Mushroom Data Analysis

Harsh Ranjan Kumar

22/09/2020

```
dataset = read.csv("data/agaricus_lepiota_data.csv")
colnames(dataset) <- c("ediblility", "cap_shape", "cap_surface", "cap_color", "bruises", "odor", "gill_a
```

Including Plots

You can also embed plots, for example:

```
##    ediblility cap_shape cap_surface cap_color bruises odor gill_attachement
## 1           e         x           s         y    true    a                f
## 2           e         b           s         w    true    l                f
## 3           p         x           y         w    true    p                f
## 4           e         x           s         g   false    n                f
## 5           e         x           y         y    true    a                f
## 6           e         b           s         w    true    a                f
## 7           e         b           y         w    true    l                f
## 8           p         x           y         w    true    p                f
## 9           e         b           s         y    true    a                f
## 10          e         x           y         y    true    l                f
##    gill_spacing gill_size gill_color stalk_shape stalk_root
## 1             c         b          k           e          c
## 2             c         b          n           e          c
## 3             c         n          n           e          e
## 4             w         b          k           t          e
## 5             c         b          n           e          c
## 6             c         b          g           e          c
## 7             c         b          n           e          c
## 8             c         n          p           e          e
## 9             c         b          g           e          c
## 10            c         b          g           e          c
##    stalk_surface_above_ring stalk_surface_below_ring stalk_color_above_ring
## 1                         s                        s                      w
## 2                         s                        s                      w
## 3                         s                        s                      w
## 4                         s                        s                      w
## 5                         s                        s                      w
## 6                         s                        s                      w
## 7                         s                        s                      w
## 8                         s                        s                      w
## 9                         s                        s                      w
## 10                        s                        s                      w
```

```
##    stalk_color_below_ring veil_type veil_color ring_number ring_type
## 1                       w         p          w           o         p
## 2                       w         p          w           o         p
## 3                       w         p          w           o         p
## 4                       w         p          w           o         e
## 5                       w         p          w           o         p
## 6                       w         p          w           o         p
## 7                       w         p          w           o         p
## 8                       w         p          w           o         p
## 9                       w         p          w           o         p
## 10                      w         p          w           o         p
##    spore_print_color population habitat
## 1                  n          n       g
## 2                  n          n       m
## 3                  k          s       u
## 4                  n          a       g
## 5                  k          n       g
## 6                  k          n       m
## 7                  n          s       m
## 8                  k          v       g
## 9                  k          s       m
## 10                 n          n       g
```

