Estimating age-at-death of humans from tooth-wear

Andrew Millard

and

Rebecca Gowland

Department of Archaeology

University of Durham

Age estimation

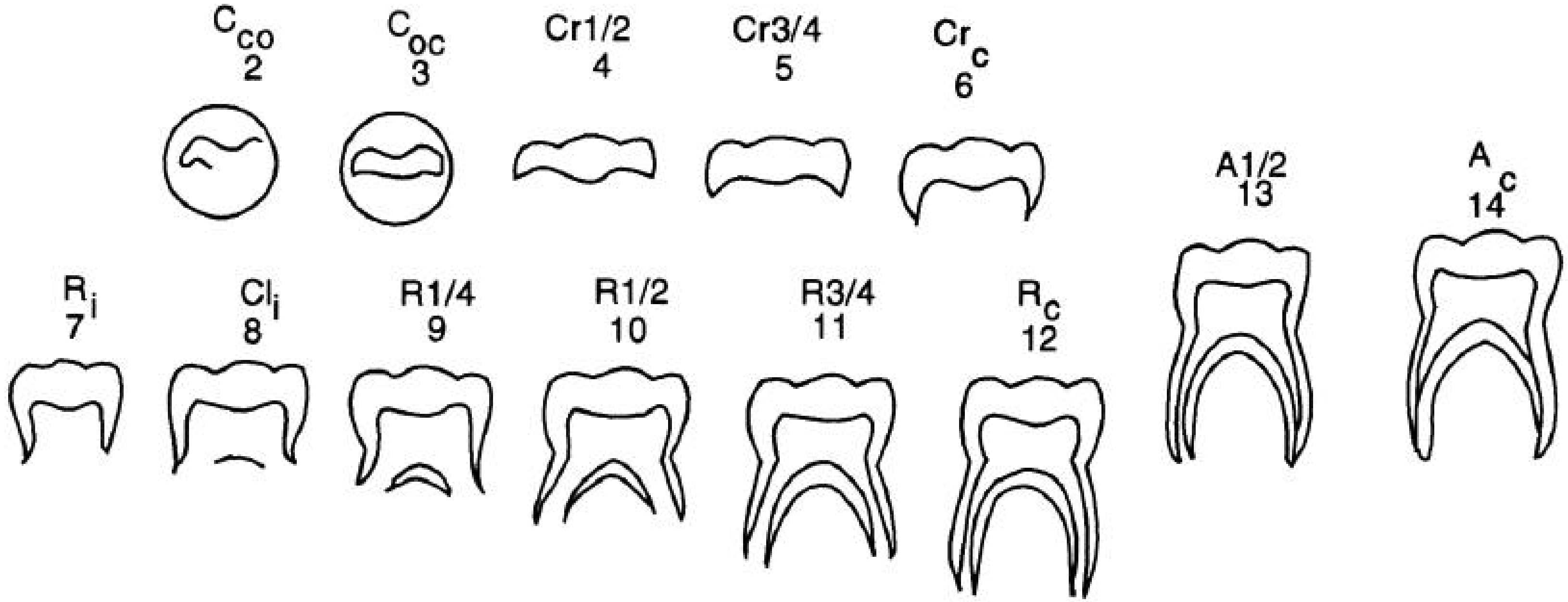
- key procedure in human osteoarchaeology
- many methods
  - most use a modern *reference population* to estimate ages of archaeological *target population*
  - for juveniles based on growth and development
    e.g. fusing of bones, development of teeth
  - for adults based on degeneration
    e.g. changes to joint surfaces, tooth-wear

