

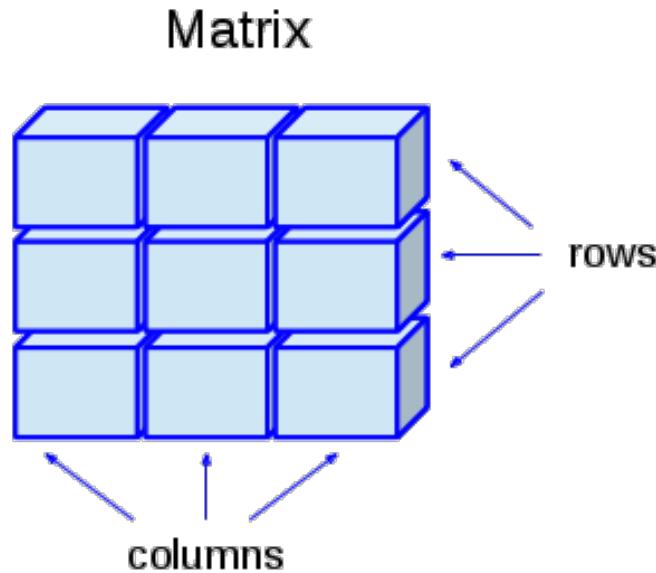


Introducción a R (parte 2)

José Luis Texcalac Sangrador

Procesamiento y visualización de datos espaciales en R

Matrices



```
> matrix(data, nrow, ncol , byrow = F)
```

```
> matrix(1:15, nrow = 3, byrow = T )
```

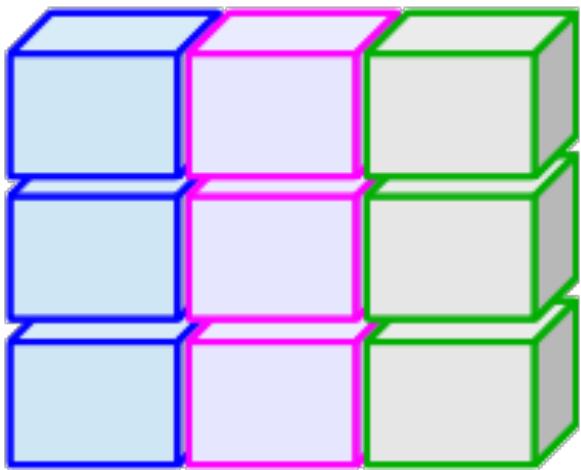
```
[,1] [,2] [,3] [,4] [,5]
[1,] 1 2 3 4 5
[2,] 6 7 8 9 10
[3,] 11 12 13 14 15
```

```
[,1] [,2] [,3] [,4]
[1,] "Brayan" "16" "167" "69.4"
[2,] "Kimberly" "14" "158" "59.6"
[3,] "Kevin" "15" "171" "74.3"
[4,] "Britany" "17" "154" "55.1"
[5,] "Brandon" "15" "165" "69.8"
[6,] "Jenifer" "16" "161" "57.4"
[7,] "Yovani" "15" "166" "64.1"
[8,] "Nicole" "18" "159" "61.1"
```



Data frame (“bases de datos”)

**Data Frame
(Table)**

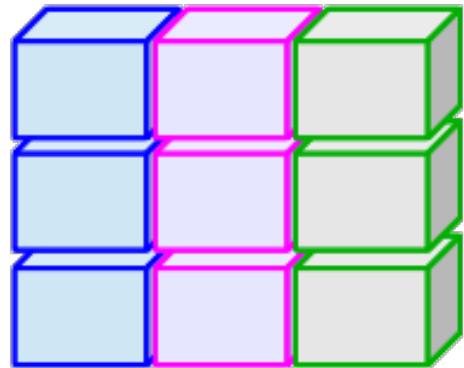


Nombre	Edad	Altura	Peso
Brayan	16	167	69.4
Kimberly	14	158	59.6
Kevin<	15	171	74.3
Britany	17	154	55.1
Brandon	15	165	69.8
Jenifer	16	161	57.4
Iker	15	166	64.1
Nicole	18	159	61.1



Data frame ("bases de datos")

Data Frame
(Table)



Nombre
Brayan
Kimberly
Kevin
Britany
Brandon
Jenifer
Iker
Nicole

Edad
16
14
15
17
15
16
15
18

Altura
167
158
171
154
165
161
166
159

Peso
69.4
59.6
74.3
55.1
69.8
57.4
64.1
61.1



Data Editor (Browse) - [auto.dta]

File Edit View Data Tools

make[1] AMC Concord

Variables

Filter variables here

Variable Label

- make Make and Model
- price Price
- mpg Mileage (mpg)
- rep78 Repair Record 1978
- headroom Headroom (in.)

Ready Vars: 12 Order: Dataset Obs: 74 Filter Off Mode: By Rows

	make	price	mpg	rep78	headroom
1	AMC Concord	4,099	22	3	
2	AMC Pacer	4,749	17	3	
3	AMC Spirit	3,799	22	.	
4	Buick Century	4,816	20	3	
5	Buick Electra	7,827	15	4	
6	Buick LeSabre	5,788	18	3	
7	Buick Opel	4,453	26	.	
8	Buick Regal	5,189	20	3	
9	Buick Riviera	10,372	16	3	
10	Buick Skylark	4,082	19	3	
11	Cad. Deville	11,385	14	3	
12	Cad. Eldorado	14,500	14	2	
13	Cad. Seville	15,906	21	3	
14	Chev. Chevette	3,299	29	3	

