# **DSS Prototype Analysis**

## Alvin Murphy

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## 1 Hypothesis

Hypotheses are "innocent until proven guilty." We'll assume that SpaceX and others have proven that DevSecOps tech can meet hard-real-time requirements but nothing available in the body of knowledge documents this.

**Hypothesis:** Modern DevSecOps architectures can be designed to meet hard-real-time latency  $(\mu)$  requirements using modern computing environments and computing infrastructure.

```
H_0: \mu \leq 500ms with jitter within latency bounds H_a: \mu > 500ms with jitter exceeding latency bounds
```

Murphy, Alvin C. and Moreland Jr, James D. 'Integrating AI Microservices into Hard-Real-Time SoS to Ensure Trustworthiness of Digital Enterprise Using Mission Engineering'. 1 Jan. 2021: 38 – 54.

```
setwd('/home/jovyan/work/data')
```

#### 2 Load Data Files

```
macData <- read.csv('DSS_SpanData-mac-2022-05-02 18_38_26_s10-5-1.csv', header = TRUE)
linpcData <- read.csv('DSS_SpanData-linuxpc-2022-06-06 17_38_29_s10-5-1.csv', header = TRUE)
rpi4Data <- read.csv('DSS_SpanData-rpi4-2022-06-06 17_52_59_s10-5-1.csv', header = TRUE)
awsEC2Data <- read.csv('DSS_SpanData-aws_ec2-2022-06-07 17_44_08_s10-5-1.csv', header = TRUE)
cci_Data <- read.csv('DSS_SpanData-odu_cci-2022-06-28 17_47_20_s10-5-1.csv', header = TRUE)</pre>
```

#### 2.1 Review and Tag MacBook Air (2017) Data

```
summary(macData)
  Trace.ID
                    Trace.name
                                       Start.time
                                                            Duration
                   Length:100
Length: 100
                                      Length: 100
                                                          Length: 100
Class :character
                                      Class :character
                                                          Class : character
                   Class :character
Mode :character
                                      Mode :character
                                                          Mode :character
                   Mode :character
 head(macData[, c(1,2)])
 head(macData[, c(3,4)])
```

	Trace.ID <chr></chr>	Trace.name <chr></chr>
1	9ee3577fb1b427bc4fc17fecc5154d7d	dss-prototype: /TE
2	f05ddc4dc13aff5c3098011b2a402401	dss-prototype: /tracks
3	2bd901fbbfc9ee8dfa7c9629d93a1567	dss-prototype: /IAD
4	69a48381a14e79da08aaa2353f7db4b2	dss-prototype: /RIC
5	e83037 dcb 9438 c04 dc12 fba 373 b5502 f	dss-prototype: /WA
6	7e381cd880adb670bb9627ca47020938	dss-prototype: /TE

#### A data.frame: $6 \times 2$

	Start.time <chr></chr>	Duration <chr></chr>
1	2022-05-02 10:25:01.366	36.0 ms
2	2022-05-02 10:25:00.309	43.3  ms
3	2022-05-02 10:24:58.818	464  ms
4	2022-05-02 10:24:57.307	494  ms
5	2022-05-02 10:24:56.128	139  ms
6	2022-05-02 10:24:55.081	30.3  ms

#### 2.1.1 Add Source Indicator to MacBook Data

```
macDataPlat <- macData
macDataPlat$platform = "2017-macbook"
macDataPlat$env = 0</pre>
```

## 2.2 Tag Linux PC (2012) Data

```
linpcDataPlat <- linpcData
linpcDataPlat$platform = "2012-linpc"
linpcDataPlat$env = 1</pre>
```

## 2.3 Tag Raspberry Pi 4 (2020) Data

```
rpi4DataPlat <- linpcData

rpi4DataPlat$platform = "2020-rpi4"
rpi4DataPlat$env = 2</pre>
```

## 2.4 Tag AWS EC2 t2.micro (2022) Data

```
awsEC2DataPlat <- awsEC2Data
awsEC2DataPlat$platform = "2022-aws-ec2"
awsEC2DataPlat$env = 3</pre>
```

#### 2.5 Tag ODU CCI (2022) Data

```
cciDataPlat <- cci_Data

cciDataPlat$platform = "2022-odu-cci"
cciDataPlat$env = 4</pre>
```

### 2.6 Merge Data Files

Here we merge data from all platforms.

```
# head(spanData[, c(4,5,6)])
# spanData
```

#### 3 Convert Data into Useable Metrics

To make the data more usable and easier to understand we apply conversions from text to numeric and add additional columns with supporting information. A **useCase** column is added to identify specific DSS request use cases; e.g. Get Dulles Airport Data. The data also indicates whether the request is managed internally or a connection to an external service is required to provided a response (i.e., https://opensky-network.org). A **numContainers** column is added to indicate the number of containers involved in providing a use case response (e.g. independent variable). An **ext** column is added to indicate whether an API external to the Docker environment is used; e.g., ext = TRUE for OpenSky API calls.

```
## Dictionary for converting data
DSSoperations <- c(
    "dss-prototype: /IAD" = "Get Dulles Airport Data (External)",
    "dss-prototype: /RIC" = "Get Richmond Airport Data (External)",
    "dss-prototype: /tracks" = "Get Stored Local DSS Tracks (Internal)",
    "dss-prototype: /TE" = "Trial Engage (Internal)",
    "dss-prototype: /WA" = "Assess Weapons (Internal)"
)
DSSuseCaseNum <- c(
    "dss-prototype: /IAD" = 4,
    "dss-prototype: /RIC" = 5,
    "dss-prototype: /tracks" = 1,
    "dss-prototype: /TE" = 2,
    "dss-prototype: /WA" = 3
)
DSSexternal <- c(
    "dss-prototype: /IAD" = TRUE,
    "dss-prototype: /RIC" = TRUE,
    "dss-prototype: /tracks" = FALSE,
    "dss-prototype: /TE" = FALSE,
    "dss-prototype: /WA" = FALSE
)
```

```
DSStraceShortName <- c(
    "dss-prototype: /IAD" = "/IAD",
    "dss-prototype: /RIC" = "/RIC",
    "dss-prototype: /tracks" = "/tracks",
    "dss-prototype: /TE" = "/TE",
    "dss-prototype: /WA" = "/WA"
)

# DSShypothesis <- c(
# Duration > 500 = FALSE
# Duration <= 500 = TRUE
# )</pre>
```

#### 3.1 Add Additional Column Descriptors

```
spanMetrics <- spanData

spanMetrics$useCase <- DSSoperations[spanMetrics$Trace.name]
spanMetrics$useCaseNum <- DSSuseCaseNum[spanMetrics$Trace.name]

spanMetrics$ext = DSSexternal[spanMetrics$Trace.name]
spanMetrics$Trace.name = DSStraceShortName[spanMetrics$Trace.name]

# truncate span ID
# spanMetrics$Trace.ID <- str_sub(spanMetrics$Trace.ID,1,4)

# summary(spanMetrics)
# head(spanMetrics)
# tail(spanMetrics)
# spanMetrics

# install.packages("tidyverse")
library(tidyverse)

# Convert character data into numeric metrics</pre>
```

```
# Convert span duration
     char = spanMetrics[index,4]
     len = str length(char)
     duration = str sub(char,1,(len-3))
     units = str_sub(char,(len-1),len)
     duration <- as.numeric(duration)</pre>
     # glimpse(duration)
     # print(units)
     if(units == 'ms') {
         duration = duration
                                        # Keep ms
     } else if (units == 'us') {
         duration = duration * 0.001
                                    # Convert µs to ms
     } else if (units == ' s') {
         duration = duration * 1000
                                         # Convert s to ms
     } else {
         print ('Unable to find specified units')
         print (units)
     spanMetrics$Duration[index] = as.numeric(duration)
  }
  # Convert Duration columns from char to numeric
  spanMetrics$Duration = as.numeric(spanMetrics$Duration)
  glimpse(spanMetrics)
Rows: 500
Columns: 9
$ Trace.ID
           <chr> "9ee3577fb1b427bc4fc17fecc5154d7d", "f05ddc4dc13aff5c309801...
$ Trace.name <chr> "/TE", "/tracks", "/IAD", "/RIC", "/WA", "/TE", "/tracks", ...
$ Start.time <chr> "2022-05-02 10:25:01.366", "2022-05-02 10:25:00.309", "2022...
$ Duration <dbl> 36.0, 43.3, 464.0, 494.0, 139.0, 30.3, 30.0, 478.0, 546.0, ...
$ platform <chr> "2017-macbook", "2017-macbook", "2017-macbook", "2017-macbo...
$ env
           $ useCase
           <chr> "Trial Engage (Internal)", "Get Stored Local DSS Tracks (In...
$ useCaseNum <dbl> 2, 1, 4, 5, 3, 2, 1, 4, 5, 3, 2, 1, 4, 5, 3, 2, 1, 4, 5, 3,...
$ ext
           <lgl> FALSE, FALSE, TRUE, TRUE, FALSE, FALSE, FALSE, TRUE, TRUE, ...
```

