabels")
p <- ggplot(projectionSeconds, aes(vector.length/1e6)) + 
  geom_ribbon(aes(ymin=min, ymax=max, 
                fill=method, group=method), alpha=1/2) + 
  geom_line(aes(y=mean, group=method, colour=method)) + 
  ggtitle("Projection Time against Vector Length (Sparsity = 10") + 
  guides(fill="none") + 
  ylab("Runtime (s)")
}

## complicated ridge regression lineplot ex. fig 3.8 from Elements of 
## Statistical Learning, Hastie et al.
myridge <- function(f, data, lambda=c(exp(-seq(-15, 15, l=200)), 0)){
  require(MASS)
  require(reshape2)
  fit <- lm.ridge(f, data, lambda)
  X <- data[ - which(names(data) == as.character(f[[2]])), ]
  Xs <- svd(scale(X)) ## my d's should come from the scaled matrix
  dsq <- Xs$d^2
  ## make the x axis degrees of freedom
  df <- sapply(lambda, function(l) sum(dsq/(dsq+l)))
  D <- data.frame(t(fit$coef), lambda, df) # scaled coefs
}
positioning.functions

molt <- melt(D,id=c("lambda","df"))
## add in the points for df=0
limpts <- transform(subset(molt,lambda==0),lambda=Inf,df=0,value=0)
`rbind`(limpts,molt)
}

data(prostate,package="ElemStatLearn")
pros <- subset(prostate,train==TRUE,select=-train)
m <- myridge(lpsa~.,pros)
library(lattice)
p <- xyplot(value~df,m,groups=variable,type="o",pch="+",
  panel=function(...){
    panel.xyplot(...)
    panel.abline(h=0)
    panel.abline(v=5,col="grey")
  },
xlim=c(-1,9),
main="Ridge regression shrinks least squares coefficients",
ylab="scaled coefficients",
sub="grey line shows coefficients chosen by cross-validation",
xlab=expression(df(lambda)))
}

library(ggplot2)
tx <- time(mdeaths)
Time <- ISOdate(floor(tx),round(tx)
uk.lung <- rbind(data.frame(Time,sex="male",deaths=as.integer(mdeaths)),
  data.frame(Time,sex="female",deaths=as.integer(fdeaths)))
p <- qplot(Time,deaths,data=uk.lung,colour=sex,geom="line")+
  xlim(ISOdate(1973,9,1),ISOdate(1980,4,1))
)

for(p in list(
data(mpg,package="ggplot2")
m <- lm(cty~displ,data=mpg)
mpgf <- fortify(m,mpg)
library(lattice)
library(latticeExtra)
p <- xyplot(cty~hwy|manufacturer,mpgf,groups=class,aspect="iso",
          panel=function(...){
            panel.xyplot(...)
            panel.abline(h=0)
            panel.abline(v=5,col="grey")
          },
xlim=c(-1,9),
main="Scatterplot Positioning Methods",
ylab="",
sub="",
xlab=expression(df(lambda)))
```
project.onto.segments

Description

Given a point and a set of line segments representing a convex or alpha hull, calculate the closest point on the segments.
**Usage**

```r
project.onto.segments(m, 
  h, debug = FALSE, 
  ...)```

**Arguments**

- `m` is 1 row, a center of a point cloud, we need to find the distance to the closest point on each segment of the convex hull.
- `h` Data frame describing the line segments of the convex or alpha hull.
- `debug`... ignored

**Author(s)**

Toby Dylan Hocking

---

**projectionSeconds**  
Timings of projection algorithms

**Description**

Timings of seconds for 3 projection algorithms.

**Usage**

```r
data(projectionSeconds)
```

**Format**

A data frame with 603 observations on the following 6 variables.

- `vector.length`  a numeric vector
- `method`  a factor with levels Heap Random Sort
- `mean`  a numeric vector
- `sd`  a numeric vector
- `min`  a numeric vector
- `max`  a numeric vector

**Source**

Mark Schmidt’s prettyPlot code for MATLAB http://www.di.ens.fr/~mschmidt/Software/prettyPlot.html
Make a Positioning Method for non-overlapping lineplot labels

**Description**

Use a QP solver to find the best places to put the points on a line, subject to the constraint that they should not overlap.

**Usage**

```r
cp.labels(target.var, lower.var, upper.var, order.labels = function(d) order(d[, target.var]), limits = NULL)
```

**Arguments**

- `target.var`: Variable name of the label target.
- `lower.var`: Variable name of the lower limit of each label bounding box.
- `upper.var`: Variable name of the upper limit of each label bounding box.
- `order.labels`: Function that takes the data.frame of labels and returns an ordering, like from the order function. That ordering will be used to reorder the rows. This is useful to e.g. break ties when two groups have exactly the same value at the endpoint near the label.
- `limits`: Function that takes the data.frame of labels an returns a numeric vector of length 2. If finite, these values will be used to add constraints to the QP: limits[1] is the lower limit for the first label’s `lower.var`, and limits[2] is the upper limit for the last labels’s `upper.var`. Or NULL for no limits.

