Perspectivas em ciências de dados na linguagem R

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Análise exploratória de dados

Manipulação de dados e estatísticas descritivas

Instalando e carregando pacotes.

```
install_if_missing_multi <- function(packages) {
  for (pkg in packages) {
    if (!require(pkg, character.only = TRUE)) {
      install.packages(pkg)
      library(pkg, character.only = TRUE)
    }
  }
}

packages <- c("rstudioapi", "modelsummary", "glmnet", "xgboost", "ranger", "nnet", "dplyr", "g

install_if_missing_multi(packages)
```

Carregando pacotes necessários às análises (é o que faço se não quero usar a função anterior).

```
library(dplyr)
library(modelsummary)
```

Carregando o conjunto de dados `mtcars`.

```
dados <- mtcars
# ?mtcars

head(dados)
```

```
                   mpg cyl disp  hp drat    wt  qsec vs am gear carb
Mazda RX4         21.0   6  160 110 3.90 2.620 16.46  0  1    4    4
Mazda RX4 Wag     21.0   6  160 110 3.90 2.875 17.02  0  1    4    4
Datsun 710        22.8   4  108  93 3.85 2.320 18.61  1  1    4    1
Hornet 4 Drive    21.4   6  258 110 3.08 3.215 19.44  1  0    3    1
Hornet Sportabout 18.7   8  360 175 3.15 3.440 17.02  0  0    3    2
Valiant           18.1   6  225 105 2.76 3.460 20.22  1  0    3    1
```

```
# https://rstudio-pubs-static.s3.amazonaws.com/61800_faea93548c6b49cc91cd0c5ef5059894.html
```

Número de dimensões do *data frame* (linhas e colunas).

```
dim(dados)
```

```
[1] 32 11
```

Acessando coluna de interesse.

```
hp <- dados$hp
hp
```

```
 [1] 110 110  93 110 175 105 245  62  95 123 123 180 180 180 205 215 230  66  52
[20]  65  97 150 150 245 175  66  91 113 264 175 335 109
```

Indexando colunas.

```
dados[,4]
```

```
 [1] 110 110  93 110 175 105 245  62  95 123 123 180 180 180 205 215 230  66  52
[20]  65  97 150 150 245 175  66  91 113 264 175 335 109
```

Indexando linhas.

```
porsche <- dados[27,]
porsche
```

```
              mpg cyl  disp hp drat   wt qsec vs am gear carb
Porsche 914-2  26   4 120.3 91 4.43 2.14 16.7  0  1    5    2
```

Indexando linhas e colunas.

```
dados[27,4]
```

```
[1] 91
```

```
dados_red <- dados[27:29, 4:5]
dados_red
```

```
                hp drat
Porsche 914-2   91 4.43
Lotus Europa   113 3.77
Ford Pantera L 264 4.22
```

```
dados[c(27,29), 4:5]
```

```
                hp drat
Porsche 914-2   91 4.43
Ford Pantera L 264 4.22
```

Repetindo operações anteriores via `dplyr`.

```
d_hp <- dados |>
  select(hp)
d_hp
```

```
                     hp
Mazda RX4           110
Mazda RX4 Wag       110
Datsun 710           93
Hornet 4 Drive      110
Hornet Sportabout   175
Valiant             105
Duster 360          245
Merc 240D            62
Merc 230             95
Merc 280            123
Merc 280C           123
Merc 450SE          180
Merc 450SL          180
Merc 450SLC         180
Cadillac Fleetwood  205
Lincoln Continental 215
Chrysler Imperial   230
Fiat 128             66
Honda Civic          52
Toyota Corolla       65
Toyota Corona        97
Dodge Challenger    150
AMC Javelin         150
Camaro Z28          245
Pontiac Firebird    175
Fiat X1-9            66
Porsche 914-2        91
Lotus Europa        113
Ford Pantera L      264
Ferrari Dino        175
Maserati Bora       335
Volvo 142E          109
```

```
# dados |>
#   pull(hp)
```

```
dados |>
  slice(27)
```

```
              mpg cyl  disp hp drat   wt qsec vs am gear carb
Porsche 914-2  26   4 120.3 91 4.43 2.14 16.7  0  1    5    2
```

```
dados |>
  select(hp) |>
  slice(27)
```

```
              hp
Porsche 914-2 91
```

```
dados |>
  select(hp,drat) |>
```

```
  slice(27:29) # slice(27,29)
```

```
                hp drat
Porsche 914-2   91 4.43
Lotus Europa   113 3.77
Ford Pantera L 264 4.22
```

Vislumbrando os dados.

```
glimpse(dados)
```

```
Rows: 32
Columns: 11
$ mpg  <dbl> 21.0, 21.0, 22.8, 21.4, 18.7, 18.1, 14.3, 24.4, 22.8, 19.2, 17.8,…
$ cyl  <dbl> 6, 6, 4, 6, 8, 6, 8, 4, 4, 6, 6, 8, 8, 8, 8, 8, 8, 4, 4, 4, 4, 8,…
$ disp <dbl> 160.0, 160.0, 108.0, 258.0, 360.0, 225.0, 360.0, 146.7, 140.8, 16…
$ hp   <dbl> 110, 110, 93, 110, 175, 105, 245, 62, 95, 123, 123, 180, 180, 180…
$ drat <dbl> 3.90, 3.90, 3.85, 3.08, 3.15, 2.76, 3.21, 3.69, 3.92, 3.92, 3.92,…
$ wt   <dbl> 2.620, 2.875, 2.320, 3.215, 3.440, 3.460, 3.570, 3.190, 3.150, 3.…
$ qsec <dbl> 16.46, 17.02, 18.61, 19.44, 17.02, 20.22, 15.84, 20.00, 22.90, 18…
$ vs   <dbl> 0, 0, 1, 1, 0, 1, 0, 1, 1, 1, 1, 0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 0,…
$ am   <dbl> 1, 1, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 0, 0,…
$ gear <dbl> 4, 4, 4, 3, 3, 3, 3, 4, 4, 4, 4, 3, 3, 3, 3, 3, 3, 4, 4, 4, 3, 3,…
$ carb <dbl> 4, 4, 1, 1, 2, 1, 4, 2, 2, 4, 4, 3, 3, 3, 4, 4, 4, 1, 2, 1, 1, 2,…
```

Estatísticas descritivas.

```
datasummary_skim(dados)
```

	Unique	Missing Pct.	Mean	SD	Min	Median	Max	Histogram
mpg	25	0	20.1	6.0	10.4	19.2	33.9	
cyl	3	0	6.2	1.8	4.0	6.0	8.0	
disp	27	0	230.7	123.9	71.1	196.3	472.0	
hp	22	0	146.7	68.6	52.0	123.0	335.0	
drat	22	0	3.6	0.5	2.8	3.7	4.9	
wt	29	0	3.2	1.0	1.5	3.3	5.4	
qsec	30	0	17.8	1.8	14.5	17.7	22.9	
vs	2	0	0.4	0.5	0.0	0.0	1.0	
am	2	0	0.4	0.5	0.0	0.0	1.0	
gear	3	0	3.7	0.7	3.0	4.0	5.0	
carb	6	0	2.8	1.6	1.0	2.0	8.0	

```
# summary(dados)
```

Conjunto de dados `penguins`.

```
glimpse(penguins)
```

```
Rows: 344
Columns: 7
$ species           <fct> Adelie, Adelie, Adelie, Adelie, Adelie, Adelie, Adel…
$ island            <fct> Torgersen, Torgersen, Torgersen, Torgersen, Torgerse…
$ bill_length_mm    <dbl> 39.1, 39.5, 40.3, NA, 36.7, 39.3, 38.9, 39.2, 34.1, …
$ bill_depth_mm     <dbl> 18.7, 17.4, 18.0, NA, 19.3, 20.6, 17.8, 19.6, 18.1, …
$ flipper_length_mm <int> 181, 186, 195, NA, 193, 190, 181, 195, 193, 190, 186…
$ body_mass_g       <int> 3750, 3800, 3250, NA, 3450, 3650, 3625, 4675, 3475, …
$ sex               <fct> male, female, female, NA, female, male, female, male…
```

Resumo das variáveis numéricas com `datasummary_skim`.

```
datasummary_skim(penguins,
                 type = "numeric")
```

	Unique	Missing Pct.	Mean	SD	Min	Median	Max	Histo
bill_length_mm	165	1	43.9	5.5	32.1	44.5	59.6	
bill_depth_mm	81	1	17.2	2.0	13.1	17.3	21.5	
flipper_length_mm	56	1	200.9	14.1	172.0	197.0	231.0	
body_mass_g	95	1	4201.8	802.0	2700.0	4050.0	6300.0	

Caso queira avaliar apenas as variáveis categóricas.

```
datasummary_skim(penguins,
                 type = "categorical")
```

		N	%
species	Adelie	152	44.2
	Chinstrap	68	19.8
	Gentoo	124	36.0
island	Biscoe	168	48.8
	Dream	124	36.0
	Torgersen	52	15.1

		N	%
sex	female	165	48.0
	male	168	48.8

Voltando aos carros. Avaliando a correlação entre as variáveis.

```
cor(dados) |>
  round(2)
```

```
       mpg   cyl  disp    hp  drat    wt  qsec    vs    am  gear  carb
mpg   1.00 -0.85 -0.85 -0.78  0.68 -0.87  0.42  0.66  0.60  0.48 -0.55
cyl  -0.85  1.00  0.90  0.83 -0.70  0.78 -0.59 -0.81 -0.52 -0.49  0.53
disp -0.85  0.90  1.00  0.79 -0.71  0.89 -0.43 -0.71 -0.59 -0.56  0.39
hp   -0.78  0.83  0.79  1.00 -0.45  0.66 -0.71 -0.72 -0.24 -0.13  0.75
drat  0.68 -0.70 -0.71 -0.45  1.00 -0.71  0.09  0.44  0.71  0.70 -0.09
wt   -0.87  0.78  0.89  0.66 -0.71  1.00 -0.17 -0.55 -0.69 -0.58  0.43
qsec  0.42 -0.59 -0.43 -0.71  0.09 -0.17  1.00  0.74 -0.23 -0.21 -0.66
vs    0.66 -0.81 -0.71 -0.72  0.44 -0.55  0.74  1.00  0.17  0.21 -0.57
am    0.60 -0.52 -0.59 -0.24  0.71 -0.69 -0.23  0.17  1.00  0.79  0.06
gear  0.48 -0.49 -0.56 -0.13  0.70 -0.58 -0.21  0.21  0.79  1.00  0.27
carb -0.55  0.53  0.39  0.75 -0.09  0.43 -0.66 -0.57  0.06  0.27  1.00
```

```
cor(dados,
    method = "spearman") |>
  round(2)
```

```
       mpg   cyl  disp    hp  drat    wt  qsec    vs    am  gear  carb
mpg   1.00 -0.91 -0.91 -0.89  0.65 -0.89  0.47  0.71  0.56  0.54 -0.66
cyl  -0.91  1.00  0.93  0.90 -0.68  0.86 -0.57 -0.81 -0.52 -0.56  0.58
disp -0.91  0.93  1.00  0.85 -0.68  0.90 -0.46 -0.72 -0.62 -0.59  0.54
hp   -0.89  0.90  0.85  1.00 -0.52  0.77 -0.67 -0.75 -0.36 -0.33  0.73
drat  0.65 -0.68 -0.68 -0.52  1.00 -0.75  0.09  0.45  0.69  0.74 -0.13
wt   -0.89  0.86  0.90  0.77 -0.75  1.00 -0.23 -0.59 -0.74 -0.68  0.50
qsec  0.47 -0.57 -0.46 -0.67  0.09 -0.23  1.00  0.79 -0.20 -0.15 -0.66
vs    0.71 -0.81 -0.72 -0.75  0.45 -0.59  0.79  1.00  0.17  0.28 -0.63
am    0.56 -0.52 -0.62 -0.36  0.69 -0.74 -0.20  0.17  1.00  0.81 -0.06
gear  0.54 -0.56 -0.59 -0.33  0.74 -0.68 -0.15  0.28  0.81  1.00  0.11
carb -0.66  0.58  0.54  0.73 -0.13  0.50 -0.66 -0.63 -0.06  0.11  1.00
```

```
datasummary_correlation(dados)
```

	mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear	carb
mpg	1	.	.	.	.	.	.	.	.	.	.
cyl	-.85	1	.	.	.	.	.	.	.	.	.
disp	-.85	.90	1	.	.	.	.	.	.	.	.
hp	-.78	.83	.79	1	.	.	.	.	.	.	.

	mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear	carb
drat	.68	-.70	-.71	-.45	1	.	.	.	.	.	.
wt	-.87	.78	.89	.66	-.71	1	.	.	.	.	.
qsec	.42	-.59	-.43	-.71	.09	-.17	1	.	.	.	.
vs	.66	-.81	-.71	-.72	.44	-.55	.74	1	.	.	.
am	.60	-.52	-.59	-.24	.71	-.69	-.23	.17	1	.	.
gear	.48	-.49	-.56	-.13	.70	-.58	-.21	.21	.79	1	.
carb	-.55	.53	.39	.75	-.09	.43	-.66	-.57	.06	.27	1

Correlação para o conjunto de dados `penguins`.

```
# cor(penguins) # dá erro devido as variáveis categóricas

penguins |>
  select(where(is.numeric)) |>
  cor(use="pairwise.complete.obs")
```

```
                  bill_length_mm bill_depth_mm flipper_length_mm body_mass_g
bill_length_mm         1.0000000    -0.2350529         0.6561813   0.5951098
bill_depth_mm         -0.2350529     1.0000000        -0.5838512  -0.4719156
flipper_length_mm      0.6561813    -0.5838512         1.0000000   0.8712018
body_mass_g            0.5951098    -0.4719156         0.8712018   1.0000000
```

Conjunto de dados iris.

```
glimpse(iris)
```

```
Rows: 150
Columns: 5
$ Sepal.Length <dbl> 5.1, 4.9, 4.7, 4.6, 5.0, 5.4, 4.6, 5.0, 4.4, 4.9, 5.4, 4.…
$ Sepal.Width  <dbl> 3.5, 3.0, 3.2, 3.1, 3.6, 3.9, 3.4, 3.4, 2.9, 3.1, 3.7, 3.…
$ Petal.Length <dbl> 1.4, 1.4, 1.3, 1.5, 1.4, 1.7, 1.4, 1.5, 1.4, 1.5, 1.5, 1.…
$ Petal.Width  <dbl> 0.2, 0.2, 0.2, 0.2, 0.2, 0.4, 0.3, 0.2, 0.2, 0.1, 0.2, 0.…
$ Species      <fct> setosa, setosa, setosa, setosa, setosa, setosa, setosa, s…
```

```
levels(iris$Species)
```

```
[1] "setosa"     "versicolor" "virginica"
```

Seleção de variáveis de forma inteligente.

```
sepal <- iris |>
  select(starts_with("Sepal"))
sepal
```

```
    Sepal.Length Sepal.Width
1            5.1         3.5
2            4.9         3.0
3            4.7         3.2
4            4.6         3.1
5            5.0         3.6
6            5.4         3.9
7            4.6         3.4
8            5.0         3.4
9            4.4         2.9
10           4.9         3.1
11           5.4         3.7
12           4.8         3.4
13           4.8         3.0
14           4.3         3.0
15           5.8         4.0
16           5.7         4.4
17           5.4         3.9
18           5.1         3.5
19           5.7         3.8
20           5.1         3.8
21           5.4         3.4
22           5.1         3.7
23           4.6         3.6
24           5.1         3.3
25           4.8         3.4
26           5.0         3.0
27           5.0         3.4
28           5.2         3.5
29           5.2         3.4
30           4.7         3.2
31           4.8         3.1
32           5.4         3.4
33           5.2         4.1
34           5.5         4.2
35           4.9         3.1
36           5.0         3.2
37           5.5         3.5
38           4.9         3.6
39           4.4         3.0
40           5.1         3.4
41           5.0         3.5
42           4.5         2.3
43           4.4         3.2
44           5.0         3.5
45           5.1         3.8
46           4.8         3.0
47           5.1         3.8
48           4.6         3.2
49           5.3         3.7
50           5.0         3.3
51           7.0         3.2
52           6.4         3.2
53           6.9         3.1
```

54	5.5	2.3
55	6.5	2.8
56	5.7	2.8
57	6.3	3.3
58	4.9	2.4
59	6.6	2.9
60	5.2	2.7
61	5.0	2.0
62	5.9	3.0
63	6.0	2.2
64	6.1	2.9
65	5.6	2.9
66	6.7	3.1
67	5.6	3.0
68	5.8	2.7
69	6.2	2.2
70	5.6	2.5
71	5.9	3.2
72	6.1	2.8
73	6.3	2.5
74	6.1	2.8
75	6.4	2.9
76	6.6	3.0
77	6.8	2.8
78	6.7	3.0
79	6.0	2.9
80	5.7	2.6
81	5.5	2.4
82	5.5	2.4
83	5.8	2.7
84	6.0	2.7
85	5.4	3.0
86	6.0	3.4
87	6.7	3.1
88	6.3	2.3
89	5.6	3.0
90	5.5	2.5
91	5.5	2.6
92	6.1	3.0
93	5.8	2.6
94	5.0	2.3
95	5.6	2.7
96	5.7	3.0
97	5.7	2.9
98	6.2	2.9
99	5.1	2.5
100	5.7	2.8
101	6.3	3.3
102	5.8	2.7
103	7.1	3.0
104	6.3	2.9
105	6.5	3.0
106	7.6	3.0
107	4.9	2.5

```
108          7.3         2.9
109          6.7         2.5
110          7.2         3.6
111          6.5         3.2
112          6.4         2.7
113          6.8         3.0
114          5.7         2.5
115          5.8         2.8
116          6.4         3.2
117          6.5         3.0
118          7.7         3.8
119          7.7         2.6
120          6.0         2.2
121          6.9         3.2
122          5.6         2.8
123          7.7         2.8
124          6.3         2.7
125          6.7         3.3
126          7.2         3.2
127          6.2         2.8
128          6.1         3.0
129          6.4         2.8
130          7.2         3.0
131          7.4         2.8
132          7.9         3.8
133          6.4         2.8
134          6.3         2.8
135          6.1         2.6
136          7.7         3.0
137          6.3         3.4
138          6.4         3.1
139          6.0         3.0
140          6.9         3.1
141          6.7         3.1
142          6.9         3.1
143          5.8         2.7
144          6.8         3.2
145          6.7         3.3
146          6.7         3.0
147          6.3         2.5
148          6.5         3.0
149          6.2         3.4
150          5.9         3.0
```

Excluindo coluna.

```
iris |>
  select(!Species)
```

```
    Sepal.Length Sepal.Width Petal.Length Petal.Width
1            5.1         3.5          1.4         0.2
2            4.9         3.0          1.4         0.2
3            4.7         3.2          1.3         0.2
4            4.6         3.1          1.5         0.2
```

5	5.0	3.6	1.4	0.2
6	5.4	3.9	1.7	0.4
7	4.6	3.4	1.4	0.3
8	5.0	3.4	1.5	0.2
9	4.4	2.9	1.4	0.2
10	4.9	3.1	1.5	0.1
11	5.4	3.7	1.5	0.2
12	4.8	3.4	1.6	0.2
13	4.8	3.0	1.4	0.1
14	4.3	3.0	1.1	0.1
15	5.8	4.0	1.2	0.2
16	5.7	4.4	1.5	0.4
17	5.4	3.9	1.3	0.4
18	5.1	3.5	1.4	0.3
19	5.7	3.8	1.7	0.3
20	5.1	3.8	1.5	0.3
21	5.4	3.4	1.7	0.2
22	5.1	3.7	1.5	0.4
23	4.6	3.6	1.0	0.2
24	5.1	3.3	1.7	0.5
25	4.8	3.4	1.9	0.2
26	5.0	3.0	1.6	0.2
27	5.0	3.4	1.6	0.4
28	5.2	3.5	1.5	0.2
29	5.2	3.4	1.4	0.2
30	4.7	3.2	1.6	0.2
31	4.8	3.1	1.6	0.2
32	5.4	3.4	1.5	0.4
33	5.2	4.1	1.5	0.1
34	5.5	4.2	1.4	0.2
35	4.9	3.1	1.5	0.2
36	5.0	3.2	1.2	0.2
37	5.5	3.5	1.3	0.2
38	4.9	3.6	1.4	0.1
39	4.4	3.0	1.3	0.2
40	5.1	3.4	1.5	0.2
41	5.0	3.5	1.3	0.3
42	4.5	2.3	1.3	0.3
43	4.4	3.2	1.3	0.2
44	5.0	3.5	1.6	0.6
45	5.1	3.8	1.9	0.4
46	4.8	3.0	1.4	0.3
47	5.1	3.8	1.6	0.2
48	4.6	3.2	1.4	0.2
49	5.3	3.7	1.5	0.2
50	5.0	3.3	1.4	0.2
51	7.0	3.2	4.7	1.4
52	6.4	3.2	4.5	1.5
53	6.9	3.1	4.9	1.5
54	5.5	2.3	4.0	1.3
55	6.5	2.8	4.6	1.5
56	5.7	2.8	4.5	1.3
57	6.3	3.3	4.7	1.6
58	4.9	2.4	3.3	1.0

