

autoplot : ready made plots with ggplot2

Deuxièmes rencontres R

Lyon, 27-28 Juillet 2013



Jean-Olivier Irisson



The problem

```
head(env, 1)
obj <- prcomp(env, scale.=T)

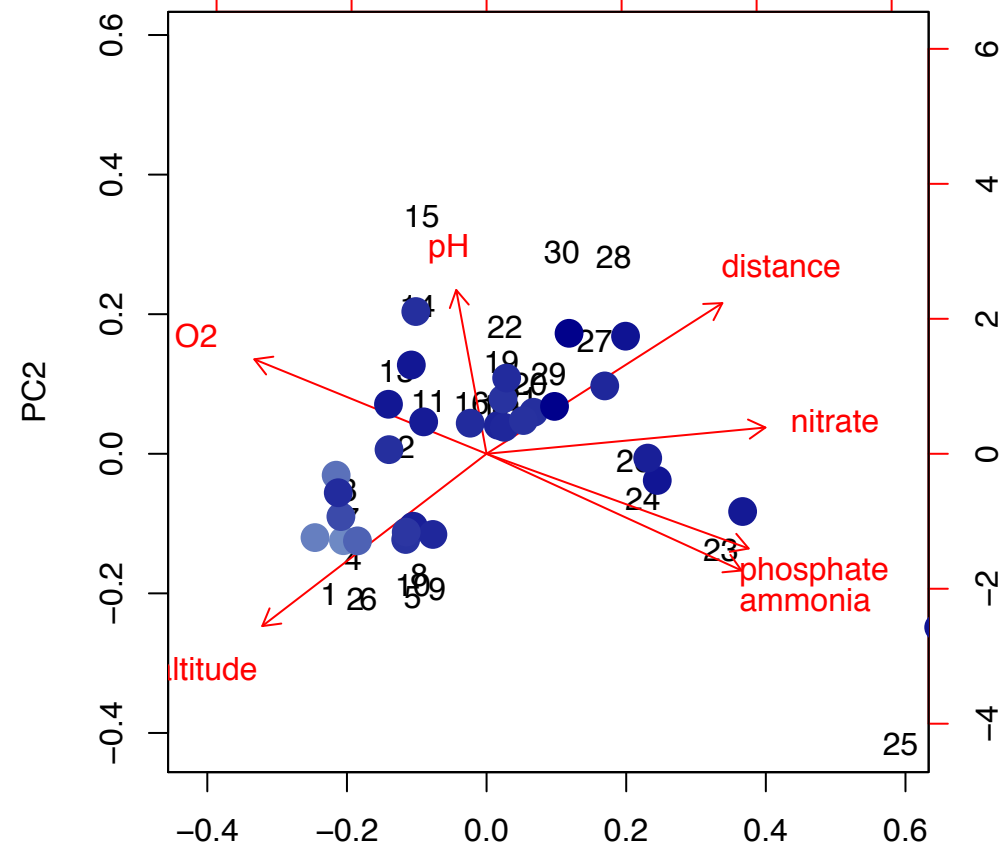
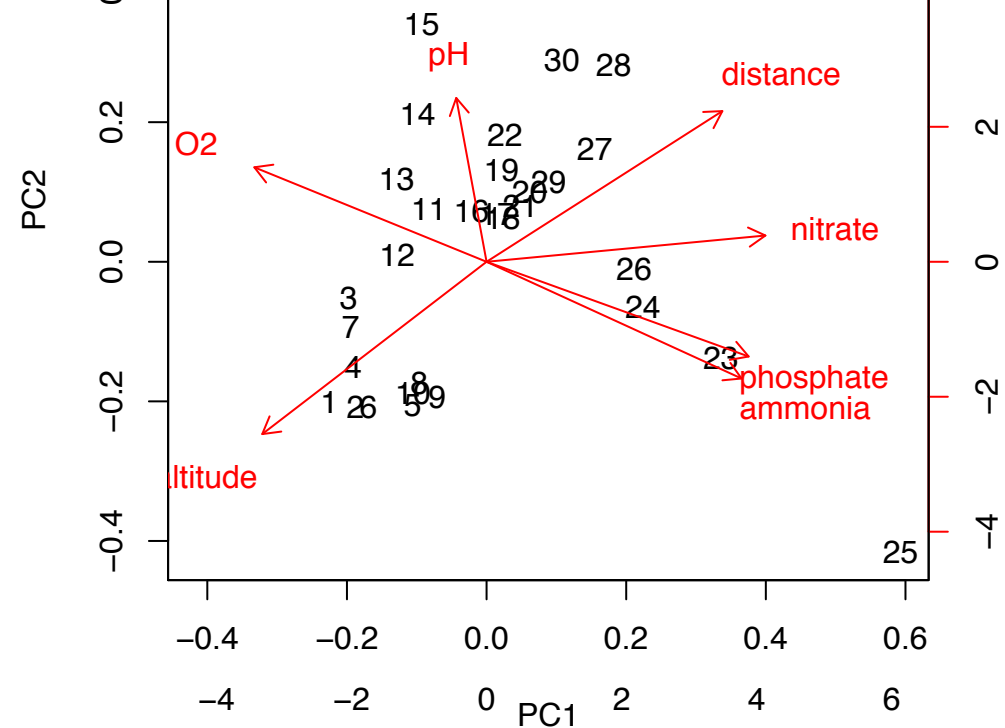
