```
> #Q1
> sample(c("H", "T"), 10, replace = TRUE)
  [1] "H" "H" "T" "H" "T" "T" "T" "T" "T"
>
```

```
#Q1
sample(c("H", "T"), 10, replace = TRUE)
```

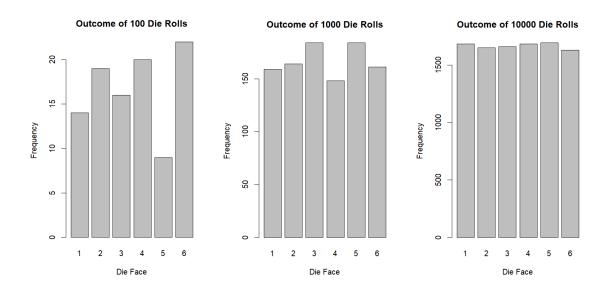
## Q2

m.trails \ r.reps		10	100	1000	10000
10	Min	0.4	0.2	0	0
	Max	0.7	0.9	1	1
100	Min	0.47	036	0.33	0.28
	Max	0.58	0.59	0.65	0.69
1000	Min	0.481	0.469	0.444	0.441
	Max	0.518	0.544	0.556	0.582
10000	Min	0.4929	0.4886	0.4841	0.4799
	Max	0.5149	0.5102	0.5157	0.5186

```
#Q3
MinAndMaxProbHeads <- function(m.trials, r.reps) {</pre>
 results <- replicate(r.reps, ProbHeads(m.trials))
 return(c(min(results), max(results)))
}
MinAndMaxProbHeads(10, 10)
MinAndMaxProbHeads(10, 100)
MinAndMaxProbHeads(10, 1000)
MinAndMaxProbHeads(10, 10000)
MinAndMaxProbHeads(100, 10)
MinAndMaxProbHeads(100, 100)
MinAndMaxProbHeads(100, 1000)
MinAndMaxProbHeads(100, 10000)
MinAndMaxProbHeads(1000, 10)
MinAndMaxProbHeads(1000, 100)
MinAndMaxProbHeads(1000, 1000)
MinAndMaxProbHeads(1000, 10000)
MinAndMaxProbHeads(10000, 10)
MinAndMaxProbHeads(10000, 100)
MinAndMaxProbHeads(10000, 1000)
MinAndMaxProbHeads(10000, 10000)
```

The gap between Min and Max seems to be getting smaller.

# Q4

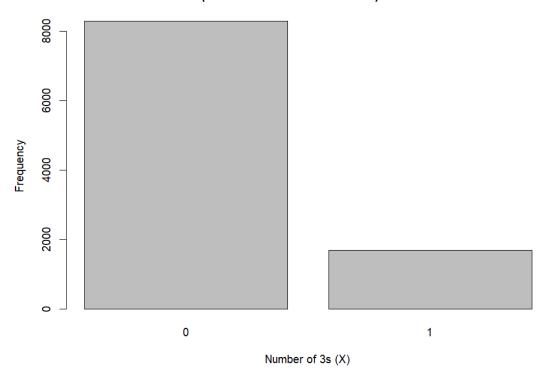


```
RollDice <- function(m.trials){
  rolls <- sample(1:6, m.trials, replace = TRUE)
  roll.table <- table(rolls)
  barplot(roll.table,
      main = paste("Outcome of", m.trials, "Die Rolls"),
      xlab = "Die Face",
      ylab = "Frequency")
}

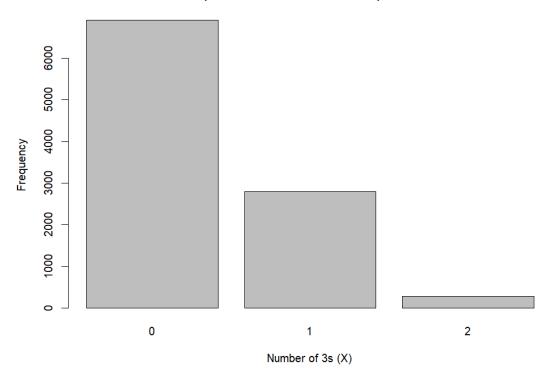
RollDice(100)
RollDice(1000)
RollDice(10000)
```

The bar chart becomes increasingly smooth and symmetric.