59	6.6	2.9	4.6	1.3
60	5.2	2.7	3.9	1.4
61	5.0	2.0	3.5	1.0
62	5.9	3.0	4.2	1.5
63	6.0	2.2	4.0	1.0
64	6.1	2.9	4.7	1.4
65	5.6	2.9	3.6	1.3
66	6.7	3.1	4.4	1.4
67	5.6	3.0	4.5	1.5
68	5.8	2.7	4.1	1.0
69	6.2	2.2	4.5	1.5
70	5.6	2.5	3.9	1.1
71	5.9	3.2	4.8	1.8
72	6.1	2.8	4.0	1.3
73	6.3	2.5	4.9	1.5
74	6.1	2.8	4.7	1.2
75	6.4	2.9	4.3	1.3
76	6.6	3.0	4.4	1.4
77	6.8	2.8	4.8	1.4
78	6.7	3.0	5.0	1.7
79	6.0	2.9	4.5	1.5
80	5.7	2.6	3.5	1.0
81	5.5	2.4	3.8	1.1
82	5.5	2.4	3.7	1.0
83	5.8	2.7	3.9	1.2
84	6.0	2.7	5.1	1.6
85	5.4	3.0	4.5	1.5
86	6.0	3.4	4.5	1.6
87	6.7	3.1	4.7	1.5
88	6.3	2.3	4.4	1.3
89	5.6	3.0	4.1	1.3
90	5.5	2.5	4.0	1.3
91	5.5	2.6	4.4	1.2
92	6.1	3.0	4.6	1.4
93	5.8	2.6	4.0	1.2
94	5.0	2.3	3.3	1.0
95	5.6	2.7	4.2	1.3
96	5.7	3.0	4.2	1.2
97	5.7	2.9	4.2	1.3
98	6.2	2.9	4.3	1.3
99	5.1	2.5	3.0	1.1
100	5.7	2.8	4.1	1.3
101	6.3	3.3	6.0	2.5
102	5.8	2.7	5.1	1.9
103	7.1	3.0	5.9	2.1
104	6.3	2.9	5.6	1.8
105	6.5	3.0	5.8	2.2
106	7.6	3.0	6.6	2.1
107	4.9	2.5	4.5	1.7
108	7.3	2.9	6.3	1.8
109	6.7	2.5	5.8	1.8
110	7.2	3.6	6.1	2.5
111	6.5	3.2	5.1	2.0
112	6.4	2.7	5.3	1.9

```
113          6.8         3.0          5.5         2.1
114          5.7         2.5          5.0         2.0
115          5.8         2.8          5.1         2.4
116          6.4         3.2          5.3         2.3
117          6.5         3.0          5.5         1.8
118          7.7         3.8          6.7         2.2
119          7.7         2.6          6.9         2.3
120          6.0         2.2          5.0         1.5
121          6.9         3.2          5.7         2.3
122          5.6         2.8          4.9         2.0
123          7.7         2.8          6.7         2.0
124          6.3         2.7          4.9         1.8
125          6.7         3.3          5.7         2.1
126          7.2         3.2          6.0         1.8
127          6.2         2.8          4.8         1.8
128          6.1         3.0          4.9         1.8
129          6.4         2.8          5.6         2.1
130          7.2         3.0          5.8         1.6
131          7.4         2.8          6.1         1.9
132          7.9         3.8          6.4         2.0
133          6.4         2.8          5.6         2.2
134          6.3         2.8          5.1         1.5
135          6.1         2.6          5.6         1.4
136          7.7         3.0          6.1         2.3
137          6.3         3.4          5.6         2.4
138          6.4         3.1          5.5         1.8
139          6.0         3.0          4.8         1.8
140          6.9         3.1          5.4         2.1
141          6.7         3.1          5.6         2.4
142          6.9         3.1          5.1         2.3
143          5.8         2.7          5.1         1.9
144          6.8         3.2          5.9         2.3
145          6.7         3.3          5.7         2.5
146          6.7         3.0          5.2         2.3
147          6.3         2.5          5.0         1.9
148          6.5         3.0          5.2         2.0
149          6.2         3.4          5.4         2.3
150          5.9         3.0          5.1         1.8
```

Estatísticas de variáveis contínuas por categoria (neste caso espécie).

```r
iris |>
  group_by(Species) |>
  summarise(xbar_c_pet = mean(Petal.Length),
            sd_c_pet = sd(Petal.Length))
```

```
# A tibble: 3 × 3
  Species    xbar_c_pet sd_c_pet
  <fct>           <dbl>    <dbl>
1 setosa           1.46    0.174
2 versicolor       4.26    0.470
3 virginica        5.55    0.552
```

Para todas as variáveis não agrupadas use `everything()`.

```
iris |>
 group_by(Species) |>
 summarise(across(everything(), list(mean=mean, sd=sd)))
```

```
# A tibble: 3 × 9
  Species    Sepal.Length_mean Sepal.Length_sd Sepal.Width_mean Sepal.Width_sd
  <fct>                  <dbl>           <dbl>            <dbl>          <dbl>
1 setosa                  5.01           0.352             3.43          0.379
2 versicolor              5.94           0.516             2.77          0.314
3 virginica               6.59           0.636             2.97          0.322
# ℹ 4 more variables: Petal.Length_mean <dbl>, Petal.Length_sd <dbl>,
#   Petal.Width_mean <dbl>, Petal.Width_sd <dbl>
```

```
penguins |>
  group_by(species, island) |>
  summarize(qtd = n(), .groups = "drop")
```

```
# A tibble: 5 × 3
  species   island      qtd
  <fct>     <fct>     <int>
1 Adelie    Biscoe       44
2 Adelie    Dream        56
3 Adelie    Torgersen    52
4 Chinstrap Dream        68
5 Gentoo    Biscoe      124
```

```
penguins |>
  group_by(species, island) |>
  summarize(prop = n()/nrow(penguins),
            .groups = "drop")
```

```
# A tibble: 5 × 3
  species   island     prop
  <fct>     <fct>     <dbl>
1 Adelie    Biscoe    0.128
2 Adelie    Dream     0.163
3 Adelie    Torgersen 0.151
4 Chinstrap Dream     0.198
5 Gentoo    Biscoe    0.360
```

```
datasets::penguins |>
  group_by(species, island) |>
  summarize(mean_mass = mean(body_mass, na.rm=T),
            sd_mass = sd(body_mass, na.rm=T),
            .groups = "drop")
```

```
# A tibble: 5 × 4
  species   island    mean_mass sd_mass
  <fct>     <fct>         <dbl>   <dbl>
1 Adelie    Biscoe        3710.    488.
2 Adelie    Dream         3688.    455.
3 Adelie    Torgersen     3706.    445.
```

```
4 Chinstrap Dream          3733.    384.
5 Gentoo    Biscoe         5076.    504.
```

```
penguins <- datasets::penguins
```

Criando novas variáveis com `mutate`.

```
dados2 <- dados |>
  mutate(hp_wt = hp/wt)
head(dados2)
```

```
                   mpg cyl disp  hp drat    wt  qsec vs am gear carb    hp_wt
Mazda RX4         21.0   6  160 110 3.90 2.620 16.46  0  1    4    4 41.98473
Mazda RX4 Wag     21.0   6  160 110 3.90 2.875 17.02  0  1    4    4 38.26087
Datsun 710        22.8   4  108  93 3.85 2.320 18.61  1  1    4    1 40.08621
Hornet 4 Drive    21.4   6  258 110 3.08 3.215 19.44  1  0    3    1 34.21462
Hornet Sportabout 18.7   8  360 175 3.15 3.440 17.02  0  0    3    2 50.87209
Valiant           18.1   6  225 105 2.76 3.460 20.22  1  0    3    1 30.34682
```

```
dados2 |>
  select(qsec, hp_wt) |>
  cor()
```

```
          qsec     hp_wt
qsec   1.000000 -0.798592
hp_wt -0.798592  1.000000
```

Conjunto de dados `starwars`.

```
glimpse(starwars)
```

```
Rows: 87
Columns: 14
$ name       <chr> "Luke Skywalker", "C-3PO", "R2-D2", "Darth Vader", "Leia Or…
$ height     <int> 172, 167, 96, 202, 150, 178, 165, 97, 183, 182, 188, 180, 2…
$ mass       <dbl> 77.0, 75.0, 32.0, 136.0, 49.0, 120.0, 75.0, 32.0, 84.0, 77.…
$ hair_color <chr> "blond", NA, NA, "none", "brown", "brown, grey", "brown", N…
$ skin_color <chr> "fair", "gold", "white, blue", "white", "light", "light", "…
$ eye_color  <chr> "blue", "yellow", "red", "yellow", "brown", "blue", "blue",…
$ birth_year <dbl> 19.0, 112.0, 33.0, 41.9, 19.0, 52.0, 47.0, NA, 24.0, 57.0, …
$ sex        <chr> "male", "none", "none", "male", "female", "male", "female",…
$ gender     <chr> "masculine", "masculine", "masculine", "masculine", "femini…
$ homeworld  <chr> "Tatooine", "Tatooine", "Naboo", "Tatooine", "Alderaan", "T…
$ species    <chr> "Human", "Droid", "Droid", "Human", "Human", "Human", "Huma…
$ films      <list> <"A New Hope", "The Empire Strikes Back", "Return of the J…
$ vehicles   <list> <"Snowspeeder", "Imperial Speeder Bike">, <>, <>, <>, "Imp…
$ starships  <list> <"X-wing", "Imperial shuttle">, <>, <>, "TIE Advanced x1",…
```

```
# ?starwars
```

Calculando imc com mutate

```
sw_ <- starwars |>
  mutate(imc = mass/(height/100)^2)

sw_ |>
  select(name, imc) |>
  head()
```

```
# A tibble: 6 × 2
  name             imc
  <chr>          <dbl>
1 Luke Skywalker  26.0
2 C-3PO           26.9
3 R2-D2           34.7
4 Darth Vader     33.3
5 Leia Organa     21.8
6 Owen Lars       37.9
```

Filtrando segundo condição de interesse.

```
sobrepeso <- sw_ |>
  select(name, imc) |>
  filter(imc >= 25 & imc < 30)

sobrepeso
```

```
# A tibble: 13 × 2
   name                   imc
   <chr>                <dbl>
 1 Luke Skywalker        26.0
 2 C-3PO                 26.9
 3 Beru Whitesun Lars    27.5
 4 Biggs Darklighter     25.1
 5 Wedge Antilles        26.6
 6 Palpatine             26.0
 7 Lando Calrissian      25.2
 8 Lobot                 25.8
 9 Ackbar                25.6
10 Wicket Systri Warrick  25.8
11 Nien Nunb             26.6
12 Darth Maul            26.1
13 Dexter Jettster       26.0
```

Separando dados da espécie “versicolor”.

```
versicolor <- iris |>
  filter(Species == "versicolor") |>
  select(!Species)
head(versicolor)
```

```
  Sepal.Length Sepal.Width Petal.Length Petal.Width
1          7.0         3.2          4.7         1.4
2          6.4         3.2          4.5         1.5
```

```
3          6.9         3.1          4.9         1.5
4          5.5         2.3          4.0         1.3
5          6.5         2.8          4.6         1.5
6          5.7         2.8          4.5         1.3
```

```
iris |>
  filter(Species == "versicolor") |>
  select(!starts_with("S"))
```

```
   Petal.Length Petal.Width
1           4.7         1.4
2           4.5         1.5
3           4.9         1.5
4           4.0         1.3
5           4.6         1.5
6           4.5         1.3
7           4.7         1.6
8           3.3         1.0
9           4.6         1.3
10          3.9         1.4
11          3.5         1.0
12          4.2         1.5
13          4.0         1.0
14          4.7         1.4
15          3.6         1.3
16          4.4         1.4
17          4.5         1.5
18          4.1         1.0
19          4.5         1.5
20          3.9         1.1
21          4.8         1.8
22          4.0         1.3
23          4.9         1.5
24          4.7         1.2
25          4.3         1.3
26          4.4         1.4
27          4.8         1.4
28          5.0         1.7
29          4.5         1.5
30          3.5         1.0
31          3.8         1.1
32          3.7         1.0
33          3.9         1.2
34          5.1         1.6
35          4.5         1.5
36          4.5         1.6
37          4.7         1.5
38          4.4         1.3
39          4.1         1.3
40          4.0         1.3
41          4.4         1.2
42          4.6         1.4
43          4.0         1.2
```

```
44           3.3          1.0
45           4.2          1.3
46           4.2          1.2
47           4.2          1.3
48           4.3          1.3
49           3.0          1.1
50           4.1          1.3
```

```
penguins |>
  group_by(species) |>
  summarise(mean(body_mass, na.rm = T))
```

```
# A tibble: 3 × 2
  species   `mean(body_mass, na.rm = T)`
  <fct>                            <dbl>
1 Adelie                           3701.
2 Chinstrap                        3733.
3 Gentoo                           5076.
```

```
penguins |>
  group_by(species) |>
  filter(body_mass > mean(body_mass, na.rm = T))
```

```
# A tibble: 159 × 8
# Groups:   species [3]
   species island    bill_len bill_dep flipper_len body_mass sex     year
   <fct>   <fct>        <dbl>    <dbl>       <int>     <int> <fct>  <int>
 1 Adelie  Torgersen     39.1     18.7         181      3750 male    2007
 2 Adelie  Torgersen     39.5     17.4         186      3800 female  2007
 3 Adelie  Torgersen     39.2     19.6         195      4675 male    2007
 4 Adelie  Torgersen     42       20.2         190      4250 <NA>    2007
 5 Adelie  Torgersen     38.6     21.2         191      3800 male    2007
 6 Adelie  Torgersen     34.6     21.1         198      4400 male    2007
 7 Adelie  Torgersen     42.5     20.7         197      4500 male    2007
 8 Adelie  Torgersen     46       21.5         194      4200 male    2007
 9 Adelie  Biscoe        35.9     19.2         189      3800 female  2007
10 Adelie  Biscoe        38.2     18.1         185      3950 male    2007
# ℹ 149 more rows
```

Análise bivariada de variáveis qualitativas.

```
penguins |>
  select(species, island) |>
  table()
```

```
           island
species     Biscoe Dream Torgersen
  Adelie        44    56        52
  Chinstrap      0    68         0
  Gentoo       124     0         0
```

```
penguins |>
  select(species, island) |>
  table()/nrow(penguins)
```

```
           island
species        Biscoe     Dream Torgersen
  Adelie    0.1279070 0.1627907 0.1511628
  Chinstrap 0.0000000 0.1976744 0.0000000
  Gentoo    0.3604651 0.0000000 0.0000000
```

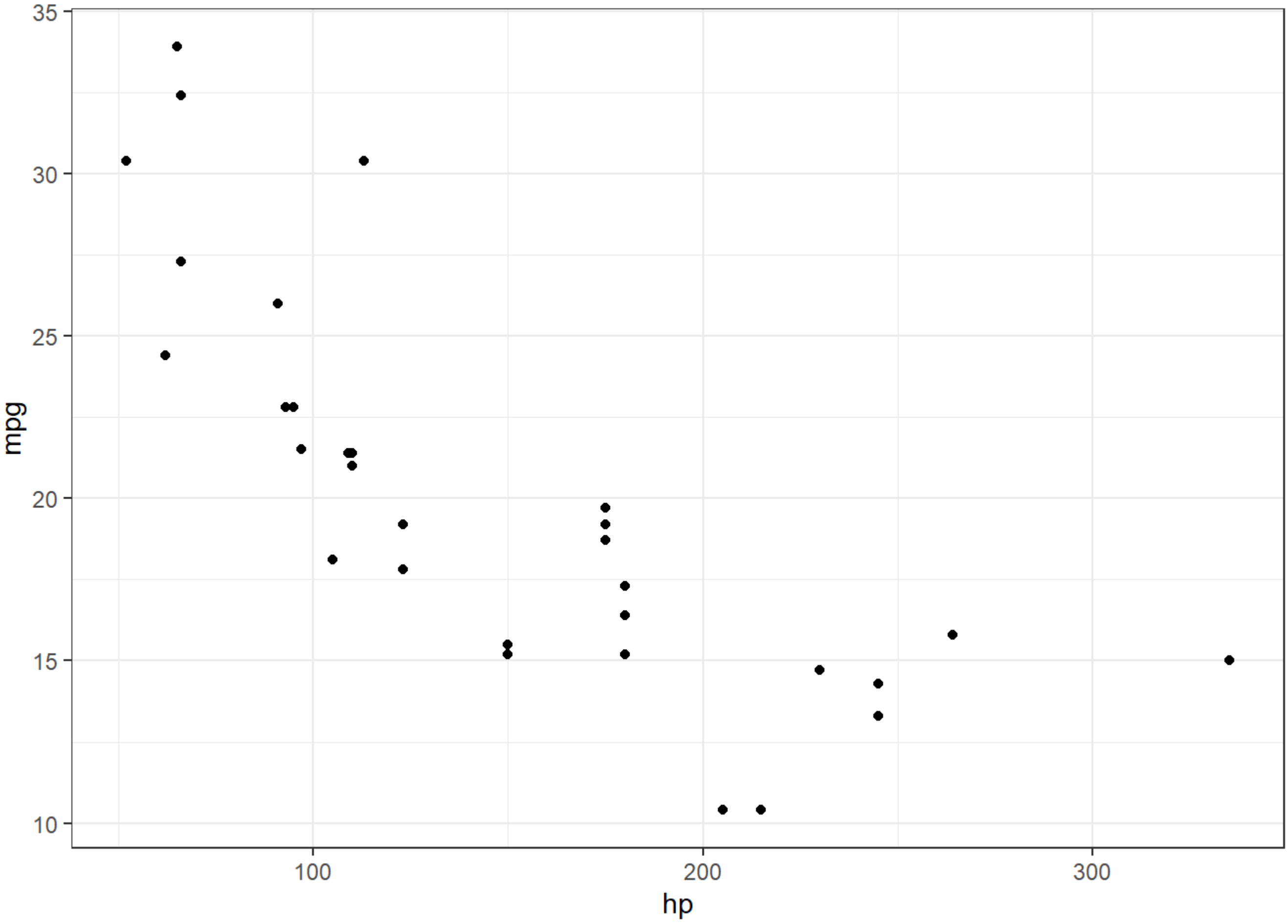
```
dados |>
  select(gear, carb) |>
  table()
```

```
    carb
gear 1 2 3 4 6 8
   3 3 4 3 5 0 0
   4 4 4 0 4 0 0
   5 0 2 0 1 1 1
```

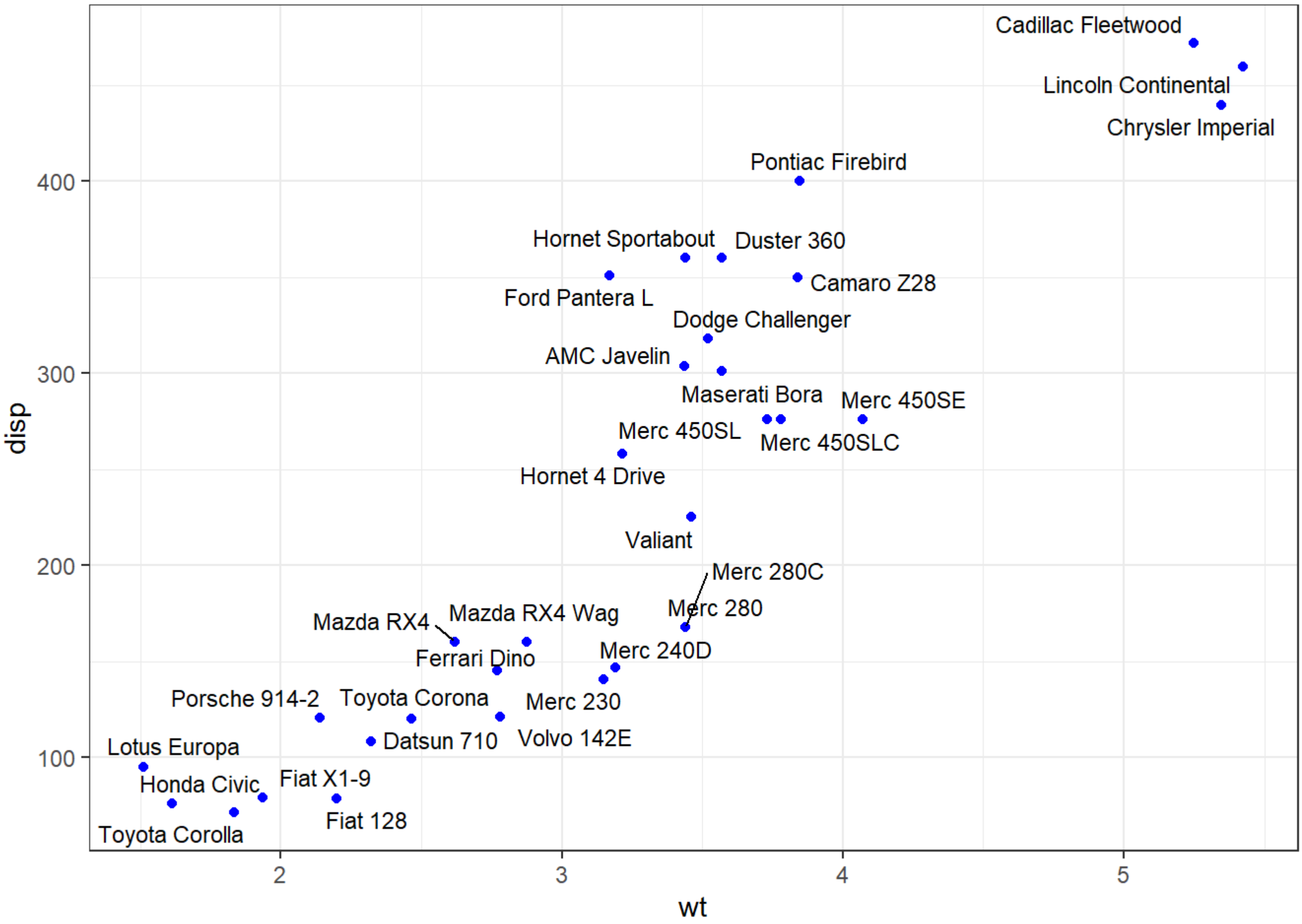
Análise gráfica

```
library(ggplot2)
library(ggrepel)
library(corrplot)
library(GGally)
library(ggridges)
```

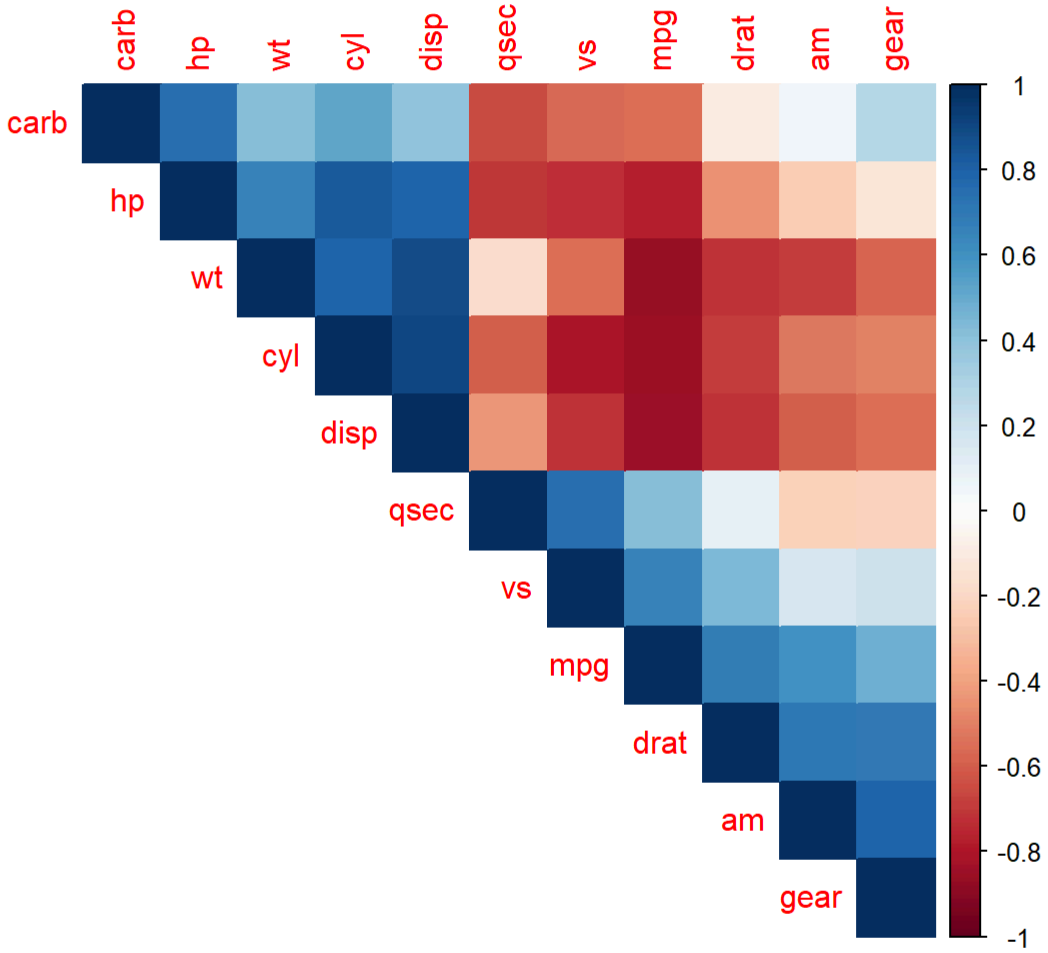
```
theme_set(theme_bw())
ggplot(data = dados,
       mapping = aes(x = hp, y = mpg)) +
  geom_point()
```



