

1.

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BioC_mirror: https://bioconductor.org  
Using Bioconductor 3.7 (BiocInstaller 1.30.0), R 3.5.1 (2018-07-02).  
Installing package(s) 'fitdistrplus'  
library(readr)  
GOOG <- read_csv("Downloads/GOOGL.csv")  
View(GOOG)  
install.packages("fitdistrplus")  
pt1=GOOG[,6]  
pt1=as.matrix(pt1)  
pt1=pt1[,1]  
pt=tail(pt1,250)  
pt1=head(pt1,250)  
rt=log(pt/pt1)  
quantile(rt,0.05)  
q005=quantile(rt,0.05)  
r=rt[rt<q005]  
Er=mean(r)  
plotdist(rt)  
descdist(rt)  
fitdist(rt,"logis")  
fitdist(rt,"norm")  
install.packages("gofest")  
library(gofest)  
ad.test(rt,"pnorm")  
ad.test(rt,"plogis",fit$estimate[1],fit$estimate[2])  
m=fit$estimate[1]  
s=fit$estimate[2]  
f=function(x){x*dlogis(x,m,s)}  
c=qlogis(0.05,m,s)  
E=integrate(f,-Inf,c)$value  
Fr=plogis(c,m,s)  
Erc=E/Fr  
Erc
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2.

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pt1=AMZN[,6]  
pt1=as.matrix(pt1)  
pt1=pt1[,1]  
pt=tail(pt1,250)  
pt1=head(pt1,250)  
rt=log(pt/pt1)  
quantile(rt,0.05)  
q005=quantile(rt,0.05)  
r=rt[rt<q005]  
Er=mean(r)  
plotdist(rt)  
descdist(rt)  
fit1=fitdist(rt,"logis")  
fit2=fitdist(rt,"norm")  
ad.test(rt,"pnorm",fit2$estimate[1],fit2$estimate[2])  
ad.test(rt,"plogis",fit1$estimate[1],fit1$estimate[2])  
ma=fit1$estimate[1]  
sa=fit1$estimate[2]
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f=function(x){x*dlogis(x,ma,sa)}
c=qlogis(0.05,ma,sa)
E=integrate(f,-Inf,c)$value
Fr=plogis(c,ma,sa)
Erc=E/Fr
Erc

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3.ptG=as.matrix(GOOG[,6])
ptG=tail(ptG[,1],250)
pt1G=head(ptG[,1],250)
ptA=pta
pt1A=pt1
i=seq(from=0,to=1,by=0.02)
ptw=w*ptG+(1-w)*ptA
pt1w=w*pt1G+(1-w)*pt1A
w=0
tRtw=matrix(0,250,50)
ptw=matrix(0,250,50)
pt1w=ptw
for(i in 1:50){
  w[i]=i*0.02
  for (j in 1:250) {
    ptw[j,i]=w[i]*ptG[j]+(1-w[i])*ptA[j]
    pt1w[j,i]=w[i]*pt1G[j]+(1-w[i])*pt1A[j]
    tRtw[j,i]=log(ptw[j,i]/pt1w[j,i])
    Esw[i]=mean(tRtw[tRtw[,i]<q005w[i],i])
  }

  q005w[i]=quantile(tRtw[,i],0.05)
}
plot(w,q005w)
plot(Esw)
plot(q005w)

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```

maxe=0
maxesw=max(Esw)
minesw=min(Esw)
for(i in 1:50){
  if(Esw[i]==maxesw) maxw=i*0.02
  if(Esw[i]==minesw) minw=i*0.02
}
maxw
minw

```