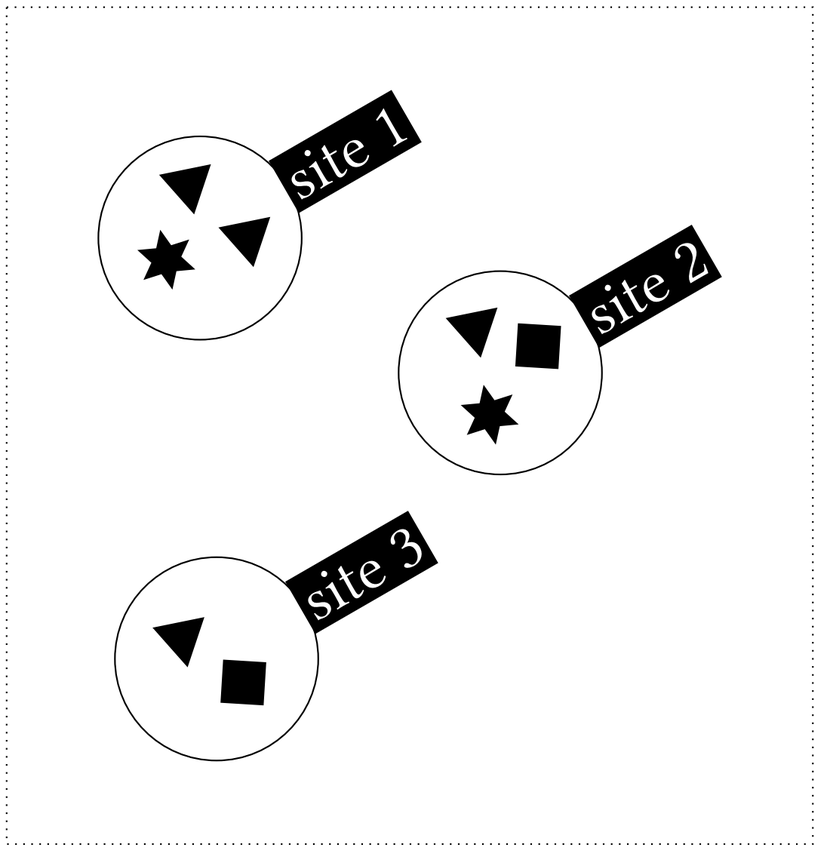
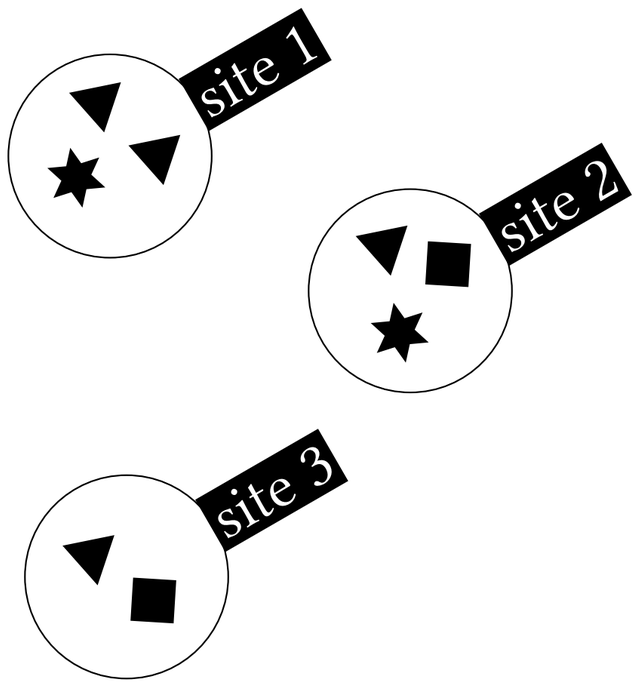
plyr

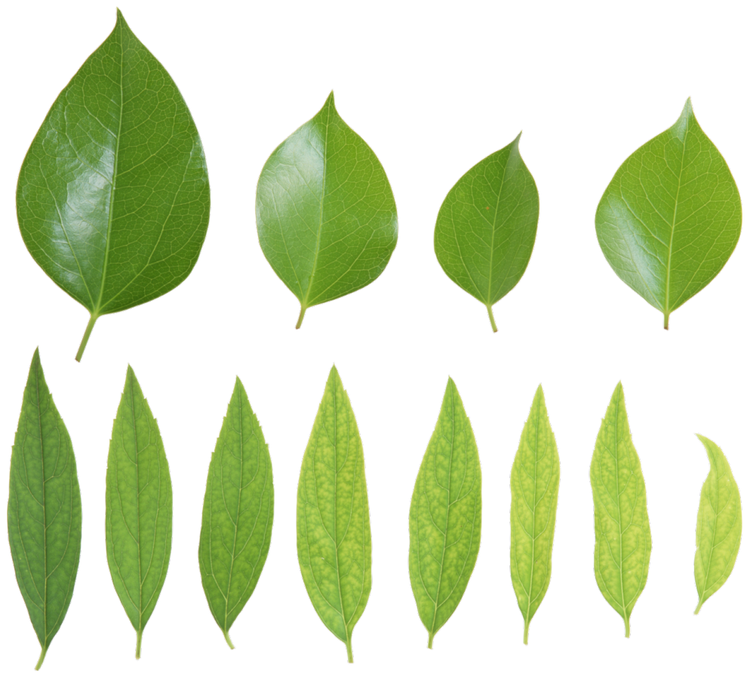
the split-apply-combine strategy

the split-apply-combine strategy ?