class(obj)
[1] "prcomp"

summary(obj)
biplot(obj)

blues <- colorRamp(
  c("lightblue", "darkblue"))

cols <- rgb(blues(allEnv$hard /
  max(allEnv$hard)), max=255)

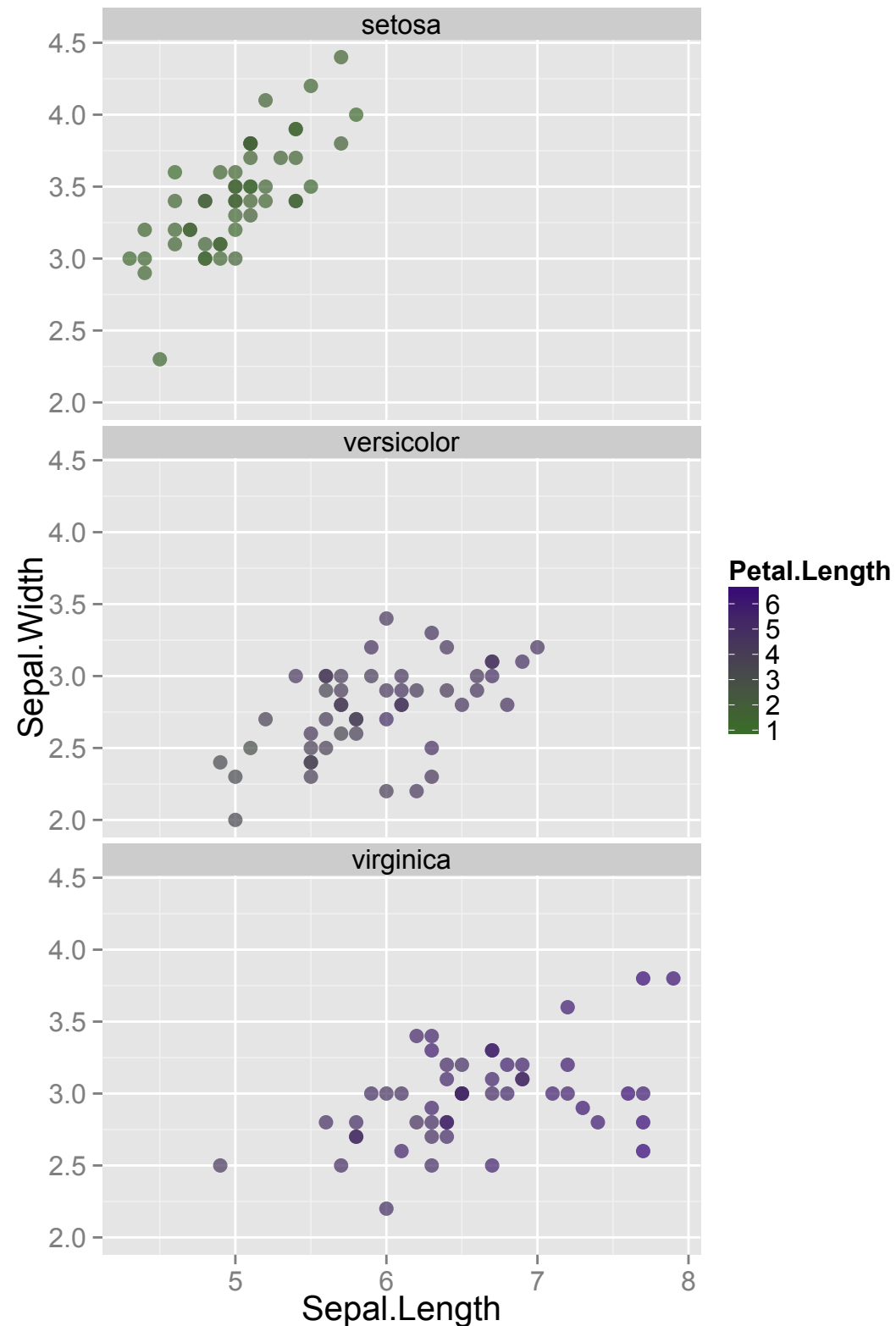
points(obj $x[,1], obj $x[,2],
  col=cols, pch=16, cex=2)
```



