setwd("C:/Users/vmc04/Documents/GitHub/wingproj/lifehist")

lifehist<-read.csv("2017\_09\_28 Life history data file.csv", header=TRUE)

lifehist$Locality=factor(lifehist$Locality, c("ARS","APR","RPV","RMO","TLC","TPN","SJU"))

head(lifehist)

#lifehist larvae life of surviving larvae to adult

lifehist$sLL= ifelse(lifehist$Adult.death!="NA",lifehist$Pupation.date-lifehist$Hatch.day ,NA)

#lifehist preadult length of life if survived to adult (time to emerge)

lifehist$Emtime= ifelse(lifehist$Adult.death!="NA",lifehist$Emergence.date-lifehist$Hatch.day ,NA)

#lifehist preadult length of life if died before adult Preadult.death

lifehist$Preadult.death=ifelse(!is.na(lifehist$PD),lifehist$PD-lifehist$Hatch.day,

ifelse(!is.na(lifehist$LD),lifehist$LD-lifehist$Hatch.day, NA))

#if adult death is NA, then Sex= NA

lifehist$Sex1=ifelse(is.na(lifehist$Adult.death), NA,ifelse(lifehist$Sex=="M",1,0))

#deathstatus is 0=for died preadult, 1= for died as adult

lifehist$Death\_stat=ifelse(is.na(lifehist$Preadult.death), 1,0)

#Rate of adult development

lifehist$AdRate<- (1/lifehist$Emtime)

#Rate of larvae development

lifehist$LarvRate<- (1/lifehist$sLL)

#length of time as pupae

lifehist$Puplen<- lifehist$Emergence.date-lifehist$Pupation.date

#Rate of pupal development

lifehist$Puprate<- (1/lifehist$Puplen)

#rate of development if died as preadult

lifehist$D.pread.rate<- (1/lifehist$Preadult.death)

#length of adult life

lifehist$AL<- lifehist$Adult.death-lifehist$Emergence.date

#print out new datafile

write.csv(lifehist,"C:/Users/vmc04/Documents/GitHub/wingproj/lifehist/2017\_10\_17 Life history data new clean file.csv")