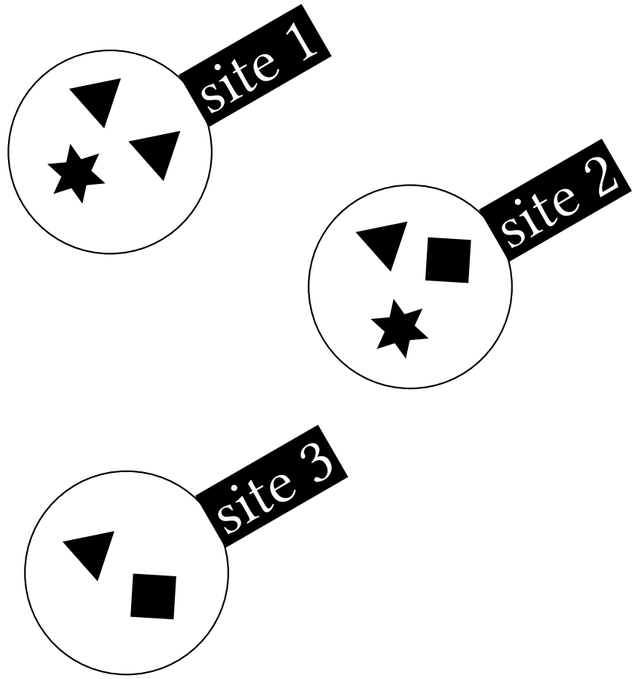


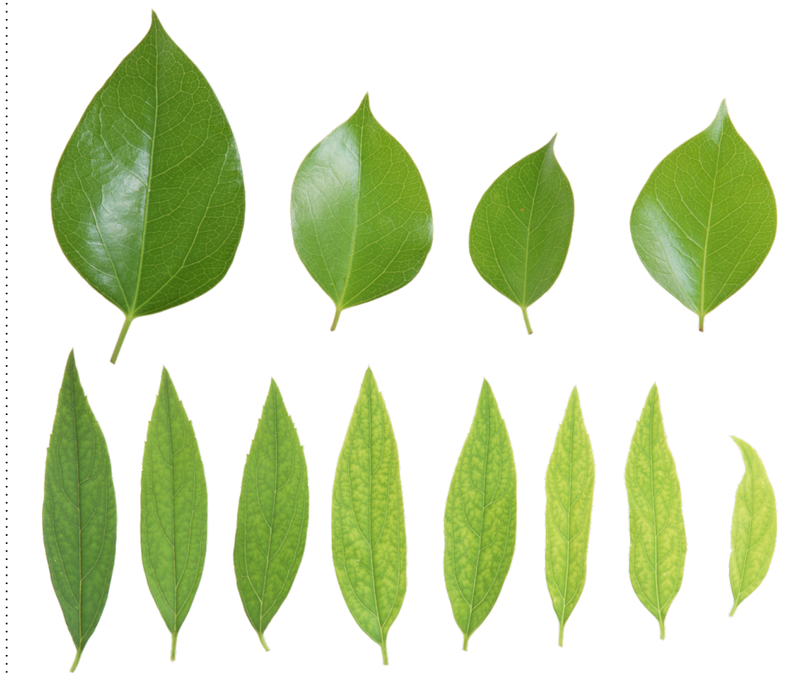
the split-apply-combine strategy ?

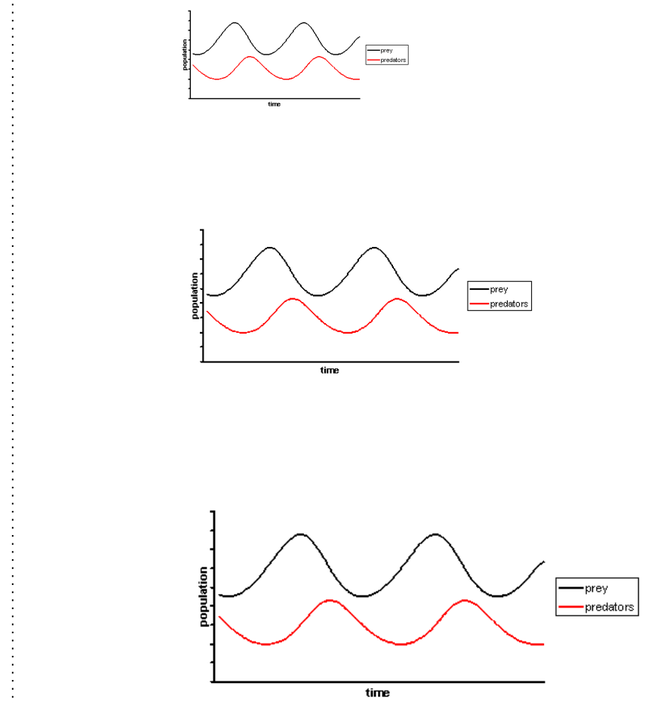




the split-apply-combine strategy ?







the split-apply-combine strategy ?

Species	Sepal.Width	Sepal.Length
setosa	3.1	4.9
setosa	3.7	5.4
versicolor	2.3	5.0
versicolor	2.7	5.6
virginica	3.0	7.2
virginica	2.8	7.4

a **data.frame** example: compute the mean Sepal.Length (*iris* dataset)

```
   Species Sepal.Width Sepal.Length
    setosa         3.1          4.9
    setosa         3.7          5.4
versicolor         2.3          5.0
versicolor         2.7          5.6
 virginica         3.0          7.2
 virginica         2.8          7.4
```

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split

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Species	Sepal.Width	Sepal.Length
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virginica	2.8	7.4

apply

`mean(Sepal.Length)`

5.006

5.936

6.588

a **data.frame** example: compute the mean Sepal.Length (*iris* dataset)

Species	Sepal.Width	Sepal.Length
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virginica	2.8	7.4

