

UNIVERSIDAD PRIVADA SAN JUAN BAUTISTA

FACULTAD DE CIENCIAS DE LA SALUD

ESCUELA PROFESIONAL DE MEDICINA HUMANA

"Año de la unidad, la paz y el desarrollo"



ASIGNATURA:

Sistematización y métodos estadísticos

INTEGRANTES:

Casas Ruiz Caro, Jhahandra Jimena

Rojas Onton , Christian Adrian

Ragas Asenjo, Sergio Henry

Robles Sevillano, Stefanny Liliana

Saico Achamizo, Karen Andrea

DOCENTES RESPONSABLE:

SEGUNDO VICENTE CASTRO LOPEZ

Integrantes:

- Casas Ruiz Caro, Jhahandra Jimena
- Rojas Onton , Christian Adrian
- Ragas Asenjo, Sergio Henry
- Robles Sevillano, Stefanny Liliana
- Saico Achamizo, Karen Andrea

Paquetes para resumir datos

Instalar paquetes

```
{r}
library(tidyverse)
library(dplyr)
```

Con tidyverse

```
{r}
#> #> bac_aguda >
#> select(edad, raza, sexo, mes, glucosa_sangre,
#>         leucocitos_lcr, células_banda_sangre_pct, neutrofilos_sangre_pct) >
#> by = neutrofilos_sangre_pct
#>
```

146 missing rows in the "neutrofilos_sangre_pct" column have been removed.

```
> library(readr)
> bac_aguda <- read_csv("Desktop/Sistematización y métodos estadísticos/estadistica_upsjb/data/bac_aguda.csv")
Rows: 581 Columns: 22
Column specification:
Delimiter: ","
chr (5): mes, raza, sexo, conjunto, meningitis_bacteriana_aguda
dbl (17): numero_caso, año, edad, leucocitos_sangre, neutrofilos_sangre_pct, células_banda_sangre_pct, glucosa_sangre, ...

i Use `spec()` to retrieve the full column specification for this data.
i Specify the column types or set `show_col_types = FALSE` to quiet this message.
> View(bac_aguda)
>
```

1. Resumen de variables categóricas

```
{r}
table(bac_aguda$meningitis_bacteriana_aguda, useNA = "ifany")
```

Ausente	Presente	<NA>
284	217	88

```
{r}
table(bac_aguda$cultivo_sangre, useNA = "ifany")
```

0	1	2	3	4	6	11	<NA>
73	39	16	8	2	8	1	434

Con tidyverse

```
{r}
#> bac_aguda >
#> select(edad, raza, sexo, mes, glucosa_sangre,
#>         leucocitos_lcr, células_banda_sangre_pct, neutrofilos_sangre_pct) >
#> by = neutrofilos_sangre_pct
#>
```

146 missing rows in the "neutrofilos_sangre_pct" column have been removed.

```
> library(readr)
> bac_aguda <- read_csv("Desktop/Sistematización y métodos estadísticos/estadistica_upsjb/data/bac_aguda.csv")
Rows: 581 Columns: 22
Column specification:
Delimiter: ","
chr (5): mes, raza, sexo, conjunto, meningitis_bacteriana_aguda
dbl (17): numero_caso, año, edad, leucocitos_sangre, neutrofilos_sangre_pct, células_banda_sangre_pct, glucosa_sangre, ...

i Use `spec()` to retrieve the full column specification for this data.
i Specify the column types or set `show_col_types = FALSE` to quiet this message.
> View(bac_aguda)
>
```

RStudio

Con tidyverse

```
{r}
boc_aguda >
  dplyr::count(cultivo_sangre, sort = TRUE)
```

A table: 8 x 2

cultivo_sangre	n
N/A	434
0	73
1	39
2	16
3	8
6	8
4	2
11	1

8 rows

Valores perdidos en proporciones

```
## Chunks 32: 2
```

Console Terminal Background Jobs

```
R - R 4.4.3 - / 
> boc_aguda >
+ select(edad, raza, sexo, mes, glucosa_sangre,
+        leucocitos_lcr, células_banda_sangre_pct, neutrofilos_sangre_pct) >
+  tbl_summary()
+   by = neutrofilos_sangre_pct
+ )
146 missing rows in the "neutrofilos_sangre_pct" column have been removed.
> library(readr)
> boc_aguda <- read_csv("Desktop/Sistematización y métodos estadísticos/estadística_upsjb/data/boc_aguda.csv")
Rows: 581 Columns: 22
-- Column specification --
```

Column specification

```
Delimiter: ","
chr (5): mes, raza, sexo, conjunto, meningitis_bacteriana_aguda
dbl (17): numero_caso, año, edad, leucocitos_sangre, neutrofilos_sangre_pct, células_banda_sangre_pct, glucosa_sangre...
```

i Use 'spec()' to retrieve the full column specification for this data.
i Specify the column types or set 'show_col_types = FALSE' to quiet this message.

```
> View(boc_aguda)
> |
```

