

RWorksheet_5

BSIT-2B

2023-12-10

##Basic Statistics

#1. Create a data frame for the table below. Show your solution.

```
students_score <- data.frame (  
  Students = c(1,2,3,4,5,6,7,8,9,10),  
  preTest = c(55,54,47,57,51,61,57,54,63,58),  
  postTest = c(61,60,56,63,56,63,59,56,62,61)  
)  
students_score
```

##	Students	preTest	postTest
## 1	1	55	61
## 2	2	54	60
## 3	3	47	56
## 4	4	57	63
## 5	5	51	56
## 6	6	61	63
## 7	7	57	59
## 8	8	54	56
## 9	9	63	62
## 10	10	58	61

#a. Compute the descriptive statistics using different packages (Hmisc and pastecs). Write the codes and
`library(Hmisc)`

```
## Warning: package 'Hmisc' was built under R version 4.3.2
```

```
##
```

```
## Attaching package: 'Hmisc'
```

```
## The following objects are masked from 'package:base':
```

```
##
```

```
##      format.pval, units
```

```
library(pastecs)
```

```
## Warning: package 'pastecs' was built under R version 4.3.2
```

```
stats_hmisc <- describe(students_score)
stats_hmisc
```

```
## students_score
##
## 3 Variables      10 Observations
## -----
## Students
##      n missing distinct      Info      Mean      Gmd      .05      .10
##      10         0         10         1       5.5     3.667     1.45     1.90
##      .25      .50      .75      .90      .95
##      3.25     5.50     7.75     9.10     9.55
##
## Value      1  2  3  4  5  6  7  8  9 10
## Frequency  1  1  1  1  1  1  1  1  1  1
## Proportion 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1
##
## For the frequency table, variable is rounded to the nearest 0
## -----
## preTest
##      n missing distinct      Info      Mean      Gmd
##      10         0         8     0.988     55.7     5.444
##
## Value      47 51 54 55 57 58 61 63
## Frequency  1  1  2  1  2  1  1  1
## Proportion 0.1 0.1 0.2 0.1 0.2 0.1 0.1 0.1
##
## For the frequency table, variable is rounded to the nearest 0
## -----
## postTest
##      n missing distinct      Info      Mean      Gmd
##      10         0         6     0.964     59.7     3.311
##
## Value      56 59 60 61 62 63
## Frequency  3  1  1  2  1  2
## Proportion 0.3 0.1 0.1 0.2 0.1 0.2
##
## For the frequency table, variable is rounded to the nearest 0
## -----
```

```
stats_pastics <- stat.desc(students_score)
stats_pastics
```

```
##           Students      preTest      postTest
## nbr.val    10.0000000  10.0000000  10.0000000
## nbr.null     0.0000000   0.0000000   0.0000000
## nbr.na       0.0000000   0.0000000   0.0000000
## min         1.0000000  47.0000000  56.0000000
## max        10.0000000  63.0000000  63.0000000
## range        9.0000000  16.0000000   7.0000000
## sum        55.0000000 557.0000000 597.0000000
## median       5.5000000  56.0000000  60.5000000
```

```
## mean      5.5000000  55.70000000  59.70000000
## SE.mean   0.9574271   1.46855938   0.89504811
## CI.mean.0.95 2.1658506   3.32211213   2.02473948
## var       9.1666667  21.56666667   8.01111111
## std.dev   3.0276504   4.64399254   2.83039063
## coef.var  0.5504819   0.08337509   0.04741023
```

##2. The Department of Agriculture was studying the effects of several levels of a fertilizer on the growth of a plant. For some analyses, it might be useful to convert the fertilizer levels to an ordered factor.

```
#a. Write the codes and describe the result.
order_fertilize <- c(10,10,10, 20,20,50,10,20,10,50,20,50,20,10)
ordered(order_fertilize)
```

```
## [1] 10 10 10 20 20 50 10 20 10 50 20 50 20 10
## Levels: 10 < 20 < 50
```

```
# the data_fertilize result shows the level as an ordered factor.
```

