

STATISTICS 641 - ASSIGNMENT 4

DUE DATE: NOON (CDT), WEDNESDAY, OCTOBER 6, 2021

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#### STAT 641 Assignment 4 ####
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# P1: ( 50 points)  A researcher is studying the relative brain weights (brain
weight divided by body weight)
# for 51 species of mammals whose litter size is 1 and for 44 species of
mammals whose average litter size is
# greater than or equal to 2.  The researcher was interested in determining
what evidence that brain sizes
# tend to be different for the two groups.  (Data from The Statistical Sleuth by
Fred Ramsey and Daniel Schafer).
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```
BrainSize = read.csv("C:/Users/jackr/OneDrive/Desktop/Graduate School Courses/
STAT 641 - Methods of STAT I/RawData/Assign3_BrainSize.csv")
BrainSize = data.frame(SmallLitter = BrainSize$Small.Litter.Size,
LargeLitter = BrainSize$Large.Litter.Size)
LLitter = na.omit(BrainSize$LargeLitter)
SLitter = BrainSize$SmallLitter
```

```
#1.)  For the Small Litter Size mammals,  answer the following questions:  The
data is given in the file:
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#      BrainWeight Data.txt in Canvas
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#(a) Compute a 10% trimmed mean, and compare it to the untrimmed sample mean.
Does this comparison suggest
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```
#      any extreme values in the data?
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mean(BrainSize$SmallLitter)
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```
mean(BrainSize$SmallLitter, trim = .10)
```

```
# the trimmed mean and the untrimmed sample mean are very similar.  This would
suggest there are few (if any)
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```
# extreme values in the data
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```
#(b)  The researcher suggested a Weibull distribution to model the data for
the Small Litter Size mammals.
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```
#      Assuming that the Weibull distribution is an appropriate model for the
Small Litter Size data,
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```
#      obtain the MLE estimates of the Weibull parameters for the Small Litter
Size data.
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library(MASS)
```

```
mle_weibull=fitdistr(BrainSize$SmallLitter,"weibull",lower=c(0,0))
```

```
# shape:
```

```
mle_weibull$estimate[1]
```

```
# scale:
```

```
mle_weibull$estimate[2]
```

```
#(c)  Estimate the probability that a randomly selected mammal with a litter
size of 1 will have a relative brain
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#      weight greater than 15, first using the Weibull model and
secondly using a distribution-free
```

```
#      estimate.
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# Weibull:
1 - pweibull(15, shape = mle_weibull$estimate[1], scale =
mle_weibull$estimate[2])
exp(-(15/mle_weibull$estimate[2])^mle_weibull$estimate[1])

# Distribution Free Estimate:
1-ecdf(BrainSize$SmallLitter)(15)

#(d) Compare the MLE estimates of  $\mu$  and  $\sigma$  based on the Weibull model to the
distribution-free
# estimates of  $\mu$  and  $\sigma$  for the Small Litter Size data.
lambda = mle_weibull$estimate[2]
k = mle_weibull$estimate[1]

lambda*gamma(1+1/k)
mean(BrainSize$SmallLitter)

sqrt((lambda^2)*(gamma(1+2/k) - (gamma(1+1/k)^2)))
sd(BrainSize$SmallLitter)

# the MLE estimates and the distribution free estimates are very similar

# (e) Compare the MLE estimates of median and IQR based on the Weibull model
to the distribution-free estimates
# of median and IQR for the Small Litter Size data.

# Distribution Free
median(BrainSize$SmallLitter)
IQR(BrainSize$SmallLitter)
quantile(BrainSize$SmallLitter)

# MLE Estimates
qweibull(.5, shape = mle_weibull$estimate[1], scale = mle_weibull$estimate[2])
qweibull(c(.25,.75), shape = mle_weibull$estimate[1], scale =
mle_weibull$estimate[2])

#2.) Without any assumed model, estimate the mean and standard deviation of
the relative brain weights for both Large
# and Small litter sizes.
mean(LLitter)
sd(LLitter)

mean(BrainSize$SmallLitter)
sd(BrainSize$SmallLitter)

# 3.) Estimate the median and MAD of the relative brain weights for both Large
and Small litter sizes.
absDevS = NULL
for(i in seq_along(SLitter)){
  absDevS[i] = abs(SLitter[i]-quantile(BrainSize$SmallLitter,.5))
}
quantile(absDevS,0.5)/.6745

```

```
absDevL = NULL
for(i in seq_along(LLitter)){
  absDevL[i] = abs(LLitter[i]-quantile(LLitter,.5))
}
quantile(absDevL,0.5)/.6745
```

# 4.) Based on your plots from Assignment #3, which pair of estimates of the center and spread in the two datasets best represents the center and spread in the two populations of relative brain weights?

# The sample mean seems to be the best estimate of the center and the MAD seems to be the best estimate of the spread because we have highly skewed data

# 5.) Using your answers from the previous three questions, suggest a relationship (if any) between litter size and relative brain weights.

# Based on the previous three questions, I would say that there is a positive relationship between average litter size and relative brain weights.

# P2. ( 30 points) Twenty-five patients diagnosed with rare skin disease are randomly assigned to two drug treatments. The following times are either the time in days from the point of randomization to either a complete recovery or censoring (as indicated by the status variable:  
# 0 means censored, i.e., time at which patient left study prior to a complete recovery, 1 means patient's time to recovery).

```
library(survival)
```

```
Time = c(180, 632, 2240, 195, 76, 70, 13, 1990, 18, 700, 210, 1296, 23)
Status = c(1,1,1,1,1,1,0,0,1,1,1,1,1)
```

```
Time2 = c(8, 852, 52, 220, 63, 8, 1976, 1296, 1460, 63, 1328, 365)
Status2 = c(0,1,1,1,1,1,0,0,1,1,1,1)
```

```
# 1.) Estimate the survival function for the two treatments.
Surv(Time, Status)
cords.surv1 <- survfit(Surv(Time, Status) ~ 1, conf.type="log-log")
summary(cords.surv1)
print(cords.surv1, print.rmean=TRUE)
```

```

Surv(Time2, Status2)
cords.surv2 <- survfit(Surv(Time2, Status2) ~ 1, conf.type="log-log")
summary(cords.surv2)
print(cords.surv2, print.rmean=TRUE)

# 2.) Compute the mean and median time to recovery for the two treatments
using the estimated survival function.

# Treatment 1: mean - 657, median - 202
# Treatment 2: mean - 731, median - 365

# 3.) Which treatment appears to be most effective in the treatment of the
skin disease?

# Treatment 1 seems to be most effective in the treatment of the skin disease
as the mean recovery
# time is lower than that of Treatment 2

# 4.) Estimate the mean and median time to recovery ignoring the censoring and
compare these values to values
#      obtained in part 2.

mean(cords.surv1$time)
median(cords.surv1$time)

mean(cords.surv2$time)
median(cords.surv2$time)

# the mean and median for treatment 1 is lower and the mean and median for
treatment 2 is higher

# P3. (20 points) Select the letter of the BEST answer.

# 1.) A
# 2.) D
# 3.) B
# 4.) C
# 5.) B

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