# CKMR model equations

## Uninformative prior

# Where,

N = adult abundance (sex-specific)

Y = number of observed matches (half siblings)

R = number of pairwise comparisons

a = older birth year,

b = younger birth year,

c = difference between older birth year and younger birth year,

*γ* = year of estimation (arbitrary),

*ɸ* = survival

## Hierarchical model

# Where,

N = adult abundance (sex-specific)

Y = number of observed matches (half siblings)

R = number of pairwise comparisons

a = older birth year,

b = younger birth year,

c = difference between older birth year and younger birth year,

*γ* = year of estimation (arbitrary),

*ɸ* = survival

**C** = conversion factor

Model

#---------------Calculating mean and sd on abundance prior------------------

#Positive comparisons

mom\_positives.gap <- positives %>% filter(Ind\_1\_mom == Ind\_2\_mom) %>%

mutate(yr\_gap = Ind\_2\_birth - Ind\_1\_birth) %>%

dplyr::select(yr\_gap) %>%

plyr::count()

#Negative comparisons

mom\_negatives.gap <- pairwise.df\_all.info %>% filter(Ind\_1\_mom != Ind\_2\_mom & Ind\_1\_birth != Ind\_2\_birth) %>% #filter for same cohort is repetitive

mutate(yr\_gap = Ind\_2\_birth - Ind\_1\_birth) %>%

dplyr::select(yr\_gap) %>%

plyr::count()

mom\_comps.gap <- mom\_positives.gap %>%

rename(yes = freq) %>%

full\_join(mom\_negatives.gap, by = "yr\_gap") %>%

rename(no = freq) %>%

mutate(yes = replace\_na(yes, 0), no = replace\_na(no, 0)) %>%

mutate(all = yes + no) %>%

filter(yes > 0)

mc <- mom\_comps.gap %>% mutate(all.adj = all \* (Adult.survival^yr\_gap)) %>%

mutate(mom.N = all.adj/yes)

mc.all <- sum(mc$all.adj)

mc.pos <- sum(mc$yes)

mc.mean <- mean(mc$mom.N)

mc.prior <- mc.all/mc.pos #Mean of normal distribution for prior on abundance

mc.sd <- sd(mc$mom.N) #standard deviation of normal distribution for prior on abundance

#------------------JAGS data---------------------------

mc.prec = 1/(mc.sd^2),

lam.tau <- 1/(0.02277^2) #Value derived from Leslie matrix

#Moms - year specific

MHSP = mom\_comps$yes, # Positive maternal half-sibs; Y

mom\_n\_comps = mom\_comps$all, # Number of total maternal comparisons; R

mom\_ys\_birth = mom\_comps$Ind\_2\_birth, # birth year of younger sib; b

mom\_os\_birth = mom\_comps$Ind\_1\_birth, # birth year of older sib; a

mom\_yrs = nrow(mom\_comps), # number of cohort comparisons to loop over

#------------------CKMR model----------------------

#PRIORS

Nf ~ dnorm(mc.prior, mc.prec)

surv ~ dbeta(1 ,1) # Uninformative prior for adult survival

lam ~ dnorm(1, lam.tau)

#Likelihood

for(i in 1:mom\_yrs){ # Loop over maternal cohort comparisons

MHSP[i] ~ dbin((surv^(mom\_ys\_birth[i] - mom\_os\_birth[i]))/(Nf\*lam^(mom\_ys\_birth[i]-est.year)), mom\_n\_comps[i]) # Sex-specific CKMR model equation

}