

COVID In Situ - Supplementary Content

Version – 15 July 2021

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1 Write-Up

1.1 Research Question

Will a structured in-situ/Quality Improvement (QI) programme result in the reduction of PLSTs over the course of 3 PDSA cycles in a non-academic Emergency Department?

1.1.1 Primary Outcome

The primary outcome of interest was the shift in the SAFER-matrix over each PDSA cycle.

1.1.2 Secondary Outcome

Secondary outcomes of interest included: (1) monitoring identified threats per cycle and (2) a review of the impact of the interventions on the primary drivers per cycle.

1.2 Simulation

1.2.1 Case

70 year old female in the Emergency Department, known to be COVID positive from prior visit, now returns in respiratory distress. Arrives by EMS on BiPAP, appearing lethargic.

(Monitor is turned on below)

Team should realize that they need to intubate. In the case, the primary airway will fail requiring the team to acquire a secondary device, which will signal the end of the case.

1.2.1.1 Patient Monitor Link <https://www.youtube.com/watch?v=A1MlmZEKTFA>

Utilized iPad or other screen device, desktop computer in room for Electronic Health Records.

1.2.2 No Go Criteria

1. Lack of staffing to run the program
2. Avoid breaks or shift change patterns
3. High clinical load or acuity
4. Avoid using low-stocked equipment (have them bring the bags but do not open them)
5. Unanticipated event that is a threat to psychological safety

Bajaj K, Minors A, Walker K, Meguerdichian M, Patterson M. “No-Go Considerations” for In Situ Simulation Safety. *Simul Healthc*. 2018 Jun;13(3):221-224. doi: 10.1097/SIH.0000000000000301. PMID: 29621037.

1.3 Debriefing

1.3.1 Pre-Brief Script

Pre-Brief Script “Hello and welcome. My name is [debriefing name], and I am from (Montefiore/White Plains/Jacobi) and would like to talk to you about an in situ simulation / quality improvement research study on COVID-19 management.

We work in a very complex healthcare environment and errors are more often secondary to problems with how our system functions rather than that of individuals. The idea of this study is to run a short simulated case in our work environment and have an open and candid discussion regarding problems that we find in our work environment. Because you are all going to be in your natural environment, you will have access to all the equipment and tools you would normally have in any clinical scenario. Your knowledge of the environment will help you navigate this scenario. Additionally, any systemic issues that need to be addressed will also surface in this scenario, we call these latent safety threats. We hope to identify, with your help, problems in our environment today so that we can start fixing them. Why is this a study? Well, we are combining in situ simulation and quality improvement tools and if successful, we believe that we should disseminate this method to the larger healthcare community.

The debriefing will look different than learner-focused debriefing that you are accustomed to our in simulation center. We have predetermined objectives that we need your feedback on, and want to hear what worked well and what could be improved. Your feedback is important to us and we will make sure to inform you of changes we make based on your feedback.

We ask you to join this study because you are a healthcare provider working in a hospital unit that treats patients with COVID-19. We hope it’s a fun and learning-friendly environment for you! We will ask you to participate in an in situ simulation here in the hospital unit and debrief today. It will take 10 minutes for the simulation and 10 minutes for the debrief. Your participation is completely voluntary and information about participation or performance will not be reported to your supervisor. The decision to participate will not affect your employment status, rights or benefits. We will not collect any personal information. The data collected be your anonymous comments and solutions on how we can improve our system. You will receive no direct benefit from this study. We will not pay you to join this study.

1.3.2 Debriefing Script

“We are going to spend the next 10 minutes debriefing the simulation. This simulation is not about your individual knowledge or skills. This focus is to improve the systems and processes in which we work and identify system issues including latent safety threats. In this scenario, we asked you to... (focus on predetermined objectives)” A plus / delta will be performed for each predetermined objective. Debriefing will document topics from the conversation.

1.3.3 Pre-Summary Script

“We discussed important safety and system issues. Before we summarize, are there any other latent safety threats or systems issues we should capture?”

If so, document.

1.3.4 Summary Script

“In this simulation, we identified the following (read the itemized list from notes, including potential solutions). Any other improvements you can think of?”

1.4 Data Collection

1.4.1 Debrief Data

We will only documenting the delta portion of the in situ simulation. However, please continue to perform the “plus” portion with the team in your debriefs.

The goal of this section is to obtain raw data so that we can categorize your findings into weighted latent safety threats.

1.4.1.1 Infection Control Delta - Infection control latent safety threats: aerosol spread, donning/doffing PPE, cross-contamination

1.4.1.2 Equipment Delta - Equipment latent safety threats: glidescope, ventilator, to-go bags

1.4.1.3 Communication Delta - communication latent safety threats: (clear team leader? clear roles? closed loop communication used? call-outs? briefs or huddles?)

1.5 SAFER-Matrix Standardization Form

1.5.1 Introduction

Dear Quality and/or ED leader.

We appreciate your time and energy in assisting us with this quality improvement project. Across five institutions, we have found the following categories of latent safety threats. However, they are not all weighted the same in regards to both their likelihood for harm OR scope. The goal of this survey is that we take a subjective assessment and make it as objective as possible across our institutions.

We will be using the SAFER matrix (<https://www.jointcommission.org/accreditation-and-certification/become-accredited/what-is-accreditation/safer-matrix-resources/>) as our guide to categorize the risks associated with our identified threats.

We appreciate your time and expertise in helping us make this data as objective as we can so that we can work on improving the quality of care delivered at each of our respective hospitals.

We expect that this will take you at least 15 minutes to complete. This program has been reviewed by the IRB at Montefiore and White Plains Hospital and is considered exempt as a quality improvement initiative.

This case focused on primary and secondary set-up for a SARS-CoV-2 intubation. A patient with known COVID was in respiratory distress requiring intubation. The primary airway would fail requiring the team to locate and plan for a secondary device.

Threats were categorized into (1) Infection Control, (2) Equipment and (3) Communication.

1.5.1.1 Likelihood of Harm What we will ask you to do is to review each category of threat and assign it a label for its likelihood of harm as either

1. High: Could directly lead to harm without need for other significant circumstances or failures. – Likely
2. Moderate: Could cause harm directly, but more likely to cause harm as a contributing factor in the presence of special circumstances or additional failures. –Possible
3. Low: Undermines safety/quality or contributes to an unsafe environment, but very unlikely to directly contribute to harm. – Rare

1.5.1.2 Scope If you spend at least >50% of your time clinically, we also ask that you also assigns a label for your perceptions of the scope of the category in your respective department. Scope is determined by the following

1. Widespread: issue is “pervasive at the organization” – Process failure/systemic failure – Majority of patients are/could be impacted
2. Pattern: issue has potential to “impact more than a limited number of patients impacted” – Process variation
3. Limited: issue is a “unique occurrence” – Outlier – Not representative of routine/regular practice

1.6 Interventions

1.6.1 Equipment Related Interventions

The primary drivers developed for equipment-related interventions included decreasing the number of (1) difficult to find equipment, (2) missing or expired equipment, and (3) equipment that were present, but staff were unfamiliar with either the location or item during the simulation.

Regarding the “number of difficult to find equipment,” during PDSA 1, a newly designed airway cart was introduced along with improved signage, including floor decals color coordinated for ease of visualization. Prior carts and “to go” bags for airway equipment were removed. For PDSA 2, an additional stylet was added into the airway cart. The idea for floor decals was inspired by the work from Hicks et al 2018 (cite).

With the “number of missing or expired equipment found,” during PDSA 1, airway cart restocking was outsourced to our transport department and an additional safety seal was implemented for quality checks. If this seal was broken, ED staff were informed to contact the transport department to have the cart removed and replaced by an additional pre-stocked cart. This process also allowed for tracking of when the cart is being used. During PDSA 2, unit clerk and staff education were put into place to reinforce contacting the transport department to replace the airway cart for quality control and restocking.

Concerning “equipment that was present, but staff were unfamiliar with the location or item,” during PDSA 1, change concepts included building an “airway menu” with images and locations for each drawer and placing it on the airway cart. Dedicated training was established for all medical staff to familiarize them with the medical carts. Signage and markers were placed on the floors for the carts for ease of identification. During PDSA 2, dedicated and continued training of medical staff occurred using “just-in-time” training and departmental meetings.

1.6.2 Infection Control Related Interventions

Primary drivers developed during the first cycle included decreasing PLSTs associated with (1) Intubation workflow, (2) Access to available PPE, and (3) Infection control related equipment. Concerning “PLSTs associated with the intubation workflow,” during the first wave, a critical airway team was developed consisting of Anesthesiologists and Emergency Physicians working together (Binder et al 2020). However, as SARS-CoV-2 volume decreased, this team was dismantled leading to confusion as to current workflows based on team debriefs. Identified through PDSA 1, an updated workflow for intubation included clear role designations and number of staff in the room consisting solely of ED staff along with RT’s. Intubation and PPE training were added to the new hires program for providers along with continued dedicated training for all medical staff. Disposal areas for laundered PPE were in every room. Continued training occurred between PDSA cycles 2-3.

For “PLSTs associated with access to available PPE,” during the first PDSA cycle, dedicated infection control carts were placed in each zone with clear signage, bright yellow floor decals. Floor decals were inspired from the previous work done by Hicks et al 2018 (cite). In addition, the PAPR system was removed and replaced

with gowns, face shields and N95 masks only. During PDSA 2, PPE gowns were placed on top of airway cart for additional ease of access and as a physical reminder for gowning before entering a room.

Finally, for “PLST attributed to infection control related equipment,” during PDSA 1, the simulation and QI team worked with the hospital’s procurement officer and reviewed current laundered gowns secondary to the threats of the gowns being difficult to remove during doffing. New gowns with Velcro for easy doffing were coordinated with the manufacturer, and after PDSA cycle 2 20,000 new gowns were circulated throughout each department. In addition, a restocking system was put into place by the unit leader in the ED.

1.6.3 Communication Related Interventions

For communication, the simulation and QI team focused primarily on role designation. Primary drivers were listed as PLSTs associated with lack of (1) role designation during a resuscitation, (2) a clear team leader or presence of shared leadership, or (3) a designated runner outside of the resuscitation room. Interventions for primary drivers remained the same. During PDSA 1, change concepts focused primarily on departmental education and reviewing threats from the simulation. Clear workflows for intubation were trained and reviewed. During PDSA 2, role labels were placed on top of airway carts, and a dedicated communication subcommittee was developed from an interprofessional group of clinical leaders within the department to address overall concerns. The subgroup created a structured team huddle program. This included reviewing a “check-in” with each staff member, reviewing safety or quality concerns and pre-designating roles in the event of an acute resuscitation. The structured huddle utilized an already established Artificial Intelligence system to send messages to teams’ handheld devices reminding them to huddle and preventing them from receiving patients for 7 minutes when huddles were activated. This also allowed for continued surveillance via tracking the huddles for the communication subgroup.

2 Load the Data

```
library(xlsx)
if (!require(qicharts)) install.packages('qicharts')

## Loading required package: qicharts

## qicharts will no longer be maintained. Please consider moving to qicharts2: https://anhoej.github.io.
library(lme4)

## Loading required package: Matrix
library(qcc)

## Package 'qcc' version 2.7

## Type 'citation("qcc")' for citing this R package in publications.
library(glmmTMB())
library(qicharts)
library(car)

## Loading required package: carData

## Registered S3 methods overwritten by 'car':
##   method                               from
##   influence.merMod                      lme4
##   cooks.distance.influence.merMod      lme4
##   dfbeta.influence.merMod              lme4
##   dfbetas.influence.merMod            lme4
```

```
library(plm)
library(ggplot2)
covid <-read.xlsx("WP_In_Situ_Data.xlsx", sheetIndex = 1, header = TRUE)
safer <-read.xlsx("WP_In_Situ_Data.xlsx", sheetIndex = 2, header = TRUE)
```

3 Diagram

3.1 DAG

```
DiagrammerR::grViz("digraph {

graph [layout = dot, rankdir = LR]
node [shape = rectangle, style = filled, fillcolor = Linen]

'PDSA Cycle' -> 'Structure Intervention'
'PDSA Cycle' -> 'Process Intervention'
'Night Shift / Day Shift' -> 'LST Count'
'Team Size' -> 'LST Count'
'Zone Location' -> 'LST Count'
'Census' -> 'LST Count'
'Perceived Workload' -> 'LST Count'
'Census' -> 'Perceived Workload'
'Attended Prior Simulation' -> 'LST Count'
'Structure Intervention' -> 'LST Count'
'Process Intervention' -> 'LST Count'

}")
```

4 Descriptive - SAFER Score

4.1 Summary PDSA 1

```
saferpdsa1<-safer$SAFER_Score[c(1:35)]
summary(saferpdsa1)
```

##	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
##	0.00	0.00	8.00	10.94	14.00	60.00

4.2 Summary PDSA 2

```
saferpdsa2<-safer$SAFER_Score[c(36:70)]
summary(saferpdsa2)
```

##	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
##	0.000	0.000	4.000	6.771	8.000	32.000

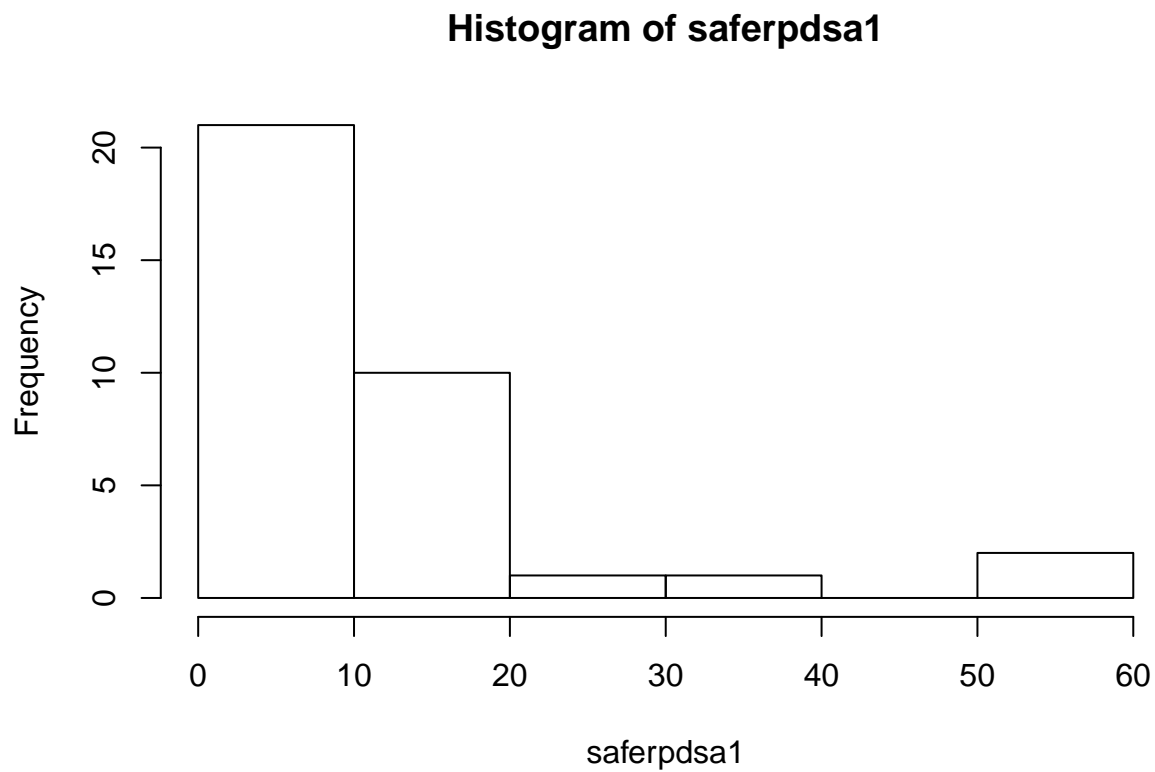
4.3 Summary PDSA 3

```
saferpdsa3<-safer$SAFER_Score[c(71:105)]  
summary(saferpdsa3)
```

