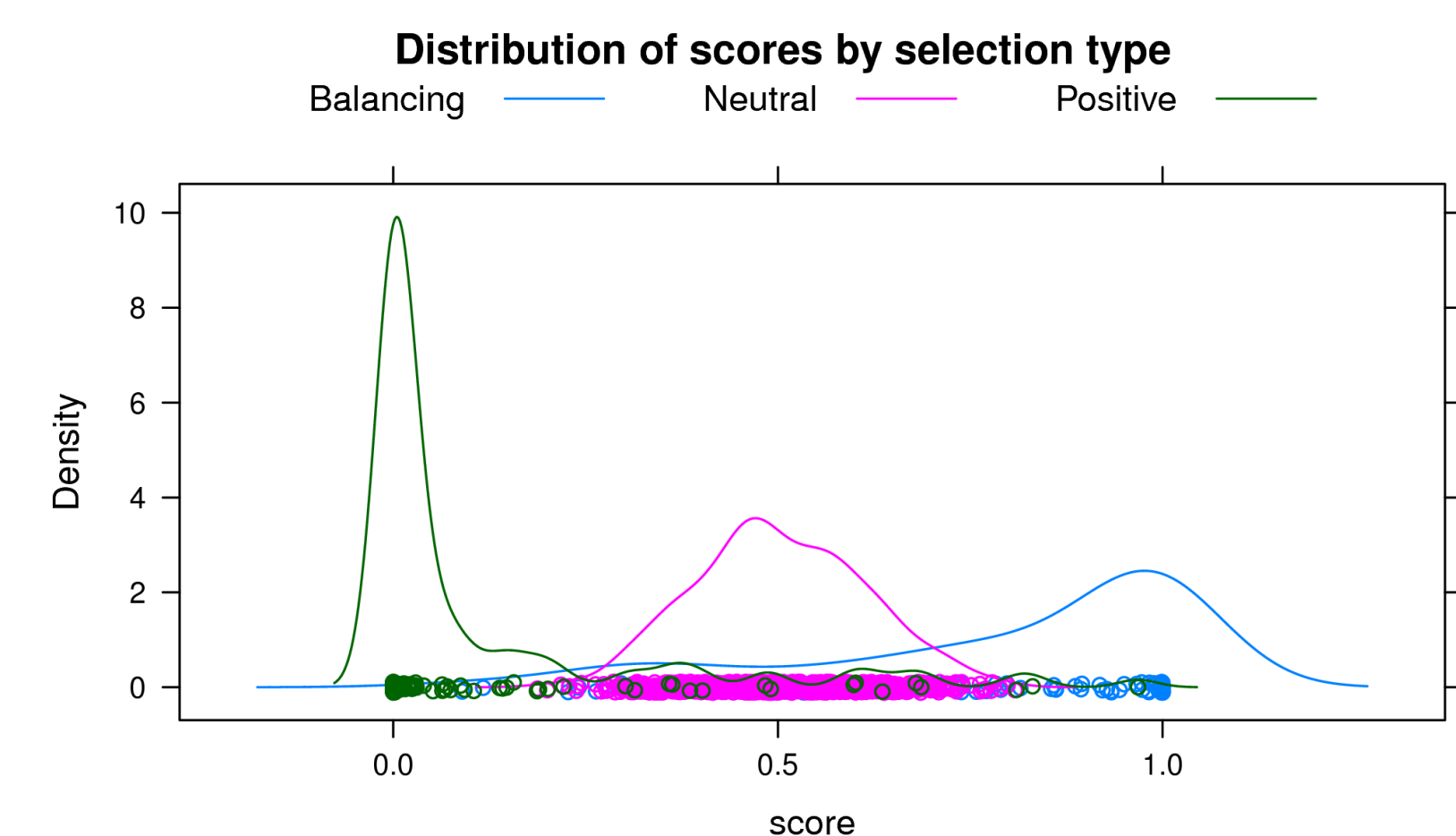


Motivation

- Direct labels are useful when legends are confusing, as below.
- The **directlabels** package makes it easy to use direct labels in everyday statistical plots with lattice [1] and ggplot2 [2].
[1] Deepayan Sarkar. Lattice: Multivariate Data Visualization with R. Springer, New York, 2008.
[2] Hadley Wickham. ggplot2: elegant graphics for data analysis. Springer, New York, 2009.