apply

`mean(Sepal.Length)`

5.006

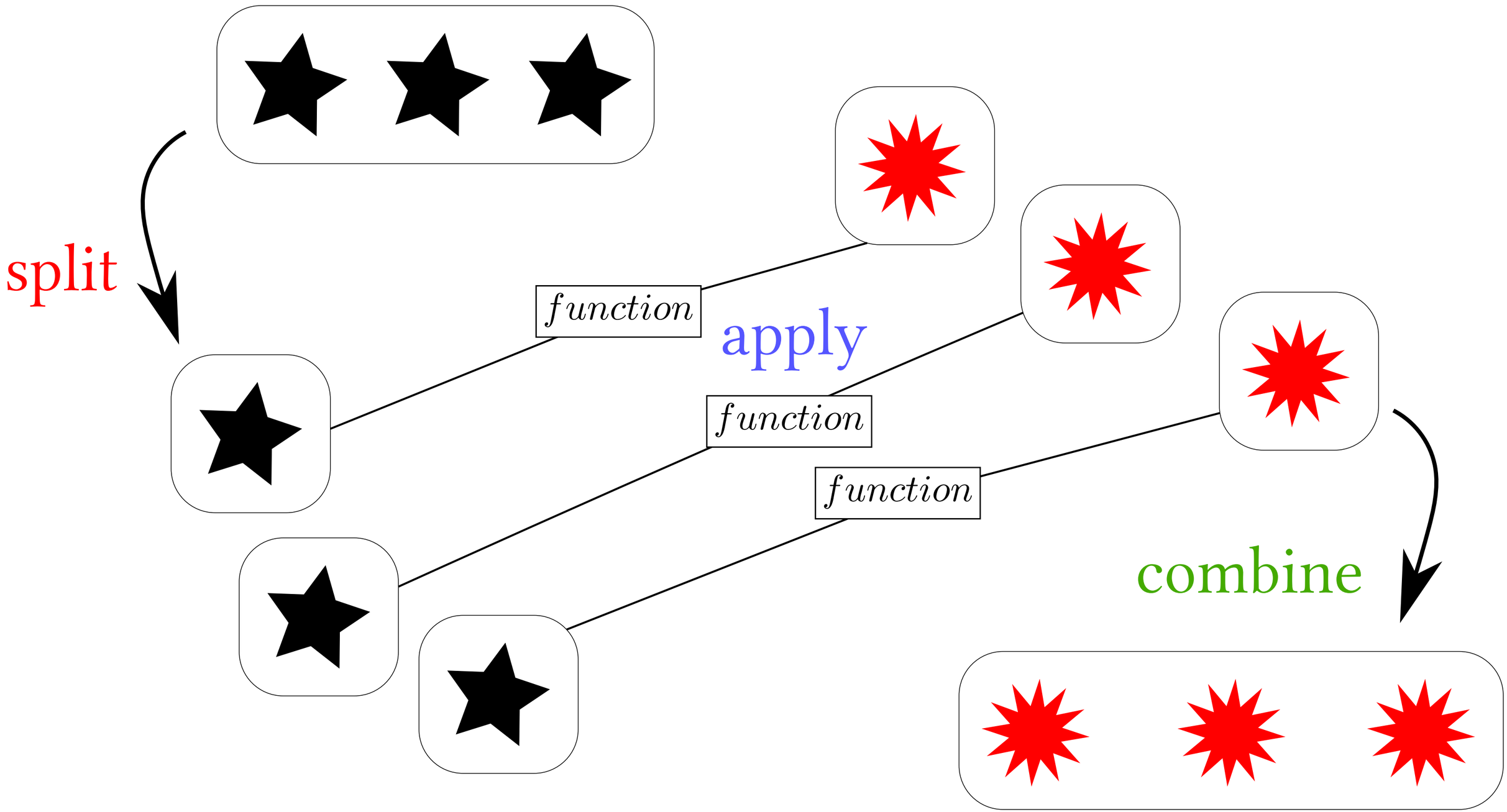
5.936

6.588

combine

Species	Length.mean
setosa	5.006
versicolor	5.936
virginica	6.588

a **collection** of things



a **collection** of things

all rows of a **matrix**

all columns of a **data.frame**

all elements of a **list**

all combinations of factors in a **data.frame**

a **collection** of things

all rows of a **matrix**	apply()
all columns of a **data.frame**	lapply() / apply()
all elements of a **list**	lapply()
all combinations of factors in a **data.frame**	aggregate()

a **collection** of things

each row of a **matrix** — apply()

each column of a **data.frame** — lapply() / apply()

each element of a **list** — lapply()

data belonging to each category in a **data.frame** — aggregate()

**ply()

**ply()

ddply()

data.frame

Species	Sepal.Width	Sepal.Length
setosa	3.1	4.9
setosa	3.7	5.4
versicolor	2.3	5.0
versicolor	2.7	5.6
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data.frame

Species	Length.mean
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**ply()

data.frame

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ddply()

data.frame

Species	Length.mean
setosa	5.006
versicolor	5.936
virginica	6.588

array (e.g. matrix)

	[,1]	[,2]	[,3]	[,4]	[,5]
[1,]	1	6	11	16	21
[2,]	2	7	12	17	22
[3,]	3	8	13	18	23
[4,]	4	9	14	19	24
[5,]	5	10	15	20	25

aaply()

array (e.g. matrix)

	[,1]
[1,]	1
[2,]	2
[3,]	3
[4,]	4
[5,]	5

**ply()

data.frame

Species	Sepal.Width	Sepal.Length
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ddply()

data.frame

Species	Length.mean
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aaply()

array (e.g. matrix)

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[1,]	1	6	11	16	21
[2,]	2	7	12	17	22
[3,]	3	8	13	18	23
[4,]	4	9	14	19	24
[5,]	5	10	15	20	25

array (e.g. matrix)

	[,1]
[1,]	1
[2,]	2
[3,]	3
[4,]	4
[5,]	5

dlply()

data.frame

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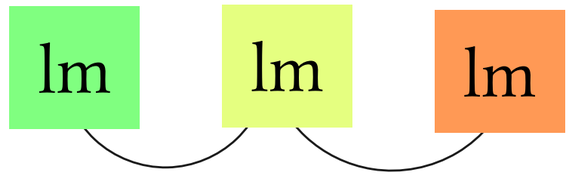
list



[1] ddply()

task: get the mean sepal length for each species

```
# Define the function to apply
mean_sep_length <- function(df) {
  mean(df[ ,'Sepal.Length'])
}
```

Species	Sepal.Width	Sepal.Length
setosa	3.1	4.9
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[1] ddply()

task: get the mean sepal length for each species

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# Define the function to apply
mean_sep_length <- function(df) {
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}
```

```
> mean_sep_length(iris)
[1] 5.843333
```

Species	Sepal.Width	Sepal.Length
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[1] ddply()

task: get the mean sepal length for each species

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# Define the function to apply
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  mean(df[ ,'Sepal.Length'])
}
```

```
> mean_sep_length(iris)
```

```
[1] 5.843333
```

```
library(plyr)
> ddply(iris, ~ Species, mean_sep_length)
```

