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```
library(readxl)
fb<- read_excel("LA MOLINA 2014 POTATO WUE (FB).xlsx",
    sheet = "fb", col_types = c("text", "text",
        "text", "text", "numeric", "numeric",
        "numeric", "numeric", "numeric",
        "numeric", "numeric", "numeric",
        "numeric", "numeric", "numeric",
        "numeric", "numeric", "numeric"))
View(fb)
str(fb)
```

```
tibble [150 × 18] (S3: tbl_df/tbl/data.frame)
 $ riego  : chr [1:150] "sequia" "sequia" "irrigado" "sequia" ...
 $ geno   : chr [1:150] "G01" "G02" "G01" "G02" ...
 $ block  : chr [1:150] "2.0" "4.0" "3.0" "1.0" ...
 $ bloque : chr [1:150] "II" "IV" "III" "I" ...
 $ spad_29: num [1:150] 56.3 52.7 49.2 55.5 58.2 43.5 57.4 56.1 61 60.3 ...
 $ spad_83: num [1:150] 41.1 47.9 41.6 44.2 32.6 37.8 42.5 35.9 57.5 41.8 ...
 $ rwc_84 : num [1:150] 61.5 63.2 67.7 64.9 74.5 ...
 $ op_84  : num [1:150] -2.43 -3.03 -2.5 -2.4 -2.27 ...
 $ leafdw : num [1:150] 13.28 9.42 18.22 8.84 14.55 ...
 $ stemdw : num [1:150] 14.87 8.63 24.19 6.58 12.63 ...
 $ rootdw : num [1:150] 3.83 2.1 3.16 2 1.83 2.83 2.28 3.65 4.04 4.17 ...
 $ tubdw  : num [1:150] 19.8 17.7 38 13.5 51.1 ...
 $ biomdw : num [1:150] 51.8 37.8 83.6 30.9 80.2 ...
 $ hi     : num [1:150] 0.45 0.43 0.455 0.437 0.638 ...
 $ ttrans : num [1:150] 4.5 3.54 8.39 2.9 7.37 ...
 $ wue    : num [1:150] 11.51 10.69 9.97 10.65 10.88 ...
 $ twue   : num [1:150] 4.4 4.99 4.53 4.65 6.94 ...
 $ lfa    : num [1:150] 2900 2619 7579 2450 5413 ...
```

Analisis de datos

```
library(tidyverse)
```

```
── Attaching core tidyverse packages ──────────────────────── tidyverse 2.0.0 ──
✓ dplyr     1.1.4     ✓ readr     2.1.5
✓ forcats   1.0.0     ✓ stringr   1.5.1
✓ ggplot2   3.5.1     ✓ tibble    3.2.1
✓ lubridate 1.9.3     ✓ tidyr     1.3.1
✓ purrr     1.0.2
── Conflicts ────────────────────────────────────────── tidyverse_conflicts() ──
✖ dplyr::filter() masks stats::filter()
✖ dplyr::lag()    masks stats::lag()
ℹ Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become
errors
```

