Functions in R

- R has many in-built functions.
- Writing new functions is also possible.
- It can be constructed using function

Functions in R: Syntax

say we are trying to find the mean of vector

```
> ourmean = function(x) {
+ sum(x)/length(x)
+ }
```

 the function will return the last computed value unless the body calls for a specific return value.

```
> x = c(1,2,3,4,4,5,5,5,5)
> ourmean(x)
[1] 3.777778
```

Functions in R

• Try to use in-built functions -R

 It does take effort to write a useful function using function that provides one single number.

Sampling from a given distribution

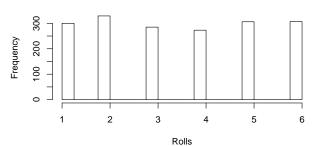
- we can use the sample function.
- takes a sample of the specified size (specified by size) from the elements of x using either with or without replacement (specified by replace).
- The optional prob argument can be used to give a vector of weights for obtaining the elements of the vector being sampled.

```
> x = c(1,2,3,4,5,6)
> probx= c(1/6,1/6,1/6,1/6,1/6,1/6)
> Rolls=sample(x, size=1800, replace=T, prob=probx)
```

Uniform(1,2,3,4,5,6)

```
> table(Rolls)
Rolls
    1    2    3    4    5    6
300 329 285 273 306 307
> hist(Rolls,breaks = seq(1,6, by=0.25))
```

Histogram of Rolls



Functions in R: Variance of Uniform

Let us try to compute the variance of x

```
> x
[1] 1 2 3 4 5 6
> ourvariance = function(x) {
+ sum((x -ourmean(x))^2)/length(x)
+ }
```

 Note that this differs from sample variance in the normalisation.

Uniform(1,2,3,4,5,6)

```
> var(Rolls)
[1] 2.980381
> ourvariance(x)
[1] 2.916667
```

ourvariance gives the variance of the uniform random variable.

Sums of Rolls

Suppose we wish to simulate in R the experiment that we did in class of Rolling a die and noting down its sum. We can use the sample, matrix and apply.

```
> x = c(1,2,3,4,5,6)
> probx= c(1/6,1/6,1/6,1/6,1/6,1/6)
> Rolls=sample(x, size=1500, replace=T, prob=probx)
> Rollm=matrix(Rolls, 5)
> # above creates a matrix 5 columns and 30 Rows
> Rollsums = apply(Rollm, 2, sum)
```

Sums of Rolls

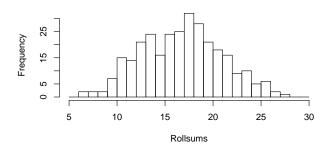
> table(Rollsums)

```
Rollsums
```

```
7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 2 2 2 7 15 14 21 24 16 24 25 32 28 21 18 16 9 10 5 6 2 1
```

> hist(Rollsums, breaks = seq(5,30, by=1))

Histogram of Rollsums



Class experiment: Sums of Rolls

This was the histogram that we got when we did the experiment of rolling a die 5times and noting down its sum.



Suppose we want to verify the below result via simulations:

Let X_1, X_2, \ldots, X_n be an i.i.d. sample of random variables whose distribution has finite expected value μ and finite variance σ^2 . Let \bar{X} represent the sample mean. Then

$$E[\bar{X}] = \mu$$
 and $SD[\bar{X}] = \frac{\sigma}{\sqrt{n}}$.

```
> x = c(1,2,3,4,5,6)
> probx= c(1/6,1/6,1/6,1/6,1/6,1/6)
```

Let us generate 3 sets of data:

500,5000,150000 samples from x and probx.

- > Rolls=sample(x,size=500,replace=T,prob=probx)
- > Rolls5000=sample(x,size=5000,replace=T,prob=probx)
- > Rolls150000=sample(x,size=150000,replace=T,prob=probx)

We split them up into sets of 5, 50, 5000 rolls.