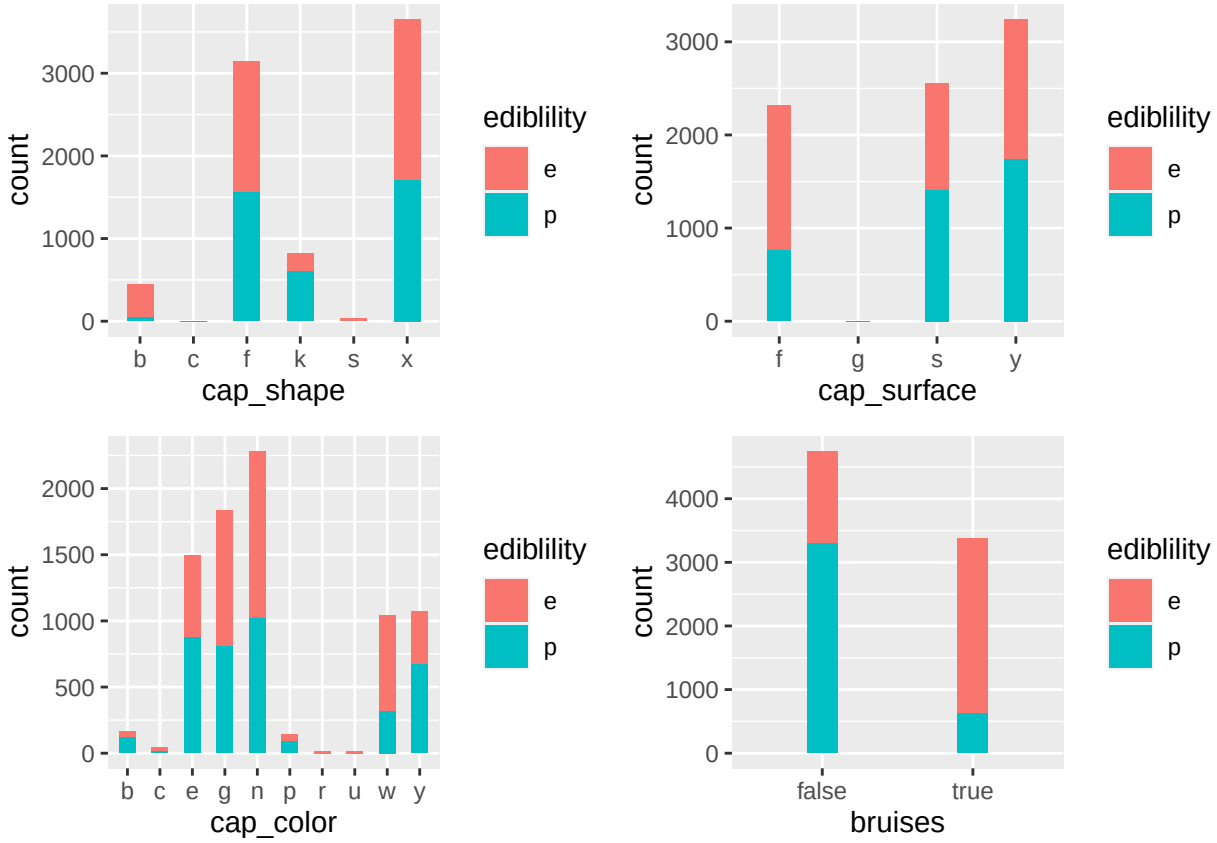
#Columns data :

1. cap-shape: bell=b, conical=c, convex=x, flat=f, knobbed=k, sunken=s
2. cap-surface: fibrous=f, grooves=g, scaly=y, smooth=s
3. cap-color: brown=n, buff=b, cinnamon=c, gray=g, green=r, pink=p, purple=u, red=e, white=w, yellow=y
4. bruises: bruises=t, no=f
5. odor: almond=a, anise=l, creosote=c, fishy=y, foul=f, musty=m, none=n, pungent=p, spicy=s
6. gill-attachment: attached=a, descending=d, free=f, notched=n
7. gill-spacing: close=c, crowded=w, distant=d
8. gill-size: broad=b, narrow=n
9. gill-color: black=k, brown=n, buff=b, chocolate=h, gray=g, green=r, orange=o, pink=p, purple=u, red=e, white=w, yellow=y
10. stalk-shape: enlarging=e, tapering=t
11. stalk-root: bulbous=b, club=c, cup=u, equal=e, rhizomorphs=z, rooted=r, missing=?
12. stalk-surface-above-ring: fibrous=f, scaly=y, silky=k, smooth=s
13. stalk-surface-below-ring: fibrous=f, scaly=y, silky=k, smooth=s
14. stalk-color-above-ring: brown=n, buff=b, cinnamon=c, gray=g, orange=o, pink=p, red=e, white=w, yellow=y
15. stalk-color-below-ring: brown=n, buff=b, cinnamon=c, gray=g, orange=o, pink=p, red=e, white=w, yellow=y
16. veil-type: partial=p, universal=u
17. veil-color: brown=n, orange=o, white=w, yellow=y
18. ring-number: none=n, one=o, two=t
19. ring-type: cobwebby=c, evanescent=e, flaring=f, large=l, none=n, pendant=p, sheathing=s, zone=z
20. spore-print-color: black=k, brown=n, buff=b, chocolate=h, green=r, orange=o, purple=u, white=w, yellow=y
21. population: abundant=a, clustered=c, numerous=n, scattered=s, several=v, solitary=y
22. habitat: grasses=g, leaves=l, meadows=m, paths=p, urban=u, waste=w, woods=d