Why ggplot?

- Visually pleasing
- Automatic everything
- Customizable after the fact

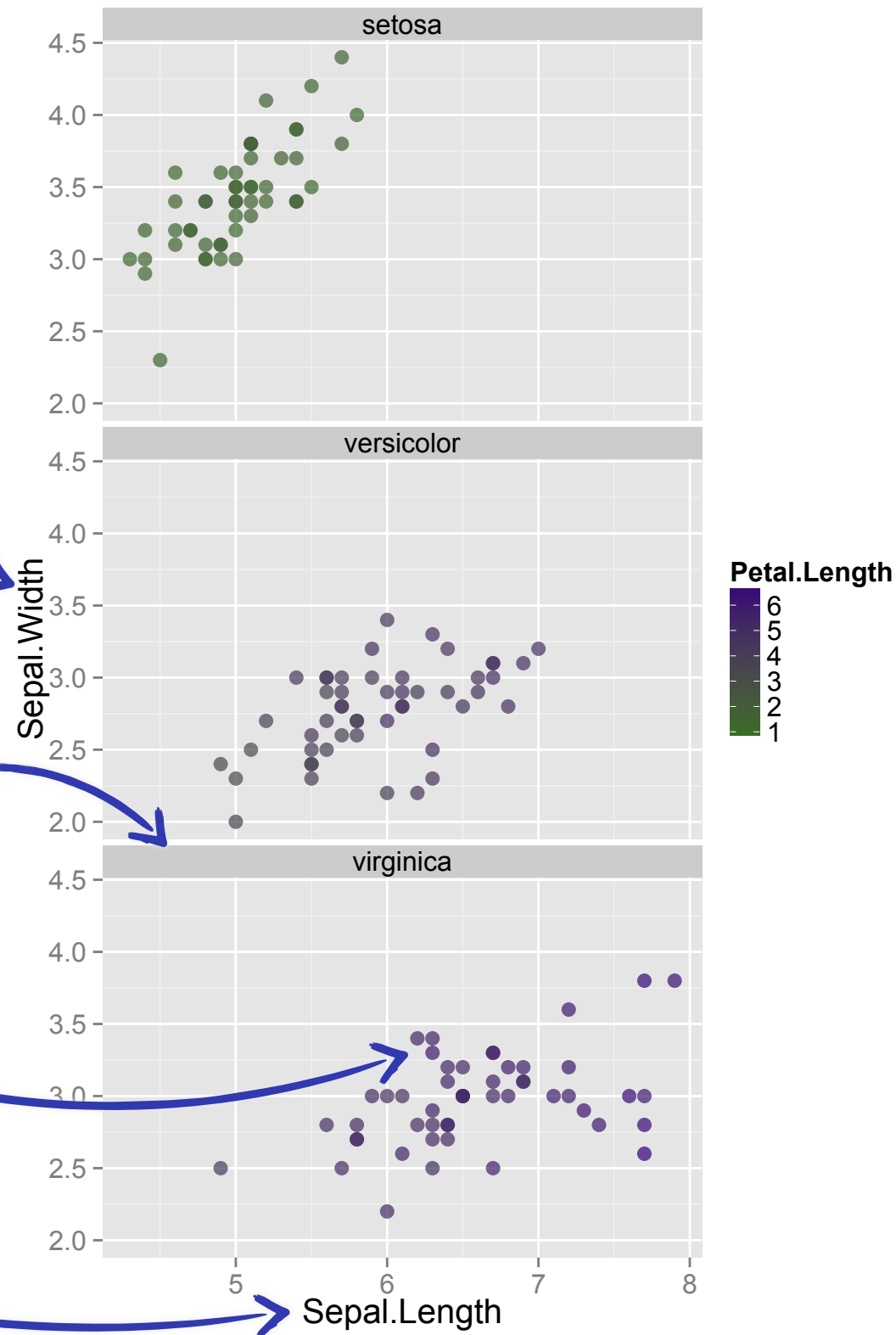
```
p <- ggplot(iris) +  
  geom_point(aes(  
    x=Sepal.Length,  
    y=Sepal.Width,  
    colour=Petal.Length),  
  alpha=0.7, size=3)  
  
p +  
  facet_wrap(~Species, ncol=1)+  
  scale_colour_continuous(  
    low="#3C6B2A", high="#350079")
```



How does ggplot2 work?

- grammar of graphics
- mapping data ↔ aesthetics

Sepal.length	Sepal.width	Petal.length	Peta.width	Species
6.0	3.0	4.8	1.8	virginica
6.4	2.9	4.3	1.3	versicol
4.6	3.6	1.0	0.2	setosa
4.3	3.0	1.1	0.1	setosa