RStudio

Valores perdidos en proporciones

```
{r}
prop.table(table(boc_aguda$cultivo_sangre, useNA = "ifany"))
```

	0	1	2	3	4	6	11
<NA>	0.125645439	0.067125645	0.027538726	0.013769363	0.003442341	0.013769363	0.001721170
0.746987952							

Porcentaje

```
{r}
round(prop.table(table(boc_aguda$cultivo_sangre, useNA = "ifany"))*100,1)
```

	0	1	2	3	4	6	11	<NA>
12.6	6.7	2.8	1.4	0.3	1.4	0.2	74.7	0.746987952

2. Resumen de variables continuas

```
## Chunks 32: 2
```

Console Terminal Background Jobs

```
R - R 4.4.3 - / 
> boc_aguda >
+ select(edad, raza, sexo, mes, glucosa_sangre,
+        leucocitos_lcr, células_banda_sangre_pct, neutrofilos_sangre_pct) >
+  tbl_summary()
+   by = neutrofilos_sangre_pct
+ )
146 missing rows in the "neutrofilos_sangre_pct" column have been removed.
> library(readr)
> boc_aguda <- read_csv("Desktop/Sistematización y métodos estadísticos/estadística_upsjb/data/boc_aguda.csv")
Rows: 581 Columns: 22
-- Column specification --
```

Column specification

```
Delimiter: ","
chr (5): mes, raza, sexo, conjunto, meningitis_bacteriana_aguda
dbl (17): numero_caso, año, edad, leucocitos_sangre, neutrofilos_sangre_pct, células_banda_sangre_pct, glucosa_sangre...
```

i Use 'spec()' to retrieve the full column specification for this data.
i Specify the column types or set 'show_col_types = FALSE' to quiet this message.

```
> View(boc_aguda)
> |
```

2. Resumen de variables continuas

```
[r]
mean(boc_aguda$leucocitos_lcr, na.rm = TRUE)
[1] 2492.898

(r)
sd(boc_aguda$leucocitos_lcr, na.rm = TRUE)
[1] 7455.422

Otras funciones que puedes encontrar útil son min(), max(), median() y IQR()

(r)
min(boc_aguda$leucocitos_lcr, na.rm = TRUE) # Proporciona el valor mínimo
IQR(boc_aguda$leucocitos_lcr, na.rm = TRUE) # Calcula el rango intercuartilico
median(boc_aguda$leucocitos_lcr, na.rm = TRUE) # Calcula la mediana
```

Chunk 32 :

```
Console Terminal Background Jobs
[R - R 4.4.3 - ~/]
> boc_aguda <- 
+ select(dad, raza, sexo, mes, glucosa_sangre,
+ leucocitos_lcr, células_bonda_sangre_pct, neutrofilos_sangre_pct) |>
+tbl_summary(
+   by = neutrofilos_sangre_pct
+ )
146 missing rows in the "neutrofilos_sangre_pct" column have been removed.
> library(readr)
> boc_aguda <- read.csv("Desktop/Sistematización y métodos estadísticos/estadística_upsjb/data/boc_aguda.csv")
Rows: 581 Columns: 22
-- Column specification --
Delimiter: ","
chr (5): dad, raza, sexo, conjunto_meningitis_bacteriana_aguda
dbl (17): numero_caso, año, eddad, leucocitos_sangre, neutrofilos_sangre_pct, células_bonda_sangre_pct, glucosa_sangre, ...
Use `spec()` to retrieve the full column specification for this data.
Specify the column types or set `show_col_types = FALSE` to quiet this message.
> View(boc_aguda)
```

La función summary() para calcular todas las medidas, a la vez.

```
[r]
summary(boc_aguda$glucosa_sangre)

Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
1     185    125    138    155    410    258
```

Media o mediana?

```
Chunk 32 :
```

```
Console Terminal Background Jobs
[R - R 4.4.3 - ~/]
> boc_aguda <- 
+ select(dad, raza, sexo, mes, glucosa_sangre,
+ leucocitos_lcr, células_bonda_sangre_pct, neutrofilos_sangre_pct) |>
+tbl_summary(
+   by = neutrofilos_sangre_pct
+ )
146 missing rows in the "neutrofilos_sangre_pct" column have been removed.
> library(readr)
> boc_aguda <- read.csv("Desktop/Sistematización y métodos estadísticos/estadística_upsjb/data/boc_aguda.csv")
Rows: 581 Columns: 22
-- Column specification --
Delimiter: ","
chr (5): dad, raza, sexo, conjunto_meningitis_bacteriana_aguda
dbl (17): numero_caso, año, eddad, leucocitos_sangre, neutrofilos_sangre_pct, células_bonda_sangre_pct, glucosa_sangre, ...
Use `spec()` to retrieve the full column specification for this data.
Specify the column types or set `show_col_types = FALSE` to quiet this message.
> View(boc_aguda)
```

Mediana o media?

```
[{r}
mean(bac_aguda$leucocitos_lcr, na.rm = T)
[1] 2492.898

{r}
median(bac_aguda$leucocitos_lcr, na.rm = T)
[1] 336.5
```

La media y mediana de la variable leucocitos_lcr son diferentes. Estos sugiere que los datos tienen una distribución asimétrica.