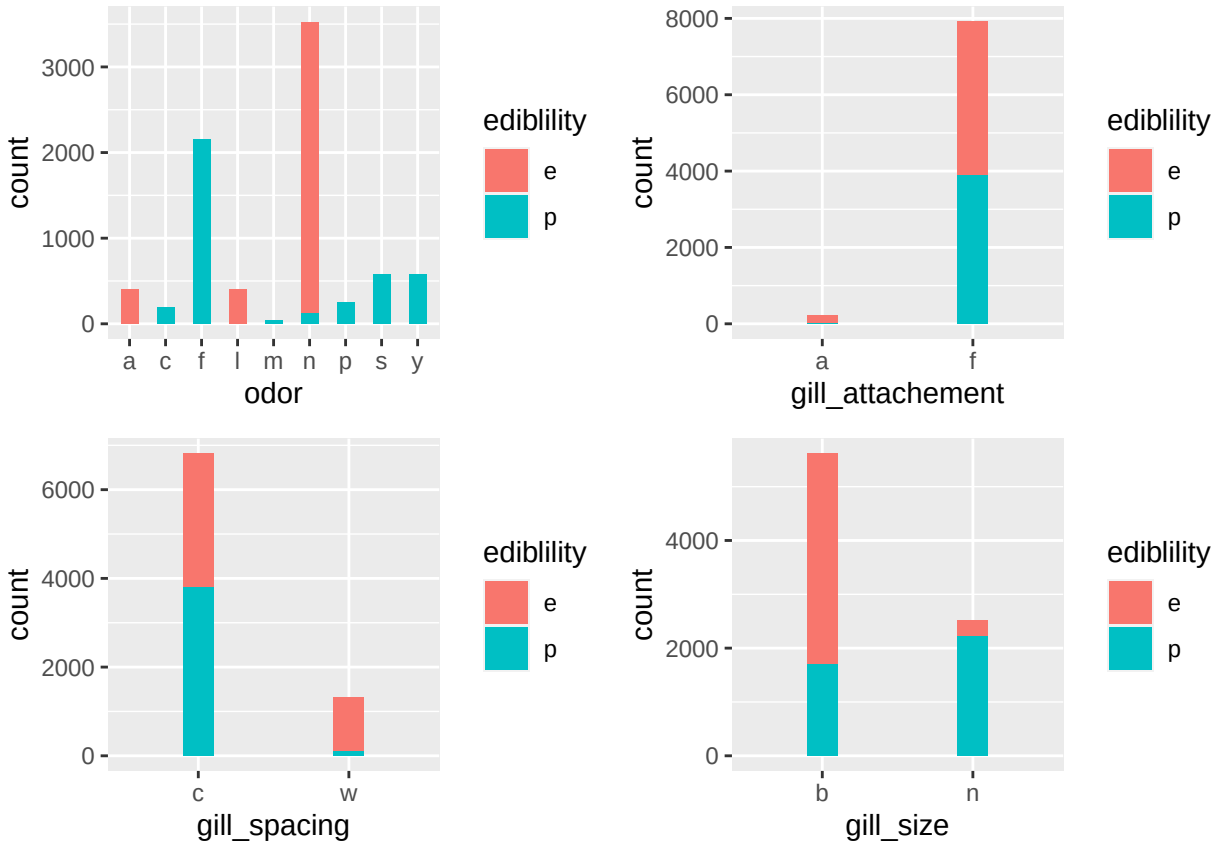
```
library(ggplot2)
library(gridExtra)
```

```
p1 = ggplot(data = dataset) +
        geom_bar(aes(cap_shape, fill = ediblility), width = 0.5)

p2  =ggplot(data = dataset) +
        geom_bar(aes(cap_surface, fill = ediblility), width = 0.3)

p3 = ggplot(data = dataset) +
        geom_bar(aes(cap_color, fill = ediblility), width = 0.5)

p4 = ggplot(data = dataset) +
        geom_bar(aes(bruises, fill = ediblility), width = 0.2)

p5 = ggplot(data = dataset) +
        geom_bar(aes(odor, fill = ediblility), width = 0.5)

p6 = ggplot(data = dataset) +
        geom_bar(aes(gill_attachement, fill = ediblility), width = 0.2)

p7 = ggplot(data = dataset) +
        geom_bar(aes(gill_spacing, fill = ediblility), width = 0.2)

p8 = ggplot(data = dataset) +
        geom_bar(aes(gill_size, fill = ediblility), width = 0.2)

p9 = ggplot(data = dataset) +
        geom_bar(aes(gill_color, fill = ediblility), width = 0.5)

p10 = ggplot(data = dataset) +
        geom_bar(aes(stalk_shape, fill = ediblility), width = 0.2)

p11 = ggplot(data = dataset) +
        geom_bar(aes(stalk_root, fill = ediblility), width = 0.5)

p12 = ggplot(data = dataset) +
        geom_bar(aes(stalk_surface_above_ring, fill = ediblility), width = 0.3)

p13 = ggplot(data = dataset) +
        geom_bar(aes(stalk_surface_below_ring, fill = ediblility), width = 0.4)

p14 = ggplot(data = dataset) +
        geom_bar(aes(stalk_color_above_ring, fill = ediblility), width = 0.5)

p15 = ggplot(data = dataset) +
        geom_bar(aes(stalk_color_below_ring, fill = ediblility), width = 0.5)

p16 = ggplot(data = dataset) +
        geom_bar(aes(veil_type, fill = ediblility), width = 0.1)

p17 = ggplot(data = dataset) +
        geom_bar(aes(veil_color, fill = ediblility), width = 0.3)
```