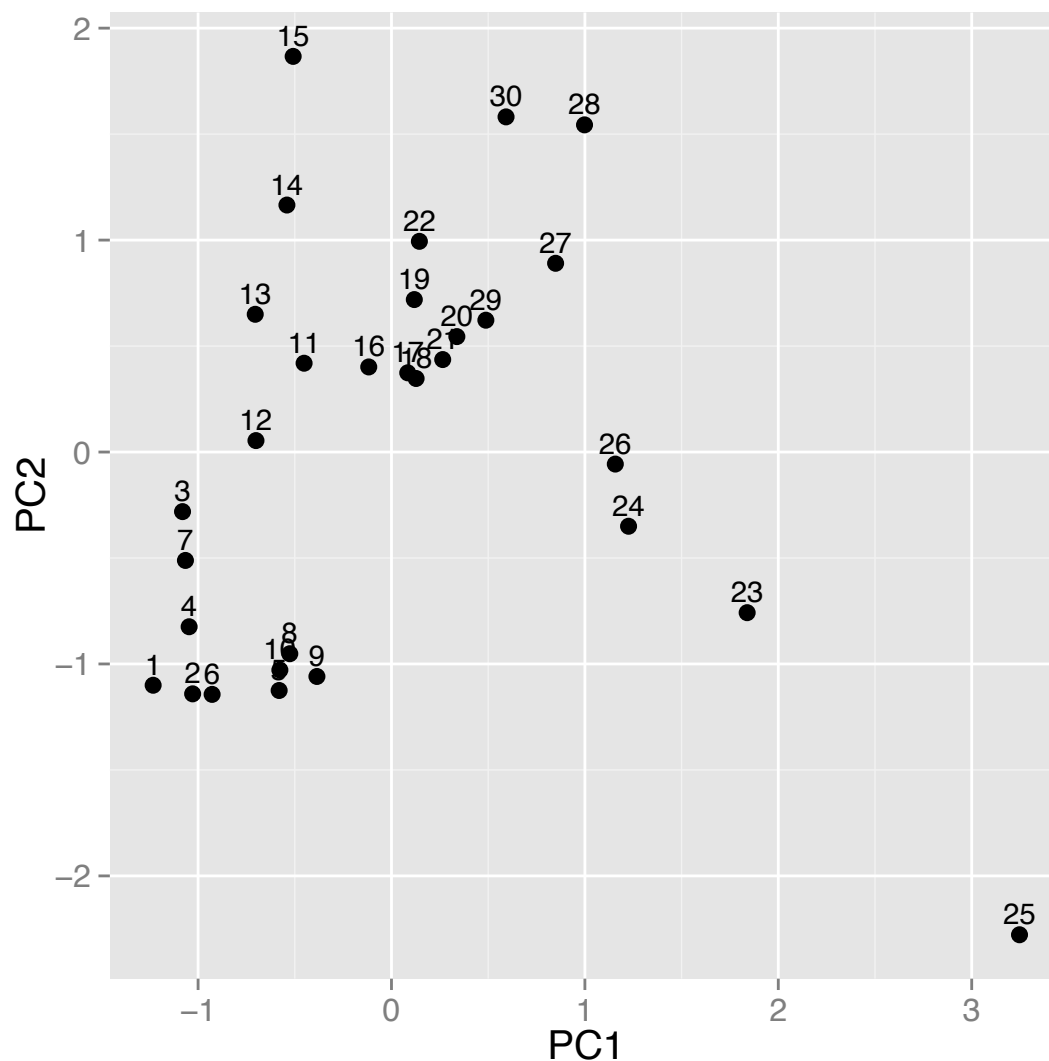
Use ggplot2 for multivariate analyses output

```
obj <- prcomp(env, scale.=T)

# prepare a data.frame
scores <- obj$x[,1:2]
lambda <- obj$sdev[1:2]
d <- data.frame(id=1:nrow(d),
  t(t(scores)/lambda))

# plot it
ggplot(d, aes(x=PC1, y=PC2)) +
  geom_point() +
  geom_text(aes(label=id),
    size=3, vjust=-0.5)

# or
autoplot(obj, type="obs")
```