Deabajo otro ejemplo con la variable glucosa_sangre

```
{r}
mean(bac_aguda$glucosa_sangre, na.rm = T)
[1] 138.0402

{r}
median(bac_aguda$glucosa_sangre, na.rm = T)
[1] 125
```

Comprobémoslo visualmente

```
par(mfrow=c(1,2)) # Configuramos e número de elementos por Figura
hist(bac_aguda$leucocitos_lcr)
hist(bac_aguda$glucosa_sangre)
```

Histogram of bac_aguda\$leucocitos

Histogram of bac_aguda\$glucosa_sangre

RStudio Environment

Integrantes:

- Paquetes para ...
- Cargando los d...
- La "estimatur..."
- 1. Resumen de...
- 2. Resumen de...
- La función ...
- ¿Mediana o m...
- [resumen] Por ...
- La "Tabla 1" co...
- Configurando ...

Data

bac_aguda 581 obs. of 22 variables

Files Plots Packages Help Viewer Presentation

Console Terminal Background Jobs

Quarto 2

Project: (None) ▾

Environment History Connections Tutorial

R - Global Environment

File New Folder New File Delete Rename More

Home Desktop Sistematización y métodos estadísticos estadistica_upsjb data

Name Size Modified

Name	Size	Modified
..	58.7 KB	Apr 17, 2025, 9:37 PM
bac_aguda.csv	41.7 KB	Apr 12, 2025, 8:10 AM
s02_treat_arritis.csv	33.6 KB	Apr 12, 2025, 8:10 AM
s02_treat_arritis.RData	12.9 KB	Apr 12, 2025, 8:10 AM
s02_treat_arritis.sav	38.6 KB	Apr 12, 2025, 8:10 AM
s02_treat_arritis.xlsx	29.9 KB	Apr 19, 2025, 7:55 AM
s03_treat_arritis.csv	38.7 KB	Apr 26, 2025, 8:02 AM
s04_diabetes.csv		

Deabajo otro ejemplo con la variable glucosa_sangre

```
{r}
mean(bac_aguda$glucosa_sangre, na.rm = T)
[1] 138.0402

{r}
median(bac_aguda$glucosa_sangre, na.rm = T)
[1] 125
```

Comprobémoslo visualmente

```
par(mfrow=c(1,2)) # Configuramos e número de elementos por Figura
hist(bac_aguda$leucocitos_lcr)
hist(bac_aguda$glucosa_sangre)
```

Histogram of bac_aguda\$leucocitos

Histogram of bac_aguda\$glucosa_sangre

RStudio Environment

Integrantes:

- Paquetes para ...
- Cargando los d...
- La "estimatur..."
- 1. Resumen de...
- 2. Resumen de...
- La función ...
- ¿Mediana o m...
- [resumen] Por ...
- La "Tabla 1" co...
- Configurando ...