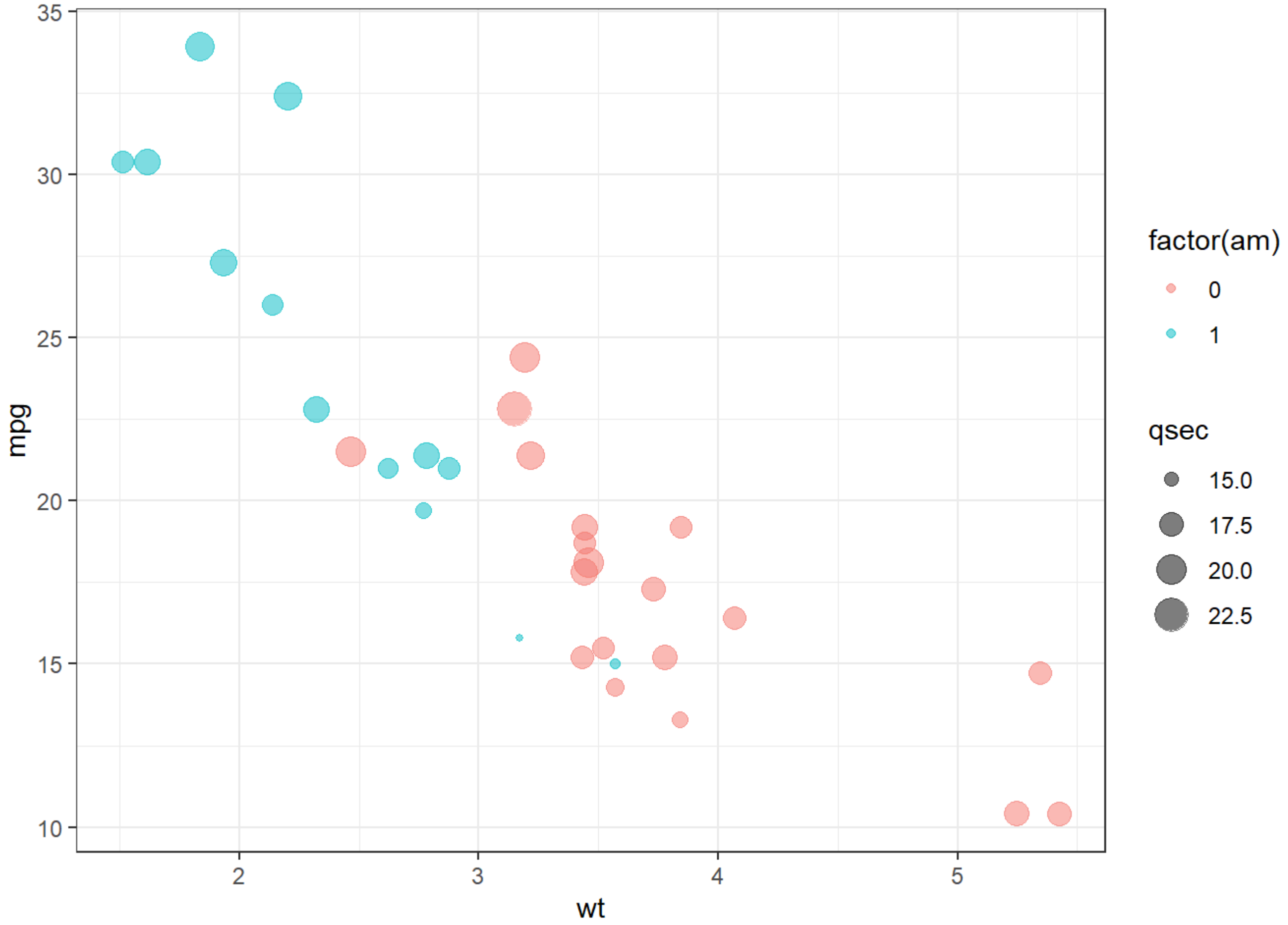

```
dados2 <- dados2 |>
  mutate(car = rownames(dados2))

p <- ggplot(dados2, aes(wt, disp, label = car)) +
  geom_point(color = "blue")

p + geom_text_repel(size = 3)
```



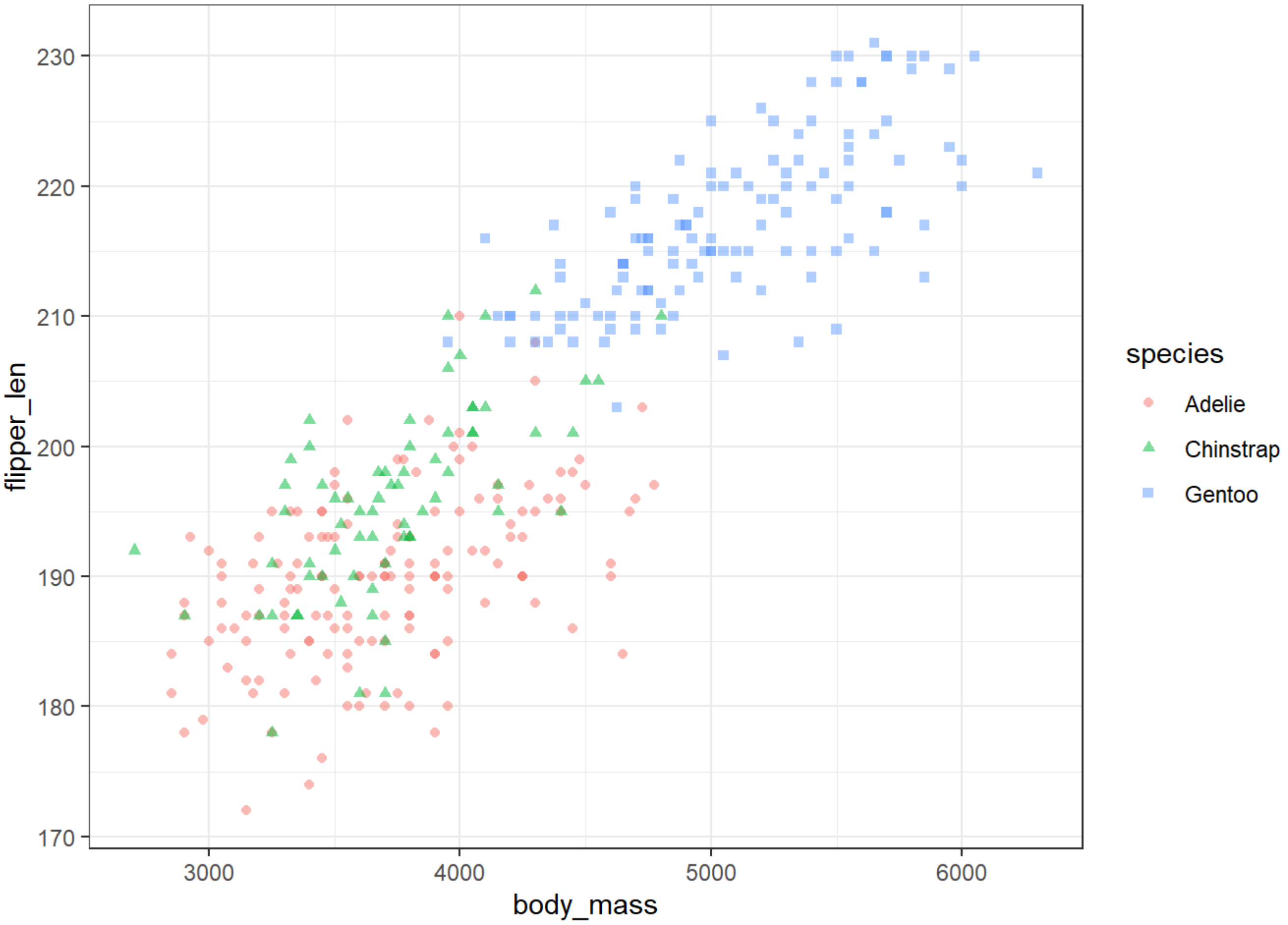

```
r <- cor(dados)

corrplot(r,
         method = "color",
         type = "upper",
         hclust.method = "centroid",
         order = "hclust")
```



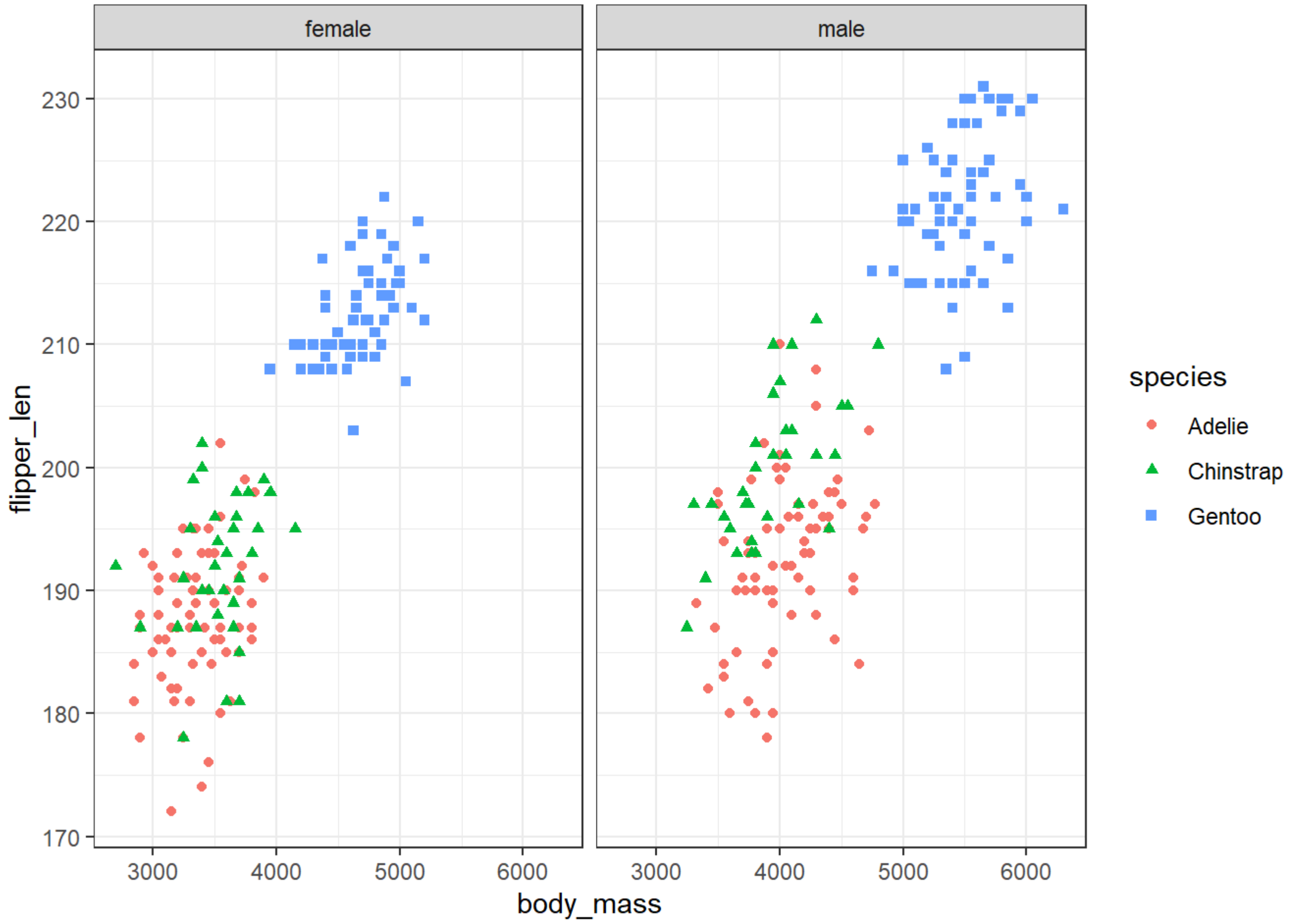

```r
ggplot(data = dados,
       mapping = aes(x = wt,
                     y = mpg,
                     size = qsec,
                     col = factor(am))) +
  geom_point(alpha = .5)
```



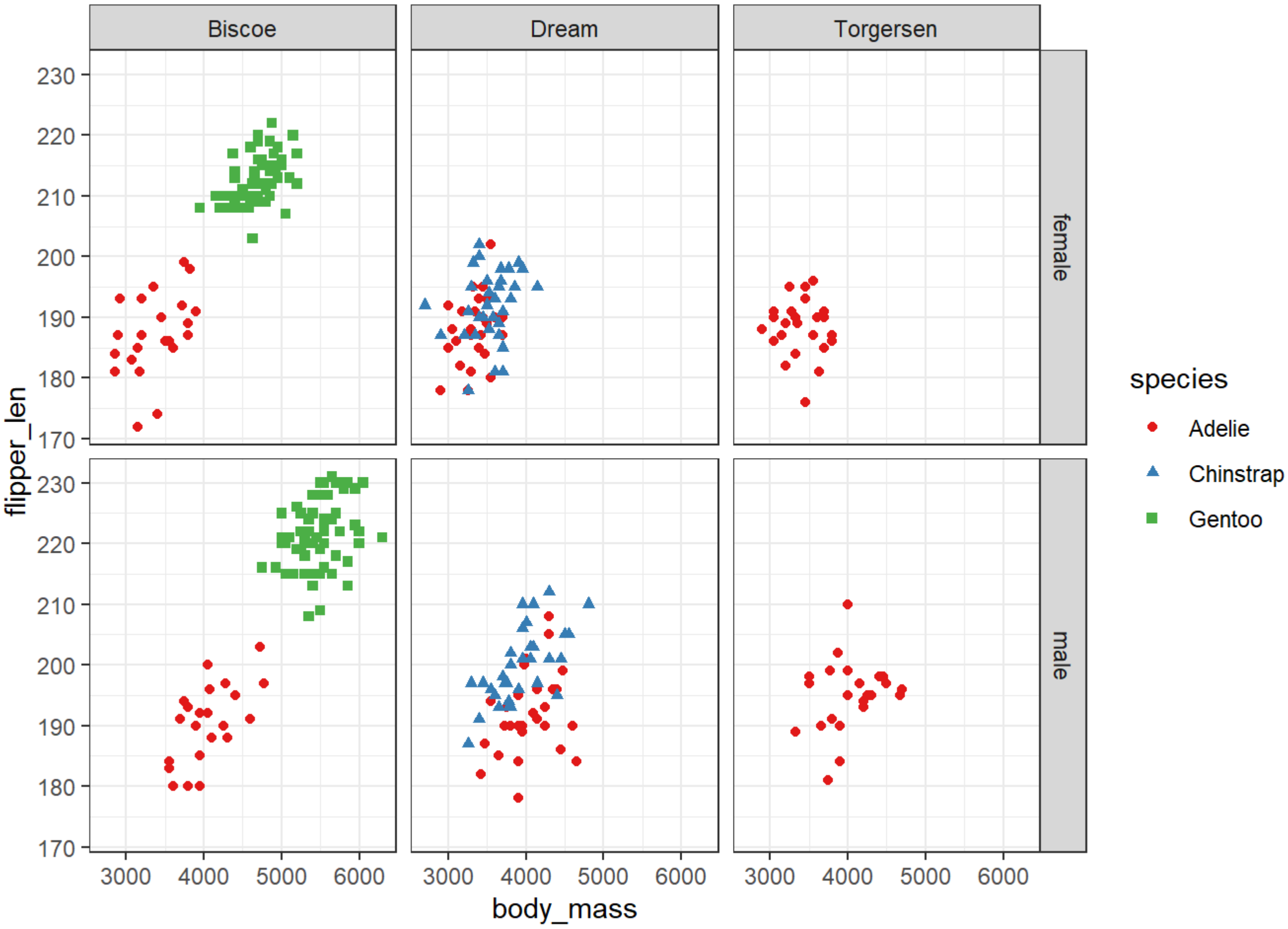

```
penguins |>
  ggplot(aes(x = body_mass, y = flipper_len,
             col = species,
             pch = species)) +
  geom_point(alpha = .5)
```



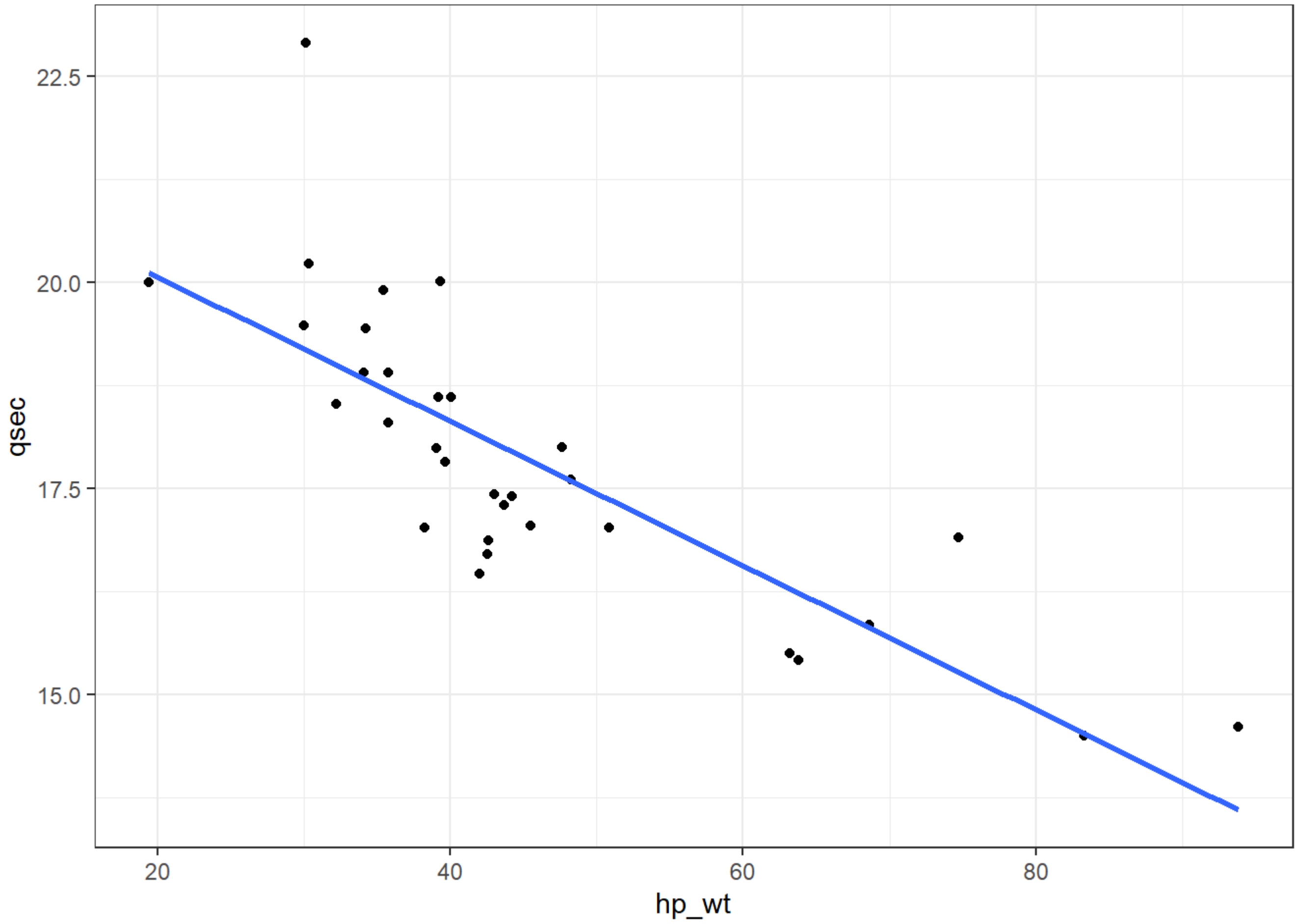

```
penguins |>
  na.exclude() |>
  ggplot(aes(x = body_mass, y = flipper_len,
             col = species,
             pch = species)) +
  facet_grid(cols = vars(sex)) +
  geom_point()
```



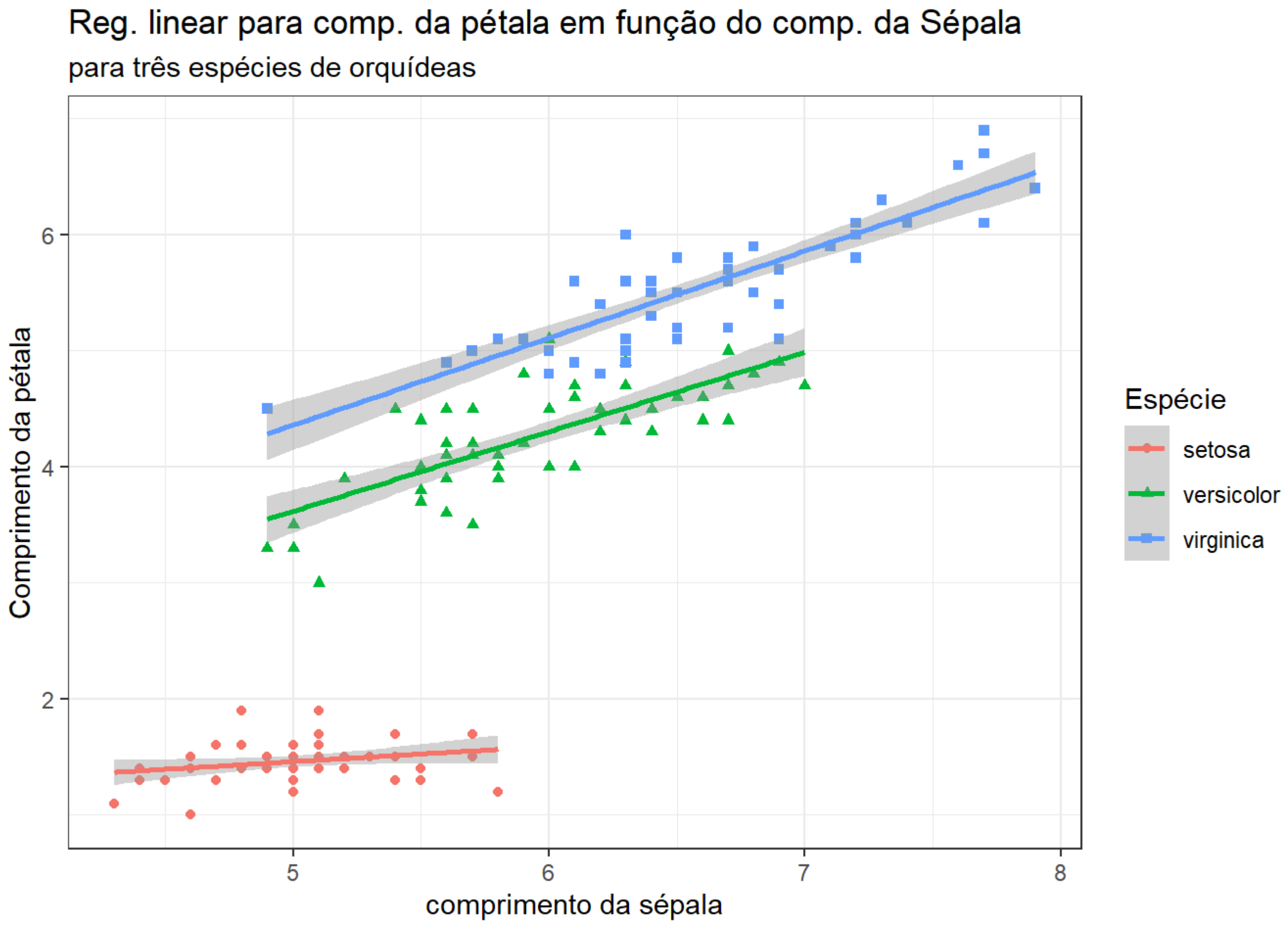

```r
penguins |>
  na.exclude() |>
  ggplot(aes(x = body_mass, y = flipper_len,
             col = species,
             pch = species)) +
  facet_grid(sex ~ island) +
  geom_point() +
  scale_color_brewer(palette="Set1")
```