Automatic

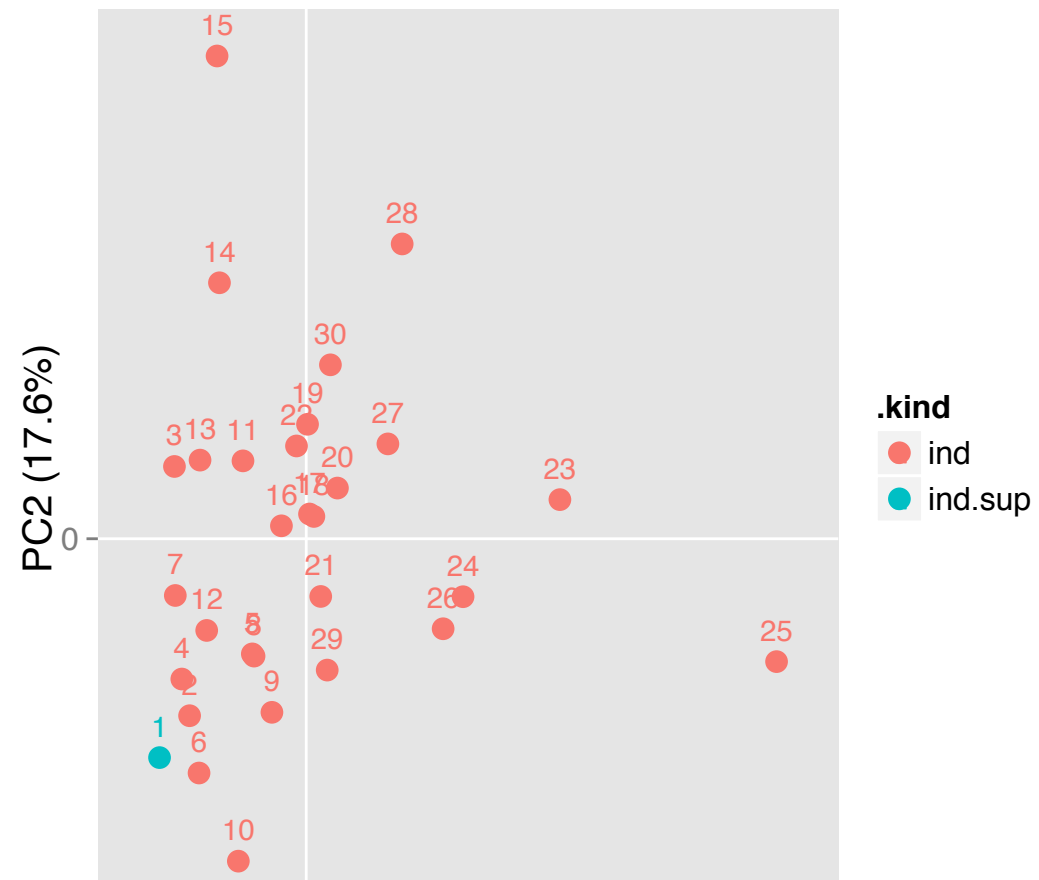
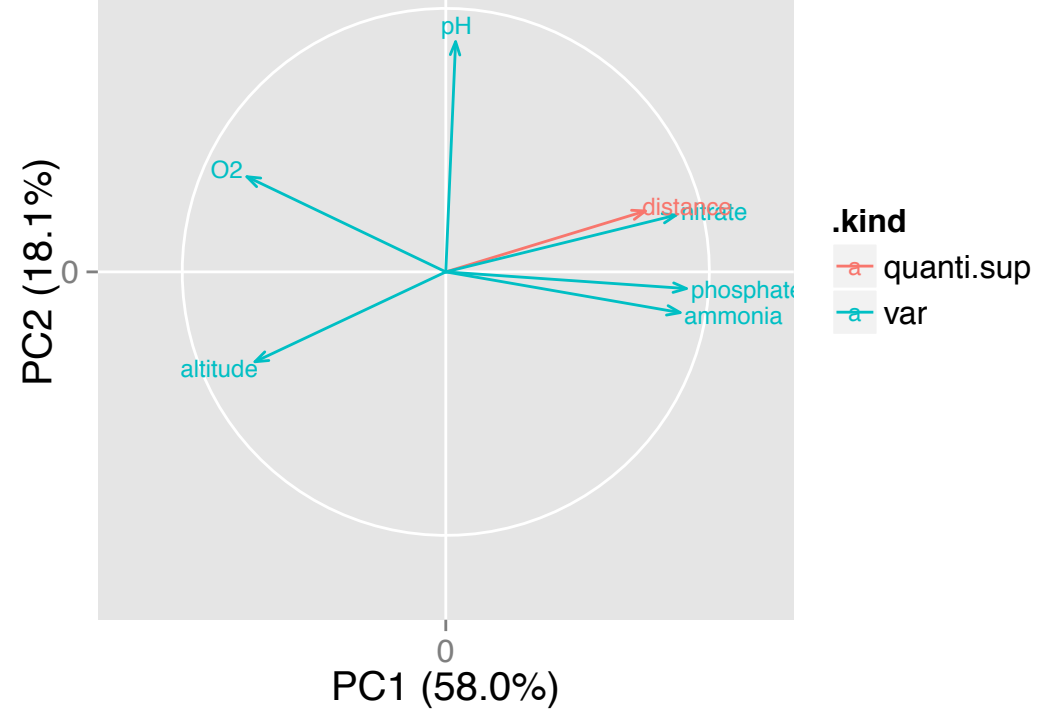
- computation of percentage of variance explained
- better scales
- automatic colours

```
library("FactoMineR")
```

```
obj <- PCA(env, graph=F,  
          quanti.sup=1, ind.sup=1)
```

```
autoplot(obj, type="var")
```

```
autoplot(obj, type="obs")
```