- > Rollm=matrix(Rolls, 5)
- > Rollm5000=matrix(Rolls5000, 50)
- > Rollm150000=matrix(Rolls150000, 5000)

Thus each gives us sets of 100,100,30 trials respectively fo 5,50,5000

Let us compute the the mean of each row which are of size 5, 50, 5000

```
> Rollmeans = apply(Rollm, 2, mean)
```

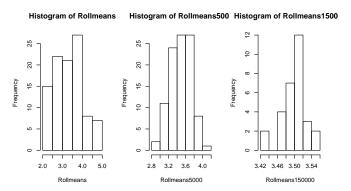
- > Rollmeans5000 = apply(Rollm5000, 2, mean)
- > Rollmeans150000 = apply(Rollm150000, 2, mean)

Mean of Rolls

```
> table(Rollmeans)
Rollmeans
 2 2.2 2.4 2.6 2.8
                    332343638 4424448
                    5 10 11 11
> table(Rollmeans5000)
Rollmeans5000
2.88 3 3.02 3.04 3.06 3.08 3.1 3.12 3.14 3.16 3.18 3.2 3.22 3.24 3.26 3.28
3.64 3.66 3.68 3.7 3.72 3.74 3.76 3.78
                                      3.8 3.82 3.84 3.86 3.88
4.02
> table(Rollmeans150000)
Rollmeans150000
3.4326 3.4334 3.4644 3.474 3.477 3.4774 3.4826 3.4828 3.4844 3.4868 3.4902
3.4912 3.4938 3.5006 3.5016 3.5028 3.503 3.505 3.507 3.508 3.5084 3.5102
 3.511 3.5172 3.5268 3.5316 3.5334 3.5482
```

Centered around 3.5

- > par(mfrow=c(1,3))
- > hist(Rollmeans)
- > hist(Rollmeans5000)
- > hist(Rollmeans150000)



Variance Reduction

Observe that there is real variance reduction in the sample means.

```
> ourvariance(x) # Variance of Uniform (1,2,3,4,5,6)
[1] 2.916667
> var(Rollmeans) # S^2, 100 Trials, mean of 5 Rolls
[1] 0.5527919
> var(Rollmeans5000)# S^2,100 Trials, mean of 50 Rolls
[1] 0.056544
> var(Rollmeans150000) # S^2, 100 Trials, mean of 5000 Rolls
[1] 0.0007484258
```

Suppose we want to verify the below result via simulations:

Let X_1, X_2, \ldots be i.i.d. random variables with finite mean μ , finite variance σ^2 . Then

$$\frac{\sqrt{n}(\bar{X}_n - \mu)}{\sigma} \stackrel{d}{\to} Z, \tag{1}$$

where $Z \sim \text{Normal } (0,1)$.

Suppose we want to verify the below result via simulations:

Let $X_1, X_2, ...$ be i.i.d. random variables with finite mean μ , finite variance σ^2 . Then

$$\frac{\sqrt{n}(\bar{X} - \mu)}{\sigma} \stackrel{d}{\to} Z, \tag{2}$$

where $ar{X} = rac{X_1 + X_2 + \ldots + X_n}{n}$ and $Z \sim$ Normal (0,1).

We could rephrase the result as:

Let $X_1, X_2,...$ be i.i.d. random variables with finite mean μ , finite variance σ^2 . Then

$$\frac{(S_n - n\mu)}{\sqrt{n}\sigma} \stackrel{d}{\to} Z, \tag{3}$$

where $S_n = X_1 + X_2 + \ldots + X_n$ and $Z \sim$ Normal (0,1).

Suppose each X_i was distributed as Bernoulli (p) random variable. Then S_n is a Binomail(n,p) random variable. Let us check for what p does

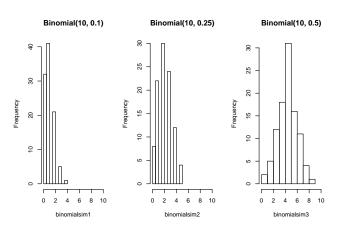
$$\frac{S_n - np}{\sqrt{np(1-p)}}$$

is close to a Normal distribution.