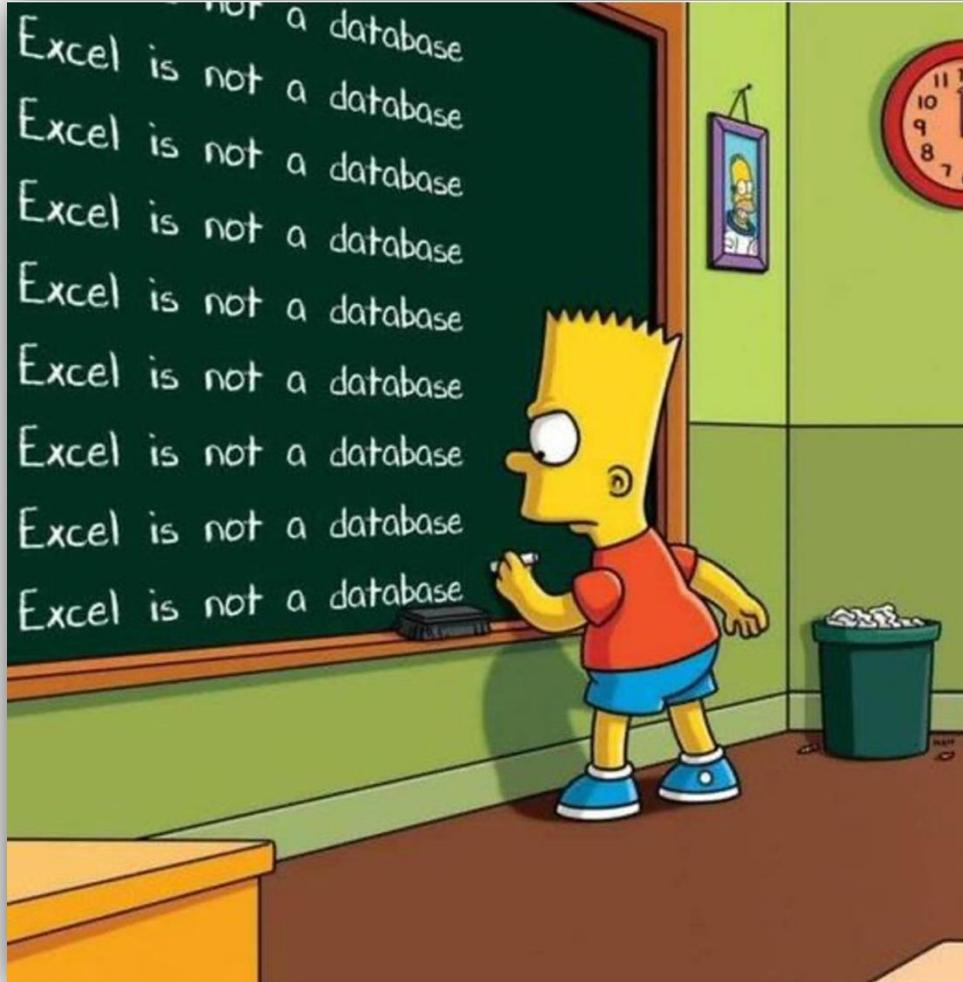
A small image of former US President Barack Obama is visible in the background of the software window, appearing to speak or gesture.



Base de datos

- Una base de datos es una colección de información organizada de tal forma que un programa de computadora pueda seleccionar rápidamente los fragmentos de datos que necesite
- Una base de datos es un sistema de archivos electrónico.
- Las bases de datos tradicionales se organizan por campos, registros y archivos.







¿les ha pasado?

A screenshot of a Microsoft Excel spreadsheet. The top menu bar shows "Paste" with a small orange icon, followed by bold ("B"), italic ("I"), and underline ("U") buttons. The formula bar displays "A1". Below the toolbar is a grid with column headers "A", "B", and "C" and row headers "1", "2", "3", "4", "5", and "6". Cell A1 is highlighted with a green border. The background of the slide features a large, faint watermark of the INSP/ESPM logo.



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> [Genome Biol.](#) 2016 Aug 23;17(1):177. doi: 10.1186/s13059-016-1044-7.

Gene name errors are widespread in the scientific literature

Mark Ziemann ¹, Yotam Eren ^{1 2}, Assam El-Osta ^{3 4}

Affiliations + expand

PMID: 27552985 PMCID: [PMC4994289](#) DOI: [10.1186/s13059-016-1044-7](#)

[Free PMC article](#)

Abstract

The spreadsheet software Microsoft Excel, when used with default settings, is known to convert gene names to dates and floating-point numbers. A programmatic scan of leading genomics journals reveals that approximately one-fifth of papers with supplementary Excel gene lists contain erroneous gene name conversions.

Keywords: Gene symbol; Microsoft Excel; Supplementary data.

Figures

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Abstract



STREAMING NEWS & INSIGHT

From Vulture's Joe Adalian

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Scientists rename human genes to stop Microsoft Excel from misreading them as dates

Sometimes it's easier to rewrite genetics than update Excel

By James Vincent | Aug 6, 2020, 8:44am EDT

- **Symbols that affect data handling and retrieval.** For example, all symbols that autoconverted to dates in Microsoft Excel have been changed (for example, SEPT1 is now SEPTIN1; MARCH1 is now MARCHF1); tRNA synthetase symbols that were also common words have been changed (for example, WARS is now WARS1; CARS is now CARS1).



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Covid: how Excel may have caused loss of 16,000 test results in England

Public Health England data error blamed on limitations of Microsoft spreadsheet

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RESEARCH ARTICLE

Gene name errors: Lessons not learned

Mandhri Abeysooriya , Megan Soria , Mary Savvy Kasu , Mark Ziemann *^{*}

Deakin University, School of Life and Environmental Sciences, Geelong, Australia

* m.ziemann@deakin.edu.au

Abstract



OPEN ACCESS

Citation: Abeysooriya M, Soria M, Kasu MS, Ziemann M (2021) Gene name errors: Lessons not learned. PLoS Comput Biol 17(7): e1008984. <https://doi.org/10.1371/journal.pcbi.1008984>

Editor: Christos A. Ouzounis, CPERI, GREECE

Received: May 4, 2021

Accepted: July 1, 2021

Published: July 30, 2021

Erroneous conversion of gene names into other dates and other data types has been a frustration for computational biologists for years. We hypothesized that such errors in supplementary files might diminish after a report in 2016 highlighting the extent of the problem. To assess this, we performed a scan of supplementary files published in PubMed Central from 2014 to 2020. Overall, gene name errors continued to accumulate unabated in the period after 2016. An improved scanning software we developed identified gene name errors in 30.9% (3,436/11,117) of articles with supplementary Excel gene lists; a figure significantly higher than previously estimated. This is due to gene names being converted not just to dates and floating-point numbers, but also to internal date format (five-digit numbers). These findings further reinforce that spreadsheets are ill-suited to use with large genomic data.