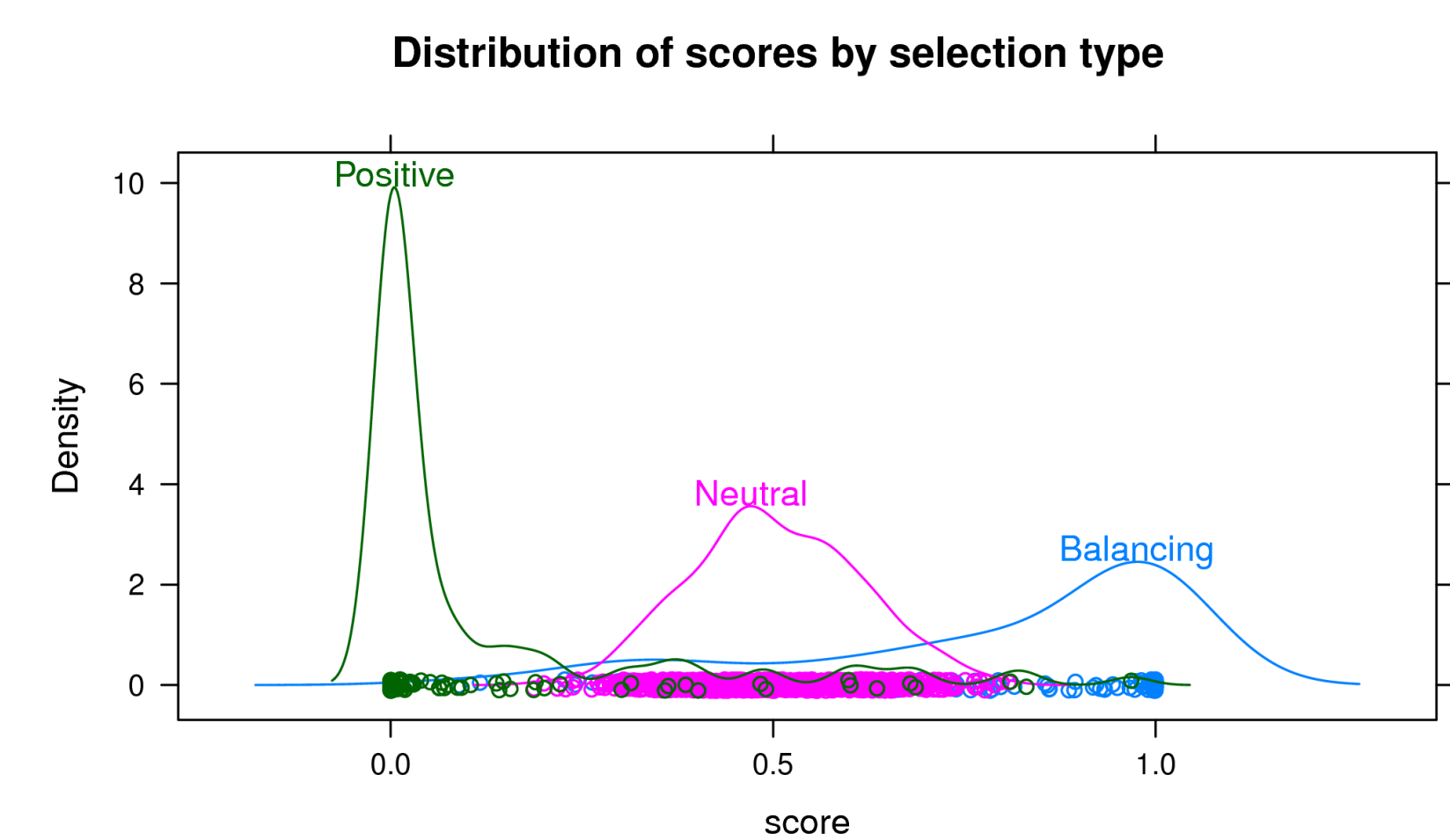
Problem 1: confusing legend!

```
library(lattice)
dens <- densityplot(~score, loci, groups=type,
  auto.key=list(space="top", columns=3))
```



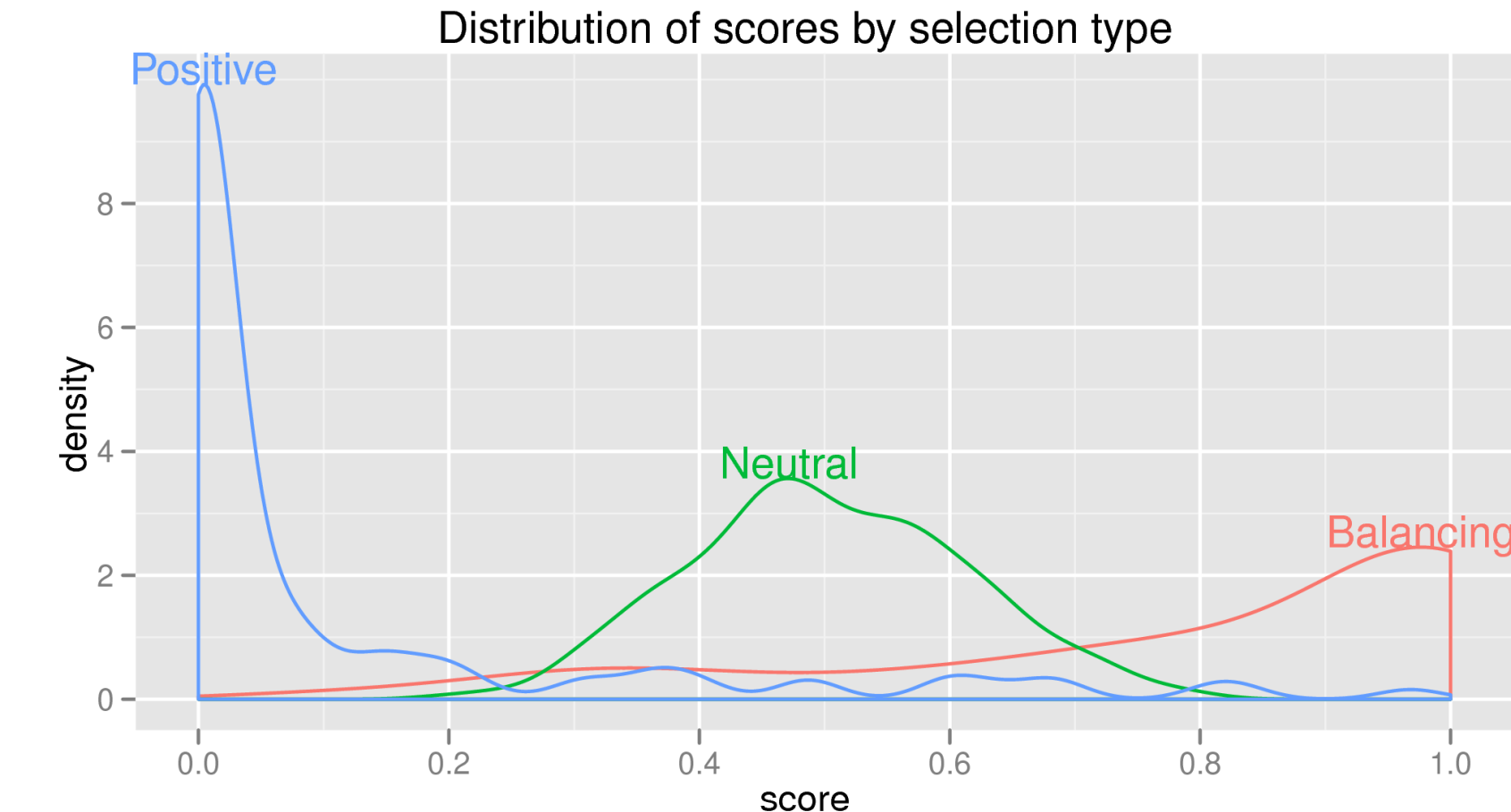
Solution: direct labels.

```
install.packages("directlabels")
library(directlabels)
direct.label(dens)
```