**Value**

Positioning Method that adjusts `target.var` so there is no overlap of the label bounding boxes, as specified by `upper.var` and `lower.var`.

**Author(s)**

Toby Dylan Hocking

**Examples**

```r
SegCost$error <- factor(SegCost$error,c("FP","FN","E","I"))
if(require(ggplot2)){
  fp.fn.colors <- c(FP="skyblue",FN="#E41A1C",I="black",E="black")
  fp.fn.sizes <- c(FP=2.5,FN=2.5,I=1,E=1)
  fp.fn.linetypes <- c(FP="solid",FN="solid",I="dashed",E="solid")
  err.df <- subset(SegCost,type!="Signal")
```
kplot <- ggplot(err.df,aes(segments,cost)) +
gem_line(aes(colour=error,size=error,linetype=error)) +
facet_grid(type~bases.per.probe) +
scale_linetype_manual(values=fp.fn.linetypes) +
scale_colour_manual(values=fp.fn.colors) +
scale_size_manual(values=fp.fn.sizes) +
scale_x_continuous(limits=c(0,20),breaks=c(1,7,20),minor_breaks=NULL) +
theme_bw()+theme(panel.margin=grid::unit(0,"lines"))

## The usual ggplot without direct labels.
print(kplot)

## Get rid of legend for direct labels.
no.leg <- kplot+guides(colour="none",linetype="none",size="none")

## Default direct labels.
direct.label(no.leg)

## Explore several options for tiebreaking and limits. First let's
## make a qp.labels Positioning Method that does not tiebreak.
no.tiebreak <- list("first.points",
"calc.boxes",
qp.labels("y","bottom","top"))
direct.label(no.leg, no.tiebreak)

## Look at the weird labels in the upper left panel. The E curve is
## above the FN curve, but the labels are the opposite! This is
## because they have the same y value on the first points, which are
## the targets for qp.labels. We need to tiebreak.
qp.break <- qp.labels("y","bottom","top",make.tiebreaker("x","y"))
tiebreak <- list("first.points",
"calc.boxes",
"qp.break")
direct.label(no.leg, tiebreak)

## Enlarge the text size and spacing.
tiebreak.big <- list("first.points",
  cex=2,
  "calc.boxes",
  dl.trans(h=1.25*h),
  "calc.borders",
  "qp.break")
direct.label(no.leg, tiebreak.big)

## Even on my big monitor, the FP runs off the bottom of the screen
## in the top panels. To avoid that you can specify a limits
## function.

## Below, the ylims function uses the limits of each panel, so
## labels appear inside the plot region. Also, if you resize your
## window so that it is small, you can see that the text size of the
## labels is decreased until they all fit in the plotting region.
reduce.cex

```r
qp.limited <- qp.labels("y","bottom","top",make.tiebreaker("x","y"),ylimits)
tiebreak.lim <- list("first.points",
                   cex=2,
                   "calc.boxes",
                   dl.trans(h=1.25*h),
                   "calc.borders",
                   "qp.limited")
direct.label(no.leg, tiebreak.lim)
```

---

**reduce.cex**

**reduce cex**

**Description**

If edges of the text are going out of the plotting region, then decrease cex until it fits. We call calc.boxes inside, so you should set cex before using this.

**Usage**

```r
reduce.cex(sides)
```

**Arguments**

- `sides` string: lr (left and right) or tb (top and bottom).

**Author(s)**

Toby Dylan Hocking

**Examples**

```r
if(require(lars) && require(ggplot2)){
  data(diabetes,package="lars",envir=environment())
  X <- diabetes$x
  colnames(X) <- paste(colnames(X), colnames(X))
  fit <- lars(X,diabetes$y,type="lasso")
  beta <- scale(coef(fit),FALSE,1/fit$normx)
  arclength <- rowSums(abs(beta))
  path.list <- list()
  for(variable in colnames(beta)){
    standardized.coef <- beta[, variable]
    path.list[[variable]] <-
      data.frame(step=seq_along(standardized.coef),
                 arclength,
                 variable,
                 standardized.coef)
  }
  path <- do.call(rbind, path.list)
```


\[ p \leftarrow \text{ggplot(path, aes(arclength, standardized.coef, colour=variable))} + \]
\[ \text{geom_line(aes(group=variable))} \]
\[ \text{## the legend isn't very helpful.} \]
\[ \text{print(p)} \]
\[ \text{## add direct labels at the end of the lines.} \]
\[ \text{direct.label(p, "last.points")} \]
\[ \text{## on my screen, some of the labels go off the end, so we can use} \]
\[ \text{## this Positioning Method to reduce the text size until the labels} \]
\[ \text{## are on the plot.} \]
\[ \text{direct.label(p, list("last.points", reduce.cex("lr")))} \]
\[ \text{## the default direct labels for lineplots are similar.} \]
\[ \text{direct.label(p)} \]

---

### reduce.cex.lr

**Description**

If edges of the text are going left or right out of the plotting region, then decrease cex until it fits.