##	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
##	0.000	0.000	0.000	4.714	6.000	36.000

4.4 Histogram PDSA 1

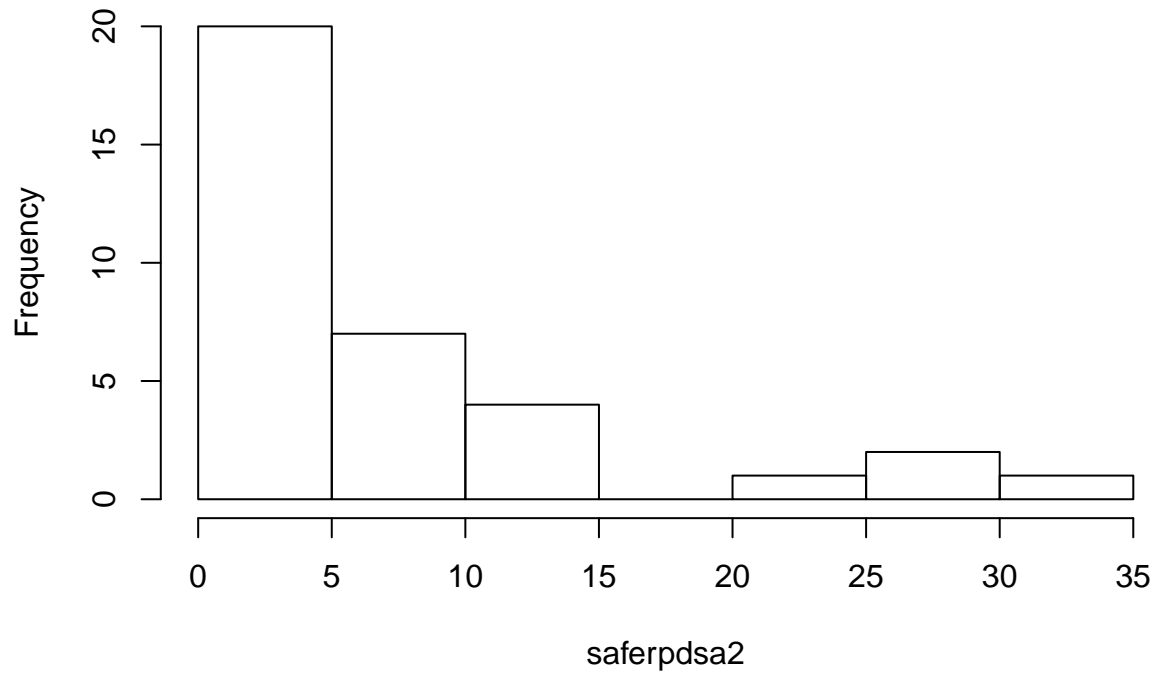
```
hist(saferpdsa1)
```



4.5 Histogram PDSA 2

```
hist(saferpdsa2)
```

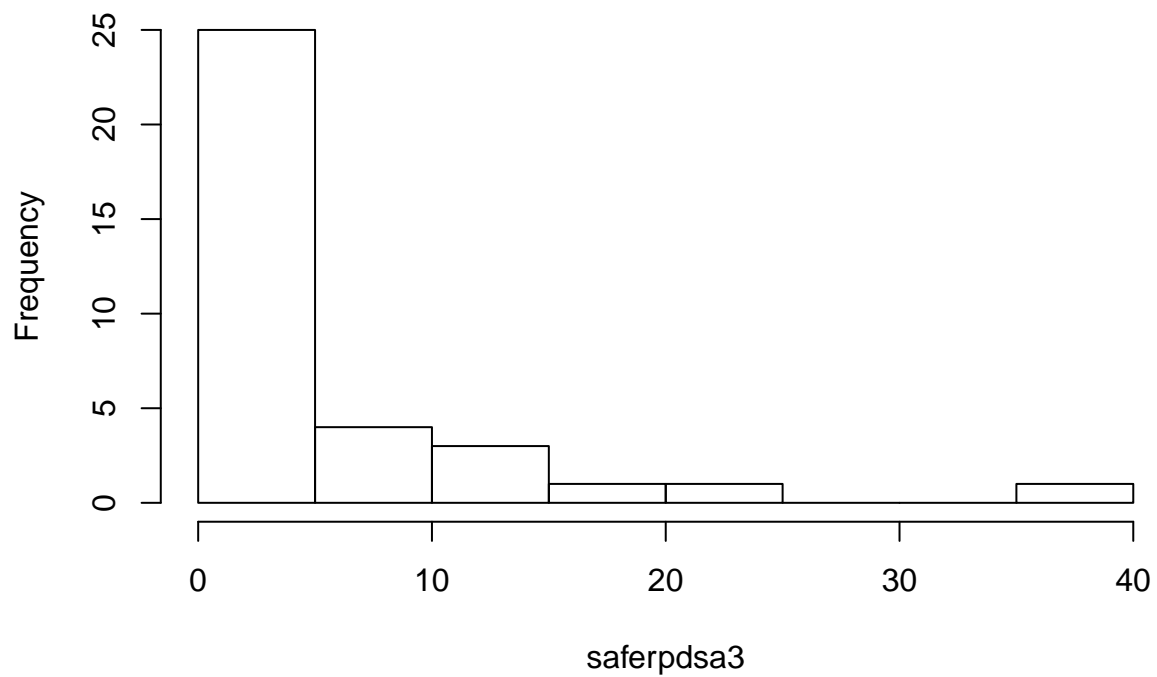
Histogram of saferpdsa2



4.6 Histogram PDSA 3

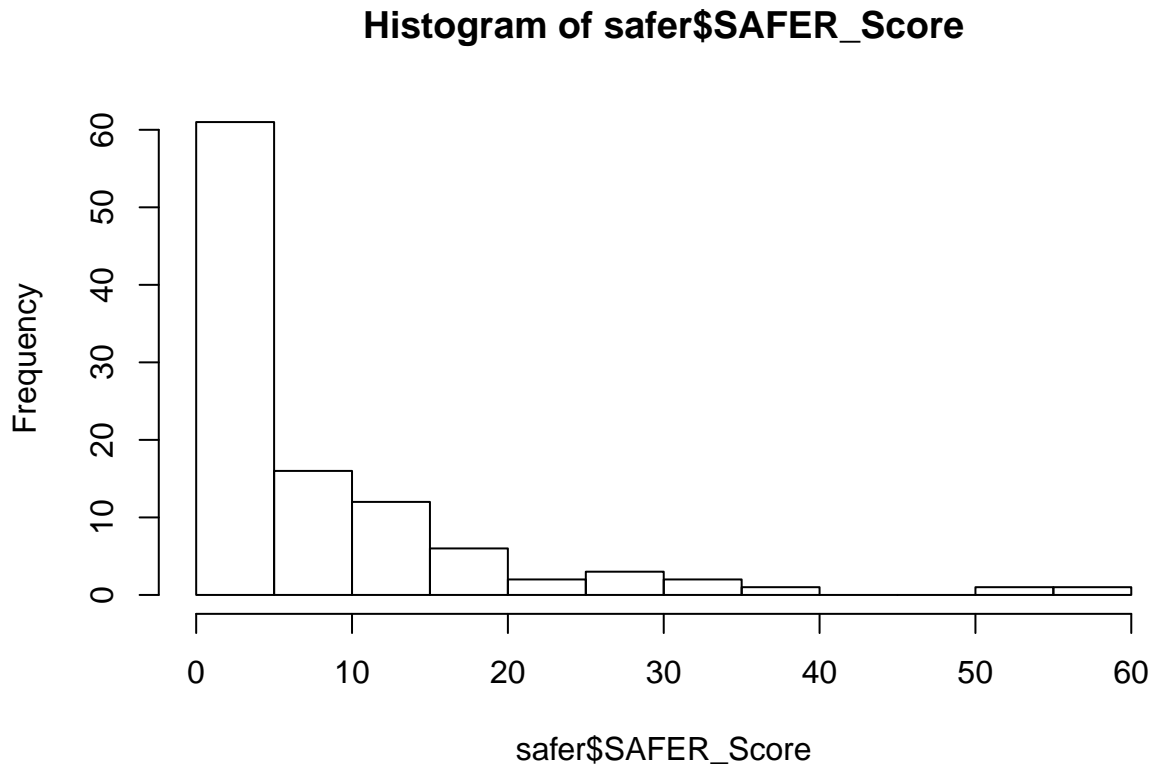
```
hist(saferpdsa3)
```

Histogram of saferpdsa3



4.7 Histogram for SAFER Score

```
hist(safer$SAFER_Score, breaks=10)
```



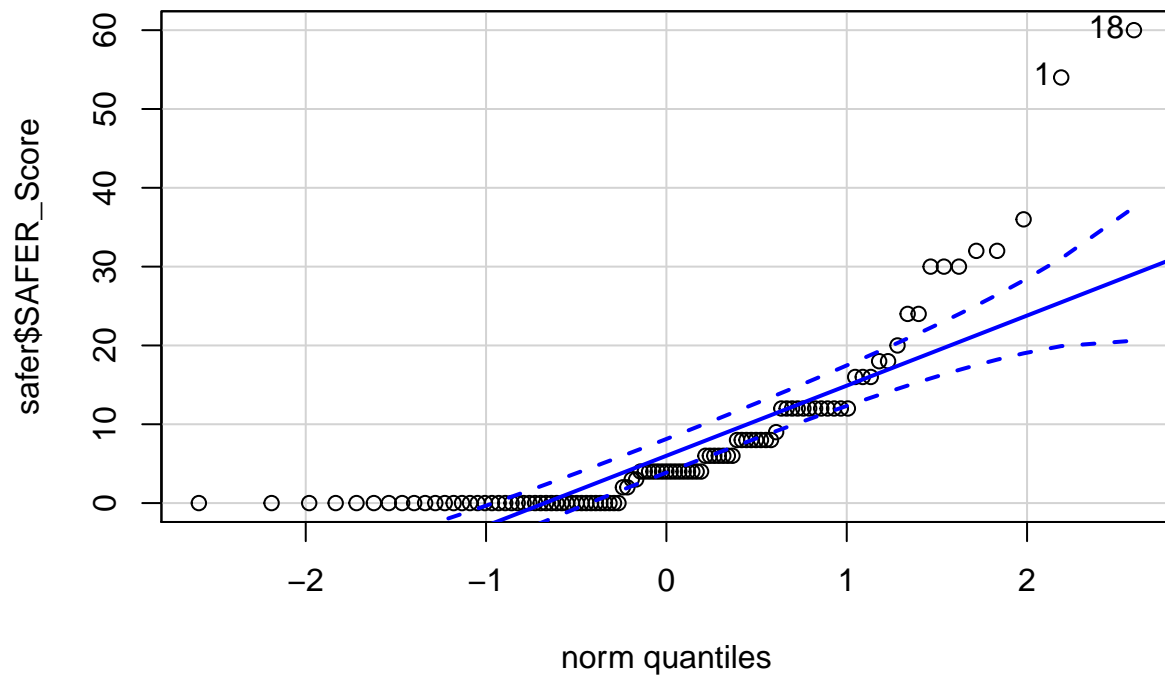
4.8 Table for SAFER Score

```
table(safer$SAFER_Score, safer$PDSA)
```

```
##
##      1  2  3
## 0  10 13 19
## 2   0  1  1
## 3   1  1  0
## 4   5  5  5
## 6   1  4  2
## 8   4  3  1
## 9   0  0  1
## 12  5  4  3
## 16  3  0  0
## 18  1  0  1
## 20  1  0  0
## 24  0  1  1
## 30  1  2  0
## 32  1  1  0
## 36  0  0  1
## 54  1  0  0
## 60  1  0  0
```

4.9 QQ Plot SAFER Score

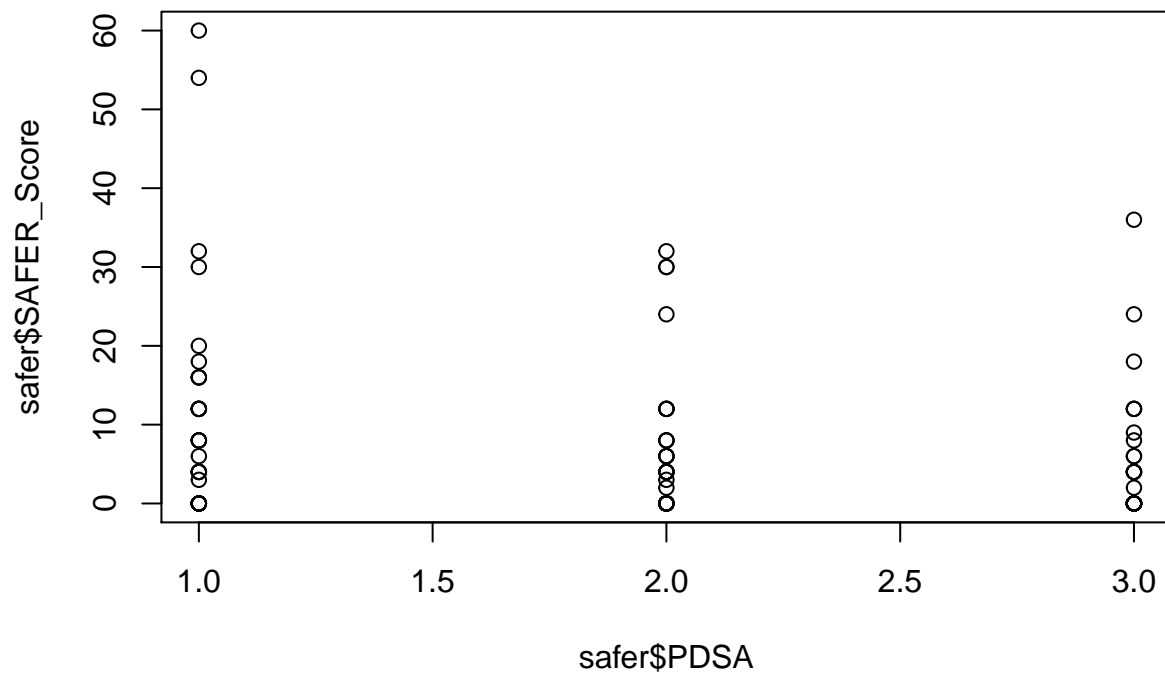
```
qqPlot(safer$SAFER_Score)
```



```
## [1] 18 1
```

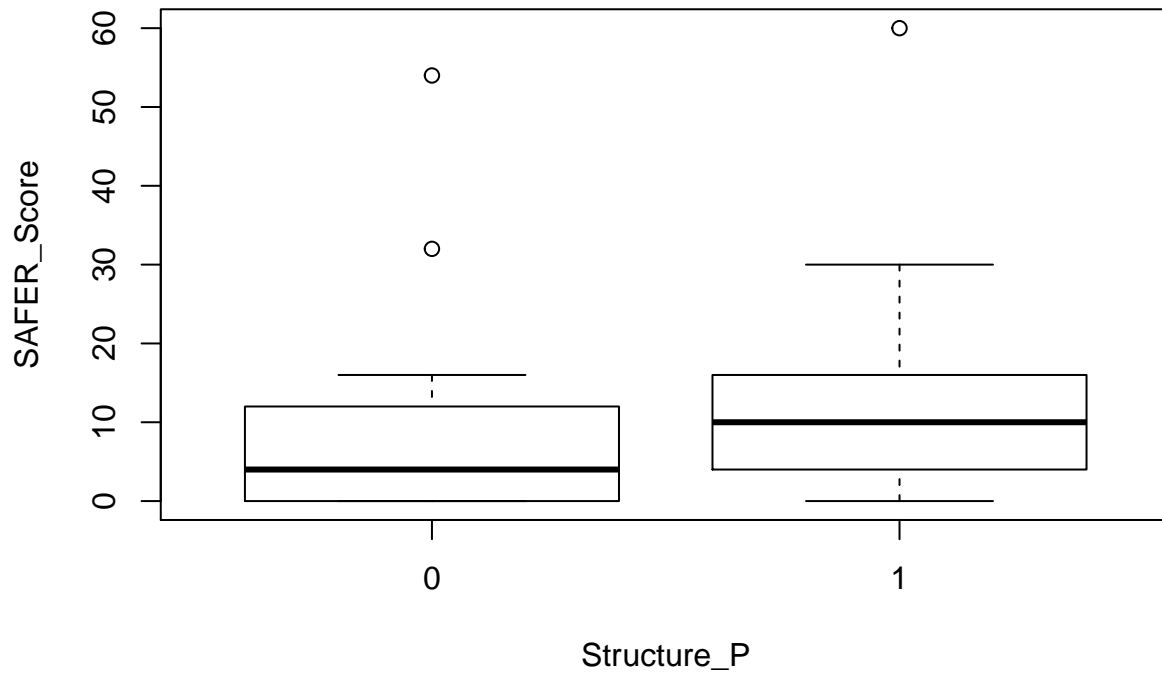
4.10 Plot of SAFER Score

```
plot(safer$PDSA, safer$SAFER_Score)
```



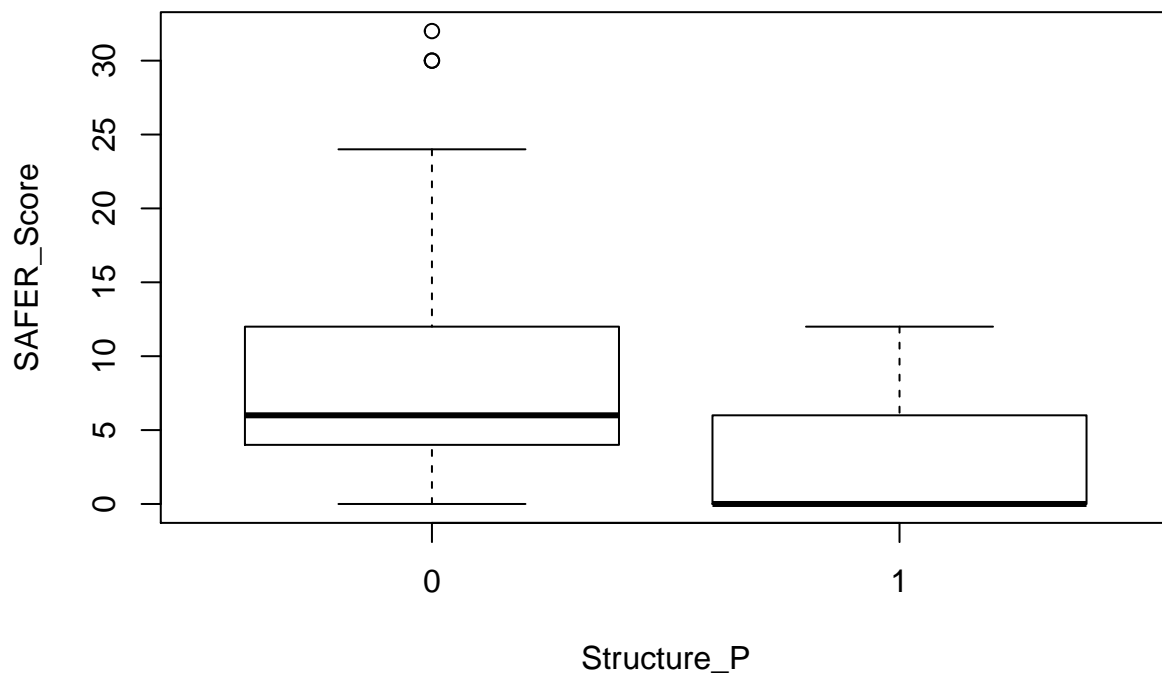
4.11 Box Plot PDSA 1

```
boxplot(SAFER_Score ~ Structure_P, data=safes[which(safes$PDSA==1),])
```



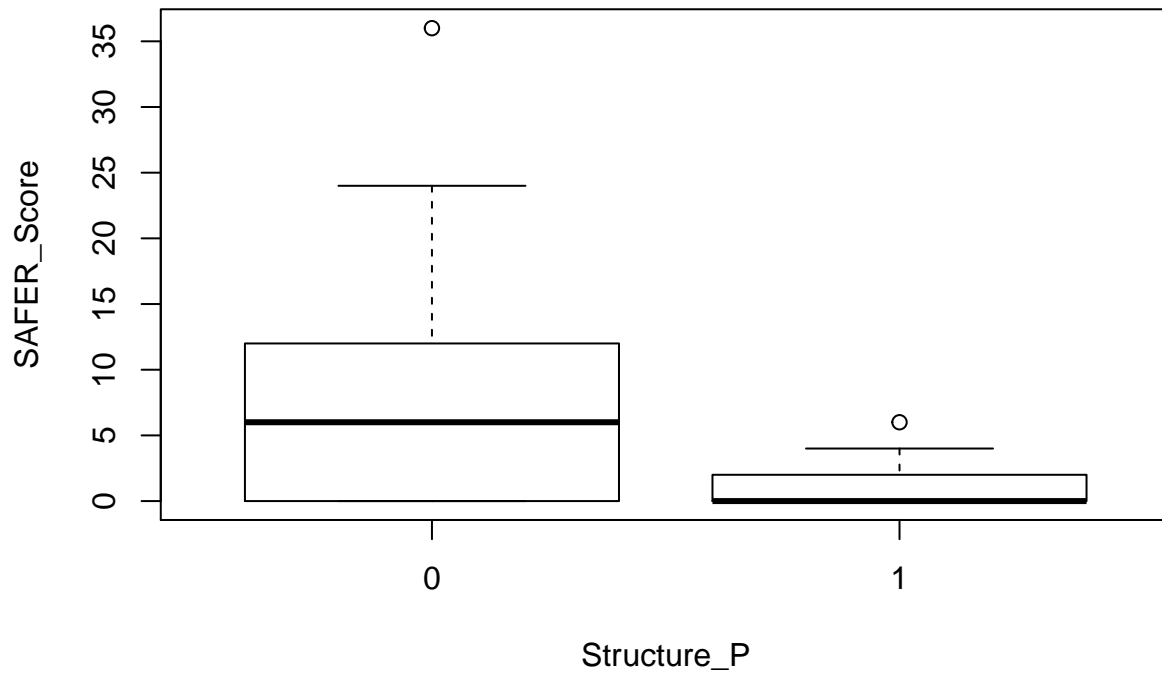
4.12 Box Plot SAFER 7 - PDSA 2

```
boxplot(SAFER_Score ~ Structure_P, data=safes[which(safes$PDSA==2),])
```



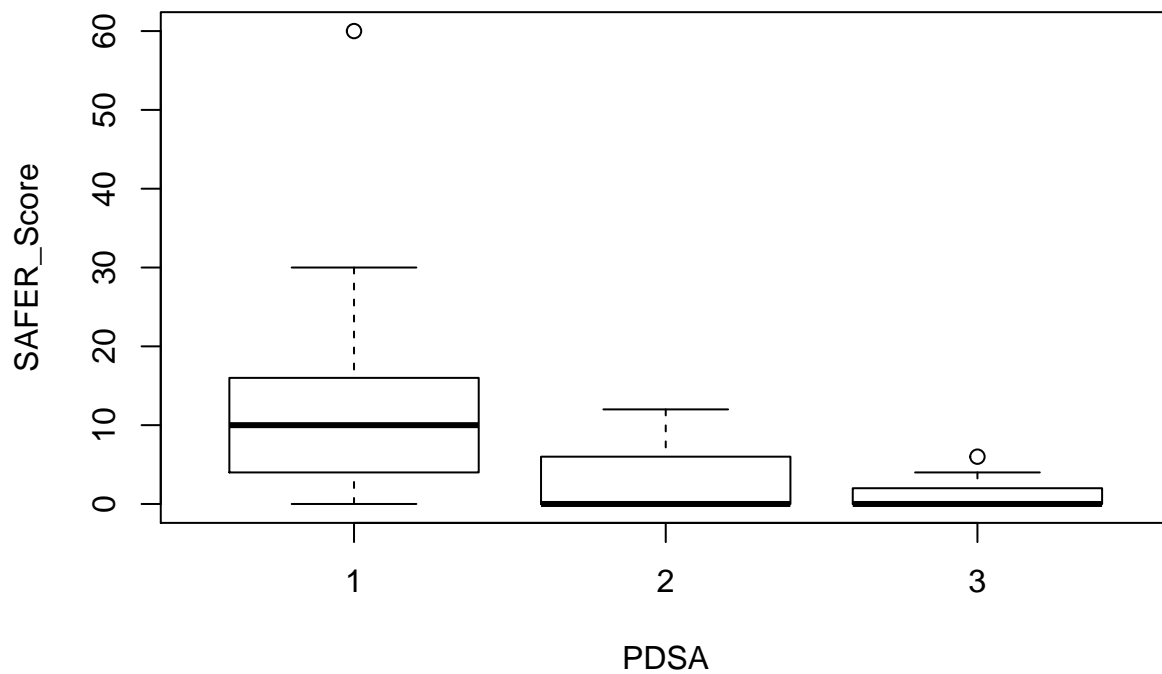
4.13 Box Plot SAFER 7 - PDSA 3

```
boxplot(SAFER_Score ~ Structure_P, data=safes[which(safes$PDSA==3),])
```

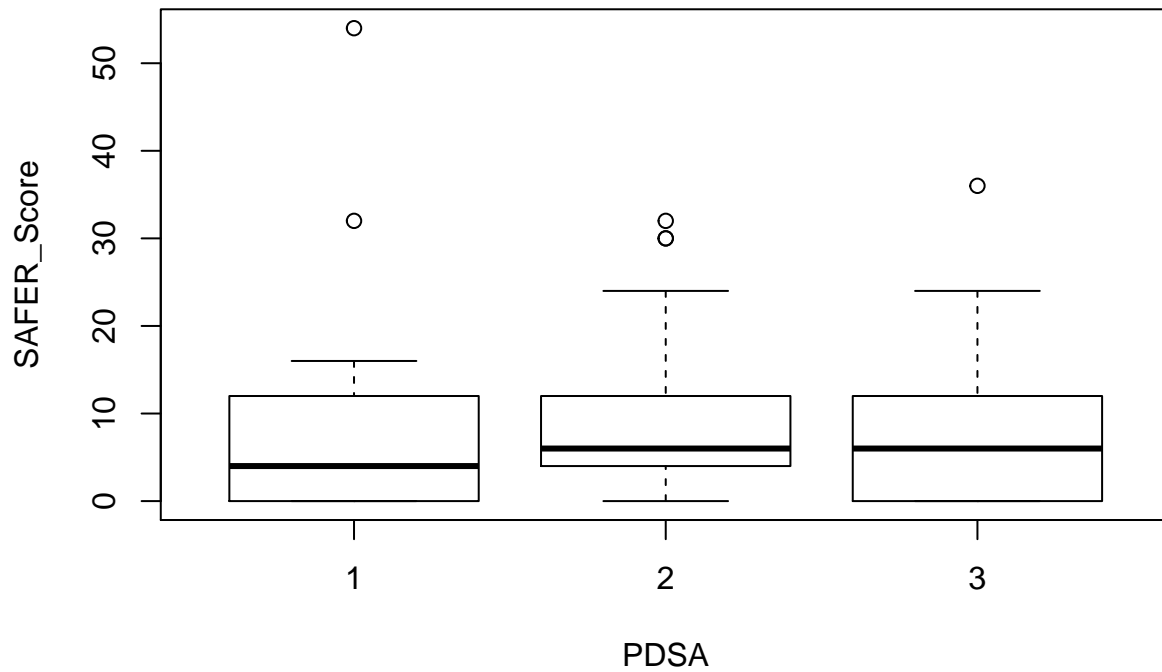


4.14 Box Plot

```
boxplot(SAFER_Score ~ PDSA, data=safes[which(safes$Structure_P==1),])
```



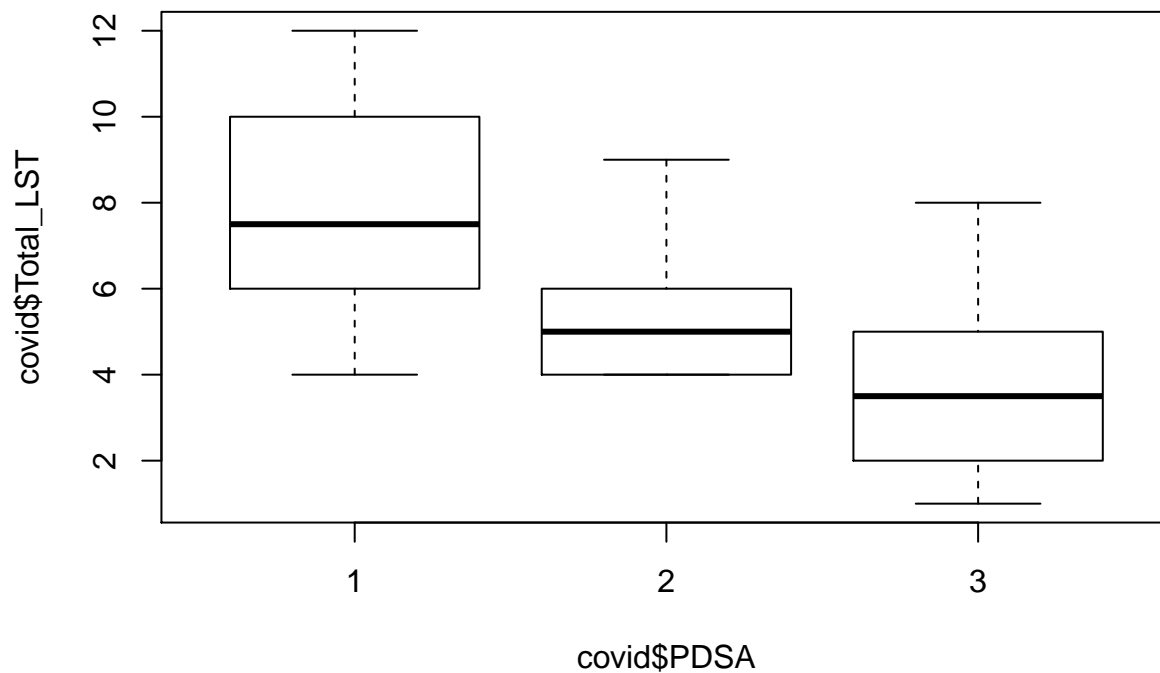
```
boxplot(SAFER_Score ~ PDSA, data=safers[which(safers$Structure_P==0),])
```