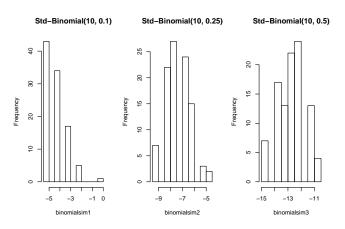
We may simulate Binomial samples either directly by rbinom command or usi ng the replicate and rbinom command.

```
> binomialsim1 = rbinom(100,10,0.1)
> # generates 100 Binomial (10,0.1) samples
>
> binomialsim2 = replicate(100, rbinom(1,10,0.25))
> # generates 100 Binomial (10,0.25) samples
>
 binomialsim3 = replicate(100, rbinom(1,10,0.5))
> # generates 100 Binomial (10,0.5) samples
```

Histogram of all three simulations

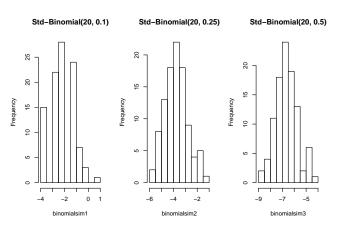


From the above it seems that at n=10 the symmetry is achieved when p=0.5 and not at p=0.1 and p=0.25

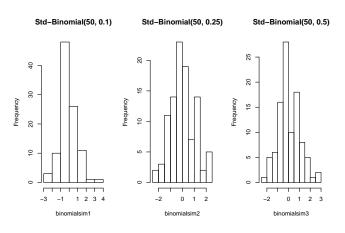


Perhaps n=10 is not large enough to see the Central Limit Theorem occurring.

Standardised Histograms: Binomial n=20 and $p=0.1,\ 0.25,\ 0.5$



n = 20 is better.



n = 50 we get closer to Normal distribution

Role of *n* versus *p*

Binomial Random variable is close to Normal when the distribution is symmetric. That is when p is close to 0.5. Otherwise the general rule that we can apply is that when

$$np \geq 5$$
 and $n(1-p) \geq 5$.

then Binomial(n,p) is close to Normal distribution.

Using the Central Limit Theorem for large n we have

$$P(\mid \frac{\sqrt{n}(\bar{X} - \mu)}{\sigma} \mid \leq 1.96) \approx 0.95$$

which is the same as saying

$$P(\mu \in \left(-\frac{1.96\sigma}{\sqrt{n}} + \bar{X}, \frac{1.96\sigma}{\sqrt{n}} + \bar{X}\right)) \approx 0.95$$

The interval $\left(-\frac{1.96\sigma}{\sqrt{n}} + \bar{X}, \frac{1.96\sigma}{\sqrt{n}} + \bar{X}\right)$ is called the 95% confidence interval for μ .

95% confidence interval for
$$\mu$$
 is $\left(-\frac{1.96\sigma}{\sqrt{n}} + \bar{X}, \frac{1.96\sigma}{\sqrt{n}} + \bar{X}\right)$

Meaning: for n large if we did m (large) repeated trials and computed the above interval for each trial then true mean would belong to approximately 95% of m intervals calculated.

The below is code for finding the confidence interval for a data x.

```
> cifn = function(x, alpha=0.95){
+ z = qnorm( (1-alpha)/2, lower.tail=FALSE)
+ sdx = sqrt(1/length(x))
+ c(mean(x) - z*sdx, mean(x) + z*sdx)
+ }
```

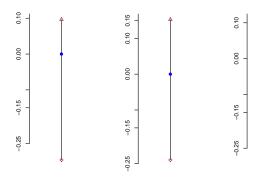
Three Confidence Intervals for Normal(0,1)

```
> x1 = rnorm(100,0,1); y = cifn(x1)
> y
[1] -0.29570433 0.09628847
> x2 = rnorm(100,0,1);z = cifn(x2)
> 7.
[1] -0.2396115 0.1523813
> x3 = rnorm(100,0,1); w = cifn(x3)
> w
[1] -0.2829300 0.1090628
```

Does 0 belong to all the three confidence intervals?