Yet customizable

```
obj <- PCA(env, graph=F)

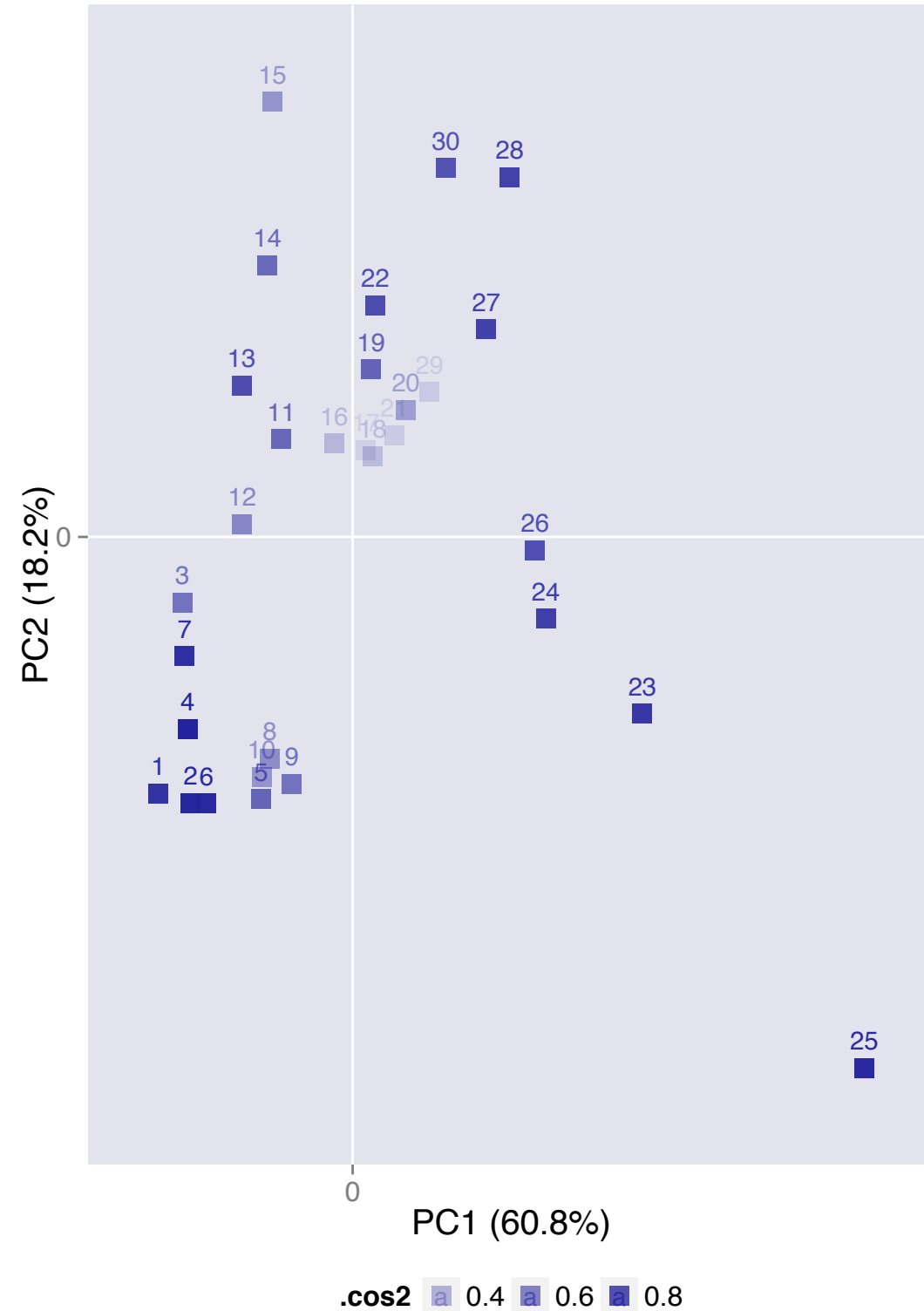
p <- autoplot(obj, type="obs",

  # map additional variables
  mapping=aes(alpha=.cos2),


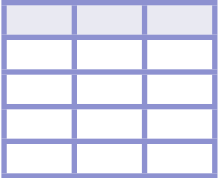

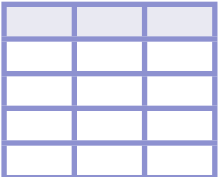
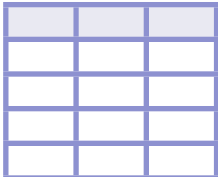
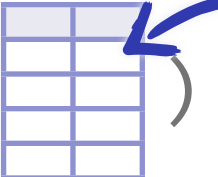
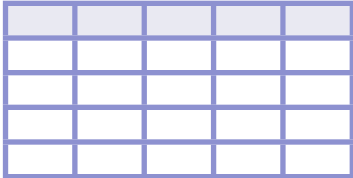
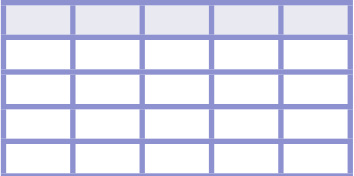
  # pass settings to ggplot calls
  shape=15, colour="#24239D"
)

# change the look after the fact
p + theme(
  panel.background=
  element_rect(fill="#E3E3EE"),
  legend.position="bottom"
)

# yay, beamer-like ggplot!
```



Two step process

```
autoplot(model=, data=, ...) {  
  fortify(model=, data=) {  
    cbind(, )  
    return()  
  }  
  ggplot(, ...) + geom_???(aes(...))  
}
```

The diagram illustrates a two-step process for data visualization. It shows a sequence of R functions: `autoplot`, `fortify`, `cbind`, `return`, and `ggplot`. Each function call is accompanied by a visual representation of its input or output. The `model` parameter is represented by a rounded rectangle icon with a smaller rectangle inside. The `data` parameter is represented by a grid icon. The `cbind` function takes two grid icons as input and returns a larger grid icon. A blue arrow points from the `cbind` function to the `return` function, indicating the flow of data. The `geom_???` function in `ggplot` is represented by a grid icon.

Map original variables, outside the analysis

```
head(env, 1)
  distance altitude pH phosphate
1         3      934 79         1
  nitrate ammonia O2
1       20        0 122
```

```
head(allEnv, 1)
  distance altitude pH phosphate
1         3      934 79         1
  nitrate ammonia O2 slope flow
1       20        0 122 6.176  84
  hard O2_demand
1   45         27
```

```
autoplot(obj, data=allEnv,
  type="obs",
  mapping=aes(alpha=.cos2,
  colour=hard)
)
```

