

R Review Session



Paleobiology

February 22, 2016

The R WorkFlow

- Step 1: What data do you currently have?
- Step 2: What data do you want to have?
- Step 3: What function do you use to get the data you want?
- Step 4: How do you get the data you have into that function?

The R Workflow

Where is the data stored?



What shape is the data in?



What size is the data?



What other information is attached to the data?



What do I want to do to the data?



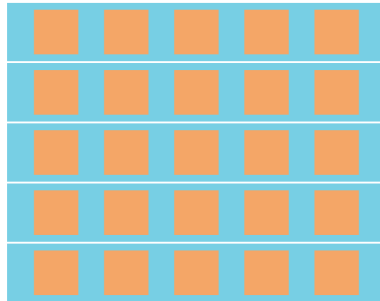
Reshape, resize, or subset the data

What shape is the data in?

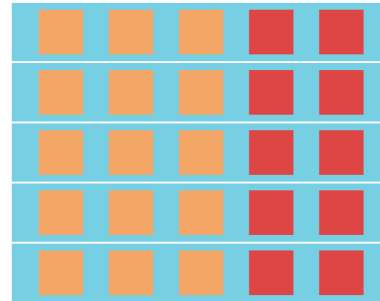
Vector



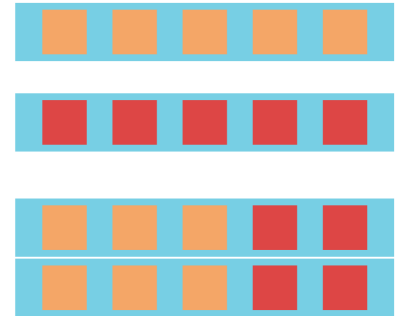
Matrix



Data Frame



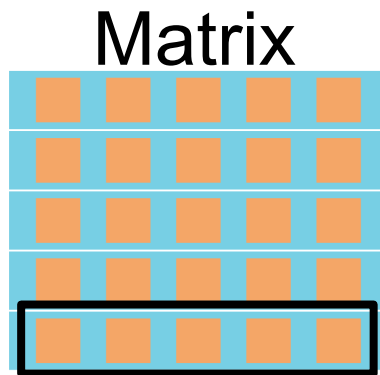
List



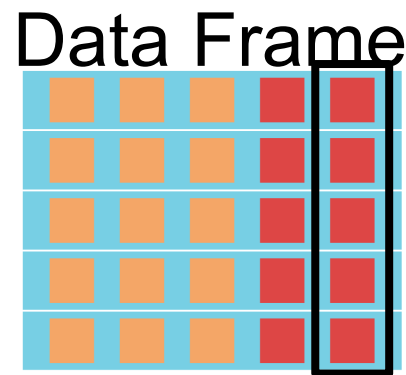
Referencing data from different shapes



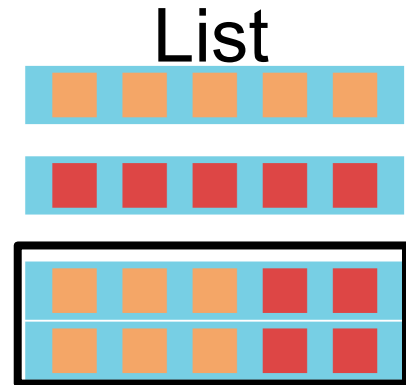
Vector[5]



Matrix[5,]

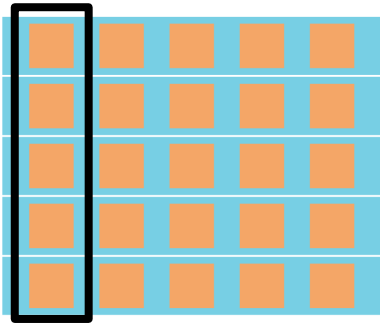


Frame[,5]

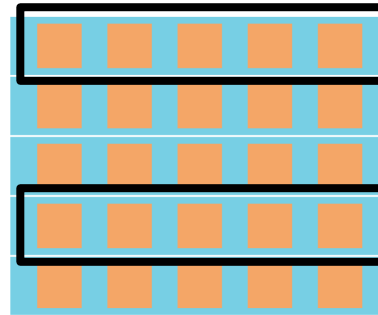


List[[3]]

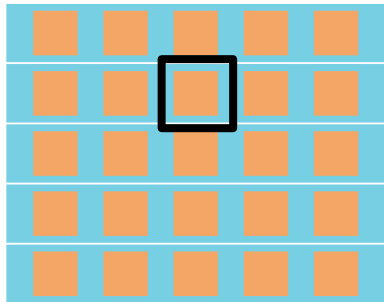
How do I reference these elements



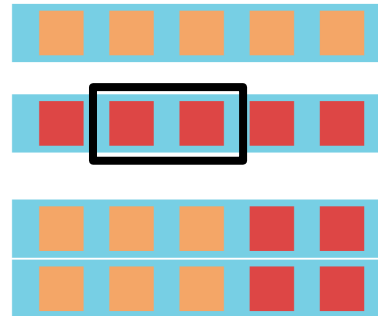
Matrix[,1]



