Testing for goodness of fit - plant germination probability.

Assuming X= Bi(30, p), where X= number of plants that germinated.

**Estimating P**

> Ob=c(3, 4, 5, 6 ,7 ,8, 9, 10, 11, 12, 13, 17)

> count=c(1, 2, 2 ,4 ,10, 16, 9 ,11 ,13 ,4 ,7, 1)

>total=sum(Ob\*count)

> total/(30\*80)

[1] 0.3054167

Thus my estimate for p=0.3054167 where p is the probability that the plant Germinates.

**Carrying out a goodness of fit test**

**Creating a suitable table to carry out the test**

> prob.type=dbinom(Ob, 30,p) # probability for each observation.

> Expected=80\*prob.type

> Expected=round(Expected)

>Expected # Determining what observations to group

[1] 0 1 3 6 9 12 13 12 9 6 4

[12] 0

>Observations=c(3,4,4,5,5,6,6,6,6,seq(7,7, length.out=10),seq(8,8, length.out=16),seq(9,9, length.out=9),seq(10,10, length.out=11),seq(11,11, length.out=13),12,12,12,12,seq(13,13, length.out=7),17)

> new.Ob=cut(Observations,breaks=c(0,6.5,7.5,8.5,9.5,10.5,11.5,30))

> T1=table(new.Ob)

T1

new.Ob

(0,6.5] (6.5,7.5] (7.5,8.5]

9 10 16

(8.5,9.5] (9.5,10.5] (10.5,11.5]

9 11 13

(11.5,30]

12

p.set=c(pbinom(6.5,30 , prob=p),dbinom(7,30 , prob=p),dbinom(8,30 , prob=p),dbinom(9,30 , prob=p),dbinom(10,30 , prob=p),dbinom(11,30 , prob=p),1-pbinom(11.5,30 , prob=p))

> Ecpt.value=80\*p.set

>Obv.value=T1

> new.table=rbind(Obv.value,Ecpt.value)

> new.table

(0,6.5] (6.5,7.5] (7.5,8.5] (8.5,9.5] (9.5,10.5] (10.5,11.5]

T1 9.00000 10.00000 16.00000 9.0000 11.00000 13.000000

Ecpt.value 11.57233 9.24133 11.68263 12.5571 11.59516 9.270061

(11.5,30]

T1 12.00000

Ecpt.value 14.08138

**Goodness fit test**

H0:Bi(30,p) is a good fit

H1: Bi(30,phat) is not a good fit.

>Chi=sum((Obv.value-Ecpt.value)^2/Ecpt.value)

> 1-pchisq(Chi,df=5)

[1] 0.4087206

Using a significance level of 0.05, we do not have sufficient evidence to to reject the null hypothesis IE the distribution fits the data.