CV for NBA clutch free throws models

Chapter 5.1: Cross-validation

The NBA clutch free throws data set has three variables for player $i = 1, \ldots, 10$:

1. Y_i is the number clutch free throws made
2. N_i is the number clutch free throws attempted
3. q_i is the proportion of the non-clutch free throws made

We model these data as

$$Y_i \sim \text{Binomial}(N_i, p_i),$$

where p_i is the true probability of making a clutch shot. The objective is to explore the relationship between clutch and overall percentages, p_i and q_i. We do this using two logistic regression models:

1. $\text{logit}(p_i) = \beta_1 + \beta_2 \text{logit}(q_i)$
2. $\text{logit}(p_i) = \beta_1 + \text{logit}(q_i)$

In both models we select uninformative priors $\beta_j \sim \text{Normal}(0, 10^2)$.

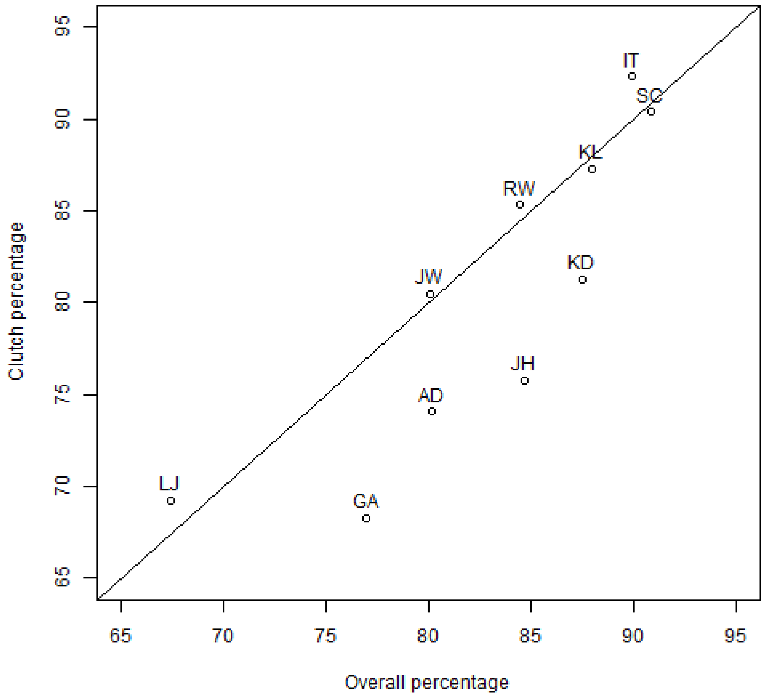
In the first model, $p_i = q_i$ if $\beta_1 = 0$ and $\beta_2 = 1$; in the second model $p_i = q_i$ if $\beta_1 = 0$. Therefore, we compare the posteriors of the β_j to these values to analyze the relationship between p_i and q_i.

Load the data

```
Y <- c(64, 72, 55, 27, 75, 24, 28, 66, 40, 13)
N <- c(75, 95, 63, 39, 83, 26, 41, 82, 54, 16)
q <- c(0.845, 0.847, 0.880, 0.674, 0.909, 0.899, 0.770, 0.801, 0.802, 0.875)

X <- log(q)-log(1-q) # X = logit(q)
```

Plot the data

```
inits   <- c("RW","JH","KL","LJ","SC","IT","GA","JW","AD","KD")
plot(100*q,100*Y/N,
     xlim=100*c(0.65,0.95),ylim=100*c(0.65,0.95),
     xlab="Overall percentage",ylab="Clutch percentage")
text(100*q,100*Y/N+1,inits)
abline(0,1)
```




```
expit <- function(x){1/(1+exp(-x))}
```

Randomly assign observations to $K = 5$ folds

```
set.seed(0820)
fold <- rep(1:5,2)
fold <- sample(fold)
fold
```