4.15 LST Count Box Plots

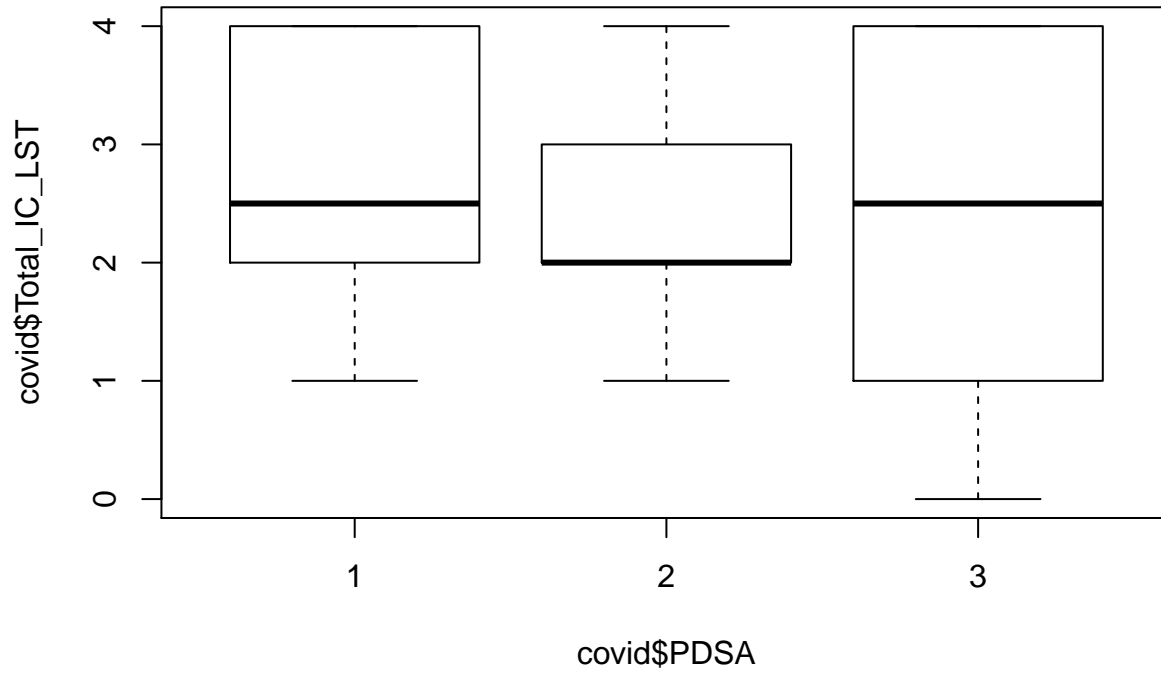
4.15.1 Total LST

```
boxplot(covid$Total_LST ~ covid$PDSA, data = covid)
```



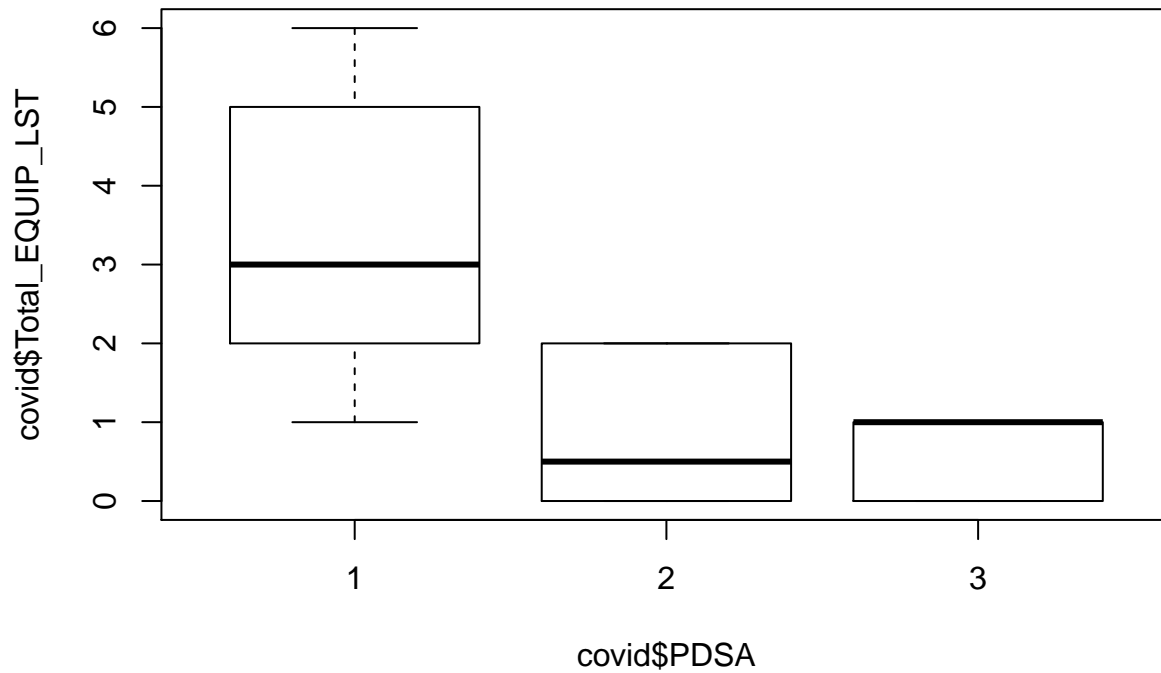
4.15.2 Infection Control LST

```
boxplot(covid$Total_IC_LST ~ covid$PDSA, data = covid)
```



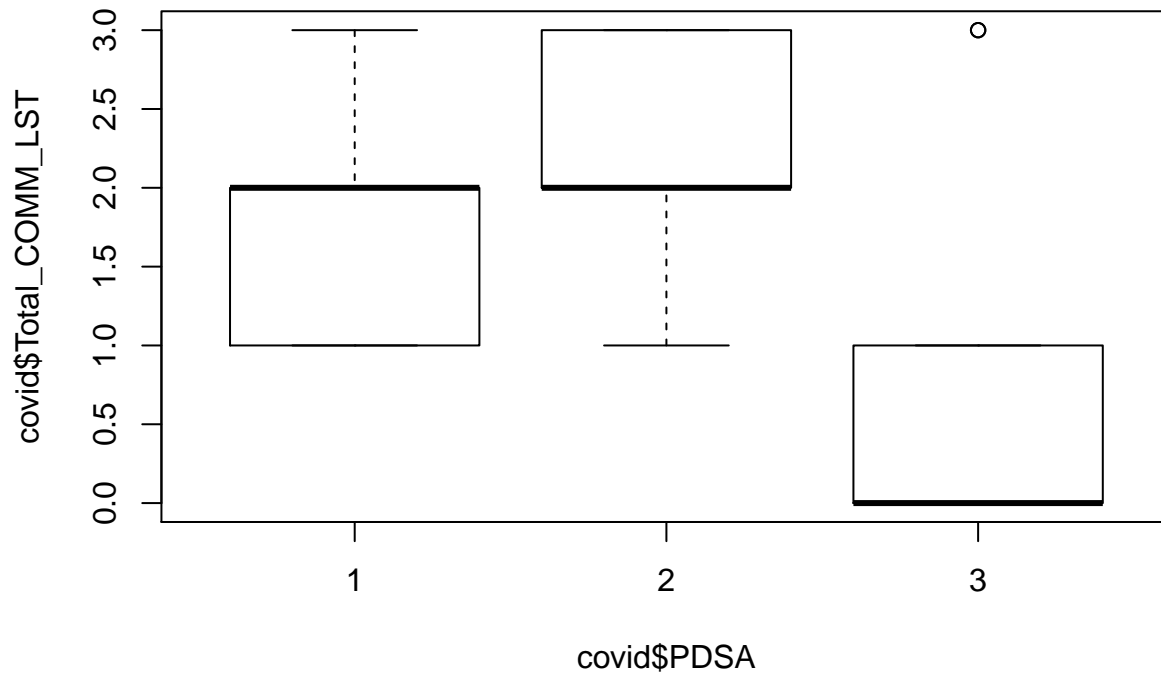
4.15.3 Equipment LST

```
boxplot(covid$Total_EQUIP_LST ~ covid$PDSA, data = covid)
```



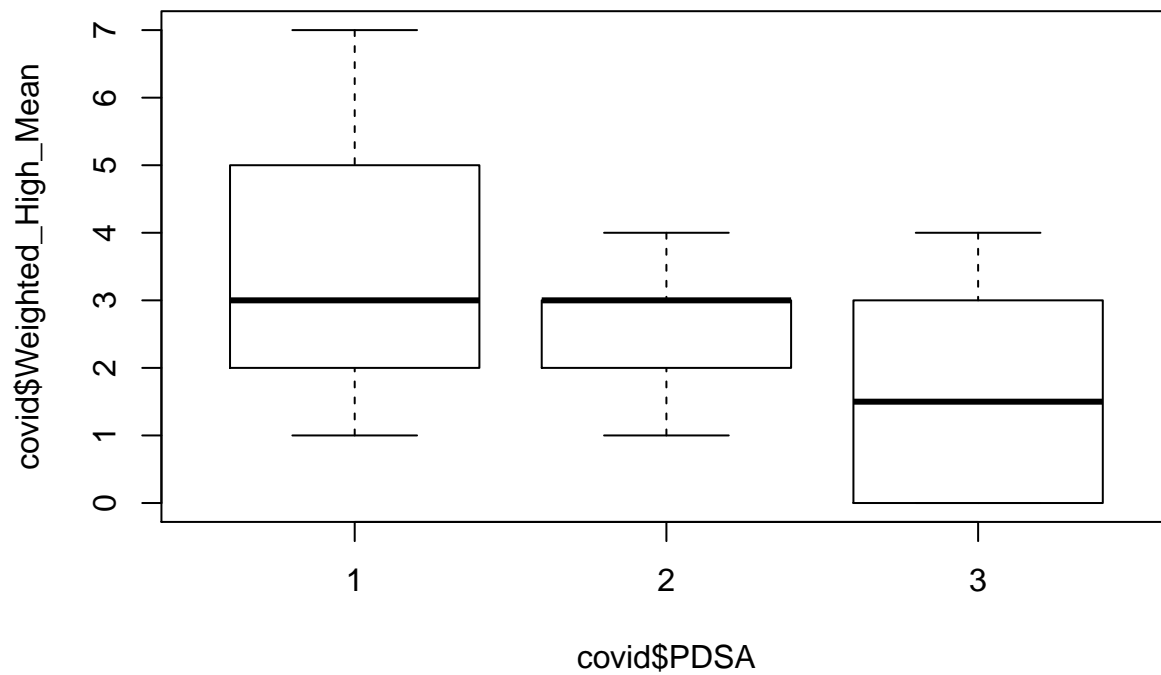
4.15.4 Communication

```
boxplot(covid$Total_COMM_LST ~ covid$PDSA, data = covid)
```



4.15.5 High Risk of Harm

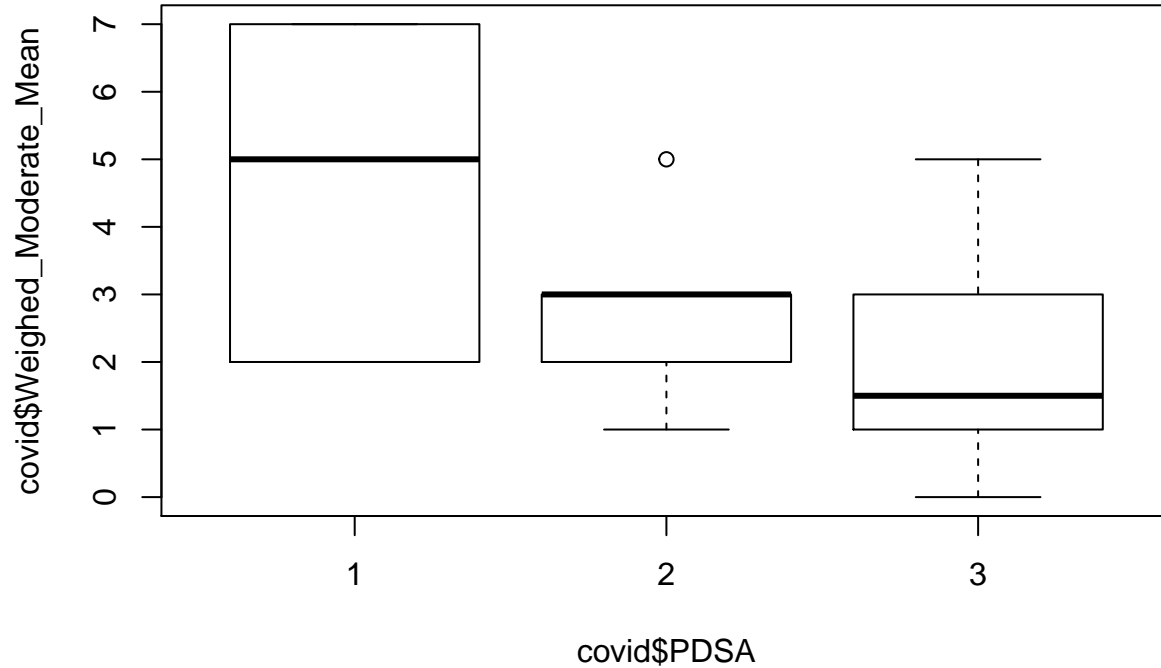
```
boxplot(covid$Weighted_High_Mean ~ covid$PDSA, data = covid)
```



Moderate Risk of Harm

###

```
boxplot(covid$Weighed_Moderate_Mean ~ covid$PDSA, data = covid)
```



5 Diagrams

5.1 Control Charts

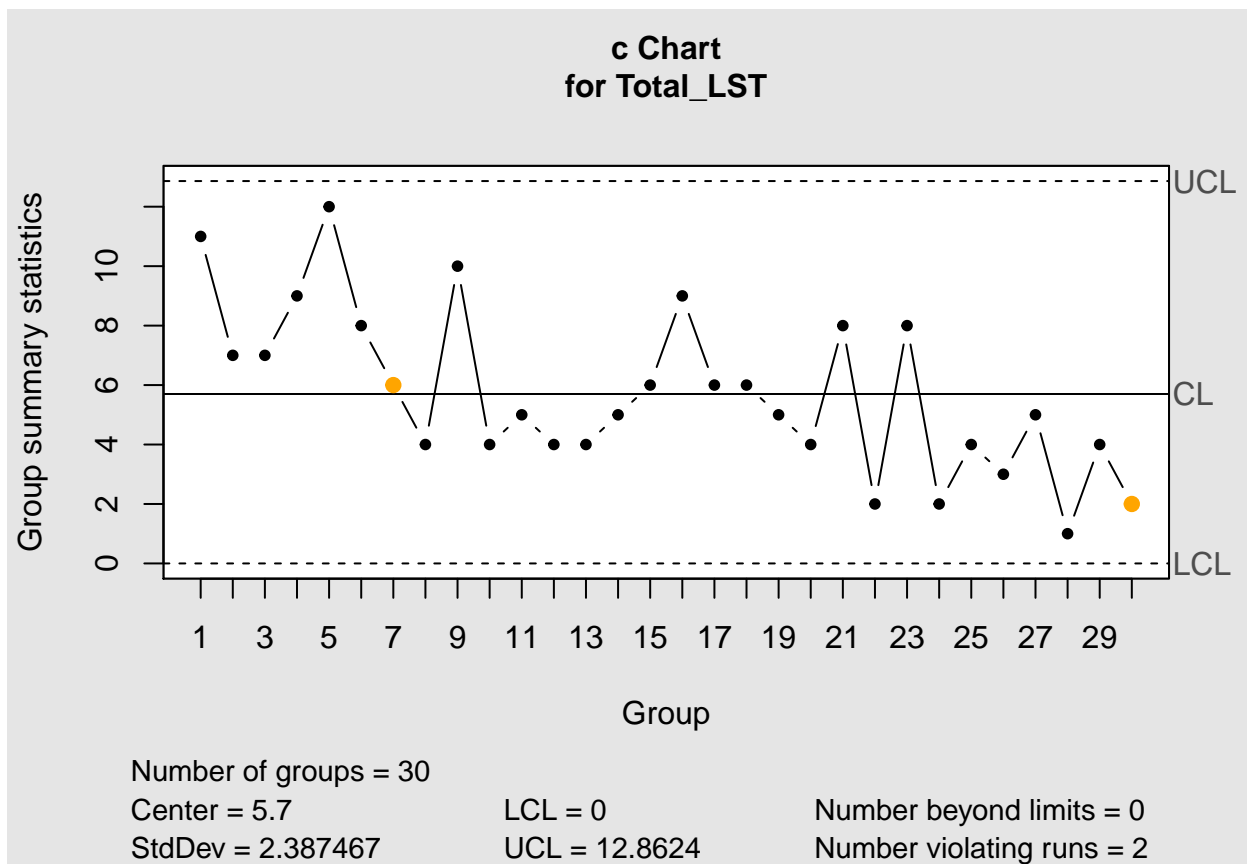
5.1.1 Total LST

```
install.packages("qcc")
```

```
## Installing package into '/home/rstudio-user/R/x86_64-pc-linux-gnu-library/3.6'  
## (as 'lib' is unspecified)
```

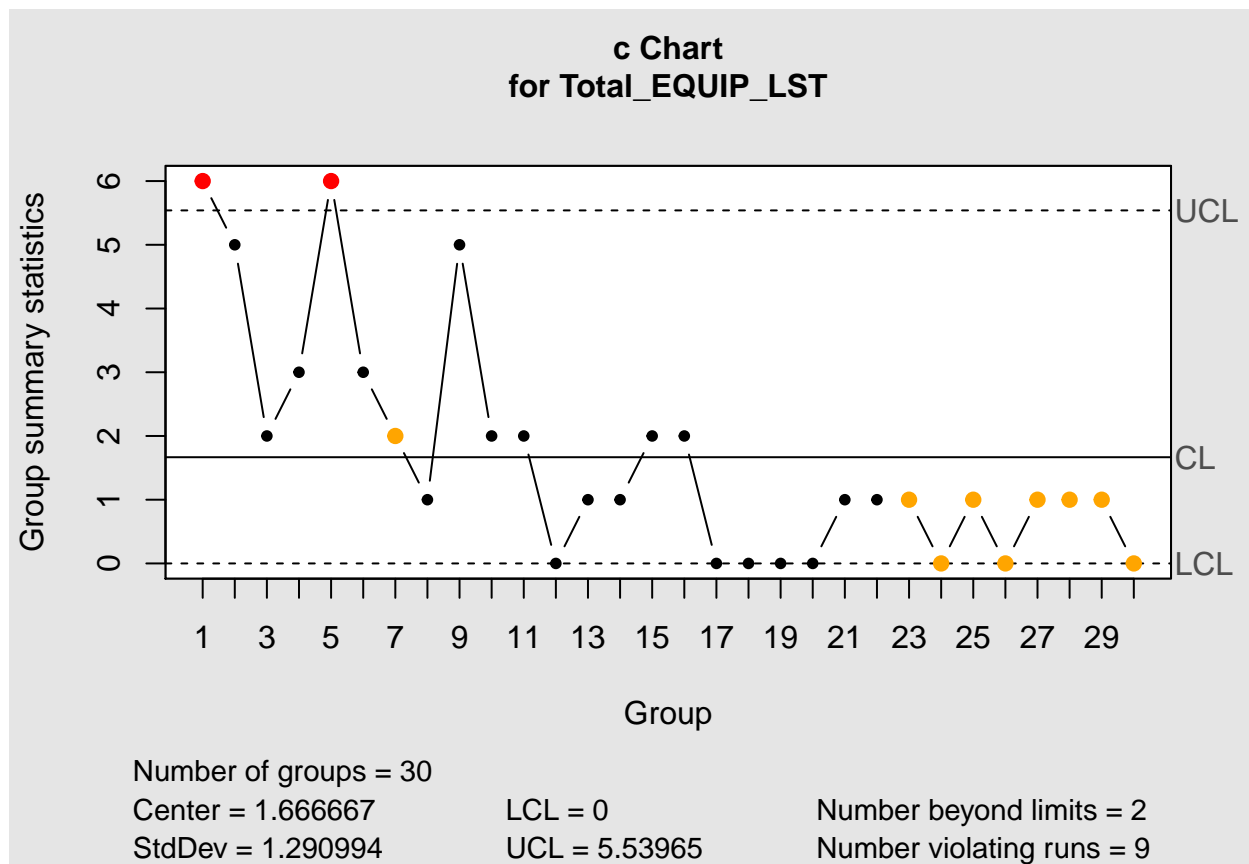
```
library(qcc)
```

```
q1 = with(covid,  
          qcc(Total_LST, type="c"))
```