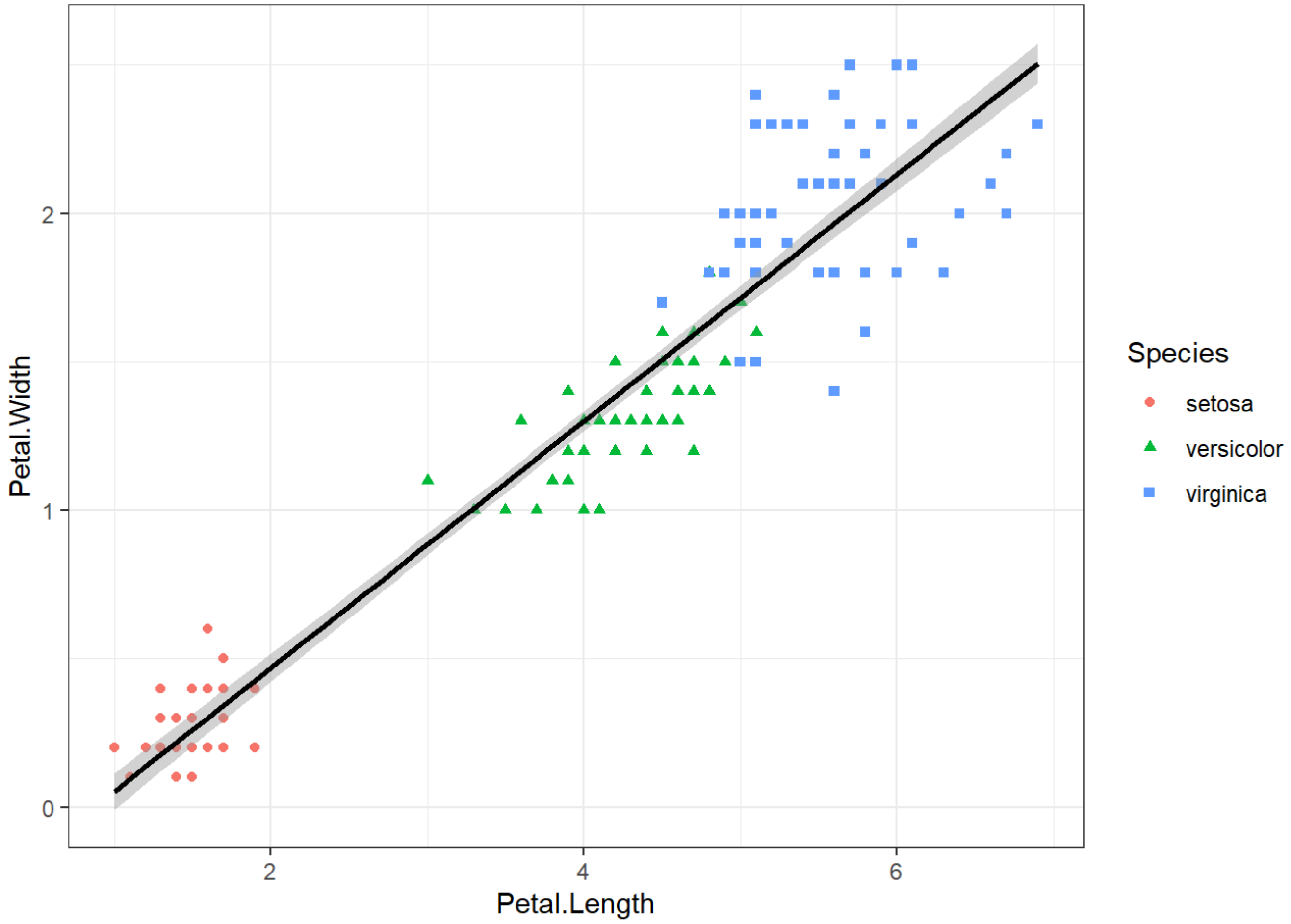

```
ggplot(data = dados2,
       aes(x = hp_wt, y = qsec)) +
  geom_point() +
  geom_smooth(method = lm, se = F)
```



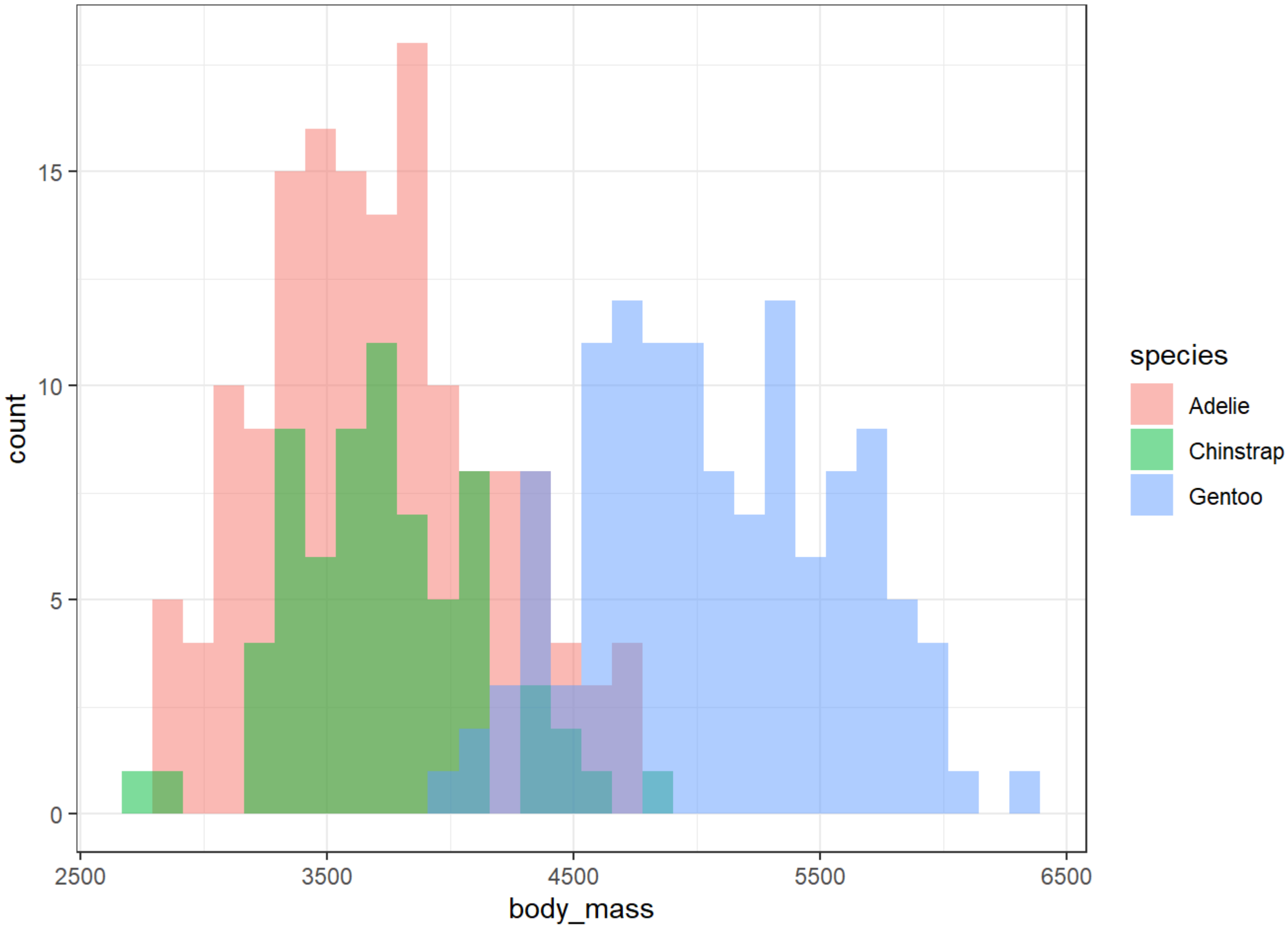

```
ggplot(iris, aes(x=Sepal.Length,
                 y=Petal.Length,
                 col = Species,
                 pch = Species)) +
  geom_point() +
  geom_smooth(method = "lm", formula = y~x) +
  labs(x = "comprimento da sépala",
       y = "Comprimento da pétala",
       col = "Espécie",
       pch = "Espécie",
       title = "Reg. linear para comp. da pétala em função do comp. da Sépala",
       subtitle = "para três espécies de orquídeas")
```



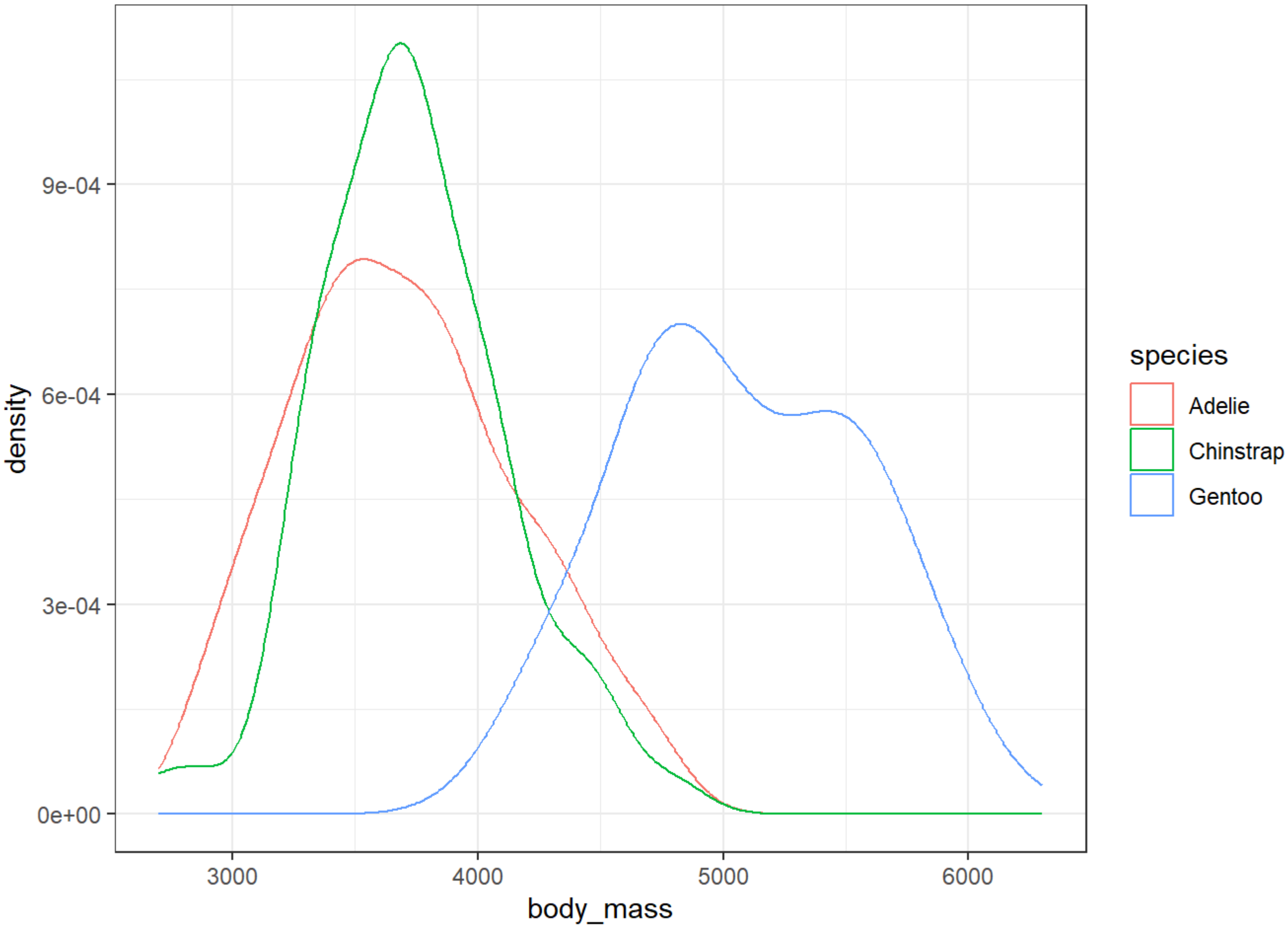

```
ggplot(iris, aes(x=Petal.Length,
                 y=Petal.Width)) +
  geom_point(aes(col = Species,
                 pch = Species)) +
  geom_smooth(method = "lm",
              formula = y~x,
              col = "black")
```



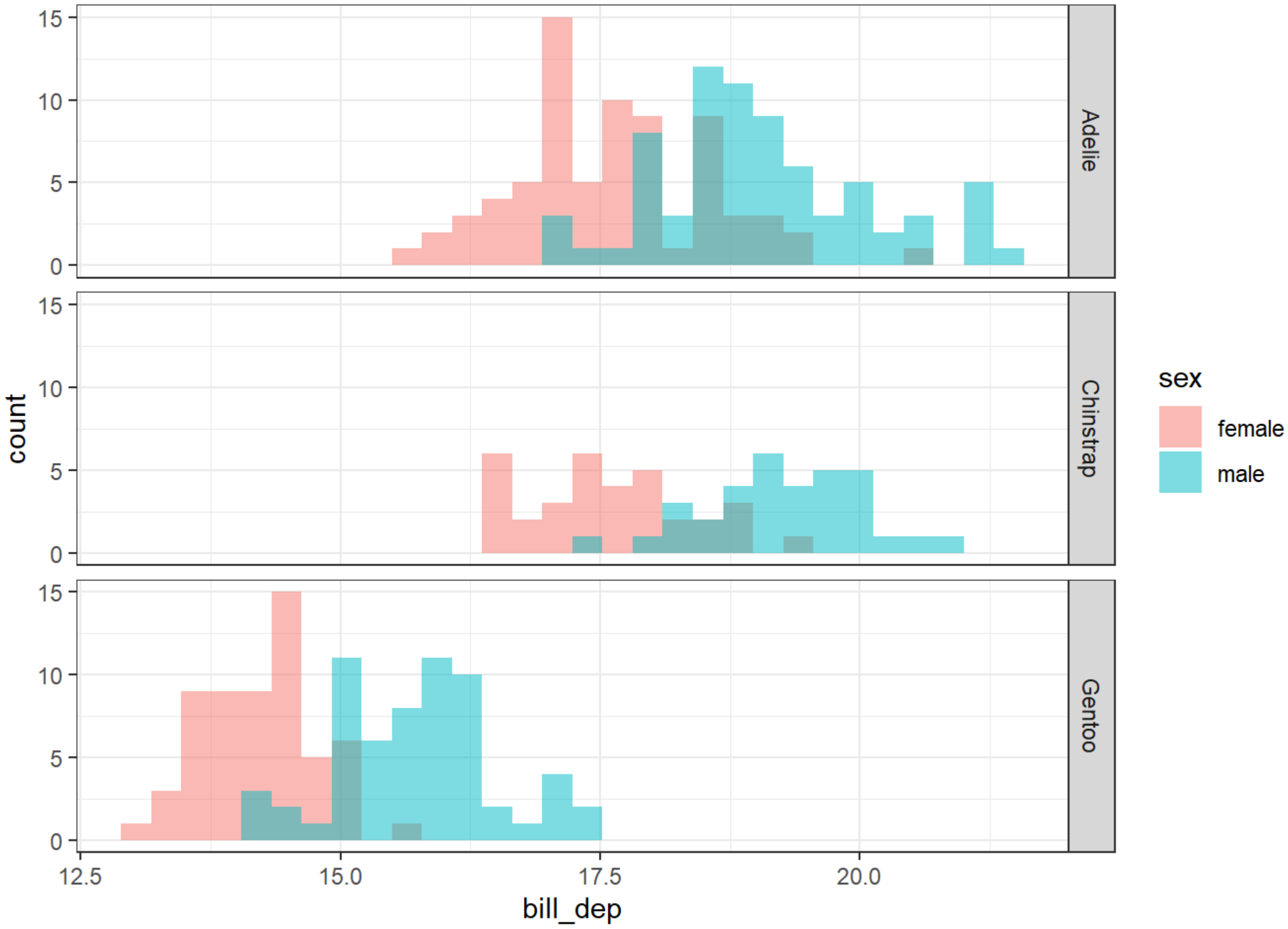

```
ggplot(penguins, aes(x = body_mass,
                     fill = species)) +
  geom_histogram(alpha = .5, position = 'identity')
```



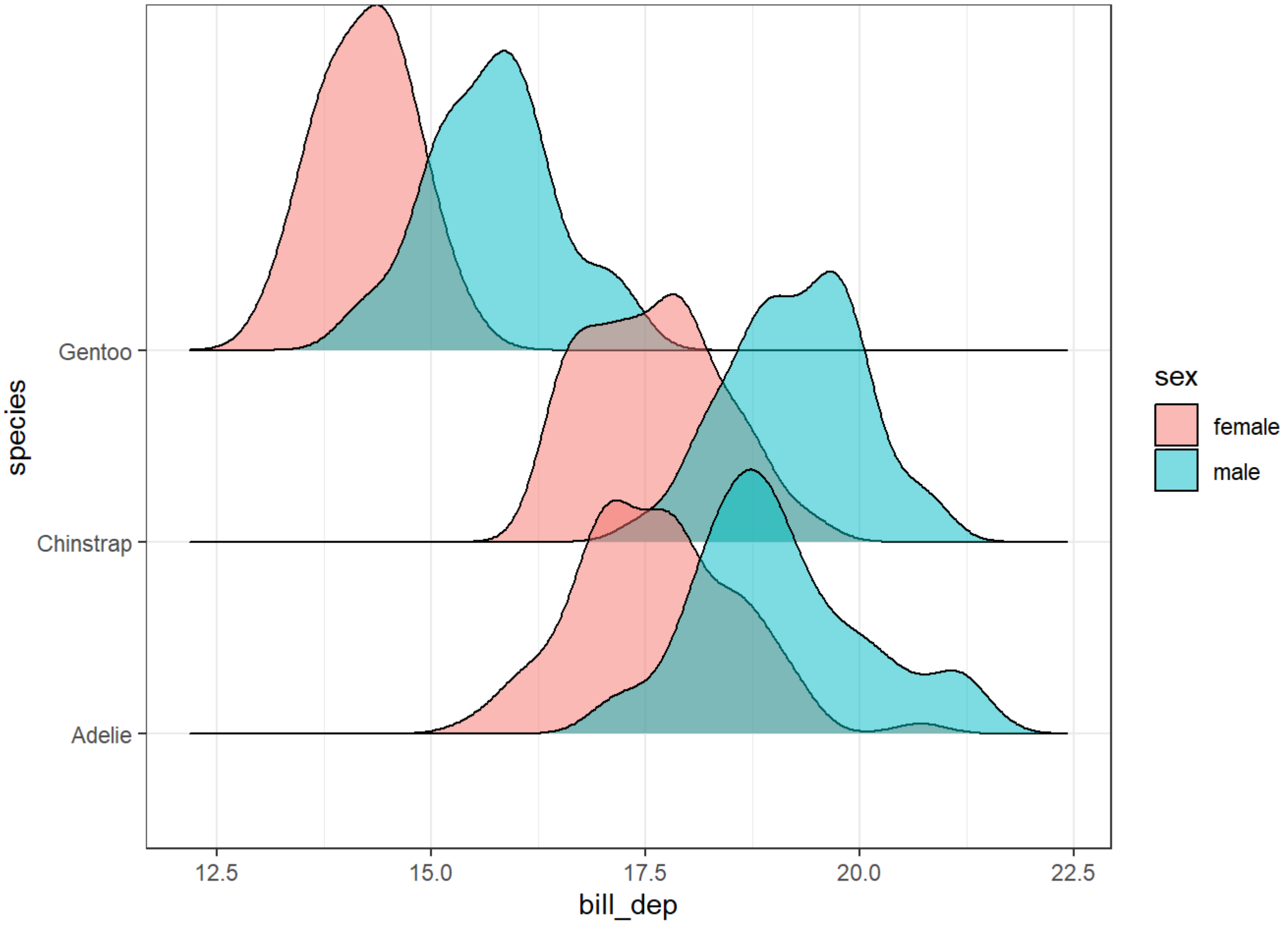

```
ggplot(penguins, aes(x = body_mass,
                     col = species)) +
  geom_density(position = 'identity')
```




```
ggplot(penguins |> na.omit(), aes(x = bill_dep,
                     fill = sex)) +
  geom_histogram(alpha = .5, position = 'identity') +
  facet_grid(rows = vars(species))
```