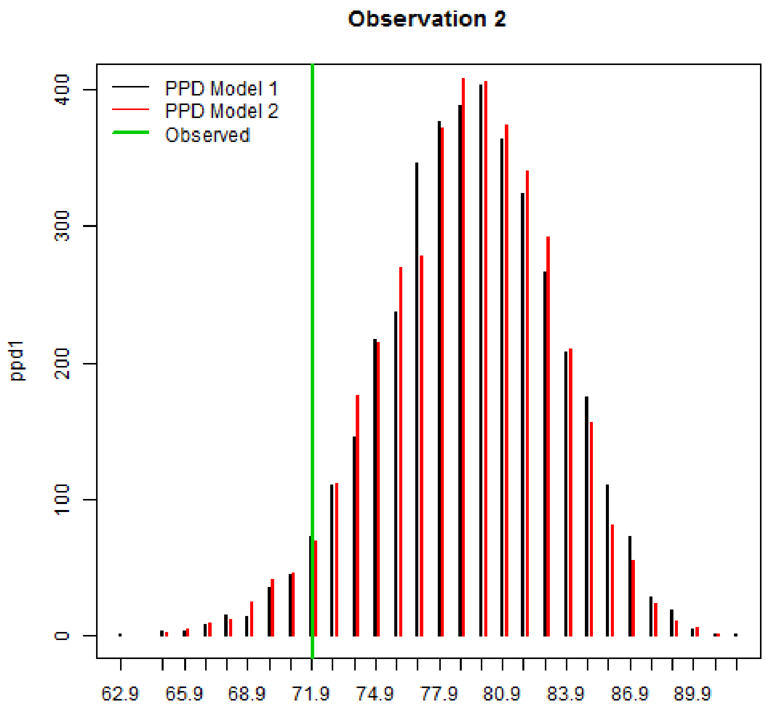
```
##  [1] 3 1 5 2 1 2 4 5 4 3
```

Fit the model and make predictions

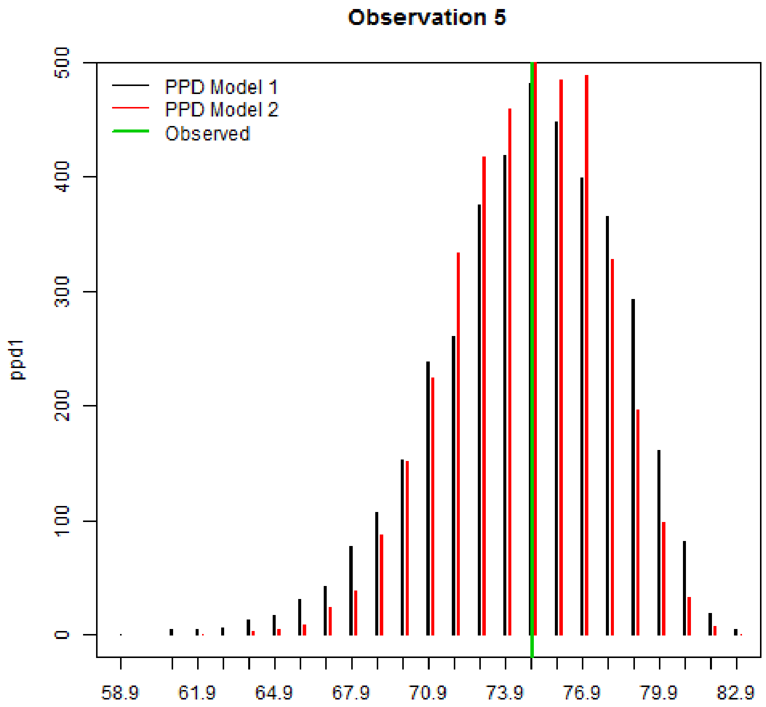
```
## Define the models in JAGS
```

```
library(rjags)

Y_mean   <- matrix(NA,10,2)
Y_median <- matrix(NA,10,2)
Y_low    <- matrix(NA,10,2)
Y_high   <- matrix(NA,10,2)

for(f in 1:5){

  # Select training data with fold not equal to f
  data   <- list(Y=Y[fold!=f],N=N[fold!=f],X=X[fold!=f],n=sum(fold!=f))
  params <- c("beta")

  # Fit model 1
  m1 <- textConnection("model{
    for(i in 1:n){
      Y[i]        ~ dbinom(p[i],N[i])
      logit(p[i]) <- beta[1] + beta[2]*X[i]
    }
    beta[1] ~ dnorm(0,0.01)
    beta[2] ~ dnorm(0,0.01)
  }")
```

```
    model1 <- jags.model(m1,data = data, n.chains=1,quiet=TRUE)
    update(model1, 10000, progress.bar="none")
    b1     <- coda.samples(model1, variable.names=params, thin=5, n.iter=20000, progress.bar="none")[[1]]

    # Fit model 2
    m2 <- textConnection("model{
     for(i in 1:n){
       Y[i]        ~ dbinom(p[i],N[i])
       logit(p[i]) <- beta + X[i]
     }
     beta ~ dnorm(0,0.01)