Age estimation

- key procedure in human osteoarchaeology
- many methods

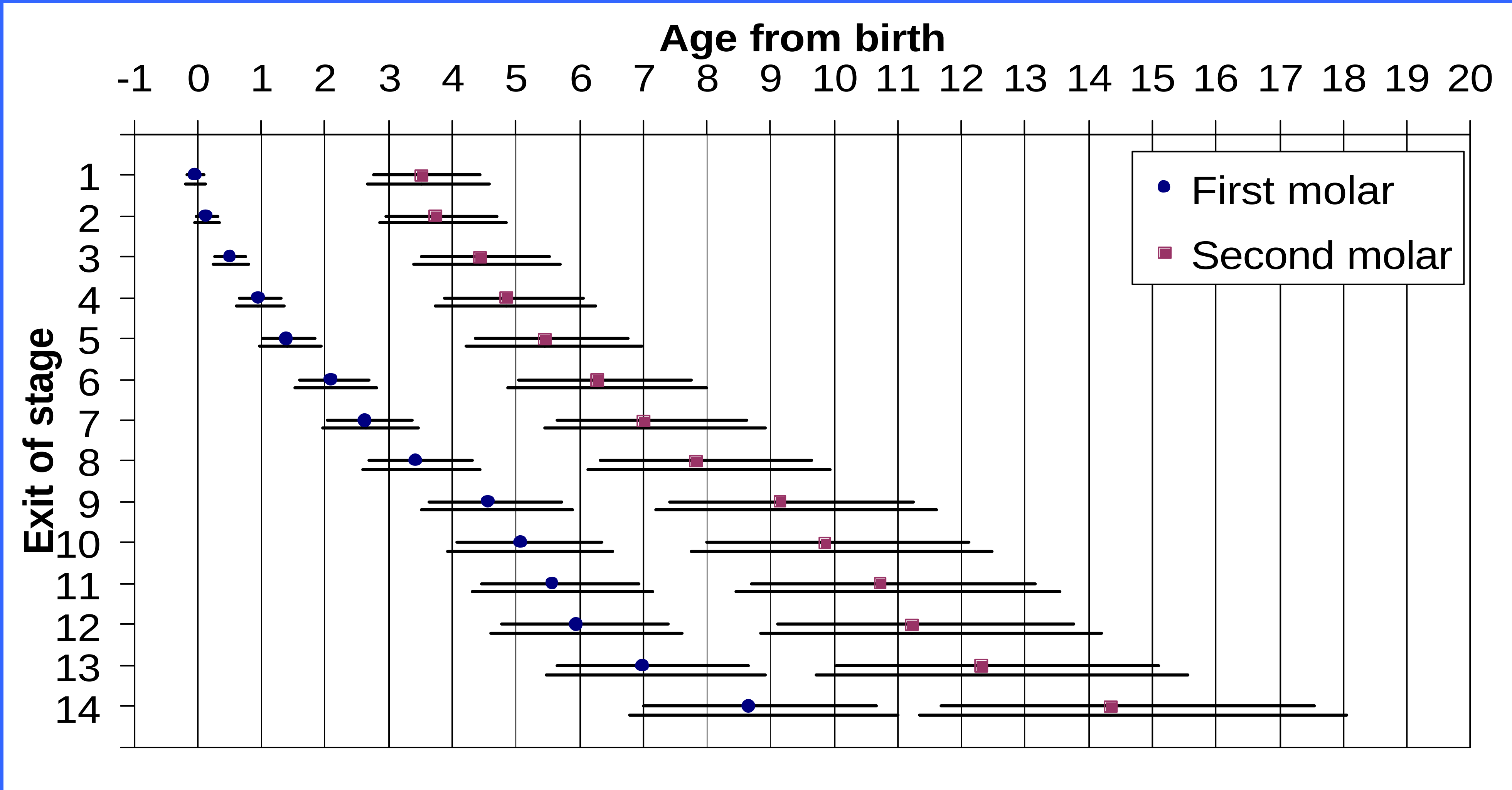
> “nearly all methods of ageing in current use do not make proper use of the statistical nature of age estimates … age estimation is a process of generating the *distribution* of possible chronological ages for a skeleton.”
>
> (Konigsberg & Holman 1999)