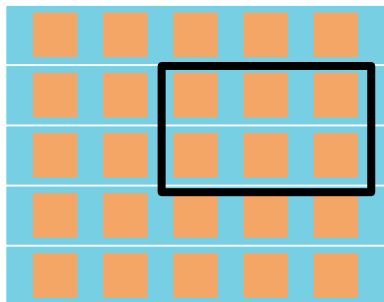
Matrix[c(1,4),]



Matrix[2,3]

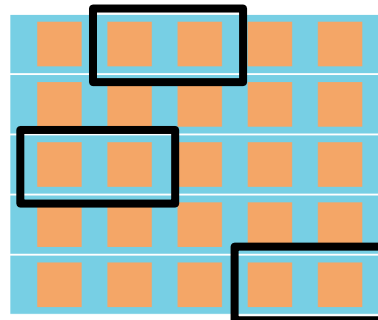


(List[[2]])[c(2,3)]



Matrix[2:3,3:5]

Matrix[c(2,3),c(3,4,5)]



Don't subscript,
use which or
subset

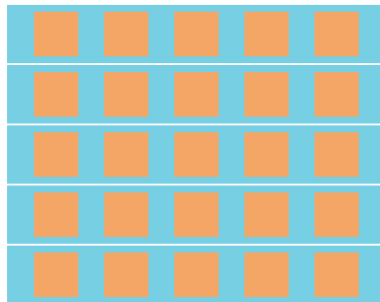
What size is the data?

Vector



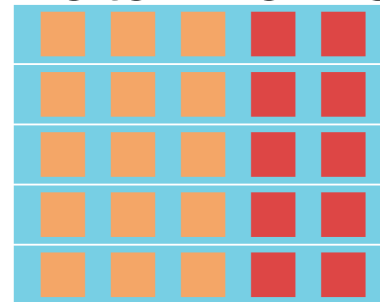
`length(Vec)`

Matrix



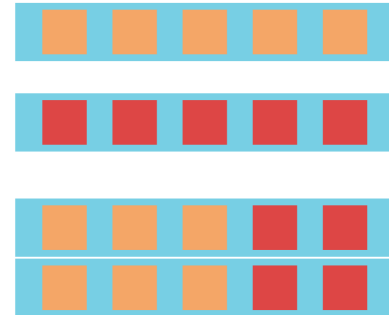
`dim(Matrix)`

Data Frame



`dim(Frame)`

List



`length(List)`

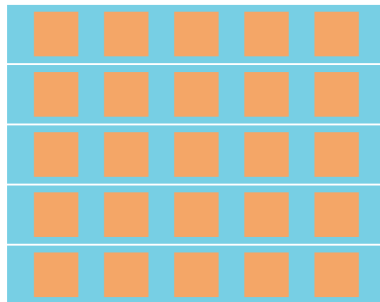
Other information in your data

Vector



`names(Vec)`

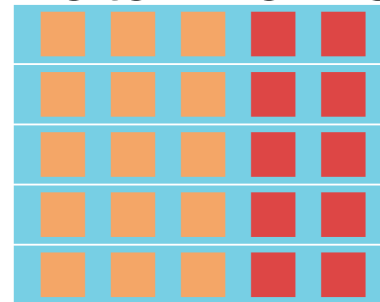
Matrix



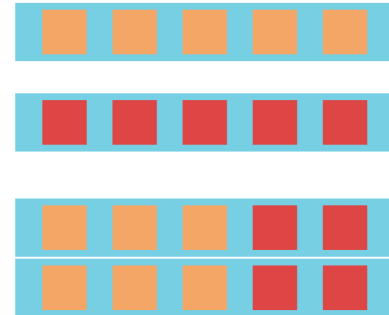
`dimnames(Matrix)`

`dimnames(Frame)`

Data Frame



List



`names(List)`

Other information in your data

Vector

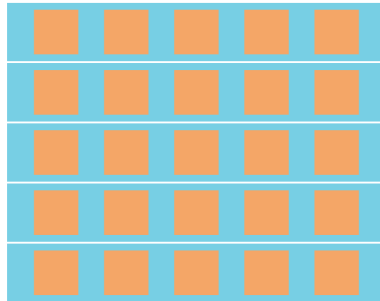


names(Vec)