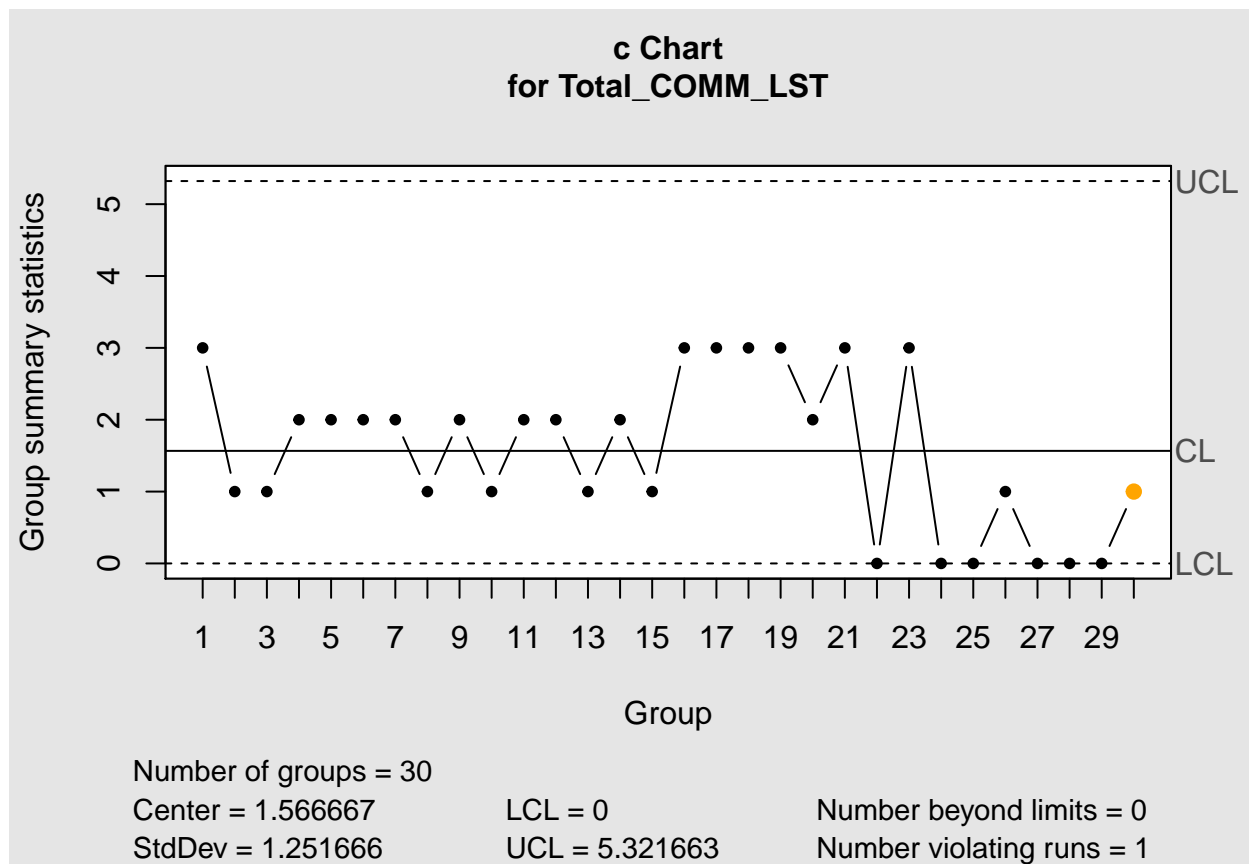
5.1.2 Total Equipment LST

```
q1 = with(covid,
  qcc(Total_EQUIP_LST, type="c"))
```



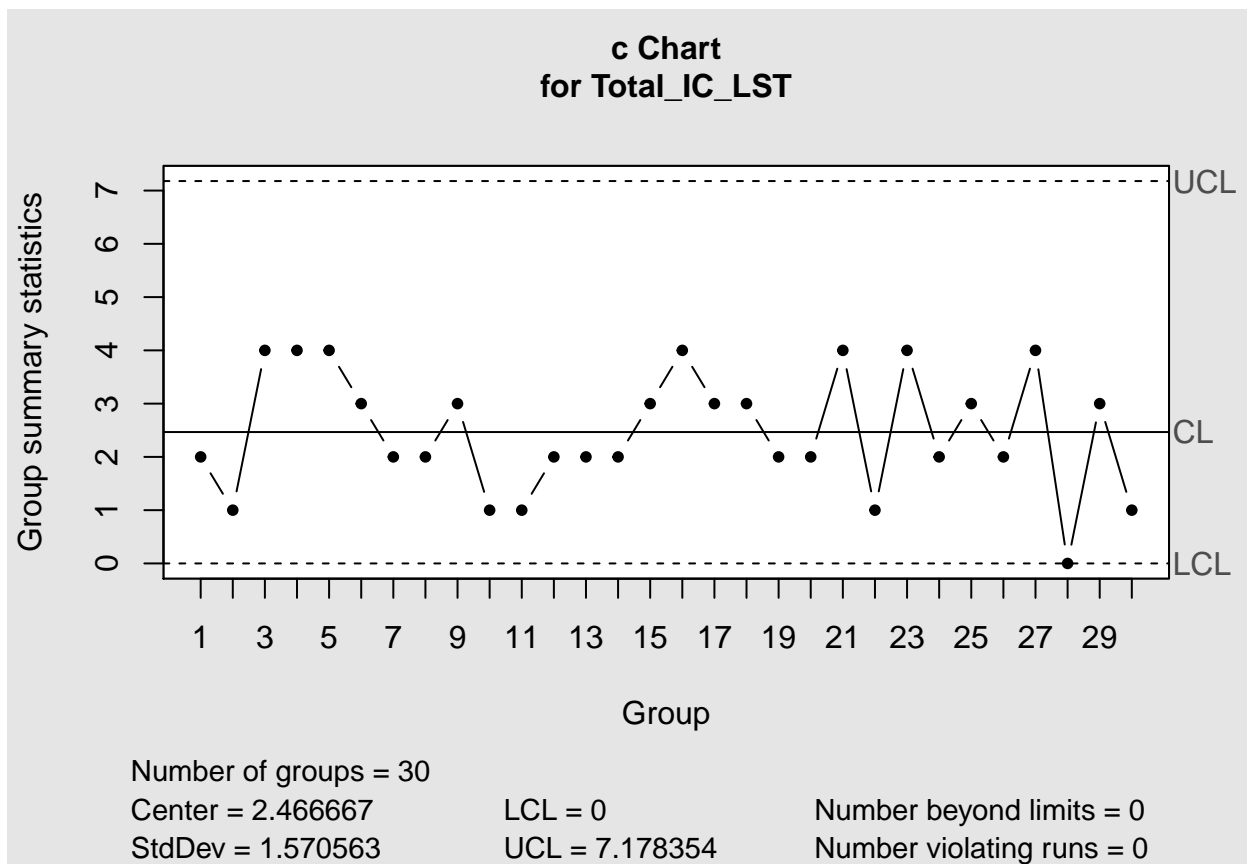
5.1.3 Total Communication LST

```
q1 = with(covid,
  qcc(Total_COMM_LST, type="c"))
```



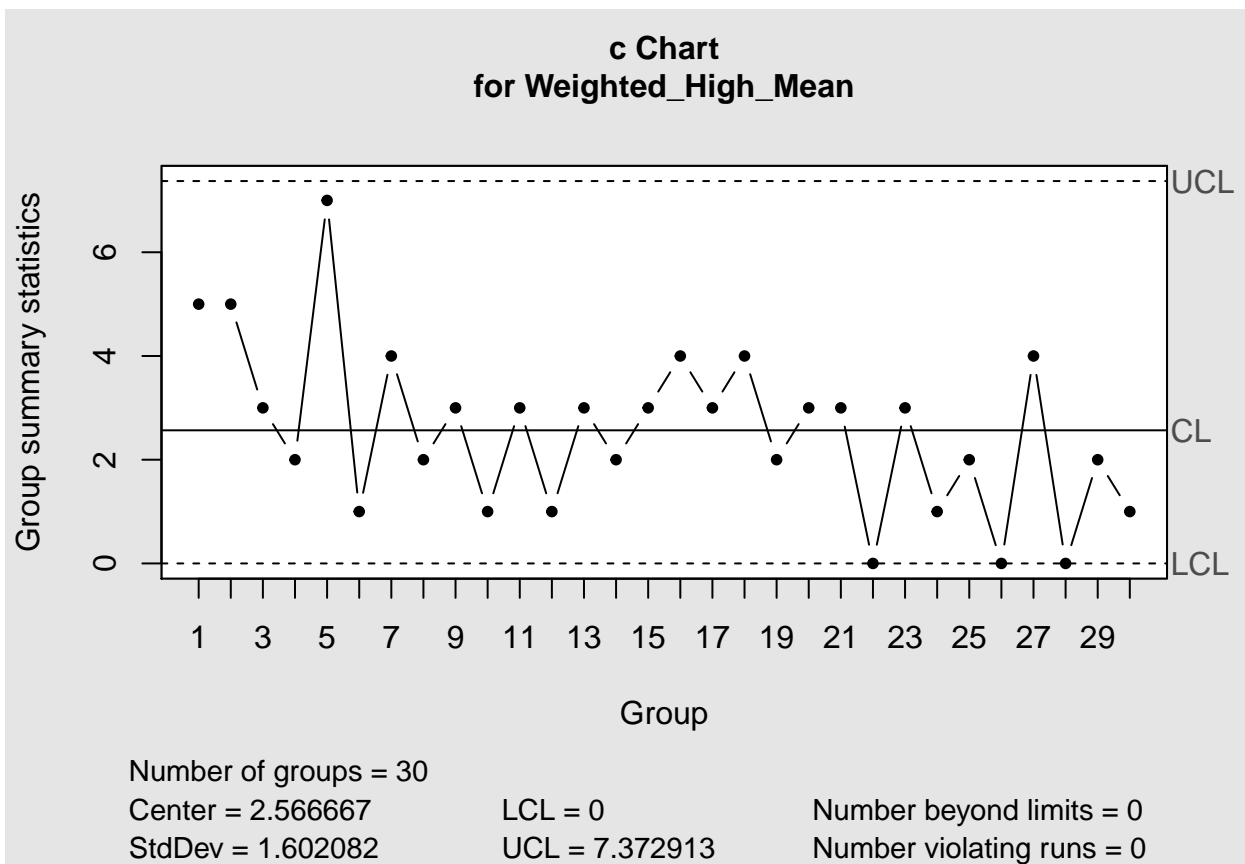
5.1.4 Total Infection Control LST

```
q1 = with(covid,
  qcc(Total_IC_LST, type="c"))
```



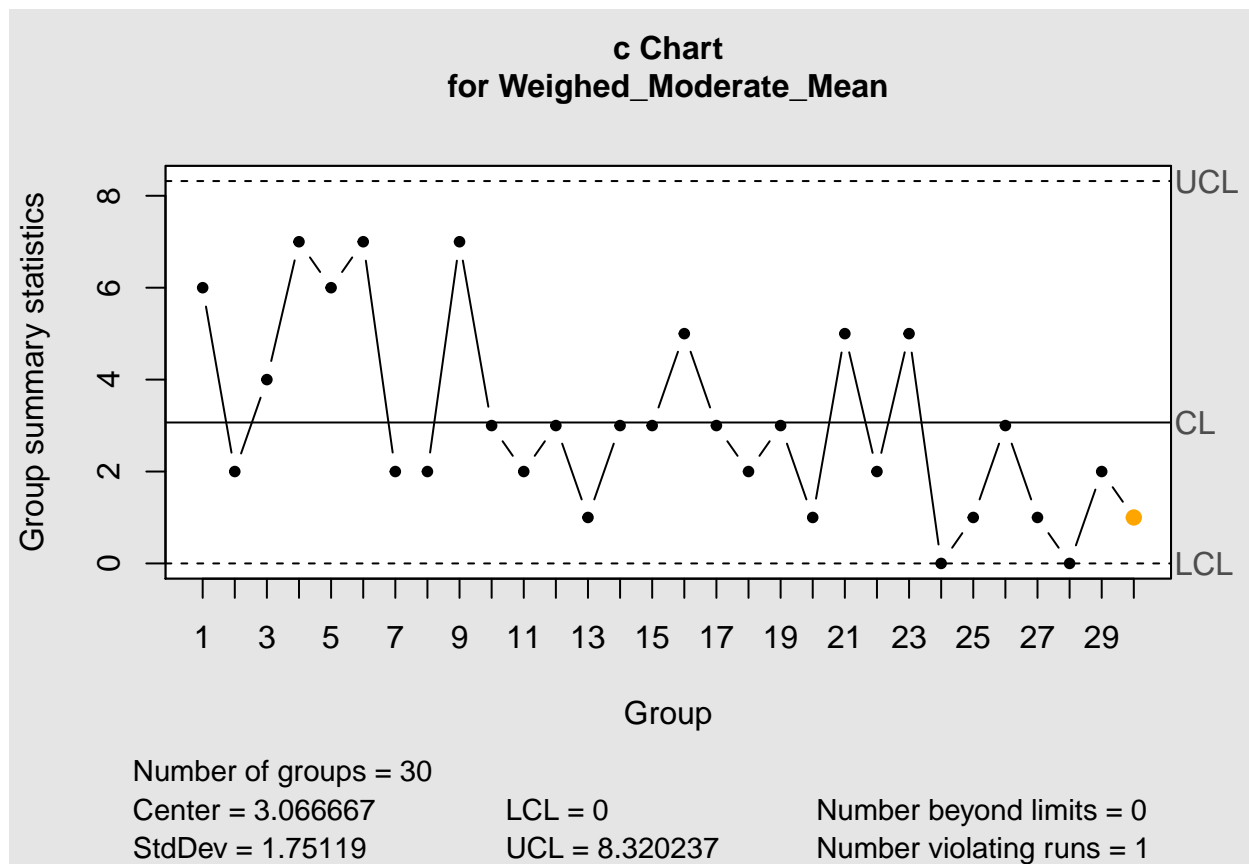
5.1.5 High Impact for Harm

```
q1 = with(covid,
  qcc(Weighted_High_Mean, type="c"))
```



5.1.6 Weighted Medium

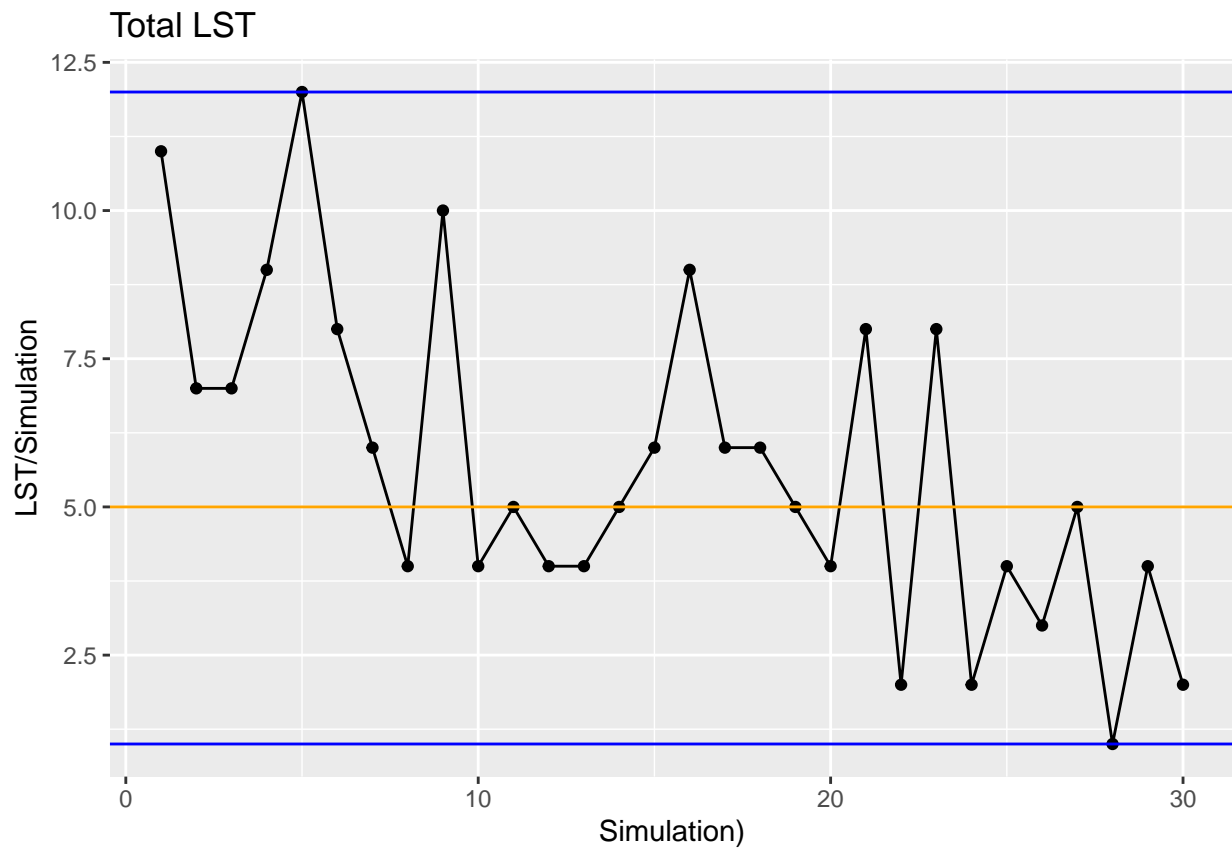
```
q1 = with(covid,
  qcc(Weighed_Moderate_Mean, type="c"))
```



5.2 Scatterplot

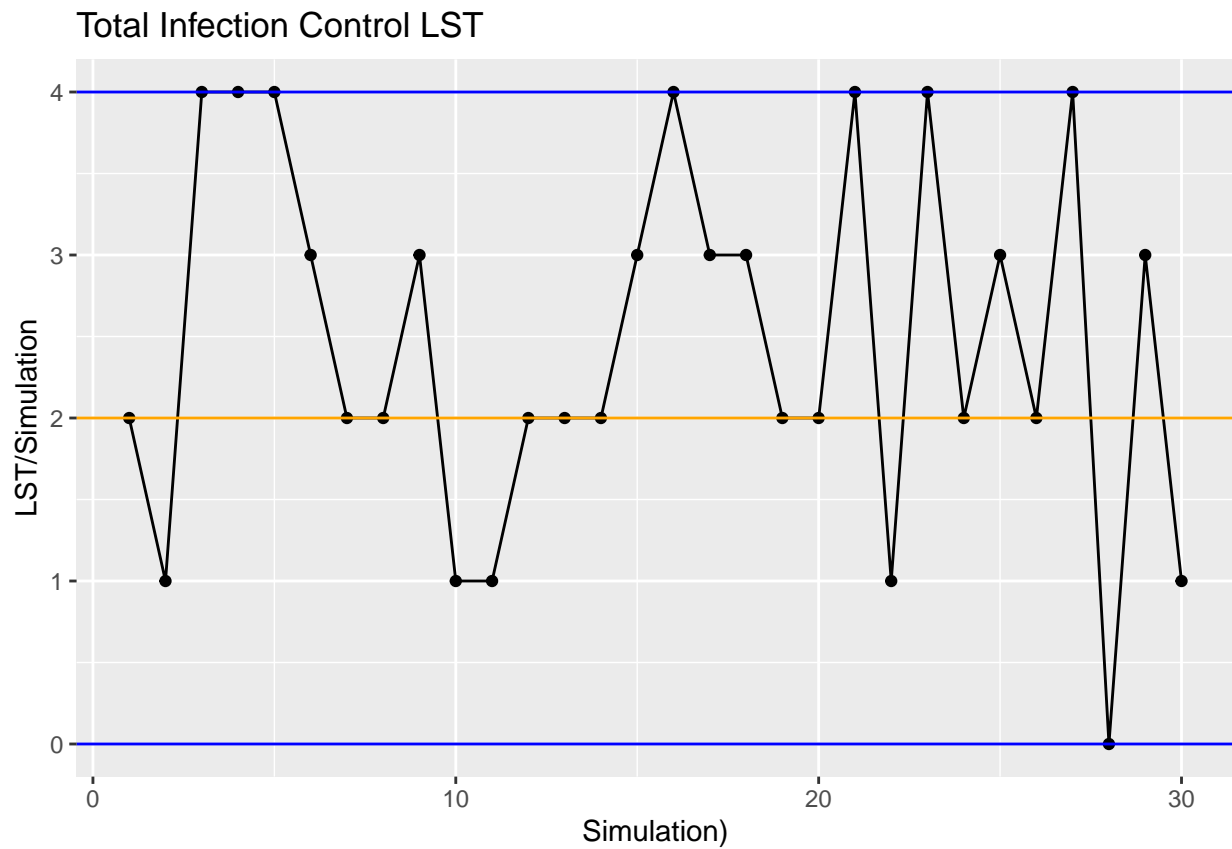
5.2.1 Total LST

```
ggplot(covid, aes(x=Simulation, y=Total_LST)) + geom_point() + geom_line() + labs(title="Total LST", x=
```