Author summary

Autocorrection is a feature of modern softwares including messaging apps, word processors and spreadsheets. These are designed to avoid data entry errors but “autocorrect”



Book1 - Microsoft Excel

The screenshot shows a Microsoft Excel spreadsheet titled "Book1 - Microsoft Excel". The data is organized into columns A through P, with rows numbered from 61 to 83. Column A contains car models, and column L contains foreign exchange rates. The data includes the following entries:

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P
61	Fiat Strada	4296	21	3	2.5	16	2130	161	36	105	3.37	Foreign				
62	Honda Accord	5799	25	5	3	10	2240	172	36	107	3.05	Foreign				
63	Honda Civic	4499	28	4	2.5	5	1760	149	34	91	3.3	Foreign				
64	Mazda GLC	3995	30	4	3.5	11	1980	154	33	86	3.73	Foreign				
65	Peugeot 604	12990	14		3.5	14	3420	192	38	163	3.58	Foreign				
66	Renault Le Car	3895	26	3	3	10	1830	142	34	79	3.72	Foreign				
67	Subaru	3798	35	5	2.5	11	2050	164	36	97	3.81	Foreign				
68	Toyota Celica	5899	18	5	2.5	14	2410	174	36	134	3.06	Foreign				
69	Toyota Corolla	3748	31	5	3	9	2200	165	35	97	3.21	Foreign				
70	Toyota Corona	5719	18	5	2	11	2670	175	36	134	3.05	Foreign				
71	VW Dasher	7140	23	4	2.5	12	2160	172	36	97	3.74	Foreign				
72	VW Diesel	5397	41	5	3	15	2040	155	35	90	3.78	Foreign				
73	VW Rabbit	4697	25	4	3	15	1930	155	35	89	3.78	Foreign				
74	VW Scirocco	6850	25	4	2	16	1990	156	36	97	3.78	Foreign				
75	Volvo 260	11995	17	5	2.5	14	3170	193	37	163	2.98	Foreign				
76																
77																
78																
79																
80																
81																
82																
83																

Sheet1 Sheet2 Sheet3

Ready Count: 12 100% STATA 12



Generando un data frame

```
> mi_df <- data.frame(nombre, peso, edad, edo_civ, titulado)  
> mi_df
```

```
> as.matrix(my_df)
```

Nombre	Edad	Altura	Peso
Brayan	16	167	69.4
Kimberly	14	158	59.6
Kevin	15	171	74.3
Britany	17	154	55.1
Brandon	15	165	69.8
Jenifer	16	161	57.4
Iker	15	166	64.1
Nicole	18	159	61.1

```
nombre edad altura peso  
1 Brayan 16 167 69.4  
2 Kimberly 14 158 59.6  
3 Kevin 15 171 74.3  
4 Britany 17 154 55.1  
5 Brandon 15 165 69.8  
6 Jenifer 16 161 57.4  
7 Iker 15 166 64.1  
8 Nicole 18 159 61.1
```



Explore su data frame

```
> class(mi_df)
```

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

```
> is(mi_df)
```

```
[1] "data.frame" "list"      "oldClass"   "vector"
```

```
> str(mi_df)
```

```
'data.frame': 8 obs. of 4 variables:  
 $ nombres: chr  "Brayan" "Kimberly" "Kevin" "Britany" ...  
 $ edad    : num  16 14 15 17 15 16 15 18  
 $ altura  : num  167 158 171 154 165 161 166 159  
 $ peso    : num  69.4 59.6 74.3 55.1 69.8 57.4 64.1 61.1
```



Explore su data frame

```
> mean(mi_df$edad, na.rm = TRUE)
```

```
[1] 15.75
```

```
> sd(mi_df$edad, na.rm = TRUE)
```

```
[1] 1.28
```

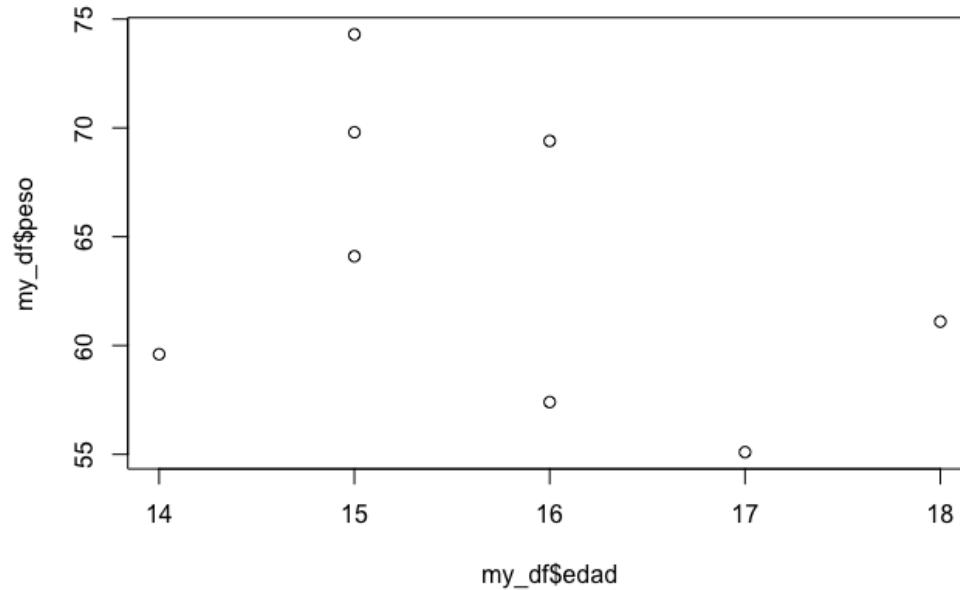
```
> summary(mi_df)
```

	nombres	edad	altura	peso
Length:	8	Min. :14.00	Min. :154.0	Min. :55.10
Class :	character	1st Qu.:15.00	1st Qu.:158.8	1st Qu.:59.05
Mode :	character	Median :15.50	Median :163.0	Median :62.60
		Mean :15.75	Mean :162.6	Mean :63.85
		3rd Qu.:16.25	3rd Qu.:166.2	3rd Qu.:69.50
		Max. :18.00	Max. :171.0	Max. :74.30



