Note

Age distribution estimation given molar stages for males and females for five ethnic groups

Upper (maxillary)

Right   Left

Lower (mandibular)

Incisors
Canines
Premolars
Molars

Authors

Senior Research Scientist Ingunn F. Tvete, The Norwegian Computing Center.

Professor Lyle W. Konigsberg, University of Illinois at Urbana-Champaign.

Reader in Dental Anthropology Helen M. Liversidge, Institute of Dentistry, Queen Mary University of London

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Authors	**Ingunn F. Tvete, Lyle W. Konigsberg, Helen M. Liversidge**
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Abstract

Teeth mature at more or less predictable rates and can therefore be used for age estimation of individuals. This note deals with deriving chronological age distributions given molar stages, and provides a mathematical framework for doing so. We describe a two-step procedure, as given by Lyle Konigsberg. We estimated chronological age distributions for molar stages for males and females for five ethnic groups. Tests for detecting differences between ethnic groups and genders are presented.

This note does not discuss how age assessment of individuals is actually done. That is, the age assessment procedure in real life is a separate issue not covered in this note.

NR **Age distribution estimation given molar stages for males and females for five ethnic groups**

Table of Content

1 Introduction

Teeth mature at more or less predictable rates and are being used for age estimation of individuals. The development of a tooth can be divided into a series of maturity stages, see Liversidge (2008) for details. In practical work, a tooth's given maturity stage is matched with a reference table of stages and from this the individual's age is estimated. Because of individual variation in the rate of tooth development, the chronological age of an individual with a given tooth in a given stage cannot be predicted accurately.

The main purpose of this note is to compare chronological age distributions for molar stages across ethnic groups. This note will hence provide an approach for deriving the conditional chronological age distribution (age conditional on molar stage). For deriving these age distributions we conducted separate analyses for males and females for different ethnic populations. We considered data from two different teeth (second and third molar in lower jaw) separately. The age range was 10 to 26 years. We will present estimated chronological age distributions for molar stage 12 (root three quarters formed) through stage14 (root apex half closed) for the second molar and stage 5 (crown half formed) through stage14 (root apex half closed) for the third molar (due to features in the estimation procedure no results for stage 15 will be given, see section 3 for details). See section 3 for further details regarding age estimation for different stages.

The data is presented in section 2 and the age estimation procedure is described in section 3. In section 4 we present the estimated age distributions given molar stage. In section 5 we consider the estimated probability for being 18 years or older for a given molar stage and in section 6 we consider possible differences between ethnic groups and genders. In section 7 contain some sensitivity analyses. A summary and discussion is given in section 8.

The statistical software R and WinBUGS have been used for deriving the age distributions, see the reference list at the end of the note for details. A probit model was fitted in R for deriving mean ages for transitions between stages and in WinBUGS age distributions given the molar stages were derived with input from the fitted probit model described as known parameters. This latter Bayesian procedure makes an a priori vague assumption regarding the age distribution. This is discussed further in section 3.

This note deals with deriving age distributions given molar stage, and provides a mathematical framework for doing so. It does not discuss how age assessment of individuals is actually done. That is, the age assessment procedure in real life is a separate issue not covered in this note.

Helen M. Liversidge has provided the data, which consist of individuals with known chronological ages and molar stage scores, were the scores were made from orthopantomograms (OPGs) of the lower jaw (mandible). The scoring was performed in collaboration with international colleagues. Lyle W. Konigsberg has provided the statistical method and helpfully shared R and WinBUGS code. Ingunn F. Tvete has conducted the analysis and written the note.

2 Data

This analysis concerns real data; initially 4561 individuals with known chronological age and developmental scores from second and third molar stages (left mandibular teeth), for details see table 3. The chronological age was calculated from date of birth and date of radiographic examination; although for some Africans (369 Nigerians and 229 South Africans) only year of birth was available. In the latter case it was assumed that they were half way into their year, i.e. if aged 7 years then he/she was assumed to be 7.5 years old. The data for analysis was collected and molars scored by Helen Liversidge in collaboration with Morenike Ukfong Folayan and Abiola Adeniyi in Nigeria, Ibrahim Ngom in Senegal, Yuko Mikami, Yuki Shimada and Kazuto Kuroe in Japan and Kalai Pearisammy in Malaysia. The molar stages range from stage 1 (crypt formation) to stage 15 (root apex closed), see Liversidge (2008) for details and further description. Part of these data have been analysed in previous work, Liversidge (2008) and Liversidge (2010). We considered the following ethnic groups:

1) Sub-Saharan African (Nigeria, South Africa and Senegal),
2) Japanese,
3) Malaysian,
4) White/European UK and
5) Bangladeshi UK.

We first present the third molar data and then the second molar data. This is because the third molar data covers most stages.