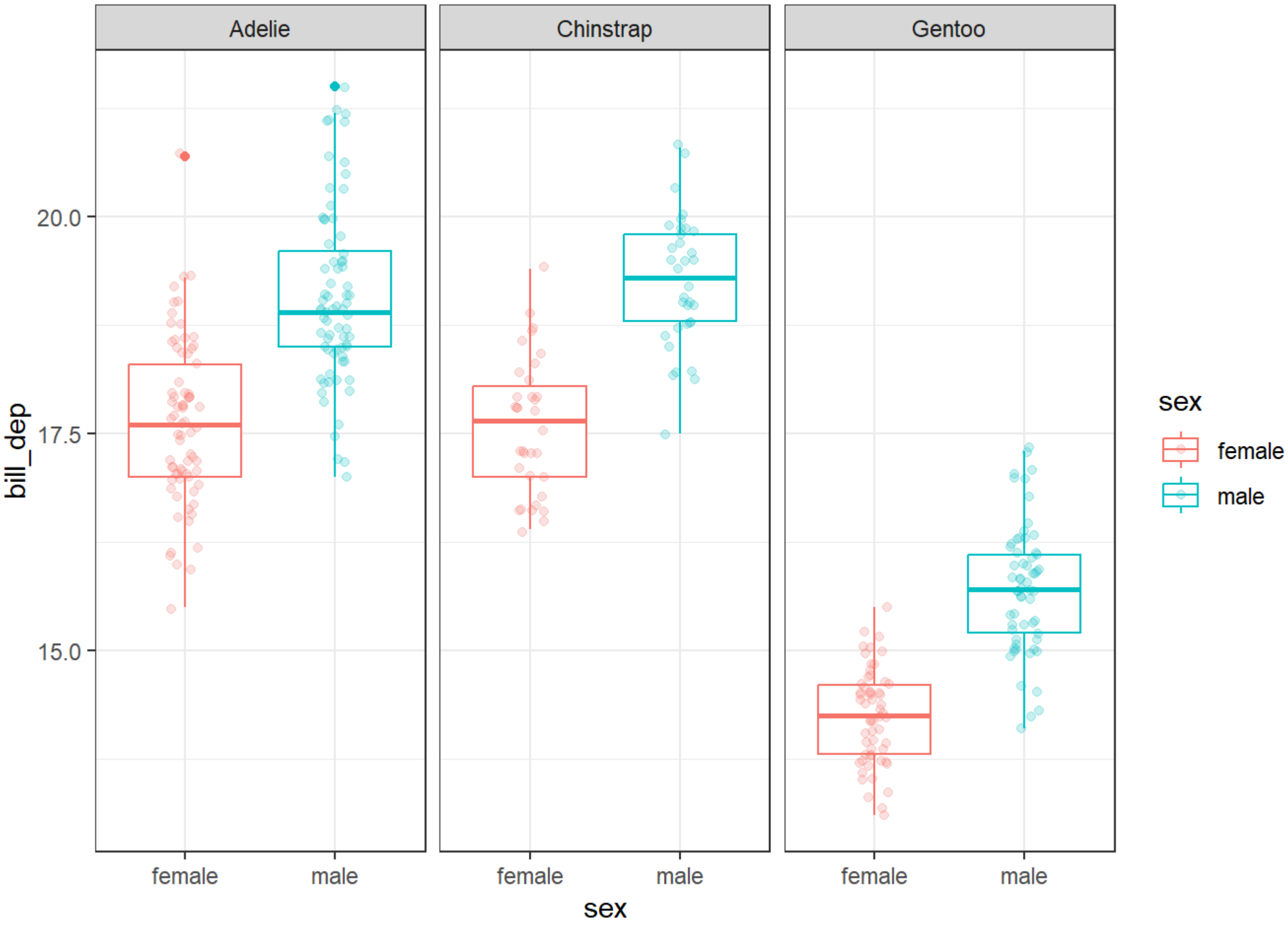



```
ggplot(penguins |>
         na.omit(),
       aes(x = bill_dep,
           y = species,
           fill = sex)) +
  geom_density_ridges(alpha = .5)
```

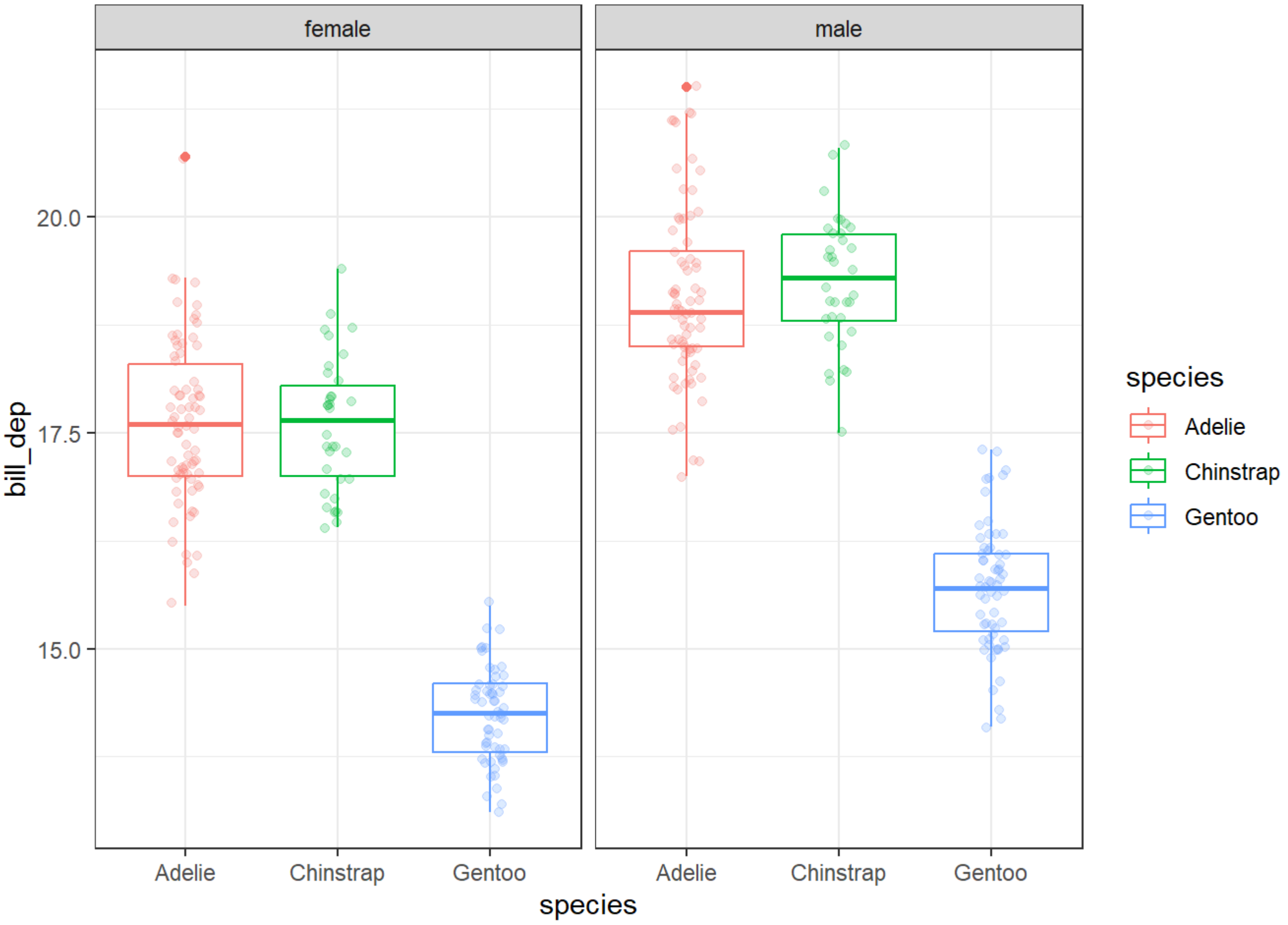


Boxplots.

```
ggplot(penguins |> na.omit(),
       aes(x = sex,
           y = bill_dep,
           col = sex)) +
  facet_grid(~species) +
  geom_boxplot() +
  geom_jitter(alpha = .2, width = .1)
```

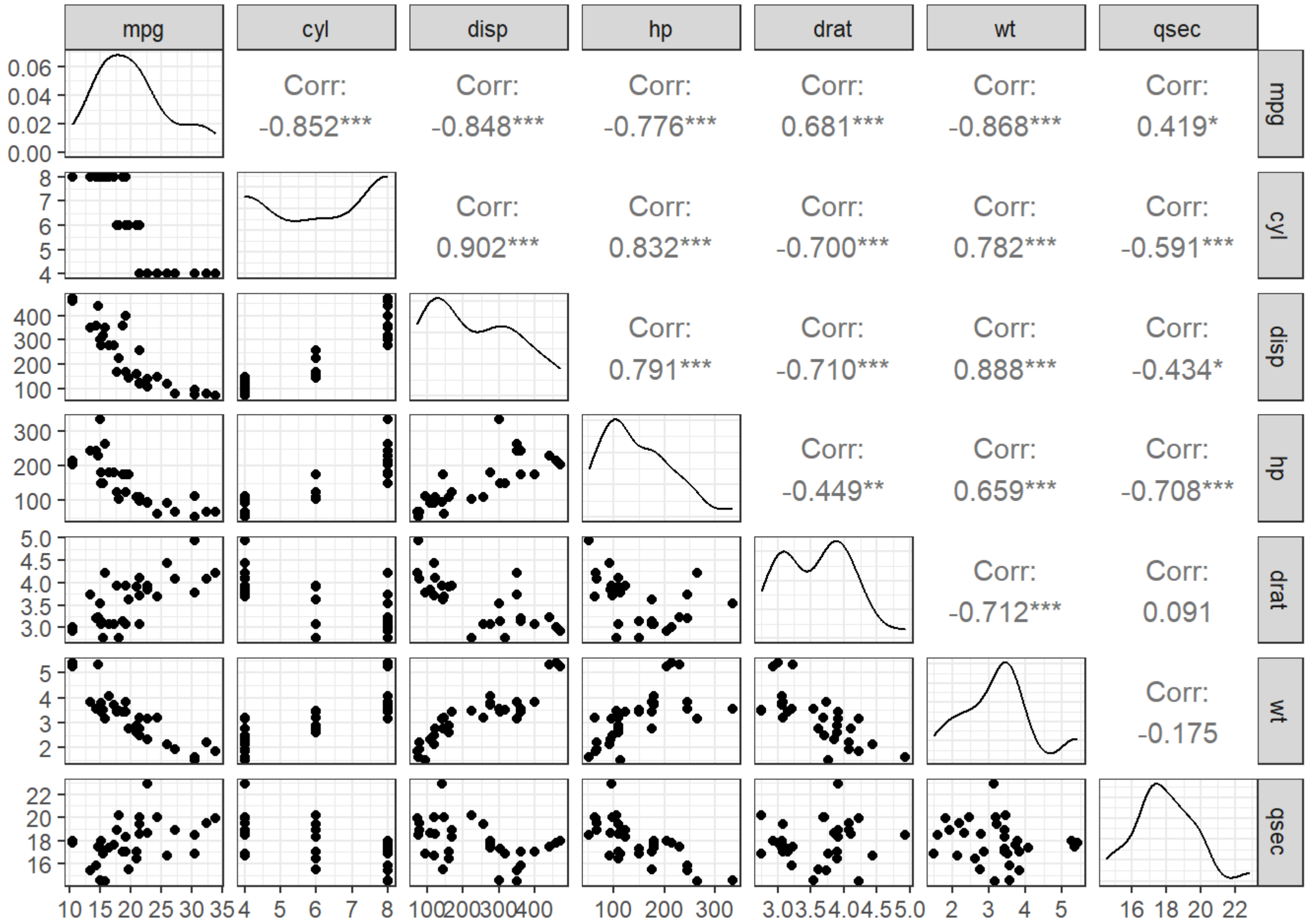



```
ggplot(penguins |> na.omit(),
       aes(x = species,
           y = bill_dep,
           col = species)) +
  facet_grid(~sex) +
  geom_boxplot() +
  geom_jitter(alpha = .2, width = .1)
```

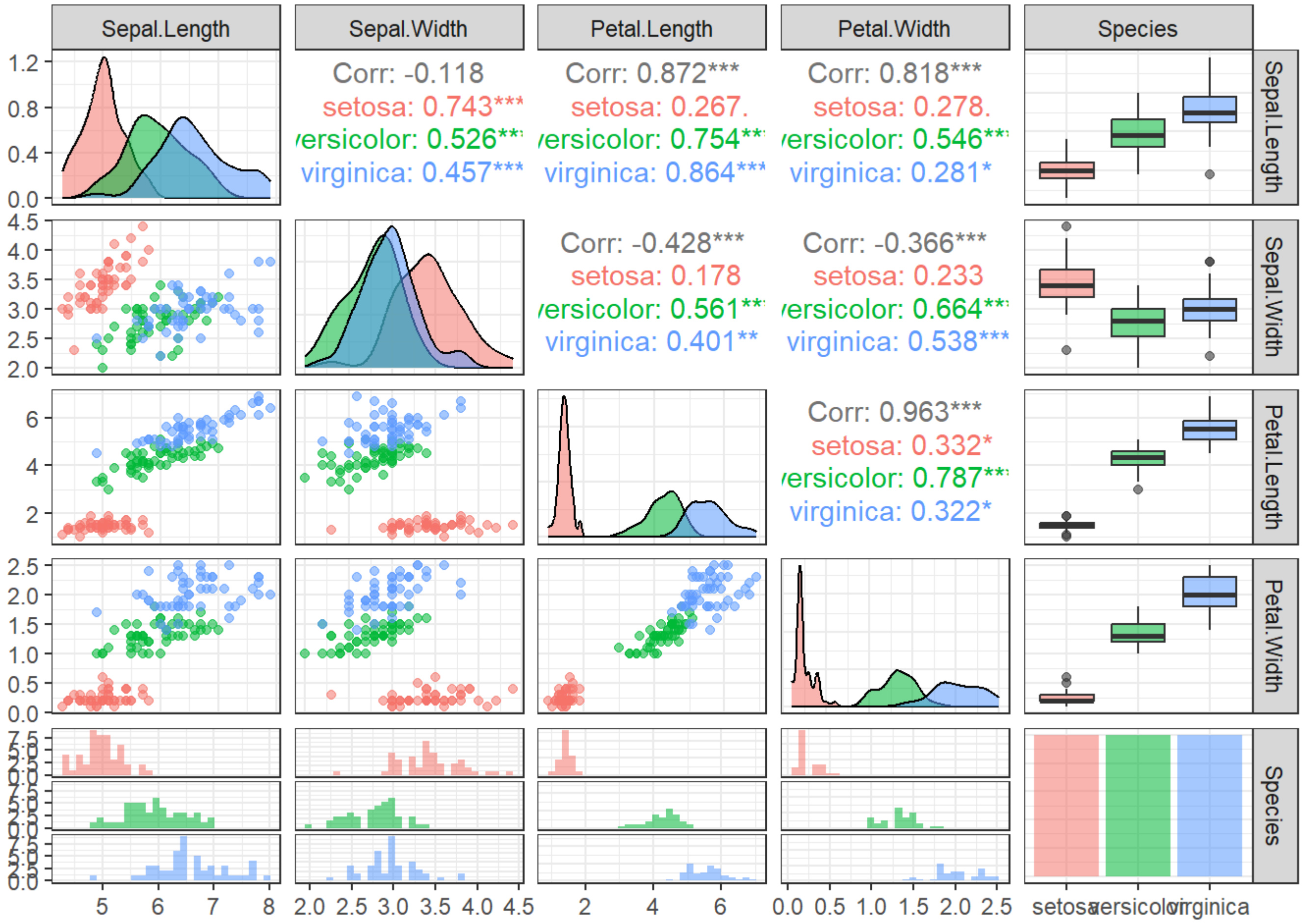


Matriz de gráficos aos pares de variáveis.

```
ggpairs(dados[,1:7], progress = F)
```

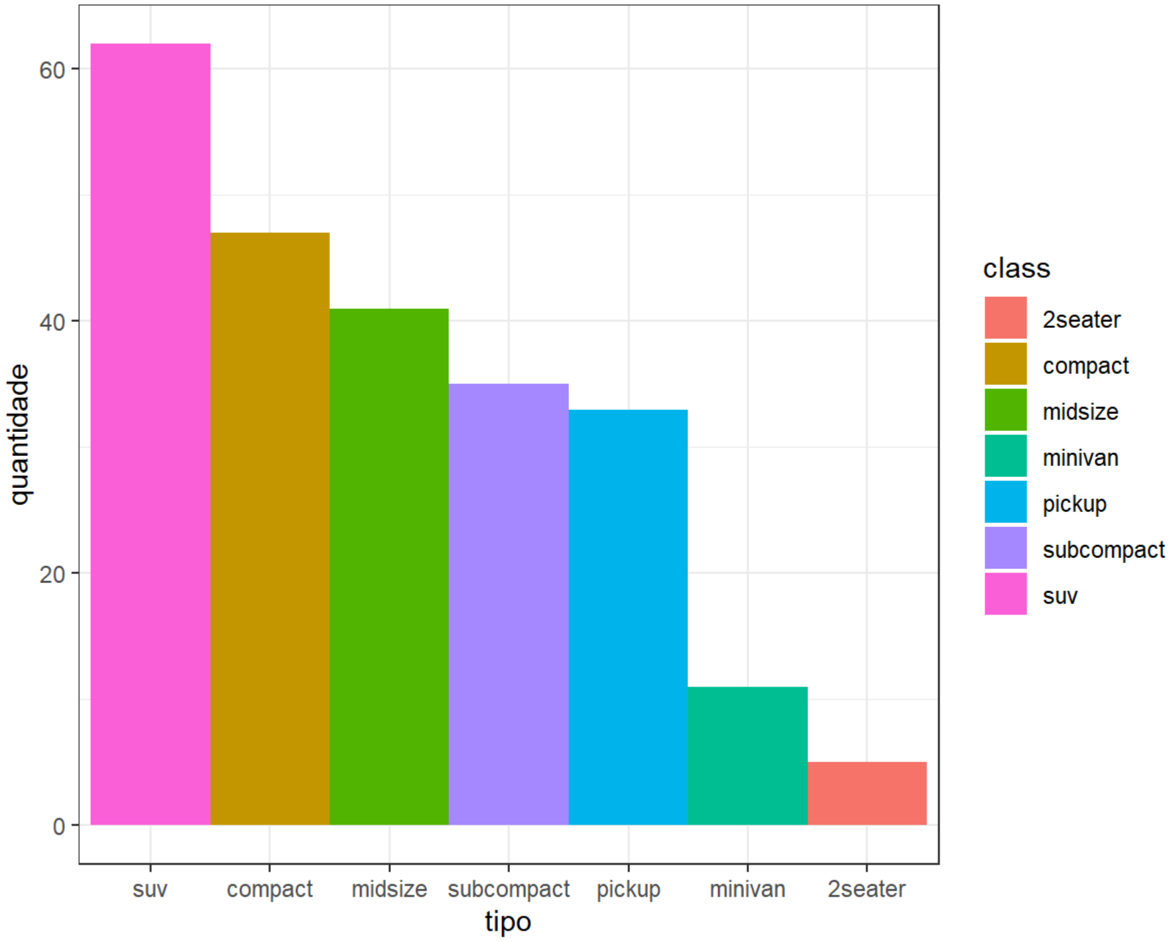



```
ggpairs(iris |> na.omit(),
        aes(color = Species,
            alpha =.5),
        progress = F)
```

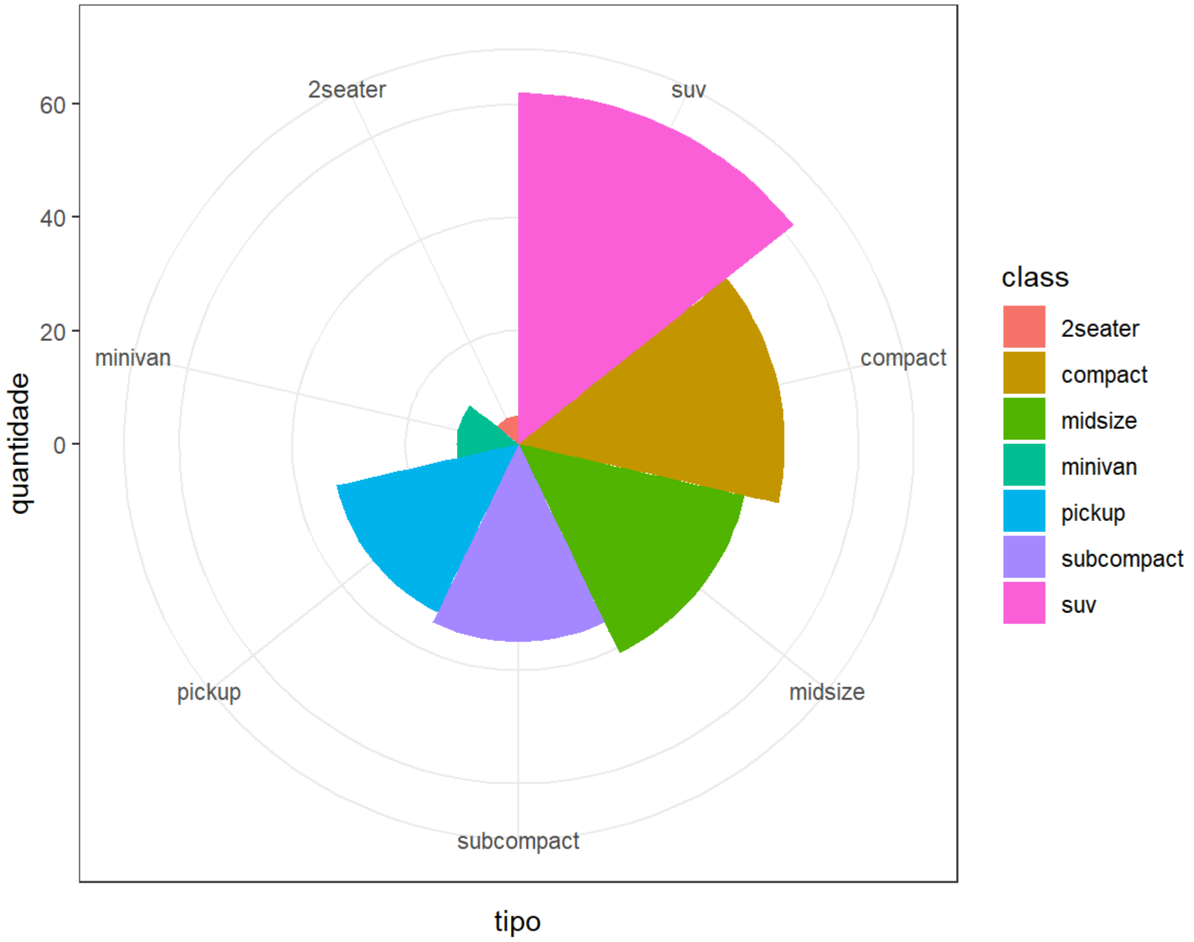


Gráficos de barras.

```
bar <- mpg |>
  count(class) |>
  ggplot(aes(x = reorder(class, -n), y = n, fill = class),
         show.legend = FALSE) +
  geom_bar(stat="identity", width = 1) +
  labs(x = "tipo", y = "quantidade") +
  theme(aspect.ratio = 1)


bar #+ coord_flip()
```




```
bar + coord_polar()
```



Aprendizado supervisionado

Regressão linear múltipla para preço do Petróleo em função do grau de pureza e teor de enxofre

```
library(AER) # USCrudes
```

