

HW2

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一、Variable Definition

```
library(dplyr)
library(Hmisc)
library(tibble)
library(knitr)
library(table1)
library(reticulate)
#
mushroom_data <- tibble::tribble(
  ~Variable, ~ "Data Type", ~"Values/Range",
  "family", "Categorical", "familyname",
  "name", "Categorical", "Mushroomvarietyname",
  "class", "Binary", "poisonous=p, edible=e",
  "cap-diameter", "Continuous", "float (cm)",
  "cap-shape", "Categorical", "{b, c, x, f, s, p, o}",
  "cap-surface", "Categorical", "{i, g, y, s, h, l, k, t, w, e}",
  "cap-color", "Categorical", "{n, b, g, r, p, u, e, w, y, l, o, k}",
  "does-bruise-bleed", "Categorical", "{t, f}",
  "gill-attachment", "Categorical", "{a, x, d, e, s, p, f, ?}",
  "gill-spacing", "Categorical", "{c, d, f}",
  "gill-color", "Categorical", "{cap-color + f}",
  "stem-height", "Continuous", "float (cm)",
  "stem-width", "Continuous", "float (mm)",
  "stem-root", "Categorical", "{b, s, c, u, e, z, r}",
  "stem-surface", "Categorical", "{cap-surface + f}",
  "stem-color", "Categorical", "{cap-color + f}",
  "veil-type", "Categorical", "{p, u}",
  "veil-color", "Categorical", "{cap-color + f}",
```

```

"has-ring", "Categorical", "{t, f}",
"ring-type", "Categorical", "{c, e, r, g, l, p, s, z, y, m, f, ?}",
"spore-print-color", "Categorical", "{cap-color}",
"habitat", "Categorical", "{g, l, m, p, h, u, w, d}",
"season", "Categorical", "{s, u, a, w}"
)
kable(mushroom_data, format = "latex", booktabs = TRUE, escape = FALSE, caption="Mushroom Variable Table",

```

表 1: Mushroom Variable Table

Variable	Data Type	Values/Range
family	Categorical	familyname
name	Categorical	Mushroomvarietyname
class	Binary	poisonous=p, edible=e
cap-diameter	Continuous	float (cm)
cap-shape	Categorical	b, c, x, f, s, p, o
cap-surface	Categorical	i, g, y, s, h, l, k, t, w, e
cap-color	Categorical	n, b, g, r, p, u, e, w, y, l, o, k
does-bruise-bleed	Categorical	t, f
gill-attachment	Categorical	a, x, d, e, s, p, f, ?
gill-spacing	Categorical	c, d, f
gill-color	Categorical	cap-color + f
stem-height	Continuous	float (cm)
stem-width	Continuous	float (mm)
stem-root	Categorical	b, s, c, u, e, z, r
stem-surface	Categorical	cap-surface + f
stem-color	Categorical	cap-color + f
veil-type	Categorical	p, u
veil-color	Categorical	cap-color + f
has-ring	Categorical	t, f
ring-type	Categorical	c, e, r, g, l, p, s, z, y, m, f, ?
spore-print-color	Categorical	cap-color
habitat	Categorical	g, l, m, p, h, u, w, d
season	Categorical	s, u, a, w

二、Data Preprocessing

```

library(dplyr)
library(Hmisc)
library(tibble)
library(tidyverse)
library(table1)
library(reticulate)

# CSV
df <- read.csv("primary_data.csv", sep = ";", stringsAsFactors = FALSE)

# []
df[] <- lapply(df, function(x) gsub("\\[|\\]", "", x))
df <- df %>%

```

```

mutate_all(~ifelse(. == "", NA, .))

split_column <- function(data, column_name) {
  data %>%
    mutate(!column_name := str_replace_all(.data[[column_name]], " ", "")) %>% #
    separate(
      !!column_name, into = c(paste0(column_name, "_Min"), paste0(column_name, "_Max")),
      sep = ",", fill = "right"
    ) %>%
    mutate(
      across(c(paste0(column_name, "_Min"), paste0(column_name, "_Max")), as.numeric)
    ) %>%
    mutate(
      !!paste0(column_name, "_Max") := ifelse(
        is.na(.data[[paste0(column_name, "_Max")]]),
        .data[[paste0(column_name, "_Min")]],
        .data[[paste0(column_name, "_Max")]]
      )
    )
}

df_clean <- df %>%
  split_column("cap.diameter") %>%
  split_column("stem.height") %>%
  split_column("stem.width")

#
write.csv(df_clean, "cleaned_data.csv", row.names = FALSE)

