

414Quiz3

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1.

- a. The mean of the samples is 0.9993, the standard deviation of the samples is 1.0189. The theoretical mean and standard deviation are both 1. The results are close to the theoretical values.
- b. The plot for Markov chain sampler indicates some correlation because the draws are not independent. The other plot does not show any correlation because draws are independent.

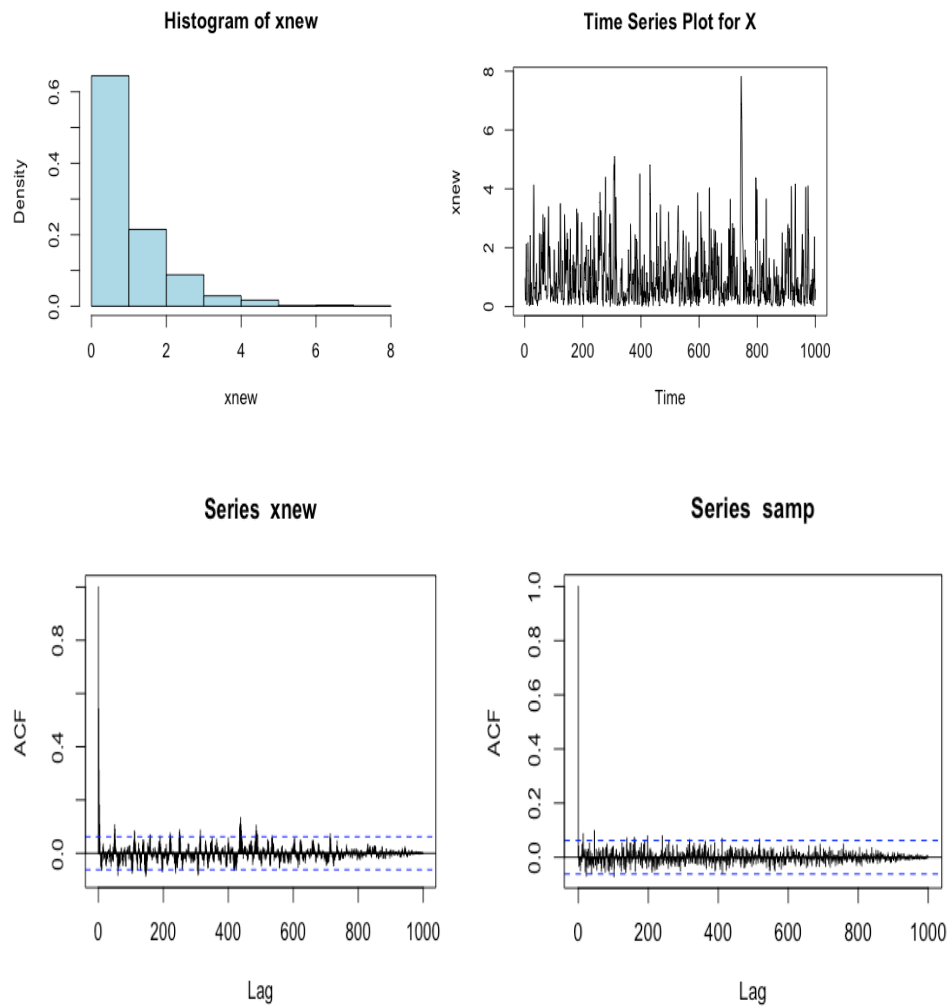
```
#a.
J = 1200
y = rep(0, J)
x = rep(0, J)
x[1] = 1
y[1] = 0.3
# run 1200 iterations
set.seed(135)
for (i in 1:(J-1)){
  y[i+1] = runif(1, 0, exp(-x[i]))
  x[i+1] = runif(1, 0, -log(y[i+1]))
}

# discard initial 200 for burnin
xnew = x[201:1200]
mean(xnew)

## [1] 0.9993493

sd(xnew)

## [1] 1.01889
```



2.

- The estimate of alpha is -0.7597, the standard error of alpha is 0.1427. The estimate of beta is 5.6922, the standard error of beta is 0.5366. $G^2 = 4.6415$ on 4 df. Because p-value is $0.3260973 > 0.05$. Reject H_0 at $\alpha = 0.05$. Therefore, this is a good fit.
- The mean of samples is 0.1345173, and the standard error of samples is 0.02166359.
- The estimate of alpha is -0.7688, the standard error of alpha is 0.1427. The estimate of beta is 5.766, the standard error of beta is 0.5414. The results are very close to the results in part a.
- The posterior mean is 0.1334 and the posterior standard error is 0.02171. The results are very close to the results in part b.
- With delta method, the estimate of standard error is 0.02178673, the value is very close to the results in b and d.

```

#a.
y = c(2, 19, 24, 49, 69, 78)
n = rep(80, 6)
x = c(-0.553, -0.113, 0.059, 0.185, 0.446, 0.753)
slogit = log((y + 0.5)/(n - y + 0.5)); ymat = cbind(y, n-y)
m1 = glm(ymat~x, family = binomial)
summary(m1)

##
## Call:
## glm(formula = ymat ~ x, family = binomial)
##
## Deviance Residuals:
##      1      2      3      4      5      6
##  0.3279  0.8810 -1.7801  0.7206  0.1772  0.1955
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -0.7597     0.1427  -5.325 1.01e-07 ***
## x              5.6922     0.5366  10.608 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 271.6730  on 5  degrees of freedom
## Residual deviance:   4.6415  on 4  degrees of freedom
## AIC: 31.898
##
## Number of Fisher Scoring iterations: 4

pchisq(4.6415, 4, lower.tail = F)

## [1] 0.3260973

#b.
phat = fitted.values(m1)
nmat = matrix(0, nrow=2, ncol=1000)
for(i in 1:1000){
  ynew = rbinom(6, n, phat)
  ymatnew = cbind(ynew, n-ynew)
  m2 = glm(ymatnew~x, family=binomial)
  nmat[,i] = m2$coef
}
LD50samp = -nmat[1,]/nmat[2,]
sd(LD50samp)

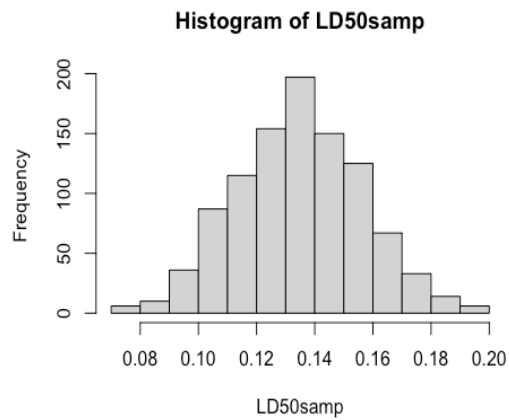
## [1] 0.02166359

mean(LD50samp)

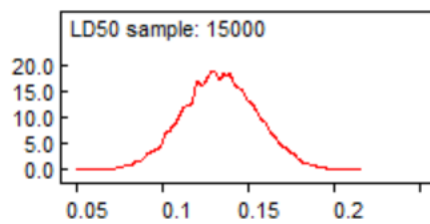
```

```
## [1] 0.1345173
```

```
hist(LD50samp)
```



#d.



#e.

```
B = c(-1/m1$coef[2], m1$coef[1]/m1$coef[2]^2)  
sqrt(B %*% vcov(m1) %*% B)
```

```
## [1,]
```

```
## [1,] 0.02178673
```