Gráfico básico

```
> plot(mi_df$edad, mi_df$peso)
```





Data frames instalados por defecto

- **R** y algunos paquetes tienen e instalan por defecto algunas mallas de datos para el análisis de datos.

```
> paquetes <- library(help = "datasets")
```

```
> head(paquetes$info[[2]])
```

[1] "AirPassengers	Monthly Airline Passenger Numbers 1949-1960"
[2] "Bjsales	Sales Data with Leading Indicator"
[3] "BOD	Biochemical Oxygen Demand"
[4] "CO2	Carbon Dioxide Uptake in Grass Plants"
[5] "ChickWeight	Weight versus age of chicks on different diets"
[6] "Dnase	Elisa assay of DNase"



Ejemplos de dataframes instalados por defecto

> AirPassengers

	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
1949	112	118	132	129	121	135	148	148	136	119	104	118
1950	115	126	141	135	125	149	170	170	158	133	114	140
1951	145	150	178	163	172	178	199	199	184	162	146	166
1952	171	180	193	181	183	218	230	242	209	191	172	194
1953	196	196	236	235	229	243	264	272	237	211	180	201
1954	204	188	235	227	234	264	302	293	259	229	203	229
1955	242	233	267	269	270	315	364	347	312	274	237	278
1956	284	277	317	313	318	374	413	405	355	306	271	306
1957	315	301	356	348	355	422	465	467	404	347	305	336
1958	340	318	362	348	363	435	491	505	404	359	310	337
1959	360	342	406	396	420	472	548	559	463	407	362	405
1960	417	391	419	461	472	535	622	606	508	461	390	432

> head(CO2, 12)

	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
7	Qn1	Quebec	nonchilled	1000	39.7
8	Qn2	Quebec	nonchilled	95	13.6
9	Qn2	Quebec	nonchilled	175	27.3
10	Qn2	Quebec	nonchilled	250	37.1
11	Qn2	Quebec	nonchilled	350	41.8
12	Qn2	Quebec	nonchilled	500	40.6





Instalar paquetes

The Comprehensive R Archive Network (CRAN)

Available CRAN Packages By Name

[A](#) [B](#) [C](#) [D](#) [E](#) [F](#) [G](#) [H](#) [I](#) [J](#) [K](#) [L](#) [M](#) [N](#) [O](#) [P](#) [Q](#) [R](#) [S](#) [T](#) [U](#) [V](#) [W](#) [X](#) [Y](#) [Z](#)

[A3](#)

[aaSEA](#)

[AATtools](#)

[ABACUS](#)

[abbyyR](#)

[abc](#)

[abc.data](#)

[ABC.RAP](#)

[abcADM](#)

[ABCanalysis](#)

[abcdeFBA](#)

[ABCoptim](#)

[ABCp2](#)

[abcf](#)

[abcrda](#)

[abctools](#)

[abd](#)

[abdiv](#)

[abe](#)

[abf2](#)

[ABHgenotypeR](#)

Accurate, Adaptable, and Accessible Error Metrics for Predictive Models

Amino Acid Substitution Effect Analyser

Reliability and Scoring Routines for the Approach-Avoidance Task

Apps Based Activities for Communicating and Understanding Statistics

Access to Abbyy Optical Character Recognition (OCR) API

Tools for Approximate Bayesian Computation (ABC)

Data Only: Tools for Approximate Bayesian Computation (ABC)

Array Based CpG Region Analysis Pipeline

Fit Accumulated Damage Models and Estimate Reliability using ABC

Computed ABC Analysis

ABCDE_FBA: A-Biologist-Can-Do-Everything of Flux Balance Analysis with this package

Implementation of Artificial Bee Colony (ABC) Optimization

Approximate Bayesian Computational Model for Estimating P2

Approximate Bayesian Computation via Random Forests

Asymptotically Bias-Corrected Regularized Linear Discriminant Analysis

Tools for ABC Analyses

The Analysis of Biological Data

Alpha and Beta Diversity Measures

Augmented Backward Elimination

Load Gap-Free Axon ABF2 Files

Easy Visualization of ABH Genotypes

https://cran.r-project.org/web/packages/available_packages_by_name.html



<https://rsanchezs.gitbooks.io/ciencia-de-datos-con-r/content/paquetes/paquetes.html>



Instalar paquetes desde el CRAN

- Ampliar las capacidades del software requiere la instalación de paquetes adicionales
- El paquete sólo se instala una vez
- No es necesario instalar en cada sesión el paquete

Estructura básica para la instalación de paquetes

```
> install.packages("nombre_paquete", dependencies = TRUE)
```

```
> install.packages("remotes", dependencies = TRUE)
```

```
> install.packages("remotes")
```

Generalmente con esto es suficiente



Instalar paquetes desde Github

- No todos los paquetes se hospedan en CRAN.
- Muchos de ellos son rutinas específicas para problemas concretos.
- Puede ser y es muy útil para ampliar las capacidades del programa.
- Los paquetes `remotes` y `devtools` nos permite instalar paquetes de GitHub.

```
> install.packages("remotes", dependencies = TRUE)
```

```
> library(remotes)
```

```
> install_github("hrbrmstr/hrbraddins")
```



¡Importante!

- Al momento de instalar un paquete puede aparecerle el mensaje que se muestra en la imagen
- Siempre seleccionar la opción “CRAN packages only” (identificar el número que corresponda)

These packages have more recent versions available.
It is recommended to update all of them.
Which would you like to update?