Data

bac_aguda 581 obs. of 22 variables

Files Plots Packages Help Viewer Presentation

Console Terminal Background Jobs

Quarto 2

Project: (None) ▾

Environment History Connections Tutorial

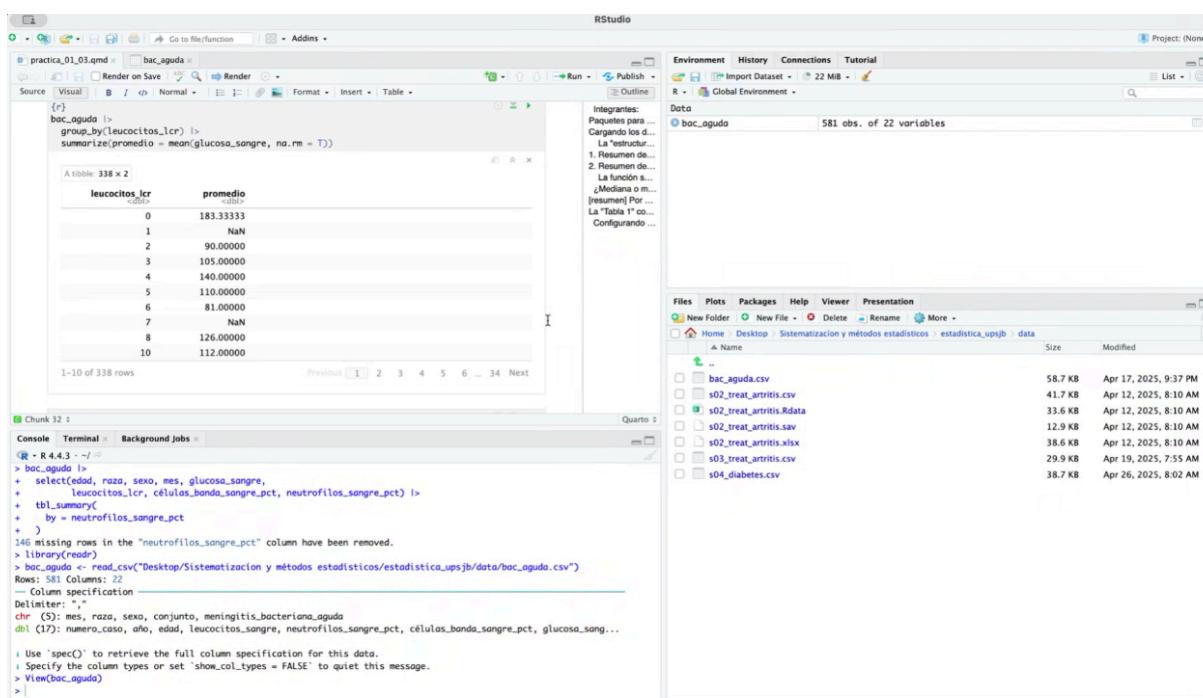
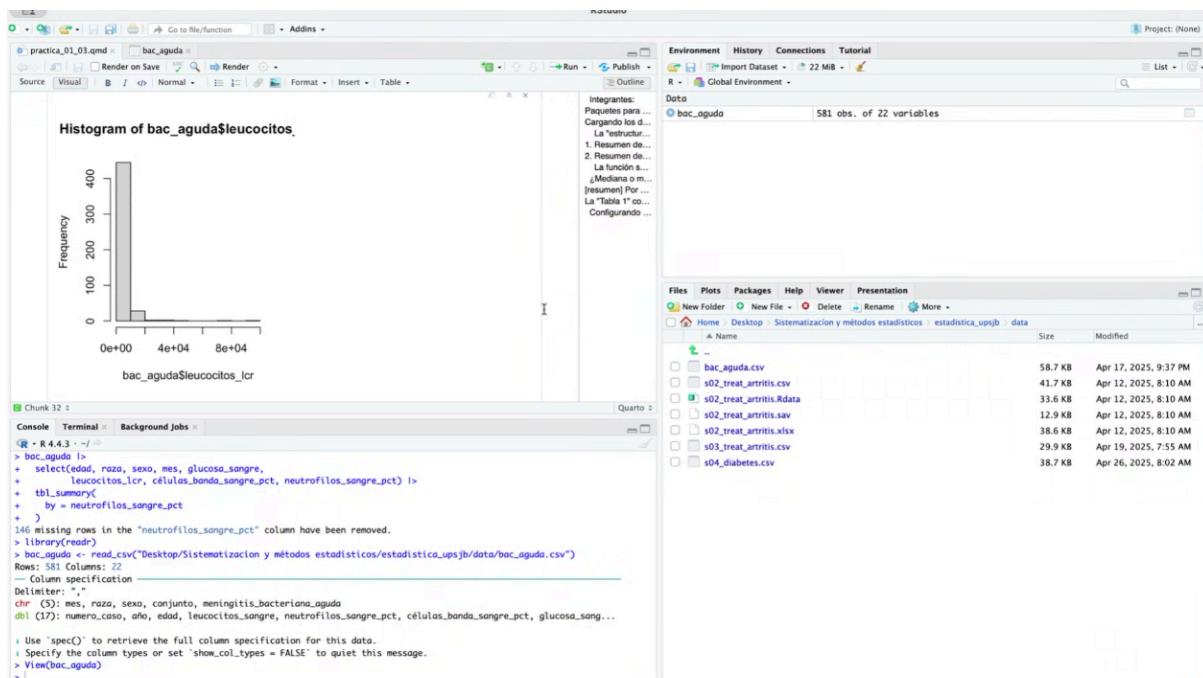
R - Global Environment

File New Folder New File Delete Rename More

Home Desktop Sistematización y métodos estadísticos estadistica_upsjb data

Name Size Modified

Name	Size	Modified
..	58.7 KB	Apr 17, 2025, 9:37 PM
bac_aguda.csv	41.7 KB	Apr 12, 2025, 8:10 AM
s02_treat_arritis.csv	33.6 KB	Apr 12, 2025, 8:10 AM
s02_treat_arritis.RData	12.9 KB	Apr 12, 2025, 8:10 AM
s02_treat_arritis.sav	38.6 KB	Apr 12, 2025, 8:10 AM
s02_treat_arritis.xlsx	29.9 KB	Apr 19, 2025, 7:55 AM
s03_treat_arritis.csv	38.7 KB	Apr 26, 2025, 8:02 AM
s04_diabetes.csv		