#### 3.2 Shapiro-Wilk Test

The null-hypothesis of this test is that the population is normally distributed. Thus, if the p value is less than the chosen alpha level, then the null hypothesis is rejected and there is evidence that the data tested are not normally distributed. On the other hand, if the p value is greater than the chosen alpha level, then the null hypothesis (that the data came from a normally distributed population) can not be rejected (e.g., for an alpha level of .05, a data set with a p value of less than .05 rejects the null hypothesis that the data are from a normally distributed population).

https://en.wikipedia.org/wiki/Shapiro-Wilk\_test

```
shapiro.test(spanMetrics$Duration)

Shapiro-Wilk normality test

data: spanMetrics$Duration
W = 0.7464, p-value < 2.2e-16</pre>
```

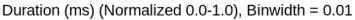
The result indicates that the data is not normally distributed and needs to be adjusted. We normalized the data between 0 and 1 to see the details.

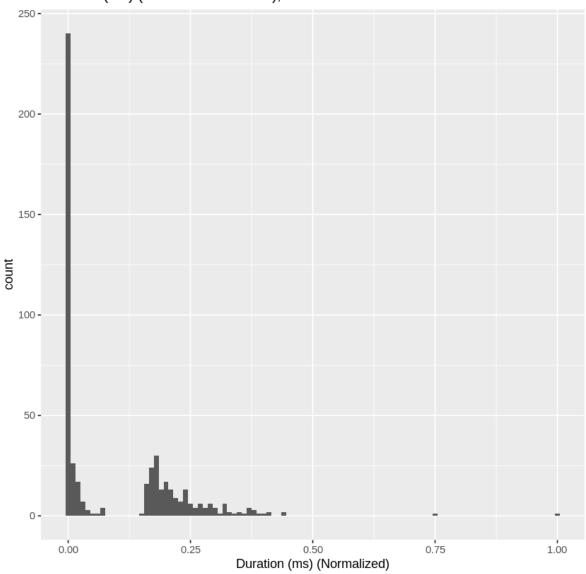
```
# create min-max-norm function
min_max_norm <- function(x) {
        (x - min(x)) / (max(x) - min(x))
}

#apply Min-Max normalization
norm_spanMetrics <- spanMetrics
norm_spanMetrics$Duration <- (spanMetrics$Duration - min(spanMetrics$Duration)) /
        (max(spanMetrics$Duration) - min(spanMetrics$Duration))</pre>
summary(norm_spanMetrics)
```

${\tt Trace.ID}$	Trace.name	Start.time	Duration	
Length:500	Length:500	Length:500	Min. :0.000000	
Class :character	Class :character	Class :character	1st Qu.:0.001568	
Mode :character	Mode :character	Mode :character	Median :0.008699	
			Mean :0.097136	
			3rd Qu.:0.188760	
			Max. :1.000000	

```
platform
                               useCase
                                                  useCaseNum
                       env
                                                                ext
Length:500
                  Min.
                         :0
                              Length:500
                                                Min.
                                                      :1
                                                             Mode :logical
Class :character
                  1st Qu.:1
                              Class :character
                                                 1st Qu.:2
                                                             FALSE:300
Mode :character
                  Median :2
                              Mode :character
                                                Median :3
                                                             TRUE :200
                  Mean :2
                                                Mean
                                                      :3
                  3rd Qu.:3
                                                 3rd Qu.:4
                                                Max.
                  Max. :4
                                                       :5
 norm_spanMetrics %>%
     ggplot(aes(Duration)) + geom_histogram(binwidth = 0.01) +
     ggtitle("Duration (ms) (Normalized 0.0-1.0), Binwidth = 0.01") +
     xlab("Duration (ms) (Normalized)")
```





```
# Add processing delay from a normal distribution
pd_spanMetrics <- spanMetrics

# pd <- rnorm(1, mean = 50, sd = 10)
pd <- rnorm(1, mean = 15, sd = 5)
# pd <- rnorm(1, mean = 10, sd = 2)
pd_spanMetrics$Duration = pd_spanMetrics$Duration + pd</pre>
```

