Revalidation of Numbers in KJA21212

This code was developed to validate the statistical figures reported in KJA21212. We can confirm that this output was consistently reproducible using R software on both a personal computer (R 4.2.1) and the Google Colaboratory cloud-based Jupyter Notebook (R 4.3.1). Under the supervision of Sang Gyu Kwak (Statistical editor of KJA), Younsuk Lee (Editor-in-Chief of KJA) developed this code, and both individuals thoroughly verified the accuracy of the output.

loading a raw data

In [1]:
```
Sys.setenv(lang = "en_US")
#
# For newly installing the required packages,
# the machine is to be connected to the internet.
#
if (!require(readxl)) install.packages("readxl")
if (!require(magrittr)) install.packages("magrittr")

library(readxl); library(magrittr)
sessionInfo()

#
#
# This script file must be placed at the same directory
# of the source Excel file ("Tejshri master chart main.xlsx").
#
#
d21212 <- readxl::read_excel("Tejshri master chart main.xlsx")
str(d21212)
```

```
Loading required package: readxl

Loading required package: magrittr
```

```
R version 4.3.1 (2023-06-16)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Ubuntu 20.04.6 LTS

Matrix products: default
BLAS:   /usr/lib/x86_64-linux-gnu/openblas-pthread/libblas.so.3
LAPACK: /usr/lib/x86_64-linux-gnu/openblas-pthread/liblapack.so.3;  LAPACK
version 3.9.0

locale:
 [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C
 [3] LC_TIME=en_US.UTF-8        LC_COLLATE=en_US.UTF-8
 [5] LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8
 [7] LC_PAPER=en_US.UTF-8       LC_NAME=C
 [9] LC_ADDRESS=C               LC_TELEPHONE=C
[11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C

time zone: Etc/UTC
tzcode source: system (glibc)

attached base packages:
[1] stats     graphics  grDevices utils     datasets  methods   base

other attached packages:
[1] magrittr_2.0.3 readxl_1.4.2

loaded via a namespace (and not attached):
 [1] digest_0.6.32    IRdisplay_1.1    utf8_1.2.3       base64enc_0.1-3
 [5] fastmap_1.1.1    cellranger_1.1.0 glue_1.6.2       htmltools_0.5.5
 [9] repr_1.1.6       lifecycle_1.0.3  cli_3.6.1        fansi_1.0.4
[13] vctrs_0.6.3      pbdZMQ_0.3-9     compiler_4.3.1   tools_4.3.1
[17] evaluate_0.21    pillar_1.9.0     crayon_1.5.2     rlang_1.1.1
[21] jsonlite_1.8.5   IRkernel_1.3.2   uuid_1.1-0
New names:
• `` -> `...19`
```

```
tibble [90 × 23] (S3: tbl_df/tbl/data.frame)
 $ SN                           : num [1:90] 1 2 3 4 5 6 7 8 9 10 ...
 $ Name                         : chr [1:90] "Manju" "Mayaram" "Shailesh"
"Alok ram" ...
 $ Age(yrs)                     : chr [1:90] "36 yrs" "53 yrs" "38 yrs" "5
3 yrs" ...
 $ Gender                       : chr [1:90] "Female" "Male" "Male" "Male"
...
 $ Height(cm)                   : chr [1:90] "155 cm" "160 cm" "176 cm" "1
62 cm" ...
 $ Weight(kg)                   : chr [1:90] "52 kg" "65 kg" "72 kg" "64 k
g" ...
 $ BMI(kg/m²)                   : chr [1:90] "21.6 kg/m²" "25.4 kg/m²" "23
.2 kg/m²" "24.4 kg/m²" ...
 $ MPG                          : num [1:90] 2 2 2 2 2 2 2 2 2 2 ...
 $ ASA Grade                    : num [1:90] 2 1 1 2 1 1 1 1 1 1 ...
 $ Proposed surgery             : chr [1:90] "Lap chole" "Lap hernia" "Lap
chole" "Lap chole" ...
 $ Duration of surgery (minutes): chr [1:90] "104 min" "135 min" "92 min"
"94 min" ...
 $ Supraglotic device used      : chr [1:90] "I gel" "I gel" "I gel" "I ge
l" ...
 $ Size                         : num [1:90] 3 4 4 4 3 3 3 3 3 3 ...
 $ Number of attempts           : num [1:90] 1 1 1 2 1 1 1 1 1 1 ...
 $ Time of insertion            : chr [1:90] "18 sec" "25 sec" "14 sec" "2
3 sec" ...
 $ Ease of insertion            : chr [1:90] "No resis" "Mild resis" "Mild
" "Moderate" ...
 $ Failure to place device      : chr [1:90] "No" "No" "No" "No" ...
 $ Oropharyngeal leak pressure  : logi [1:90] NA NA NA NA NA NA ...
 $ ...19                        : num [1:90] 14 12 11 14 23 18 22 22 25 16
...
 $ Airway manouvers reqd.       : chr [1:90] "No" "No" "No" "Yes" ...
 $ Type of manouver             : chr [1:90] "Nil" "Nil" "Nil" "Inserted f
urther" ...
 $ Ease of placing gastric tube : chr [1:90] "Easy" "Moderate" "Easy" "Eas
y" ...
 $ Complications                : chr [1:90] "No" "nausea" "No" "sore thro
at" ...
```