```
library(googlesheets4)
```

Importar datos

```
#url <- ""
```

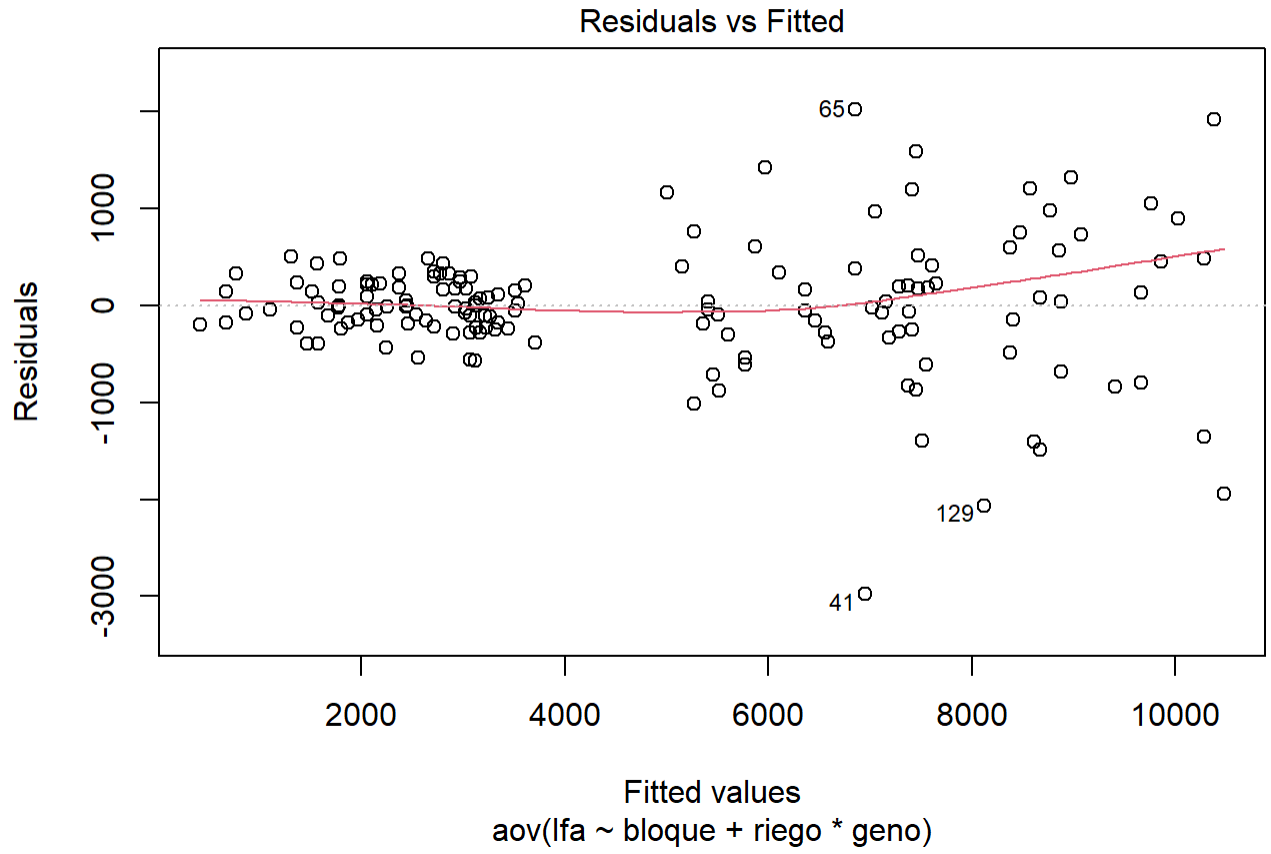
```
  #gs <- as_sheets_id(url)
#fb <- range_read(gs,"fb")
#str(fb)
```

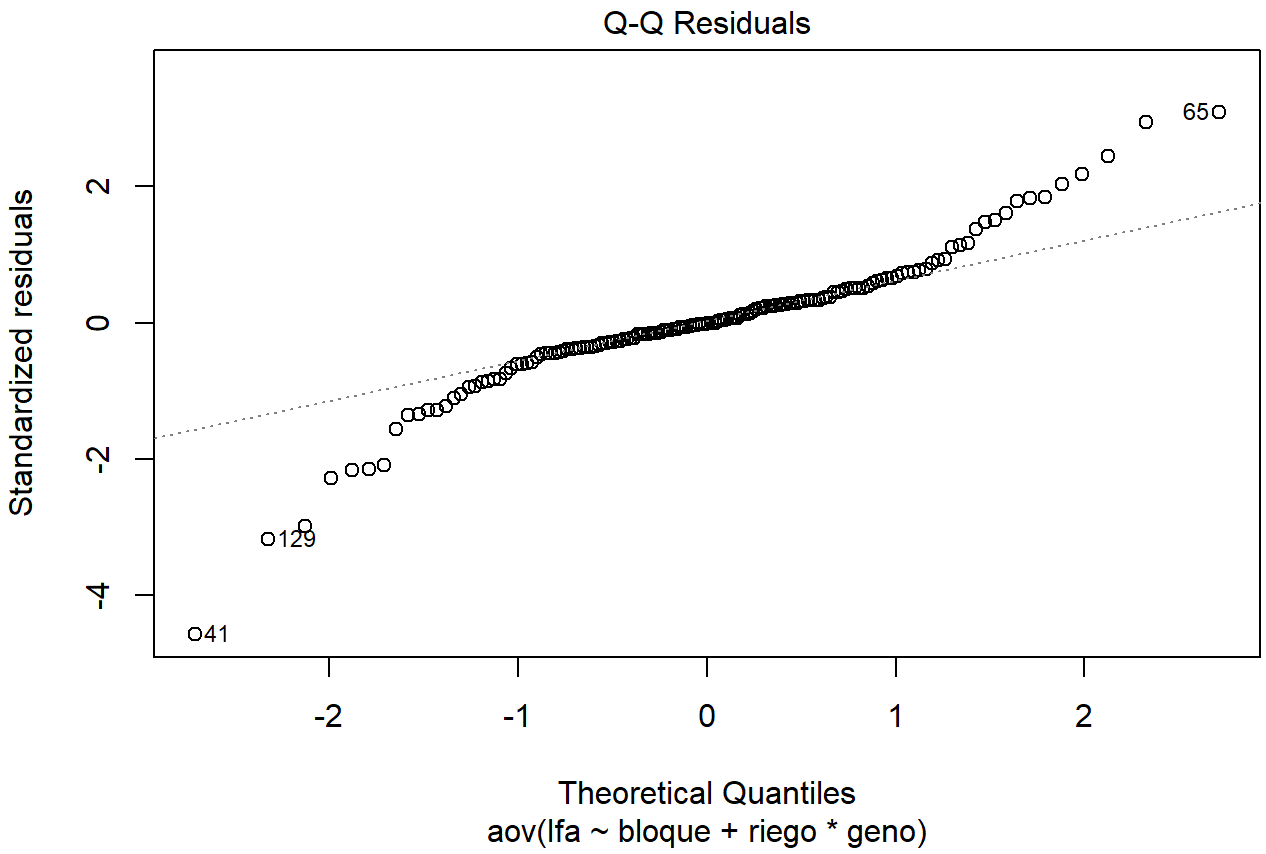
Modelo estadistico

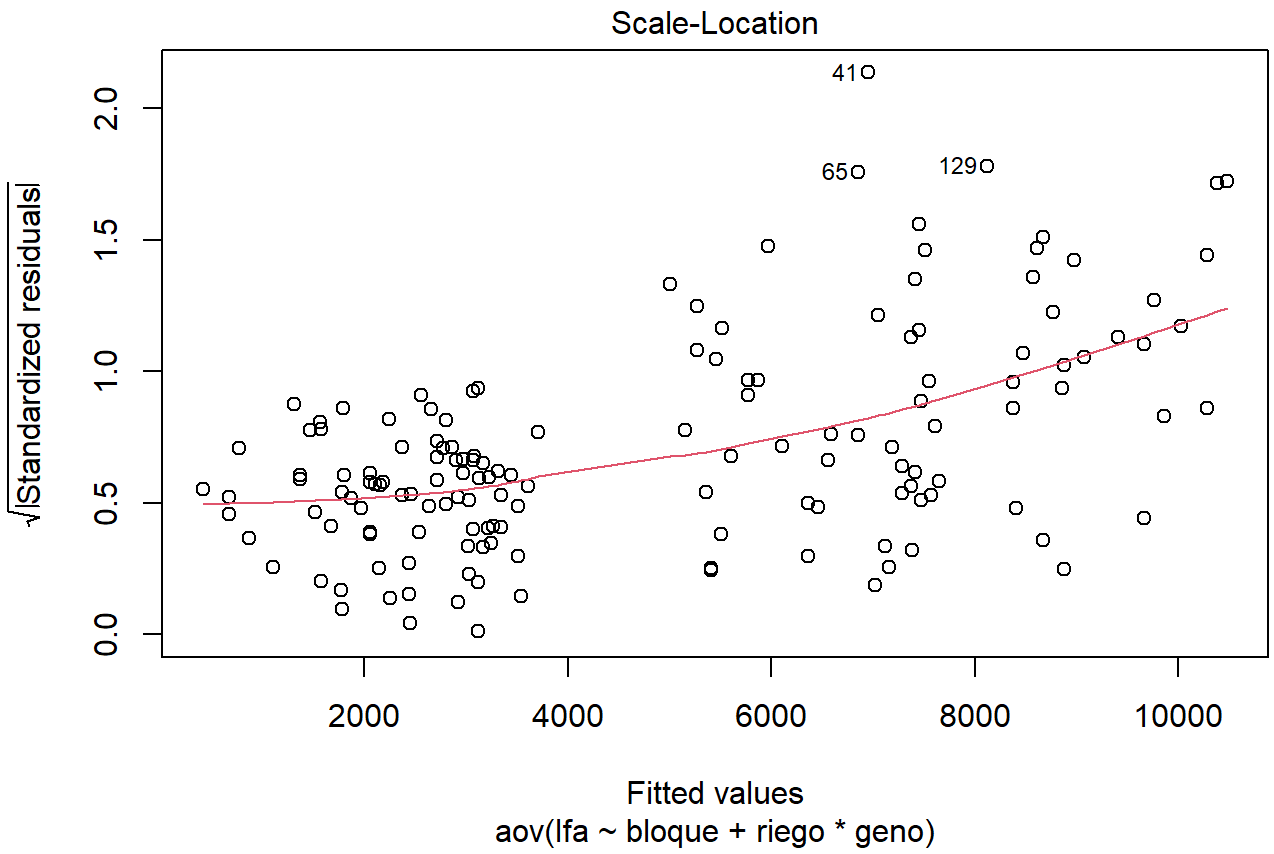
```
modelo <- aov(formula = lfa ~ bloque + riego*geno, data = fb)