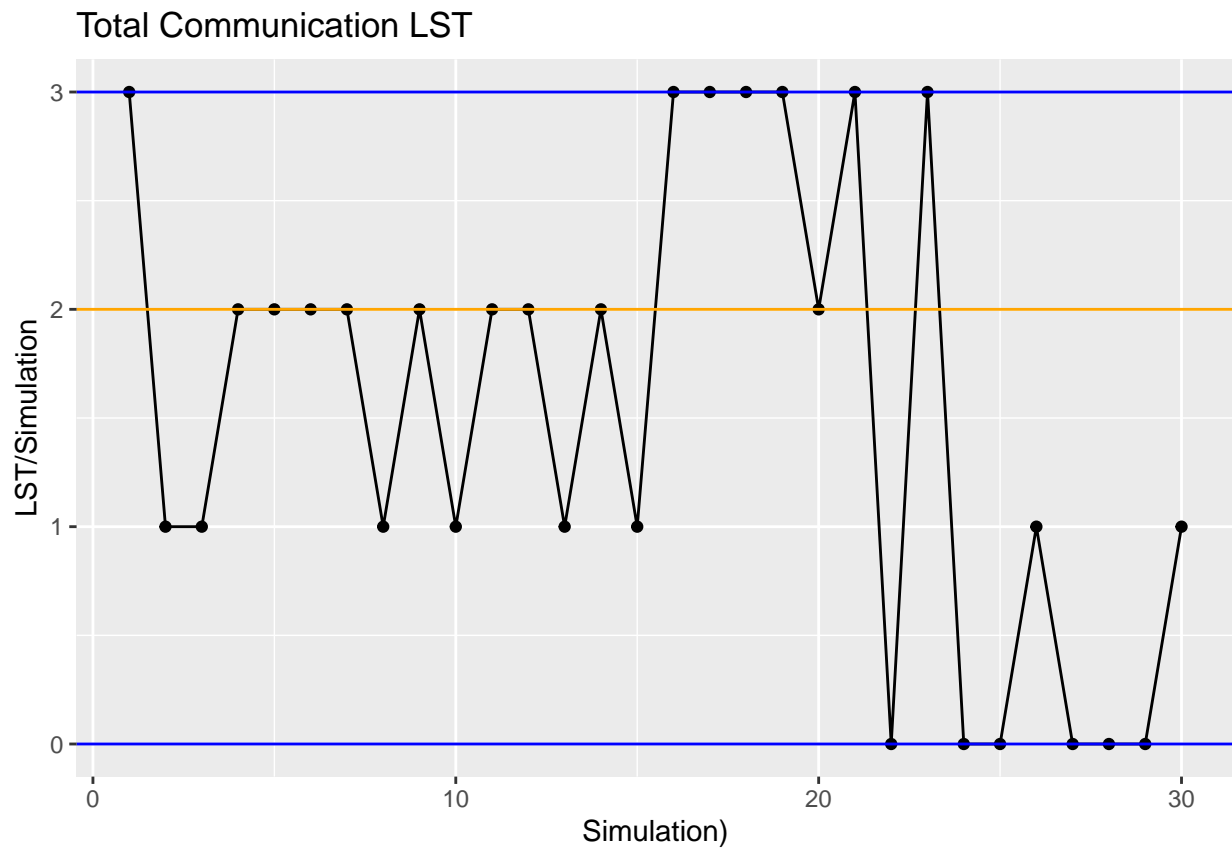
```
### Infection Control LST
```

```
ggplot(covid, aes(x=Simulation, y=Total_IC_LST)) + geom_point() + geom_line() + labs(title="Total Infection Control LST")
```



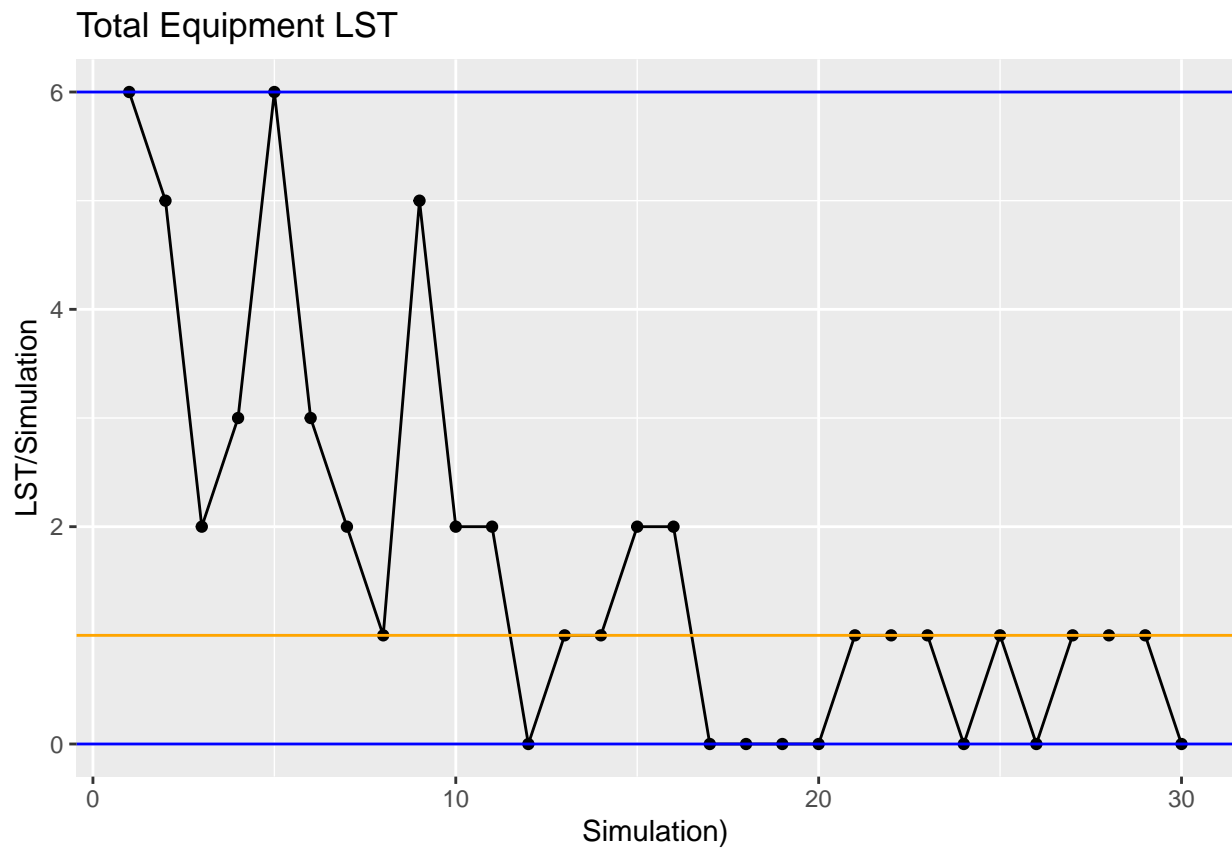
5.2.2 Total Communication LST

```
ggplot(covid, aes(x=Simulation, y=Total_COMM_LST)) + geom_point() + geom_line() + labs(title="Total Comm
```



5.2.3 Total Equipment LST

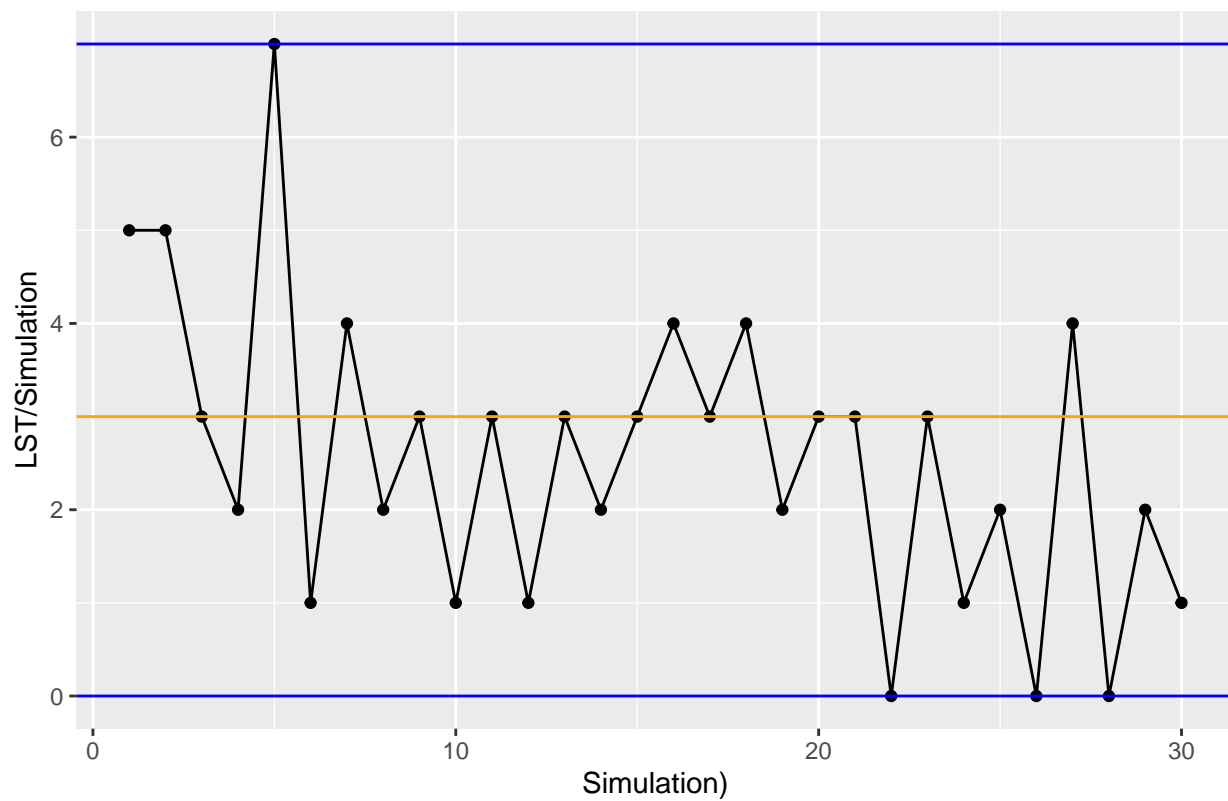
```
ggplot(covid, aes(x=Simulation, y=Total_EQUIP_LST)) + geom_point() + geom_line() + labs(title="Total Equipm
```



5.2.4 High Impact of Patient Harm

```
ggplot(covid, aes(x=Simulation, y=covid$Weighted_High_Mean)) + geom_point() + geom_line() + labs(title=
```

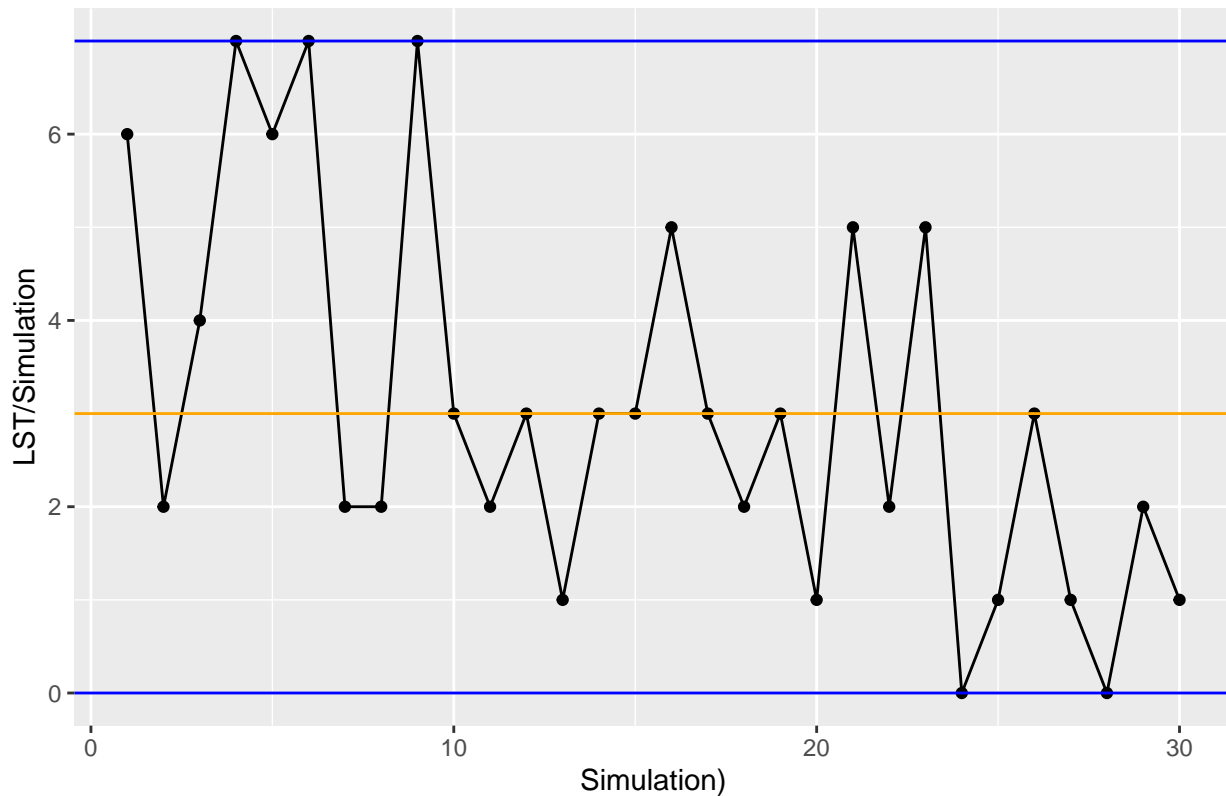
LST with High Impact of Patient Harm



5.2.5 Moderate Impact of Patient Harm

```
ggplot(covid, aes(x=Simulation, y=covid$Weighed_Moderate_Mean)) + geom_point() + geom_line() + labs(title="Moderate Impact of Patient Harm")
```

LST with Moderate Impact of Patient Harm



6 SAFER Matrix - REGRESSION ANALYSIS

6.1 Model 1 - Univariate Analysis

```
library(plm)
safer1 <- lm(SAFER_Score ~ PDSA, data = safer)
summary(safer1)
```

```
##
## Call:
## lm(formula = SAFER_Score ~ PDSA, data = safer)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -10.590   -6.590   -3.476    1.638    49.410
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   13.705     2.766   4.955 2.85e-06 ***
## PDSA          -3.114     1.280  -2.432  0.0167 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 10.71 on 103 degrees of freedom
```

```
## Multiple R-squared:  0.05432,    Adjusted R-squared:  0.04514
## F-statistic: 5.916 on 1 and 103 DF,  p-value: 0.01672
```

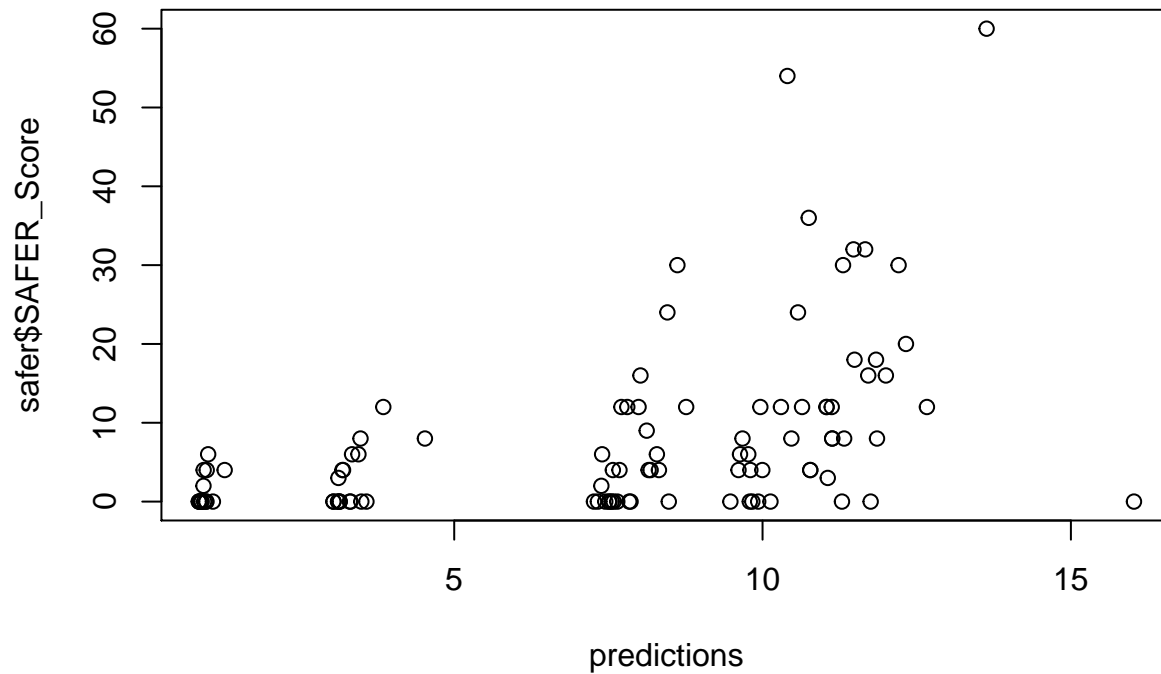
6.2 Model 2 - Negative Binomial Regression

Unable to run a Poisson regression as variance does not equal the mean. Our data has under dispersion secondary to zero inflation. Therefore, we do not meet the equi-dispersion assumption. The negative binomial regression model was chosen as it does not require the variance = mean assumption.

```
model2 <- (glmmTMB(SAFER_Score ~ PDSA * Structure_P + Category + (1 | Threat), data = safer, family = n
summary(model2)
```

```
## Family: nbinom2 ( log )
## Formula:          SAFER_Score ~ PDSA * Structure_P + Category + (1 | Threat)
## Data: safer
##
##      AIC      BIC   logLik deviance df.resid
##    593.7    615.0   -288.9    577.7      97
##
## Random effects:
##
## Conditional model:
##   Groups Name      Variance Std.Dev.
## Threat (Intercept) 0.07444  0.2728
## Number of obs: 105, groups: Threat, 36
##
## Overdispersion parameter for nbinom2 family (): 0.481
##
## Conditional model:
##                                Estimate Std. Error z value Pr(>|z|)
## (Intercept)                   2.31365    0.63124   3.665 0.000247 ***
## PDSA                          0.01635    0.27363   0.060 0.952357
## Structure_P                   1.67931    0.93685   1.792 0.073054 .
## CategoryEquipment             -0.27607    0.55846  -0.494 0.621068
## CategoryInfection Control -0.25510    0.43432  -0.587 0.556973
## PDSA:Structure_P             -1.28078    0.38996  -3.284 0.001022 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

predictions <- predict(model2, type="response")
plot(predictions,safer$SAFER_Score)
```



6.2.1 Assumptions

6.2.1.1 DHARma High p value means that the results are no overdispersion or underdispersion.

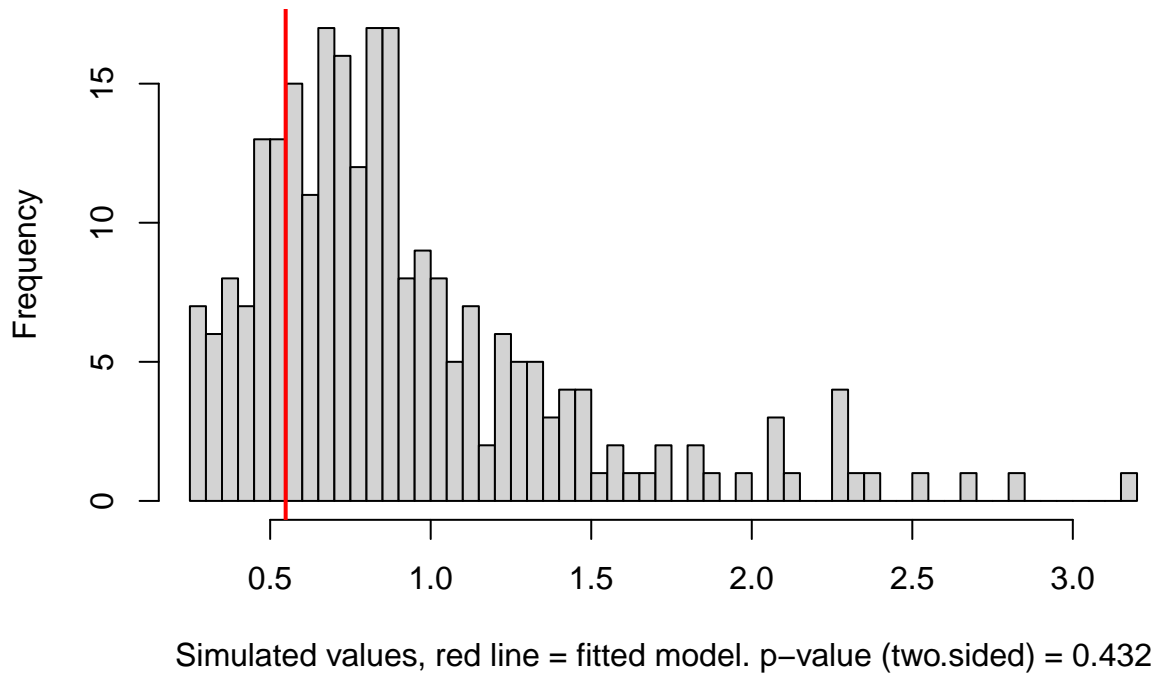
Reference: <https://cran.r-project.org/web/packages/DHARma/vignettes/DHARma.html>

```
library(DHARma)
```

```
## This is DHARma 0.4.1. For overview type '?DHARma'. For recent changes, type news(package = 'DHARma')
```

```
testDispersion(model2)
```


DHARMA nonparametric dispersion test via sd of residuals fitted vs. simulated



```
##
## DHARMA nonparametric dispersion test via sd of residuals fitted vs.
## simulated
##
## data: simulationOutput
## dispersion = 0.60076, p-value = 0.432
## alternative hypothesis: two.sided
?testDispersion
```