- 1: All
- 2: CRAN packages only
- 3: None
- 4: rlang (1.0.2 -> 1.0.3) [CRAN]
- 5: rprojroot (2.0.2 -> 2.0.3) [CRAN]
- 6: waldo (0.3.1 -> 0.4.0) [CRAN]
- 7: ps (1.7.0 -> 1.7.1) [CRAN]
- 8: processx (3.5.3 -> 3.6.1) [CRAN]
- 9: pkgload (1.2.4 -> 1.3.0) [CRAN]



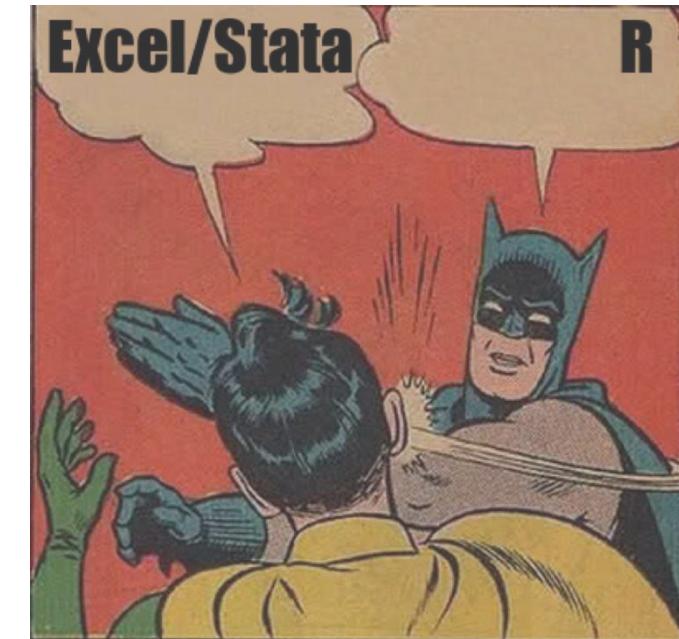
Su turno

```
> install_github("sctyner/memer")
```

```
> library(memer)
```

```
> meme_get("BatmanRobin") %>%
  meme_text_batman(batman = "R",
                    robin = "Excel/Stata",
                    size = 40)
```

```
> install_github("texcalac/addinsTex")
```





¿Dudas y/o comentarios?



Introducción al Tidy Data

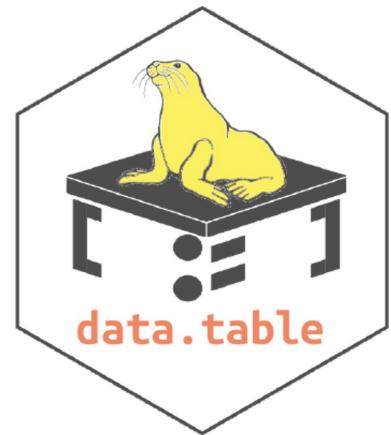
José Luis Texcalac Sangrador

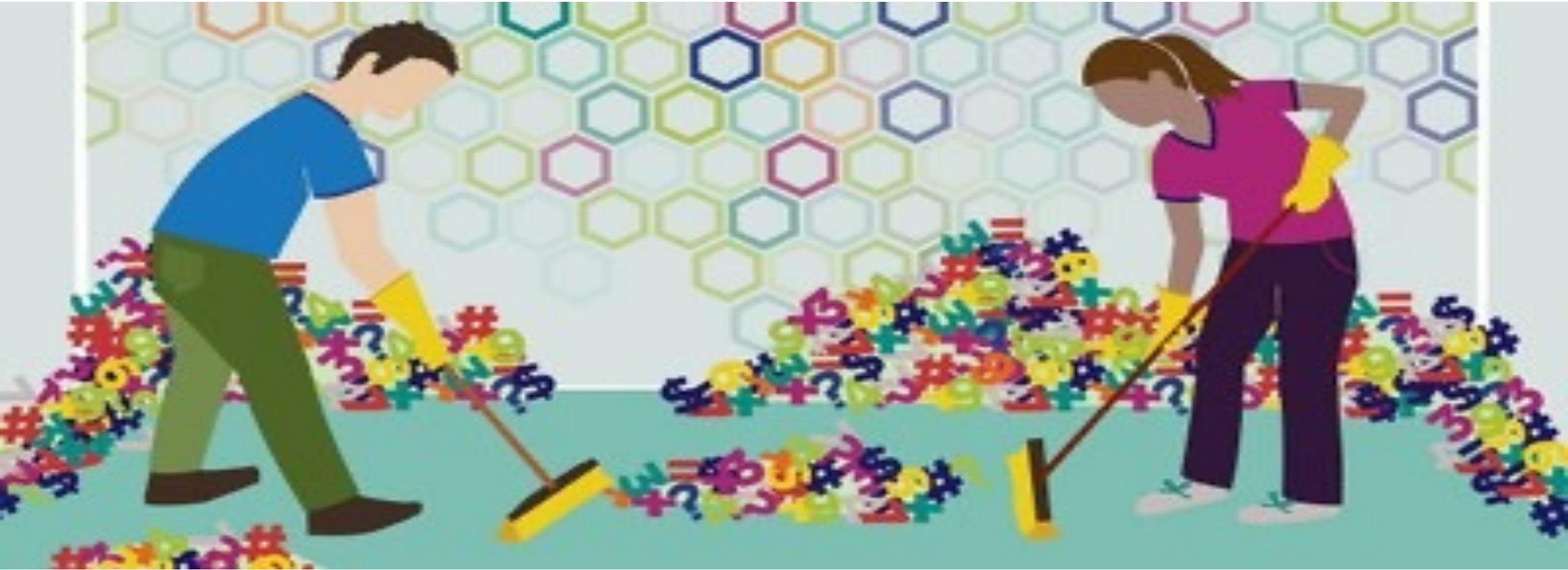
Procesamiento y visualización de datos espaciales en R



Tidyverse

- Actualmente en **R** predominan tres entornos de trabajo, con sus respectivas librerías, que nos permiten programar y manipular la información.
- Cada una tiene sus propias ventajas y desventajas, así como la forma de abordar la manipulación de datos.
- Para este curso, adoptaremos la filosofía de **Tidyverse**.