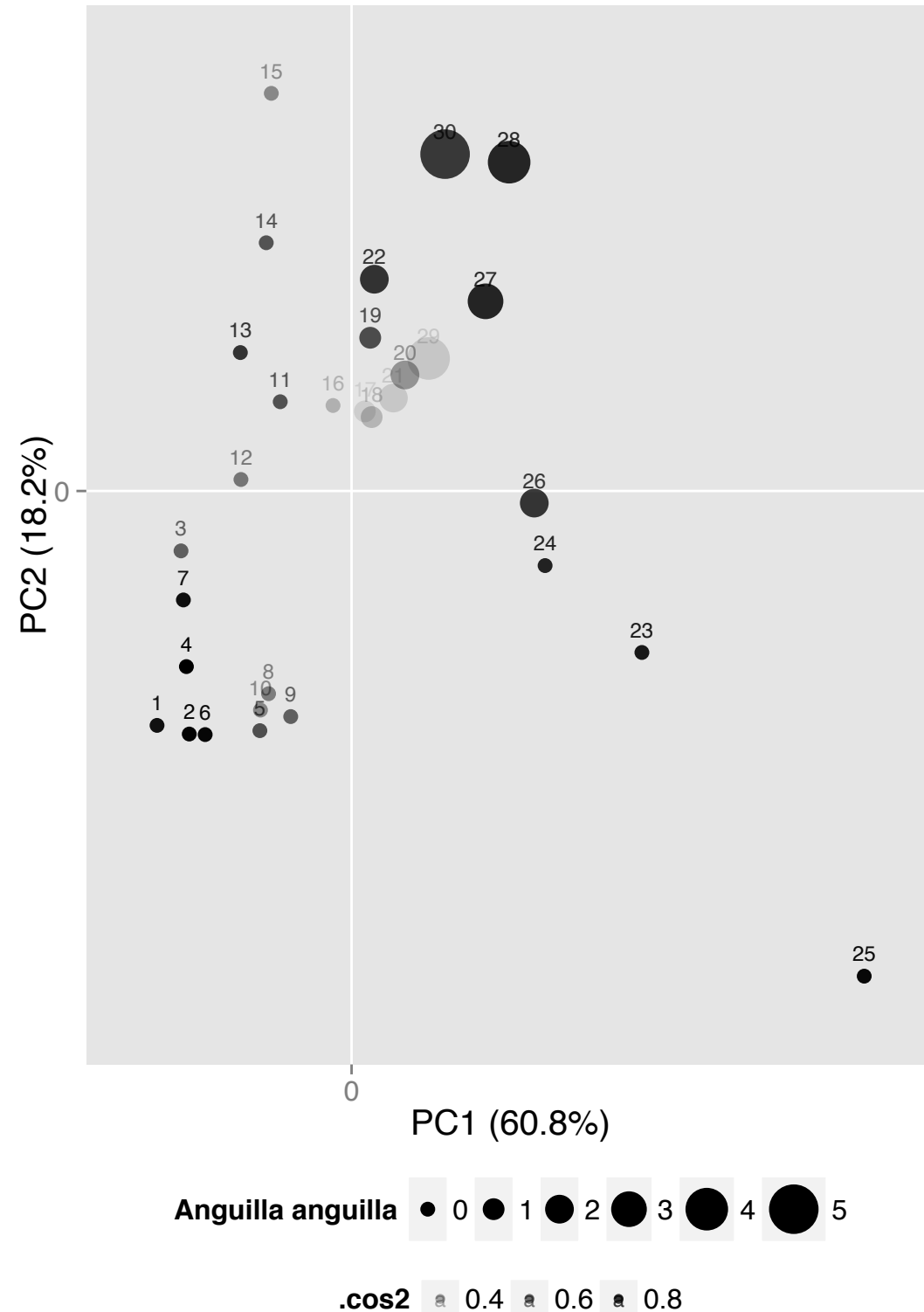
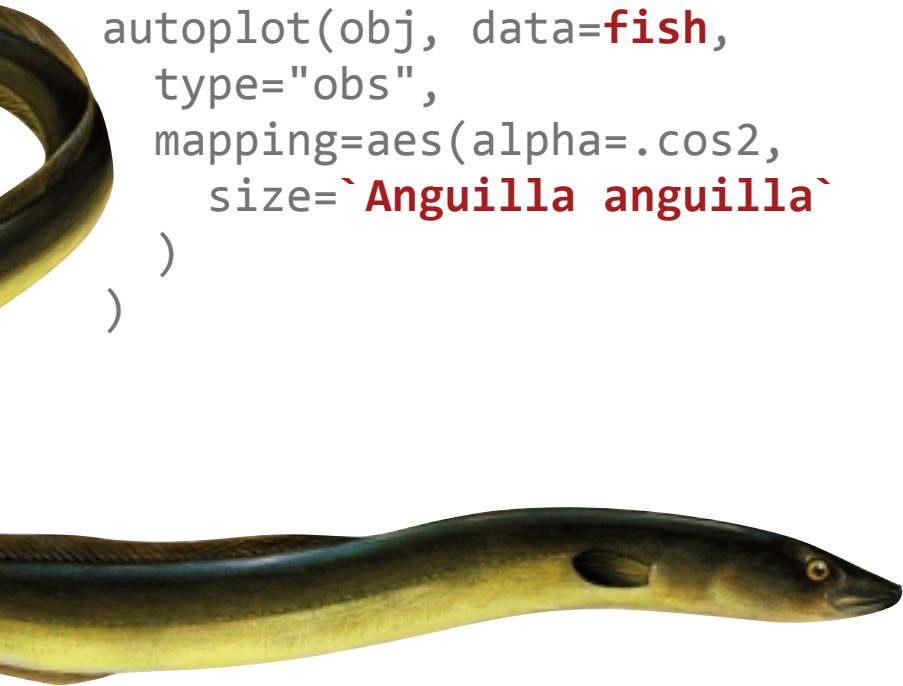


Map variables from other datasets

```
dim(env)  
[1] 30 7
```

```
dim(fish)  
[1] 30 27
```

```
autoplot(obj, data=fish,  
  type="obs",  
  mapping=aes(alpha=.cos2,  
    size=`Anguilla anguilla`  
  )  
)
```