In [2]:
```
# Tidying the 19th column name
colnames(d21212)[19] <- "OLP"
```

In [3]:
```
# loading library
library(magrittr)
```

In [4]:
```
# Factoring and ordering the SGA Group
# 30 individuals per each sga group
sga <- factor(d21212$"Supraglotic device used",
    levels = c("I gel", "lma supreme", "Ambu aura gain"))
table(sga)
```

```
sga
        I gel     lma supreme Ambu aura gain
           30              30              30
```

Table 1

Table 1. Demographic Data and Preoperative Assessment of the Study Groups

	Group I (n = 30)	Group L (n = 30)	Group A (n = 30)	P value
Age (yr)	40.2 ± 11.6	42.0 ± 11.5	40.6 ± 15.7	0.852
Sex (F/M)	24/6	25/5	24/6	0.130
Height (cm)	155.7 ± 9.8	156.0 ± 8.5	159.8 ± 8.5	0.157
Weight (kg)	58.9 ± 6.3	59.7 ± 5.2	59.1 ± 5.5	0.866
BMI (kg/m^2)	24.6 ± 4.2	24.8 ± 3.9	23.3 ± 3.4	0.302
Mallampati score (I/II/III)	0/28/2	7/20/3	5/23/2	0.086
ASA PS (I/II/III)	18/12/0	11/12/7	12/13/5	0.070

Values are presented as mean ± SD or number. Group I: i-gel, Group L: LMA Supreme, Group A: Ambu AuraGain. BMI: body mass index, ASA PS: American Society of Anesthesiologists physical status classification.

In [5]:
```
# age: (mean, sd)
# Printed numbers are slightly different from the R output.
#
Age <- as.numeric(gsub("[a-zA-Z]", "", d21212$"Age(yrs)"))
rbind(tapply(Age, sga, mean), tapply(Age, sga, sd))
aov(Age ~ sga) %>% summary
```

A matrix: 2 × 3 of type dbl

I gel	lma supreme	Ambu aura gain
40.20000	42.03333	40.20000
11.57405	11.52055	14.81472

```
            Df Sum Sq Mean Sq F value Pr(>F)
sga          2     67   33.61   0.207  0.813
Residuals   87  14099  162.05
```

In [6]:
```
# sex
table(d21212$Gender, sga)
# clean labeling
# Printed p-value (0.130) is quite different from the R output.
#
clean_gender <- ifelse(grepl("^f", tolower(d21212$Gender)), "F", "M")
clean_gender %>% table(sga) %>% print %>% chisq.test
```

```
        sga
         I gel lma supreme Ambu aura gain
  Fem        0           0              1
  femal      0           0              1
  female     0          19             21
  Female    24           6              1
  male       2           5              6
  Male       4           0              0
```

```
   sga
.   I gel lma supreme Ambu aura gain

  F    24          25             24
  M     6           5              6
        Pearson's Chi-squared test

data:  .
X-squared = 0.14504, df = 2, p-value = 0.93
```