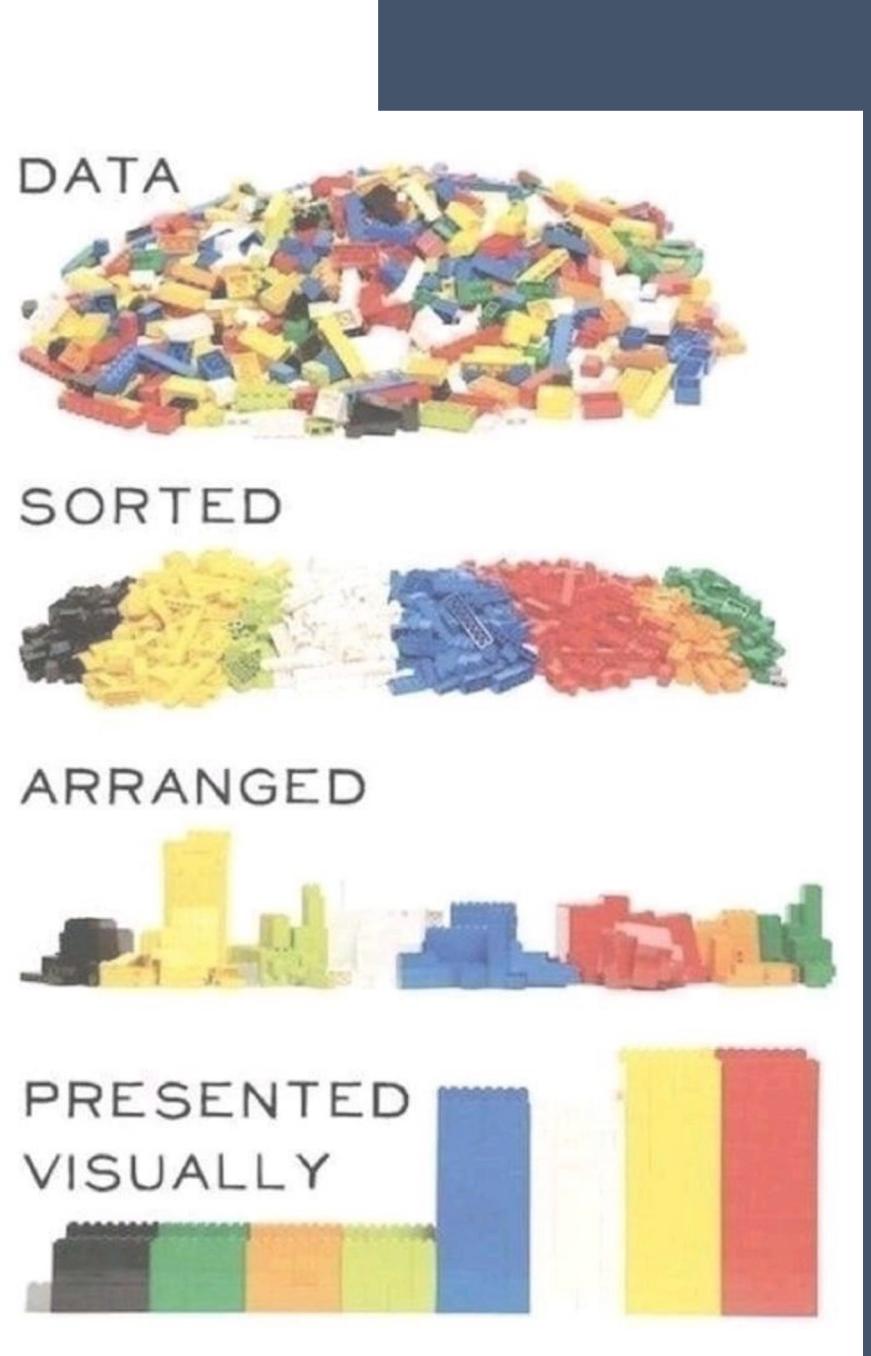


Hadley Wickham, gestor de esta filosofía en la ciencia de datos, recuerda que uno de sus principales problemas en el trabajo con datos era la gran cantidad de tiempo que se tenía que invertir para ordenar y analizar la información través de las herramientas de R y RStudio.



Tidy data

- Este antecedente le llevó a gestar la idea de **data tidyng** o **tidy data**, es decir:
- “Estructurar un conjunto de datos (data) para facilitar su análisis”
- El concepto de **tidy data** implica una forma estandarizada de vincular la estructura de un conjunto de datos (su disposición física), con su semántica (su significado).





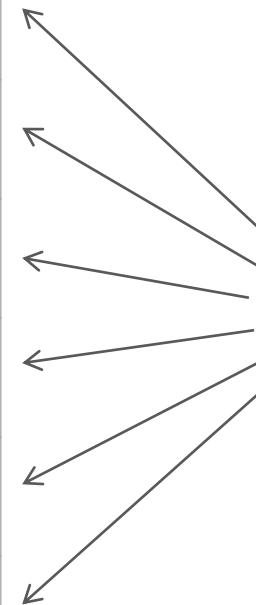
tidy data

Cada celda es un valor e indica la intersección entre una variable y una observación



Cada columna es una variable

nombre	edad	peso
Kevin	17	64.3
Brayan	16	61.7
Kimberly	15	51.9
Britany	16	59.3
Brandon	17	69.1
Melany	16	61.6



Cada fila es una observación



tidy data

Dataset: Colección de valores (tabla, malla de datos, data frame)

nombre	edad	peso
Kevin	17	64.3
Brayan	16	61.7
Kimberly	15	51.9
Britany	16	59.3
Brandon	17	69.1
Melany	16	61.6



tidy data

Dataset: Colección de valores (tabla, malla de datos, data frame)

