



- Full sibs i and j do not inherit the same sample of alleles from parent s and d
- Breeding values for i and j :

$$u_i = \frac{1}{2} u_s + \frac{1}{2} u_d + \boxed{m_i}$$

$$u_j = \frac{1}{2} u_s + \frac{1}{2} u_d + \boxed{m_j}$$

→ Mendelian

Sampling Term
and it corresponds
to the derivation of
a single breeding value
from the full sib average

Matrix in R:

`mat <- matrix(olata = c(1:9)`

`{nrow = 3
ncol = 3}`

mat has 3 rows and
3 columns

1 1 2 3

numbers to be
placed in
the matrix