    }")
    model2 <- jags.model(m2,data = data, n.chains=1,quiet=TRUE)
    update(model2, 10000, progress.bar="none")
    b2     <- coda.samples(model2, variable.names=params, thin=5, n.iter=20000, progress.bar="none")[[1]]

    # Make predictions
    for(i in 1:10){if(fold[i]==f){
       Y_mod1         <- rbinom(nrow(b1),N[i],expit(b1[,1] + b1[,2]*X[i]))
       Y_mean[i,1]    <- mean(Y_mod1)
       Y_median[i,1] <- median(Y_mod1)
       Y_low[i,1]     <- quantile(Y_mod1,0.025)
       Y_high[i,1]    <- quantile(Y_mod1,0.975)

       Y_mod2         <- rbinom(length(b2),N[i],expit(b2 + X[i]))
       Y_mean[i,2]    <- mean(Y_mod2)
       Y_median[i,2] <- median(Y_mod2)
       Y_low[i,2]     <- quantile(Y_mod2,0.025)
       Y_high[i,2]    <- quantile(Y_mod2,0.975)

       ppd1 <- table(Y_mod1-0.1)
       ppd2 <- table(Y_mod2+0.1) # Add 0.1 to avoid overlap

       plot(ppd1,main=paste("Observation", i))
       lines(ppd2,col=2)
       abline(v=Y[i],lwd=2,col=3)

       legend("topleft",c("PPD Model 1","PPD Model 2","Observed"),lwd=c(1,1,2),col=1:3,bty="n")
    }}

    rm(model1)
    rm(model2)
}
```