Variable: Contiene todos los valores que miden el mismo atributo entre todas las unidades de observación

nombre	edad	peso
Kevin	17	64.3
Brayan	16	61.7
Kimberly	15	51.9
Britany	16	59.3
Brandon	17	69.1
Melany	16	61.6



tidy data

Dataset: Colección de valores (tabla, malla de datos, data frame)

Variable: Contiene todos los valores que miden el mismo atributo entre todas las unidades de observación

Observación: Contiene todos los valores medidos, en todos los atributos, en la misma unidad de observación

nombre	edad	peso
Kevin	17	64.3
Brayan	16	61.7
Kimberly	15	51.9
Britany	16	59.3
Brandon	17	69.1
Melany	16	61.6



tidy data

Dataset: Colección de valores (tabla, malla de datos, data frame)

Variable: Contiene todos los valores que miden el mismo atributo entre todas las unidades de observación

Observación: Contiene todos los valores medidos, en todos los atributos, en la misma unidad de observación

Valor: Intersección entre la variable y la observación

nombre	edad	peso
Kevin	17	64.3
Brayan	16	61.7
Kimberly	15	51.9
Britany	16	59.3
Brandon	17	69.1
Melany	16	61.6



messy data

Los encabezados son
valores, no atributos



nombre	edad	peso	lacio	rizado	ondulado
Kevin	17	64.3	0	1	0
Brayan	16	61.7	0	0	0
Kimberly	15	51.9	1	0	0
Britany	16	59.3	0	0	0
Brandon	17	69.1	0	0	1
Melany	16	61.6	0	0	0



Datos wide y
long

wide

id	x	y	z
1	a	c	e
2	b	d	f

long

id key val

1	x	a
2	x	b
1	y	c
2	y	d
1	z	e
2	z	f



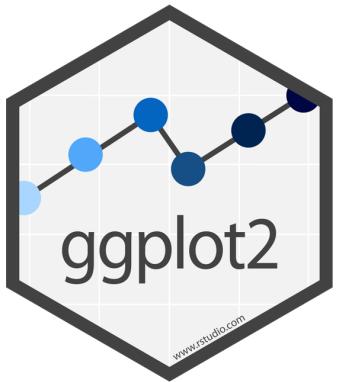
Datos wide y long

Site	2013	2014	2015
CAM	51.0	42.8	39.9
FAC	48.3	39.0	36.6
IZT	44.6	39.3	35.0

Site	Year	PM10
CAM	2013	51.0
FAC	2013	48.3
IZT	2013	44.6
CAM	2014	42.8
FAC	2014	39.0
IZT	2014	39.3
CAM	2015	39.9
FAC	2015	36.6
IZT	2015	35.0



Paquetes base





Su turno...

- Desde la consola de **R** instale los siguientes paquetes del CRAN:
 - tidyverse, lubridate, readxl, haven, janitor.

```
> install.packages("tidyverse", dependencies = TRUE)
```





```
install.packages("tidyverse")
```

Es equivalente a:

```
install.packages("ggplot2")
install.packages("dplyr")
install.packages("tidyr")
install.packages("readr")
install.packages("purrr")
install.packages("tibble")
install.packages("stringr")
install.packages("forcats")
```

```
library(tidyverse)
```

Es equivalente a:

```
library(ggplot2)
library(dplyr)
library(tidyr)
library(readr)
library(purrr)
library(tibble)
library(stringr)
library(forcats)
```



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install.packages("tidyverse")
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Es equivalente a:

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```
install.packages("purrr")
```

```
install.packages("tibble")
```

```
install.packages("stringr")
```

```
install.packages("forcats")
```

```
library(tidyverse)
```

Es equivalente a:

```
R version 4.1.1 (2021-08-10) -- "Kick Things"  
Copyright (C) 2021 The R Foundation for Statistical Computing  
Platform: x86_64-apple-darwin17.0 (64-bit)
```

R es un software libre y viene sin GARANTIA ALGUNA.
Usted puede redistribuirlo bajo ciertas circunstancias.
Escriba 'license()' o 'licence()' para detalles de distribucion.

R es un proyecto colaborativo con muchos contribuyentes.
Escriba 'contributors()' para obtener más información y
'citation()' para saber cómo citar R o paquetes de R en publicaciones.

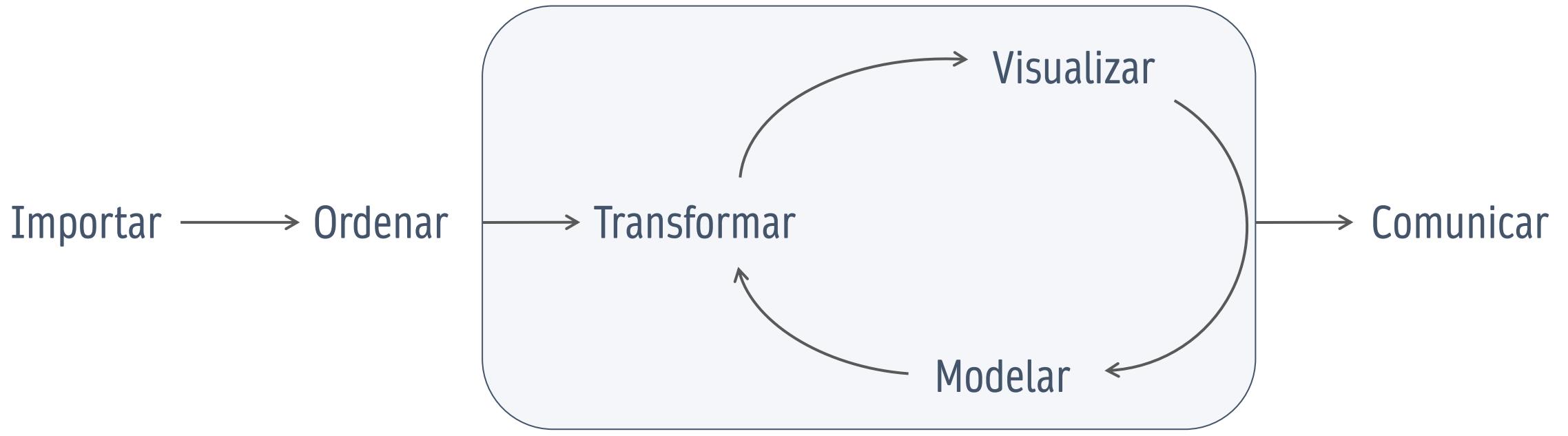
Escriba 'demo()' para demostraciones, 'help()' para el sistema on-line de ayuda,
o 'help.start()' para abrir el sistema de ayuda HTML con su navegador.
Escriba 'q()' para salir de R.