##3. Abdul Hassan, president of Floor Coverings Unlimited, has asked you to study the exercise levels undertaken by 10 subjects were “l”, “n”, “n”, “i”, “l”, “l”, “n”, “n”, “i”, “l” ; n=none, l=light, i=intense.

```
# a. What is the best way to represent this in R?
exe_levels <- c("l", "n", "n", "i", "l", "l", "n", "n", "i", "l")
exe_factor <- factor(exe_levels, levels = c("n", "l", "i"), labels = c("none", "light", "intense"))
exe_factor
```

```
## [1] light none none intense light light none none intense
## [10] light
## Levels: none light intense
```

4. Sample of 30 tax accountants from all the states and territories of Australia and their individual state of origin is specified by a character vector of state mnemonics as:

```
#a. Apply the factor function and factor level. Describe the results.
#the factor_with_level variable result is factor with level.

aussie_state <- c("tas", "sa", "qld", "nsw", "nsw", "nt", "wa", "wa", "qld",
                  "vic", "nsw", "vic", "qld", "qld", "sa", "tas", "sa", "nt",
                  "wa", "vic", "qld", "nsw", "nsw", "wa", "sa", "act", "nsw",
                  "vic", "vic", "act")
aussie_state
```

```
## [1] "tas" "sa" "qld" "nsw" "nsw" "nt" "wa" "wa" "qld" "vic" "nsw" "vic"
## [13] "qld" "qld" "sa" "tas" "sa" "nt" "wa" "vic" "qld" "nsw" "nsw" "wa"
## [25] "sa" "act" "nsw" "vic" "vic" "act"
```

```
factor_and_level <- factor(aussie_state, levels = c("act", "nsw", "nt", "qld", "sa", "tas", "vic", "wa"))
factor_and_level
```

```
## [1] tas sa qld nsw nsw nt wa wa qld vic nsw vic qld qld sa tas sa nt wa
## [20] vic qld nsw nsw wa sa act nsw vic vic act
## Levels: act nsw nt qld sa tas vic wa
```

##5. From #4 - continuation:

```
aussie_incomes <- c(60, 49, 40, 61, 64, 60, 59, 54,
                    62, 69, 70, 42, 56, 61, 61, 61, 58, 51, 48,
                    65, 49, 49, 41, 48, 52, 46, 59, 46, 58, 43)
aussie_incomes
```

```
## [1] 60 49 40 61 64 60 59 54 62 69 70 42 56 61 61 61 58 51 48 65 49 49 41 48 52
## [26] 46 59 46 58 43
```

a. Calculate the sample mean income for each state we can now use the special function tapply():

```
incmeans <- tapply(aussie_incomes, factor_and_level, mean)
incmeans
```

```
##      act      nsw      nt      qld      sa      tas      vic      wa
## 44.50000 57.33333 55.50000 53.60000 55.00000 60.50000 56.00000 52.25000
```

b. Copy the results and interpret.

#The result has the means of each states that has factor with levels

##6. Calculate the standard errors of the state income means (refer again to number 3)

#stdError <- function(x) sqrt(var(x)/length(x)) Note: After this assignment, the standard errors are ca

#a. What is the standard error? Write the codes.

```
stdErrors <- function(x) sqrt(var(x)/length(x))
stdErrors
```

```
## function(x) sqrt(var(x)/length(x))
```

```
incster <- tapply(aussie_incomes, factor_and_level, stdErrors)
incster
```

```
##      act      nsw      nt      qld      sa      tas      vic      wa
## 1.500000 4.310195 4.500000 4.106093 2.738613 0.500000 5.244044 2.657536
```

#b. Interpret the result.

#It displays the state income means' computed standard errors. The sample mean income is a reasonably a

#7. Use the titanic dataset.

#a. subset the titanic dataset of those who survived and not survived. Show the codes and its result.

```
library(datasets)
```

```
data(Titanic)
```

```
Titanic<-as.data.frame(Titanic)
```

```
subset_titanic<-subset(Titanic, Survived=="Yes")
```

```
subset_titanic
```