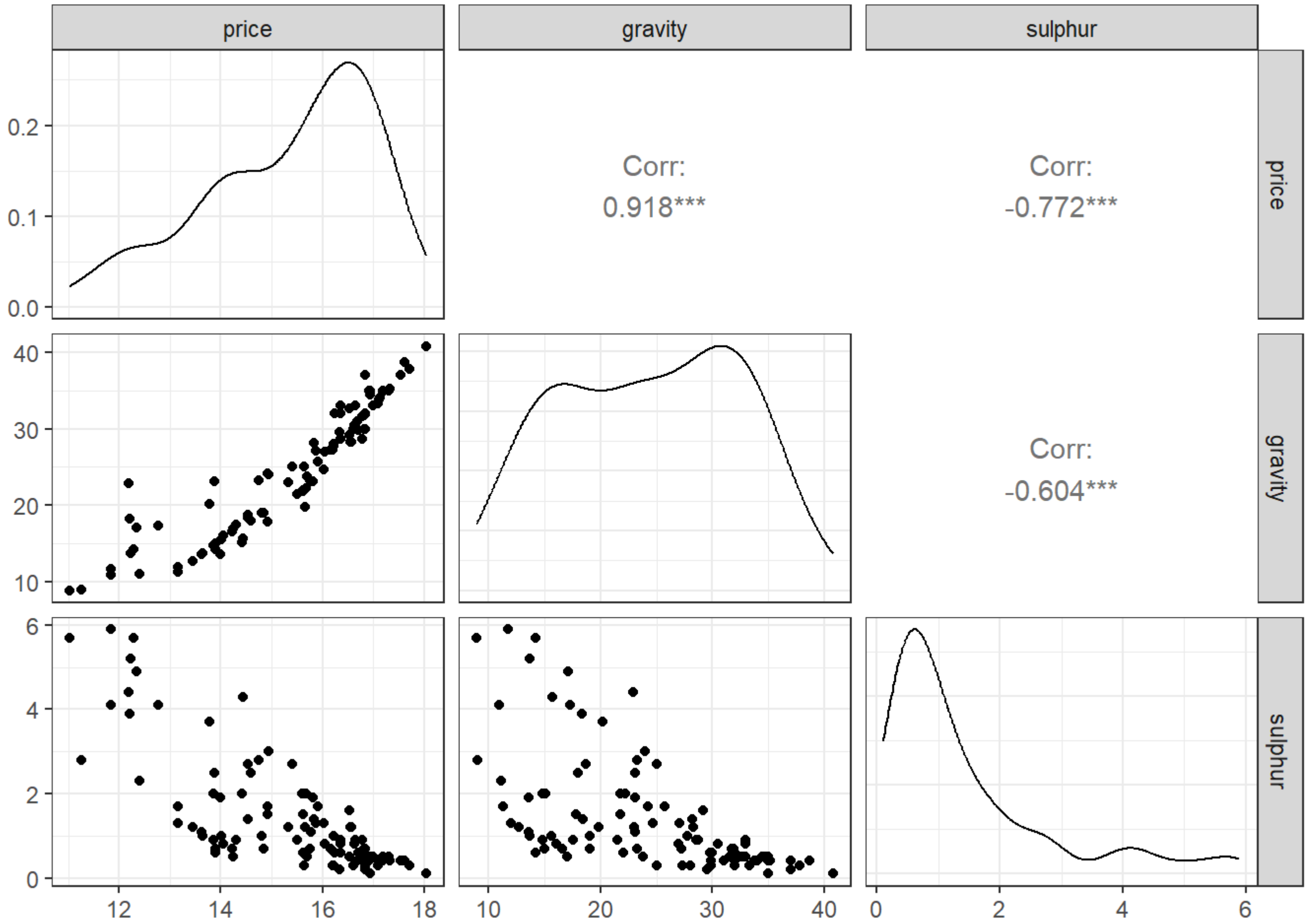
Dados de purza, teor de enxofre e preço de 99 poços de Petróleo dos EUA.

```
data("USCrudes") # sempre que usar dados de um pacote específico
glimpse(USCrudes)
```

```
Rows: 99
Columns: 3
$ price   <dbl> 13.86, 16.82, 13.65, 16.53, 15.66, 16.16, 18.05, 14.93, 16.57,…
$ gravity <dbl> 14.8, 31.7, 13.7, 29.2, 19.8, 27.2, 40.8, 24.2, 28.3, 32.6, 16…
$ sulphur <dbl> 2.0, 0.7, 1.0, 1.6, 1.2, 0.7, 0.1, 1.7, 1.2, 0.5, 0.7, 4.3, 0.…
```

```
# ?USCrudes
```

```
ggpairs(USCrudes, progress = F)
```



Seprando dados de treino e teste.

```
treino <- sample(nrow(USCrudes),
                 0.8*nrow(USCrudes),
                 replace = F)

dados.treino <- USCrudes[treino,]
dados.teste <- USCrudes[-treino,]
```

Modelo de regressão múltipla.

```
lm1 <- lm(price ~ scale(gravity) + scale(sulphur), dados.treino)
summary(lm1)
```

```
Call:
lm(formula = price ~ scale(gravity) + scale(sulphur), data = dados.treino)

Residuals:
     Min       1Q   Median       3Q      Max 
-1.64184 -0.27941 -0.01474  0.28608  1.62328 

Coefficients:
               Estimate Std. Error t value Pr(>|t|)    
(Intercept)    15.28430    0.05879  259.99  < 2e-16 ***
scale(gravity)  1.15659    0.07426   15.57  < 2e-16 ***
scale(sulphur) -0.60080    0.07426   -8.09 7.39e-12 ***
```

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.5225 on 76 degrees of freedom
Multiple R-squared:  0.9051,    Adjusted R-squared:  0.9026
F-statistic: 362.6 on 2 and 76 DF,  p-value: < 2.2e-16
```

Métricas de desempenho para avaliar o modelo.

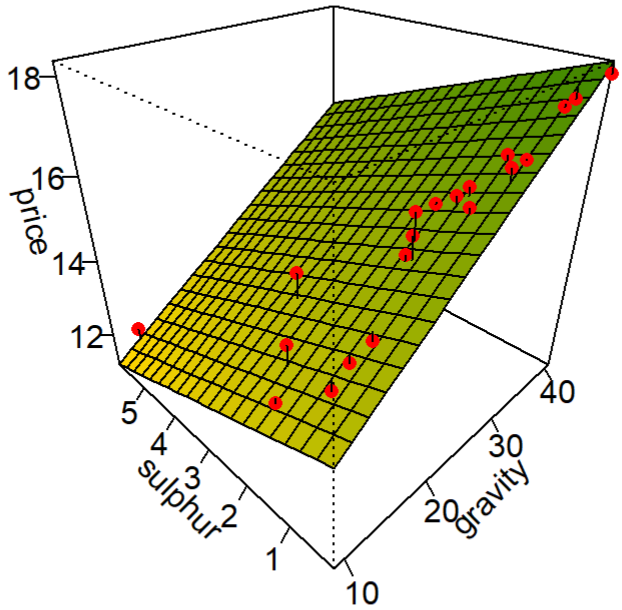
```r
metrics <- function(obs, pred) {

  RSE <- sum((obs - pred)^2)
  SST <- sum((obs - mean(obs))^2)
  R2 <- 1 - RSE/SST

  MAE <-  mean(abs(obs - pred))

  RMSE <- sqrt(mean((obs - pred)^2))

  return(
    data.frame(RMSE = RMSE,
               MAE = MAE,
               R2 = R2))
}
```

```r
pred <- predict(lm1, newdata = dados.teste)

metrics(dados.teste$price, pred)
```

```
       RMSE       MAE        R2
1 0.2992358 0.2476817 0.9654462
```

```r
xs <- seq(min(USCrudes$gravity), max(USCrudes$gravity), length = 20)
ys <- seq(min(USCrudes$sulphur), max(USCrudes$sulphur), length = 20)
xys <- expand.grid(xs,ys)
colnames(xys) <- c("gravity", "sulphur")

zs <- matrix(predict(lm1, xys), nrow = length(xs))

n.cols <- 100
palette <- colorRampPalette(c("gold", "chartreuse4"))(n.cols)
zfacet <- zs[-1, -1] + zs[-1, -20] + zs[-20, -1] + zs[-20, -20]
facetcol <- cut(zfacet, n.cols)

par(mfrow = c(1,1))
p1 <- persp(x=xs, y=ys, z=zs, theta=-45, phi=30, ticktype='detailed',
            xlab="gravity", ylab="sulphur", zlab="price", col = palette[facetcol])

obs <- with(USCrudes[-treino,], trans3d(gravity,sulphur,price,p1))

pred <- with(USCrudes[-treino,], trans3d(gravity,sulphur,predict(lm1,newdata = USCrudes[-trein
```

```
points(obs, col = "red", pch = 16)
segments(obs$x, obs$y, pred$x, pred$y)
```



Usando pacote tidymodels para testar distintos modelos

```
library(tidymodels)
library(finetune) # para grid search
```

```
set.seed(16)
dados_split <- initial_split(USCrudes,
                             prop = 0.75)

dados_train <- training(dados_split)
dados_test  <- testing(dados_split)

set.seed(17)
dados_folds <-
  vfold_cv(v = 5, dados_train)
```

```
normalized_rec <-
  recipe(price ~ .,
         data = dados_train) |>
  step_normalize(all_numeric_predictors())
```

```
linear_reg_spec <-
  linear_reg(penalty = tune(), mixture = tune()) |>
  set_engine("glmnet")

rforest_spec <- rand_forest(mtry = tune(), min_n = tune(), trees = tune()) |>
  set_engine("ranger") |>
  set_mode("regression")

xgb_spec <- # evolution of GBM
  boost_tree(tree_depth = tune(), learn_rate = tune(), loss_reduction = tune(),
             min_n = tune(), sample_size = tune(), trees = tune()) |>
  set_engine("xgboost") |>
  set_mode("regression")

nnet_spec <-
  mlp(hidden_units = tune(), penalty = tune(), epochs = tune()) |>
  set_engine("nnet", MaxNWts = 2600) |>
  set_mode("regression")

nnet_param <-
  nnet_spec |>
  extract_parameter_set_dials() |>
  update(hidden_units = hidden_units(c(1, 27)))
```

```
normalized <-
  workflow_set(
    preproc = list(normalized = normalized_rec),
    models = list(linear_reg = linear_reg_spec,
                  rforest = rforest_spec,
                  neural_network = nnet_spec)
  )
normalized
```

```
# A workflow set/tibble: 3 × 4
  wflow_id                  info             option    result
  <chr>                     <list>           <list>    <list>
1 normalized_linear_reg     <tibble [1 × 4]> <opts[0]> <list [0]>
2 normalized_rforest        <tibble [1 × 4]> <opts[0]> <list [0]>
3 normalized_neural_network <tibble [1 × 4]> <opts[0]> <list [0]>
```

```
all_workflows <-
  bind_rows(normalized) |>
  # Make the workflow ID's a little more simple:
  mutate(wflow_id = gsub("(simple_)|(normalized_)", "", wflow_id))
all_workflows
```

```
# A workflow set/tibble: 3 × 4
  wflow_id       info             option    result
  <chr>          <list>           <list>    <list>
1 linear_reg     <tibble [1 × 4]> <opts[0]> <list [0]>
2 rforest        <tibble [1 × 4]> <opts[0]> <list [0]>
3 neural_network <tibble [1 × 4]> <opts[0]> <list [0]>
```

```
race_ctrl <-
  control_race(
    save_pred = TRUE,
    parallel_over = "everything",
    save_workflow = TRUE
  )

race_results <-
  all_workflows |>
  workflow_map(
    "tune_race_anova",
    seed = 1503,
    resamples = dados_folds,
    grid = 25,
    control = race_ctrl
  )
```

```
collect_metrics(race_results) |>
  filter(.metric == "rmse") |>
  arrange(mean)
```

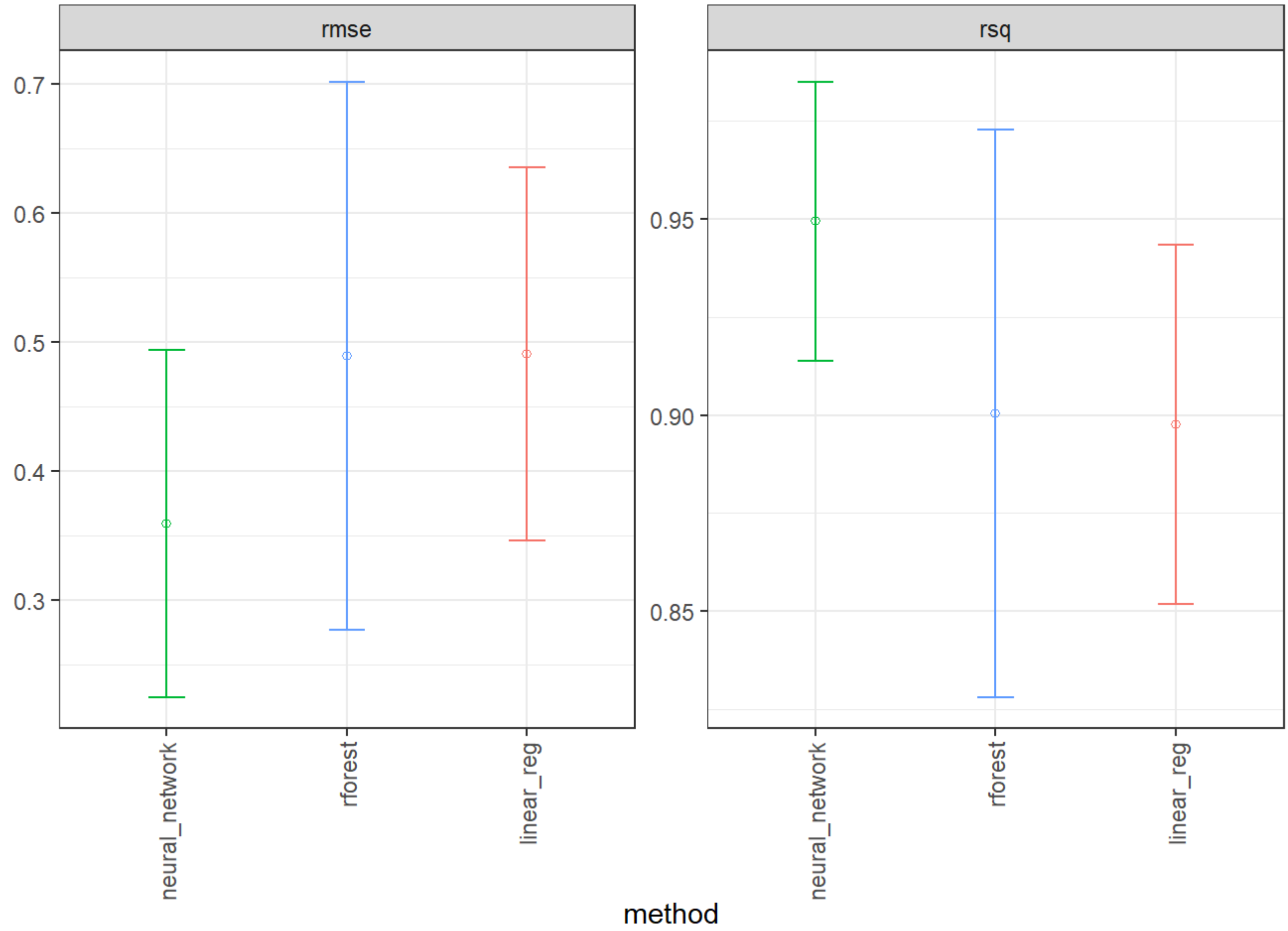
```
# A tibble: 47 × 9
   wflow_id       .config   preproc model .metric .estimator  mean     n std_err
   <chr>          <chr>     <chr>   <chr> <chr>   <chr>      <dbl> <int>   <dbl>
 1 neural_network Preproce… recipe  mlp   rmse    standard   0.359     5  0.0687
 2 neural_network Preproce… recipe  mlp   rmse    standard   0.360     5  0.0736
 3 neural_network Preproce… recipe  mlp   rmse    standard   0.368     5  0.0716
 4 neural_network Preproce… recipe  mlp   rmse    standard   0.376     5  0.0654
 5 neural_network Preproce… recipe  mlp   rmse    standard   0.453     5  0.0747
 6 neural_network Preproce… recipe  mlp   rmse    standard   0.461     5  0.0939
 7 neural_network Preproce… recipe  mlp   rmse    standard   0.480     5  0.0798
 8 neural_network Preproce… recipe  mlp   rmse    standard   0.482     5  0.0763
 9 rforest        Preproce… recipe  rand… rmse    standard   0.489     5  0.108
10 linear_reg     Preproce… recipe  line… rmse    standard   0.491     5  0.0738
# ℹ 37 more rows
```

```
collect_metrics(race_results) |>
  filter(.metric == "rsq") |>
  arrange(desc(mean))
```

```
# A tibble: 47 × 9
   wflow_id       .config   preproc model .metric .estimator  mean     n std_err
   <chr>          <chr>     <chr>   <chr> <chr>   <chr>      <dbl> <int>   <dbl>
 1 neural_network Preproce… recipe  mlp   rsq     standard   0.949     5  0.0182
 2 neural_network Preproce… recipe  mlp   rsq     standard   0.949     5  0.0174
 3 neural_network Preproce… recipe  mlp   rsq     standard   0.946     5  0.0178
 4 neural_network Preproce… recipe  mlp   rsq     standard   0.946     5  0.0186
 5 neural_network Preproce… recipe  mlp   rsq     standard   0.918     4  0.0271
 6 neural_network Preproce… recipe  mlp   rsq     standard   0.917     5  0.0245
 7 neural_network Preproce… recipe  mlp   rsq     standard   0.914     5  0.0261
 8 neural_network Preproce… recipe  mlp   rsq     standard   0.913     5  0.0263
 9 neural_network Preproce… recipe  mlp   rsq     standard   0.907     4  0.0306
```

```
10 neural_network Preproce… recipe  mlp   rsq     standard   0.904     5  0.0245
# ℹ 37 more rows
```

```
IC_rmse <- collect_metrics(race_results) |>
  filter(.metric == "rmse") |>
  group_by(wflow_id) |>
  filter(mean == min(mean)) |>
  group_by(wflow_id) |>
  arrange(mean) |>
  ungroup()

IC_r2 <- collect_metrics(race_results) |>
  filter(.metric == "rsq") |>
  group_by(wflow_id) |>
  filter(mean == max(mean)) |>
  group_by(wflow_id) |>
  arrange(desc(mean)) |>
  ungroup()

IC2 <- bind_rows(IC_rmse, IC_r2)

ggplot(IC2, aes(x = factor(wflow_id, levels = unique(wflow_id)), y = mean)) +
  facet_wrap(~.metric, scales = "free") +
  geom_point(stat="identity", aes(color = wflow_id), pch = 1) +
  geom_errorbar(stat="identity", aes(color = wflow_id,
                                     ymin=mean-1.96*std_err,
                                     ymax=mean+1.96*std_err), width=.2) +
  labs(y = "", x = "method") + theme_bw() +
  theme(legend.position = "none",
        axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1))
```



Classificação de espécies de árvores frutíferas considerando características dimensionais de folhas

```
folhas <- read.csv("folhas.csv", header = T)
head(folhas)
```

```
  especie      area perimetro raiomedio    raiosd   raiomin   raiomax eixomaior
1  goiaba 2.3587161  5.575758 0.9105212 0.1573576 0.6948606 1.1568970  2.313212
2  goiaba 2.2907601  5.818182 0.9124121 0.1605576 0.6507515 1.2462788  2.232667
3  goiaba 1.8871878  5.103030 0.8239879 0.1680606 0.5723879 1.1024121  2.146024
4  goiaba 1.2324738  5.224242 0.7478909 0.2848121 0.2493576 1.2367152  2.335758
5  goiaba 0.9707225  3.684848 0.6013455 0.1543394 0.3110061 0.8603394  1.675248
6  goiaba 2.1489390  6.072727 0.9169333 0.2829576 0.4715758 1.4316727  2.711770
  ecentricidade
1         0.789
2         0.763
3         0.819
4         0.941
5         0.868
6         0.909
```

```
glimpse(folhas)
```

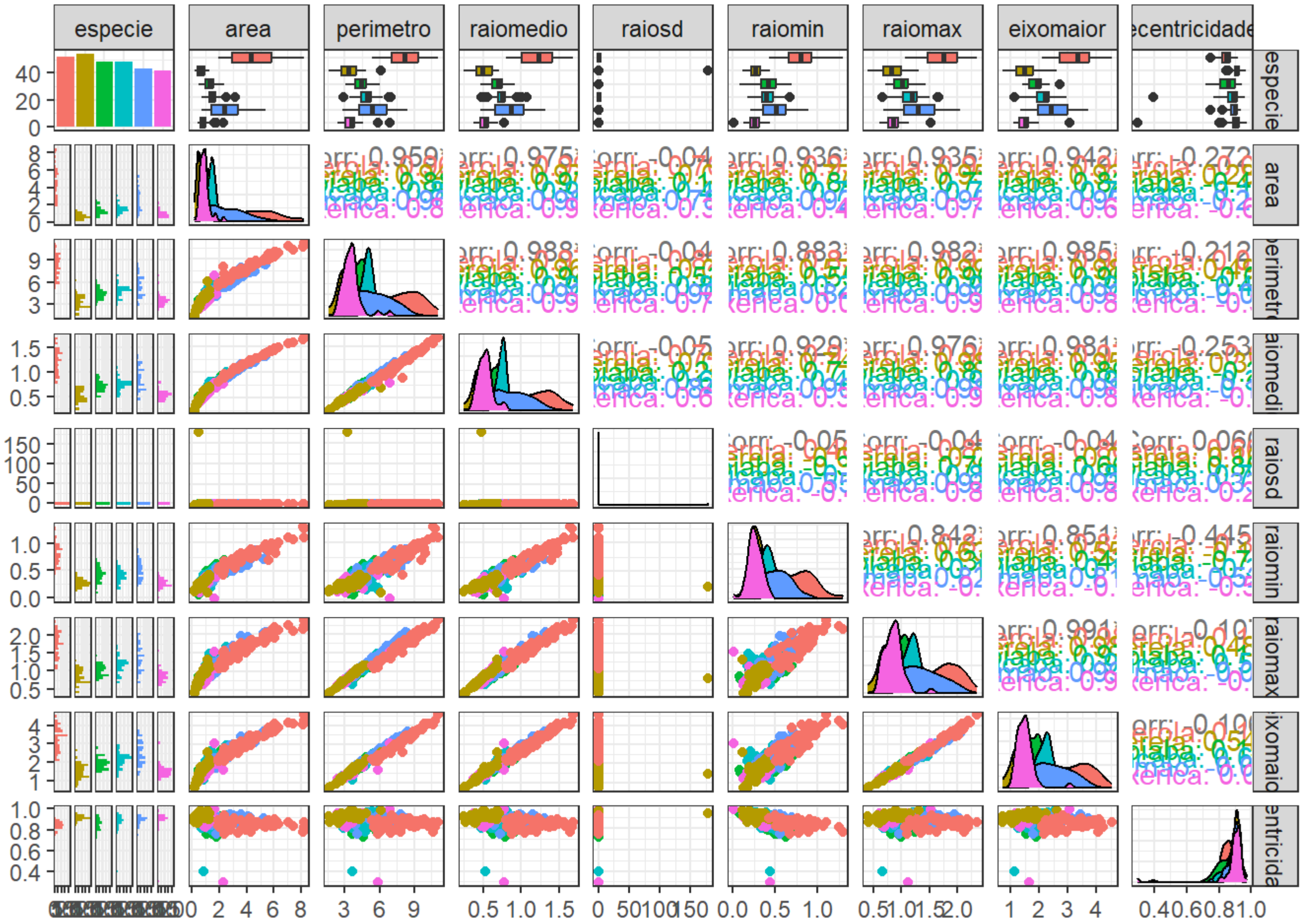
```
Rows: 287
Columns: 9
```

```
$ especie       <chr> "goiaba", "goiaba", "goiaba", "goiaba", "goiaba", "goiab…
$ area          <dbl> 2.3587161, 2.2907601, 1.8871878, 1.2324738, 0.9707225, 2…
$ perimetro     <dbl> 5.575758, 5.818182, 5.103030, 5.224242, 3.684848, 6.0727…
$ raiomedio     <dbl> 0.9105212, 0.9124121, 0.8239879, 0.7478909, 0.6013455, 0…
$ raiosd        <dbl> 0.15735758, 0.16055758, 0.16806061, 0.28481212, 0.154339…
$ raiomin       <dbl> 0.6948606, 0.6507515, 0.5723879, 0.2493576, 0.3110061, 0…
$ raiomax       <dbl> 1.1568970, 1.2462788, 1.1024121, 1.2367152, 0.8603394, 1…
$ eixomaior     <dbl> 2.313212, 2.232667, 2.146024, 2.335758, 1.675248, 2.7117…
$ ecentricidade <dbl> 0.789, 0.763, 0.819, 0.941, 0.868, 0.909, 0.841, 0.798, …
```

```
datasummary_skim(folhas)
```

	Unique	Missing Pct.	Mean	SD	Min	Median	Max	Histogram
area	287	0	1.9	1.6	0.2	1.3	8.2	
perimetro	265	0	5.0	2.0	1.6	4.5	11.1	
raiomedio	287	0	0.8	0.3	0.2	0.7	1.7	
raiosd	287	0	0.8	10.5	0.1	0.2	178.0	
raiomin	285	0	0.4	0.2	0.0	0.4	1.3	
raiomax	287	0	1.2	0.4	0.4	1.1	2.4	
eixomaior	287	0	2.1	0.8	0.7	2.0	4.5	
ecentricidade	142	0	0.9	0.1	0.3	0.9	1.0	
especie	N	%						
acerola	52	18.1						
cereja	54	18.8						
goiaba	48	16.7						
jabuticaba	48	16.7						
limao	43	15.0						
mexerica	42	14.6						

```
ggpairs(folhas, aes(col = especie), progress = F)
```




```
set.seed(16)
dados_split2 <- initial_split(folhas,
                              prop = 0.75)

dados_train2 <- training(dados_split2)
dados_test2  <- testing(dados_split2)

set.seed(17)
dados_folds2 <-
  vfold_cv(v = 5, dados_train2)
```

```
normalized_rec <-
  recipe(especie ~ .,
         data = dados_train2) |>
  step_normalize(all_numeric_predictors())
```

Métodos de classificação.