Species	V1
1 setosa	5.006
2 versicolor	5.936
3 virginica	6.588

Species	Sepal.Width	Sepal.Length
setosa	3.1	4.9
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versicolor	2.3	5.0
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virginica	2.8	7.4

a **data.frame** example: compute the mean Sepal.Length (*iris* dataset)

Species	Sepal.Width	Sepal.Length
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virginica	2.8	7.4

split

Species	Sepal.Width	Sepal.Length
setosa	3.1	4.9
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versicolor	2.3	5.0
versicolor	2.7	5.6

Species	Sepal.Width	Sepal.Length
virginica	3.0	7.2
virginica	2.8	7.4

apply

```
mean_sep_length
```

5.006

5.936

6.588

combine

Species	V1
setosa	5.006
versicolor	5.936
virginica	6.588

[1]ddply()

Your turn

task: get the mean **petal** length for each species

[1]ddply()

task: get the mean petal length for each species

```
# Define the function to apply
mean_pet_length <- function(df) {
  mean(df[ ,'Petal.Length'])
}
```

```
> mean_pet_length(iris)
```

```
[1] 3.758
```

```
library(plyr)
> ddply(iris, ~ Species, mean_pet_length)
```

```
     Species    V1
1     setosa 1.462
2 versicolor 4.260
3  virginica 5.552
```

[1]ddply()

task: get the mean petal length for each species

```
# Define the function to apply
mean_pet_length <- function(df) {
  mean(df[ ,'Petal.Length'])
}
```

NO NAME HERE...

```
> mean_pet_length(iris)
```

```
[1] 3.758
```

...MEANS NO NAME THERE

```
library(plyr)
> ddply(iris, ~ Species, mean_pet_length)
```

```
     Species    V1
1     setosa 1.462
2 versicolor 4.260
3  virginica 5.552
```

[1]ddply()

task: get the mean petal length for each species

```
# Define the function to apply
mean_pet_length <- function(df) {
  data.frame(length = mean(df[ ,'Petal.Length']))
}
```

[1] ddply()

task: get the mean petal length for each species

```
# Define the function to apply
mean_pet_length <- function(df) {
  data.frame(length = mean(df[ ,'Petal.Length']))
}
```

```
> mean_pet_length(iris)
```

```
  length
1  3.758
```

[1] ddply()

task: get the mean petal length for each species

```
# Define the function to apply
mean_pet_length <- function(df) {
  data.frame(length = mean(df[ ,'Petal.Length']))
}
```

```
> mean_pet_length(iris)
```

```
  length
1  3.758
```

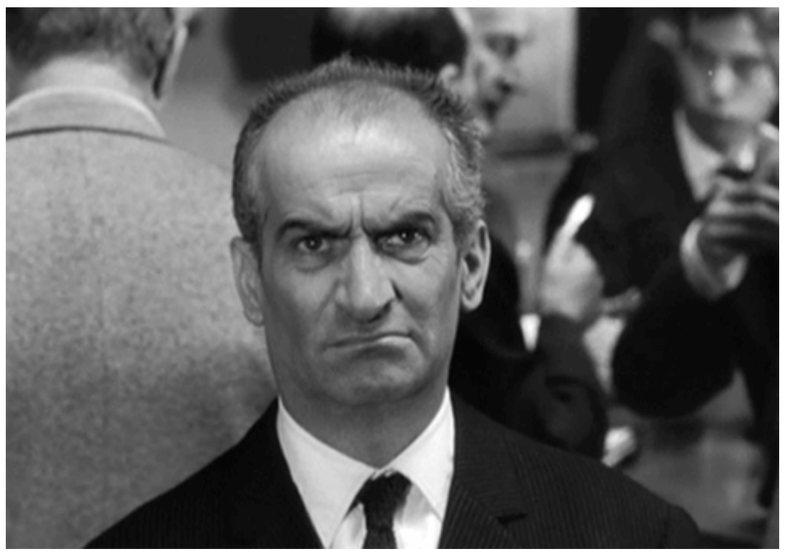
```
library(plyr)
> ddply(iris, ~ Species, mean_pet_length)
```

```
     Species  length
1     setosa   1.462
2 versicolor   4.260
3  virginica   5.552
```

[2]ddply()

(a bit) more complicated

task: get the mean **sepal length** and **width** for each species



[2] ddply()

task: get the mean **sepal length** and **width** for each species

```
# Define the function to apply
mean_sep_dims <- function(df) {
  data.frame(length = mean(df[ ,'Sepal.Length']))
}
```

[2] ddply()

task: get the mean **sepal length** and **width** for each species

```
# Define the function to apply
mean_sep_dims <- function(df) {
  data.frame(length = mean(df[ ,'Sepal.Length']),
             width  = mean(df[ ,'Sepal.Width']))
}
```

[2] ddply()

task: get the mean **sepal length** and **width** for each species

```
# Define the function to apply
mean_sep_dims <- function(df) {
  data.frame(length = mean(df[ ,'Sepal.Length']),
             width  = mean(df[ ,'Sepal.Width']))
}
```

```
> mean_sep_dims(iris)
```

```
     length    width
1 5.843333 3.057333
```

[2] ddply()

task: get the mean **sepal length** and **width** for each species

```
# Define the function to apply
mean_sep_dims <- function(df) {
  data.frame(length = mean(df[ ,'Sepal.Length']),
             width  = mean(df[ ,'Sepal.Width']))
}
> mean_sep_dims(iris)
     length    width
1 5.843333 3.057333

library(plyr)
> ddply(iris, ~ Species, mean_sep_dims)
     Species length width
1     setosa  5.006 3.428
2 versicolor  5.936 2.770
3  virginica  6.588 2.974
```

Your turn

task: get the mean **petal length and width** for each species

[3]ddply()

```
# Define the function to apply
mean_sep_dims <- function(df) {
  c(mean(df[ ,'Sepal.Length']), mean(df[ ,'Sepal.Width']))
}
```