anova(modelo)
```

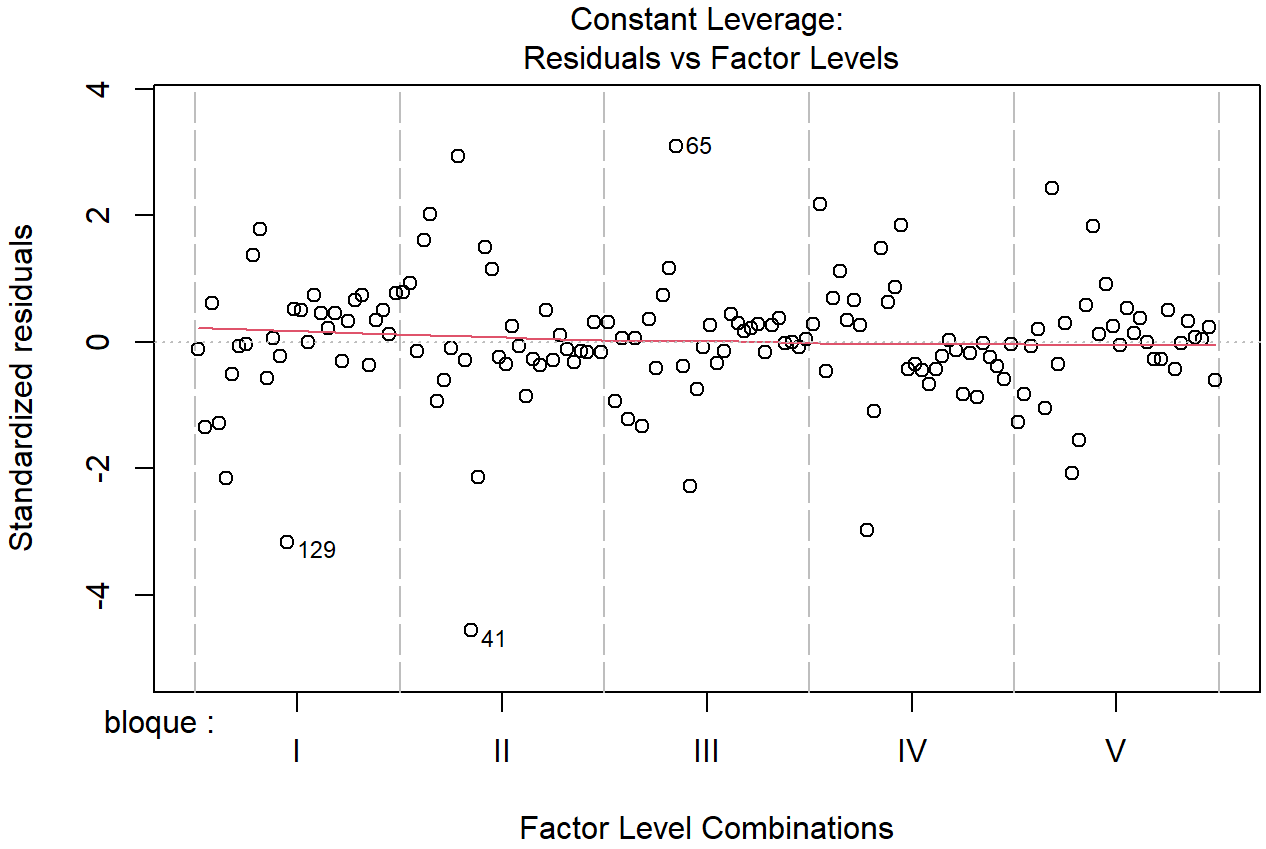
```
Analysis of Variance Table