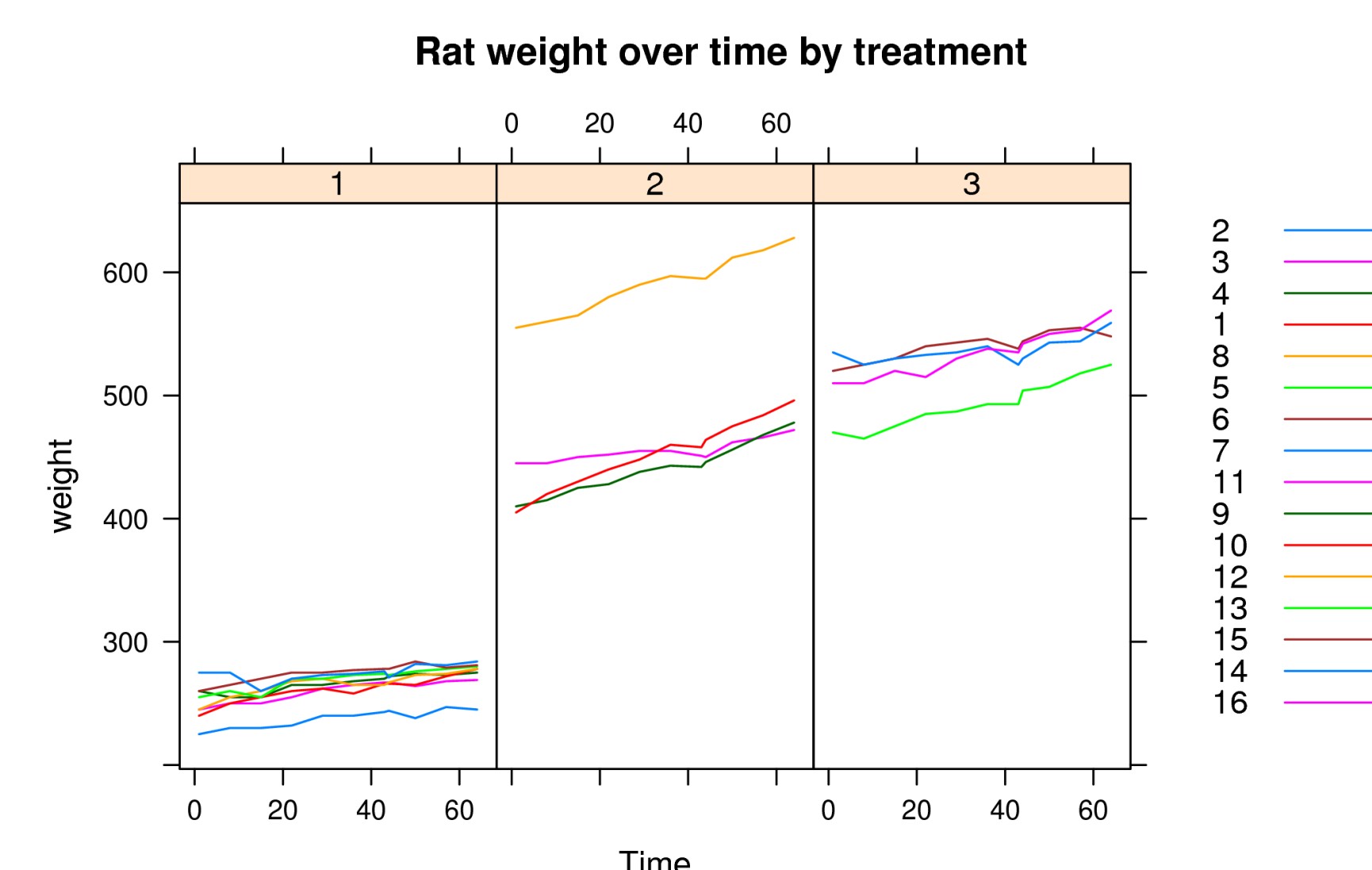
Also works with ggplot2!

```
library(ggplot2)
direct.label(qplot(score, data=loci,
  color=type, geom="density"))
```