[3]ddply()

```
# Define the function to apply
mean_sep_dims <- function(df) {
  c(mean(df[ ,'Sepal.Length']), mean(df[ ,'Sepal.Width']))
}

> mean_sep_dims(iris)
                                    [1] 5.843333 3.057333
```

[3]ddply()

```
# Define the function to apply
mean_sep_dims <- function(df) {
  c(mean(df[ ,'Sepal.Length']), mean(df[ ,'Sepal.Width']))
}

> mean_sep_dims(iris)
[1] 5.843333 3.057333
```

```
> library(plyr)
> ddply(iris, ~ Species, mean_sep_dims)
```

	Species	V1	V2
1	setosa	5.006	3.428
2	versicolor	5.936	2.770
3	virginica	6.588	2.974

[3]ddply()

```
# Define the function to apply
mean_sep_dims <- function(df) {
  c(mean(df[ ,'Sepal.Length']), mean(df[ ,'Sepal.Width']))
}

> mean_sep_dims(iris)
                                    [1] 5.843333 3.057333
```

```
> library(plyr)
> ddply(iris, ~ Species, mean_sep_dims)
```

Species	V1	V2
setosa	5.006	3.428
versicolor	5.936	2.770
virginica	6.588	2.974

[3]ddply()

The most unambiguous behaviour is achieved when [the function to apply] returns a data frame - in that case pieces will be combined...

(from ?ddply)

-> Always return a **data.frame** [with **names**, ndlr]

... do not program by coincidence

[https://pragprog.com/the-pragmatic-programmer/extracts/coincidence]

[3bis]ddply()

Make it short: use `summarise()`


```
> ddply(iris, ~ Species, summarise,
        length = mean(Sepal.Length),
        width  = mean(Sepal.Width))

     Species length width
1     setosa  5.006 3.428
2 versicolor  5.936 2.770
3  virginica  6.588 2.974
```

-> Do the same with Petals

[4]ddply()

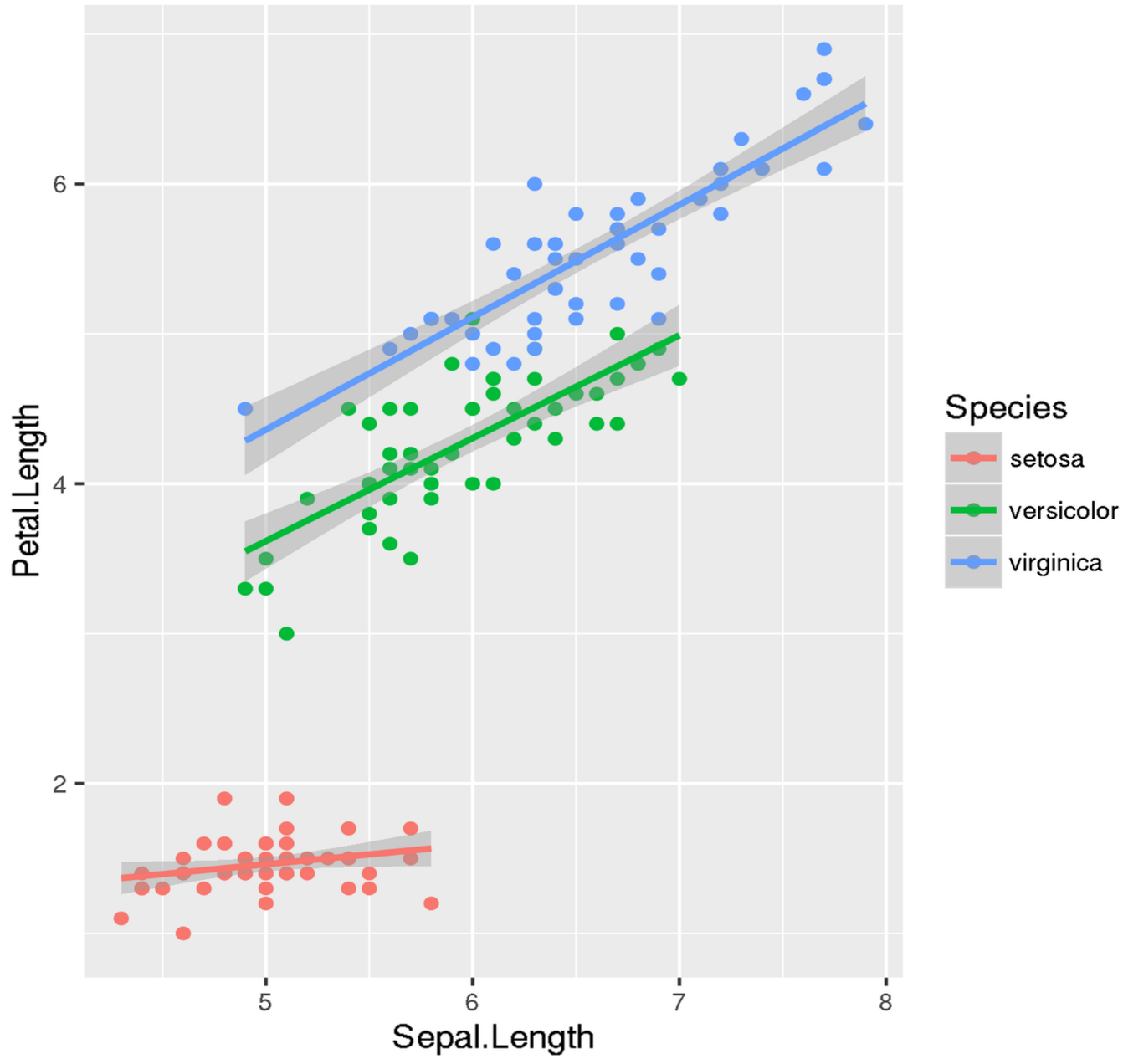
(a bit) more complicated

task: explore the **Petal length ~ Sepal length** relationship

[4] ddply()

task: explore the **Petal length ~ Sepal length** relationship

```
ggplot(iris, aes(Sepal.Length, Petal.Length, color = Species)) +
  geom_point() +
  geom_smooth(method = 'lm')
```



[4] ddply()

task: explore the **Petal length ~ Sepal length** relationship

get the coefficients of a linear regression (example for all species altogether)

```
iris_model <- lm(Petal.Length ~ Sepal.Length,
   data = iris)
coeffs <- coefficients(iris_model)
```

write this within a function that returns a data.frame !