```
lreg_spec <-
  multinom_reg(penalty = tune(), mixture = tune()) |>
  set_engine("glmnet")

tree_spec <- decision_tree(tree_depth = tune(), min_n = tune(), cost_complexity = tune()) |>
  set_engine("rpart") |>
  set_mode("classification")
```

```
rforest_spec <- rand_forest(mtry = tune(), min_n = tune(), trees = tune()) |>
  set_engine("ranger") |>
  set_mode("classification")

svm_r_spec <-
  svm_rbf(cost = tune(), rbf_sigma = tune()) |>
  set_engine("kernlab") |>
  set_mode("classification")

svm_p_spec <-
  svm_poly(cost = tune(), degree = tune()) |>
  set_engine("kernlab") |>
  set_mode("classification")
```

Definindo o `worflow`, o qual contém os modelos e a receita.

```
normalized2 <-
  workflow_set(
    preproc = list(normalized = normalized_rec),
    models = list(lreg = lreg_spec,
                  tree = tree_spec,
                  rforest = rforest_spec,
                  SVM_radial = svm_r_spec,
                  SVM_poly = svm_p_spec
                  )
  )
normalized2
```

```
# A workflow set/tibble: 5 × 4
  wflow_id              info             option    result
  <chr>                 <list>           <list>    <list>
1 normalized_lreg       <tibble [1 × 4]> <opts[0]> <list [0]>
2 normalized_tree       <tibble [1 × 4]> <opts[0]> <list [0]>
3 normalized_rforest    <tibble [1 × 4]> <opts[0]> <list [0]>
4 normalized_SVM_radial <tibble [1 × 4]> <opts[0]> <list [0]>
5 normalized_SVM_poly   <tibble [1 × 4]> <opts[0]> <list [0]>
```

Fazendo modificação no nome dos modelos para simplificá-los.

```
all_workflows2 <-
  bind_rows(normalized2) |>
  # Make the workflow ID's a little more simple:
  mutate(wflow_id = gsub("(simple_)|(normalized_)", "", wflow_id))
all_workflows2
```

```
# A workflow set/tibble: 5 × 4
  wflow_id   info             option    result
  <chr>      <list>           <list>    <list>
1 lreg       <tibble [1 × 4]> <opts[0]> <list [0]>
2 tree       <tibble [1 × 4]> <opts[0]> <list [0]>
3 rforest    <tibble [1 × 4]> <opts[0]> <list [0]>
4 SVM_radial <tibble [1 × 4]> <opts[0]> <list [0]>
5 SVM_poly   <tibble [1 × 4]> <opts[0]> <list [0]>
```

Grid search e validação cruzada.

```
race_ctrl2 <-
  control_race(
    save_pred = TRUE,
    parallel_over = "everything",
    save_workflow = TRUE
  )

race_results2 <-
  all_workflows2 |>
  workflow_map(
    "tune_race_anova",
    seed = 1503,
    resamples = dados_folds2,
    grid = 25,
    control = race_ctrl2
  )
```

Extraindo métricas para avaliar os resultados da validação cruzada.

```
collect_metrics(race_results2) |>
  filter(.metric == "accuracy") |>
  arrange(desc(mean))
```

```
# A tibble: 34 × 9
   wflow_id .config         preproc model .metric .estimator  mean     n std_err
   <chr>    <chr>           <chr>   <chr> <chr>   <chr>      <dbl> <int>   <dbl>
 1 lreg     Preprocessor1_… recipe  mult… accura… multiclass 0.842     5  0.0225
 2 lreg     Preprocessor1_… recipe  mult… accura… multiclass 0.837     5  0.0285
 3 SVM_poly Preprocessor1_… recipe  svm_… accura… multiclass 0.837     5  0.0127
 4 lreg     Preprocessor1_… recipe  mult… accura… multiclass 0.833     5  0.0225
 5 lreg     Preprocessor1_… recipe  mult… accura… multiclass 0.833     5  0.0225
 6 lreg     Preprocessor1_… recipe  mult… accura… multiclass 0.833     5  0.0298
 7 lreg     Preprocessor1_… recipe  mult… accura… multiclass 0.823     5  0.0189
 8 lreg     Preprocessor1_… recipe  mult… accura… multiclass 0.814     5  0.0195
 9 lreg     Preprocessor1_… recipe  mult… accura… multiclass 0.809     5  0.0171
10 lreg     Preprocessor1_… recipe  mult… accura… multiclass 0.805     5  0.0158
# ℹ 24 more rows
```

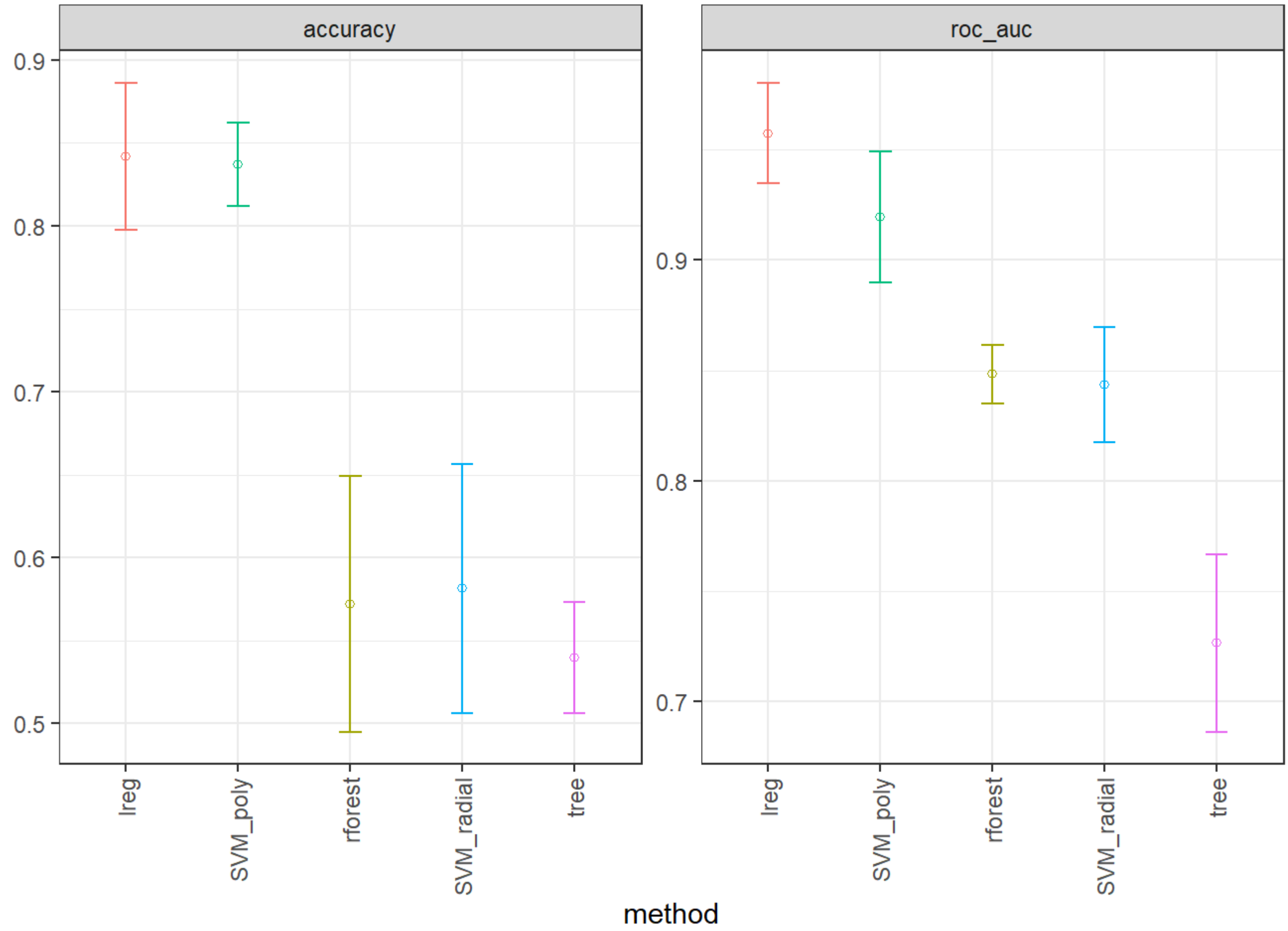
```
collect_metrics(race_results2) |>
  filter(.metric == "roc_auc") |>
  arrange(desc(mean))
```

```
# A tibble: 34 × 9
   wflow_id .config         preproc model .metric .estimator  mean     n std_err
   <chr>    <chr>           <chr>   <chr> <chr>   <chr>      <dbl> <int>   <dbl>
 1 lreg     Preprocessor1_… recipe  mult… roc_auc hand_till  0.964     5 0.0105
 2 lreg     Preprocessor1_… recipe  mult… roc_auc hand_till  0.963     5 0.0104
 3 lreg     Preprocessor1_… recipe  mult… roc_auc hand_till  0.963     5 0.0102
 4 lreg     Preprocessor1_… recipe  mult… roc_auc hand_till  0.963     5 0.0103
 5 lreg     Preprocessor1_… recipe  mult… roc_auc hand_till  0.963     5 0.0108
```

```
 6 lreg      Preprocessor1_… recipe  mult… roc_auc hand_till  0.963      5 0.0113
 7 lreg      Preprocessor1_… recipe  mult… roc_auc hand_till  0.963      5 0.0111
 8 lreg      Preprocessor1_… recipe  mult… roc_auc hand_till  0.963      5 0.0112
 9 lreg      Preprocessor1_… recipe  mult… roc_auc hand_till  0.962      5 0.0110
10 lreg      Preprocessor1_… recipe  mult… roc_auc hand_till  0.962      5 0.00985
# ℹ 24 more rows
```

Visualizando desempenho dos métodos.

```
IC_rmse <- collect_metrics(race_results2) |>
  filter(.metric == "roc_auc") |>
  group_by(wflow_id) |>
  filter(mean == min(mean)) |>
  group_by(wflow_id) |>
  arrange(desc(mean)) |>
  ungroup()

IC_r2 <- collect_metrics(race_results2) |>
  filter(.metric == "accuracy") |>
  group_by(wflow_id) |>
  filter(mean == max(mean)) |>
  group_by(wflow_id) |>
  arrange(desc(mean)) |>
  ungroup()

IC <- bind_rows(IC_rmse, IC_r2)

ggplot(IC, aes(x = factor(wflow_id, levels = unique(wflow_id)), y = mean)) +
  facet_wrap(~.metric, scales = "free") +
  geom_point(stat="identity", aes(color = wflow_id), pch = 1) +
  geom_errorbar(stat="identity", aes(color = wflow_id,
                                     ymin=mean-1.96*std_err,
                                     ymax=mean+1.96*std_err), width=.2) +
  labs(y = "", x = "method") + theme_bw() +
  theme(legend.position = "none",
        axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1))
```




```
best_roc_auc <-
  race_results2 |>
  extract_workflow_set_result("lreg") |>
  select_best(metric = "roc_auc")
best_roc_auc
```

```
# A tibble: 1 × 3
       penalty mixture .config
         <dbl>   <dbl> <chr>
1 0.0000000121   0.683 Preprocessor1_Model17
```

Previsão e desempenho para dados de teste.

Modelo final.

```
last_mod <-
  multinom_reg(penalty = 1.211528e-08, mixture = 0.6833333) |>
  set_engine("glmnet",
             importance = "impurity") |>
  set_mode("classification")

last_workflow <-
  extract_workflow(all_workflows2, "lreg") |>
  update_model(last_mod)

set.seed(345)
```

```
last_fit <-
  last_workflow |>
  last_fit(dados_split2)

last_fit
```

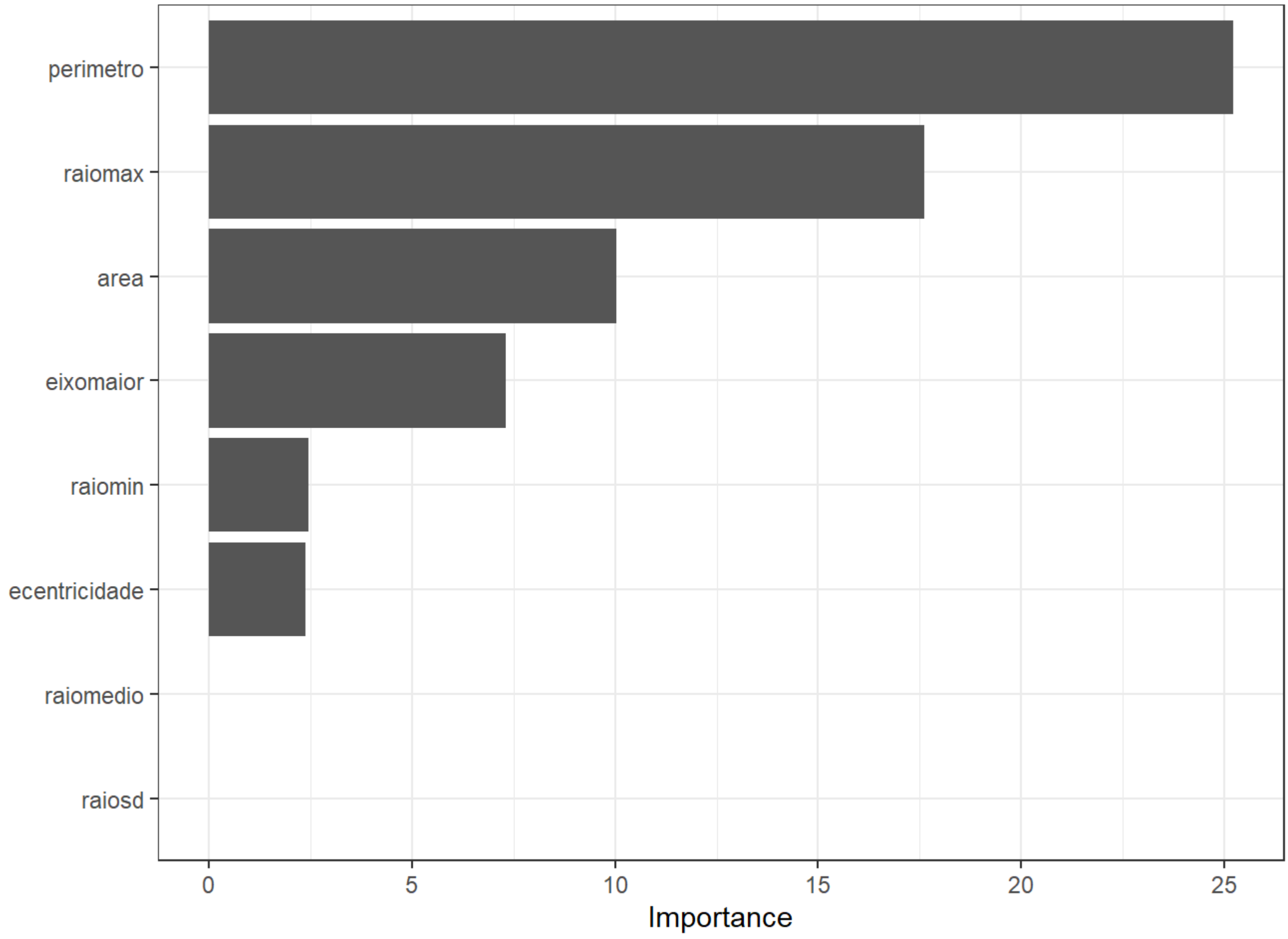
```
# Resampling results
# Manual resampling
# A tibble: 1 × 6
  splits            id               .metrics .notes   .predictions .workflow
  <list>            <chr>            <list>   <list>   <list>       <list>
1 <split [215/72]> train/test split <tibble> <tibble> <tibble>     <workflow>
```

```
last_fit |>
  collect_metrics()
```

```
# A tibble: 3 × 4
  .metric     .estimator .estimate .config
  <chr>       <chr>          <dbl> <chr>
1 accuracy    multiclass     0.847 Preprocessor1_Model1
2 roc_auc     hand_till      0.981 Preprocessor1_Model1
3 brier_class multiclass     0.106 Preprocessor1_Model1
```

Importância das variáveis no modelo.

```
library(vip)
last_fit |>
  extract_fit_parsnip() |>
  vip(num_features = 20) + theme_bw()
```



Séries temporais

```
library(fpp3)
library(zoo)
```

Leitura dos dados.

```
voosbr <- read.csv("voosbr_ts.csv", header = T)
```

Transformando dados em série temporal.

```
voosbr_ts <- voosbr |>
  mutate(data = yearmonth(paste(data, " 01"), format = "%Y %b %d")) |>
  as_tsibble(index = data)
```

Plotando até ano 2019.