Response: lfa
             Df    Sum Sq   Mean Sq   F value Pr(>F)
bloque        4   3435339    858835    1.5616 0.1892
riego         1 788556926 788556926 1433.7957 <2e-16 ***
geno         14 261729564  18694969   33.9922 <2e-16 ***
riego:geno   14 108147972   7724855   14.0457 <2e-16 ***
Residuals   116  63797516    549979
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
plot(modelo)
```




Q-Q Residuals
Standardized residuals
Theoretical Quantiles
aov(lfa ~ bloque + riego * geno)
65
129
41
2
0
-2
-4
-2
-1
0
1
2


Scale-Location
41
65
129
√|Standardized residuals|
0.0
0.5
1.0
1.5
2.0
2000
4000
6000
8000
10000
Fitted values
aov(lfa ~ bloque + riego * geno)



Comparacion de medias

```
library(agricolae)
mc <- agricolae::duncan.test(y= modelo
                             ,trt = c("riego","geno"))

mc
```

```
$statistics
   MSerror  Df     Mean       CV
  549978.6 116 4806.708 15.42855

$parameters
    test     name.t ntr alpha
  Duncan riego:geno  30  0.05

$duncan
      Table CriticalRange
2  2.801028      928.9779
3  2.947907      977.6910
4  3.045555     1010.0768
5  3.117189     1033.8343
6  3.172876     1052.3034
7  3.217864     1067.2239
```

```
8  3.255217     1079.6123
9  3.286875     1090.1118
10 3.314137     1099.1534
11 3.337915     1107.0395
12 3.358871     1113.9897
13 3.377500     1120.1683
14 3.394183     1125.7013
15 3.409216     1130.6870
16 3.422835     1135.2039
17 3.435231     1139.3152
18 3.446561     1143.0726
19 3.456952     1146.5191
20 3.466514     1149.6904
21 3.475338     1152.6169
22 3.483500     1155.3239
23 3.491071     1157.8346
24 3.498115     1160.1708
25 3.504650     1162.3382
26 3.510752     1164.3621
27 3.516453     1166.2529
28 3.521778     1168.0190
29 3.526793     1169.6820
30 3.531442     1171.2240