[4] ddply()

task: explore the **Petal length ~ Sepal length** relationship

get the coefficients of a linear regression (example for all species altogether)

```
iris_model <- lm(Petal.Length ~ Sepal.Length,
   data = iris)
coeffs <- coefficients(iris_model)
```

write this within a function that returns a data.frame !

```
get_coeffs <- function(df) {
  model <- lm(Petal.Length ~ Sepal.Length, data = df)
  coeffs <- coefficients(model)

  # coeffs is a vector -> convert to data.frame
  data.frame(slope     = coeffs["Sepal.Length"],
             intercept = coeffs["(Intercept)"])
}
```

[4] ddply()

task: explore the **Petal length ~ Sepal length** relationship

```
get_coeffs <- function(df) {
  model <- lm(Petal.Length ~ Sepal.Length, data = df)
  coeffs <- coefficients(model)

  # coeffs is a vector -> convert to data.frame
  data.frame(slope     = coeffs["Sepal.Length"],
             intercept = coeffs["(Intercept)"])
}
```

```
> ddply(iris, ~ Species, get_coeffs)
```

	Species	slope	intercept
1	setosa	0.1316317	0.8030518
2	versicolor	0.6864698	0.1851155
3	virginica	0.7500808	0.6104680

Your turn

task: get the coefficients of the **Petal.Width ~ Sepal.Width** relationship for each species

[5] ddply()

What if my task takes a lot of time ?

e.g. get bootstrapped estimates of slope coefficients (Petal.Length ~ Sepal.Length)

```
> source('http://alex.lecairn.org/boot_iris.R')

> ddply(iris, ~ Species, get_boot_coeffs)
```

data.frame with 3000 rows and 3 columns

[5]ddply()

What if my task takes a lot of time ?

Solution 1: report about the time it takes and go get a coffee

```
ddply(iris, ~ Species, get_boot_coeffs,
      .progress = 'time')
```

(try also .progress = 'tk' or 'win')

[5]ddply()

What if my task takes a lot of time ?

Solution 1: report about the time it takes and go get a coffee

```
ddply(iris, ~ Species, get_boot_coeffs,
      .progress = 'time')
```

(try also .progress = 'tk' or 'win')

Solution 2: use parallel computing

```
library(doParallel)
registerDoParallel(cl = makeCluster(2))

ddply(iris, ~ Species, get_boot_coeffs,
      .parallel = TRUE)
```

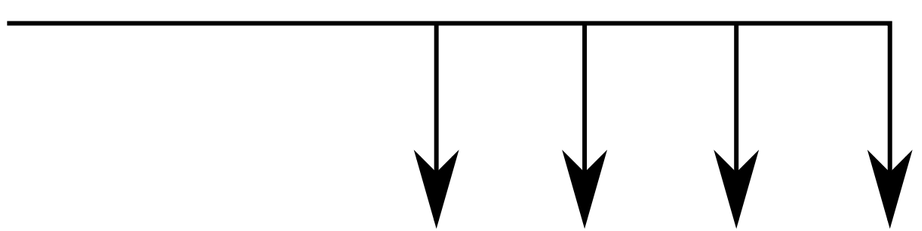
WHAT IF I DDPLY DOES NOT DO IT ?

WHAT IF I DDPLY DOES NOT DO IT ?

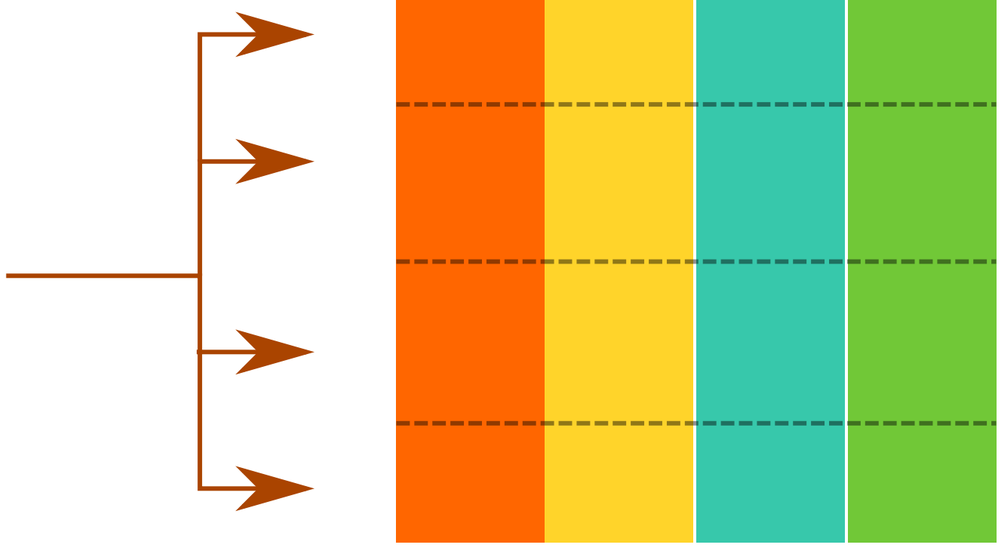
YOU PROBABLY WANT TO REFORMAT YOUR DATA, BUT....

a*ply: apply on all **rows of a data.frame**
rows or columns of a matrix

```
a*ply(matrix, 2, mean)
```



```
a*ply(matrix, 1, mean)
```



e.g. Compute abundances of species in a community matrix

```
> library(vegan)
> data(dune)
> dune <- as.matrix(dune)
```

species ->

<- sites

	Achimill	Agrostol	Airaprae	Alopgeni	Anthodor	Bellpere	Bromhord	Chenalbu	Cirsarve	Comapalu	Eleopalu	Elymr
1	1	0	0	0	0	0	0	0	0	0	0	
2	3	0	0	2	0	3	4	0	0	0	0	
3	0	4	0	7	0	2	0	0	0	0	0	
4	0	8	0	2	0	2	3	0	2	0	0	
5	2	0	0	0	4	2	2	0	0	0	0	
6	2	0	0	0	3	0	0	0	0	0	0	