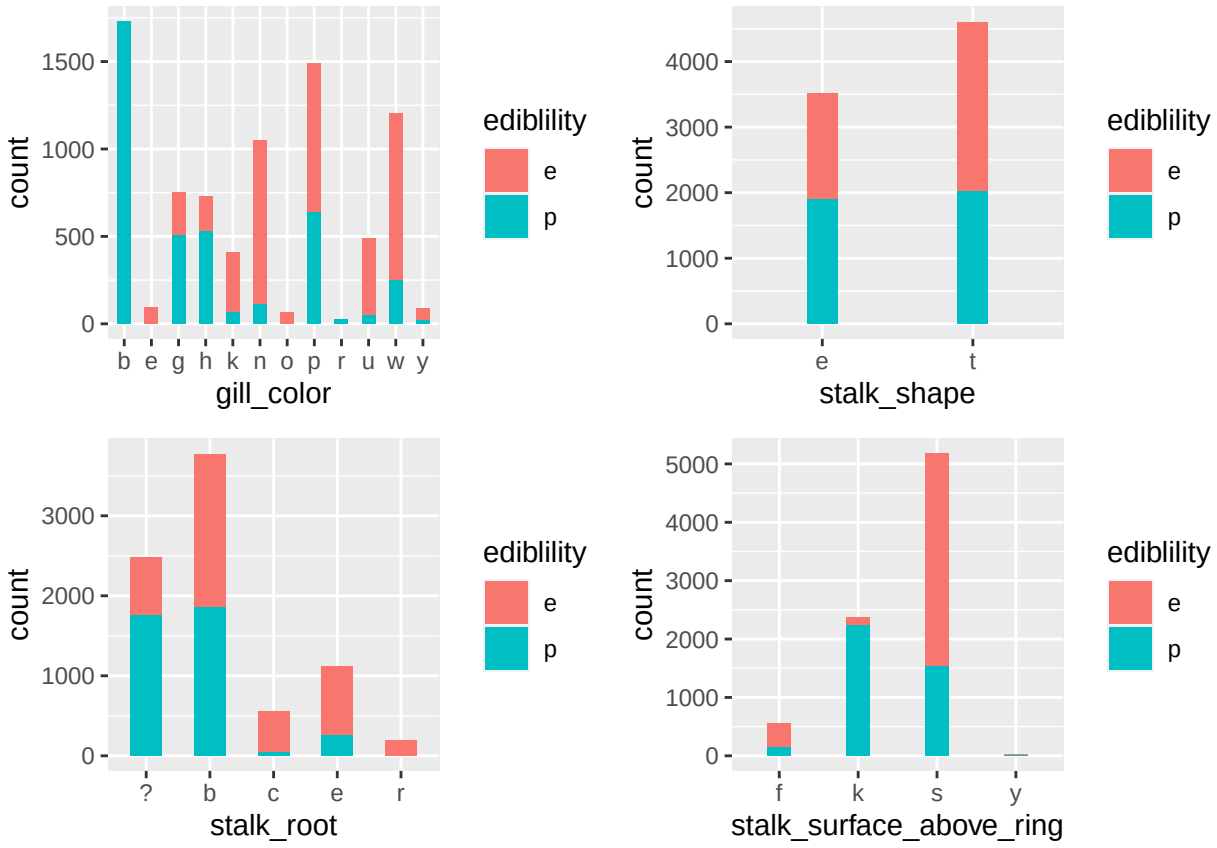
```
p18 = ggplot(data = dataset) +
        geom_bar(aes(ring_number, fill = ediblility), width = 0.3)

p19 = ggplot(data = dataset) +
        geom_bar(aes(ring_type, fill = ediblility), width = 0.4)

p20 = ggplot(data = dataset) +
        geom_bar(aes(spore_print_color, fill = ediblility), width = 0.5)

p21 = ggplot(data = dataset) +
        geom_bar(aes(population, fill = ediblility), width = 0.4)

p22 = ggplot(data = dataset) +
        geom_bar(aes(habitat, fill = ediblility), width = 0.5)

grid.arrange(p1, p2, p3, p4)
```