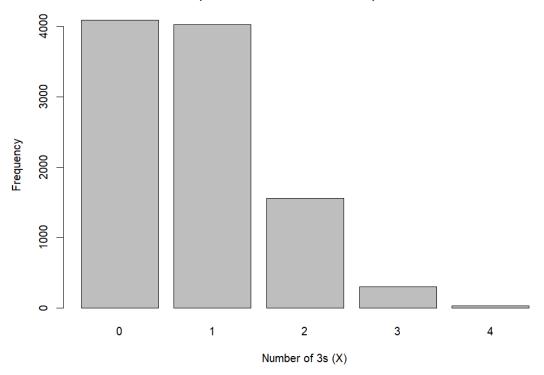
### Distribution of X (number of 3s out of 1 dice) Based on 10000 Trials



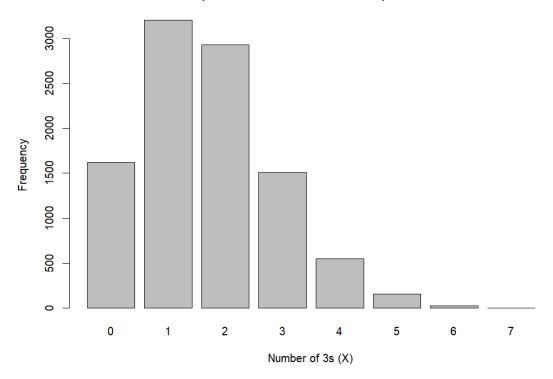
### Distribution of X (number of 3s out of 2 dice) Based on 10000 Trials



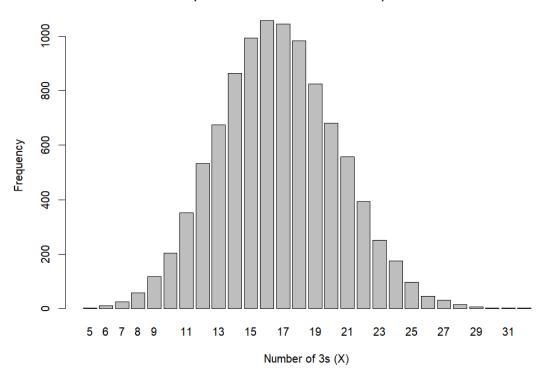
## Distribution of X (number of 3s out of 5 dice) Based on 10000 Trials



## Distribution of X (number of 3s out of 10 dice) Based on 10000 Trials



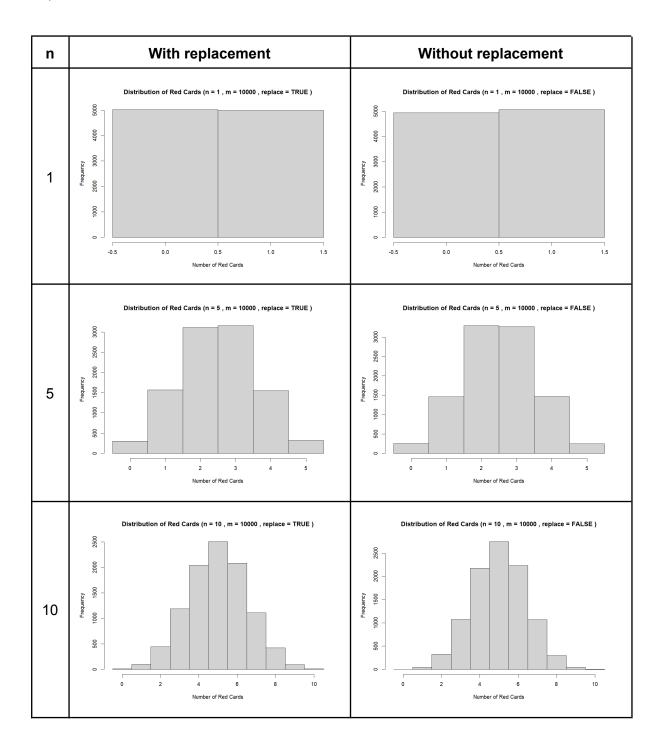
#### Distribution of X (number of 3s out of 100 dice) Based on 10000 Trials