"a community matrix"

e.g. Compute abundances of species in a community matrix

species ->

<- sites

	Achimill	Agrostol	Airaprae	Alopgeni	Anthodor	Bellpere	Bromhord	Chenalbu	Cirsarve	Comapalu	Eleopalu	Elymr
1	1	0	0	0	0	0	0	0	0	0	0	
2	3	0	0	2	0	3	4	0	0	0	0	
3	0	4	0	7	0	2	0	0	0	0	0	
4	0	8	0	2	0	2	3	0	2	0	0	
5	2	0	0	0	4	2	2	0	0	0	0	
6	2	0	0	0	3	0	0	0	0	0	0	

```
> aaply(dune, 2, mean) # average species abundance (column sums)
```

```
> aaply(dune, 1, mean) # average site abundance (row sums)
```

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3	0	4	0	7	0	2	0	0	0	0	0	
4	0	8	0	2	0	2	3	0	2	0	0	
5	2	0	0	0	4	2	2	0	0	0	0	
6	2	0	0	0	3	0	0	0	0	0	0	

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Your turn: do the same with **adply**

-> what changes ?

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2	3	0	0	2	0	3	4	0	0	0	0	
3	0	4	0	7	0	2	0	0	0	0	0	
4	0	8	0	2	0	2	3	0	2	0	0	
5	2	0	0	0	4	2	2	0	0	0	0	
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2	3	0	0	2	0	3	4	0	0	0	0	
3	0	4	0	7	0	2	0	0	0	0	0	
4	0	8	0	2	0	2	3	0	2	0	0	
5	2	0	0	0	4	2	2	0	0	0	0	
6	2	0	0	0	3	0	0	0	0	0	0	

Multi-argument example: `diversity(data, index = 'Shannon')`

```
> aaply(dune, 1, diversity, index = 'Simpson')
```

Your turn: do the same with **adply**

-> what changes ?

But really, use (long) data.frames !

- native to R
- reliable combine behavior
- integrates well with ggplot
- everything works with d.f.
- more expressive

...

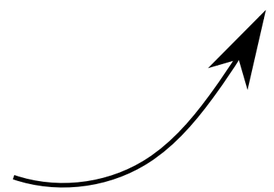
But really, use (long) data.frames !

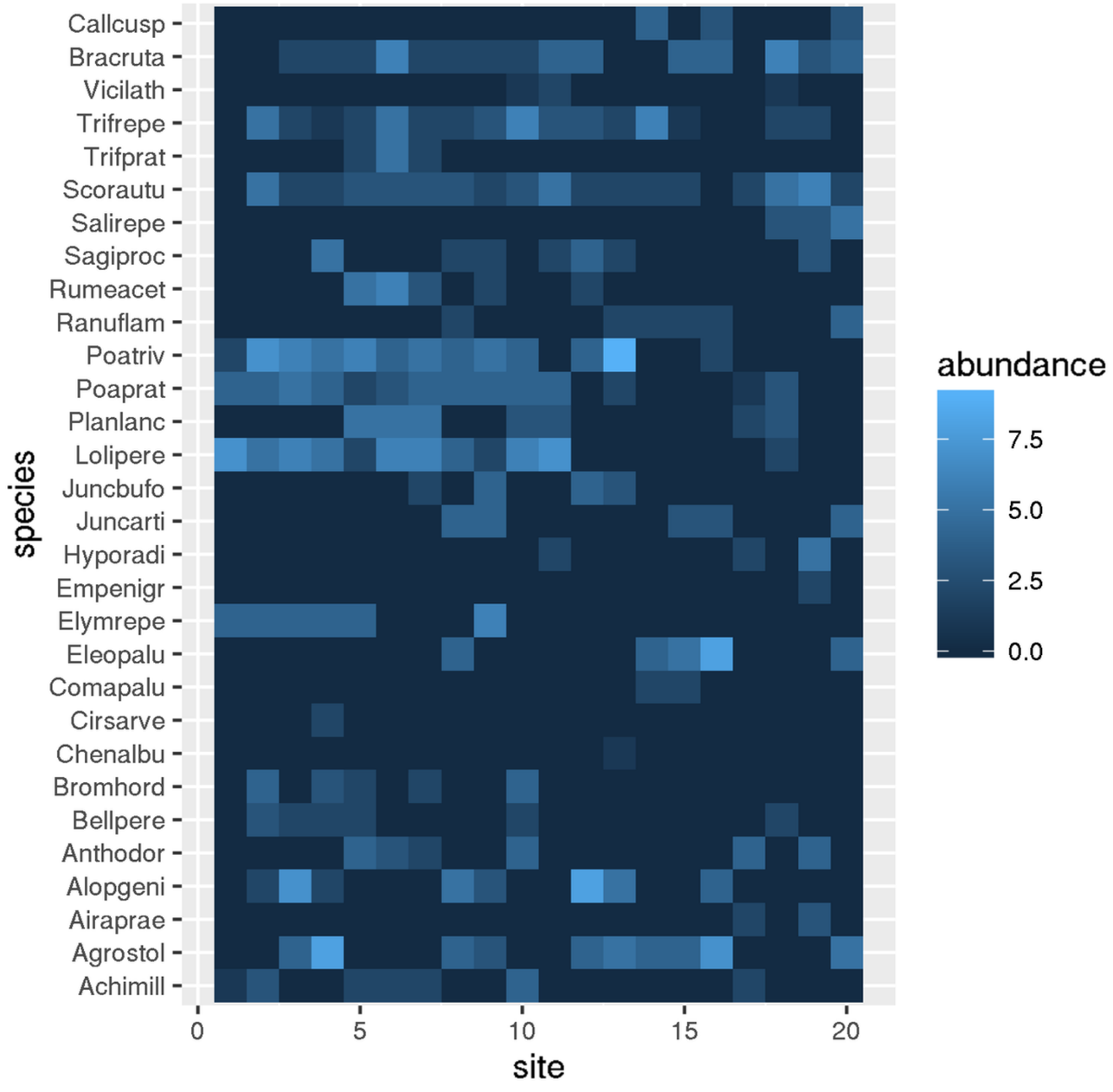
- native to R
- reliable combine behavior
- integrates well with ggplot
- everything works with d.f.
- more expressive

