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#This code runs the two genotype simulation contained in Collins,  
Jason, Boris Baer and E. Juerg Weber (2013) Economic Growth and  
Evolution: Parental Preferences for Quality and Quantity of  
Offspring, Macroeconomic Dynamics (forthcoming)
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# For further information, contact Jason Collins at  
jason@jasoncollins.org, or visit Evolving Economics http://  
www.jasoncollins.org
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```
#load BB package - used for solving nonlinear equations  
library(BB)
```

```
#initial conditions
```

```
A<-1  
g<-0  
ea<-0  
eb<-0  
e<-0  
La<-0.007  
Lb<-0.7  
L<-La+Lb  
qa<-La/L  
qb<-Lb/L  
za<-1.25  
zb<-1.25  
na<-1  
nb<-1
```

```
#parameters
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```
Ba<-1  
Bb<-0.9  
alpha<-0.4  
Tau<-0.2  
rho<-0.99  
a<-rho*Tau  
m<-2  
gamma<-0.259  
k<-8.885139596  
r<-0.108150721  
X<-1  
sc<-1  
zsc<-sc/(1-gamma)  
time<-200 #number of generations
```

```
#Build data frame which will be used to store results  
Growth<-data.frame(time=0, A, g, ea, eb, La, Lb, na, nb, za, zb)
```

```
#establish a loop  
for (t in 1:time) {
```

```
# population
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```
La<-na*La  
Lb<-nb*Lb  
L<-La+Lb
```

```

qa<-La/L
qb<-Lb/L

# technology in this period (based on education given to children in
last period)
e<-qa*ea+qb*eb
g<-k*e^0.5
A<-(1+g)*A

# human capital
ha<-(m*ea+a)/(ea+r*g+a)
hb<-(m*eb+a)/(eb+r*g+a)

#level of education of each genotype
ea<-max(0, (1/(2*m))*((Ba*m*r*g+Ba*m*a-Ba*a-m*r*g-a*m-a)+(((Ba*m*r*g
+Ba*m*a-Ba*a-m*r*g-a*m-a)^2+4*m*(Ba*m*r*g* Tau+Ba*m*a* Tau-Ba*a* Tau-
a*r*g-a^2))^0.5)))
eb<-max(0, (1/(2*m))*((Bb*m*r*g+Bb*m*a-Bb*a-m*r*g-a*m-a)+(((Bb*m*r*g
+Bb*m*a-Bb*a-m*r*g-a*m-a)^2+4*m*(Bb*m*r*g* Tau+Bb*m*a* Tau-Bb*a* Tau-
a*r*g-a^2))^0.5)))

#calculate possibilities for income for genotype a (and given
zb=za*hb/ha)
#if subsistence constraint binding for neither
zaa1b1<-(((A*X)/(L*(1-gamma)*(qa*ha+(1-qa)*hb)))^alpha)*ha
zba1b1<-zaa1b1*hb/ha
if(zaa1b1>=zsc & zba1b1>=zsc) za<-zaa1b1

#if subsistence constraint binding for type b
fzaa1b2<-function(zaa1b2){
y<-(((A*X)/(L*((1-gamma)*qa*ha)+(1-qa)*sc/zaa1b2*ha)))^alpha)*ha-
zaa1b2
y
}
ansfzaa1b2<-multiStart(c(0.2,1,10,100),fzaa1b2, control=list(M=200),
quiet=TRUE)
zaa1b2<-max(ansfzaa1b2$par[,1], ansfzaa1b2$par[,2], ansfzaa1b2$par[,
3], ansfzaa1b2$par[,4])
zba1b2<-zaa1b2*hb/ha
if(zaa1b2>=zsc & zba1b2>=sc & zba1b2<zsc) za<-zaa1b2

#if subsistence constraint binding for both types
fzaa2b2<-function(zaa2b2){
y<-(((A*X)/(L*((sc/zaa2b2*qa*ha)+(1-qa)*sc/zaa2b2*ha)))^alpha)*ha-
zaa2b2
y
}
ansfzaa2b2<-multiStart(c(0.2,1,10,100),fzaa2b2, control=list(M=200),
quiet=TRUE)
zaa2b2<-max(ansfzaa2b2$par[,1], ansfzaa2b2$par[,2], ansfzaa2b2$par[,
3], ansfzaa2b2$par[,4])
zba2b2<-zaa2b2*hb/ha
if(zaa2b2>=sc & zaa2b2<zsc & zba2b2>=sc & zba2b2<zsc) za<-zaa2b2
if(zaa2b2<sc) za<-0

```

```

#given income for genotype a, calculate income for genotype b
zb<-za*hb/ha

#population growth
if(za>=zsc) na<-gamma/(Tau+ea)
if(za<zsc & za>sc) na<-(1-(sc/za))/(Tau+ea)
if(za<=sc) na<-0
if(zb>=zsc) nb<-gamma/(Tau+eb)
if(zb<zsc & za>sc) nb<-(1-(sc/zb))/(Tau+eb)
if(zb<=sc) nb<-0

Growth<-rbind(Growth, c(t, A, g, ea, eb, La, Lb, na, nb, za, zb))
}

write.table(Growth,file="Growth.txt", sep = ",")

Growth

```