6.2.1.2 Dispersion Plot The plot of the dispersion demonstrates no significant problems detected.

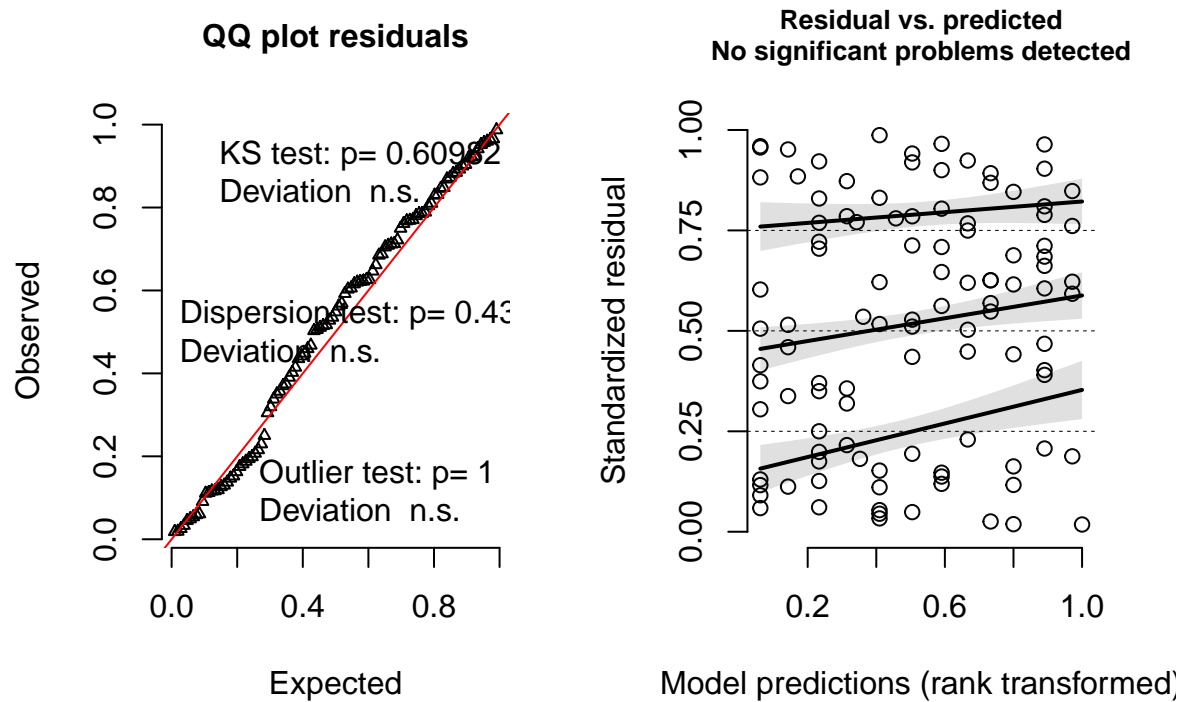
When interpreting DHARMA residuals, the residuals are expected to follow a uniform distribution instead of the normal distribution, and are standardized to values between 0 and 1. Fig 5 shows that there is no over/under dispersion or zero-inflation in the model.

https://www.researchgate.net/figure/Residual-plot-Note-When-interpreting-DHARMA-residuals-the-residuals-are-expected-to_fig1_335670195

```
simulationOutput <- simulateResiduals(fittedModel = model2, plot = F)

plot(simulationOutput)
```

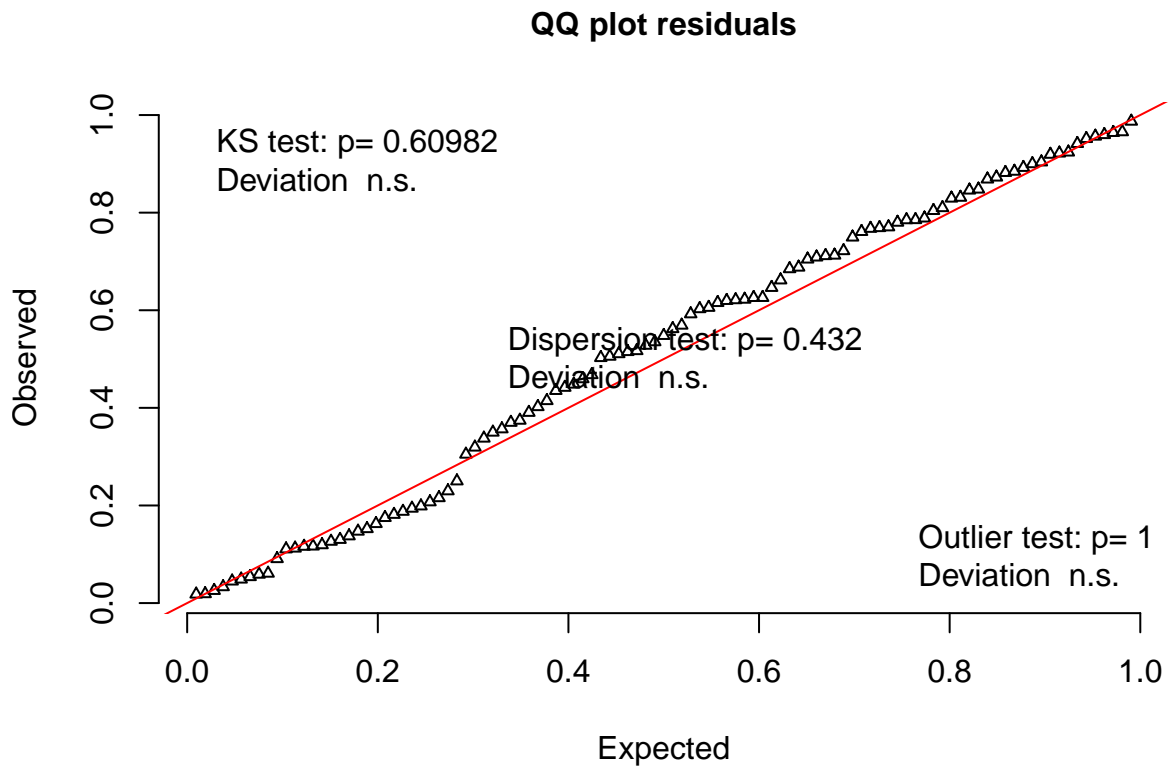
DHARMA residual diagnostics



6.2.1.3 Uniformity <https://online.stat.psu.edu/stat415/book/export/html/838>

If p value is high, then fit is fine.

```
testUniformity(model2)
```

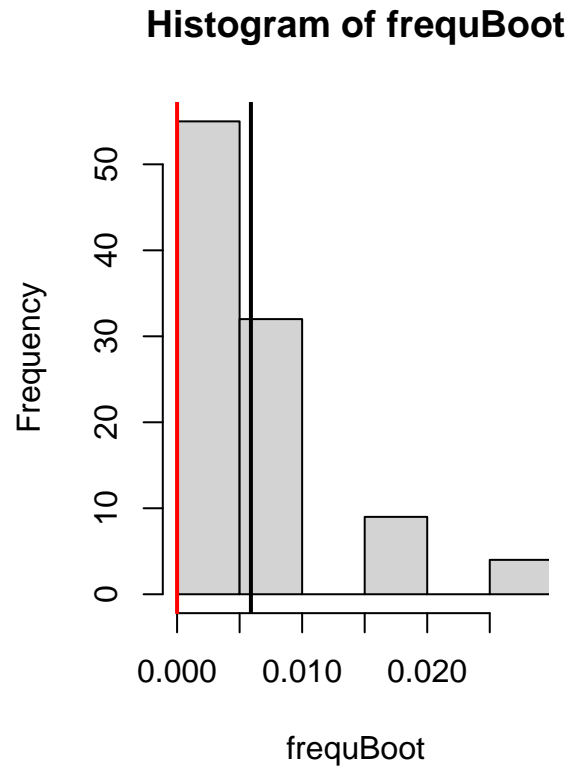
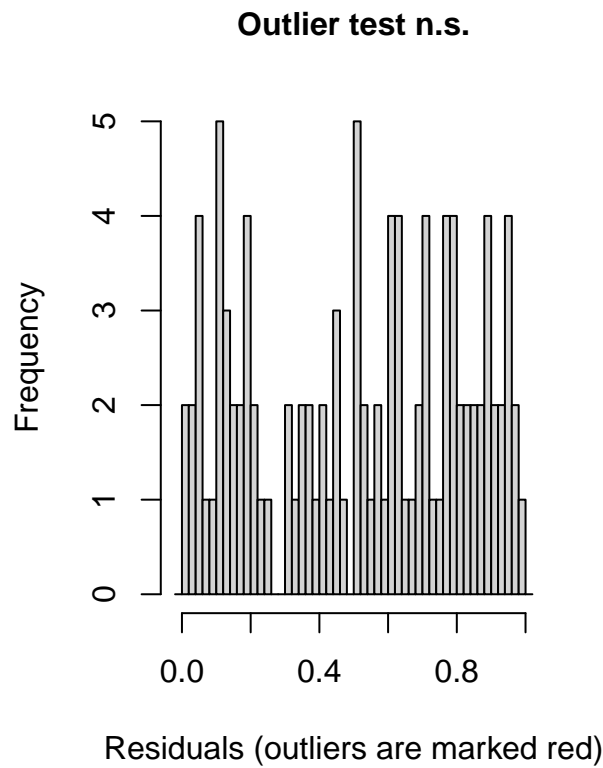


```
##
## One-sample Kolmogorov-Smirnov test
##
## data: simulationOutput$scaledResiduals
## D = 0.0742, p-value = 0.6098
## alternative hypothesis: two-sided
```

6.2.1.4 Outliers “Both binomial or bootstrap generate a null expectation, and then test for an excess or lack of outliers. Per default, `testOutliers()` looks for both, so if you get a significant p-value, you have to check if you have too many or too few outliers”

<https://www.rdocumentation.org/packages/DHARMA/versions/0.3.3.0/topics/testOutliers>

```
testOutliers(model2)
```

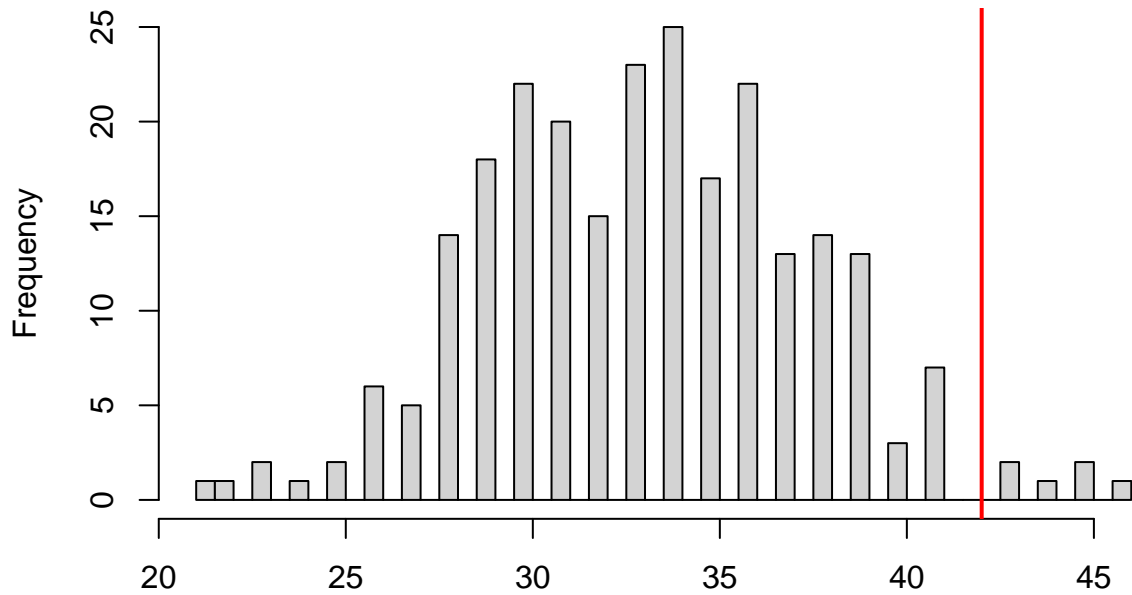


```
##
## DHARMA bootstrapped outlier test
##
## data: model2
## outliers at both margin(s) = 0, observations = 105, p-value = 1
## alternative hypothesis: two.sided
## percent confidence interval:
## 0.00000000 0.02857143
## sample estimates:
## outlier frequency (expected: 0.0059047619047619 )
## 0
```

6.2.1.5 Zero Inflation Although many observations scored zero, we did not use a zero inflation model secondary to not having true zeros and fake zeros.

```
testZeroInflation(model2)
```

DHARMA zero-inflation test via comparison to expected zeros with simulation under H0 = fitted model



Simulated values, red line = fitted model. p-value (two.sided) = 0.048

```
##
## DHARMA zero-inflation test via comparison to expected zeros with
## simulation under H0 = fitted model
##
## data: simulationOutput
## ratioObsSim = 1.2625, p-value = 0.048
## alternative hypothesis: two.sided
?testZeroInflation
```

6.2.1.6 Residuals 1 <https://bmcmedresmethodol.biomedcentral.com/articles/10.1186/s12874-020-01055-2>

```
resid(model2)
```

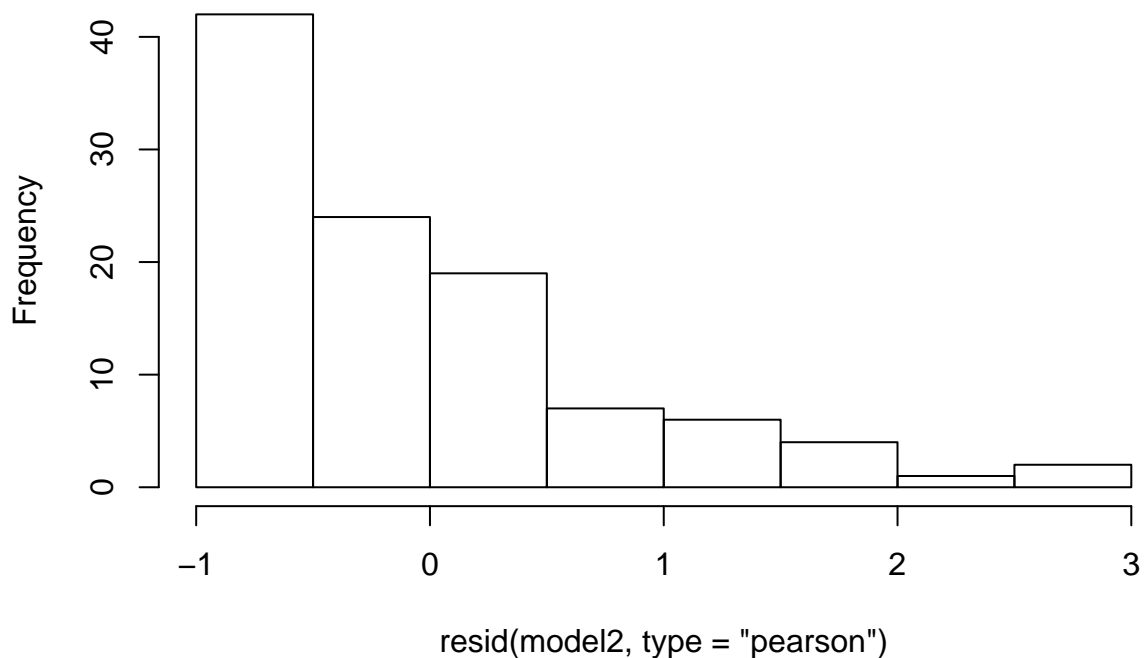
```
##          1          2          3          4          5          6
## 43.5970585  4.0001455  7.6746910 -4.1848206 -1.3984729 -3.1289807
##          7          8          9         10         11         12
## -3.1289807 -7.8599863 -8.4793919 -11.2877380 -7.5858687 -7.2662271
##          13         14         15         16         17         18
##  7.9799148 -7.3291345 17.7939090 -3.3230721  0.9623463 46.3669494
##          19         20         21         22         23         24
##  4.2864305  6.1599871 -0.6652546  0.9623463 -6.7735365 -8.0574486
##          25         26         27         28         29         30
## -7.5554483 -6.7735365 -11.7530470 20.5253599 -5.8024858 -1.6747679
##          31         32         33         34         35         36
## -5.6103133  1.7018999  0.8782624 -16.0227810 -9.4782647 13.4255878
##          37         38         39         40         41         42
## -3.4938912  4.5193391 -4.3197302 -7.5204212 -3.1428184 -3.1428184
```

```
##          43          44          45          46          47          48
##  4.0104583 21.3808431  0.8123486  4.2890942 -5.3859956 -4.1522795
##          49          50          51          52          53          54
## -7.4499399  2.5530062  0.8023703 -3.1170277  8.1500335 -3.3079060
##          55          56          57          58          59          60
##  2.6563865 -3.5766613 -3.1170277 -3.0424411 -0.1226178 -3.6799840
##          61          62          63          64          65          66
## -3.0424411 -3.3190544 20.3362246  2.0359408 -9.8342362 -3.7687191
##          67          68          69          70          71          72
## -2.4678427 18.6949439  3.4751749 -3.6344940 25.2512908  3.0133269
##          73          74          75          76          77          78
## -0.9829368 15.5431365 -7.6443795 -0.8875303 -0.8875303  0.8787675
##          79          80          81          82          83          84
##  3.2387744 -0.9001911 -7.8380039 -7.5077383 -2.2866527 -3.5727365
##          85          86          87          88          89          90
## -0.9734293 -0.9030090 -0.8802470 -1.0872285  1.0658491 -0.9442347
##          91          92          93          94          95          96
##  4.9899527 -0.8802470 -0.8591838 -0.8818256  4.1934275 -0.8591838
##          97          98          99         100         101         102
##  3.0627008 -3.8560283 -10.1282959 -5.9963329 -9.9297360  1.3596169
##          103         104         105
##  6.5086038  2.7221917 -9.7932984
```

```
library(statmod)
```

```
##
## Attaching package: 'statmod'
## The following object is masked from 'package:glmmTMB':
##
##      tweedie
hist(resid(model2,type = "pearson"))
```

Histogram of resid(model2, type = "pearson")



Based on the above, residuals are normally distributed.

6.2.1.7 Q Residuals <https://www.rdocumentation.org/packages/statmod/versions/1.4.35/topics/qresiduals>

```
install.packages("AER")
```

```
## Installing package into '/home/rstudio-user/R/x86_64-pc-linux-gnu-library/3.6'  
## (as 'lib' is unspecified)
```

```
library(AER)
```

```
## Loading required package: lmtest
```

```
## Loading required package: zoo
```

```
##
```

```
## Attaching package: 'zoo'
```

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

```
##
```

```
## as.Date, as.Date.numeric
```

```
## Loading required package: sandwich
```

```
## Loading required package: survival
```

```
try(dispersiontest(model6))
```

```
## Error in dispersiontest(model6) : object 'model6' not found
```

6.2.2 Model 3: Negative Binomial with random effects

Error message secondary to (1) singular fit - one of the variables is perfectly predicting an outcome. Uses an estimation strategy to fit a model, if unable to find, may cause error.

Has similar results with a higher AIC then the negative binomial.

```
model3<-glmer.nb(SAFER_Score ~ PDSA * Structure_P + Category + (1 | Threat), data = safer)
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :  
## Model failed to converge with max|grad| = 0.00854785 (tol = 0.001, component 1)
```

```
## boundary (singular) fit: see ?isSingular
```

```
summary(model3)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace  
## Approximation) [glmerMod]  
## Family: Negative Binomial(0.4716) ( log )  
## Formula: SAFER_Score ~ PDSA * Structure_P + Category + (1 | Threat)  
## Data: safer  
##
```

```
##      AIC      BIC    logLik deviance df.resid  
##    593.8    615.0   -288.9    577.8      97  
##
```

```
## Scaled residuals:
```

```
##      Min       1Q   Median       3Q      Max  
## -0.6764 -0.6405 -0.3268  0.3221  3.0983  
##
```

```
## Random effects:
```

```
## Groups Name      Variance Std.Dev.  
## Threat (Intercept) 0.04355  0.2087  
## Number of obs: 105, groups: Threat, 36  
##
```

```
## Fixed effects:
```

```
##              Estimate Std. Error z value Pr(>|z|)  
## (Intercept)      2.319911   0.635594   3.650 0.000262 ***  
## PDSA              0.008693   0.272671   0.032 0.974567  
## Structure_P       1.634457   0.917527   1.781 0.074851 .  
## CategoryEquipment -0.259168   0.547738  -0.473 0.636098  
## CategoryInfection Control -0.238031  0.422342  -0.564 0.573027  
## PDSA:Structure_P  -1.266751   0.385470  -3.286 0.001015 **  
## ---
```

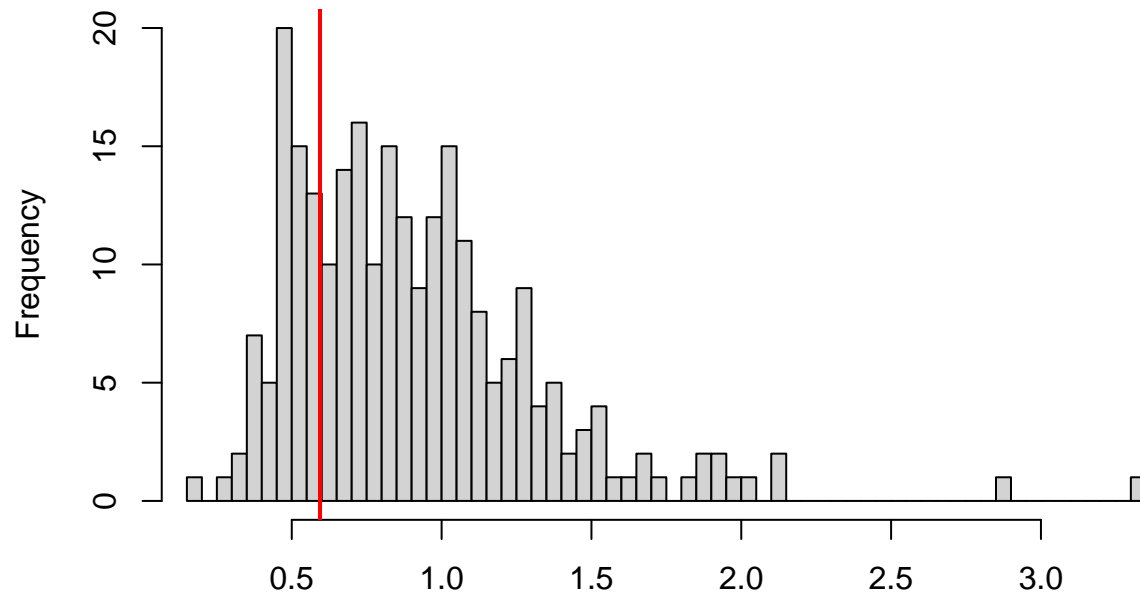
```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##
```

```
## Correlation of Fixed Effects:
```

```
##              (Intr) PDSA   Strc_P CtgrE CtgrIC  
## PDSA          -0.838  
## Structure_P   -0.598  0.653  
## CtgrEqpmnt    -0.091 -0.144 -0.472  
## CtgrInfctC    -0.220 -0.141 -0.222  0.584  
## PDSA:Strc_P   0.585 -0.722 -0.880  0.200  0.160
```

```
testDispersion(model3)
```