...

```
> # transform into long data.frame
> library(reshape2)
> dune <- melt(dune)
> names(dune) <- c('site', 'species', 'abundance')
```

	site	species	abundance
1	1	Achimill	1
2	1	Agrostol	0
3	1	Airaprae	0
4	1	Alopgeni	0
5	1	Anthodor	0
6	1	Bellpere	0
7	2	Achimill	3
8	2	Agrostol	0
9	2	Airaprae	0
10	2	Alopgeni	2
11	2	Anthodor	0
12	2	Bellpere	3
13	3	Achimill	0
14	3	Agrostol	4
15	3	Airaprae	0
16	3	Alopgeni	7
17	3	Anthodor	0






```
> # transform into long data.frame
> library(reshape2)
> dune <- melt(dune)
> names(dune) <- c('site', 'species'

> ggplot(dune) +
>   geom_tile(aes(x = site, y = species, fill = abundance))
```

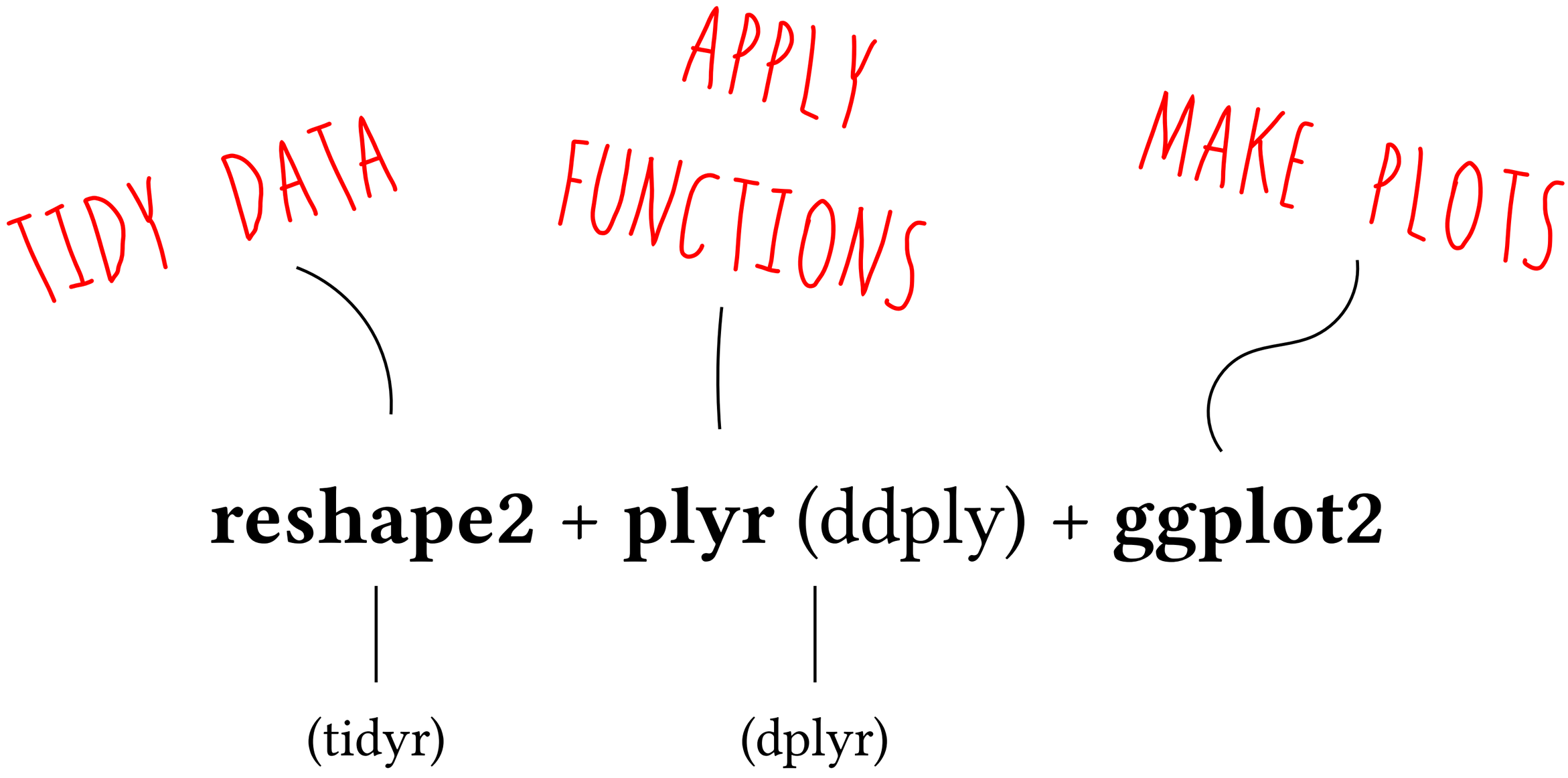
```
> # transform into long data.frame
> library(reshape2)
> dune <- melt(dune)
> names(dune) <- c('site', 'species', 'abundance')

> ddply(dune, ~ species, summarise, ab = mean(abundance)) # mean by species

> ddply(dune, ~ site, summarise, ab = mean(abundance)) # mean by site
```

```
    site  species abundance
1      1 Achimill         1
2      1 Agrostol         0
3      1 Airaprae         0
4      1 Alopgeni         0
5      1 Anthodor         0
6      1 Bellpere         0
7      2 Achimill         3
8      2 Agrostol         0
9      2 Airaprae         0
10     2 Alopgeni         2
11     2 Anthodor         0
12     2 Bellpere         3
13     3 Achimill         0
14     3 Agrostol         4
15     3 Airaprae         0
16     3 Alopgeni         7
17     3 Anthodor         0
```

The modern R workflow



(thank you)