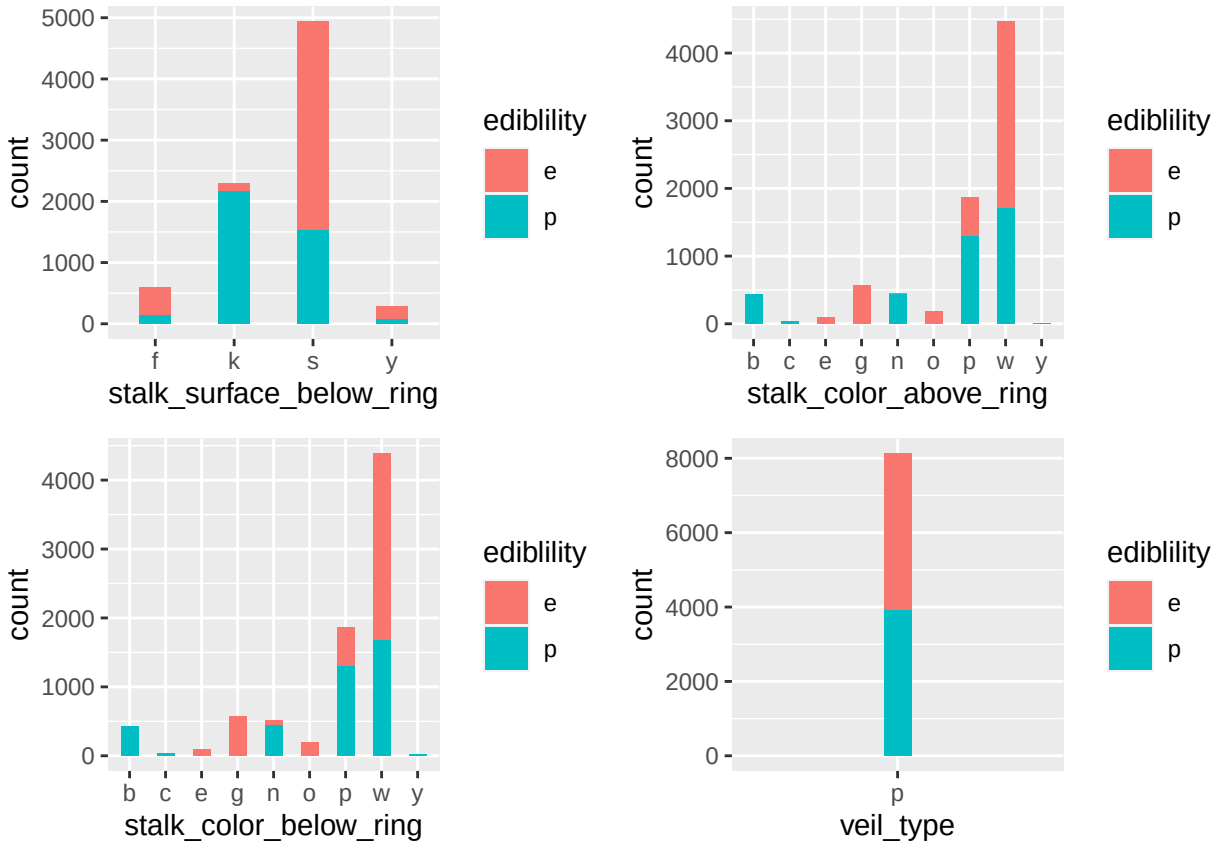

```
grid.arrange(p5, p6, p7, p8)
```