In [7]:
```
# height
summary(d21212$"Height(cm)")
# tidying and summarizing
height <- gsub("[a-zA-Z]", "", d21212$"Height(cm)") %>% as.numeric
summary(height)
# Printed numbers are slightly different from the R output.
#
rbind(tapply(height, sga, mean), tapply(height, sga, sd))
aov(height ~ sga) %>% summary
```

```
  Length     Class      Mode
      90 character character
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 138.0   155.0   158.0   157.2   161.5   176.0
```

A matrix: 2 × 3 of type dbl

	I gel	lma supreme	Ambu aura gain
	155.733333	156.033333	159.800000
	9.874849	8.547971	8.575828

```
            Df Sum Sq Mean Sq F value Pr(>F)
sga          2    308  154.08   1.893  0.157
Residuals   87   7080   81.38
```

In [8]:
```
# weight
summary(d21212$"Weight(kg)")
# tidying and summarizing
weight <- gsub("[a-zA-Z]", "",
    d21212$"Weight(kg)") %>% as.numeric
summary(weight)
# Printed numbers are slightly different from the R output.
#
rbind(tapply(weight, sga, mean), tapply(weight, sga, sd))
aov(weight ~ sga) %>% summary
```

```
  Length     Class      Mode
      90 character character
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 47.00   55.00   60.00   59.29   64.00   72.00
```

A matrix: 2 × 3 of type dbl

I gel	lma supreme	Ambu aura gain
58.966667	59.733333	59.166667
6.359806	5.205656	5.583741

```
            Df Sum Sq Mean Sq F value Pr(>F)
sga          2    9.5    4.74   0.144  0.866
Residuals   87 2863.0   32.91
```

In [9]:
```
# bmi
summary(d21212$"BMI(kg/m²)")
bmi <- substr(d21212$"BMI(kg/m²)", 1,
    nchar(d21212$"BMI(kg/m²)") - 5) %>% as.numeric
summary(bmi)
# Printed numbers are slightly different from the R output.
#
rbind(tapply(bmi, sga, mean), tapply(bmi, sga, sd))
aov(bmi ~ sga) %>% summary
```

```
   Length     Class      Mode
       90 character character
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  15.80   21.52   24.20   24.27   26.35   33.60
```

A matrix: 2 × 3 of type dbl

I gel	lma supreme	Ambu aura gain
24.636667	24.813333	23.370000
4.279662	3.981226	3.440644

```
            Df Sum Sq Mean Sq F value Pr(>F)
sga          2   37.2   18.59   1.213  0.302
Residuals   87 1334.1   15.34
```

In [10]:
```
# mallampati score
# MPG?
# Chisquared test produces may-be-incorrect result.
#
table(d21212$MPG, sga) %>% print %>% chisq.test
table(d21212$MPG, sga) %>% fisher.test
```

```
   sga
    I gel lma supreme Ambu aura gain
  1     0           7              5
  2    28          20             23
  3     2           3              2
```

```
Warning message in chisq.test(.):
“Chi-squared approximation may be incorrect”
        Pearson's Chi-squared test

data:  .
X-squared = 8.166, df = 4, p-value = 0.08568
```

```
        Fisher's Exact Test for Count Data

data:  .
p-value = 0.03549
alternative hypothesis: two.sided
```

In [11]:
```
# asa ps
# Chisquared test produces may-be-incorrect result.
#
table(d21212$"ASA Grade", sga) %>% print %>% chisq.test
table(d21212$"ASA Grade", sga) %>% fisher.test
```

```
  sga
   I gel lma supreme Ambu aura gain
1    18          11             12
2    12          12             13
3     0           7              5
Warning message in chisq.test(.):
“Chi-squared approximation may be incorrect”
        Pearson's Chi-squared test

data:  .
X-squared = 8.6516, df = 4, p-value = 0.07042
        Fisher's Exact Test for Count Data

data:  .
p-value = 0.043
alternative hypothesis: two.sided
```