#### glimpse(pd\_spanMetrics)

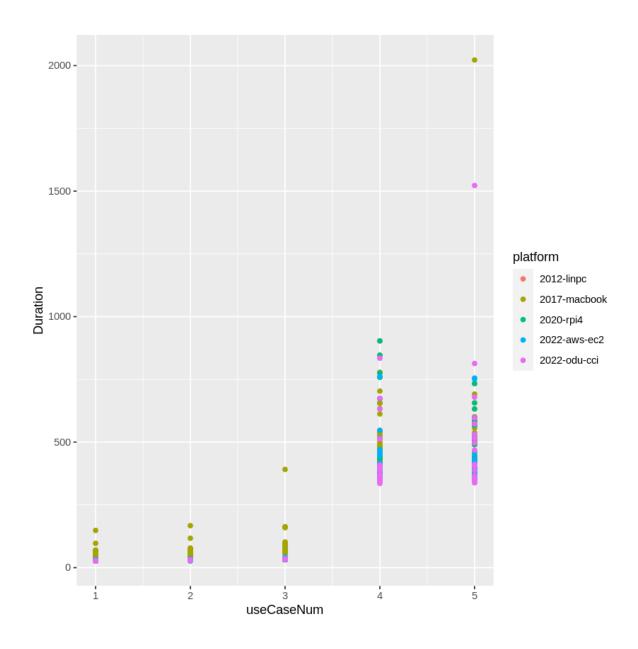
```
Rows: 500
Columns: 10
$ Trace.ID
            <chr> "9ee3577fb1b427bc4fc17fecc5154d7d", "f05ddc4dc13aff5c309801...
$ Trace.name <chr> "/TE", "/tracks", "/IAD", "/RIC", "/WA", "/TE", "/tracks", ...
$ Start.time <chr> "2022-05-02 10:25:01.366", "2022-05-02 10:25:00.309", "2022...
$ Duration <dbl> 58.27631, 65.57631, 486.27631, 516.27631, 161.27631, 52.576...
$ platform <chr> "2017-macbook", "2017-macbook", "2017-macbook", "2017-macbook",
            $ env
            <chr> "Trial Engage (Internal)", "Get Stored Local DSS Tracks (In...
$ useCase
$ useCaseNum <dbl> 2, 1, 4, 5, 3, 2, 1, 4, 5, 3, 2, 1, 4, 5, 3, 2, 1, 4, 5, 3,...
            <lg1> FALSE, FALSE, TRUE, TRUE, FALSE, FALSE, FALSE, TRUE, TRUE, ...
$ hthreshold <1gl> TRUE, TRUE, TRUE, TRUE, TRUE, TRUE, TRUE, TRUE, FALSE, TRUE...
  shapiro.test(pd_spanMetrics$Duration)
   Shapiro-Wilk normality test
data: pd_spanMetrics$Duration
W = 0.7464, p-value < 2.2e-16
  pd_spanMetrics$hthreshold = TRUE
  # Assess hypothesis threshold of 500 ms
  for(index in 1:nrow(pd_spanMetrics)) {
                                             # for-loop over rows
      if(pd_spanMetrics[index,4] > 500) {
          pd_spanMetrics[index,10] = FALSE
          # spanMetrics$hthreshold = FALSE
      } else {
      pd_spanMetrics[index,10] = TRUE
      # spanMetrics$hthreshold = TRUE
  }
  glimpse(pd_spanMetrics)
  # view(spanMetrics)
```

```
Rows: 500
Columns: 10
$ Trace.ID <chr> "9ee3577fb1b427bc4fc17fecc5154d7d", "f05ddc4dc13aff5c309801...
$ Trace.name <chr> "/TE", "/tracks", "/IAD", "/RIC", "/WA", "/TE", "/tracks", ...
$ Start.time <chr> "2022-05-02 10:25:01.366", "2022-05-02 10:25:00.309", "2022...
$ Duration <dbl> 58.27631, 65.57631, 486.27631, 516.27631, 161.27631, 52.576...
$ platform <chr> "2017-macbook", "2017-ma
$ env
                                      <chr> "Trial Engage (Internal)", "Get Stored Local DSS Tracks (In...
$ useCase
$ useCaseNum <dbl> 2, 1, 4, 5, 3, 2, 1, 4, 5, 3, 2, 1, 4, 5, 3, 2, 1, 4, 5, 3,...
                                      <lg1> FALSE, FALSE, TRUE, TRUE, FALSE, FALSE, FALSE, TRUE, TRUE, ...
$ ext
$ hthreshold <lgl> TRUE, TRUE, TRUE, FALSE, TRUE, TRUE, TRUE, FALSE, FALSE, TR...
       # sort span metrics by use case number
       spanMetricsA <- arrange(pd_spanMetrics, useCaseNum)</pre>
       # head(spanMetricsA[, c(2,3,4,5)])
       # head(spanMetricsA[, c(6,7,8,9)])
       # spanMetricsA
```

#### 3.3 Exploratory Analysis Plots

```
# spanMetricsNum <- spanMetricsA %>%
# dplyr::select(useCaseNum, env, ext, Duration)
# dplyr::select(Duration, useCaseNum, env)

qplot(useCaseNum, Duration, data = spanMetricsA, colour = platform)
```



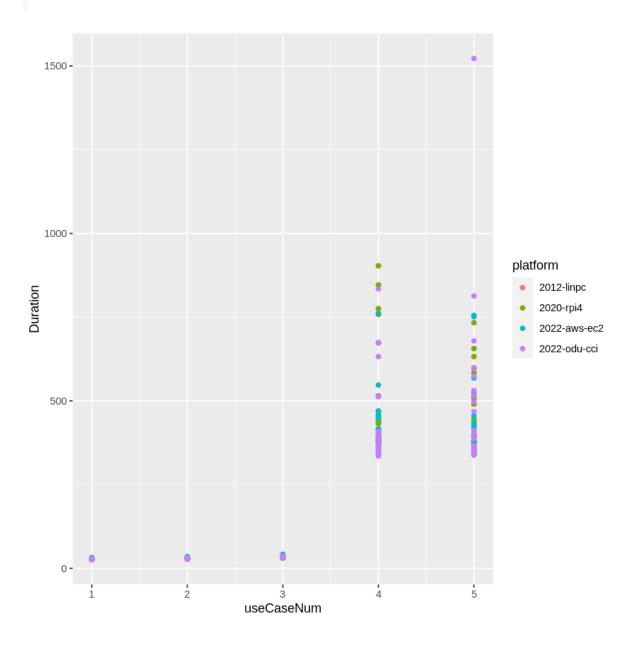
#### 3.4 Remove Macbook Data from Development Platform

Here we remove the data from the Macbook development platform. The qplot shows that the Mac implementation of Docker adds latency within the Docker environment. In non-linux based plaforms, a Docker desktop running a virtual machine is required to provided that Docker capability that is native to Linux platforms. The Mac is considered to be the development environment and not representative of the integration and production environments.

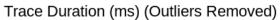
 $https://dev.to/ericnograles/why-is-docker-on-macos-so-much-worse-than-linux-flh \\ https://collabnix.com/how-docker-for-mac-works-under-the-hood/$ 

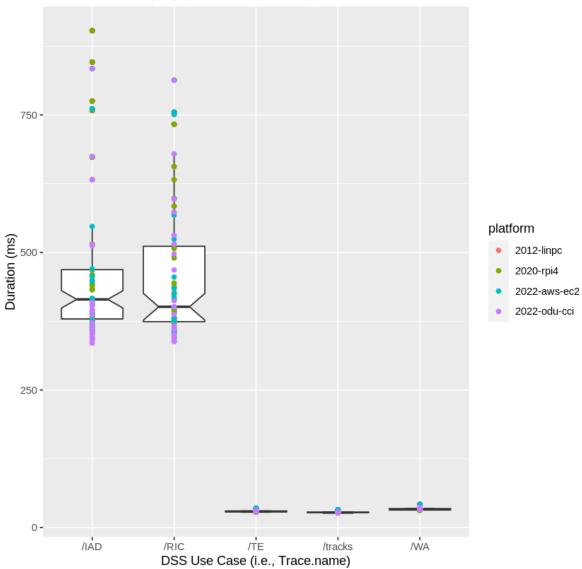
```
noMacSpan <- spanMetricsA[!spanMetricsA$env == 0,]

qplot(useCaseNum, Duration, data = noMacSpan, colour = platform)</pre>
```



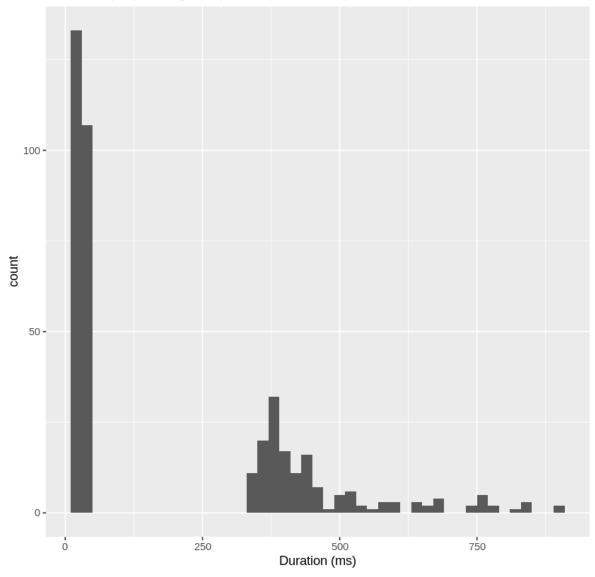
```
# par(mfrow=c(2,1))
  # hist(spanMetricsA$Duration, counts = 5)
  # spanMetricsA %>%
        ggplot(aes(Trace.name, Duration)) +
        stat_boxplot(notch="FALSE") + geom_point() +
        ggtitle("Duration of Endpoint Responses from Trace")
  # # notch went outside hinges. Try setting notch=FALSE.
  # Remove outliers
  aSpan <- noMacSpan
  outliers <- boxplot(aSpan$Duration, plot = FALSE)$out
  outliers
  aSpan <- aSpan[-which(aSpan$Duration %in% outliers),]
1522.27631116584\\
  aSpan %>%
      ggplot(aes(Trace.name, Duration)) +
      stat_boxplot(notch="TRUE") + geom_point(aes(colour = platform)) +
      ggtitle("Trace Duration (ms) (Outliers Removed)") +
      ylab("Duration (ms)") +
      xlab("DSS Use Case (i.e., Trace.name)")
  # If notch went outside hinges. Try setting notch=FALSE.
```





```
aSpan %>%
    ggplot(aes(Duration)) + geom_histogram(binwidth = 20) +
    ggtitle("Duration (ms) Histogram (Outliers Removed), Binwidth = 20") +
    xlab("Duration (ms)")
```