Output is a
vector of
names

Matrix



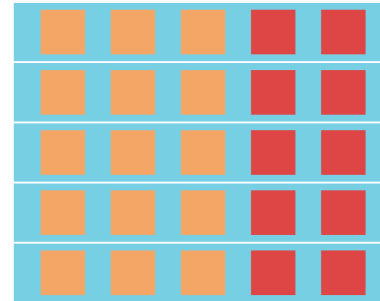
dimnames(Matrix)

dimnames(Frame)



Output is ***list***
of names

Data Frame



List



names(List)

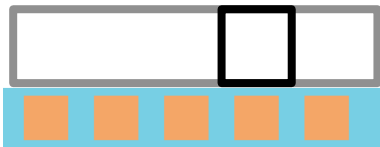


Output is a
vector of
names

Other information in your data

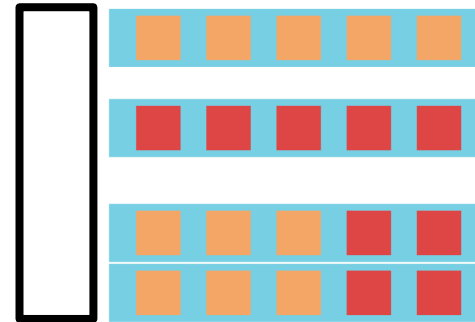


names(Vec)

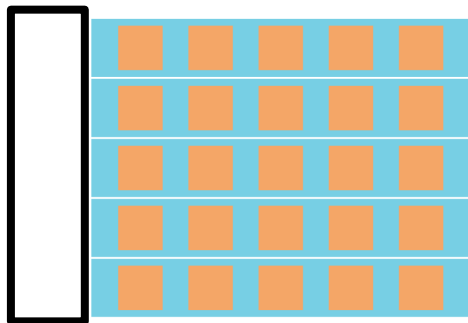


names(Vec)[4]

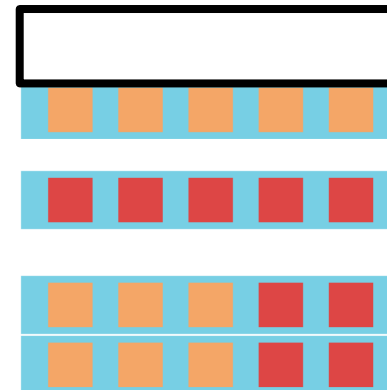
names(Vec[4])



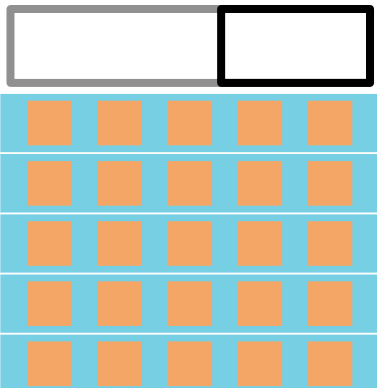
names(List)



Dimnames(Matrix)[[1]]



names(List[[1]])



Dimnames(Matrix)[[2]][c(3,4)]

Dimnames(Matrix)[[2]][3:4]

What I am getting at

- Every time you perform an action in R, a new object is created (but not necessarily saved)
- This new object, can also be subscripted.
- Therefore, you want to understand the shape of ***everything*** that you produce in R

What I am getting at

- Every time you perform an action in R, a new object is created (but not necessarily saved)
- This new object, can also be subscripted.
- Therefore, you want to understand the shape of ***everything*** that you produce in R

A simple example.

```
> c(1, 2, 3, 4, 5)^2  
[1] 1  4  9 16 25
```

What I am getting at

- Every time you perform an action in R, a new object is created (but not necessarily saved)
- This new object, can also be subscripted.
- Therefore, you want to understand the shape of ***everything*** that you produce in R

A simple example.

```
> c(1, 2, 3, 4, 5)^2  
[1] 1  4  9 16 25
```

A simple example.

```
> (c(1, 2, 3, 4, 5)^2) [5]  
[1] 25
```

Parting tips

- Always check the data shape and size before you do anything else
- Try subscripting before you reach for something more advanced like `subset()` or `which()`.
- Remember your answers can also be subscripted.
- Different functions take different shaped data. 9 times out of 10, if your function is giving you an error, it is because you gave it the wrong shape.

Parting tips

- R reads words without “ ” as objects. You need to use “ ” whenever you are **not** referencing an object.

```
Object<-5
```

```
Object
```

```
[1] 5
```

```
“Object”
```

```
[1] “Object”
```

- You can add/subtract/multiply/divide two objects of **identical** size and shape

```
c(1,2,3,4,5) + c(1,2,3,4,5)
```

```
[1] 2, 4, 6, 8, 10
```

- In other words, you may not need to do any subscripting at all.