Tooth development

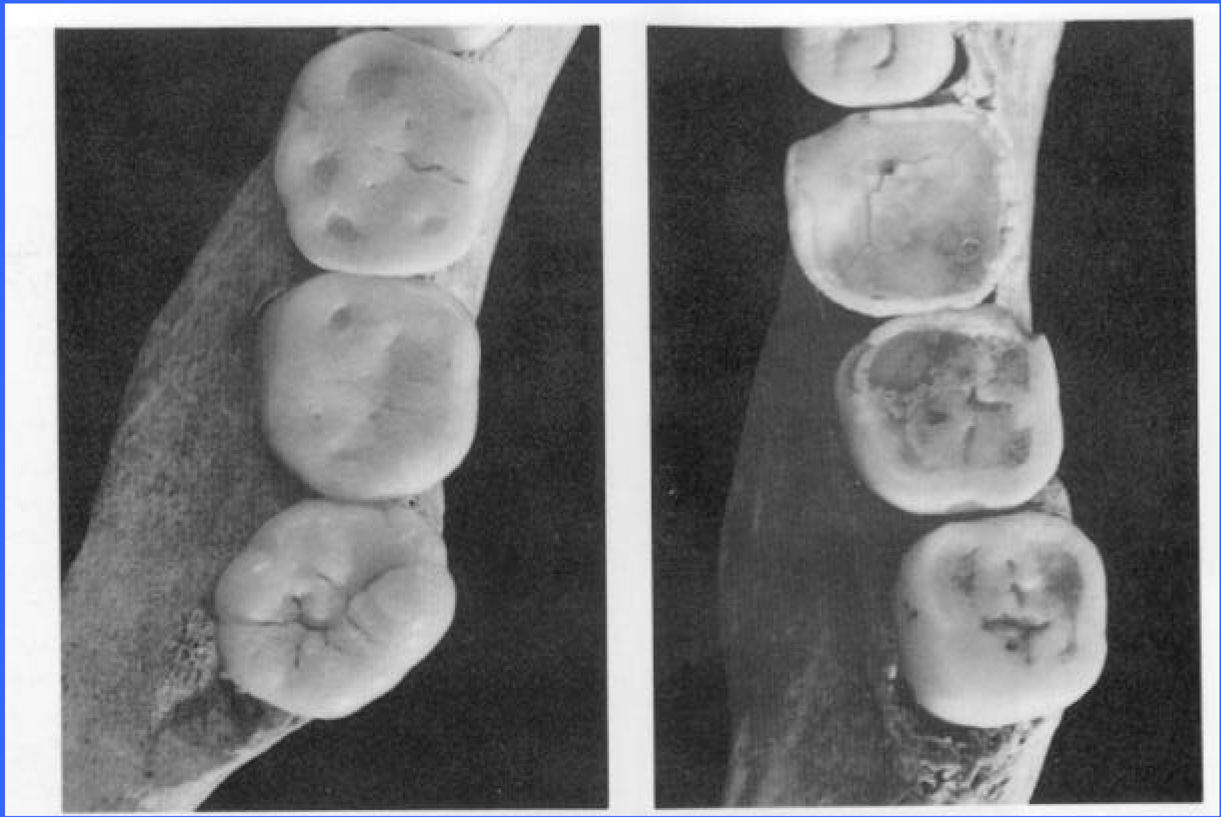


Code	Stage	Code	Stage
1	Initial cusp formation	8	Initial cleft formation
2	Coalescence of cusps	9	Root length 1/4
3	Cusp outline complete	10	Root length 1/2
4	Crown 1/2 complete	11	Root length 3/4
5	Crown 3/4 complete	12	Root length complete
6	Crown complete	13	Apex 1/2 closed
7	Initial root formation	14	Apex closed