DHARMA nonparametric dispersion test via sd of residuals fitted vs. simulated



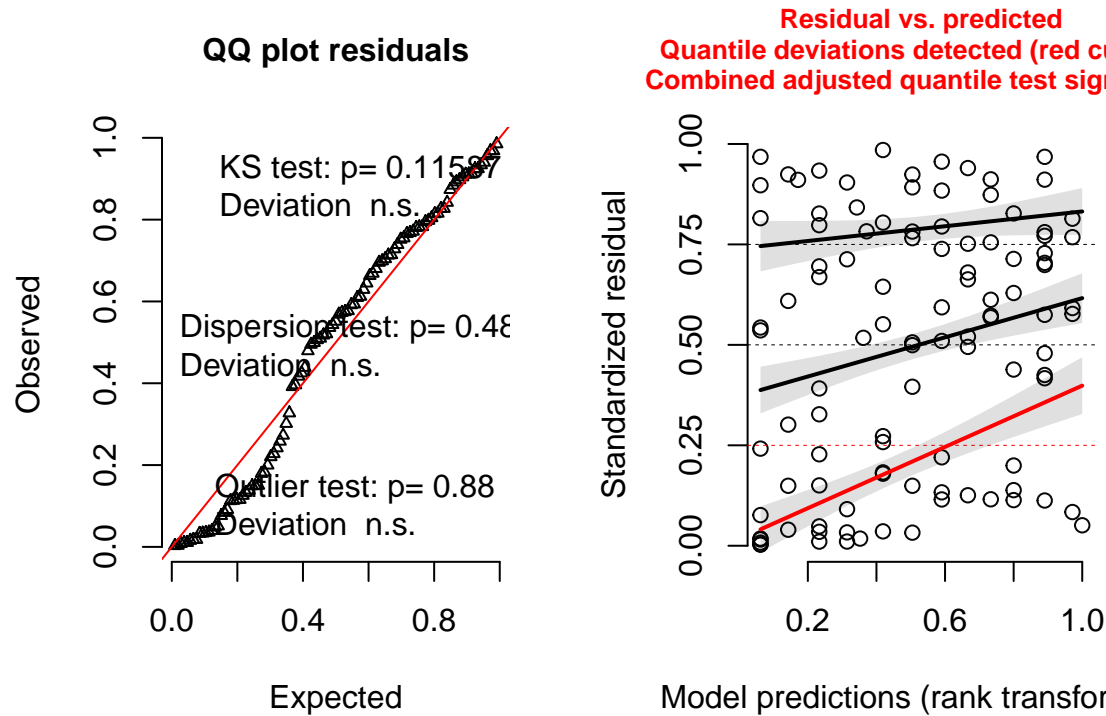
6.2.2.1 Assumptions

Simulated values, red line = fitted model. p-value (two.sided) = 0.488

```
##  
## DHARMA nonparametric dispersion test via sd of residuals fitted vs.  
## simulated  
##  
## data: simulationOutput  
## dispersion = 0.65319, p-value = 0.488  
## alternative hypothesis: two.sided
```

```
simulationOutput1 <- simulateResiduals(fittedModel = model3, plot = F)  
plot(simulationOutput1)
```

DHARMA residual diagnostics



6.2.2.2 Dispersion Plot

7 LST Count Data

To study the change in PLST across this program, I have a data frame where each row corresponds a simulation (Simulation) carried out during a PDSA cycle (1, 2, or 3).

7.1 Total

7.1.1 By PDSA

```
summary(covid1 <- lm(covid$Total_LST ~ covid$Shift + covid$Census + covid$PWL + covid$Team_Size + covid$Simulation))
```

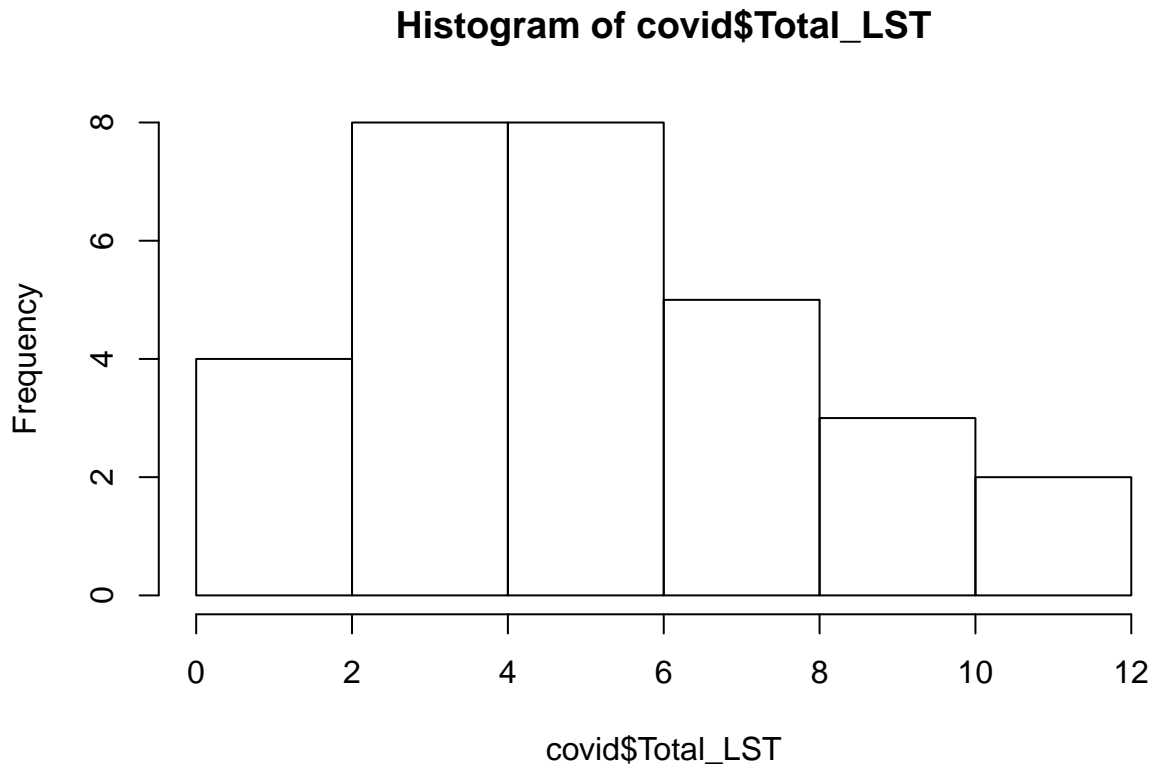
```
##
## Call:
## lm(formula = covid$Total_LST ~ covid$Shift + covid$Census + covid$PWL +
##      covid$Team_Size + covid$Attended.Prior + covid$Short + covid$Step_out +
##      covid$Simulation, data = covid)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.4021 -1.6586  0.2889  1.2255  3.5946
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      7.42690     3.02504   2.455  0.0229 *
## covid$Shift       1.05735     1.12239   0.942  0.3569
## covid$Census      0.01546     0.08420   0.184  0.8561
```

```
## covid$PWL          0.18466    0.56356    0.328    0.7464
## covid$Team_Size    0.12971    0.42030    0.309    0.7607
## covid$Attended.PriorYes -0.72525    1.32672   -0.547    0.5904
## covid$ShortYes     -0.45452    1.94648   -0.234    0.8176
## covid$Step_outYes  -1.86520    1.63892   -1.138    0.2679
## covid$Simulation   -0.19776    0.07873   -2.512    0.0203 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.335 on 21 degrees of freedom
## Multiple R-squared:  0.4804, Adjusted R-squared:  0.2824
## F-statistic: 2.427 on 8 and 21 DF,  p-value: 0.0495

library(car)
```

7.1.2 Histogram

```
hist(covid$Total_LST)
```



7.1.3 Bonferroni

```
library(car)
outlierTest(covid1)

## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 23  1.75687          0.09424          NA
```

7.1.4 Heteroskedasticity

```
ncvTest(covid1)
```

```
## Non-constant Variance Score Test
## Variance formula: ~ fitted.values
## Chisquare = 0.2585913, Df = 1, p = 0.61109
```

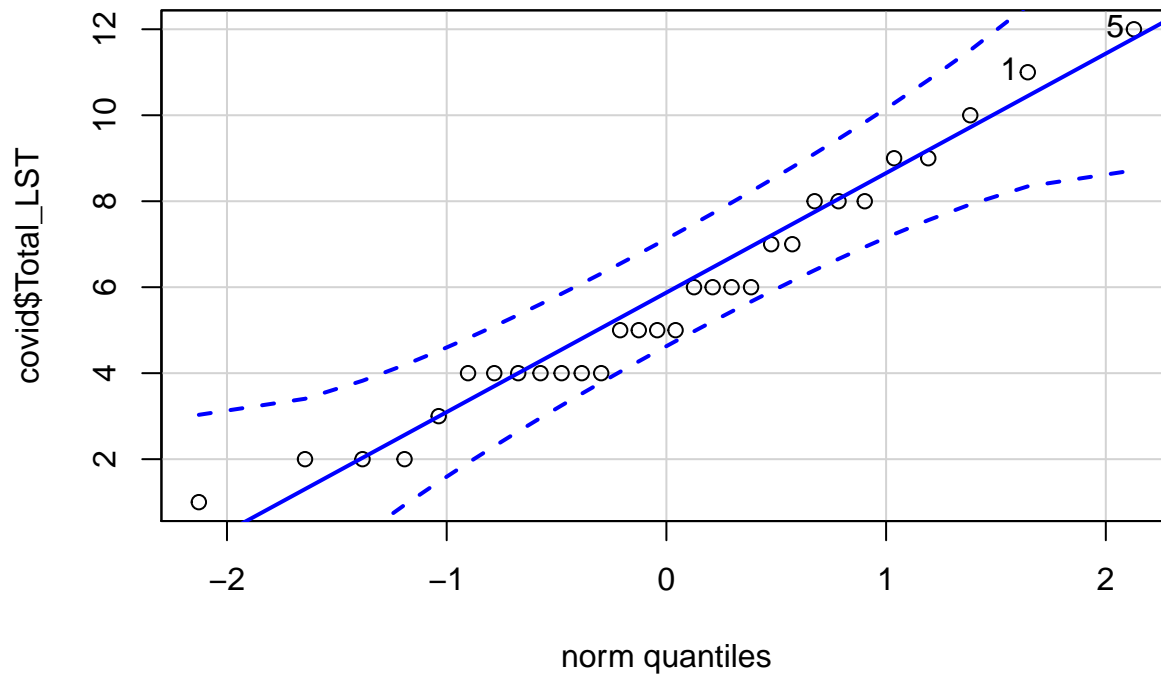
7.1.5 Multicollinearity

```
vif(covid1)
```

```
##          covid$Shift          covid$Census          covid$PWL
##          1.733305          1.530080          1.817887
## covid$Team_Size covid$Attended.Prior covid$Short
##          1.322237          2.249620          1.297464
## covid$Step_out covid$Simulation
##          1.330479          2.555586
```

7.1.6 Normality of Residuals

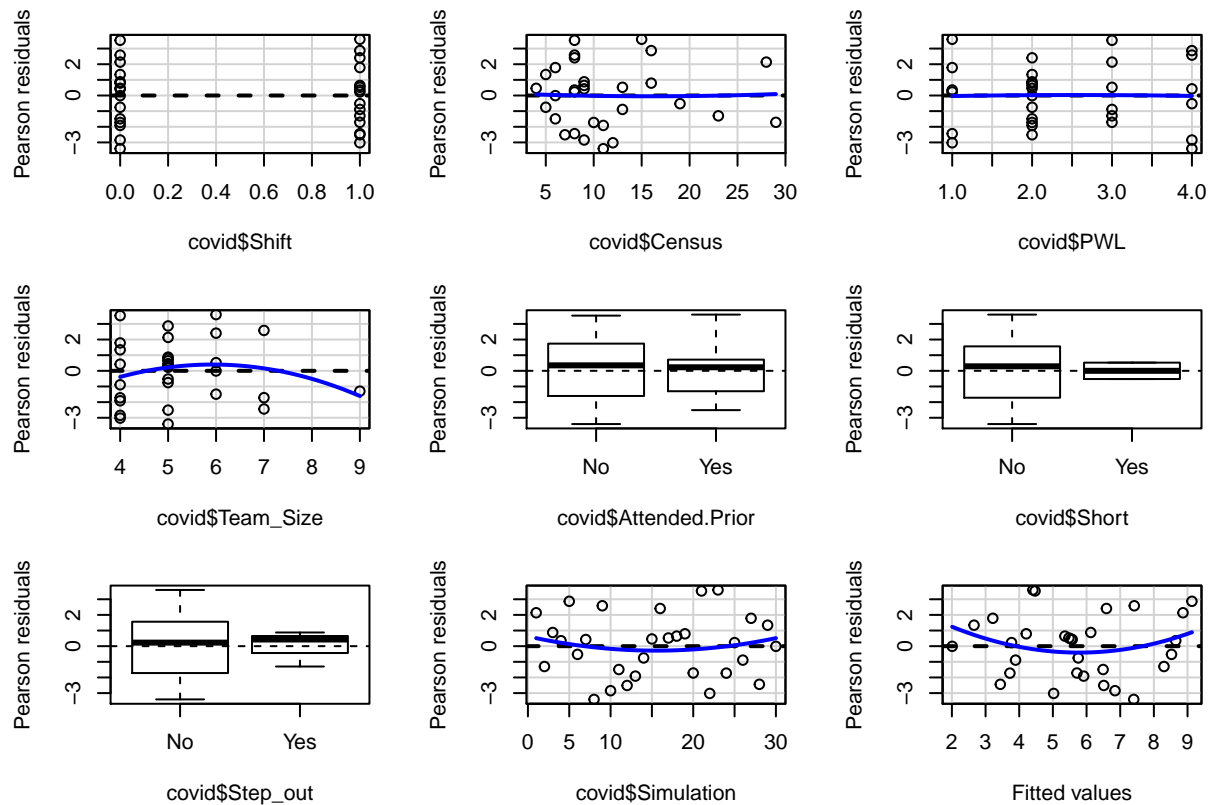
```
qqPlot(covid$Total_LST)
```



```
## [1] 5 1
```

7.1.7 Residual Plots

```
residualPlots(covid1)
```



```
##               Test stat Pr(>|Test stat|)
## covid$Shift      0.9036      0.3770
## covid$Census     0.0971      0.9236
## covid$PWL       -0.0698      0.9450
## covid$Team_Size  -1.4597      0.1599
## covid$Attended.Prior
## covid$Short
## covid$Step_out
## covid$Simulation  0.6537      0.5207
## Tukey test       1.1002      0.2712
```

7.1.8 Shapiro Wilk Test

```
shapiro.test(covid$Total_LST)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  covid$Total_LST
## W = 0.9601, p-value = 0.3115
```

```
shapiro.test(resid(covid1))
```

```
##
##  Shapiro-Wilk normality test
##
## data:  resid(covid1)
## W = 0.96863, p-value = 0.5024
```

```
library(MASS)
step(covid1)
```

7.1.8.1 STEP Feature Total

```
## Start: AIC=58.17
## covid$Total_LST ~ covid$Shift + covid$Census + covid$PWL + covid$Team_Size +
## covid$Attended.Prior + covid$Short + covid$Step_out + covid$Simulation
##
##           Df Sum of Sq  RSS   AIC
## - covid$Census      1    0.184 114.65 56.222
## - covid$Short       1    0.297 114.77 56.251
## - covid$Team_Size    1    0.519 114.99 56.309
## - covid$PWL          1    0.585 115.06 56.326
## - covid$Attended.Prior 1    1.629 116.10 56.597
## - covid$Shift        1    4.838 119.31 57.415
## - covid$Step_out     1    7.060 121.53 57.969
## <none>                114.47 58.173
## - covid$Simulation    1   34.393 148.86 64.055
##
## Step: AIC=56.22
## covid$Total_LST ~ covid$Shift + covid$PWL + covid$Team_Size +
## covid$Attended.Prior + covid$Short + covid$Step_out + covid$Simulation
##
##           Df Sum of Sq  RSS   AIC
## - covid$Short      1    0.311 114.97 54.303
## - covid$Team_Size   1    0.699 115.35 54.404
## - covid$PWL         1    0.882 115.54 54.451
## - covid$Attended.Prior 1    1.493 116.15 54.610
## - covid$Shift       1    5.531 120.19 55.635
## - covid$Step_out    1    7.173 121.83 56.042
## <none>              114.65 56.222
## - covid$Simulation  1   37.473 152.13 62.706
##
## Step: AIC=54.3
## covid$Total_LST ~ covid$Shift + covid$PWL + covid$Team_Size +
## covid$Attended.Prior + covid$Step_out + covid$Simulation
##
##           Df Sum of Sq  RSS   AIC
## - covid$PWL         1    0.632 115.60 52.467
## - covid$Team_Size    1    0.740 115.70 52.495
## - covid$Attended.Prior 1    1.571 116.53 52.710
## - covid$Shift        1    5.248 120.21 53.642
## - covid$Step_out     1    6.904 121.87 54.052
## <none>              114.97 54.303
## - covid$Simulation  1   37.210 152.17 60.715
##
## Step: AIC=52.47
## covid$Total_LST ~ covid$Shift + covid$Team_Size + covid$Attended.Prior +
## covid$Step_out + covid$Simulation
##
##           Df Sum of Sq  RSS   AIC
## - covid$Team_Size    1    0.770 116.37 50.666
```

```

## - covid$Attended.Prior 1      1.508 117.10 50.856
## - covid$Shift          1      4.715 120.31 51.666
## - covid$Step_out       1      7.201 122.80 52.280
## <none>                  115.60 52.467
## - covid$Simulation      1     50.032 165.63 61.256
##
## Step: AIC=50.67
## covid$Total_LST ~ covid$Shift + covid$Attended.Prior + covid$Step_out +
## covid$Simulation
##
##           Df Sum of Sq  RSS    AIC
## - covid$Attended.Prior 1      1.130 117.50 48.956
## - covid$Shift          1      5.720 122.09 50.106
## - covid$Step_out       1      6.565 122.93 50.313
## <none>                  116.37 50.666
## - covid$Simulation      1     55.803 172.17 60.418
##
## Step: AIC=48.96
## covid$Total_LST ~ covid$Shift + covid$Step_out + covid$Simulation
##
##           Df Sum of Sq  RSS    AIC
## - covid$Shift          1      4.616 122.11 48.112
## - covid$Step_out       1      6.842 124.34 48.654
## <none>                  117.50 48.956
## - covid$Simulation      1     98.443 215.94 65.214
##
## Step: AIC=48.11
## covid$Total_LST ~ covid$Step_out + covid$Simulation
##
##           Df Sum of Sq  RSS    AIC
## - covid$Step_out       1      7.485 129.60 47.897
## <none>                  122.11 48.112
## - covid$Simulation      1     95.072 217.19 63.387
##
## Step: AIC=47.9
## covid$Total_LST ~ covid$Simulation
##
##           Df Sum of Sq  RSS    AIC
## <none>                  129.6 47.897
## - covid$Simulation      1     90.702 220.3 61.814
##
## Call:
## lm(formula = covid$Total_LST ~ covid$Simulation, data = covid)
##
## Coefficients:
## (Intercept) covid$Simulation
##      8.8138      -0.2009

```

7.2 Infection Control

Perceived workload removed secondary to being correlated to PDSA

```
summary(covid2 <- lm(covid$Total_IC_LST ~ covid$PDSA + covid$Shift + covid$Census + covid$Team_Size + c

##
## Call:
## lm(formula = covid$Total_IC_LST ~ covid$PDSA + covid$Shift +
##     covid$Census + covid$Team_Size + covid$Attended.Prior + covid$Short +
##     covid$Step_out, data = covid)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.0480 -0.7001  0.1076  0.6223  1.8831
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      4.47712     1.40513   3.186  0.00427 **
## covid$PDSA       -0.26762     0.36773  -0.728  0.47443
## covid$Shift       0.82879     0.53376   1.553  0.13475
## covid$Census     -0.03067     0.03996  -0.768  0.45087
## covid$Team_Size  -0.28361     0.21409  -1.325  0.19886
## covid$Attended.PriorYes -0.22435     0.60710  -0.370  0.71525
## covid$ShortYes    0.25837     0.93660   0.276  0.78523
## covid$Step_outYes -0.03153     0.81433  -0.039  0.96947
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.181 on 22 degrees of freedom
## Multiple R-squared:  0.1816, Adjusted R-squared:  -0.07886
## F-statistic: 0.6972 on 7 and 22 DF,  p-value: 0.674
```

7.2.1 Bonferroni

```
outlierTest(covid2)

## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 22 -2.224443          0.037216          NA
```

7.2.2 Heteroskedasticity

```
ncvTest(covid2)

## Non-constant Variance Score Test
## Variance formula: ~ fitted.values
## Chisquare = 0.02679208, Df = 1, p = 0.86998
```