RStudio

Source: `boc_aguda >`

```
practica_01_03.qmd | bac_aguda
R | R 4.4.3 - /-
> boc_aguda >
+ select(edad, raza, sexo, mes, glucosa_sangre,
+        leucocitos_lcr, células_banda_sangre_pct, neutrofilos_sangre_pct) >
+ tbl_summary()
+   by = neutrofilos_sangre_pct
+ )
146 missing rows in the "neutrofilos_sangre_pct" column have been removed.
> library(tidyverse)
> boc_aguda <- read_csv("Desktop/Sistematización y métodos estadísticos/estadística_upsjb/data/boc_aguda.csv")
Rows: 581 Columns: 22
-- Column specification --
Delimiter: ","
chr (5): mes, raza, sexo, conjunto, meningitis_bacteriana_aguda
dbl (17): numero_caso, año, edad, leucocitos_sangre, neutrofilos_sangre_pct, células_banda_sangre_pct, glucosa_sangre...
# Use 'spec()' to retrieve the full column specification for this data.
# Specify the column types or set 'show_col_types = FALSE' to quiet this message.
> view(boc_aguda)
> |
```

Data: `boc_aguda` 581 obs. of 22 variables

Integrantes:

- Paquetes para ...
- Cargando los d...
- La "estructur...
- 1. Resumen de...
- 2. Resumen de...
- La función s...
- Medición o m...
- [resumen] Por...
- La Tabla 1" co...
- Configurando ...

A table: 412 x 3 Groups: leucocitos_lcr [338]

leucocitos_lcr	tinción_gram	promedio
0	0	225.0000
0	1	200.0000
0	NA	125.0000
1	NA	NaN
2	0	90.0000
2	NA	NaN
3	0	105.0000
3	NA	NaN
4	1	140.0000
4	NA	NaN

Console | Terminal | Background Jobs |

Files Plots Packages Help Viewer Presentation

Project: (None)

Home Desktop Sistematización y métodos estadísticos estadística_upsjb data

- bac_aguda.csv 58.7 KB Apr 17, 2025, 9:37 PM
- s02_treat_arritis.csv 41.7 KB Apr 12, 2025, 8:10 AM
- s02_treat_arritis.rdata 33.6 KB Apr 12, 2025, 8:10 AM
- s02_treat_arritis.sav 12.9 KB Apr 12, 2025, 8:10 AM
- s02_treat_arritis.xlsx 38.6 KB Apr 12, 2025, 8:10 AM
- s03_treat_arritis.csv 29.9 KB Apr 19, 2025, 7:55 AM
- s04_diabetes.csv 38.7 KB Apr 26, 2025, 8:02 AM

RStudio

Source: `boc_aguda >`

```
[resumen] Por otra variable
```

(r)
`boc_aguda >`
`group_by(tinción_gram) >`
`summarise(n_observ = n(),`
`porcentaje = (n_observ / nrow(boc_aguda))*100)`

A table: 8 x 3

tinción_gram	n_observ	porcentaje
0	116	19.9655766
1	48	8.2616179
2	16	2.7538726
3	4	0.6884682
4	76	13.0808950
5	7	1.2048193
6	1	0.1721170
NA	313	53.8726334

Console | Terminal | Background Jobs |

Files Plots Packages Help Viewer Presentation

Project: (None)

Home Desktop Sistematización y métodos estadísticos estadística_upsjb data

- bac_aguda.csv 58.7 KB Apr 17, 2025, 9:37 PM
- s02_treat_arritis.csv 41.7 KB Apr 12, 2025, 8:10 AM
- s02_treat_arritis.rdata 33.6 KB Apr 12, 2025, 8:10 AM
- s02_treat_arritis.sav 12.9 KB Apr 12, 2025, 8:10 AM
- s02_treat_arritis.xlsx 38.6 KB Apr 12, 2025, 8:10 AM
- s03_treat_arritis.csv 29.9 KB Apr 19, 2025, 7:55 AM
- s04_diabetes.csv 38.7 KB Apr 26, 2025, 8:02 AM

RStudio Project: (None)

Source: `boc_aguda > group_by(leucocitos_lcr, tinción_gran) > summarise(cultivo_sangre= mean(glucosa_sangre, na.rm = TRUE), DE = sd(glucosa_sangre, na.rm = TRUE), hematies_lcr = max(glucosa_sangre, na.rm = TRUE))`

Data: `boc_aguda` 581 obs. of 22 variables

Integrantes: Paquetes para... Cargando los d... La "estructur... 1. Resumen de... 2. Resumen de... La función a... [Mediana o m... [resumen] Por ... La "Tabla 1" co... Configurando ...

A table: 412 x 5 Groups: leucocitos_lcr [318]

leucocitos_lcr	tinción_gran	cultivo_sangre	DE	hematies_lcr
0	0	225.0000	N/A	225
0	1	200.0000	N/A	200
0	NA	125.0000	N/A	125
1	NA	NaN	I	-Inf
2	0	90.0000	N/A	90
2	NA	NaN	N/A	-Inf
3	0	105.0000	56.568542	145
3	NA	NaN	N/A	-Inf
4	1	140.0000	N/A	140
4	NA	NaN	N/A	-Inf