Table 2

Table 2. Comparisons of Various Parameters between the Study Groups

	Group I (n = 30)	Group L (n = 30)	Group A (n = 30)	P value
Size of device (size 3/4)	24/6	25/5	23/7	0.812
Number of attempts (1/2)	29/1	25/5	26/4	0.232
Insertion time (s)	16.9 ± 4.9	19.6 ± 5.2	22.1 ± 5.7	0.001
OLP (cmH_2O)	9.4 ± 6.1	24.1 ± 6.3	29.8 ± 3.0	< 0.001
Ease of insertion (1/2/3/4)*	25/3/2/0	24/3/3/0	23/6/1/0	0.630
Failed insertion/device failure during surgery	0/0	0/0	0/0	1.000
Airway maneuver requirement	2	1	3	0.585
Gastric tube insertion difficulty	1	0	0	0.364

Values are presented as number or mean ± SD. Group I: i-gel, Group L: LMA Supreme, Group A: Ambu AuraGain. OLP: oropharyngeal leak pressure. *Ease of insertion was graded as 1 = no resistance, 2 = minimal resistance, 3 = moderate resistance, and 4 = unable to place the device.

In [12]:
```
# size of device (3/4)
table(d21212$Size, sga) %>% print %>% chisq.test
```

```
  sga
   I gel lma supreme Ambu aura gain
3    24          25             23
4     6           5              7
```

```
        Pearson's Chi-squared test

data:  .
X-squared = 0.41667, df = 2, p-value = 0.8119
```

In [13]:
```
# number of attempts (1/2)
# Chisquared test produces may-be-incorrect result.
#
table(d21212$"Number of attempts", sga) %>% print %>% chisq.test
table(d21212$"Number of attempts", sga) %>% fisher.test
```

```
  sga
   I gel lma supreme Ambu aura gain
1    29          25             26
2     1           5              4
Warning message in chisq.test(.):
“Chi-squared approximation may be incorrect”
        Pearson's Chi-squared test

data:  .
X-squared = 2.925, df = 2, p-value = 0.2317
        Fisher's Exact Test for Count Data

data:  .
p-value = 0.3278
alternative hypothesis: two.sided
```

In [14]:
```
# insertion time (s)
summary(d21212$"Time of insertion")
time_insertion <- gsub("sec|secs", "",
    d21212$"Time of insertion") %>% as.numeric
summary(time_insertion)
# Printed numbers are slightly different from the R output.
#
rbind(tapply(time_insertion, sga, mean),
    tapply(time_insertion, sga, sd))
aov(time_insertion ~ sga) %>% summary
```

```
  Length     Class      Mode
      90 character character
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  10.00   15.00   19.00   19.57   24.75   33.00
```

A matrix: 2 × 3 of type dbl

I gel	lma supreme	Ambu aura gain
16.933333	19.666667	22.100000
4.926587	5.261004	5.737655

```
            Df Sum Sq Mean Sq F value  Pr(>F)
sga          2  400.9  200.43   7.085 0.00141 **
Residuals   87 2461.2   28.29
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

In [15]:
```
# OLP
# note: The authors have corrected
#   one of the OLP values in the table.
# Printed numbers are still slightly different from the R output.
#
rbind(tapply(d21212$OLP, sga, mean), tapply(d21212$OLP, sga, sd))
aov(d21212$OLP ~ sga) %>% summary
```

A matrix: 2 × 3 of type dbl

I gel	lma supreme	Ambu aura gain
19.466667	24.166667	29.866667
6.174102	6.308633	3.048271

```
            Df Sum Sq Mean Sq F value   Pr(>F)
sga          2   1627   813.7   27.99 4.11e-10 ***
Residuals   87   2529    29.1
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

In [22]:
```
# ease of insertion (1/2/3/4)
table(d21212$"Ease of insertion")
# Raw data for the "ease of insertion" contain
#    4 different levels,
#    which can be reduced to 3 levels
#    (because "severe" does not exist)
#    such as "no" (1), "mild" (2), "moderate" (3)
ease <- ifelse(grepl("mild",
    tolower(d21212$"Ease of insertion")), 2,
    ifelse(grepl("no",
        tolower(d21212$"Ease of insertion")), 1, 3))
table(ease, sga) %>% print %>% chisq.test
table(ease, sga) %>% fisher.test
# OK
```

```
     mild       Mild Mild resis   Moderate   No resis
        5          1          6          6         72
    sga
ease I gel lma supreme Ambu aura gain
   1    25          24             23
   2     3           3              6
   3     2           3              1
Warning message in chisq.test(.):
“Chi-squared approximation may be incorrect”
        Pearson's Chi-squared test

data:  .
X-squared = 2.5833, df = 4, p-value = 0.6298
        Fisher's Exact Test for Count Data

data:  .
p-value = 0.7001
alternative hypothesis: two.sided
```