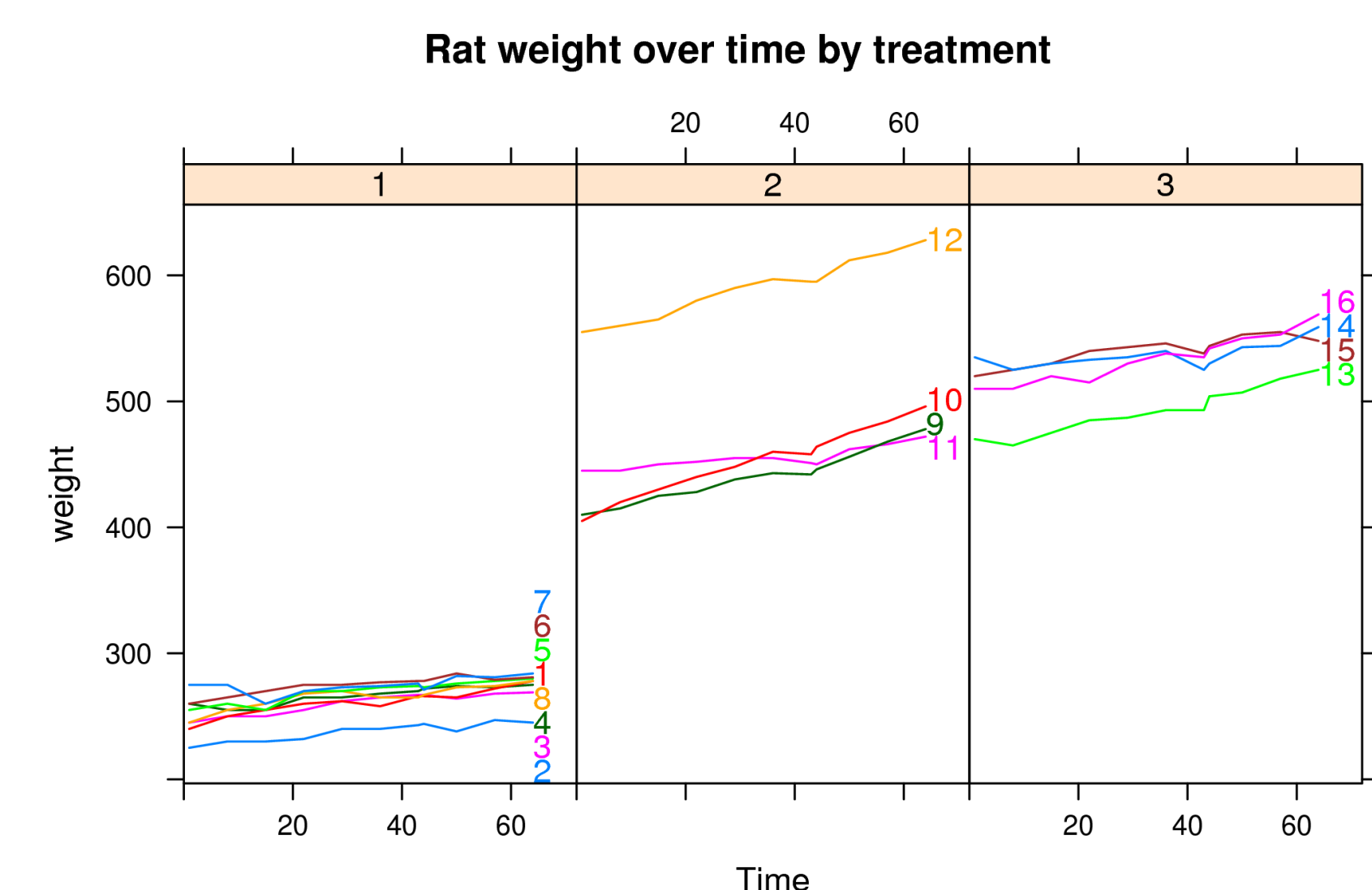
Problem 2: too many legend classes!

```
data(BodyWeight, package="nlme")
ratplot <- xyplot(weight~Time|Diet, BodyWeight,
  groups=Rat, type="l", layout=c(3,1), auto.key=
  list(space="right", points=FALSE, lines=TRUE))
```



Solution: direct labels.