Duration (ms) Histogram (Outliers Removed), Binwidth = 20



summary(aSpan)
sd(aSpan\$Duration)

${\tt Trace.ID}$	Trace.name	Start.time	Duration		
Length:399	Length:399	Length:399	Min. : 26.57		
Class :character	Class :character	Class :character	1st Qu.: 28.32		
Mode :character	Mode :character	Mode :character	Median : 33.38		

Mean :203.15 3rd Qu.:386.78 Max. :903.28

useCase useCaseNumplatform env Length: 399 :1.000 Min. :1.000 Length:399 Min. Class : character 1st Qu.:1.500 Class : character 1st Qu.:2.000 Median :2.000 Mode :character Mode :character Median :3.000 Mean :2.496 Mean :2.995 3rd Qu.:3.000 3rd Qu.:4.000 Max. :4.000 Max. :5.000

ext hthreshold
Mode:logical Mode:logical
FALSE:240 FALSE:41
TRUE:159 TRUE:358

#### 229.448905568277

```
# dnorm_aSpan <- aSpan
# dnorm_aSpan$Duration <- dnorm(dnorm_aSpan$Duration,mean=180.874,sd=229.4489)

# dnorm_aSpan %>%
# ggplot(aes(Duration)) + geom_histogram() +
# ggtitle("Duration (ms) Histogram (w dnorm, Binwidth = 20") +
# xlab("Duration (ms)")

# shapiro.test(dnorm_aSpan$Duration)

# ggpairs(spanMetricsNum, title="correlogram with ggpairs()")
```

#### 3.4.1 mclust

Used mclust to verify the separation of internal and external models as indicated from the useCaseNum vs. Duration plot; i.e. use cases 4 and 5 use an external API.

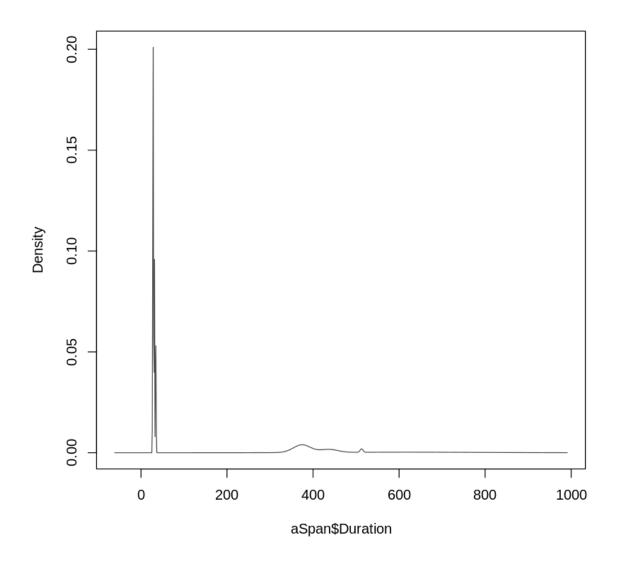
The library mclust is a contributed R package for model-based clustering, classification, and density estimation based on finite normal mixture modelling. It provides functions for parameter estimation via the EM algorithm for normal mixture models with a variety of covariance structures, and functions for simulation from these models.

Scrucca L., Fop M., Murphy T. B. and Raftery A. E. (2016) mclust 5: clustering, classification and density estimation using Gaussian finite mixture models The R Journal 8/1, pp. 289-317

```
install.packages("mclust")
library(mclust, quietly = TRUE)
```

#### 3.4.2 Mclust Univariate Analysis of Duration

```
mod4 <- densityMclust(aSpan$Duration)</pre>
```



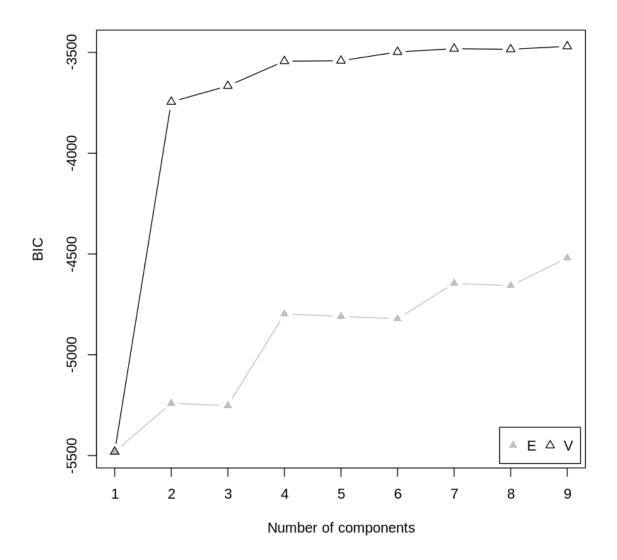
## summary(mod4)

Density estimation via Gaussian finite mixture modeling

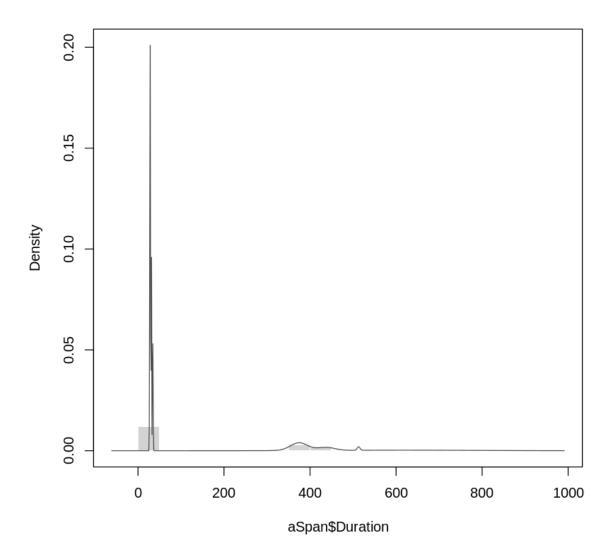
 ${\tt Mclust\ V\ (univariate,\ unequal\ variance)\ model\ with\ 9\ components:}$ 

```
log-likelihood n df     BIC     ICL
      -1656.953 399 26 -3469.619 -3511.198

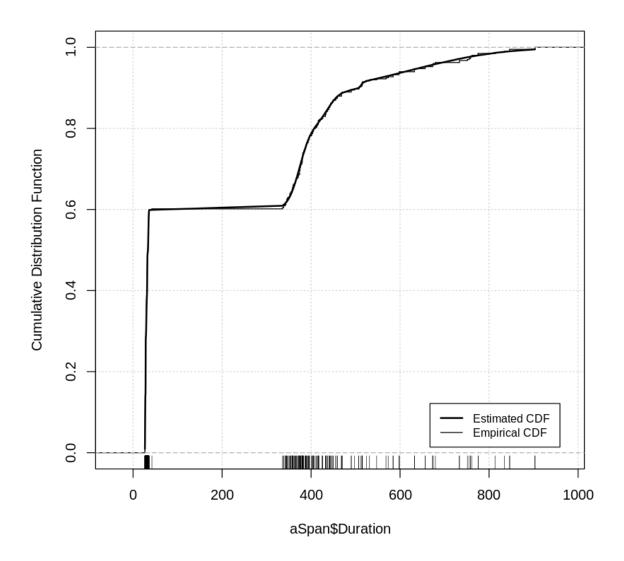
plot(mod4, what ="BIC")
```



