# CKMR model equations

**Maternal half-sibling**

**Mother-offspring**

**Father half-sibling/parent-offspring**

# Where,

**YHS a,b** = number of observed half-sibling matches between cohorts born in year a (older) and year b (younger).

**δ** = potential mortality years

**ɸ(δ)** = annual survival over year gap δ,

**γ** = year of estimation (arbitrary),

**NB***γ*= number of breeders in year *γ*

**λ(b-*γ*)** = population growth between the birth year of cohort b and γ

**Ra,b** = total number of pairwise comparisons between individuals sampled in year a and year b (na\*nb)

**ψ** = proportion of population that exhibits biennial breeding

**ζ** = percentage of total population available to breed

We account for skipped-breeding with parameter ψ, which represents the proportion of the population that breeds on a biennial cycle. This introduces a subtle difference between the HS probabilities and the PO probabilities, as we are now estimating the number of breeding individuals with the HS model, whereas the PO model estimates the total number of adults, whether they bred or not. We account for this by including a parameter ζ, which is the proportion of the total adult population that bred in year γ.

In the HS model, δ represents the number of years between the birth year of cohort a and cohort b; in the PO model, δ represents the number of years between the parent capture year and the offspring birth. If the parent was captured after the offspring birth year and was mature during the year the offspring was born, then we know the individual was a potential parent to that offspring in its birth year, and δ is set to 0, thereby reducing the numerator to 1.