In [17]:
```
# failed insertion/device failure during surgery
d21212$"Failure to place device" %>% table
# OK
```

```
.
no No
 4 86
```

In [18]:
```
# airway maneuver requirement
table(d21212$"Airway manouvers reqd." == "Yes", sga)
table(tolower(d21212$"Type of manouver") == "nil", sga)
# Printed numbers are incorrect.
# Individuals who required additional airway maneuver
# are 2, not 3 in the group A.
```

```
      sga
       I gel lma supreme Ambu aura gain
 FALSE    28          29             28
 TRUE      2           1              2
      sga
       I gel lma supreme Ambu aura gain
 FALSE     2           1              2
 TRUE     28          29             28
```

In [23]:
```
# gastric tube insertion difficulty
table(tolower(d21212$"Ease of placing gastric tube") == "easy",
    sga) %>% print %>% chisq.test
table(tolower(d21212$"Ease of placing gastric tube") == "easy",
     sga) %>% fisher.test
# Chisquare approximation may be incorrect.
```

```
      sga
       I gel lma supreme Ambu aura gain
 FALSE     1           0              0
 TRUE     29          30             30
Warning message in chisq.test(.):
“Chi-squared approximation may be incorrect”
        Pearson's Chi-squared test

data:  .
X-squared = 2.0225, df = 2, p-value = 0.3638
        Fisher's Exact Test for Count Data

data:  .
p-value = 1
alternative hypothesis: two.sided
```

Table 3

Table 3. Adverse Events (Inadequate Oxygenation/Ventilation) and Complications

	Group I (n = 30)	Group L (n = 30)	Group A (n = 30)	P value
Adverse events (inadequate oxygenation/ventilation)*	0	0	0	1.000
Intraoperative complications				0.873
Blood staining	0	1	0	
Nausea	3	3	4	
Sore throat	4	4	3	

Values are presented as number. Group I: i-gel, Group L: LMA Supreme, Group A: Ambu AuraGain. *Inadequate oxygenation/ventilation consists of an inability to generate 6–8 ml/kg tidal volume during positive pressure ventilation, a rise in end-tidal carbon dioxide > 50 mmHg despite airway maneuvers/device adjustments, or SpO_2 < 90%.

In [20]:
```
# adverse events
# all of them are zeros
```

In [21]:
```
# intraoperative complications
# Each complication is so independent
#   that it must be analyzed separately.
# Even the printed incidences are incorrect:
# Numbers for nausea must be 4, 3, and 4 for the groups I, L, and A
# Numbers for sore throat must be 3, 4, and 4, respectively.
table(d21212$"Complications")
blood <- ifelse(d21212$"Complications" == "blood staining", 1, 0)
nausea <- ifelse(d21212$"Complications" == "nausea", 1, 0)
sore_throat <- ifelse(d21212$"Complications" == "sore throat", 1, 0)
table(blood, sga) %>% print %>% fisher.test
table(nausea, sga) %>% print %>% fisher.test
table(sore_throat, sga) %>% print %>% fisher.test
```

```
blood staining         nausea             no             No    sore throat
             1             10             54             14             11
     sga
blood I gel lma supreme Ambu aura gain
    0    30          29             30
    1     0           1              0
        Fisher's Exact Test for Count Data

data:  .
p-value = 1
alternative hypothesis: two.sided
      sga
nausea I gel lma supreme Ambu aura gain
     0    26          27             27
     1     4           3              3
        Fisher's Exact Test for Count Data

data:  .
p-value = 1
alternative hypothesis: two.sided
```

```
           sga
sore_throat I gel lma supreme Ambu aura gain
          0    27          26             26
          1     3           4              4
        Fisher's Exact Test for Count Data

data:  .
p-value = 1
alternative hypothesis: two.sided
```

{End of the script}

Younsuk Lee, M.D., Ph.D.

Sang Gyu Kwak, Ph.D.