Confidence Intervals Plots

The below is a plot of the three confidence intervals computed in the previous slide.

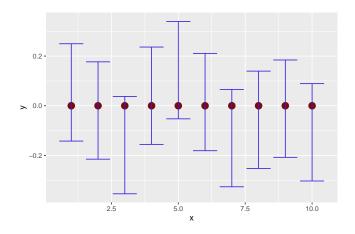


Confidence Intervals: 10 Trials

We generate 10 trials of 100 samples from Normal(0,1) and compute the confidence intervals using the function defined earlier.

```
> normaldata = replicate(10, rnorm(100,0,1),
+ simplify=FALSE)
> cidata = sapply(normaldata, cifn)
It is easy to check how many of them contain 0.
> TRUEIN = cidata[1,]*cidata[2,]<0</pre>
> table(TRUEIN)
TRUEIN
TRUE
  10
```

Confidence Intervals: 10 Trials

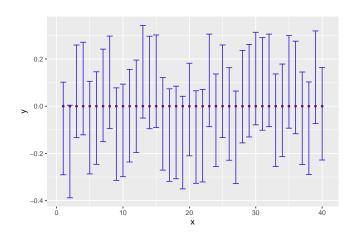


Confidence Intervals: 40 Trials

We generate 10 trials of 100 samples from Normal(0,1) and compute the confidence intervals using the function defined earlier.

```
> normaldata = replicate(40, rnorm(100,0,1),
+ simplify=FALSE)
> cidata = sapply(normaldata, cifn)
It is easy to check how many of them contain 0.
> TRUEIN = cidata[1,]*cidata[2,]<0</pre>
> table(TRUEIN)
TRUEIN
TRUE
  40
```

Confidence Intervals: 40 trials Plot

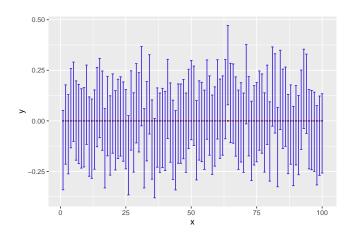


Confidence Intervals: 100 Trials

We generate 100 trials of 100 samples from Normal(0,1) and compute the confidence intervals using the function defined earlier.

```
> normaldata = replicate(100, rnorm(100,0,1),
+ simplify=FALSE)
> cidata = sapply(normaldata, cifn)
It is easy to check how many of them contain 0.
> TRUEIN = cidata[1,]*cidata[2,]<0</pre>
> table(TRUEIN)
TRUEIN
FALSE TRUE
         99
```

Confidence Intervals: 100 Trials

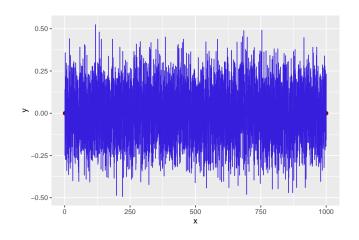


Confidence Intervals: 1000 Trials

We generate 1000 trials of 100 samples from Normal(0,1) and compute the confidence intervals using the function defined earlier.

```
> normaldata = replicate(1000, rnorm(100,0,1),
+ simplify=FALSE)
> cidata = sapply(normaldata, cifn)
It is easy to check how many of them contain 0.
> TRUEIN = cidata[1,]*cidata[2,]<0</pre>
> table(TRUEIN)
TRUEIN
FALSE
      TRUE
   51
        949
```

Confidence Intervals: 1000 Trials



95% confidence interval for
$$\mu$$
 is $\left(-\frac{1.96\sigma}{\sqrt{n}} + \bar{X}, \frac{1.96\sigma}{\sqrt{n}} + \bar{X}\right)$

Meaning: for n large if we did m (large) repeated trials and computed the above interval for each trial then true mean would belong to approximately 95% of m intervals calculated.

Thus numerically the above meaning seems to hold for a Normal population.