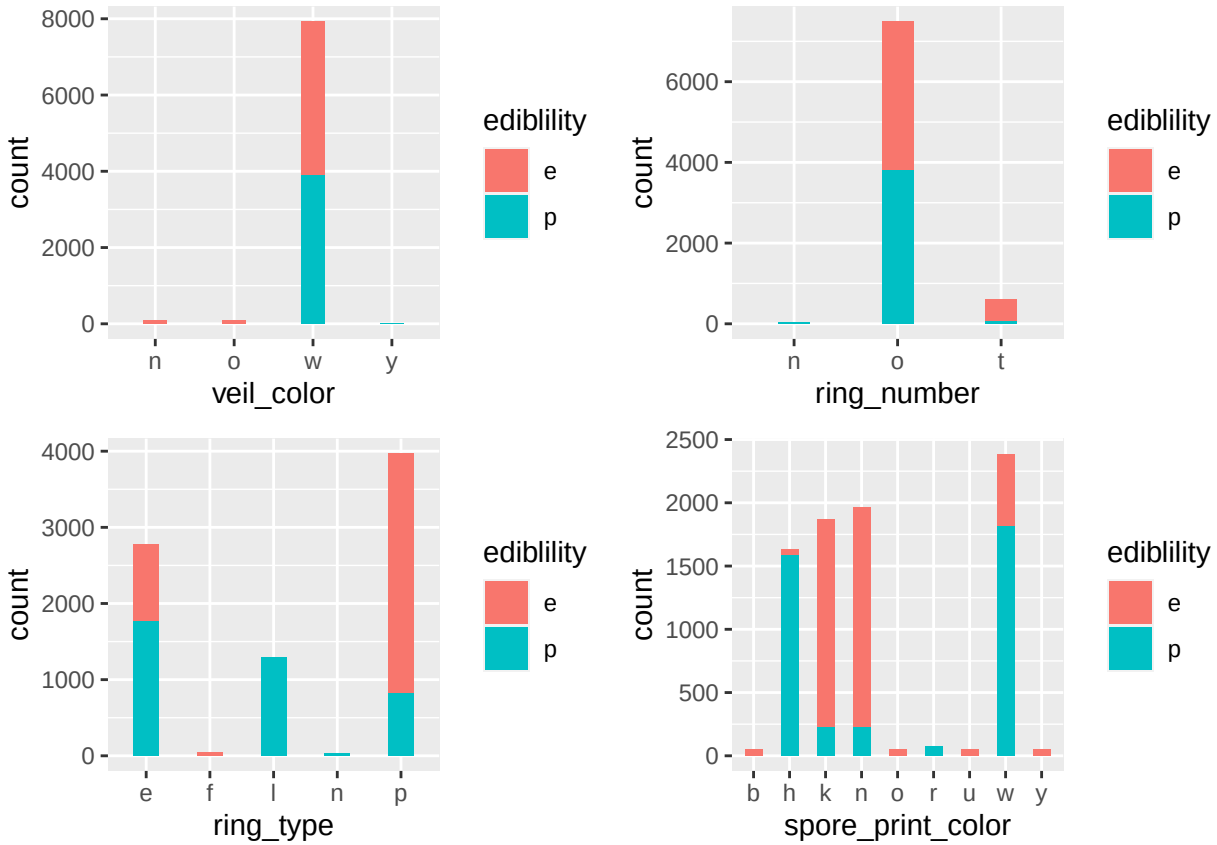

```
grid.arrange(p9, p10, p11, p12)
```