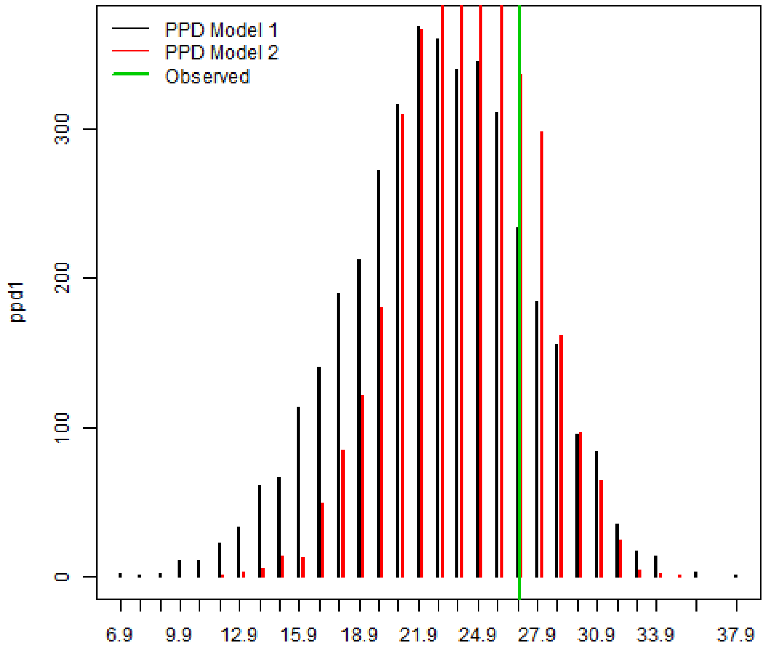


Observation 2
PPD Model 1
PPD Model 2
Observed
ppd1
0
100
200
300
400
62.9
65.9
68.9
71.9
74.9
77.9
80.9
83.9
86.9
89.9

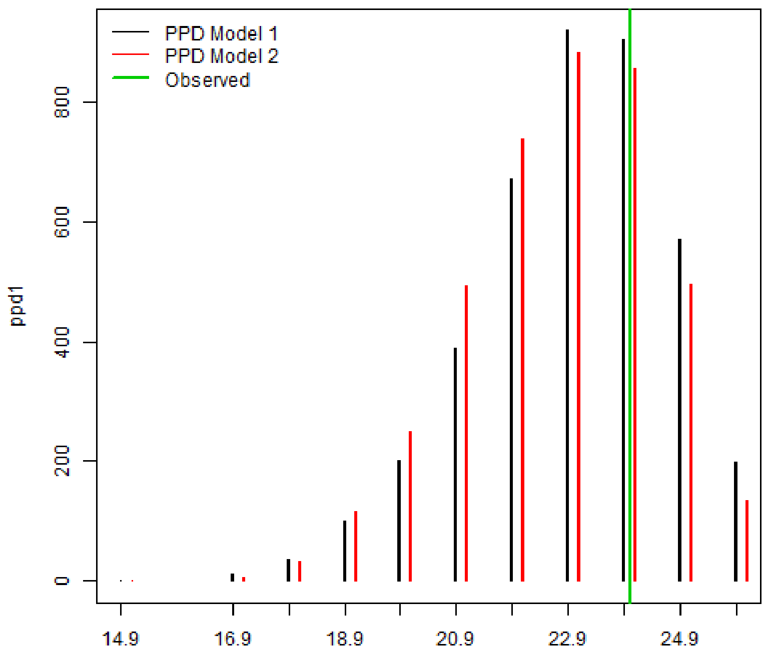


Observation 5
PPD Model 1
PPD Model 2
Observed
ppd1
0
100
200
300
400
500
58.9
61.9
64.9
67.9
70.9
73.9
76.9
79.9
82.9