```

三、Data Description

```

library(Hmisc)
library(knitr)
df <- read.csv("cleaned_data.csv")
library(dplyr)
df<-df %>%
  mutate(across(-c(cap.diameter_Min, cap.diameter_Max, stem.height_Min, stem.height_Max, stem.width_Min, stem.w
df<-df %>%
  mutate(across(c(family, name), as.character))
df<-df %>%
  mutate(across(c(cap.diameter_Min, cap.diameter_Max, stem.height_Min, stem.height_Max, stem.width_Min, stem.w

desc_stats <- Hmisc::describe(df)
desc_stats

```

df

26 Variables	173 Observations
--------------	------------------

family

n missing distinct

173 0 23

lowest : Amanita Family Bolbitius Family Bolete Family Bracket Fungi Chanterelle Family
highest: Russula Family Saddle-Cup Family Stropharia Family Tricholoma Family Wax Gill Family

name

 n missing distinct
173 0 173

lowest : Amethyst Deceiver Aniseed Funnel Cap Apricot Fungus Bare-toothed Russula
highest: Yellow-gilled Russula Yellow-staining Mushroom Yellow-stemmed Bell Cap Yellow Swamp Russula

class

 n missing distinct
173 0 2

Value e p
Frequency 77 96
Proportion 0.445 0.555

cap.diameter_Min

n	missing	distinct	Info	Mean	pMedian	Gmd	.05
173	0	14	0.976	4.043	3.5	3.038	1
.10	.25	.50	.75	.90	.95		
1	2	3	5	7	8		

Value	0.4	0.5	0.7	1.0	2.0	3.0	4.0	5.0	6.0	7.0	8.0
Frequency	2	4	1	17	39	24	26	29	11	4	9
Proportion	0.012	0.023	0.006	0.098	0.225	0.139	0.150	0.168	0.064	0.023	0.052

Value	10.0	12.0	50.0
Frequency	4	2	1
Proportion	0.023	0.012	0.006

For the frequency table, variable is rounded to the nearest 0

cap.diameter_Max

n	missing	distinct	Info	Mean	pMedian	Gmd	.05
173	0	20	0.991	9.435	8.5	6.548	2
.10	.25	.50	.75	.90	.95		
3	5	8	12	15	20		

Value	1.0	1.3	1.5	2.0	3.0	4.0	5.0	6.0	7.0	8.0	9.0
Frequency	3	1	4	7	6	12	18	16	7	16	3
Proportion	0.017	0.006	0.023	0.040	0.035	0.069	0.104	0.092	0.040	0.092	0.017

Value	10.0	12.0	14.0	15.0	18.0	20.0	25.0	30.0	50.0
Frequency	28	18	3	15	3	5	5	2	1
Proportion	0.162	0.104	0.017	0.087	0.017	0.029	0.029	0.012	0.006

For the frequency table, variable is rounded to the nearest 0

cap.shape

 n missing distinct

173	0	27
-----	---	----

lowest : b b, f b, f, s b, x b, x, f
highest: x, f x, f, s x, o x, p x, s

Cap.surface

n	missing	distinct
133	40	40

lowest : d d, e, y, i d, k d, k, s d, s
highest: t, w, d w w, t y y, s

cap.color

n	missing	distinct
173	0	67

lowest : b b, p, e, y b, u e e, n
highest: y y, n y, o y, o, g, n, r y, o, r, n

does.bruise.or.bleed

n	missing	distinct
173	0	2

Value f t
Frequency 143 30
Proportion 0.827 0.173

gill.attachment

n	missing	distinct
145	28	8

Value a a, d d e f p s x
Frequency 32 8 25 16 10 17 16 21
Proportion 0.221 0.055 0.172 0.110 0.069 0.117 0.110 0.145

gill.spacing

n	missing	distinct
102	71	3

Value c d f
Frequency 70 22 10
Proportion 0.686 0.216 0.098

gill.color

n	missing	distinct
173	0	59

lowest : b b, p, w b, u e f
highest: y, n y, o, e y, r y, r, k y, w

stem.height_Min

n	missing	distinct	Info	Mean	pMedian	Gmd	.05
173	0	12	0.957	4.306	4	2.233	2.0
.10	.25	.50	.75	.90	.95		

	2.0	3.0	4.0	5.0	6.8	8.0					
Value	0	1	2	3	4	5	6	7	8	10	12
Frequency	3	2	21	38	52	24	15	3	7	5	1
Proportion	0.017	0.012	0.121	0.220	0.301	0.139	0.087	0.017	0.040	0.029	0.006

Value	15
Frequency	2
Proportion	0.012

For the frequency table, variable is rounded to the nearest 0

```
stem.height_Max
  n missing distinct      Info      Mean  pMedian      Gmd      .05
173      0       19    0.977    8.873      8      4.37    4.0
.10    .25    .50    .75    .90    .95
5.0     6.0     8.0    10.0   14.8   15.0
```