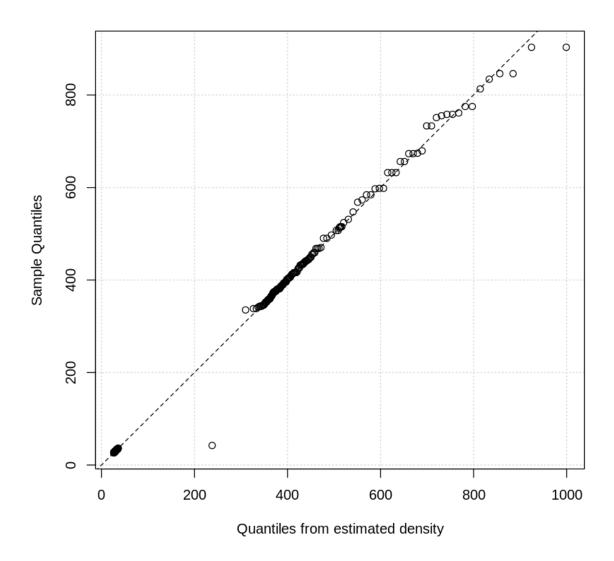
```
plot(mod4, what = "density", data = aSpan$Duration, breaks = 20)
```



```
plot(mod4, what = "diagnostic", type = "cdf")
```



```
plot(mod4, what = "diagnostic", type = "qq")
```



#### 3.4.3 Mclust Multivariate Analysis

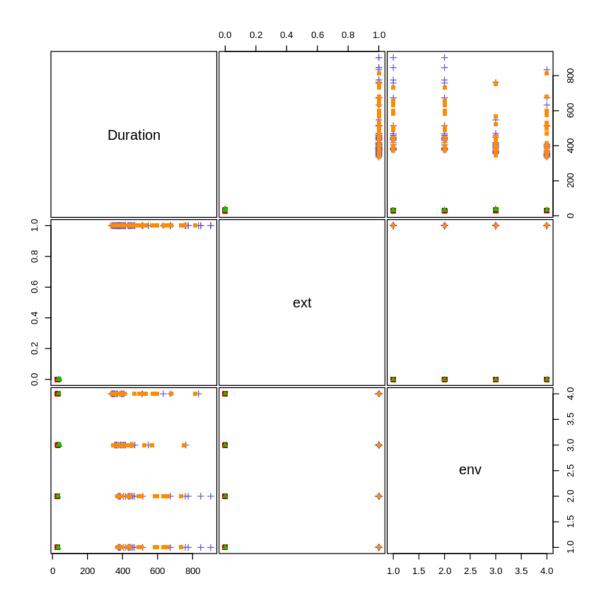
```
uc <- aSpan$useCaseNum # Trace.name is char, used uc num conversion

X <- aSpan %>%
    # dplyr::select(useCaseNum, env, ext, Duration)
    dplyr::select(Duration, ext, env)
```

```
# dplyr::select(Duration)
head(X)
clPairs(X, uc)
```

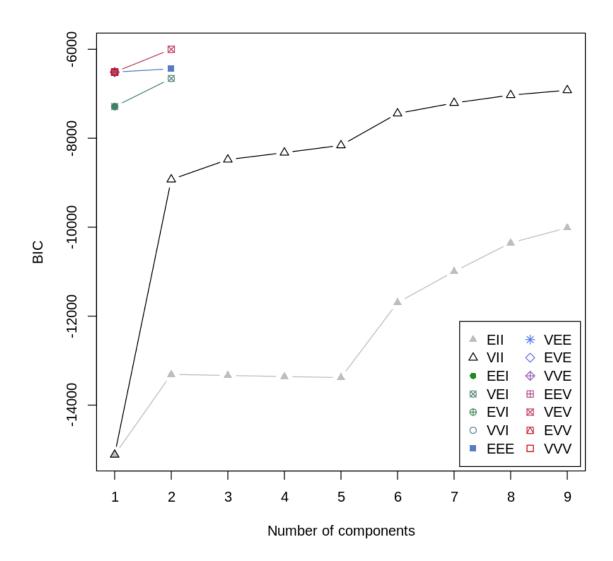
A data.frame:  $6 \times 3$ 

	Duration <dbl></dbl>	ext <lgl></lgl>	env <dbl></dbl>
21	27.17631	FALSE	1
22	26.70631	FALSE	1
23	26.94631	FALSE	1
24	26.95631	FALSE	1
25	27.00631	FALSE	1
26	27.16631	FALSE	1



```
# spanMclust <- Mclust(aSpan)
# spanMclust <- Mclust(X)
# summary(spanMclust)
# plot(spanMclust, what = c("classification"))

BIC <- mclustBIC(X)
plot(BIC)</pre>
```



## summary(BIC)

#### Best BIC values:

 VEV,2
 EEE,2
 EEE,1

 BIC
 -6000.192
 -6437.9228
 -6512.9492

 BIC diff
 0.000
 -437.7311
 -512.7575

Note that 2 is included within the list of best Bayesian Information Criterion (BIC) values.

```
# mod1 <- Mclust(X, x = BIC)
# summary(mod1, parameters = TRUE)

# plot(mod1, what = "classification")

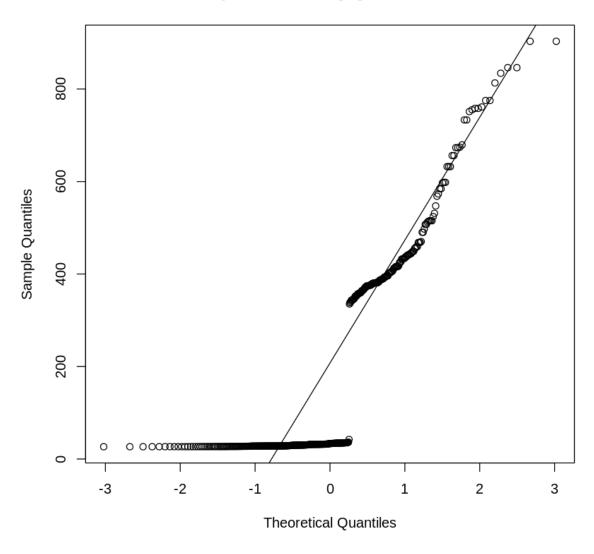
# plot(mod1, what = "uncertainty")

# ICL <- mclustICL(X)
# summary(ICL)
# plot(ICL)

# LRT <- mclustBootstrapLRT(X, modelName = "VEV")
# LRT

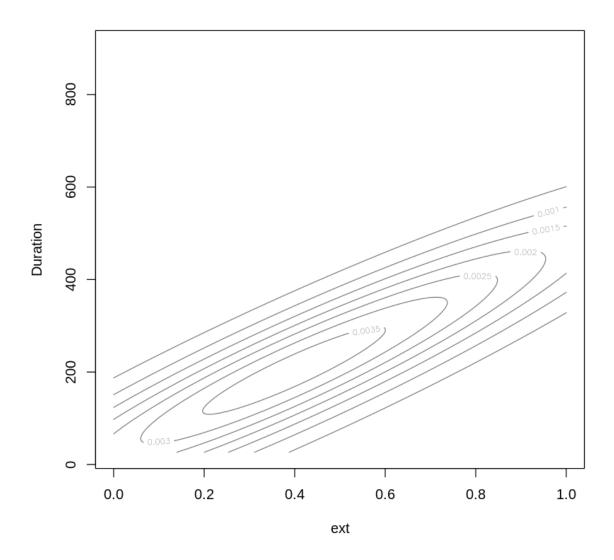
qqnorm(aSpan$Duration, main="Span Duration Q-Q Norm Plot")
qqline(aSpan$Duration)</pre>
```