##	Class	Sex	Age	Survived	Freq
## 17	1st	Male	Child	Yes	5
## 18	2nd	Male	Child	Yes	11
## 19	3rd	Male	Child	Yes	13
## 20	Crew	Male	Child	Yes	0
## 21	1st	Female	Child	Yes	1
## 22	2nd	Female	Child	Yes	13
## 23	3rd	Female	Child	Yes	14
## 24	Crew	Female	Child	Yes	0
## 25	1st	Male	Adult	Yes	57
## 26	2nd	Male	Adult	Yes	14
## 27	3rd	Male	Adult	Yes	75
## 28	Crew	Male	Adult	Yes	192
## 29	1st	Female	Adult	Yes	140
## 30	2nd	Female	Adult	Yes	80
## 31	3rd	Female	Adult	Yes	76
## 32	Crew	Female	Adult	Yes	20

```
not_subset_titanic<- subset(Titanic, Survived == "No")
```

```
not_subset_titanic
```

##	Class	Sex	Age	Survived	Freq
## 1	1st	Male	Child	No	0
## 2	2nd	Male	Child	No	0
## 3	3rd	Male	Child	No	35
## 4	Crew	Male	Child	No	0
## 5	1st	Female	Child	No	0
## 6	2nd	Female	Child	No	0
## 7	3rd	Female	Child	No	17
## 8	Crew	Female	Child	No	0
## 9	1st	Male	Adult	No	118
## 10	2nd	Male	Adult	No	154
## 11	3rd	Male	Adult	No	387
## 12	Crew	Male	Adult	No	670
## 13	1st	Female	Adult	No	4
## 14	2nd	Female	Adult	No	13
## 15	3rd	Female	Adult	No	89
## 16	Crew	Female	Adult	No	3

##8. The data sets are about the breast cancer Wisconsin. The samples arrive periodically as Dr. Wolberg reports his clinical cases.

```
library(readr)
csv.file<-"breastcancer_wisconsin.csv"
breastcancer_wisconsin<-read.csv("breastcancer_wisconsin.csv")
breastcancer_wisconsin
```

##	id	clump_thickness	size_uniformity	shape_uniformity	marginal_adhesion
## 1	1000025	5	1	1	1
## 2	1002945	5	4	4	5
## 3	1015425	3	1	1	1
## 4	1016277	6	8	8	1
## 5	1017023	4	1	1	3
## 6	1017122	8	10	10	8
## 7	1018099	1	1	1	1
## 8	1018561	2	1	2	1
## 9	1033078	2	1	1	1
## 10	1033078	4	2	1	1
## 11	1035283	1	1	1	1
## 12	1036172	2	1	1	1
## 13	1041801	5	3	3	3
## 14	1043999	1	1	1	1
## 15	1044572	8	7	5	10
## 16	1047630	7	4	6	4
## 17	1048672	4	1	1	1
## 18	1049815	4	1	1	1
## 19	1050670	10	7	7	6
## 20	1050718	6	1	1	1
## 21	1054590	7	3	2	10
## 22	1054593	10	5	5	3
## 23	1056784	3	1	1	1
## 24	1057013	8	4	5	1
## 25	1059552	1	1	1	1
## 26	1065726	5	2	3	4
## 27	1066373	3	2	1	1
## 28	1066979	5	1	1	1
## 29	1067444	2	1	1	1
## 30	1070935	1	1	3	1
## 31	1070935	3	1	1	1
## 32	1071760	2	1	1	1
## 33	1072179	10	7	7	3
## 34	1074610	2	1	1	2
## 35	1075123	3	1	2	1
## 36	1079304	2	1	1	1
## 37	1080185	10	10	10	8
## 38	1081791	6	2	1	1
## 39	1084584	5	4	4	9
## 40	1091262	2	5	3	3
## 41	1096800	6	6	6	9
## 42	1099510	10	4	3	1
## 43	1100524	6	10	10	2
## 44	1102573	5	6	5	6
## 45	1103608	10	10	10	4
## 46	1103722	1	1	1	1
## 47	1105257	3	7	7	4