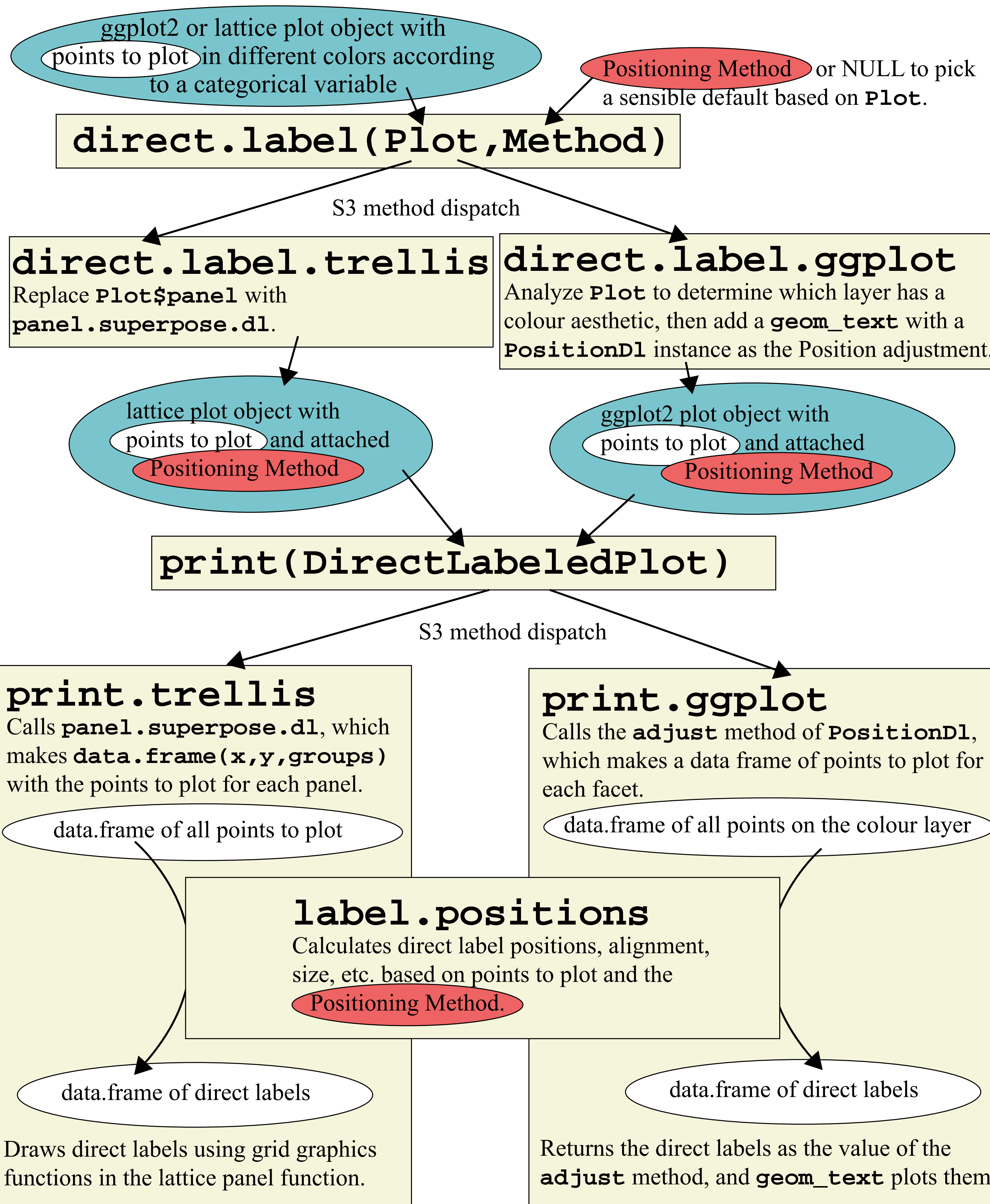
```
direct.label(update(ratplot, xlim=c(0, 72)),
  last.qp)
```



- labels are unambiguous and do not overlap.
- allows perception of group order.

Modular package design

- The **directlabels** package assumes the plot is an object and we can extract the data to plot.
- **direct.label** S3 methods are implemented for lattice and ggplot2. These methods implement framework-specific plot analysis and drawing.
- Positioning Methods calculate label positions, independently of the plot framework.



Positioning Methods

A Positioning Method is a list that describes where to draw the direct labels, based on the data.
- Elements of the Positioning Method are applied sequentially to the data, starting with the data.frame of all points to plot.
- Elements can be functions or named constants.
- The functions must apply some transformation to the data.frame, i.e. the **endpoints** function below simply returns the points with the largest x value.
- The **gapply** function can be used to apply a Positioning Method to each group of points independently, as in the **group.endpoints** function below.
- Named constants are written to the data.frame, as **rot** and **hjust** below.

```
library(reshape)
VADF <- melt(VADeaths)
names(VADF) <- c("age", "population", "death.rate")
dp <- ggplot(VADF) +
  aes(death.rate, age, colour=population) +
  geom_line(aes(group=population)) +
  geom_point() + xlim(8, 84)
```

```

endpoints <- function(Points, ...){
  subset(Points, x=max(x))
}
group.endpoints <- function(Points, ...){
  gapply(Points, endpoints)
}

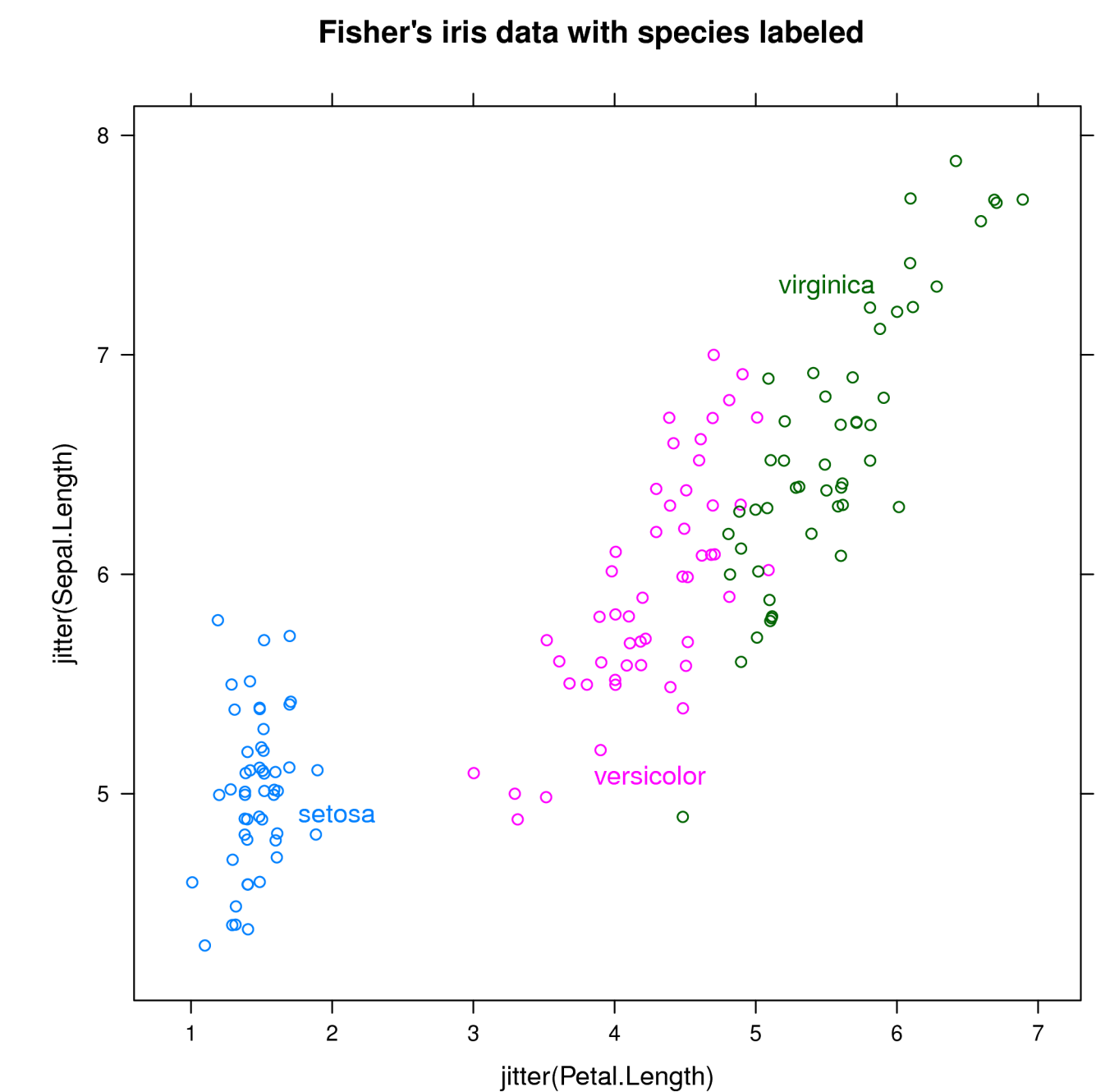
direct.label(dp, list("group.endpoints",
  rot=30, hjust=-0.1))
  