Age thresholds for development



Tooth wear

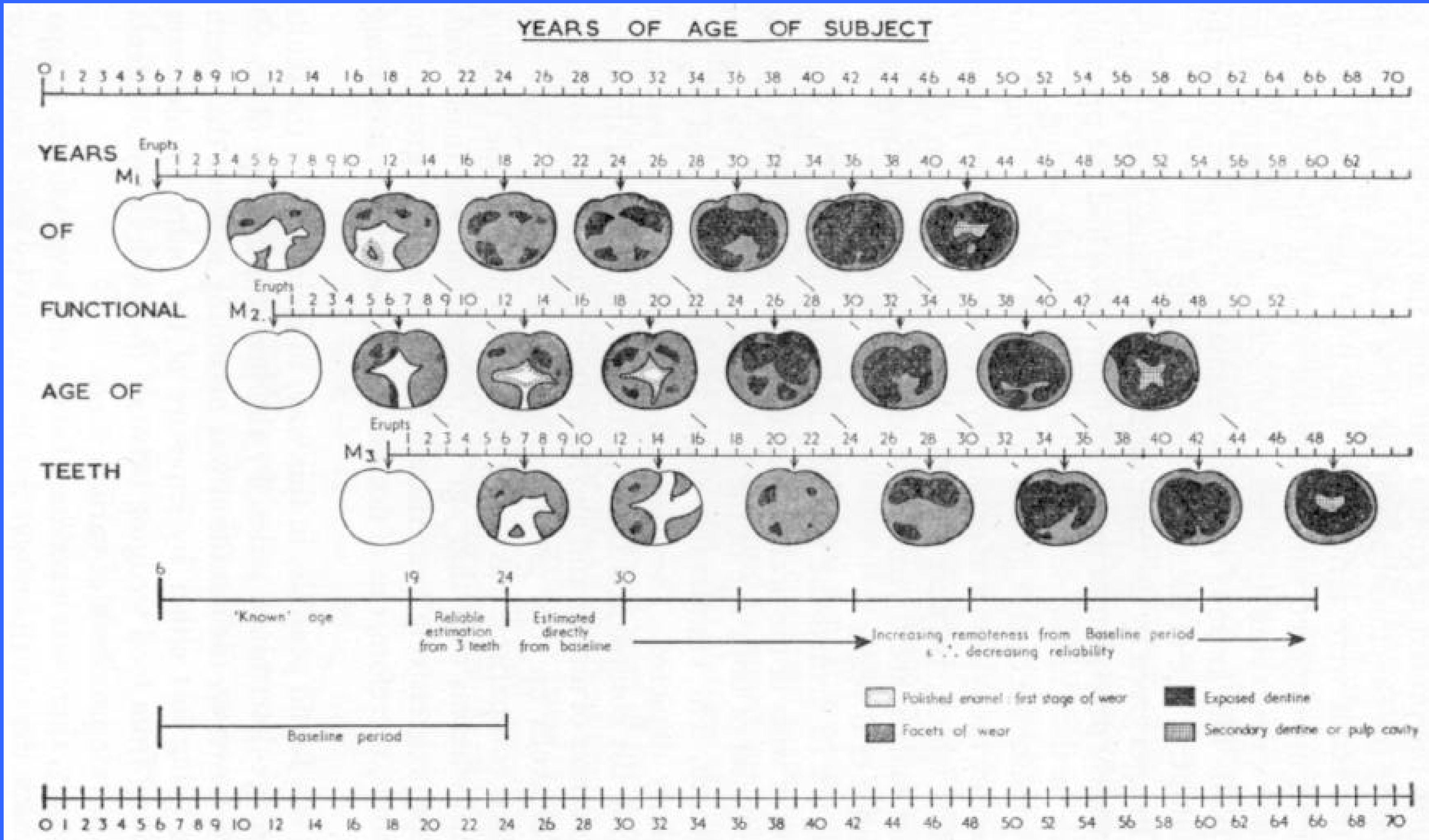


approx. 18 years approx. 40-50 years

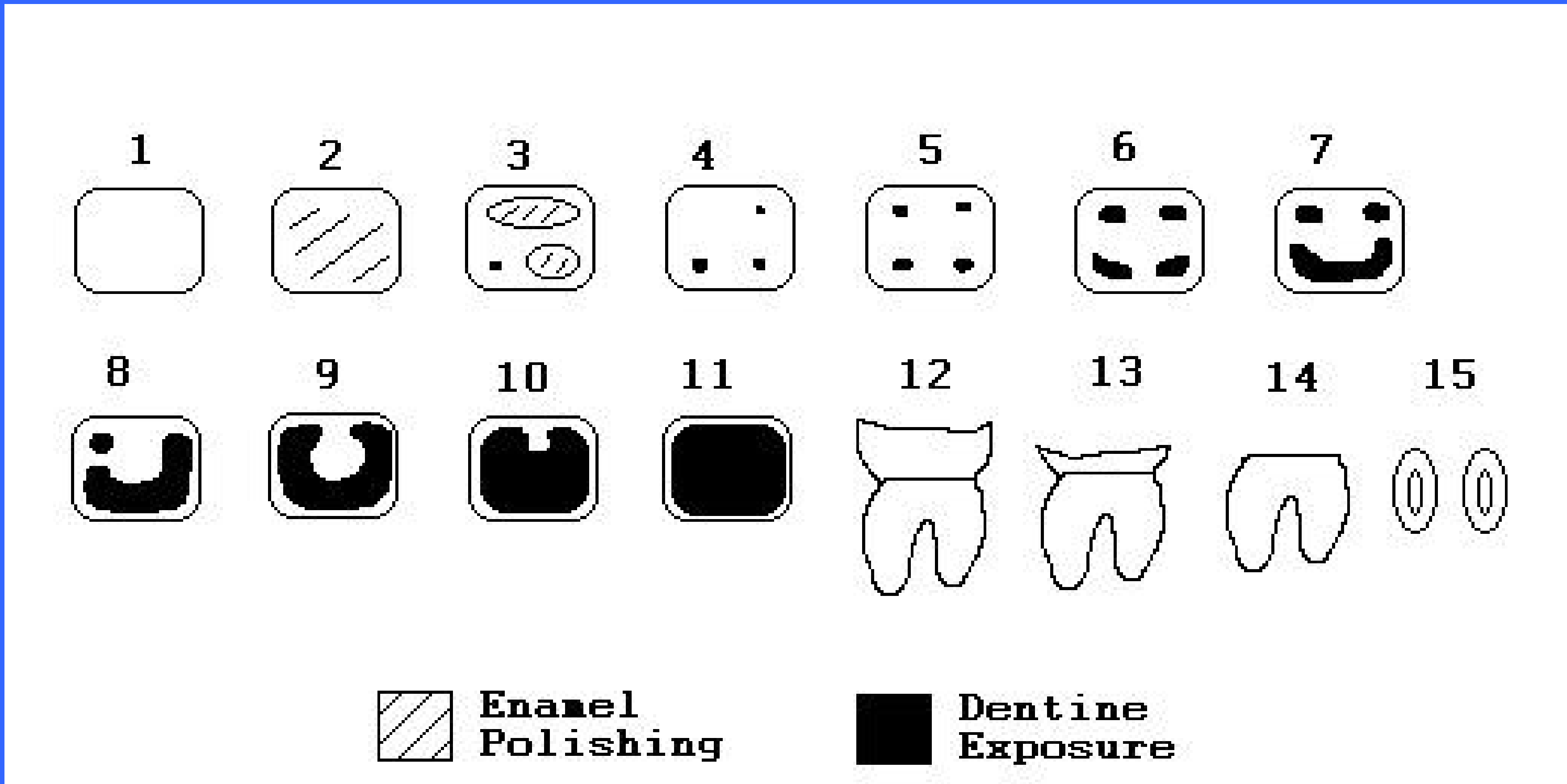
Ageing from tooth wear

- No reference population
- Miles’ (1963) method
  - age younger people from tooth development
  - M1, M2 and M3 erupt at ~6 year intervals
  - estimate ages for early wear stages on M1 & M2
  - assume same wear stage at same functional age
  - 18-24 and 24-30 year olds can be aged
  - extrapolate to older and older ages

Miles' method



Tooth wear thresholds



Model for development ages

Generic model for tooth development and wear:

$$\text{logit}(Q_{i,j,k}) = d \times [\ln(q_i) - \ln(g_{j,k})]$$

$$p_{i,j,k} = Q_{i,j,k-1} - Q_{i,j,k}$$

where

q_i is the age of individual i in years from conception

$g_{j,k}$ is the mean threshold for tooth j leaving stage k

d is the discriminability which measures the population variability

The data

- Recorded >1000 individuals from AD 300-500
- 488 suitable individuals (i.e. molars with no significant caries, no ante-mortem loss)
- recorded stage of development of upper permanent dentition and lower incisors
- recorded wear of all molars present
- much tooth loss: 23% of development data missing, 22% of wear data missing