## 48	1105524	1	1	1	1
## 49	1106095	4	1	1	3
## 50	1106829	7	8	7	2
## 51	1108370	9	5	8	1
## 52	1108449	5	3	3	4
## 53	1110102	10	3	6	2
## 54	1110503	5	5	5	8
## 55	1110524	10	5	5	6
## 56	1111249	10	6	6	3
## 57	1112209	8	10	10	1
## 58	1113038	8	2	4	1
## 59	1113483	5	2	3	1
## 60	1113906	9	5	5	2
## 61	1115282	5	3	5	5
## 62	1115293	1	1	1	1
## 63	1116116	9	10	10	1
## 64	1116132	6	3	4	1
## 65	1116192	1	1	1	1
## 66	1116998	10	4	2	1
## 67	1117152	4	1	1	1
## 68	1118039	5	3	4	1
## 69	1120559	8	3	8	3
## 70	1121732	1	1	1	1
## 71	1121919	5	1	3	1
## 72	1123061	6	10	2	8
## 73	1124651	1	3	3	2
## 74	1125035	9	4	5	10
## 75	1126417	10	6	4	1
## 76	1131294	1	1	2	1
## 77	1132347	1	1	4	1
## 78	1133041	5	3	1	2
## 79	1133136	3	1	1	1
## 80	1136142	2	1	1	1
## 81	1137156	2	2	2	1
## 82	1143978	4	1	1	2
## 83	1143978	5	2	1	1
## 84	1147044	3	1	1	1
## 85	1147699	3	5	7	8
## 86	1147748	5	10	6	1
## 87	1148278	3	3	6	4
## 88	1148873	3	6	6	6
## 89	1152331	4	1	1	1
## 90	1155546	2	1	1	2
## 91	1156272	1	1	1	1
## 92	1156948	3	1	1	2
## 93	1157734	4	1	1	1
## 94	1158247	1	1	1	1
## 95	1160476	2	1	1	1
## 96	1164066	1	1	1	1
## 97	1165297	2	1	1	2
## 98	1165790	5	1	1	1
## 99	1165926	9	6	9	2
## 100	1166630	7	5	6	10
## 101	1166654	10	3	5	1

## 102	1167439	2	3	4	4
## 103	1167471	4	1	2	1
## 104	1168359	8	2	3	1
## 105	1168736	10	10	10	10
## 106	1169049	7	3	4	4
## 107	1170419	10	10	10	8
## 108	1170420	1	6	8	10
## 109	1171710	1	1	1	1
## 110	1171710	6	5	4	4
## 111	1171795	1	3	1	2
## 112	1171845	8	6	4	3
## 113	1172152	10	3	3	10
## 114	1173216	10	10	10	3
## 115	1173235	3	3	2	1
## 116	1173347	1	1	1	1
## 117	1173347	8	3	3	1
## 118	1173509	4	5	5	10
## 119	1173514	1	1	1	1
## 120	1173681	3	2	1	1
## 121	1174057	1	1	2	2
## 122	1174057	4	2	1	1
## 123	1174131	10	10	10	2
## 124	1174428	5	3	5	1
## 125	1175937	5	4	6	7
## 126	1176406	1	1	1	1
## 127	1176881	7	5	3	7
## 128	1177027	3	1	1	1
## 129	1177399	8	3	5	4
## 130	1177512	1	1	1	1
## 131	1178580	5	1	3	1
## 132	1179818	2	1	1	1
## 133	1180194	5	10	8	10
## 134	1180523	3	1	1	1
## 135	1180831	3	1	1	1
## 136	1181356	5	1	1	1
## 137	1182404	4	1	1	1
## 138	1182410	3	1	1	1
## 139	1183240	4	1	2	1
## 140	1183246	1	1	1	1
## 141	1183516	3	1	1	1
## 142	1183911	2	1	1	1
## 143	1183983	9	5	5	4
## 144	1184184	1	1	1	1
## 145	1184241	2	1	1	1
## 146	1184840	1	1	3	1
## 147	1185609	3	4	5	2
## 148	1185610	1	1	1	1
## 149	1187457	3	1	1	3
## 150	1187805	8	8	7	4
## 151	1188472	1	1	1	1
## 152	1189266	7	2	4	1
## 153	1189286	10	10	8	6
## 154	1190394	4	1	1	1
## 155	1190485	1	1	1	1