```

Helper functions

- **d1.trans** ($x=x+0.1$) shifts direct labels to the right.
- **d1.move** ("suv", $x=20, y=10, hjust=0$) updates the direct label for the "suv" group.
- **d1.combine** (method1, method2) provides direct labels from both methods.
- **calc.bboxes** calculates bounding boxes for labels, adding columns **w**, **h**, **top**, **bottom**, **right**, and **left**.
- **draw.rects** draws grey boxes around the current labels. This is useful for debugging.
- **ahull.points** and **chull.points** calculate the alpha-hull and convex hull of some points.
- **project.onto.segments** finds the closest point on the hull from the mean of a point cloud.

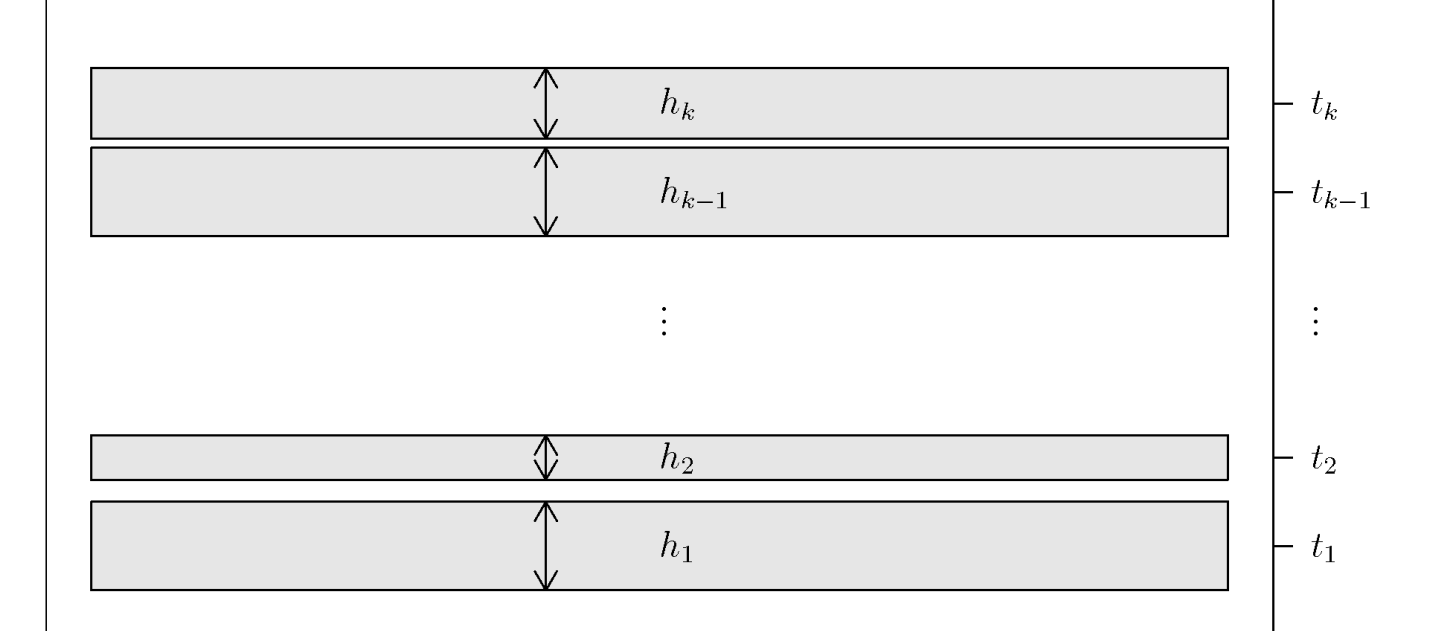
Smart labels

- In lattice panel functions we can calculate the bounding box of each label using grid functions **stringHeight**, **stringWidth**, **convertHeight**, and **convertWidth**.
- Smart Positioning Methods take advantage of this information to avoid collisions with points and other labels.
- For example, in the scatterplot below we recursively perform a grid search to find good label positions.