1-10 of 412 rows

Previous: 1 2 3 4 5 6 7 8 9 10 Next

Console: Terminal Background jobs

```
R - R 4.4.3 - / 
> boc_aguda >
+ select(edad, raza, sexo, mes, glucosa_sangre,
+        leucocitos_lcr, células_banda_sangre_pct, neutrofilos_sangre_pct) >
+   tbl_summary(
+     by = neutrofilos_sangre_pct
+   )
146 missing rows in the "neutrofilos_sangre_pct" column have been removed.
> library(readr)
> boc_aguda <- read_csv("Desktop/Sistematización y métodos estadísticos/estadística_upsjb/data/boc_aguda.csv")
Rows: 581 Columns: 22
- Column specification -
```

RStudio Project: (None)

Source: `práctica_01_03.qmd` bac_aguda

Data: `boc_aguda` 581 obs. of 22 variables

Integrantes: Paquetes para... Cargando los d... La "estructur... 1. Resumen de... 2. Resumen de... La función a... [Mediana o m... [resumen] Por ... La "Tabla 1" co... Configurando ...

Estadística descriptiva condicional: resumen por grupo de estado de diabetes

```
{r}
boc_aguda >
  group_by(tinción_gran) >
  summarise(proteína_lcr = max(leucocitos_lcr[glucosa_sangre == "Sí"], na.rm = TRUE),
            células_banda_sangre_pct = max(leucocitos_lcr[glucosa_sangre == "No"], na.rm = TRUE),
            neutrofilos_sangre_pct = mean(leucocitos_lcr[glucosa_sangre == "Sí"], na.rm = TRUE),
            monocitos_lcr_pct = mean(leucocitos_lcr[glucosa_sangre == "No"], na.rm = TRUE))
```

A table: 8 x 5

tinción_gran	proteína_lcr	células_banda_sangre...	neutrofilos_sangre_pct	monocitos_lcr_pct
0	-Inf	-Inf	NaN	
1	-Inf	-Inf	NaN	
2	-Inf	-Inf	NaN	
3	-Inf	-Inf	NaN	
4	-Inf	-Inf	NaN	
5	-Inf	-Inf	NaN	
6	-Inf	-Inf	NaN	
NA	-Inf	-Inf	NaN	

8 rows | 1-4 of 5 columns

Percentiles

```
{r}
Console: Terminal Background jobs
```

```
R - R 4.4.3 - / 
<--> ./jupyter/notebook/notebooks/01%20-%20Sistematizaci%F3n%20y%20m%F3tods%20estad%C3%ADsticos/bac_aguda.R
#> #> (17): numero_caso, año, edad, leucocitos_sangre, neutrofilos_sangre_pct, células_banda_sangre_pct, glucosa_sang...
```

i Use 'spec()' to retrieve the full column specification for this data.
i Specify the column types or set 'show_col_types = FALSE' to quiet this message.
> View(boc_aguda)

RStudio

practica_01_03.qmd

Source Visual B I Normal Format Insert Table

Percentiles

```
{r}
bac_aguda >
  filter(meningitis_bacteriana_aguda == "Presente") >
  group_by(sexo)
summarize(p25 = quantile(glucosa_lcr, probs = 0.25, na.rm=T),
          p50 = quantile(glucosa_lcr, probs = 0.50, na.rm=T),
          p75 = quantile(glucosa_lcr, probs = 0.75, na.rm=T))
```

A tibble: 2 × 4

sexo	p25	p50	p75
2	15	32	65.0
Femenino	15	40	63.5

2 rows

Using across() for multiple descriptive statistics for multiple variables

```
{r}
bac_aguda >
  group_by(meningitis_bacteriana_aguda) >
  summarize(across(.cols = c(glucosa_sangre, linfocitos_lcr_pct,
                           monocitos_lcr_pct, neutrofilos_sangre_pct, leucocitos_lcr),
               .fns = list("promedio" = mean, "DE" = sd,
                          "maximo" = max),
               na.rm = TRUE))
```

tbl_df

Quarto 2

Console Terminal Background Jobs

R 4.4.3 - /home/rafael/Desktop/Sistematización y métodos estadísticos/estadistica_upsjb

practica_01_03.qmd

bac_aguda

Use 'spec()' to retrieve the full column specification for this data.
Specify the column types or set 'show_col_types = FALSE' to quiet this message.

View(bac_aguda)

RStudio

practica_01_03.qmd

Source Visual B I Normal Format Insert Table

Integrantes

```
{r}
bac_aguda >
  group_by(meningitis_bacteriana_aguda) >
  summarize(across(.cols = c(glucosa_sangre, linfocitos_lcr_pct,
                           monocitos_lcr_pct, neutrofilos_sangre_pct, leucocitos_lcr),
               .fns = list("promedio" = mean, "DE" = sd,
                          "maximo" = max),
               na.rm = TRUE))
```

tbl_df

A tibble: 3 × 16

meningitis_bacteriana_aguda	glucosa_sangre_promedio	glucosa_sangre_DE
Absente	120.1127	32.07197
Presente	158.6452	62.23862
NA	137.8772	64.64299

3 rows | 3-13 of 16 columns

{r}
bac_aguda >
 group_by(meningitis_bacteriana_aguda) >
 summarize(across(.cols = where(is.numeric),
 .fns = list("promedio" = mean, "DE" = sd,
 "maximo" = max),
 na.rm = TRUE))

A tibble: 3 × 52

meningitis_bacteriana_aguda	numero_caso_promedio	numero_caso_DE
-----------------------------	----------------------	----------------

Quarto 2

Console Terminal Background Jobs

R 4.4.3 - /home/rafael/Desktop/Sistematización y métodos estadísticos/estadistica_upsjb

practica_01_03.qmd

bac_aguda

Use 'spec()' to retrieve the full column specification for this data.
Specify the column types or set 'show_col_types = FALSE' to quiet this message.