## 156	1192325	5	5	5	6
## 157	1193091	1	2	2	1
## 158	1193210	2	1	1	1
## 159	1193683	1	1	2	1
## 160	1196295	9	9	10	3
## 161	1196915	10	7	7	4
## 162	1197080	4	1	1	1
## 163	1197270	3	1	1	1
## 164	1197440	1	1	1	2
## 165	1197510	5	1	1	1
## 166	1197979	4	1	1	1
## 167	1197993	5	6	7	8
## 168	1198128	10	8	10	10
## 169	1198641	3	1	1	1
## 170	1199219	1	1	1	2
## 171	1199731	3	1	1	1
## 172	1199983	1	1	1	1
## 173	1200772	1	1	1	1
## 174	1200847	6	10	10	10
## 175	1200892	8	6	5	4
## 176	1200952	5	8	7	7
## 177	1201834	2	1	1	1
## 178	1201936	5	10	10	3
## 179	1202125	4	1	1	1
## 180	1202812	5	3	3	3
## 181	1203096	1	1	1	1
## 182	1204242	1	1	1	1
## 183	1204898	6	1	1	1
## 184	1205138	5	8	8	8
## 185	1205579	8	7	6	4
## 186	1206089	2	1	1	1
## 187	1206695	1	5	8	6
## 188	1206841	10	5	6	10
## 189	1207986	5	8	4	10
## 190	1208301	1	2	3	1
## 191	1210963	10	10	10	8
## 192	1211202	7	5	10	10
## 193	1212232	5	1	1	1
## 194	1212251	1	1	1	1
## 195	1212422	3	1	1	1
## 196	1212422	4	1	1	1
## 197	1213375	8	4	4	5
## 198	1213383	5	1	1	4
## 199	1214092	1	1	1	1
## 200	1214556	3	1	1	1
## 201	1214966	9	7	7	5
## 202	1216694	10	8	8	4
## 203	1216947	1	1	1	1
## 204	1217051	5	1	1	1
## 205	1217264	1	1	1	1
## 206	1218105	5	10	10	9
## 207	1218741	10	10	9	3
## 208	1218860	1	1	1	1
## 209	1218860	1	1	1	1

## 210	1219406	5	1	1	1
## 211	1219525	8	10	10	10
## 212	1219859	8	10	8	8
## 213	1220330	1	1	1	1
## 214	1221863	10	10	10	10
## 215	1222047	10	10	10	10
## 216	1222936	8	7	8	7
## 217	1223282	1	1	1	1
## 218	1223426	1	1	1	1
## 219	1223793	6	10	7	7
## 220	1223967	6	1	3	1
## 221	1224329	1	1	1	2
## 222	1225799	10	6	4	3
## 223	1226012	4	1	1	3
## 224	1226612	7	5	6	3
## 225	1227210	10	5	5	6
## 226	1227244	1	1	1	1
## 227	1227481	10	5	7	4
## 228	1228152	8	9	9	5
## 229	1228311	1	1	1	1
## 230	1230175	10	10	10	3
## 231	1230688	7	4	7	4
## 232	1231387	6	8	7	5
## 233	1231706	8	4	6	3
## 234	1232225	10	4	5	5
## 235	1236043	3	3	2	1
## 236	1241232	3	1	4	1
## 237	1241559	10	8	8	2
## 238	1241679	9	8	8	5
## 239	1242364	8	10	10	8
## 240	1243256	10	4	3	2
## 241	1270479	5	1	3	3
## 242	1276091	3	1	1	3
## 243	1277018	2	1	1	1
## 244	128059	1	1	1	1
## 245	1285531	1	1	1	1
## 246	1287775	5	1	1	2
## 247	144888	8	10	10	8
## 248	145447	8	4	4	1
## 249	167528	4	1	1	1
## 250	169356	3	1	1	1
## 251	183913	1	2	2	1
## 252	191250	10	4	4	10
## 253	1017023	6	3	3	5
## 254	1100524	6	10	10	2
## 255	1116116	9	10	10	1
## 256	1168736	5	6	6	2
## 257	1182404	3	1	1	1
## 258	1182404	3	1	1	1
## 259	1198641	3	1	1	1
## 260	242970	5	7	7	1
## 261	255644	10	5	8	10
## 262	263538	5	10	10	6
## 263	274137	8	8	9	4