Value	0	2	3	4	5	6	7	8	9	10	11
Frequency	3	1	2	6	14	25	16	37	2	35	1
Proportion	0.017	0.006	0.012	0.035	0.081	0.145	0.092	0.214	0.012	0.202	0.006

Value	12	14	15	18	20	25	30	35
Frequency	12	1	10	1	4	1	1	1
Proportion	0.069	0.006	0.058	0.006	0.023	0.006	0.006	0.006

For the frequency table, variable is rounded to the nearest 0

```
stem.width_Min
  n missing distinct      Info      Mean  pMedian      Gmd      .05
173      0       16    0.98    8.529      8    6.804      1
.10    .25    .50    .75    .90    .95
2       4       8      10     19     20
```

Value	0.0	0.5	1.0	2.0	3.0	4.0	5.0	6.0	7.0	8.0	10.0
Frequency	3	1	9	18	12	12	19	7	1	10	42
Proportion	0.017	0.006	0.052	0.104	0.069	0.069	0.110	0.040	0.006	0.058	0.243

Value	12.0	15.0	20.0	30.0	40.0
Frequency	1	20	16	1	1
Proportion	0.006	0.116	0.092	0.006	0.006

For the frequency table, variable is rounded to the nearest 0

```
stem.width_Max
  n missing distinct      Info      Mean  pMedian      Gmd      .05
173      0       21    0.992   15.79     14   13.49      2
.10    .25    .50    .75    .90    .95
3       8      12      20     30     40
```

lowest : 0 1 2 3 4, highest: 40 50 60 80 100

```
stem.root
  n missing distinct
```


Frequency	6	1	137	2	2	2	1	1	2	1	2
Proportion	0.036	0.006	0.825	0.012	0.012	0.012	0.006	0.006	0.012	0.006	0.012

Value	r	z
Frequency	3	6
Proportion	0.018	0.036

```
Spore.print.color
  n missing distinct
18    155         8
```

Value	g	k	k, r	k, u	n	p	p, w	w
Frequency	1	5	1	1	3	3	1	3
Proportion	0.056	0.278	0.056	0.056	0.167	0.167	0.056	0.167

```
habitat
  n missing distinct
173     0        21
```

lowest : d	d, h	g	g, d	g, d, h
highest: m	m, d	m, h	p, d	w

```
season
  n missing distinct
173     0        10
```

Value	a	a, w	s	s, a, w	s, u	s, u, a
Frequency	16	15	1	1	3	5
Proportion	0.092	0.087	0.006	0.006	0.017	0.029

Value	s, u, a, w	u	u, a	u, a, w
Frequency	13	1	106	12
Proportion	0.075	0.006	0.613	0.069

四、Table One

```
library(table1)
df$class<-ifelse(df$class=="e","Edible","Poisonous")
options(table1.longtable= TRUE)
table1(~ cap.diameter_Min+cap.diameter_Max+stem.height_Min+stem.height_Max+stem.width_Min+stem.width_Max)
```


	Edible	Poisonous	Overall
	(N=77)	(N=96)	(N=173)
cap.diameter_Min			
Mean (SD)	4.75 (5.74)	3.47 (2.27)	4.04 (4.22)
Median [Min, Max]	4.00 [0.500, 50.0]	3.00 [0.400, 10.0]	3.00 [0.400, 50.0]
cap.diameter_Max			
Mean (SD)	10.9 (7.29)	8.29 (5.58)	9.44 (6.50)
Median [Min, Max]	10.0 [1.50, 50.0]	7.00 [1.00, 30.0]	8.00 [1.00, 50.0]
stem.height_Min			
Mean (SD)	4.52 (2.20)	4.14 (2.31)	4.31 (2.26)
Median [Min, Max]	4.00 [2.00, 15.0]	4.00 [0, 15.0]	4.00 [0, 15.0]
stem.height_Max			
Mean (SD)	9.58 (5.03)	8.30 (4.03)	8.87 (4.53)
Median [Min, Max]	8.00 [3.00, 35.0]	8.00 [0, 20.0]	8.00 [0, 35.0]
stem.width_Min			
Mean (SD)	10.1 (6.80)	7.26 (5.71)	8.53 (6.36)
Median [Min, Max]	10.0 [1.00, 40.0]	5.00 [0, 20.0]	8.00 [0, 40.0]
stem.width_Max			
Mean (SD)	18.6 (15.7)	13.5 (11.8)	15.8 (13.9)
Median [Min, Max]	15.0 [1.00, 100]	10.0 [0, 60.0]	12.0 [0, 100]