## **Span Duration Q-Q Norm Plot**



```
# head(aSpan)

aSpan_Density <- aSpan %>%
    # dplyr::select(useCaseNum, env, ext, Duration)
    dplyr::select(ext, Duration)
    # dplyr::select(Duration)
```



## 4 Separating Internal from External Data

#### 4.1 Internal Data

```
# Separate Internal Data
# Could use ext == FALSE
tracksSpanData = subset(aSpan, useCaseNum == 1)
TE_SpanData = subset(aSpan, useCaseNum == 2)
WA_SpanData = subset(aSpan, useCaseNum == 3)
internalSpanData <- rbind(tracksSpanData, TE_SpanData, WA_SpanData)</pre>
dssSpanData <- rbind(TE_SpanData, WA_SpanData)</pre>
# Remove Outliers
# outliers <- boxplot(internalSpanData$Duration, plot = FALSE)$out
# outliers
# iSpan <- iSpan[-which(iSpan$Duration %in% outliers),]</pre>
# outliers <- which(internalSpanData$Duration > 50) #outlier rows
# outliers
# iSpan <- internalSpanData[!outliers,]</pre>
# iSpan <- dssSpanData[!dssSpanData$Duration > 50,]
# iSpan <- internalSpanData[!internalSpanData$Duration > 50,]
    # Remove if duration is greater than a value
iSpan <- internalSpanData
summary(iSpan)
sd(iSpan$Duration)
```

```
Trace.ID
                  Trace.name
                                  Start.time
                                                       Duration
Length: 240
                 Length:240
                                 Length:240
                                                   Min. :26.57
Class : character Class : character Class : character 1st Qu.:27.99
Mode :character Mode :character Mode :character Median :29.35
                                                    Mean :30.02
                                                    3rd Qu.:31.89
                                                    Max.
                                                          :42.28
                                 useCase
                                                  useCaseNum
 platform
Length: 240
                 Min. :1.00 Length:240
                                                Min. :1
```

```
      Class : character
      1st Qu.:1.75
      Class : character
      1st Qu.:1

      Mode : character
      Median : 2.50
      Mode : character
      Median : 2

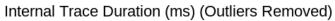
      Mean : 2.50
      Mean : 2
      3rd Qu.:3

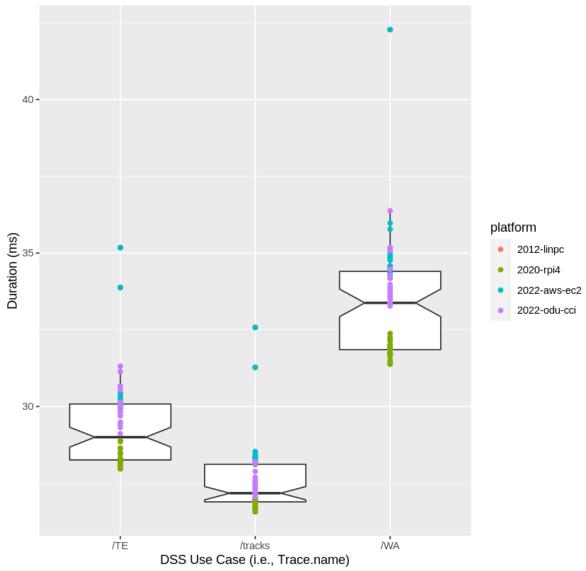
      Max. : 4.00
      Max. : 3
```

ext hthreshold
Mode:logical Mode:logical
FALSE:240 TRUE:240

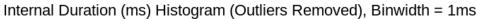
#### 2.77664210997812

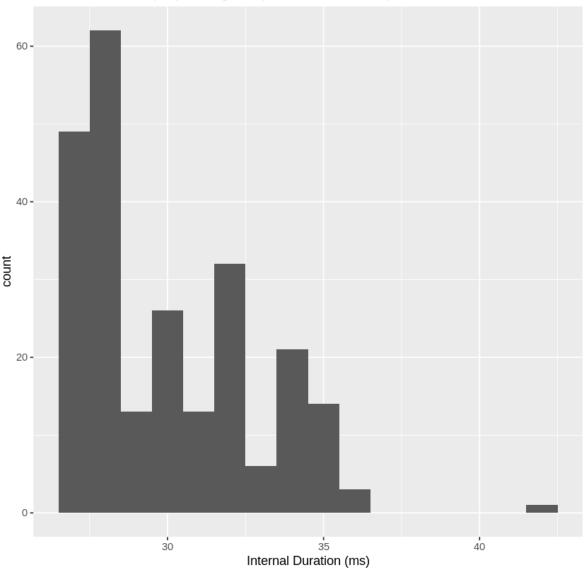
```
iSpan %>%
    ggplot(aes(Trace.name, Duration)) +
    stat_boxplot(notch="TRUE") + geom_point(aes(colour = platform)) +
    ggtitle("Internal Trace Duration (ms) (Outliers Removed)") +
    ylab("Duration (ms)") +
    xlab("DSS Use Case (i.e., Trace.name)")
```





```
iSpan %>%
    ggplot(aes(Duration)) + geom_histogram(binwidth = 1) +
    ggtitle("Internal Duration (ms) Histogram (Outliers Removed), Binwidth = 1ms") +
    xlab("Internal Duration (ms)")
```





```
# dnorm_iSpan <- iSpan
# dnorm_iSpan$Duration <- dnorm(dnorm_iSpan$Duration,mean=7.745,sd=2.776)

# dnorm_iSpan %>%
# ggplot(aes(Duration)) + geom_histogram() +
# ggtitle("Duration (ms) Histogram (w dnorm, Binwidth = auto") +
# xlab("Duration (ms)")
```

```
# shapiro.test(dnorm_iSpan$Duration)
```

Note that the histogram plot indicates that the data is not normally distributed and will need a transformation to enable application of statistics.

#### 4.2 External Data

```
RIC_SpanData = subset(aSpan, useCaseNum == 5)
IAD_SpanData = subset(aSpan, useCaseNum == 4)

externalSpanData <- rbind(RIC_SpanData, IAD_SpanData)

# Remove outliers
# outliers <- boxplot(externalSpanData$Duration, plot = FALSE)$out
# outliers

eSpan <- externalSpanData
# eSpan <- eSpan[-which(eSpan$Duration %in% outliers),]

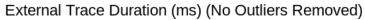
summary(eSpan)
sd(eSpan$Duration)</pre>
```