## 264	303213	10	4	4	10
## 265	314428	7	9	4	10
## 266	1182404	5	1	4	1
## 267	1198641	10	10	6	3
## 268	320675	3	3	5	2
## 269	324427	10	8	8	2
## 270	385103	1	1	1	1
## 271	390840	8	4	7	1
## 272	411453	5	1	1	1
## 273	320675	3	3	5	2
## 274	428903	7	2	4	1
## 275	431495	3	1	1	1
## 276	432809	3	1	3	1
## 277	434518	3	1	1	1
## 278	452264	1	1	1	1
## 279	456282	1	1	1	1
## 280	476903	10	5	7	3
## 281	486283	3	1	1	1
## 282	486662	2	1	1	2
## 283	488173	1	4	3	10
## 284	492268	10	4	6	1
## 285	508234	7	4	5	10
## 286	527363	8	10	10	10
## 287	529329	10	10	10	10
## 288	535331	3	1	1	1
## 289	543558	6	1	3	1
## 290	555977	5	6	6	8
## 291	560680	1	1	1	1
## 292	561477	1	1	1	1
## 293	563649	8	8	8	1
## 294	601265	10	4	4	6
## 295	606140	1	1	1	1
## 296	606722	5	5	7	8
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## 609	10	10	10	1	1	4
## 610	2	1	1	1	1	2
## 611	3	10	7	1	2	4
## 612	5	2	8	5	1	4
## 613	6	10	10	10	10	4
## 614	2	1	2	1	1	2
## 615	1	1	2	1	1	2
## 616	2	1	2	1	1	2
## 617	2	1	2	1	1	2
## 618	1	?	1	1	1	2
## 619	2	1	2	1	1	2
## 620	2	1	2	1	1	2
## 621	2	1	2	1	1	2
## 622	3	2	6	1	1	2
## 623	2	1	2	1	1	2
## 624	2	1	1	1	1	2
## 625	1	1	2	1	1	2
## 626	3	4	1	1	1	2
## 627	7	6	7	7	3	4
## 628	2	5	1	1	1	2
## 629	2	1	1	1	1	2
## 630	2	1	1	1	1	2
## 631	2	1	1	1	1	2
## 632	2	1	2	1	1	2
## 633	2	1	1	1	1	2
## 634	5	3	5	10	1	4
## 635	2	1	1	1	1	2
## 636	2	1	1	1	1	2
## 637	7	1	10	10	3	4
## 638	2	2	2	1	1	2
## 639	2	1	1	1	1	2
## 640	2	1	1	1	1	2
## 641	2	1	1	1	1	2
## 642	2	1	2	1	1	2
## 643	2	1	2	1	1	2