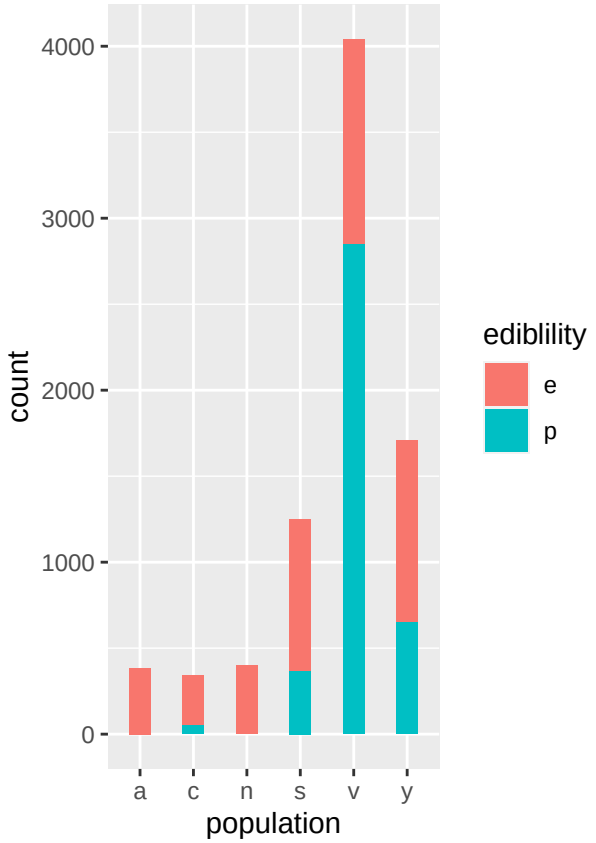

```
grid.arrange(p13, p14, p15, p16)
```

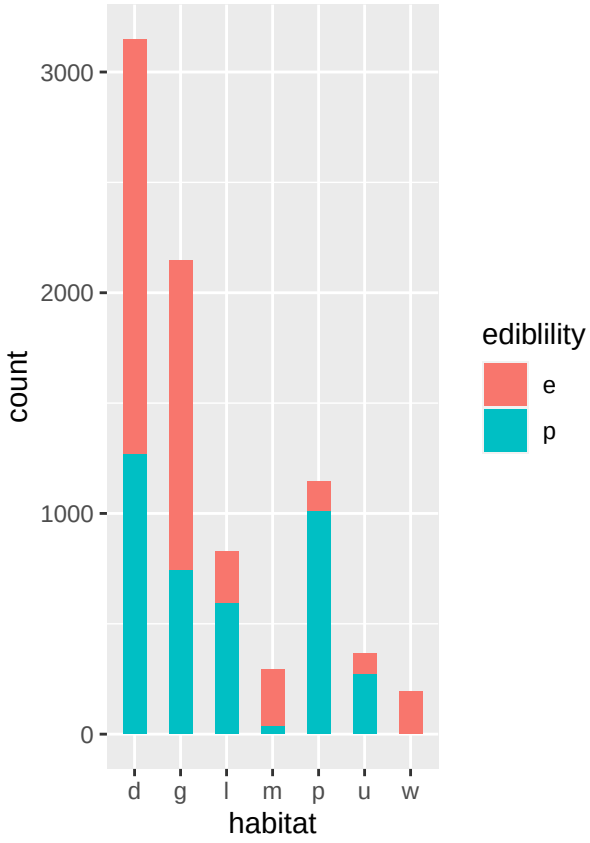



```
grid.arrange(p17, p18, p19, p20)
```




```
grid.arrange(p21, p22, nrow = 1)
```


4000
3000
2000
1000
0
count
a
c
n
s
v
y
population
ediblility
e
p


3000
2000
1000
0
count
d
g
l
m
p
u
w
habitat
ediblility
e
p