$means
                   lfa        std r      se     Min      Max     Q25      Q50
irrigado:G01  7377.892  583.61443 5 331.656 6539.86  7982.73 7038.08  7578.79
irrigado:G02  5779.562 1127.71742 5 331.656 4631.00  7392.38 5162.74  5233.55
irrigado:G03  5416.770   89.80871 5 331.656 5305.77  5545.69 5369.88  5412.51
irrigado:G04  9668.932  945.94448 5 331.656 8569.08 10811.84 8867.03  9791.10
irrigado:G05  8878.756 1235.57574 5 331.656 7205.94 10291.06 8189.67  8913.12
irrigado:G06  7455.364 1009.33982 5 331.656 6576.65  9040.06 6857.13  6938.90
irrigado:G07  1374.156  411.10652 5 331.656 1065.26  1989.25 1068.97  1140.05
irrigado:G08  7286.826  282.80318 5 331.656 6998.00  7643.80 7012.74  7310.01
irrigado:G09 10287.712 1548.81007 5 331.656 8533.54 12296.22 8924.78 10764.71
irrigado:G10  5271.344  822.34789 5 331.656 4249.18  6164.24 4743.16  5171.21
irrigado:G11  6854.880 1888.72290 5 331.656 3966.33  8867.09 6210.41  7225.02
irrigado:G12  7417.258  946.24681 5 331.656 6111.43  8603.78 7164.03  7194.26
irrigado:G13  8672.380 1015.60193 5 331.656 7180.79  9743.70 8256.98  8750.00
irrigado:G14  8384.132 1473.21710 5 331.656 6049.52  9776.01 7895.00  8978.89
irrigado:G15  6367.026  107.45072 5 331.656 6270.00  6522.46 6302.79  6304.88
sequia:G01    3039.588  115.85242 5 331.656 2900.00  3203.70 2994.58  2999.66
sequia:G02    2717.050  281.05239 5 331.656 2449.59  3063.35 2487.28  2618.85
sequia:G03    2059.052  179.44660 5 331.656 1811.97  2274.48 1953.50  2107.76
sequia:G04    2978.712  302.61678 5 331.656 2511.13  3263.70 2889.83  3010.27
sequia:G05    1783.678  120.66794 5 331.656 1657.64  1967.49 1700.00  1771.80
sequia:G06    3348.074  165.94367 5 331.656 3159.54  3550.19 3198.96  3381.68
sequia:G07     680.734  335.90739 5 331.656  216.31  1097.98  495.83   782.10
sequia:G08    2373.624  260.99914 5 331.656 2021.37  2697.93 2278.60  2319.71
sequia:G09    3073.322  198.12400 5 331.656 2781.32  3238.41 2961.78  3150.00
sequia:G10    2924.648  235.40497 5 331.656 2541.12  3136.07 2909.10  2940.95
sequia:G11    2062.412  317.51100 5 331.656 1556.38  2301.31 1942.23  2237.88
sequia:G12    2446.404   37.06811 5 331.656 2400.00  2487.78 2425.26  2438.98
sequia:G13    3126.100   47.70803 5 331.656 3062.34  3191.97 3110.00  3120.00
sequia:G14    3514.338  217.30731 5 331.656 3318.36  3811.99 3326.93  3449.76
sequia:G15    1580.506  248.79682 5 331.656 1176.63  1814.84 1560.00  1601.06
                  Q75
irrigado:G01  7750.00
irrigado:G02  6478.14
irrigado:G03  5450.00
irrigado:G04 10305.61
```

```
irrigado:G05  9793.99
irrigado:G06  7864.08
irrigado:G07  1607.25
irrigado:G08  7469.58
irrigado:G09 10919.31
irrigado:G10  6028.93
irrigado:G11  8005.55
irrigado:G12  8012.79
irrigado:G13  9430.43
irrigado:G14  9221.24
irrigado:G15  6435.00
sequia:G01    3100.00
sequia:G02    2966.18
sequia:G03    2147.55
sequia:G04    3218.63
sequia:G05    1821.46
sequia:G06    3450.00
sequia:G07     811.45
sequia:G08    2550.51
sequia:G09    3235.10
sequia:G10    3096.00
sequia:G11    2274.26
sequia:G12    2480.00
sequia:G13    3146.19
sequia:G14    3664.65
sequia:G15    1750.00

$comparison
NULL

$groups
                 lfa groups
irrigado:G09 10287.712      a
irrigado:G04  9668.932     ab
irrigado:G05  8878.756     bc
irrigado:G13  8672.380      c
irrigado:G14  8384.132     cd
irrigado:G06  7455.364     de
irrigado:G12  7417.258     de
irrigado:G01  7377.892     de
irrigado:G08  7286.826     ef
irrigado:G11  6854.880     ef
irrigado:G15  6367.026     fg
irrigado:G02  5779.562     gh
irrigado:G03  5416.770     gh
irrigado:G10  5271.344      h
sequia:G14    3514.338      i
sequia:G06    3348.074     ij
sequia:G13    3126.100    ijk
sequia:G09    3073.322    ijk
sequia:G01    3039.588    ijk
sequia:G04    2978.712    ijk
sequia:G10    2924.648    ijk
sequia:G02    2717.050   ijkl
sequia:G12    2446.404  ijklm
sequia:G08    2373.624  jklmn
sequia:G11    2062.412   klmn
sequia:G03    2059.052   klmn
sequia:G05    1783.678    lmn
sequia:G15    1580.506    mno
irrigado:G07  1374.156     no
```