**Usage**

```
reduce.cex.lr(d, ...)  
```

**Arguments**

- `d`
- `...`

**Author(s)**

- Toby Dylan Hocking

---

### reduce.cex.tb

**Description**

If edges of the text are going over the top or bottom of the plotting region, then decrease cex until it fits.

**Usage**

```
reduce.cex.tb(d, ...)  
```
**Arguments**

d  

**Author(s)**

Toby Dylan Hocking

---

**rhtmlescape**  

**Description**

for standards compliance we should escape <>&

**Usage**

rhtmlescape(code)

**Arguments**

code  

**Value**

Standards compliant HTML to display.

**Author(s)**

Toby Dylan Hocking

---

**right.points**

**Description**

Positioning Method for the last of a group of points.

**Usage**

right.points(d, ...)

**Arguments**

d  

...
Author(s)
Toby Dylan Hocking

Description
Draw a speech polygon to the last point.

Usage
"right.polygons"

SegCost
Cost of segmentation models

Description
20 segmentation models were fit to 2 simulated signals, and several different error measures were used to quantify the model fit.

Usage
data(SegCost)

Format
A data frame with 560 observations on the following 5 variables.

- bases.per.probe: a factor with levels 374 7: the sampling density of the signal.
- segments: numeric: the model complexity measured using number of segments.
- cost: numeric: the cost value.
- error: a factor with levels E FP FN I: what kind of error? FP = False Positive, FN = False Negative, I = Imprecision, E = Error (sum of the other terms).

Source
smart.grid  

**Description**
Search the plot region for a label position near the center of each point cloud.

**Usage**
```
"smart.grid"
```

---

static.labels  

**Description**

to hard-code label positions...

**Usage**
```
static.labels(x, y, groups, ...)
```

**Arguments**

- `x`
- `y`
- `groups`
- `...`

**Author(s)**

Toby Dylan Hocking
**Description**

Support Vector Machine density estimation (1-SVM) was applied to a set of negative control samples, and then used to test on a positive control.

**Usage**

data(svmtrain)

**Format**

A data frame with 378 observations on the following 5 variables.

- **replicate**: a factor with levels 1 2 3, the experimental replicate. We fit 1-SVM models to each replicate separately.
- **rate**: a numeric vector, the percent of observations that were outside the trained model.
- **data**: a factor with levels KIF11 test train, which set of observations did we measure. test and train are each 50% random splits of the negative controls in the experiment, and KIF11 is the positive control in the experiment.
- **gamma**: a numeric vector, the tuning parameter of the radial basis function kernel.
- **nu**: a numeric vector, the regularization parameter of the 1-SVM.

**Description**

Label the tops, bump labels up to avoid other labels, then to the side to avoid collisions with points.

**Usage**

top.bumptwice(d, debug = FALSE, ...)

**Arguments**

- **d**
- **debug**
- ...

**Author(s)**

Toby Dylan Hocking
Description

Label the tops, but bump labels up to avoid collisions.

Usage

"top.bumpup"

Description

Positioning Method for the top of a group of points.

Usage

top.pieces(d, ...)

Arguments

d
...

Author(s)

Toby Dylan Hocking

Description

Positioning Method for the top of a group of points.

Usage

top.points(d, ...)

Arguments

d
...

Author(s)

Toby Dylan Hocking
top.polygons

Arguments

d
...

Author(s)

Toby Dylan Hocking

Description

Draw a speech polygon to the top point.

Usage

"top.polygons"

top.qp

top qp

Description

Label points at the top, making sure they don’t collide.

Usage

"top.qp"
uselegend.ggplot

Description
Show the ggplot2 legend, for comparison.

Usage
uselegend.ggplot(p, ...)

Arguments
p The ggplot object.
... Ignored.

Author(s)
Toby Dylan Hocking

uselegend.trellis

Description
Add a legend to a trellis plot, for comparison.

Usage
uselegend.trellis(p, ...)

Arguments
p The trellis object.
... Ignored.

Author(s)
Toby Dylan Hocking
**vertical.qp**

**Description**

Make a Positioning Function from a set of points on a vertical line that will be spaced out using *qp.labels*.

**Usage**

`vertical.qp(M)`

**Arguments**

*M*

**Author(s)**

Toby Dylan Hocking

---

**visualcenter**

**Description**

Point in the middle of the min and max for each group.

**Usage**

`visualcenter(d, ...)`

**Arguments**

*d*

*...

**Author(s)**

Toby Dylan Hocking
xlimits

Description
Return the positions of the plot horizontal limits in cm, for use as the limit argument to `qp.labels`.

Usage
xlimits(...)

Arguments
...

Author(s)
Toby Dylan Hocking

ylimits

Description
Return the positions of the plot vertical limits in cm, for use as the limit argument to `qp.labels`.

Usage
ylimits(...)

Arguments
...

Author(s)
Toby Dylan Hocking
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