```
voosbr_ts |>
  filter(year(data)<2020) |>
  autoplot(Passageiros) +
  labs(title="Passageiros em vôos no Brasil", x="")
```

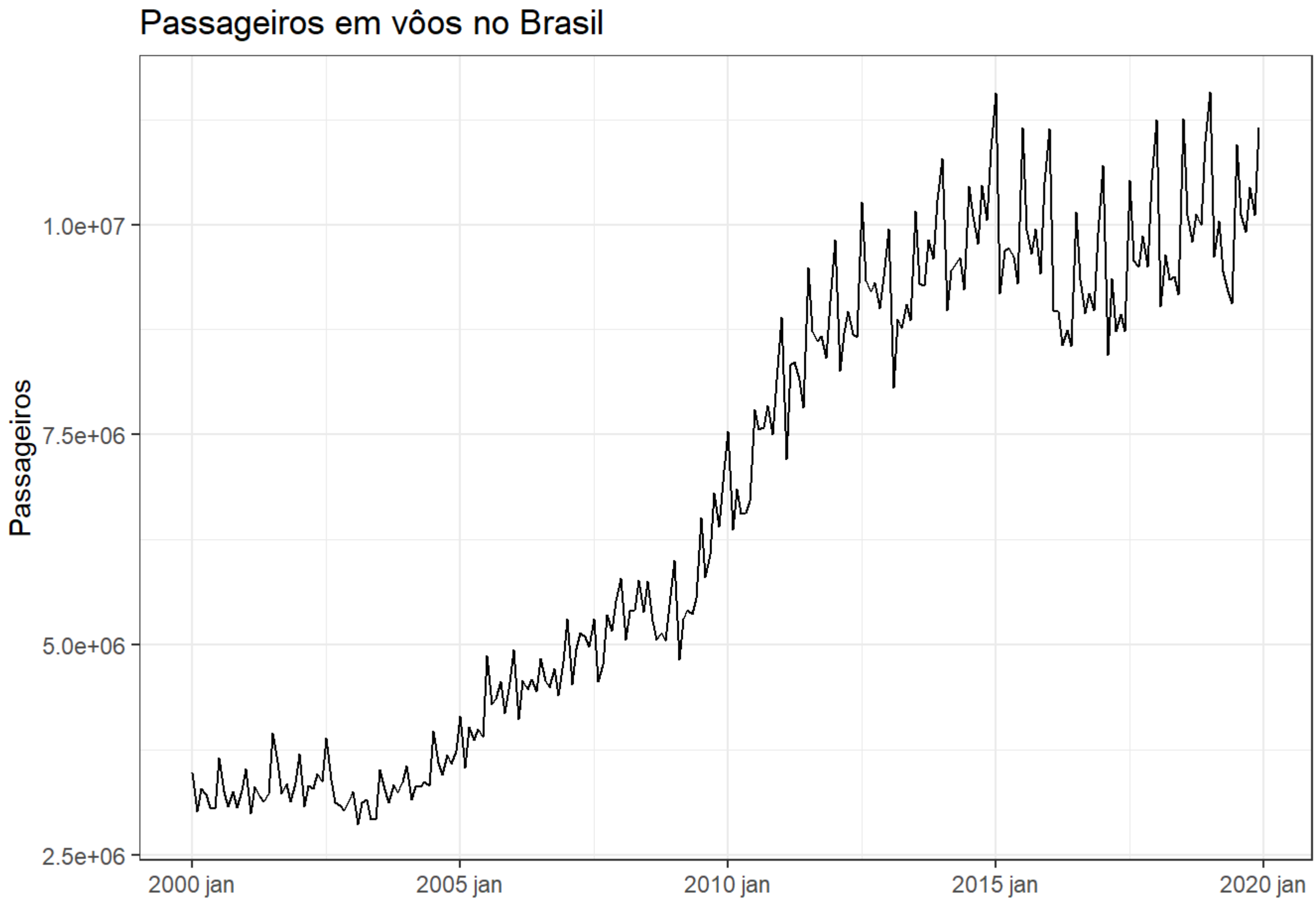
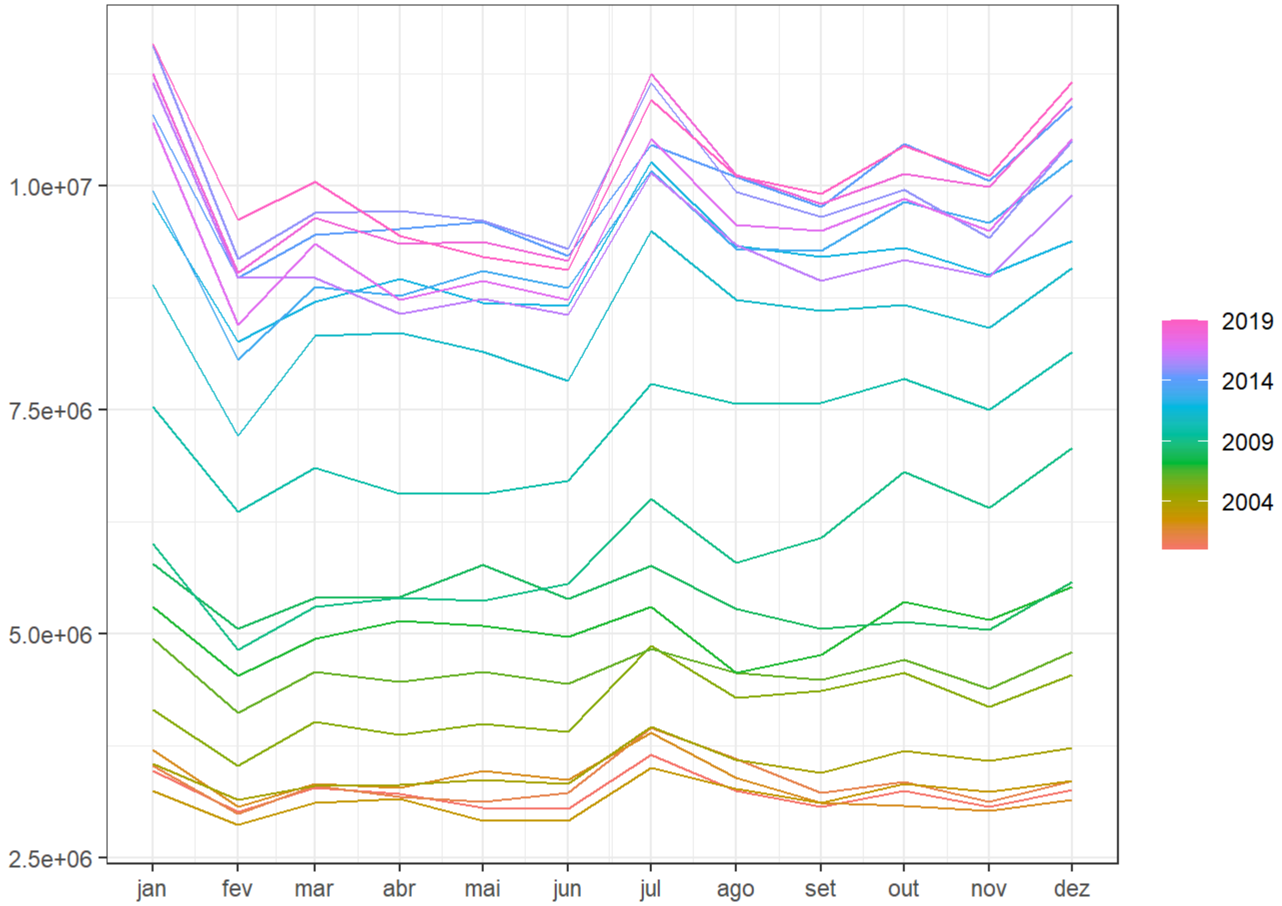


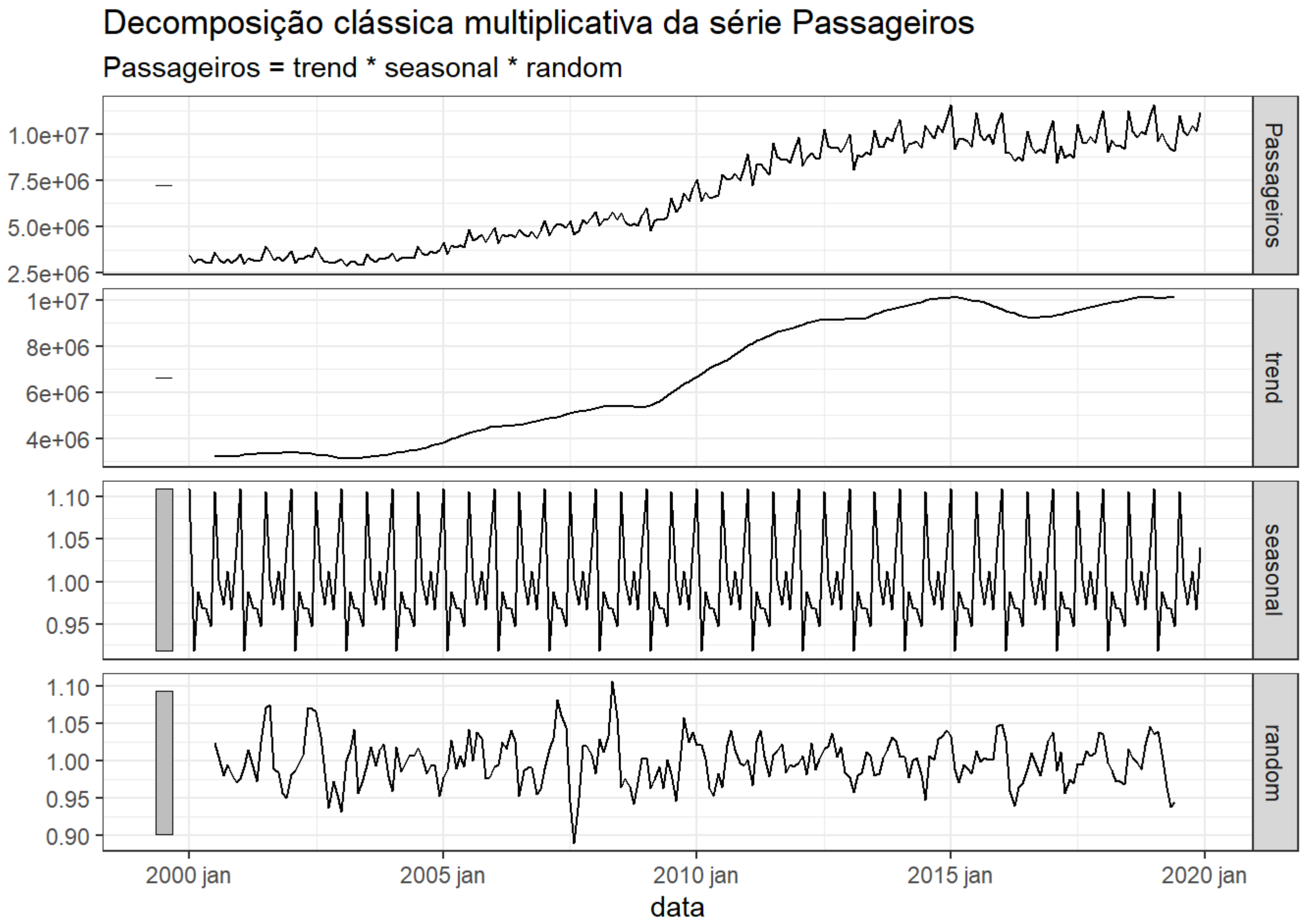
Gráfico sazonal.

```
voosbr_ts |>
  filter(year(data)<2020) |>
  gg_season(Passageiros) + labs(x="", y = "")
```



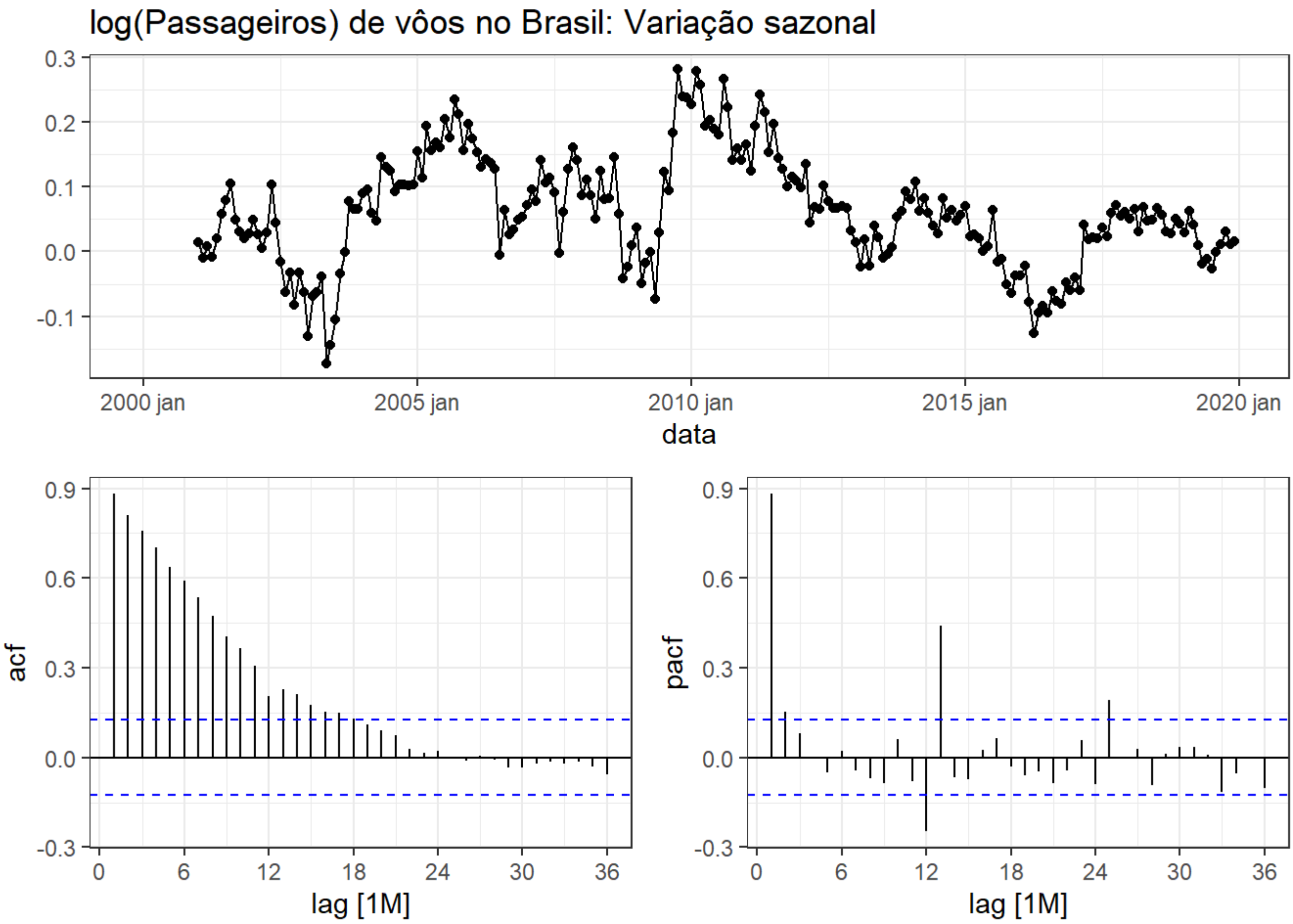
Decomposição clássifca multiplicativa.

```
voosbr_ts |>
  filter(year(data)<2020) |>
  model(
    classical_decomposition(Passageiros, type = "multiplicative")
  ) |>
  components() |>
  autoplot() +
  labs(title = "Decomposição clássica multiplicativa da série Passageiros")
```



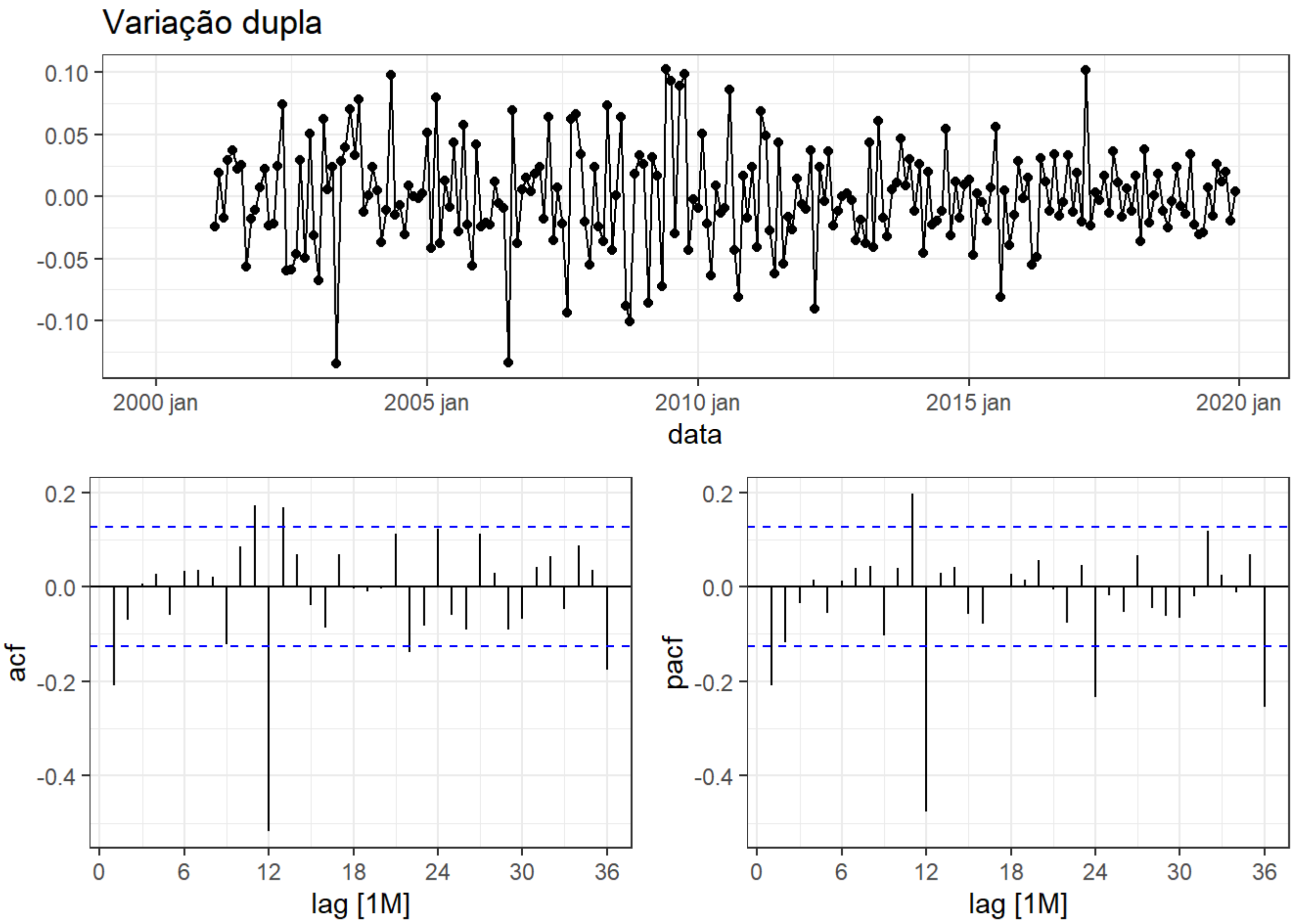
Variação sazonal da série de log(passageiros) em vôos do Brasil e correlogramas de ACF e PACF.

```
voosbr_ts  |>
  filter(year(data)<2020) |>
  gg_tsdisplay(difference(log(Passageiros), 12),
               plot_type='partial', lag=36) +
  labs(title="log(Passageiros) de vôos no Brasil: Variação sazonal", y="")
```



Série transformada com diferenciação simples e sazonal, além dos correlogramas de ACF e PACF.

```
voosbr_ts  |>
  filter(year(data)<2020) |>
  gg_tsdisplay(difference(log(Passageiros), 12) |> difference(),
               plot_type='partial', lag=36) +
  labs(title="Variação dupla", y="")
```



Testando modelos.

```
fit6 <- voosbr_ts  |>
  filter(year(data)<2020) |>
  model(
    arima011011 = ARIMA(log(Passageiros) ~ pdq(0,1,1) + PDQ(0,1,1)),
    arima110210 = ARIMA(log(Passageiros) ~ pdq(1,1,0) + PDQ(2,1,0)),
    auto = ARIMA(log(Passageiros), stepwise = FALSE, approx = FALSE)
  )

fit6 |> pivot_longer(everything(), names_to = "Modelo",
                     values_to = "Ordem")
```

```
# A mable: 3 x 2
# Key:     Modelo [3]
  Modelo                          Ordem
  <chr>                         <model>
1 arima011011 <ARIMA(0,1,1)(0,1,1)[12]>
2 arima110210 <ARIMA(1,1,0)(2,1,0)[12]>
3 auto        <ARIMA(1,1,1)(0,1,1)[12]>
```

Resultado dos três modelos.

```
glance(fit6) |> arrange(AICc) |> select(.model:BIC)
```

```
# A tibble: 3 × 6
  .model       sigma2 log_lik   AIC  AICc   BIC
```

```
  <chr>          <dbl>   <dbl> <dbl> <dbl> <dbl>
1 auto         0.00104    455.  -902.  -902.  -889.
2 arima011011 0.00105    454.  -902.  -901.  -891.
3 arima110210 0.00118    444.  -880.  -880.  -866.
```

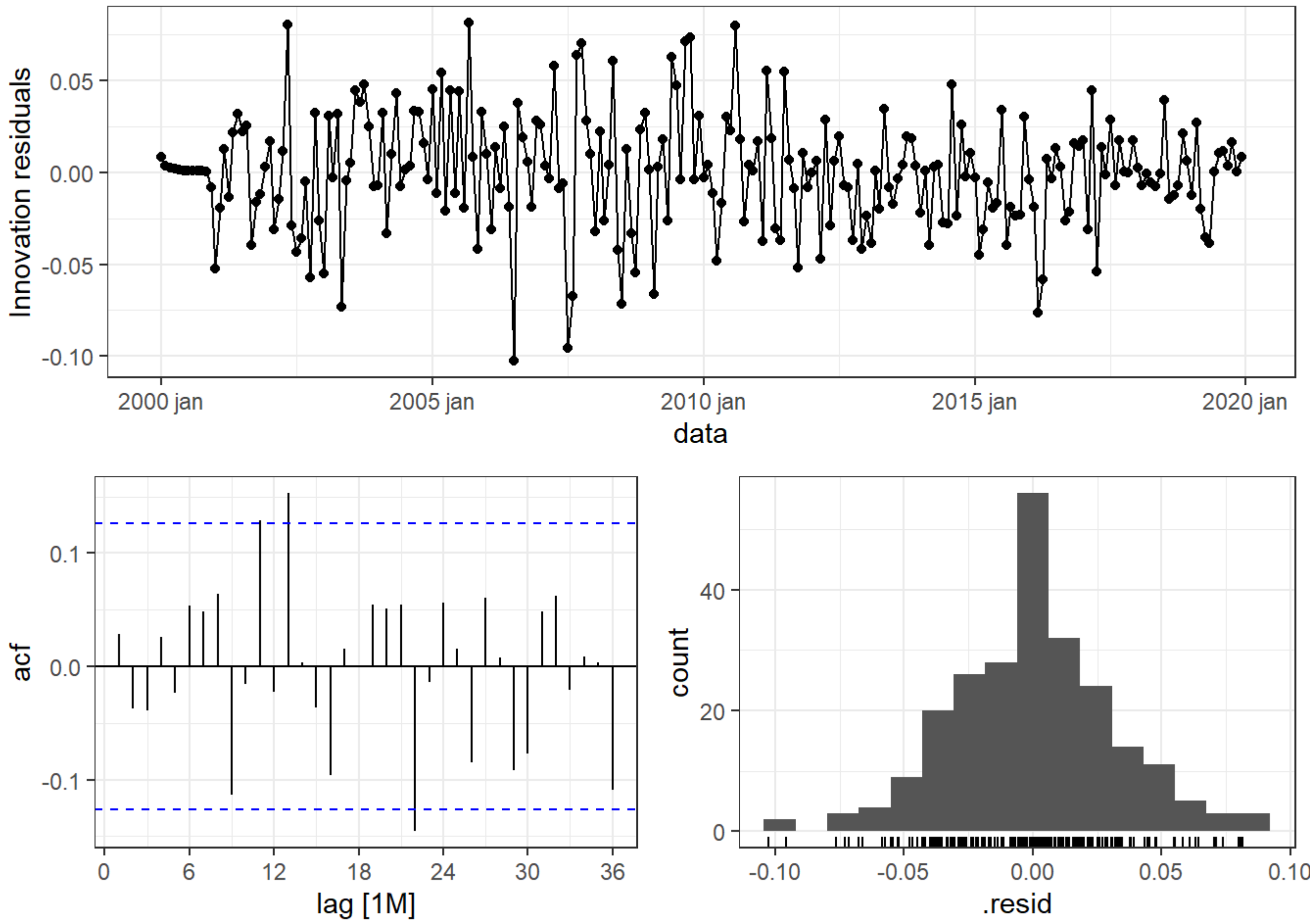
Coeficientes do modelo automático.

```
report(fit6 |> select(auto))
```

```
Series: Passageiros
Model: ARIMA(1,1,1)(0,1,1)[12]
Transformation: log(Passageiros)

Coefficients:
         ar1      ma1     sma1
      0.5214  -0.6437  -0.7410
s.e.  0.2121   0.1859   0.0584

sigma^2 estimated as 0.001045:  log likelihood=455.1
AIC=-902.2   AICc=-902.02   BIC=-888.5
```

Gráficos de resíduos.

```
fit6 |> select(auto) |> gg_tsresiduals(lag=36)
```



Teste de Ljung-Box para os resíduos do modelo.

```
augment(fit6) |>
  filter(.model == "auto") |>
  features(.innov, ljung_box, lag=24, dof=3)
```

```
# A tibble: 1 × 3
  .model lb_stat lb_pvalue
  <chr>    <dbl>     <dbl>
1 auto      28.8     0.120
```

Previsão 3 anos à frente.

```
forecast(fit6, h=36) |>
  filter(.model=='auto') |>
  autoplot(voosbr_ts |>
  filter(year(data)<2020)) +
  labs(title = "Passageiros em vôos do Brasil",
       y="Passageiros")
```