Easily visualize several results

```
scores <- as.matrix(fortify(...
```

```
# un-constrained clustering  
clust <- hclust(  
  dist(scores), method="ward")  
env$clust <- cutree(clust, 5)  
# clustering based on distance  
library("mvpart")  
dClust <- mvpart(  
  scores ~ distance,  
  data=env, size=5)  
env$dclust <- dClust$where
```

```
autoplot(obj, data=env,  
  type="obs",  
  mapping=aes(alpha=.cos2,  
    colour=clust,  
    shape=dclust)
```

```
)
```



Homogenization at little cost

- **Several** fortify methods

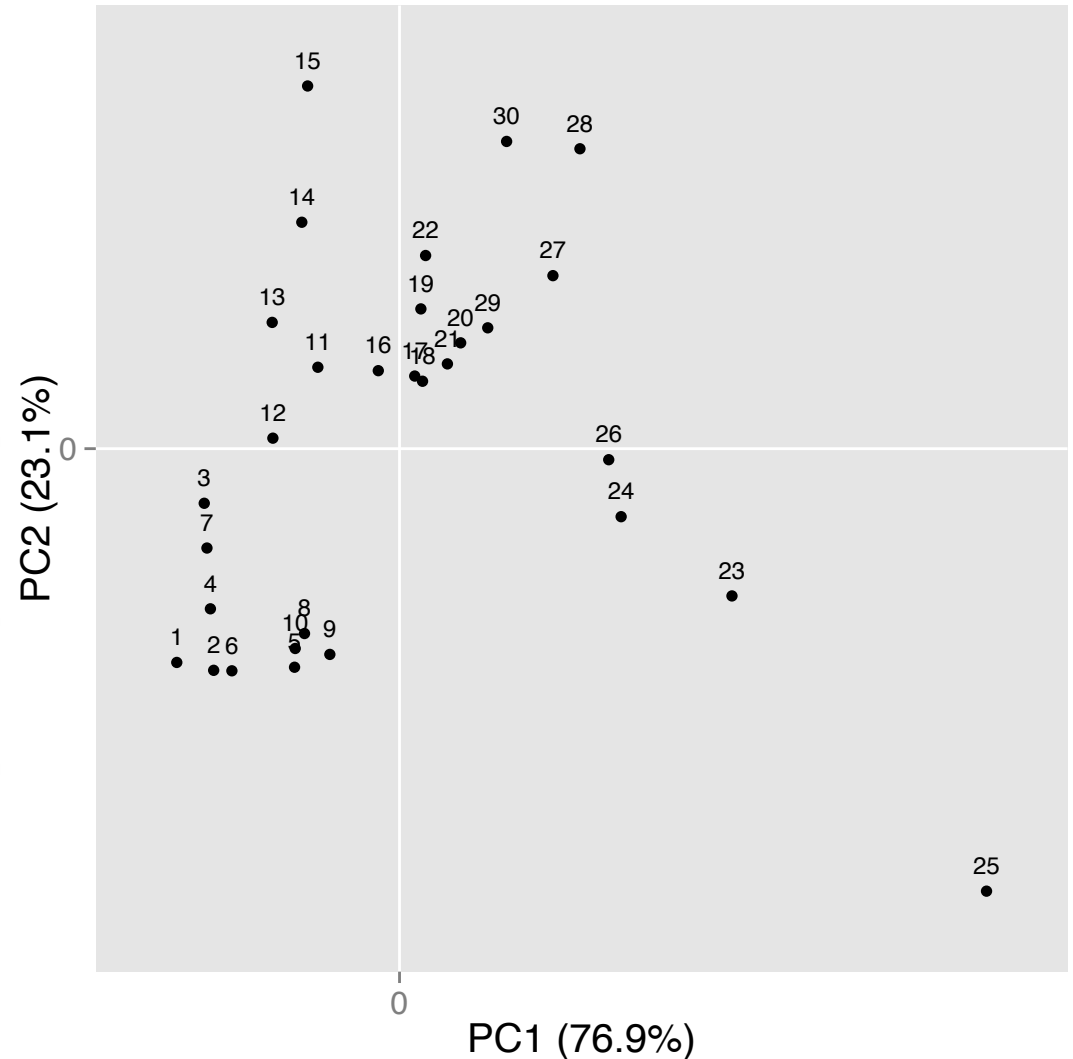
- **One** plotting function

```
obj <- stats::prcomp(env,  
  scale.=TRUE)  
autoplot(obj, type="obs")
```

```
obj <- FactoMineR::PCA(env,  
  graph=FALSE)  
autoplot(obj, type="obs")
```

```
obj <- pcaMethods::pca(env,  
  scale="uv")  
autoplot(obj, type="obs")
```

- **In progress:** `fortify.pca` (ade4)
and `fortify.rda` (vegan)



Future directions

- Scaling + biplot in PCA
- More multivariate functions (CA, MCA are in progress)
- Code `autoplot.lm()` (`fortify.lm()` is already in `ggplot2`)
- Quantile regression (`rq`, `rqs`)
- Bayesian stats (`mcmc`)

■ <https://github.com/jiho/autoplot>

```
library("devtools")
install_github("autoplot", "jiho")
```