## 644	2	1	1	1	1	2
## 645	2	1	1	1	1	2
## 646	2	1	2	1	1	2
## 647	2	1	1	1	1	2
## 648	2	1	1	1	1	2
## 649	10	2	10	10	10	4
## 650	2	1	2	1	1	2
## 651	3	4	1	1	1	2
## 652	2	1	2	1	1	2
## 653	2	1	2	2	1	2
## 654	2	1	2	1	1	2
## 655	2	1	3	1	1	2
## 656	2	1	2	1	1	2
## 657	2	1	2	1	1	2
## 658	8	1	3	6	1	2
## 659	3	10	7	2	3	4
## 660	2	1	1	1	1	2
## 661	2	1	2	1	1	2
## 662	2	1	3	1	1	2
## 663	2	1	2	1	1	2
## 664	2	1	2	1	1	2
## 665	2	1	2	1	1	2
## 666	2	1	1	1	1	2
## 667	2	1	1	1	2	2
## 668	2	1	3	1	1	2
## 669	6	1	7	10	3	4
## 670	5	5	7	10	1	4
## 671	5	8	7	4	1	4
## 672	2	1	3	1	1	2
## 673	2	1	3	1	1	2
## 674	3	1	1	1	1	2
## 675	2	1	2	1	1	2
## 676	2	1	1	1	1	2
## 677	2	1	2	1	1	2
## 678	2	1	1	1	1	2
## 679	2	1	1	1	1	2
## 680	2	1	1	1	1	2
## 681	5	10	10	10	7	4
## 682	4	10	5	6	3	4
## 683	2	1	3	2	1	2
## 684	2	1	1	1	1	2
## 685	2	1	1	1	1	2
## 686	2	1	1	1	1	2
## 687	2	1	1	1	1	2
## 688	2	1	2	3	1	2
## 689	2	1	1	1	1	2
## 690	2	1	1	1	8	2
## 691	2	1	1	1	1	2
## 692	4	5	4	4	1	4
## 693	2	1	1	1	1	2
## 694	2	1	2	1	2	2
## 695	3	2	1	1	1	2
## 696	2	1	1	1	1	2
## 697	7	3	8	10	2	4

```
## 698          3          4          10          6          1          4
## 699          4          5          10          4          1          4
```

```
summary(breastcancer_wisconsin)
```

```
##          id          clump_thickness  size_uniformity  shape_uniformity
## Min.     : 61634  Min.     : 1.000  Min.     : 1.000  Min.     : 1.000
## 1st Qu.: 870688  1st Qu.: 2.000  1st Qu.: 1.000  1st Qu.: 1.000
## Median : 1171710 Median : 4.000  Median : 1.000  Median : 1.000
## Mean    : 1071704 Mean    : 4.418  Mean    : 3.134  Mean    : 3.207
## 3rd Qu.: 1238298 3rd Qu.: 6.000  3rd Qu.: 5.000  3rd Qu.: 5.000
## Max.    :13454352 Max.    :10.000  Max.    :10.000  Max.    :10.000
## marginal_adhesion epithelial_size  bare_nucleoli      bland_chromatin
## Min.     : 1.000  Min.     : 1.000  Length:699        Min.     : 1.000
## 1st Qu.: 1.000  1st Qu.: 2.000  Class :character  1st Qu.: 2.000
## Median : 1.000  Median : 2.000  Mode  :character  Median : 3.000
## Mean    : 2.807  Mean    : 3.216                      Mean    : 3.438
## 3rd Qu.: 4.000  3rd Qu.: 4.000                      3rd Qu.: 5.000
## Max.    :10.000  Max.    :10.000                      Max.    :10.000
## normal_nucleoli    mitoses          class
## Min.     : 1.000  Min.     : 1.000  Min.     :2.00
## 1st Qu.: 1.000  1st Qu.: 1.000  1st Qu.:2.00
## Median : 1.000  Median : 1.000  Median :2.00
## Mean    : 2.867  Mean    : 1.589  Mean    :2.69
## 3rd Qu.: 4.000  3rd Qu.: 1.000  3rd Qu.:4.00
## Max.    :10.000  Max.    :10.000  Max.    :4.00
```

```
#a. describe what is the dataset all about.
```

```
#It displays the state income means' computed standard errors. The sample mean income is a reasonably a
```

```
#d. Compute the descriptive statistics using different packages. Find the values of:
```

```
#d.1 Standard error of the mean for clump thickness.
```

```
clumpThickness_dataset <- breastcancer_wisconsin$clump_thickness
stdError_clump_thickness <- stdErrors(clumpThickness_dataset)
stdError_clump_thickness
```

```
## [1] 0.1065011
```

```
#d.2 Coefficient of variability for Marginal Adhesion.
```

```
marginalAdhesion_data <- breastcancer_wisconsin$marginal_adhesion
mean <- mean(marginalAdhesion_data)
sd <- sd(marginalAdhesion_data)
cv <- sd / mean
cv
```

```
## [1] 1.017283
```

```
cv<-cv*100 #getting the percentage
cv
```

```
## [1] 101.7283
```



```
#d.3 Number of null values of Bare Nuclei.
```

```
bareNuclei_data <- breastcancer_wisconsin$bare_nucleoli  
numNull_values <- sum(is.na(bareNuclei_data))  
numNull_values
```

```
## [1] 15
```

```
#d.4 Mean and standard deviation for Bland Chromatin
```

```
blandChromatin_data <- breastcancer_wisconsin$bland_chromatin  
mean_blandChromatin <- mean(blandChromatin_data)  
sd_blandChromatin <- sd(blandChromatin_data)  
mean_blandChromatin
```

```
## [1] 3.437768
```

```
sd_blandChromatin
```

```
## [1] 2.438364
```

```
#d.5 Confidence interval of the mean for Uniformity of Cell Shape
```

```
#Using t.test function
```

```
shapeUniformity_data <- breastcancer_wisconsin$shape_uniformity  
confidence_Interval <- t.test(shapeUniformity_data, na.rm = TRUE)$conf.int  
confidence_Interval
```

```
## [1] 2.986741 3.428138
```

```
## attr("conf.level")
```

```
## [1] 0.95
```

```
#d. How many attributes?
```

```
length(breastcancer_wisconsin)
```

```
## [1] 11
```

```
names(breastcancer_wisconsin)
```

```
## [1] "id" "clump_thickness" "size_uniformity"  
## [4] "shape_uniformity" "marginal_adhesion" "epithelial_size"  
## [7] "bare_nucleoli" "bland_chromatin" "normal_nucleoli"  
## [10] "mitoses" "class"
```

```
#e. Find the percentage of respondents who are malignant. Interpret the results
```

```
percentage_malignant <- sum(breastcancer_wisconsin$class == 4) / nrow(breastcancer_wisconsin) * 100  
percentage_malignant
```

```
## [1] 34.47783
```