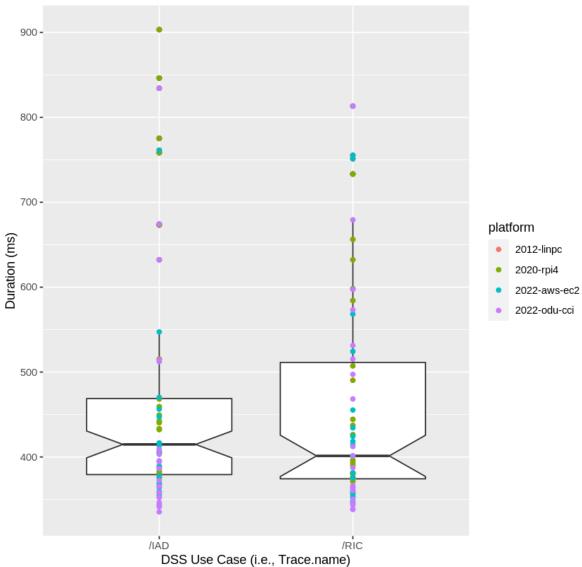
Trace.ID	Trac	Trace.name		Start.time		Duration	
Length: 159	Lengt	h:159	Ler	ngth:159	Min	. :335.3	
Class : characte	er Class	Class :character		· ·		r 1st Qu.:375.3	
Mode :characte	er Mode	:characte	r Mod	le :characte	er Med	ian :409.3	
					Mea	n:464.5	
					3rd	Qu.:507.3	
					Max	. :903.3	
platform		env	use(	Case	useC	aseNum	
Length: 159	Min.	:1.000	Length	n:159	Min.	:4.000	
Class : characte	er 1st Q	u.:1.500	Class	:character	1st Qu	.:4.000	
Mode :characte	er Media	n:2.000	Mode	:character	Median	:4.000	
	Mean	:2.491			Mean	:4.497	
	3rd Q	u.:3.000			3rd Qu	.:5.000	
	Max.	:4.000			Max.	:5.000	
ext	hthreshol	d					
Mode:logical	Mode :log	ical					
TRUE:159	FALSE:41						

#### TRUE :118

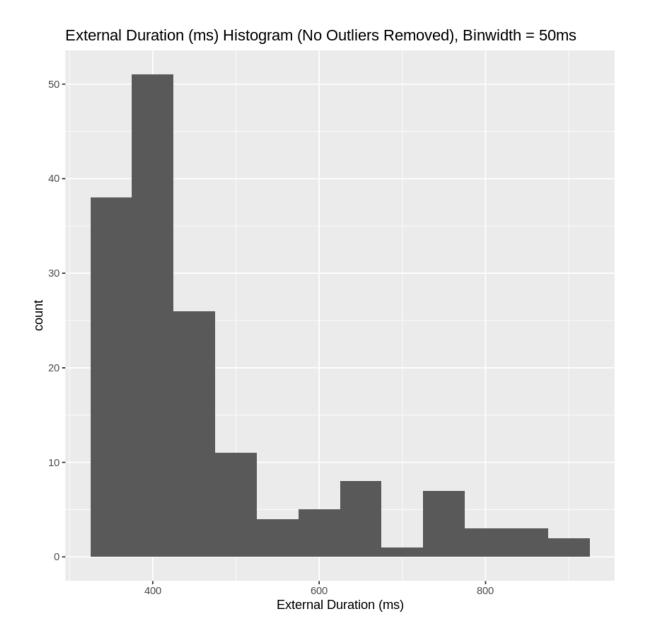
#### 135.466366505137

```
eSpan %>%
    ggplot(aes(Trace.name, Duration)) +
    stat_boxplot(notch="TRUE") + geom_point(aes(colour = platform)) +
    ggtitle("External Trace Duration (ms) (No Outliers Removed)") +
    ylab("Duration (ms)") +
    xlab("DSS Use Case (i.e., Trace.name)")
```





```
eSpan %>%
    ggplot(aes(Duration)) + geom_histogram(binwidth = 50) +
    ggtitle("External Duration (ms) Histogram (No Outliers Removed), Binwidth = 50ms") +
    xlab("External Duration (ms)")
```



Note that the histogram plot of the external data indicates that the data is not normally distributed and will need a transformation to enable application of statistics.

# 5 Transformation and Normality Testing of the Data

The histograms of the internal and external span data imply that a log transform is needed; however, we need to look at cube and sqrt transforms. A Box-Cox transformation may also

need to be explored. Once that data has been transformed, we shall use a Shapiro-Wilk test to assess whether or not the data is normally distributed.

#### 5.1 Box-Cox Transformation

Box and Cox (1964) developed a family of transformations designed to reduce nonnormality of the errors in a linear model. Applying this transform often reduces non-linearity as well, and heteroscedascity.

The idea is to transform the response variable Y to a replacement response variable  $Y_i^{(\lambda)}$ , leaving the right-hand side of the regression model unchanged, so that the regression residuals become normally-distributed. Note that the regression coefficients will also change, because the response variable has changed; therefore, the regression coefficients must be interpreted with respect to the transformed variable. Also, any predictions made with the model have to be back-transformed, to be interpreted in the original units.

The standard (simple) Box-Cox transform is:

$$Y_i^{(\lambda)} = \begin{cases} \frac{Y_i^{\lambda} - 1}{\lambda}, & (\lambda \neq 0) \\ log(Y_i), & (\lambda = 0) \end{cases}$$

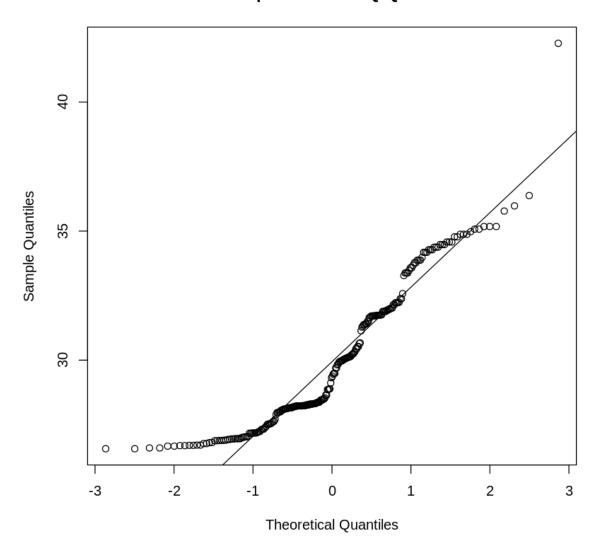
Box, G. E. P., & Cox, D. R. (1964). An Analysis of Transformations. Journal of the Royal Statistical Society, Series B (Metholological), 26(2), 211-252.

 $http://www.css.cornell.edu/faculty/dgr2/\_static/files/R\_html/Transformations.html$ 

# 5.2 Data Transformations and Hypothesis Testing (Internal Data)

qqnorm(iSpan\$Duration, main="Internal Span Duration Q-Q Norm Plot")
qqline(iSpan\$Duration)

# Internal Span Duration Q-Q Norm Plot



# 5.2.1 Sqrt-Log-Cube Transformations

```
# sqrt_iSpan <- iSpan
# sqrt_iSpan$Duration=sqrt(sqrt_iSpan$Duration)

# log_iSpan <- iSpan
# log_iSpan$Duration=log(log_iSpan$Duration + 1) # Natural Log</pre>
```

```
# log10_iSpan <- iSpan
# log10_iSpan$Duration=log10(log10_iSpan$Duration + 1) # Log Base 10
# log2_iSpan <- iSpan
# log2_iSpan$Duration=log2(log2_iSpan$Duration + 1) # Log Base 2

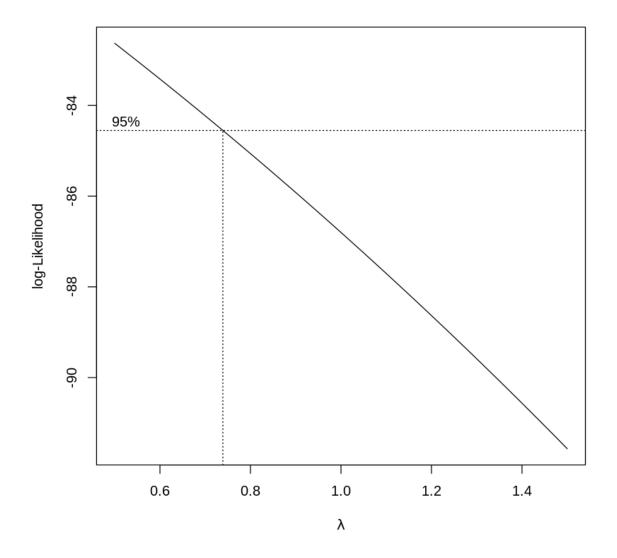
# cube_iSpan <- iSpan
# cube_iSpan$Duration=cube_iSpan$Duration^(1/3)

# par(mfrow=c(2,2))
# hist(iSpan$Duration, counts = 10)
# hist(log_iSpan$Duration)
# hist(log10_iSpan$Duration)
# hist(log2_iSpan$Duration)</pre>
```