View(bac_aguda)

The figure shows a screenshot of the RStudio interface. On the left, there are two code chunks. The top one uses `gtsummary` to create a table from a dataset named `bac_aguda`. The table has three columns: `meningitis_bacteriana_aguda`, `numero_caso_promedio`, and `numero_caso_DE`. The bottom code chunk shows the basic usage of `gtsummary`.

On the right, there is a file browser window titled "Quarto 2" showing files in the directory `estadistica_upsjb > data`. The files listed are:

Name	Size	Modified
<code>bac_aguda.csv</code>	58.7 KB	Apr 17, 2025, 9:37 PM
<code>s02_treat_arritis.csv</code>	41.7 KB	Apr 12, 2025, 8:10 AM
<code>s02_treat_arritis.Rdata</code>	33.6 KB	Apr 12, 2025, 8:10 AM
<code>s02_treat_arritis.sav</code>	12.9 KB	Apr 12, 2025, 8:10 AM
<code>s02_treat_arritis.xlsx</code>	38.6 KB	Apr 12, 2025, 8:10 AM
<code>s03_treat_arritis.csv</code>	29.9 KB	Apr 19, 2025, 7:55 AM
<code>s04_diabetes.csv</code>	38.7 KB	Apr 26, 2025, 8:02 AM

The screenshot shows the RStudio interface with the following components:

- Top Bar:** Shows tabs for "practica_01_03.qmd" and "bac_aguda.r".
- Left Panel:** Contains a "library(gtsummary)" section and a "Table 1 básica" section.
- Table 1 básica:** A data summary table with the following data:

Characteristic	N = 581 ¹
edad	3 (1, 21)
Unknown	81
raza	
Blanco	210 (42%)
Negro	286 (58%)
Unknown	85
sexo	
2	221 (44%)
Femenino	279 (56%)
Unknown	81
- Right Panel:** Shows the "Integrantes" (Members) of the "bac_aguda" package, which includes "Paquetes para...", "Cargar los paquetes...", "La "entregar()", "1. Resumen de...", "2. Resumen de...", "La función s...", "[Usted ha hecho...]", "[resumen] Por...", "La "Tabla 1" co...", and "Configurando...".
- Bottom Panel:** Shows the "Files" tab of the file browser with the following files:

Name	Size	Modified
..	58.7 KB	Apr 17, 2025, 9:37 PM
bac_aguda.csv	41.7 KB	Apr 12, 2025, 8:10 AM
s02_treat_arritis.csv	33.6 KB	Apr 12, 2025, 8:10 AM
s02_treat_arritis.Rdata	12.9 KB	Apr 12, 2025, 8:10 AM
s02_treat_arritis.sav	38.6 KB	Apr 12, 2025, 8:10 AM
s02_treat_arritis.xlsx	29.9 KB	Apr 19, 2025, 7:55 AM
s03_treat_arritis.csv	38.7 KB	Apr 26, 2025, 8:02 AM
s04_diabetes.csv		
- Console:** Shows the command "View(bac_aguda)" and its output.

RStudio interface showing the environment and file browser.

Environment:

- Data: `bac_aguda` (581 obs. of 22 variables)

File Browser:

- Home > Desktop > Sistematización y métodos estadísticos > estadistica_upsjb > data
- Files: `bac_aguda.csv`, `s02_treat_arthritis.Rdata`, `s02_treat_arthritis.csv`, `s02_treat_arthritis.sav`, `s02_treat_arthritis.xlsx`, `s03_treat_arthritis.csv`, `s04_diabetes.csv`

Console:

```

practica_01_03.qmd | bac_aguda
Source Visual B I <> Normal • Format • Insert • Table • Run • Publish • Outline
tbl_summary(
  by = neutrofilos_sangre_pct
)
>


| Characteristic     | 0        | 6        | 7        | 11       | 13       | 18       | 20       | 21       |
|--------------------|----------|----------|----------|----------|----------|----------|----------|----------|
| N = 2 <sup>t</sup> | 2 (1, 3) | 0 (0, 0) | 0 (0, 0) | 1 (1, 1) | 1 (1, 1) | 0 (0, 0) | 1 (0, 2) | 0 (0, 1) |
| edad               |          |          |          |          |          |          |          |          |
| Raza               |          |          |          |          |          |          |          |          |
| Blanco             | 0 (0%)   | 0 (0%)   | 1 (100%) | 1 (50%)  | 1 (100%) | 0 (0%)   | 1 (50%)  | 2 (50%)  |
| Negro              | 2 (100%) | 2 (100%) | 0 (0%)   | 1 (50%)  | 0 (0%)   | 1 (100%) | 1 (50%)  | 2 (50%)  |
| Unknown            | 0        | 0        | 0        | 0        | 0        | 0        | 0        | 0        |
| Sexo               |          |          |          |          |          |          |          |          |
| 2                  | 1 (50%)  | 0 (0%)   | 1 (100%) | 0 (0%)   | 1 (100%) | 0 (0%)   | 1 (50%)  | 3 (75%)  |


```

Pero las tablas deben ser autoexplicativas...