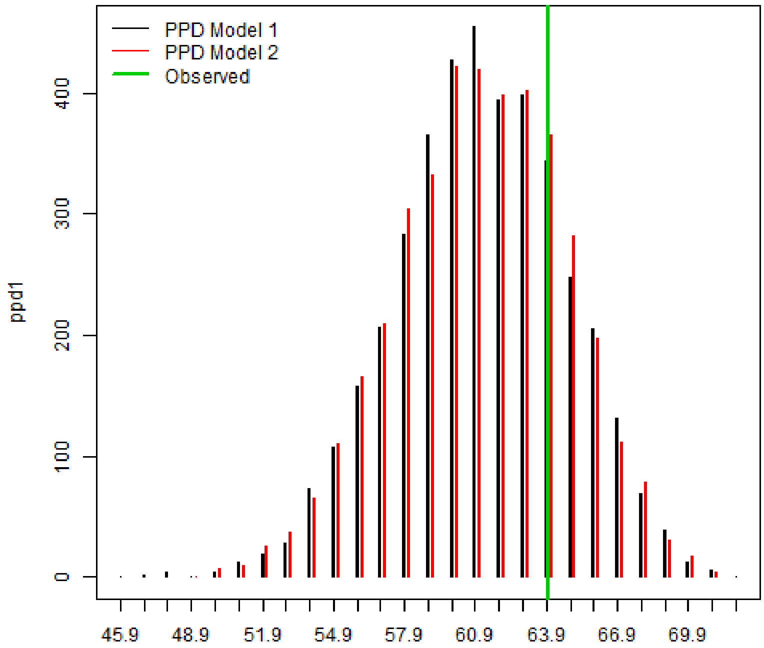
Observation 4



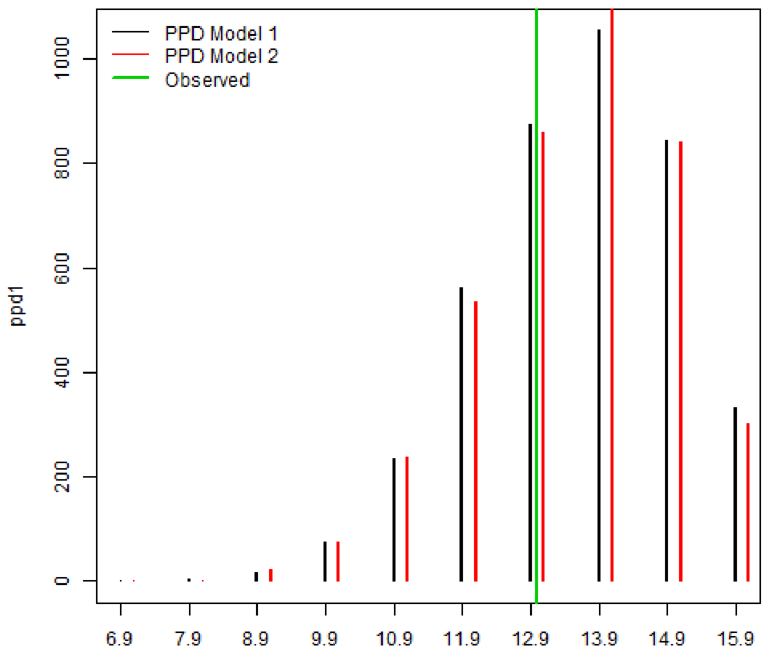
Observation 6



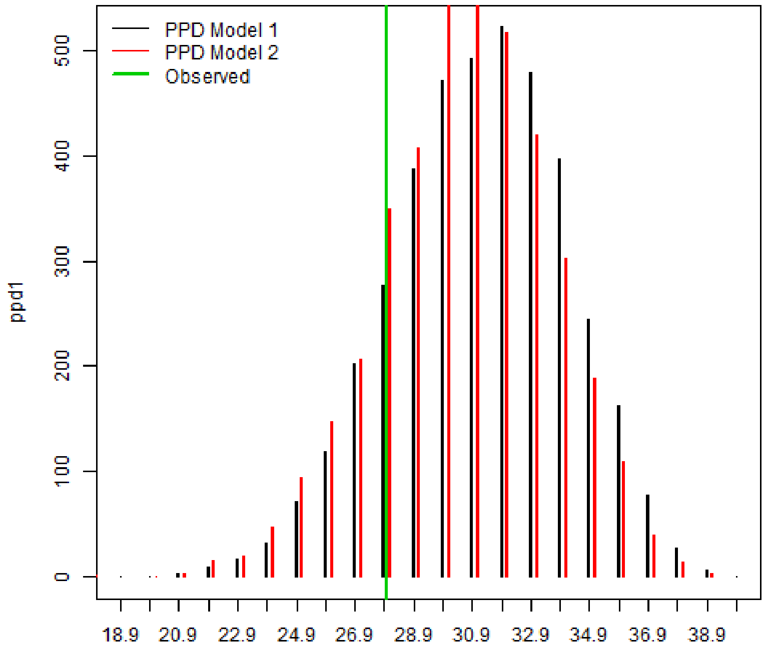
Observation 1



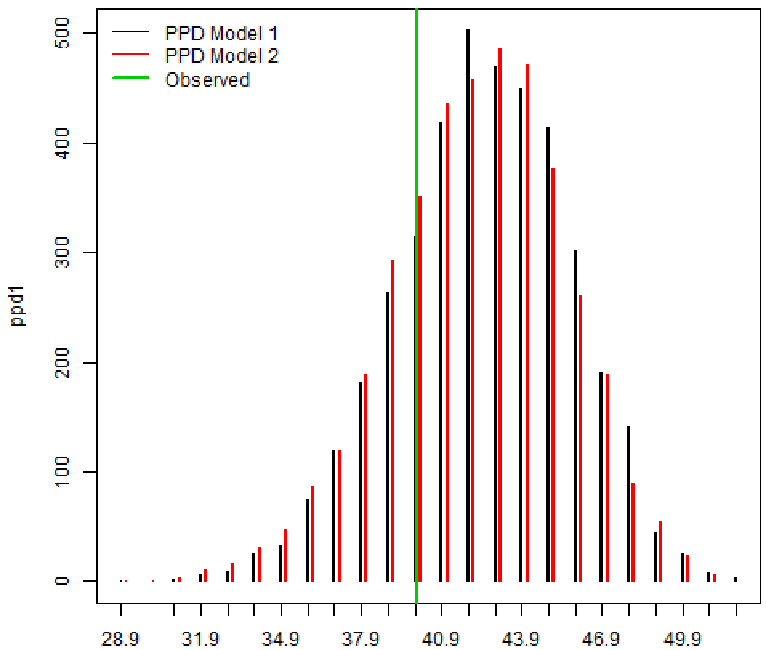
Observation 10



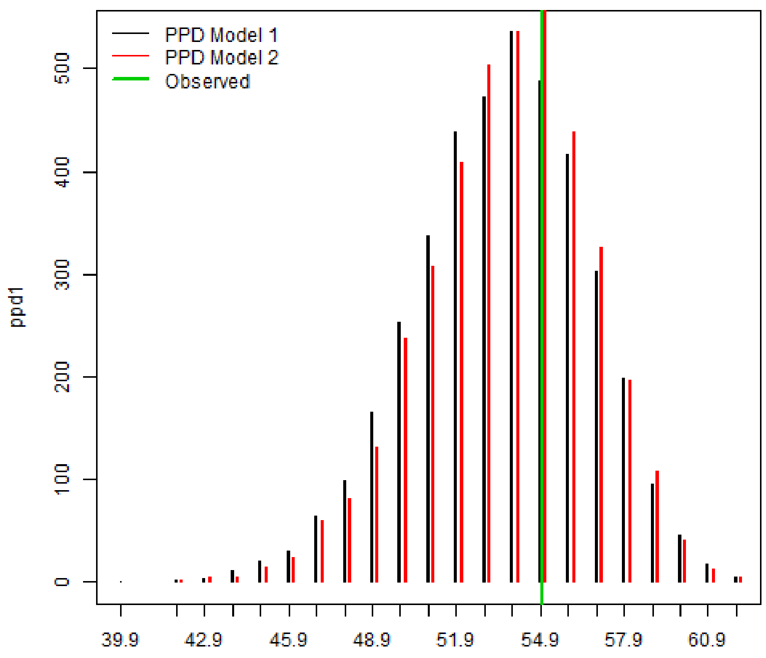
Observation 7



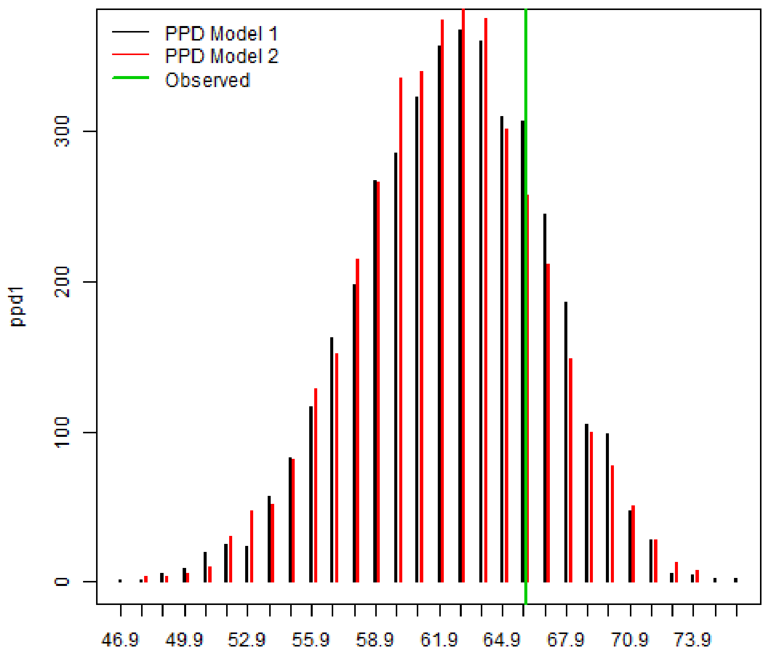
Observation 9



Observation 3

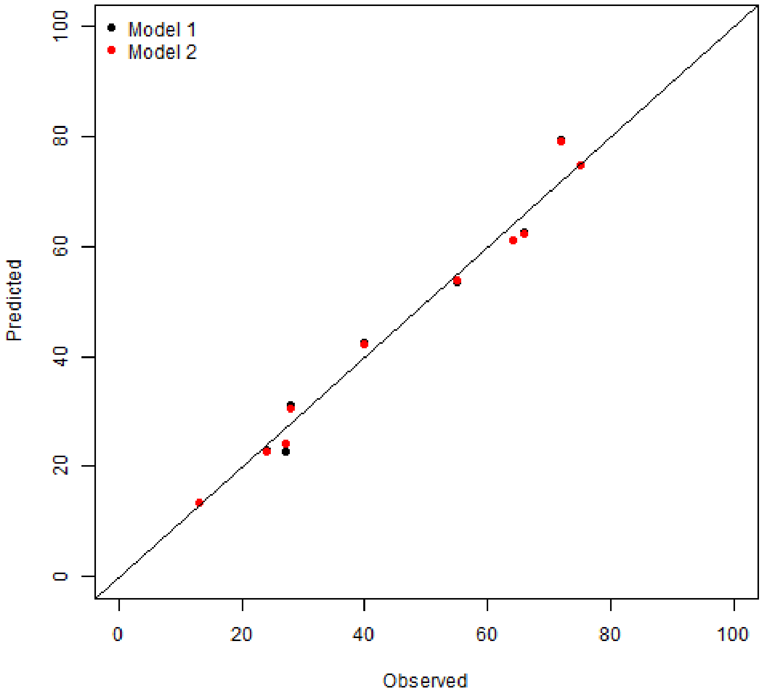


Observation 8




```
## Summarize results
```

```r
y     <- cbind(Y,Y) # Make data the same size/format as predictions
BIAS  <- colMeans(Y_mean-Y)
MSE   <- colMeans((Y_mean-Y)^2)
MAD   <- colMeans(abs(Y_mean-Y))
COV   <- colMeans( (Y_low <= Y) & (Y <= Y_high))
WIDTH <- colMeans(Y_high-Y_low)

plot(Y,Y_mean[,1],pch=19,
     xlim=c(0,100),ylim=c(0,100),
     xlab="Observed",ylab="Predicted")
points(Y,Y_mean[,2],col=2,pch=19)
abline(0,1)
legend("topleft",c("Model 1","Model 2"),pch=19,col=1:2,bty="n")
```




```r
OUT   <- cbind(BIAS,MSE,MAD,COV,WIDTH)
OUT   <- round(OUT,2)
kable(OUT)
```

BIAS	MSE	MAD	COV	WIDTH
0.04	11.14	2.69	1	12.50
0.06	9.68	2.48	1	11.71

Summary: Both models give coverage 1.00. Model 2 has smaller MSE, MAD and interval width. This is a very small dataset so it is hard to be definitive, but it seems model 2 is preferred.

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