Our Bayesian approach

Priors:

q_i : uniform on (0,100)

model life table prior possible

$g_{j,k}$: known for development

d : approximated from Moorees *et al.* (1963)

missing data has prior implied by prior on q

Results:

posterior confidence ranges for ages from birth

Bayesian version of Miles' method

- model as for development
- regression to estimate thresholds
- relate M1, M2 and M3 thresholds via functional ages:

$$g_{j,k} = g_{j,1} + a_j \times (g_{M1,k} - g_{M1,1}), \qquad j=M2, M3$$

- prior on $g_{M1,k}$ is $g_{M1,k-1} < g_{M1,k} < g_{M1,k+1}$ with 0 and 100 as limits on first and last values
- $a_j = 1$ or from Miles $a_{M2} = 6/6.5$, $a_{M3} = 6/7$
- calculate stepwise through ages like Miles

Implementation

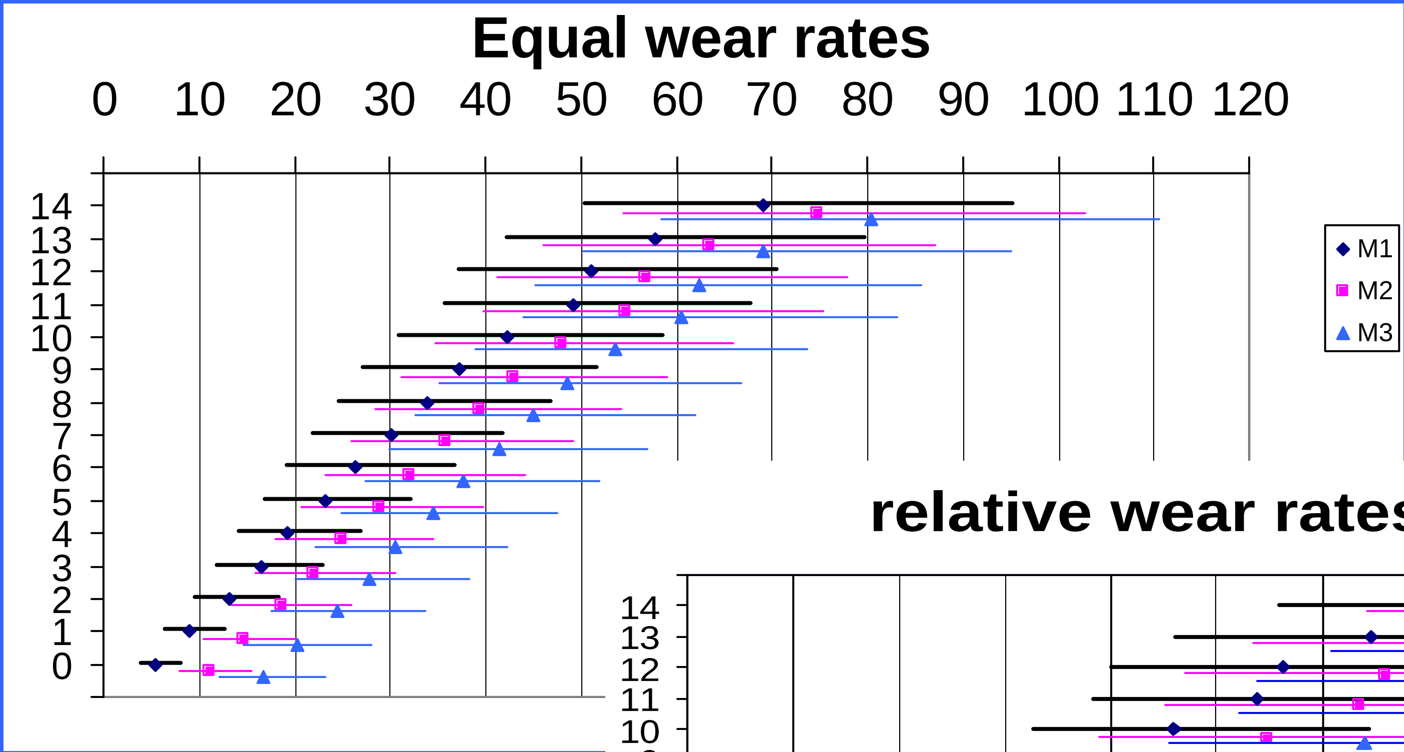
Series of WinBUGS models derived from *Bones* example:

