

object m61r

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1 Introduction

Object m61r is an object that enables all the function present in m61r, and in addition, allows a sort of pipe.

The purpose of this package is informative.

2 Example 1: pipeline with 1 step cache

```
> co2 <- m61r(CO2)
> co2$filter(~Plant %in% c("Qn1", "Qc3"))
> co2$mutate(z1=~uptake/conc, y=~conc/100)
> co2$group_by(~c(Type, Treatment))
> co2$summarise(foo=~mean(z1), bar=~sd(y))
> co2 # print results
```

	Type	Treatment	foo	bar
1	Quebec	nonchilled	0.1079993	3.177263
2	Quebec	chilled	0.1009081	3.177263

```
> head(co2) # back to normal
```

	Plant	Type	Treatment	conc	uptake
1	Qn1	Quebec	nonchilled	95	16.0
2	Qn1	Quebec	nonchilled	175	30.4
3	Qn1	Quebec	nonchilled	250	34.8
4	Qn1	Quebec	nonchilled	350	37.2
5	Qn1	Quebec	nonchilled	500	35.3
6	Qn1	Quebec	nonchilled	675	39.2

```
>
>
```

3 Example 2: get only a data.frame as result

```
> co2 <- m61r(CO2)
> co2$filter(~Plant %in% c("Qn1", "Qc3"))
> co2$transmutate(z1=~uptake/conc, y=~conc/100)
> tmp <- co2[] # get only the data.frame and not the whole m61r object
> head(tmp)
```

```
      z1    y
1 0.16842105 0.95
2 0.17371429 1.75
3 0.13920000 2.50
4 0.10628571 3.50
5 0.07060000 5.00
6 0.05807407 6.75
```

```
> class(tmp)
```

```
[1] "data.frame"
```

```
>
```

4 Example 3: manipulation of a m61r object

```
> co2 <- m61r(CO2)
> head(co2)
```

```
  Plant  Type  Treatment  conc  uptake
1  Qn1  Quebec nonchilled   95   16.0
2  Qn1  Quebec nonchilled  175   30.4
3  Qn1  Quebec nonchilled  250   34.8
4  Qn1  Quebec nonchilled  350   37.2
5  Qn1  Quebec nonchilled  500   35.3
6  Qn1  Quebec nonchilled  675   39.2
```

```
> names(co2)
```

```
[1] "Plant"      "Type"      "Treatment" "conc"      "uptake"
```

```
> dim(co2)
```

```
[1] 84 5
```

```
> co2[1,]
```

```

Plant  Type  Treatment conc uptake
1  Qn1 Quebec nonchilled  95    16

> head(co2[,2:3])

  Type  Treatment
1 Quebec nonchilled
2 Quebec nonchilled
3 Quebec nonchilled
4 Quebec nonchilled
5 Quebec nonchilled
6 Quebec nonchilled

> co2[1:10,1:3]

  Plant  Type  Treatment
1   Qn1 Quebec nonchilled
2   Qn1 Quebec nonchilled
3   Qn1 Quebec nonchilled
4   Qn1 Quebec nonchilled
5   Qn1 Quebec nonchilled
6   Qn1 Quebec nonchilled
7   Qn1 Quebec nonchilled
8   Qn2 Quebec nonchilled
9   Qn2 Quebec nonchilled
10  Qn2 Quebec nonchilled

> co2[1,"Plant"]

  Plant
1   Qn1

> str(co2)

Classes 'm61r', 'environment' <environment: 0x56080dfd9328>

> co2[1,"conc"] <- 100
> co2[1,] # w/temporary change

  Plant  Type  Treatment conc uptake
1   Qn1 Quebec nonchilled 100    16

> co2[1,] # back to normal

  Plant  Type  Treatment conc uptake
1   Qn1 Quebec nonchilled  95    16

```

```

> # WARNING: Keep the brackets to manipulate the intern data.frame
> co2[] <- co2[-1,]
> co2[1:3,] # temporary result

```

```

  Plant  Type  Treatment conc uptake
1  Qn1 Quebec nonchilled  175  30.4
2  Qn1 Quebec nonchilled  250  34.8
3  Qn1 Quebec nonchilled  350  37.2

```

```

> co2[1:3,] # back to normal

```

```

  Plant  Type  Treatment conc uptake
1  Qn1 Quebec nonchilled   95  16.0
2  Qn1 Quebec nonchilled  175  30.4
3  Qn1 Quebec nonchilled  250  34.8

```

```

> # ... OR you will destroy co2, and only keep the data.frame
> # co2 <- co2[-1,]
> # class(co2) # data.frame
>
> # cloning
> foo <- co2 # This will only create
>           # a second variable that points
>           # on the same object (i.e not cloning)
> str(co2)

```

```
Classes 'm61r', 'environment' <environment: 0x56080dfd9328>
```

```
> str(foo)
```

```
Classes 'm61r', 'environment' <environment: 0x56080dfd9328>
```

```

> # Instead, cloning into a new environment
> foo <- co2$clone()
> str(co2)

```

```
Classes 'm61r', 'environment' <environment: 0x56080dfd9328>
```

```
> str(foo)
```

```
Classes 'm61r', 'environment' <environment: 0x56080f305c38>
```

```
>
```