```
sequia:G07     680.734      o

attr(,"class")
[1] "group"
```

```
str(mc)
```

```
List of 6
 $ statistics:'data.frame': 1 obs. of  4 variables:
  ..$ MSerror: num 549979
  ..$ Df     : int 116
  ..$ Mean   : num 4807
  ..$ CV     : num 15.4
 $ parameters:'data.frame': 1 obs. of  4 variables:
  ..$ test  : chr "Duncan"
  ..$ name.t: chr "riego:geno"
  ..$ ntr   : int 30
  ..$ alpha : num 0.05
 $ duncan    :'data.frame': 29 obs. of  2 variables:
  ..$ Table        : num [1:29] 2.8 2.95 3.05 3.12 3.17 ...
  ..$ CriticalRange: num [1:29] 929 978 1010 1034 1052 ...
 $ means     :'data.frame': 30 obs. of  9 variables:
  ..$ lfa: num [1:30] 7378 5780 5417 9669 8879 ...
  ..$ std: num [1:30] 583.6 1127.7 89.8 945.9 1235.6 ...
  ..$ r  : int [1:30] 5 5 5 5 5 5 5 5 5 5 ...
  ..$ se : num [1:30] 332 332 332 332 332 ...
  ..$ Min: num [1:30] 6540 4631 5306 8569 7206 ...
  ..$ Max: num [1:30] 7983 7392 5546 10812 10291 ...
  ..$ Q25: num [1:30] 7038 5163 5370 8867 8190 ...
  ..$ Q50: num [1:30] 7579 5234 5413 9791 8913 ...
  ..$ Q75: num [1:30] 7750 6478 5450 10306 9794 ...
 $ comparison: NULL
 $ groups    :'data.frame': 30 obs. of  2 variables:
  ..$ lfa   : num [1:30] 10288 9669 8879 8672 8384 ...
  ..$ groups: chr [1:30] "a" "ab" "bc" "c" ...
 - attr(*, "class")= chr "group"
```

```
library(emmeans)
```

```
Welcome to emmeans.
Caution: You lose important information if you filter this package's results.
See '? untidy'
```

```
library(multcomp)
```

```
Loading required package: mvtnorm
Loading required package: survival
Loading required package: TH.data
Loading required package: MASS

Attaching package: 'MASS'
The following object is masked from 'package:dplyr':

    select

Attaching package: 'TH.data'
The following object is masked from 'package:MASS':