`iplot <- xyplot(jitter(Sepal.Length)~ jitter(Petal.Length), iris, groups=Species)`
`direct.label(iplot, smart.grid)`



Optimal labels

Let $t_1 \leq \dots \leq t_k$ be the target locations for each of the k direct labels, and let h_1, \dots, h_k be the heights of the corresponding labels.



The optimal direct labels do not overlap, and are as close as possible to the target locations:

$$\min_{b \in \mathbb{R}^k} \sum_{i=1}^k (b_i - t_i)^2 = \|b - t\|^2 \quad (1)$$

subject to $b_{i+1} \geq b_i + h_{i+1}/2 + h_i/2, \forall i = 1, \dots, k-1$

This is a quadratic program (QP) that we can solve using `quadprog::solve.QP()` and we can use the optimal b for the direct label positions. To use the solver, we must write the QP in standard form:

$$\min_{b \in \mathbb{R}^k} \frac{1}{2} b^T b - t^T b \quad (2)$$

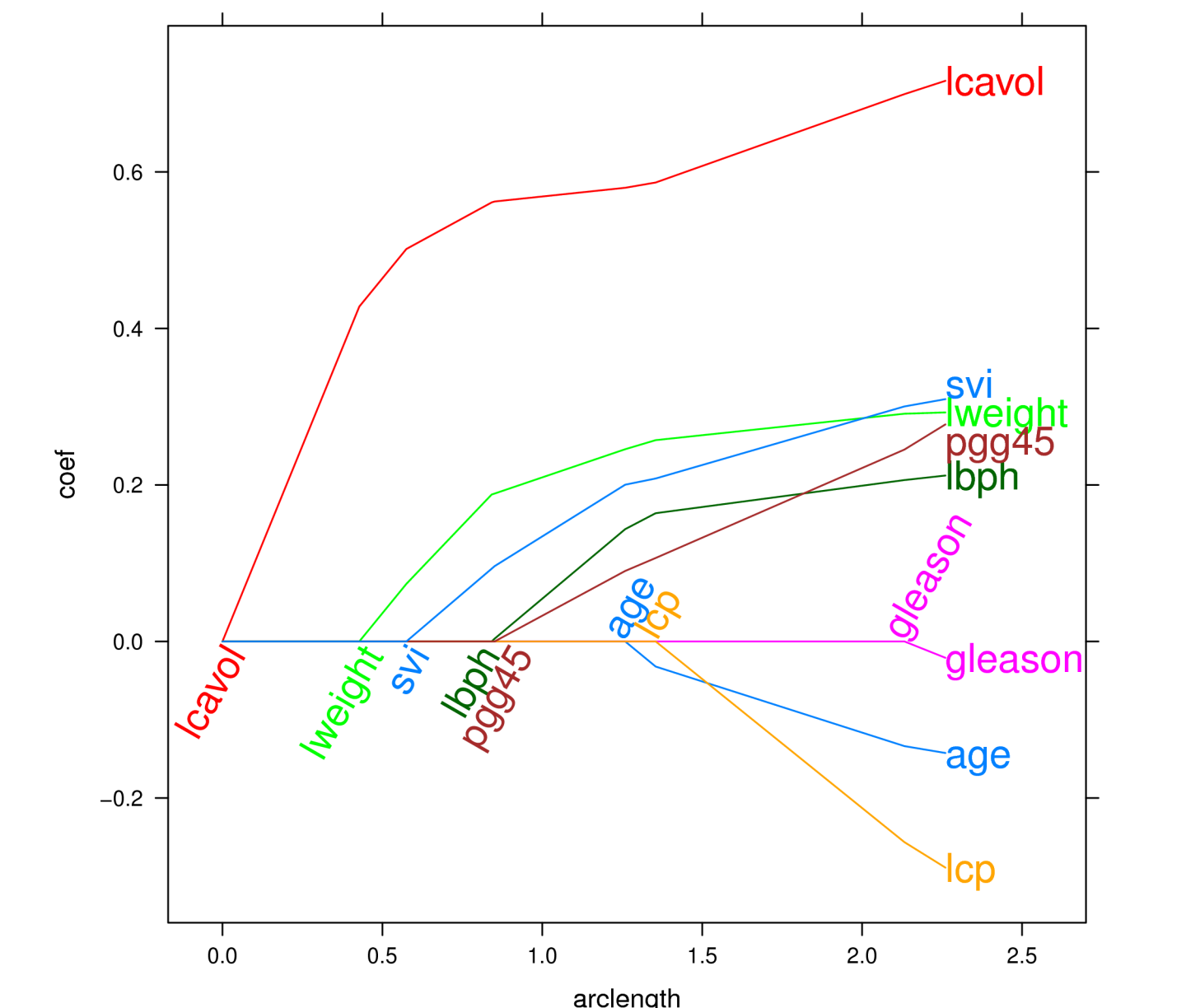
subject to $A b = \begin{bmatrix} -1 & 1 & 0 \\ 0 & -1 & 1 \\ \vdots & \vdots & \vdots \\ 0 & -1 & 1 \end{bmatrix} \begin{bmatrix} b_1 \\ \vdots \\ b_k \end{bmatrix} \geq \begin{bmatrix} (h_1 + h_2)/2 \\ \vdots \\ (h_{k-1} + h_k)/2 \end{bmatrix}$