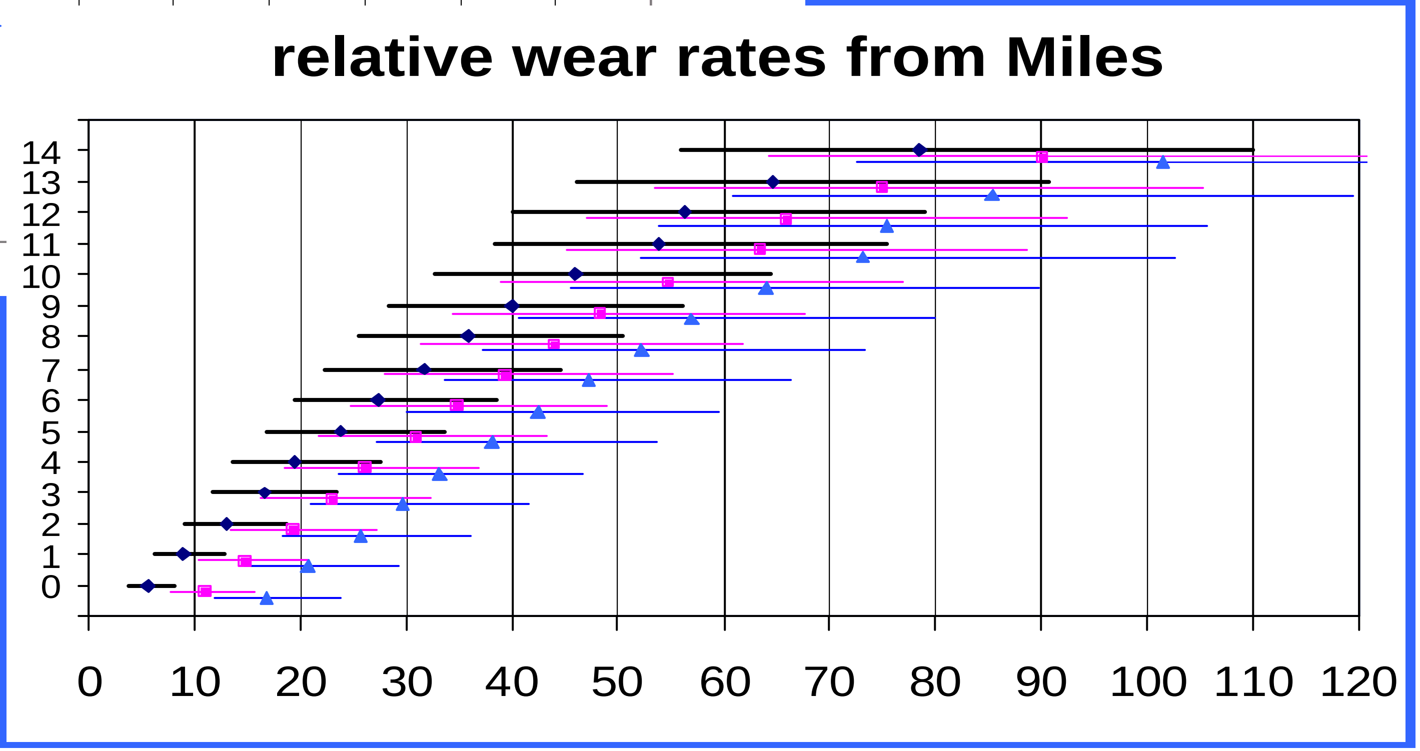
- 0: development alone where incomplete development
- 1: regression for thresholds 1-5
- 2: regression for thresholds 6-12 using mean γ from 1
- 3: regression for thresholds 13-15 using mean γ from 2