    geyser
```

```r
library(tidyverse)
library(inti)
```

```
Loading required package: shiny
```

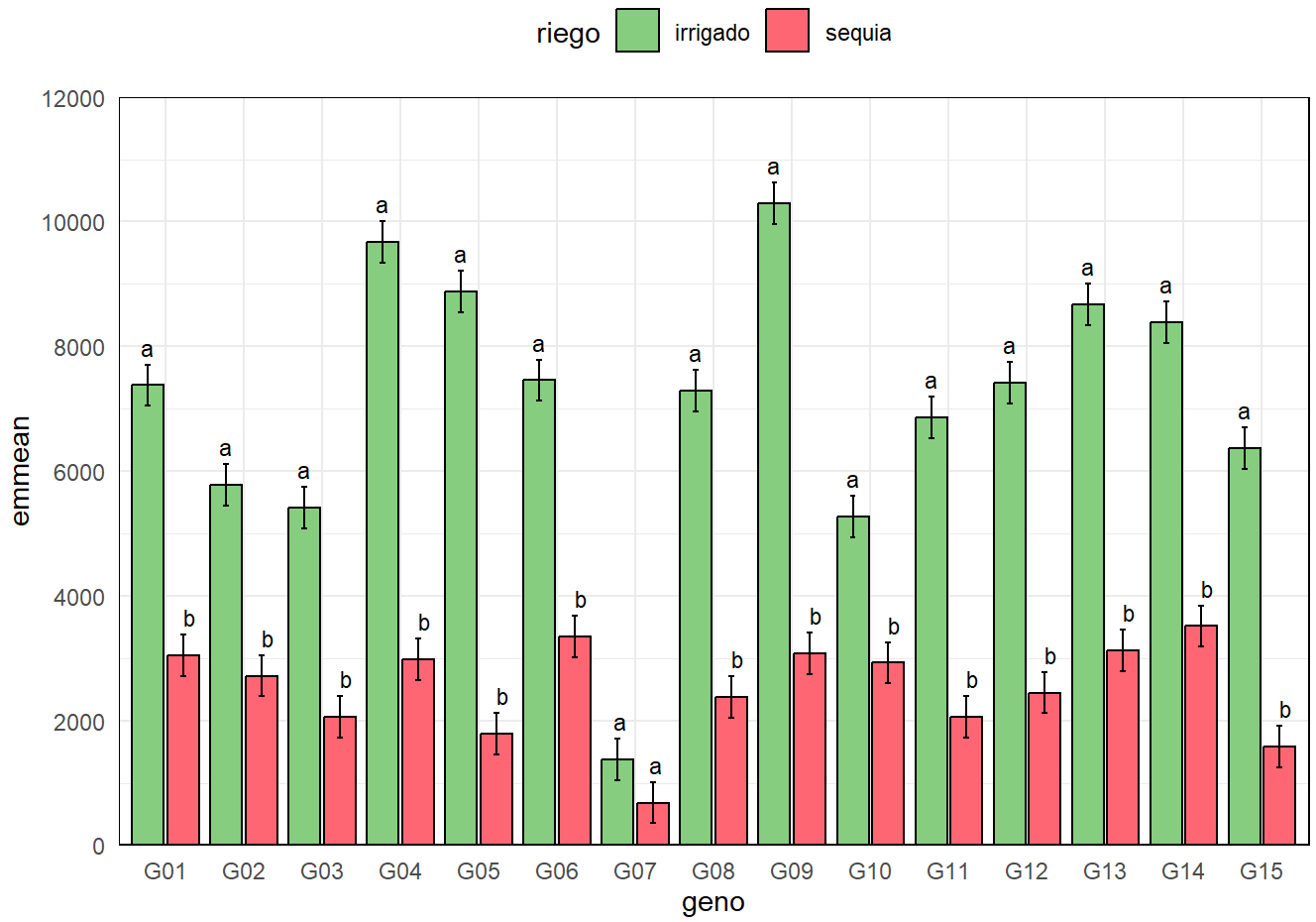
```r
mc <- emmeans(modelo, ~ riego | geno)
mc_cld <- mc %>%
  cld(Letters = letters, reversed = TRUE)

mc_cld
```

```
geno = G01:
 riego    emmean  SE  df lower.CL upper.CL .group
 irrigado   7378 332 116   6721.0     8035  a
 sequia     3040 332 116   2382.7     3696   b

geno = G02:
 riego    emmean  SE  df lower.CL upper.CL .group
 irrigado   5780 332 116   5122.7     6436  a
 sequia     2717 332 116   2060.2     3374   b

geno = G03:
 riego    emmean  SE  df lower.CL upper.CL .group
 irrigado   5417 332 116   4759.9     6074  a
 sequia     2059 332 116   1402.2     2716   b

geno = G04:
 riego    emmean  SE  df lower.CL upper.CL .group
 irrigado   9669 332 116   9012.0    10326  a
 sequia     2979 332 116   2321.8     3636   b

geno = G05:
 riego    emmean  SE  df lower.CL upper.CL .group
 irrigado   8879 332 116   8221.9     9536  a
 sequia     1784 332 116   1126.8     2441   b

geno = G06:
 riego    emmean  SE  df lower.CL upper.CL .group
 irrigado   7455 332 116   6798.5     8112  a
 sequia     3348 332 116   2691.2     4005   b

geno = G07:
 riego    emmean  SE  df lower.CL upper.CL .group
 irrigado   1374 332 116    717.3     2031  a
 sequia      681 332 116     23.8     1338  a

geno = G08:
 riego    emmean  SE  df lower.CL upper.CL .group
 irrigado   7287 332 116   6629.9     7944  a
 sequia     2374 332 116   1716.7     3031   b

geno = G09:
 riego    emmean  SE  df lower.CL upper.CL .group
 irrigado  10288 332 116   9630.8    10945  a
 sequia     3073 332 116   2416.4     3730   b

geno = G10:
 riego    emmean  SE  df lower.CL upper.CL .group
 irrigado   5271 332 116   4614.5     5928  a
 sequia     2925 332 116   2267.8     3582   b
```

```
geno = G11:
 riego    emmean  SE  df lower.CL upper.CL .group
 irrigado   6855 332 116   6198.0     7512  a
 sequia     2062 332 116   1405.5     2719   b

geno = G12:
 riego    emmean  SE  df lower.CL upper.CL .group
 irrigado   7417 332 116   6760.4     8074  a
 sequia     2446 332 116   1789.5     3103   b

geno = G13:
 riego    emmean  SE  df lower.CL upper.CL .group
 irrigado   8672 332 116   8015.5     9329  a
 sequia     3126 332 116   2469.2     3783   b

geno = G14:
 riego    emmean  SE  df lower.CL upper.CL .group
 irrigado   8384 332 116   7727.2     9041  a
 sequia     3514 332 116   2857.5     4171   b

geno = G15:
 riego    emmean  SE  df lower.CL upper.CL .group
 irrigado   6367 332 116   5710.1     7024  a
 sequia     1581 332 116    923.6     2237   b