```
> library(tidyverse)
— Attaching packages ————— tidyverse 1.3.1 —
✓ ggplot2 3.3.5   ✓ purrr  0.3.4
✓ tibble  3.1.4   ✓ dplyr   1.0.7
✓ tidyr   1.1.3   ✓ stringr 1.4.0
✓ readr   2.0.1   ✓ forcats 0.5.1
— Conflicts ————— tidyverse_conflicts() —
✖ dplyr::filter() masks stats::filter()
✖ dplyr::lag()    masks stats::lag()
```

Librerías ampliadas tidyverse

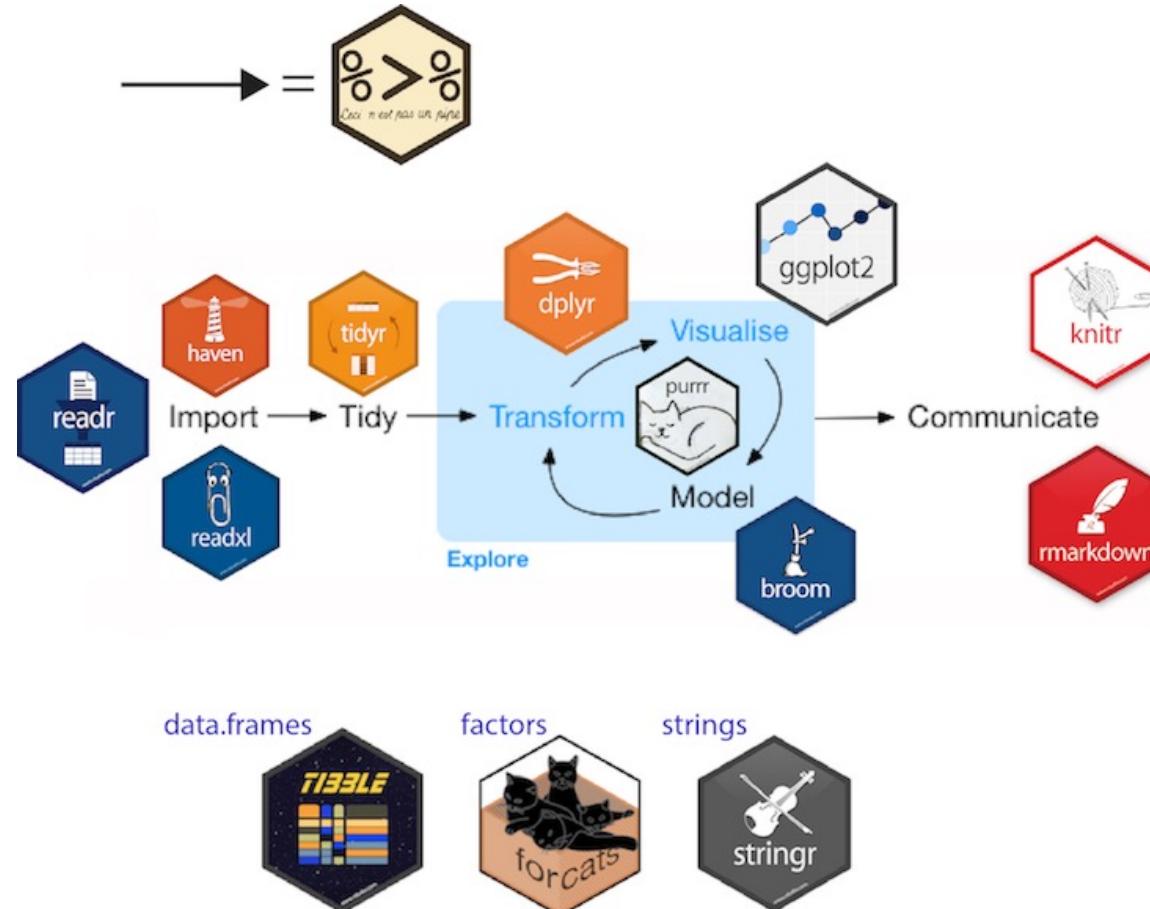


Flujo de trabajo



Programar

Flujo de trabajo usando paquetes





Pipe

El operador `%>%` simplifica y concatena múltiples funciones

```
mi_dia <- veo_tv(paseo_perro(regreso(trabajo(traslado(despierto(😊))))))
```

😊 %>%

despierto %>%

traslado %>%

trabajo %>%

regreso %>%

paseo_perro %>%

veo_tv

malla_datos %>%

filtro %>%

genero_variables %>%

agrupo %>%

paso_a_wide %>%

genero_variables %>%

selecciono_columnas



Insertar pipe

command

+

shift ↑

+

M



Mac

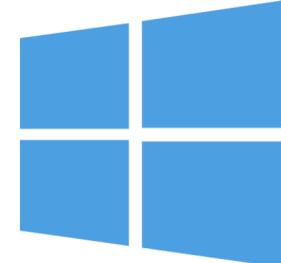
Ctrl

+

Shift

+

M



Windows



Insertar operador de asignación <-

option
option

+

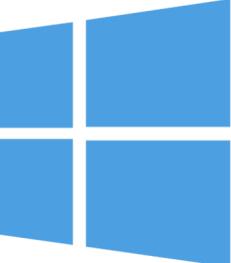
-



Mac

Alt

+



Windows



Using = instead of <- for assignment

