#code for Jaffe et al

library(coxme)

library(car)

library(survival)

#####Experiment 1#############

#data = "expt1"

#explain censoring

expt1$status<-ifelse(expt1$Emergence==18000,0,1)

#test proportional odds assumption

testfit<-coxph(Surv(Emergence,status)~Genotype+frailty(Day),data=expt1)

cox.zph(testfit)

#test for genotype differences

m0<-coxme(Surv(Emergence,status)~1+(1|Genotype)+(1|Day)+(1|Individual),data=expt1)

m0.noG<-coxme(Surv(Emergence,status)~1+(1|Day)+(1|Individual),data=expt1)

#test effect of genotype using likelihood ratio test

anova(m0,m0.noG)

#same approach for effects of Day and Individual

#extract intercept estimates for each genotype to choose for Experiment 2

gs<-ranef(fg1)$Genotype

#####Experiment 2 full model######

#data = "expt2"

#explain censoring

expt2$status<-ifelse(expt2$Time==18000,0,1)

#test proportional odds assumption

testfit <- coxph(Surv(Time,status)~median.partnerG+median.sameG+frailty(Trial) , expt2 = expt2)

cox.zph(testfit,global=T)

#medians refer to the median behavior of same-genotype and partner-genotype group members

m1<-coxme(Surv(Time,status)~median.partnerG+median.sameG+(1|Genotype)+(1|PartnerG)+(1|Trial),expt2=expt2)

#test median.partnerG x Genotype with independent slopes and intercepts

m1.1<-coxme(Surv(Time,status)~median.partnerG+median.sameG+(median.PartnerG|Genotype)+(1|Genotype)+(1|PartnerG)+(1|Trial),expt2=expt2)

#compare models

anova(m1,m1.1)

#correlated slopes and intercepts

m1.2<-coxme(Surv(Time,status)~median.partnerG+median.sameG+(1+median.PartnerG|Genotype)+(1|PartnerG)+(1|Trial),expt2=expt2)

anova(m1.1,m1.2)

#test median.sameG x Genotype with independent slopes and intercepts

m2<-coxme(Surv(Time,status)~median.partnerG+median.sameG+(median.sameG|Genotype)+(1|Genotype)+(1|PartnerG)+(1|Trial),expt2=expt2)

anova(m1,m2)

#correlated slopes and intercepts

m2.1<-coxme(Surv(Time,status)~median.partnerG+median.sameG+(1+median.sameG|Genotype)+(1|PartnerG)+(1|Trial),expt2=expt2)

anova(m2,m2.1)

#test effect of focal genotype

m1.noG<-coxme(Surv(Time,status)~median.partnerG+median.sameG+(1|PartnerG)+(1|Trial),expt2=expt2)

anova(m1,m1.noG)

#test partner genotype

m1.noPG<-coxme(Surv(Time,status)~median.partnerG+median.sameG+(1|Genotype)+(1|Trial),expt2=expt2)

anova(m1,m1.noPG)

#final model = m2. fixed effect inference

Anova(m2,type="3")

######Experiment 2: single-genotype models#####

#test effect of partner genotype for focal genotype NM-14

m14.1<-coxme(Surv(Time,status)~median.partnerG+median.sameG+(1|PartnerG)+(1|Trial),expt2=expt2[which(expt2$Genotype=='14'),])

m14.2<-coxme(Surv(Time,status)~median.partnerG+median.sameG+(1|Trial),expt2=expt2[which(expt2$Genotype=='14'),])

anova(m14.1,m14.2)

#fixed effect inference

Anova(m14.2,type="3")

#repeat for the other 3 genotypes

#fin