#Accordingly, the result 34.47783 indicates that roughly 34.48% of the participants in the dataset on b

##9. Export the data abalone to the Microsoft excel file. Copy the codes.

```
library("AppliedPredictiveModeling")
```

```
## Warning: package 'AppliedPredictiveModeling' was built under R version 4.3.2
```

```
data("abalone")
View(abalone)
head(abalone)
```

```
##   Type LongestShell Diameter Height WholeWeight ShuckedWeight VisceraWeight
## 1    M      0.455    0.365  0.095     0.5140      0.2245      0.1010
## 2    M      0.350    0.265  0.090     0.2255      0.0995      0.0485
## 3    F      0.530    0.420  0.135     0.6770      0.2565      0.1415
## 4    M      0.440    0.365  0.125     0.5160      0.2155      0.1140
## 5    I      0.330    0.255  0.080     0.2050      0.0895      0.0395
## 6    I      0.425    0.300  0.095     0.3515      0.1410      0.0775
##   ShellWeight Rings
## 1      0.150     15
## 2      0.070      7
## 3      0.210      9
## 4      0.155     10
## 5      0.055      7
## 6      0.120      8
```

```
summary(abalone)
```

```
##   Type      LongestShell      Diameter      Height      WholeWeight
## F:1307  Min.   :0.075    Min.   :0.0550  Min.   :0.0000  Min.   :0.0020
## I:1342  1st Qu.:0.450    1st Qu.:0.3500  1st Qu.:0.1150  1st Qu.:0.4415
## M:1528  Median :0.545    Median :0.4250  Median :0.1400  Median :0.7995
##        Mean   :0.524    Mean   :0.4079  Mean   :0.1395  Mean   :0.8287
##        3rd Qu.:0.615    3rd Qu.:0.4800  3rd Qu.:0.1650  3rd Qu.:1.1530
##        Max.   :0.815    Max.   :0.6500  Max.   :1.1300  Max.   :2.8255
## ShuckedWeight VisceraWeight ShellWeight Rings
## Min.   :0.0010  Min.   :0.0005  Min.   :0.0015  Min.   : 1.000
## 1st Qu.:0.1860  1st Qu.:0.0935  1st Qu.:0.1300  1st Qu.: 8.000
## Median :0.3360  Median :0.1710  Median :0.2340  Median : 9.000
## Mean   :0.3594  Mean   :0.1806  Mean   :0.2388  Mean   : 9.934
## 3rd Qu.:0.5020  3rd Qu.:0.2530  3rd Qu.:0.3290  3rd Qu.:11.000
## Max.   :1.4880  Max.   :0.7600  Max.   :1.0050  Max.   :29.000
```

```
abalone_excel<-"C:/Users/missy/OneDrive/Documents/Github/RWorksheets_Sadsad/Worksheet#5/abaloneData.xls"
install.packages("writexl")
```

```
## Installing package into 'C:/Users/missy/AppData/Local/R/win-library/4.3'
## (as 'lib' is unspecified)
```

```
## package 'writexl' successfully unpacked and MD5 sums checked
##
## The downloaded binary packages are in
## C:\Users\missy\AppData\Local\Temp\Rtmpg319Da\downloaded_packages
```

```
library(writexl)
```

```
## Warning: package 'writexl' was built under R version 4.3.2
```

```
write_xlsx(abalone, abalone_excel)
```