RStudio interface showing the environment and file browser.

Environment:

- Data: `bac_aguda` (581 obs. of 22 variables)

File Browser:

- Home > Desktop > Sistematización y métodos estadísticos > estadistica_upsjb > data
- Files: `bac_aguda.csv`, `s02_treat_arthritis.Rdata`, `s02_treat_arthritis.csv`, `s02_treat_arthritis.sav`, `s02_treat_arthritis.xlsx`, `s03_treat_arthritis.csv`, `s04_diabetes.csv`

Console:

```

practica_01_03.qmd | bac_aguda
Source Visual B I <> Normal • Format • Insert • Table • Run • Publish • Outline
theme_gtsummary_language(language = "es") # idioma es = español
theme_gtsummary_journal(journal = "jama")
Setting theme "language: es"Setting theme "JAMA"

(bac_aguda) >
  select(edad, raza, sexo, mes, glucosa_sangre,
         leucocitos_lcr, células_banda_sangre_pct, neutrofilos_sangre_pct) >
  tbl_summary(
    by = neutrofilos_sangre_pct
  )
>


| Característica     | 0 | 6     | 7     | 11    | 13    | 18    | 20    | 21    | 24  |
|--------------------|---|-------|-------|-------|-------|-------|-------|-------|-----|
| N = 2 <sup>t</sup> | 2 | N = 2 | N = 1 | N = 2 | N = 1 | N = 1 | N = 2 | N = 4 | N = |


```

Pero las tablas deben ser autoexplicativas...

Configurando el estilo e idioma

```

(r) theme_gtsummary_language(language = "es") # idioma es = español
theme_gtsummary_journal(journal = "jama")
Setting theme "language: es"Setting theme "JAMA"

(r) 
bac_aguda >
  select(edad, raza, sexo, mes, glucosa_sangre,
         leucocitos_lcr, células_banda_sangre_pct, neutrofilos_sangre_pct) >
  tbl_summary(
    by = neutrofilos_sangre_pct
  )
>


| Característica     | 0 | 6     | 7     | 11    | 13    | 18    | 20    | 21    | 24  |
|--------------------|---|-------|-------|-------|-------|-------|-------|-------|-----|
| N = 2 <sup>t</sup> | 2 | N = 2 | N = 1 | N = 2 | N = 1 | N = 1 | N = 2 | N = 4 | N = |


```

Pero las tablas deben ser autoexplicativas...

RStudio interface showing a script file (practica_01_03.qmd) and a data viewer.

Script Content:

```

practica_01_03.qmd: bac_aguda x
Source | Visual | B | I | Normal | Format | Insert | Table | Run | Publish | Outline
selected(edad, raza, sexo, mes, glucosa_sangre,
        leucocitos_lcr, células_banda_sangre_pct, neutrofilos_sangre_pct) >
tbl_summary(
  by = neutrofilos_sangre_pct
)

```

Data Viewer:

Integrantes:
Paquetes para ...
Cargando los d...
La "estructur...
El resumen...
2. Resumen de...
La función s...
Mediana o m...
[resumen] Por ...
La "Tabla 1" co...
Configurando ...

Data:

boc_aguda 581 obs. of 22 variables

Característica	N = 0	N = 6	N = 7	N = 11	N = 13	N = 18	N = 20	N = 21	N = 24
edad, Mediana (IQR)	2 (1 - 3)	0 (0 - 0)	0 (0 - 0)	1 (1 - 1)	1 (1 - 1)	0 (0 - 0)	1 (0 - 2)	0 (0 - 1)	7 (C - 14)
raza, n (%)									
Blanco	0 (0)	0 (0)	1 (100)	1 (50)	1 (100)	0 (0)	1 (50)	2 (50)	3 (10)
Negro	2 (100)	2 (100)	0 (0)	1 (50)	0 (0)	1 (100)	1 (50)	2 (50)	0 (10)
Desconocido	0	0	0	0	0	0	0	0	0
sexo, n (%)									
	1	0	1	0	1	0	1	0	1

Console Output:

```

R 4.4.3 -->
> use_foreign_parallel()
> dbi::dbList()
[1]: numero_caso, año, edad, leucocitos_sangre, neutrofilos_sangre_pct, células_banda_sangre_pct, glucosa_sang...
> View(boc_aguda)
> 

```