R-code.R

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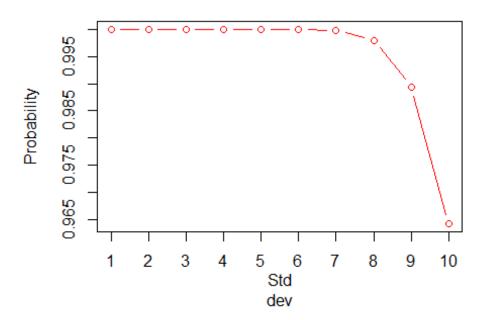
```
trials=10000
# number of simulations
avg=80
# mean of distribution
stdev=c(1:10)
# range of standard deviation values
cnt=0
m=0
ct=0
cnt1=0
m1=0
n=0
Q = 75
# specify Q value
Q_1=(Q+5)
Q_2 = (Q-15)
Q_3 = (Q-25)
d < -c()
# create empty vector
fn<-c()
count=j=0
for (x in min(stdev):max(stdev)){
  d<-c()
  set.seed(123)
  # to reproduce particular sequence of random numbers
  for (j1 in 1:trials){
    k<-round(c(rnorm(24,avg,x)),digits = 2)</pre>
    # simulate data using mean and standard deviation and
     # round it to 2 digits
    d<-cbind(d,t(t(k)))</pre>
  }
  write.table(rbind(paste0("Trial# ",c(1:trials)),d),
               paste0("stdev_", x,".csv"),
               sep = ",",row.names=F,col.names=F)
  # write a .csv file with name stdev_ with x value in the end
  d < -list(d)
  names(d)=paste("d",x,sep = "_")
  # create d with x value in the end
  list2env(d,envir = .GlobalEnv)
}
gh<-data.frame()</pre>
for (x in min(stdev):max(stdev)){
```

```
gh s1<-replicate(trials,0)</pre>
# create a column vector with number of rows equal to the variable trails
# and fill it with zero's
gh_s2<-replicate(trials,0)</pre>
gh_s3<-replicate(trials,0)</pre>
Cum_prob1<-replicate(trials,0)</pre>
Cum_prob<-replicate(trials,0)</pre>
for (j in 1:trials){
  count=0
  d<-get(paste0("d_",x,sep=""))</pre>
  # if j=1, x=1 then get d_1
  for (i in 1:6){
    if (d[i,j]>Q_1){
      # checking first six values in d greater than (Q+5)
      count=count+1
    }
  }
  if (count==6){
    gh_s1[j]=1
    # checking S1 criteria
  if(gh_s1[j]==0){
    # s1 criteria fail
    (cnt=m=0)
    for (i in 1:12){
      if (d[i,j]>Q_2){
        # checking if first 12 values in d are greater than (Q-15)
        cnt=cnt+1
      if (mean(d[1:12,j])>=Q){
        # checking if average of first 12 in d are greater than or equal
          # to Q
        m=1
        cnt=cnt*m
        if (cnt==12){
          gh s2[j]=1
          # checking for S2 criteria
        }
      }
    }
  if (gh_s2[j]==0 && gh_s1[j]==0) {
    # if failing in S1 and S2 stages
    ct=cnt1=n=m1=0
    for (b in 1:24){
      if (d[b,j]>Q_3){
        # checking if 24 in d are greater than (Q-25)
        ct=ct+1
      if (d[b,j]>Q_2){
```

```
cnt1=cnt1+1
        }
      }
      if (mean(d[1:24,j]) >= Q){
        m1=1
      if (cnt1>=22){
        # check atleast 22 are greater than (Q-15)
        # checking if average of 24 are greater than Q
      }
      ct=ct*m1*n
      if (ct==24){
        gh_s3[j]=1
        # checking S3 criteria
      if(gh_s1[j]==0 \&\& gh_s2[j]==0 \&\& gh_s3[j]==0){
        gh<-rbind(gh,c(x,j))
        # lists all trials numbers which fail to meet acceptance criteria
      }
    }
    Cum\_prob1[j] = (sum(gh\_s1[j],gh\_s2[j],gh\_s3[j]))
    # to calculate cumulative probability as function of trial number
    if (j>1){Cum prob[j]=sum(Cum prob1)/j}else{Cum prob[j]=Cum prob1[j]}
  }
  pdf(file=paste0("stdev_",x,".pdf"))
  plot(Cum prob,ylim = c(0,1),xlab = "Trials", ylab = "Cumulative
Probability",
       main = paste0("Std dev ", x))
  dev.off()
  write.table(cbind(c(1:trials),gh_s1,gh_s2,gh_s3,Cum_prob),
              paste0("All stages stdev_",x,".csv"),
              sep =
                ",",row.names=F,col.names=c('Trial#','S1','S2','S3','Cum Prob
'))
  # write .csv file
  options(scipen = 999)
  # disable scientific notation
  fn<-rbind(fn,c(avg, x, sum(gh_s1)/trials, sum(gh_s2)/trials,</pre>
                 sum(gh_s3)/trials, sum(gh_s1,gh_s2,gh_s3)/trials))
  # calculate probability of meeting acceptance criteria at every stage and
  # final passing probability
}
hder<-c("Avg", "Stddev", "S1", "S2", "S3", "Final")
result<-as.data.frame(fn)
names(result)<-hder</pre>
print(result)
##
      Avg Stddev
                     S1
                             S2
                                    S3 Final
               1 0.0153 0.9847 0.0000 1.0000
## 1
```

```
## 2
       80
               2 0.0154 0.9846 0.0000 1.0000
## 3
       80
               3 0.0154 0.9846 0.0000 1.0000
               4 0.0154 0.9846 0.0000 1.0000
## 4
       80
## 5
       80
               5 0.0154 0.9838 0.0008 1.0000
## 6
               6 0.0154 0.9778 0.0068 1.0000
       80
## 7
               7 0.0154 0.9524 0.0320 0.9998
       80
               8 0.0154 0.9010 0.0816 0.9980
## 8
       80
## 9
       80
               9 0.0154 0.8289 0.1451 0.9894
## 10
              10 0.0154 0.7300 0.2188 0.9642
      80
names(gh)<-c("Stdev","Trial#")</pre>
plot(result$Stddev,result$Final,type="b",cex=1,col="red",pch=1,xlab = "Std
dev", ylab="Probability",
     main = paste("Dissolution passing probability when mean is",
                  avg),xaxt="none")
axis(1, seq(1,10,1))
```

Dissolution passing probability when mean is 80



```
write.csv(result,paste0("Final.csv"))
write.csv(gh,paste0("Fail trails",".csv"))
```