where A is the $k \times k-1$ constraint coefficient matrix:

$$A = \begin{bmatrix} -1 & 1 & 0 \\ 0 & -1 & 1 \\ \vdots & \vdots & \vdots \\ 0 & -1 & 1 \end{bmatrix} = \begin{bmatrix} 0 & \dots & 0 \\ 1 & 0 & \\ \vdots & \vdots & \vdots \\ 0 & \dots & 1 \end{bmatrix} - \begin{bmatrix} 1 & & 0 \\ & \dots & \\ & & 1 \end{bmatrix} \quad (3)$$

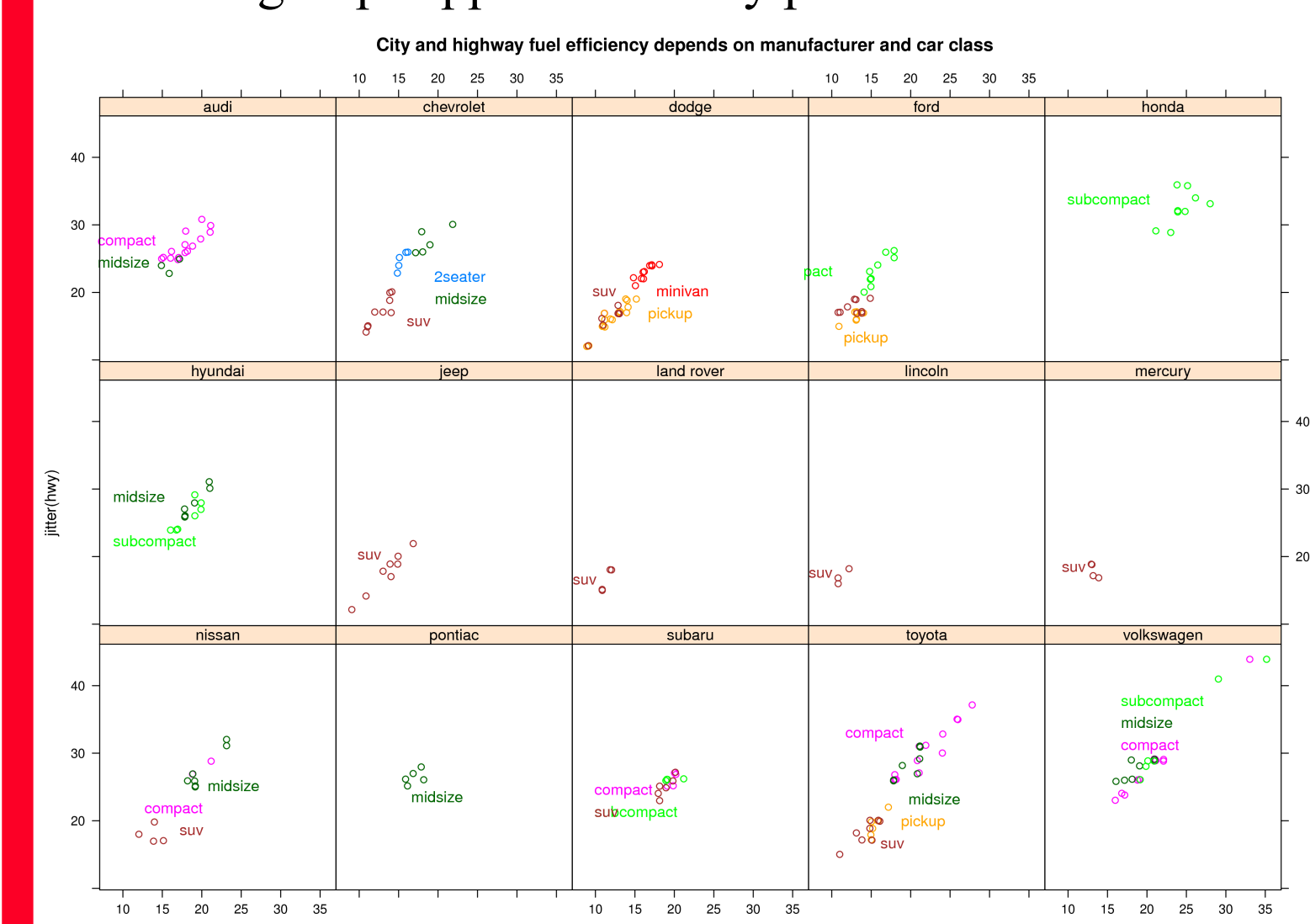
```
path <- xyplot(coef~arclength,
  prostate.path, groups=variable, type="l")
direct.label(path,
  dl.combine(lasso.labels, last.qp))
```

Direct labeled lasso path visualizes important predictors of prostate cancer



Limitation: cluttered panels

Legends preferable for multipanel displays, unless only a subset of groups appears in every panel.



Future work

- ggplot2 support for fontface and fontfamily options?
- ggplot2 support for Smart Positioning Methods? Write a custom grid grob that recalculates position when redrawn?
- automatic scale adjustment for direct label visibility?