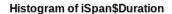
#### 5.2.2 Box-Cox Transformation

```
library("MASS")

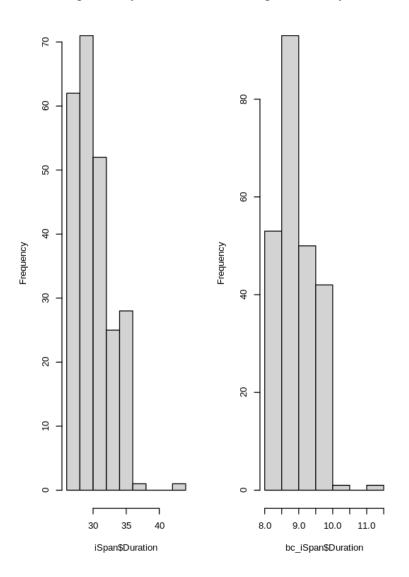
bc_iSpan = iSpan
x <- bc_iSpan$Duration
bc = boxcox(lm(x ~ 1), seq(0.5,1.5,.1))
# bc = boxcox(lm(x ~ bcData$useCaseNum))
lambda <- bc$x[which.max(bc$y)]
new_x_exact <- (x ^ lambda - 1) / lambda</pre>
```



```
bc_iSpan$Duration = new_x_exact
par(mfrow=c(1,3))
hist(iSpan$Duration)
hist(bc_iSpan$Duration)
```



#### Histogram of bc\_iSpan\$Duration



## 5.2.3 Shapiro-Wilk Normality Test

```
shapiro.test(iSpan$Duration)

# shapiro.test(log_iSpan$Duration)
# shapiro.test(log10_iSpan$Duration)
# shapiro.test(log2_iSpan$Duration)
```

```
# shapiro.test(sqrt_iSpan$Duration)
# shapiro.test(cube_iSpan$Duration)
shapiro.test(bc_iSpan$Duration)

Shapiro-Wilk normality test

data: iSpan$Duration
W = 0.9075, p-value = 5.081e-11

Shapiro-Wilk normality test

data: bc_iSpan$Duration
W = 0.91486, p-value = 1.783e-10
```

With all p-values > 0.05 we fail to reject the null hypothesis and assume we have a normal distribution.

"if the p value is greater than the chosen alpha level, then the null hypothesis (that the data came from a normally distributed population) can not be rejected"

#### 5.2.4 Hypothesis Testing (Need to Correct Issue)

We will use a Student's t-Test to test the hypothesis on **normal** internal span data. Our mean is 500 ms (e.g.  $\mu = 0.5$  seconds) and our null hypothesis is less than 500 ms.

```
mu = 0.5
x = cube_iSpan$Duration
cube_mu = mu^(1/3)
t.test(x=x, mu=cube_mu, alternative = 'greater')
```

ERROR: Error in eval(expr, envir, enclos): object 'cube\_iSpan' not found

With a p-value of  $\_\_\_$  > 0.05 we reject the null hypothesis, i.e. we assume that latency will be greater than 500 ms.

"If the p value is greater than the chosen alpha level, then the null hypothesis (that latency is < 500 ms) can not be rejected"

## 5.3 Data Transformations and Hypothesis Testing (External Data)

```
qqnorm(eSpan$Duration, main="External Span Duration Q-Q Norm Plot")
qqline(eSpan$Duration)
```

#### 5.3.1 Sqrt-Log-Cube Transformations

```
sqrt_eSpan <- eSpan
sqrt_eSpan$Duration=sqrt(sqrt_eSpan$Duration)

log_eSpan <- eSpan
log_eSpan$Duration=log(log_eSpan$Duration + 1) # Natural Log
log10_eSpan <- eSpan
log10_eSpan$Duration=log10(log10_eSpan$Duration + 1) # Log Base 10
log2_eSpan <- iSpan
log2_eSpan$Duration=log2(log2_eSpan$Duration + 1) # Log Base 2

cube_eSpan <- eSpan
cube_eSpan$Duration=cube_eSpan$Duration^(1/3)

par(mfrow=c(2,2))
hist(eSpan$Duration, counts = 50)
hist(log_eSpan$Duration)
hist(log10_eSpan$Duration)
hist(log2_eSpan$Duration)</pre>
```

#### 5.3.2 Box-Cox Transformation

```
bc_eSpan = eSpan
x <- bc_eSpan$Duration
bc = boxcox(lm(x ~ 1), seq(-3,3,.1))
# bc = boxcox(lm(x ~ bcData$useCaseNum))
lambda <- bc$x[which.max(bc$y)]
new_x_exact <- (x ^ lambda - 1) / lambda

bc_eSpan$Duration = new_x_exact
par(mfrow=c(1,3))
hist(eSpan$Duration)</pre>
```

```
hist(bc_eSpan$Duration)
```

#### 5.3.3 Shapiro-Wilk Normality Test

```
shapiro.test(eSpan$Duration)
shapiro.test(log_eSpan$Duration)
shapiro.test(log10_eSpan$Duration)
shapiro.test(log2_eSpan$Duration)
shapiro.test(sqrt_eSpan$Duration)
shapiro.test(cube_eSpan$Duration)
shapiro.test(bc_eSpan$Duration)
```

With a p-value of  $\_\_\_$  < 0.05 we reject the null hypothesis, i.e. we assume that we do not have a normal distribution.

"if the p value is greater than the chosen alpha level, then the null hypothesis (that the data came from a normally distributed population) can not be rejected"

### 5.3.4 Hypothesis Testing (Update and Correct)

We will use a Student's t-Test to test the hypothesis on external span data. Our mean is 500 ms (e.g.  $\mu = 0.5$  seconds) and our null hypothesis is less than 500 ms.

```
mu = 0.5

x = eSpan$Duration
t.test(x=x, mu=mu, alternative = 'greater')

# binom.test(420, 500, p = 0.95,
# alternative = c("greater"),
# conf.level = 0.95)

binom.test(418, 500, p = 0.95, alternative = "greater")
```

With a p-value of  $\_\_\_$  > 0.05 we fail to reject the null hypothesis, i.e. we assume that 500 ms can be maintained for external service requests.

"If the p value is greater than the chosen alpha level, then the null hypothesis (that latency is < 500 ms) can not be rejected"

#### 6 Observations

### 6.1 General Discussion of Normality

It was required to separate external data from internal to establish normality of the data samples. The internal data set required transformation to establish normality, while the external data did not require a transformation.

## 6.2 Hypothesis Results (Update to Reflect Results)

Hypothesis testing using the Student's t-Test indicates that latency constraints of 500 ms can be maintained internally and external. However, serveral external samples were greater than 500 ms. This is most likely due to the non-deterministic nature of internet (e.g. http) requests. Within the internal environment, data is directly routed between microservices within the Docker environment within a private network. The data shows that a container based microservice architecture can meet the requirement; however, care must be taken to manage processing per container that may increase container response times.

## 6.3 DSS Prototype Environment

The non deterministic nature of the Docker environment on the MacBook laptop significantly affected the ability to assess deterministic behavior. Boxplots of data inclusive of what was sampled from the MacBook clearly depicted this issue. Linux platforms truly run a container as intended; however, non-linux platform require the use of a Linux based Virtual Machine on top of the host OS to implement containers. While the MacBook met the needs for rapid software development, the use of a separate integration and test environment was clearly validated through the collected data.