CKMR model equations

# Where,

Y = number of observed matches (half siblings)

a = older birth year,

b = younger birth year,

*γ* = year of estimation (arbitrary),

N*γ* = number of females in estimation year,

λ(b – *γ*) = population change between year of estimation and birth year b,

ϕ (b-a) = expected survival from birth year a (older) to birth year b (younger),

= total number of comparisons between individuals born in year a and individuals born in year b.

Model

model {

Nf ~ dnorm(0, tau) # why not make this negative binomial?

Nm ~ dnorm(0, tau) # ditto

surv ~ dbeta(1, 1)

for (i in 1:mom\_yrs) {

MHSP[i] ~ dbin((surv^(mom\_ys\_birth[i] - mom\_os\_birth[i]))/(Nf \* lam^(mom\_ys\_birth[i] - min\_cohort)), mom\_n\_comps[i])

}

for (j in 1:dad\_yrs) {

FHSP[j] ~ dbin((surv^(dad\_ys\_birth[j] - dad\_os\_birth[j]))/(Nm \* lam^(dad\_ys\_birth[j] - min\_cohort)), dad\_n\_comps[j])

}

}

Nf # number of mature females in estimation year [i.e. *Nγ*]

Nm # number of mature males in estimation year

surv # annual survival of mature males and females

mom\_yrs # number of comparison years to loop over [e.g., *a* vs *b*]

MHSP # observed positive maternal half-sibs [i.e. ]

surv^( mom\_ys\_birth[i] - mom\_os\_birth[i]) # expected survival of mature female between comparison years [i.e. ]

lam^(mom\_ys\_birth[i] - min\_cohort) # expected population change between estimation year and younger sibling year [i.e. λ(b – *γ*)]

mom\_n\_comps # number of maternal comparisons between specified years [i.e. ]