Missing values handled easily

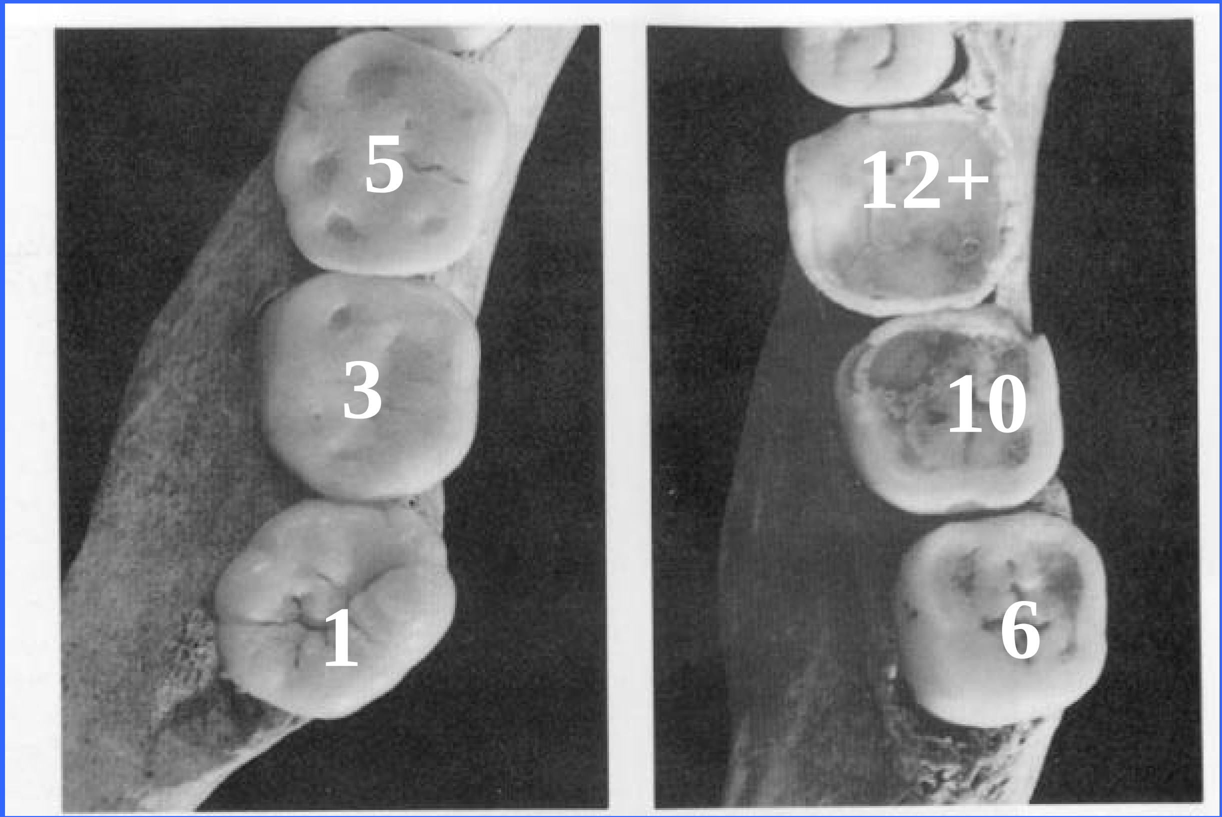
Use age divided by 10 to improve convergence

Toothwear ageing results





Tooth wear results



approx. 18 years approx. 40-50 years

our estimates:	18-22 years	43-54 years	(equal rates)
	17-21 years	48-61 years	(Miles' Rates)

Problems and limitations

- estimating a_j from data produces large values
- discriminability assumed constant for all wear stages and molars
- assume thresholds in different teeth are independent
  - known not to be true for eruption
- use of logit rather than probit

Future development

- Comparisons with other ageing methods
- Combination with other ageing methods
- Hyperpriors on q :
  - current method estimates individual ages
  - palaeodemographers are interested in the population age distribution: put a prior on that
- Extension to other species

Conclusions

- Our Bayesian method gives:
  - more realistic age estimation, with less underestimation of age
  - accounts for missing data
  - improved estimates of uncertainties
  - ability to estimate other age-dependent population parameters