7.2.3 Multicollinearity

```
vif(covid2)

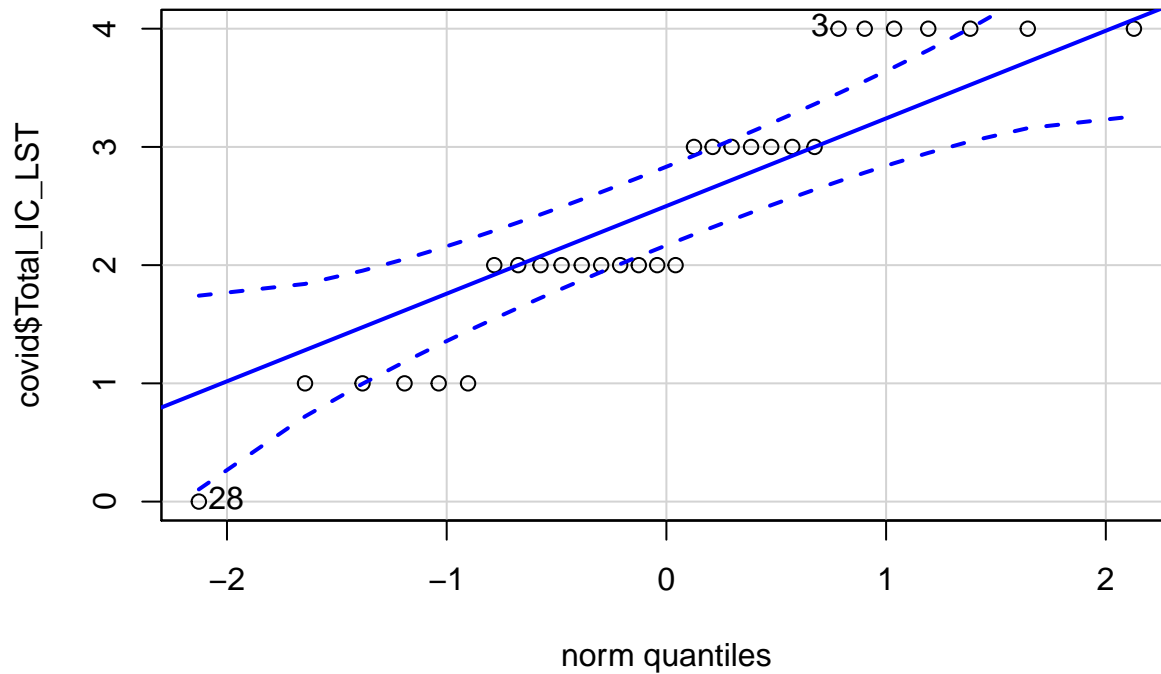
##              covid$PDSA              covid$Shift              covid$Census
```



```
##          1.940337          1.532976          1.347618
## covid$Team_Size covid$Attended.Prior covid$Short
##          1.341683          1.842170          1.174808
## covid$Step_out
##          1.284544
```

7.2.4 Normality of Residuals

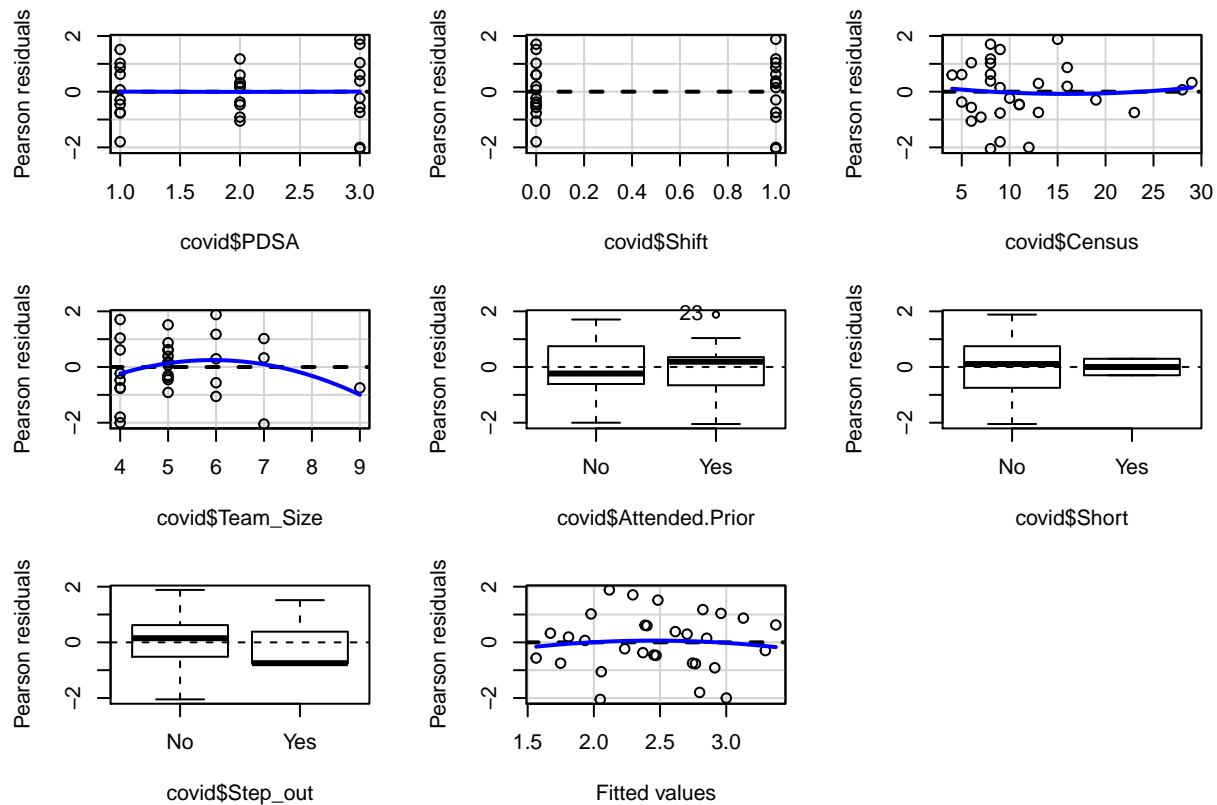
```
qqPlot(covid$Total_IC_LST)
```



```
## [1] 28 3
```

7.2.5 Residual Plots

```
residualPlots(covid2)
```



```
##               Test stat Pr(>|Test stat|)
## covid$PDSA      0.0250      0.98026
## covid$Shift     1.6319      0.11760
## covid$Census    0.3107      0.75912
## covid$Team_Size -1.7220      0.09976 .
## covid$Attended.Prior
## covid$Short
## covid$Step_out
## Tukey test      -0.3662      0.71421
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

7.2.6 Shapiro Wilke Test

```
shapiro.test(covid$Total_IC_LST)

##
##  Shapiro-Wilk normality test
##
## data:  covid$Total_IC_LST
## W = 0.90212, p-value = 0.009467
```

7.3 Equipment LST

```
summary(covid3 <- lm(covid$Total_EQUIP_LST ~ covid$PDSA + covid$Shift + covid$Census + covid$Team_Size +
```

```
##
## Call:
## lm(formula = covid$Total_EQUIP_LST ~ covid$PDSA + covid$Shift +
##      covid$Census + covid$Team_Size + covid$Attended.Prior + covid$Short +
##      covid$Step_out, data = covid)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.36610 -0.69150 -0.01784  0.42785  2.29954
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      1.58507     1.42084   1.116  0.27664
## covid$PDSA       -0.82531     0.37184  -2.220  0.03707 *
## covid$Shift       0.73118     0.53972   1.355  0.18925
## covid$Census      0.04768     0.04041   1.180  0.25063
## covid$Team_Size   0.32115     0.21649   1.483  0.15214
## covid$Attended.PriorYes -1.93021     0.61389  -3.144  0.00471 **
## covid$ShortYes    -1.14233     0.94708  -1.206  0.24056
## covid$Step_outYes -0.58197     0.82343  -0.707  0.48714
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.194 on 22 degrees of freedom
## Multiple R-squared:  0.6542, Adjusted R-squared:  0.5442
## F-statistic: 5.945 on 7 and 22 DF,  p-value: 0.0005693
```

7.3.1 Bonferroni

```
outlierTest(covid3)

## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 1 2.991066      0.0069625      0.20887
```

7.3.2 Heteroskedasticity

```
ncvTest(covid3)

## Non-constant Variance Score Test
## Variance formula: ~ fitted.values
## Chisquare = 4.850783, Df = 1, p = 0.027634
```

7.3.3 Multicollinearity

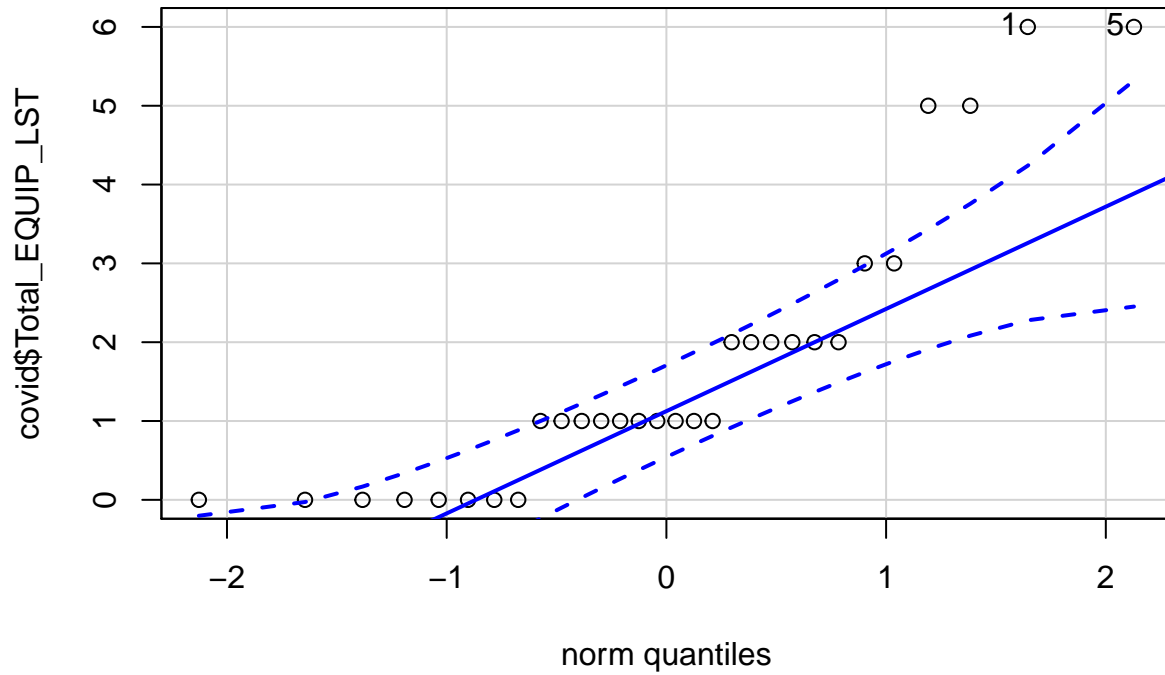
```
vif(covid3)

##          covid$PDSA          covid$Shift          covid$Census
##          1.940337          1.532976          1.347618
##          covid$Team_Size covid$Attended.Prior          covid$Short
```

```
##          1.341683          1.842170          1.174808
## covid$Step_out
##          1.284544
```

7.3.4 Normality of Residuals

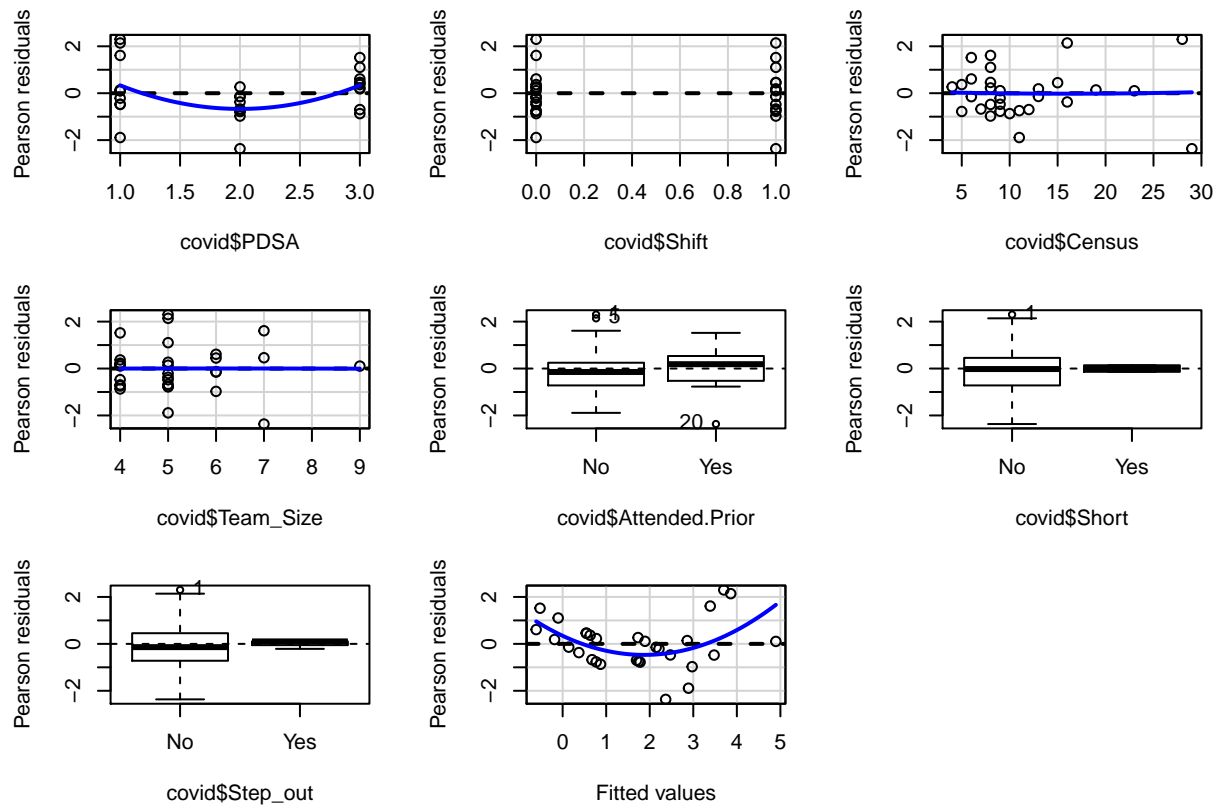
```
qqPlot(covid$Total_EQUIP_LST)
```



```
## [1] 1 5
```

7.3.5 Residual Plots

```
residualPlots(covid3)
```



```
##                               Test stat Pr(>|Test stat|)
## covid$PDSA                    2.6984      0.013458 *
## covid$Shift                   1.6164      0.120928
## covid$Census                  0.0779      0.938636
## covid$Team_Size              -0.0099      0.992202
## covid$Attended.Prior
## covid$Short
## covid$Step_out
## Tukey test                    3.2391      0.001199 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

7.3.6 Shapiro Wilke Test

```
shapiro.test(covid$Total_EQUIP_LST)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  covid$Total_EQUIP_LST
## W = 0.80509, p-value = 8.127e-05
```

7.4 Communication LST

Perceived workload removed secondary to correlation with PDSA

```
summary(covid4 <- lm(covid$Total_COMM_LST ~ covid$PDSA + covid$Shift + covid$Census + covid$Team_Size +
##
## Call:
## lm(formula = covid$Total_COMM_LST ~ covid$PDSA + covid$Shift +
##      covid$Census + covid$Team_Size + covid$Attended.Prior + covid$Short +
##      covid$Step_out, data = covid)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.2488 -0.5767 -0.2274  0.5563  2.2299
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      2.19754    1.24413   1.766  0.0912 .
## covid$PDSA       -0.62092    0.32560  -1.907  0.0697 .
## covid$Shift      -0.28951    0.47260  -0.613  0.5464
## covid$Census      0.02538    0.03538   0.717  0.4807
## covid$Team_Size   0.05806    0.18956   0.306  0.7622
## covid$Attended.PriorYes 0.59403    0.53754   1.105  0.2811
## covid$ShortYes    0.50092    0.82929   0.604  0.5520
## covid$Step_outYes -0.84201    0.72102  -1.168  0.2554
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.045 on 22 degrees of freedom
## Multiple R-squared:  0.2795, Adjusted R-squared:  0.05028
## F-statistic: 1.219 on 7 and 22 DF,  p-value: 0.334
```

7.4.1 Bonferroni

```
outlierTest(covid4)

## No Studentized residuals with Bonferroni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferroni p
## 21 2.688547      0.013755      0.41264
```

7.4.2 Heteroskedasticity

```
ncvTest(covid4)

## Non-constant Variance Score Test
## Variance formula: ~ fitted.values
## Chisquare = 3.027363, Df = 1, p = 0.081871
```

7.4.3 Multicollinearity

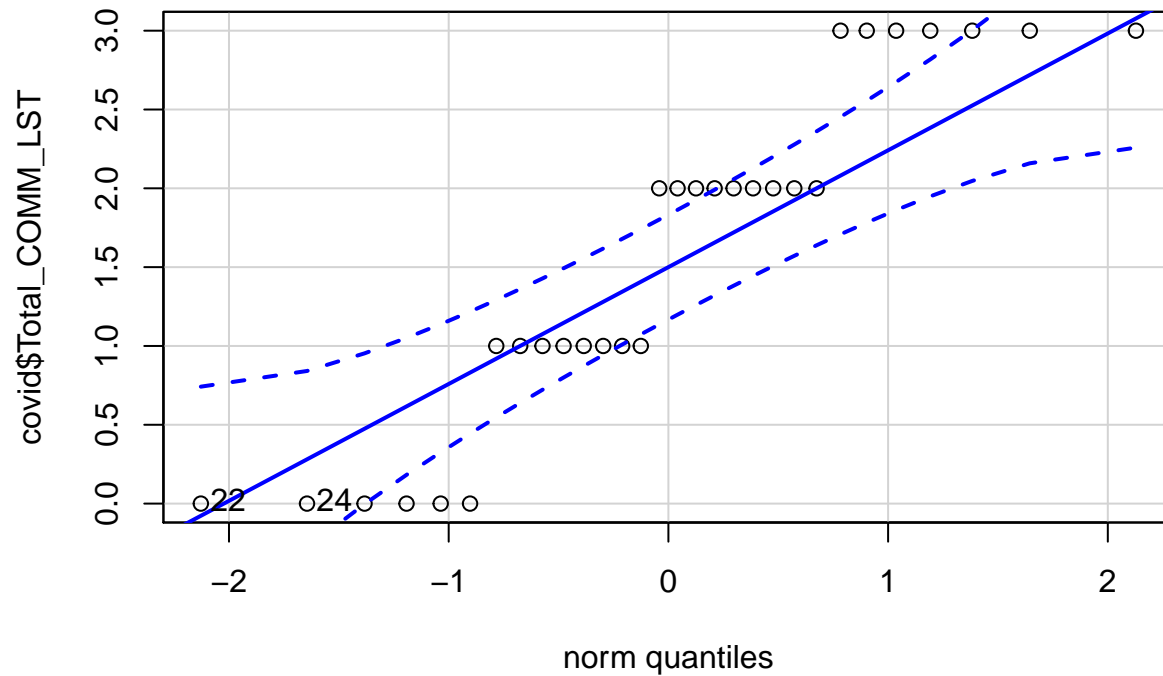
```
vif(covid4)

##              covid$PDSA              covid$Shift              covid$Census
```

```
##          1.940337          1.532976          1.347618
## covid$Team_Size covid$Attended.Prior covid$Short
##          1.341683          1.842170          1.174808
## covid$Step_out
##          1.284544
```

7.4.4 Normality of Residuals

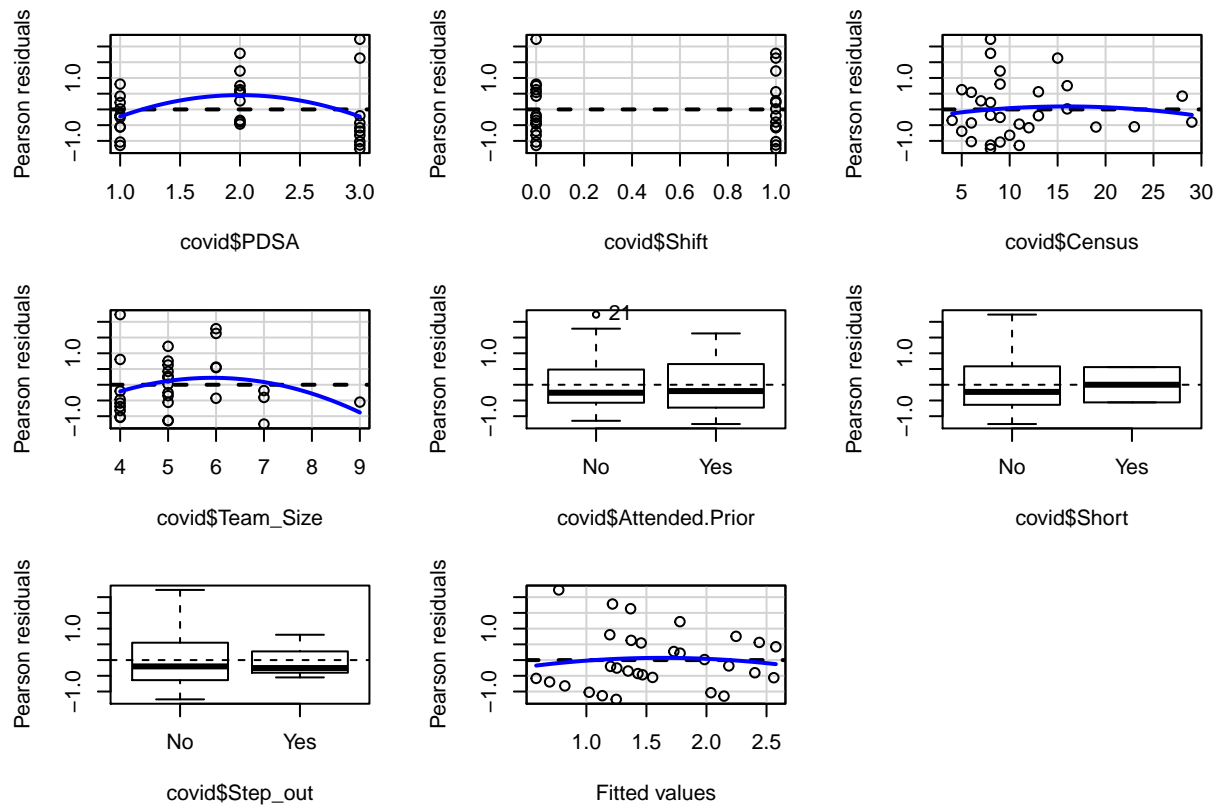
```
qqPlot(covid$Total_COMM_LST)
```



```
## [1] 22 24
```

7.4.5 Residual Plots

```
residualPlots(covid4)
```



```
##               Test stat Pr(>|Test stat|)
## covid$PDSA      -1.9587      0.06356 .
## covid$Shift       0.1684      0.86788
## covid$Census     -0.4157      0.68182
## covid$Team_Size  -1.7192      0.10029
## covid$Attended.Prior
## covid$Short
## covid$Step_out
## Tukey test      -0.6325      0.52708
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

7.4.6 Shapiro Wilke Test

```
shapiro.test(covid$Total_COMM_LST)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  covid$Total_COMM_LST
## W = 0.87297, p-value = 0.001952
```