Results are averaged over the levels of: bloque
Confidence level used: 0.95
significance level used: alpha = 0.05
NOTE: If two or more means share the same grouping symbol,
      then we cannot show them to be different.
      But we also did not show them to be the same.
```

Grafico

```
library(inti)

plot_smr(data = mc_cld
         , type = "bar"
         , x = "geno"
         , y = "emmean"
         , group = "riego"
         , sig = ".group"
         , error = "SE"
         , ylimits = c(0, 12000, 2000))
```




```
ggplot(mc_cld, aes(x = geno, y = emmean, fi11 = riego)) +
  geom_bar(stat = "identity") +
  theme_minimal() +
  labs(title = "Grafico de barras", x = "Categoria", y = "valores")
```

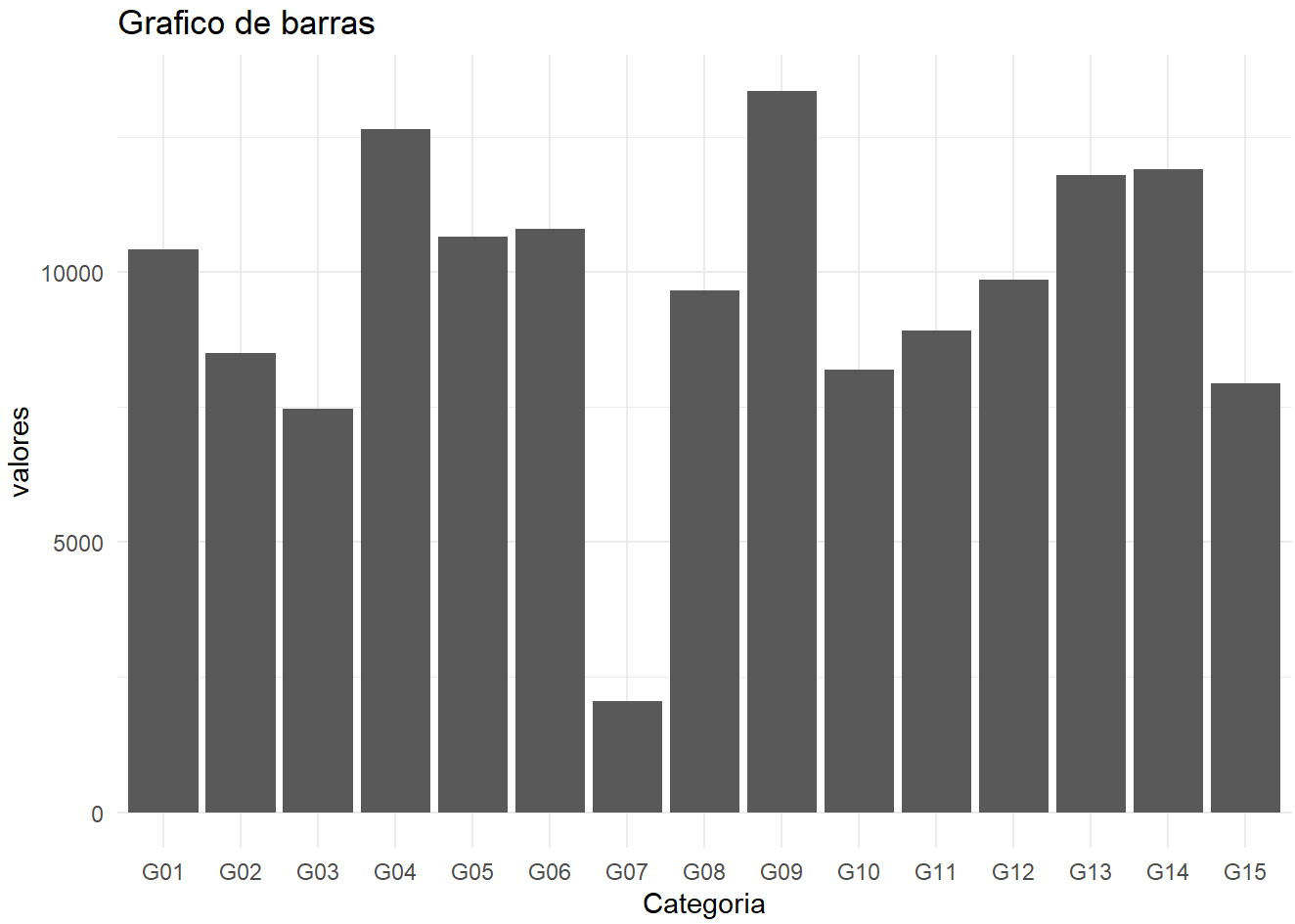


Grafico de barras
valores
10000
5000
0
G01
G02
G03
G04
G05
G06
G07
G08
G09
G10
G11
G12
G13
G14
G15
Categoria