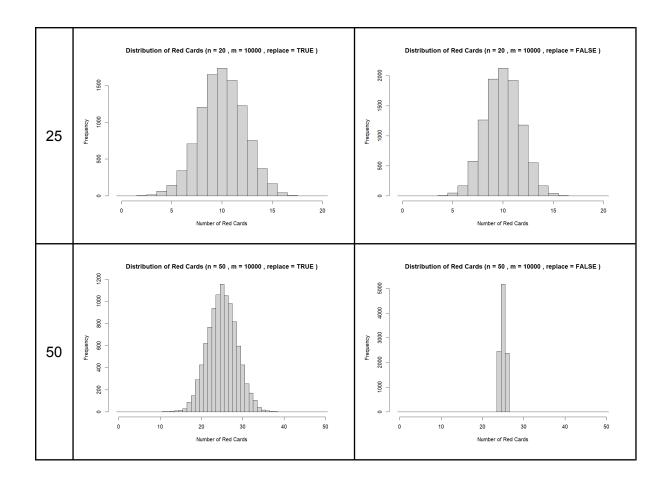


#Q5
RollSomeDice <- function(m.trials, n.dice){
 X <- numeric(m.trials)

```
for(i in 1:m.trials){
  rolls <- sample(1:6, n.dice, replace=TRUE)
  X[i] \leftarrow sum(rolls == 3)
 X.table <- table(X)
 barplot(X.table,
      main = paste("Distribution of X (number of 3s out of",
              n.dice,
              "dice) Based on",
              m.trials,
              "Trials"),
      xlab = "Number of 3s (X)",
      ylab = "Frequency")
 return(X.table)
set.seed(69)
RollSomeDice(10000, 1)
RollSomeDice(10000, 2)
RollSomeDice(10000, 5)
RollSomeDice(10000, 10)
RollSomeDice(10000, 100)
```

Their skewness decreases and at the end becomes a normal distribution.





```
#Q6
DrawCards <- function(m.trials, n.cards, replace){</pre>
 deck <- c(rep("R", 26), rep("B", 26))
 results <- replicate(
  m.trials.
  sum(sample(deck, n.cards, replace = replace) == "R")
 hist(
  results,
  breaks = seq(-0.5, n.cards + 0.5, 1),
  main = paste("Distribution of Red Cards (n =",
          n.cards,
           ", m =",
          m.trials,
          ", replace =",
          replace, ")"),
  xlab = "Number of Red Cards")
}
DrawCards(10000, 1, TRUE)
DrawCards(10000, 5, TRUE)
DrawCards(10000, 10, TRUE)
DrawCards(10000, 20, TRUE)
DrawCards(10000, 50, TRUE)
```

DrawCards(10000, 1, FALSE)
DrawCards(10000, 5, FALSE)
DrawCards(10000, 10, FALSE)
DrawCards(10000, 20, FALSE)
DrawCards(10000, 50, FALSE)

With replacement, the sampling distribution becomes increasingly close to a normal distribution. Without replacement, the unusual counts decrease until they are eventually concentrated in the middle. I think the reason is that for sampling without replacement, by the end, you will almost always draw out all the red cards, so in each trial, the number of red cards drawn tends to be similar, making the distribution more concentrated.