2.1 The third molar data
Table 1 displays the number of males and females in each of the five ethnic groups.

Table 1. Number of records for males and females for the five different ethnicities for the third molar.					
Ethnic group					
	Sub-Saharan African	Japanese	Malaysian	White/ European UK	Bangladeshi UK
Males	649	193	402	413	317
Females	718	307	554	579	298

Figure 1 and 2 display the actual age versus developmental stage for each ethnic group for males and females respectively. When plotting these data *overplotting*, that is plotting individuals with same age and stage on top of each other, could give a wrongful picture of the amount of data at each age and stage. It is therefore useful to jitter the data and hence making it easier to see the age versus stage-pattern. (Still, it is important to remember jittering means adding additional noise to the data –this is solely for easy visualization of data).
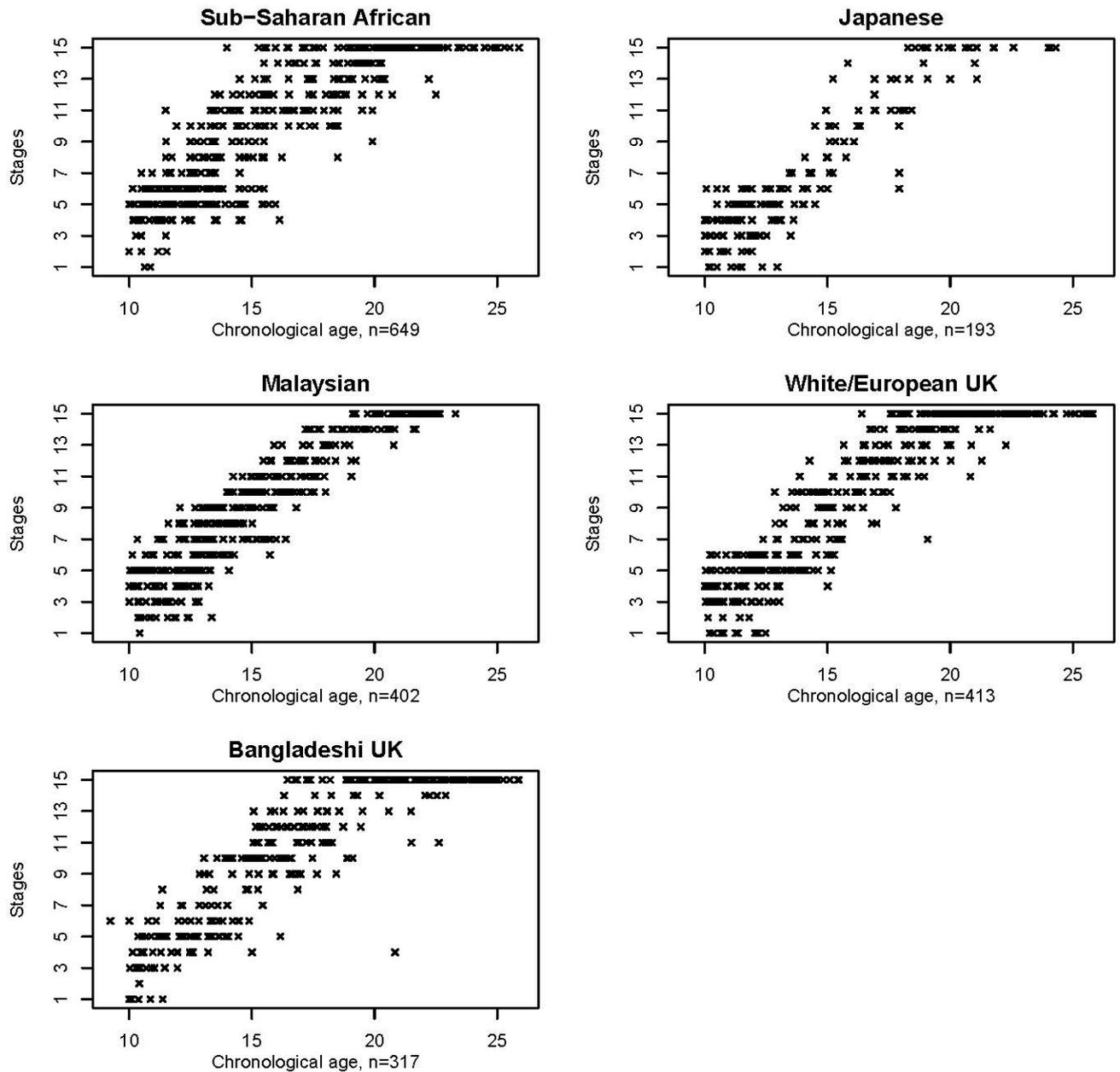
Figure 1. The chronological age versus developmental stage for the third molar for males (clusters of data points indicate several observations).

We see in figure 1 that there were few recordings for Japanese males, especially for the later molar stages, compared to the other ethnic groups. We therefore omit the Japanese recordings for males from the analysis. All the five ethnic groups are analysed for females.

For some of the ethnic groups there were few recordings for stages one and two. For simplicity we have therefore merged these two stages into one stage. The focus is to derive age distributions for later stages so this is unproblematic. For a discussion on this, see the sensitivity analyses in section 7.

Molar 3, females
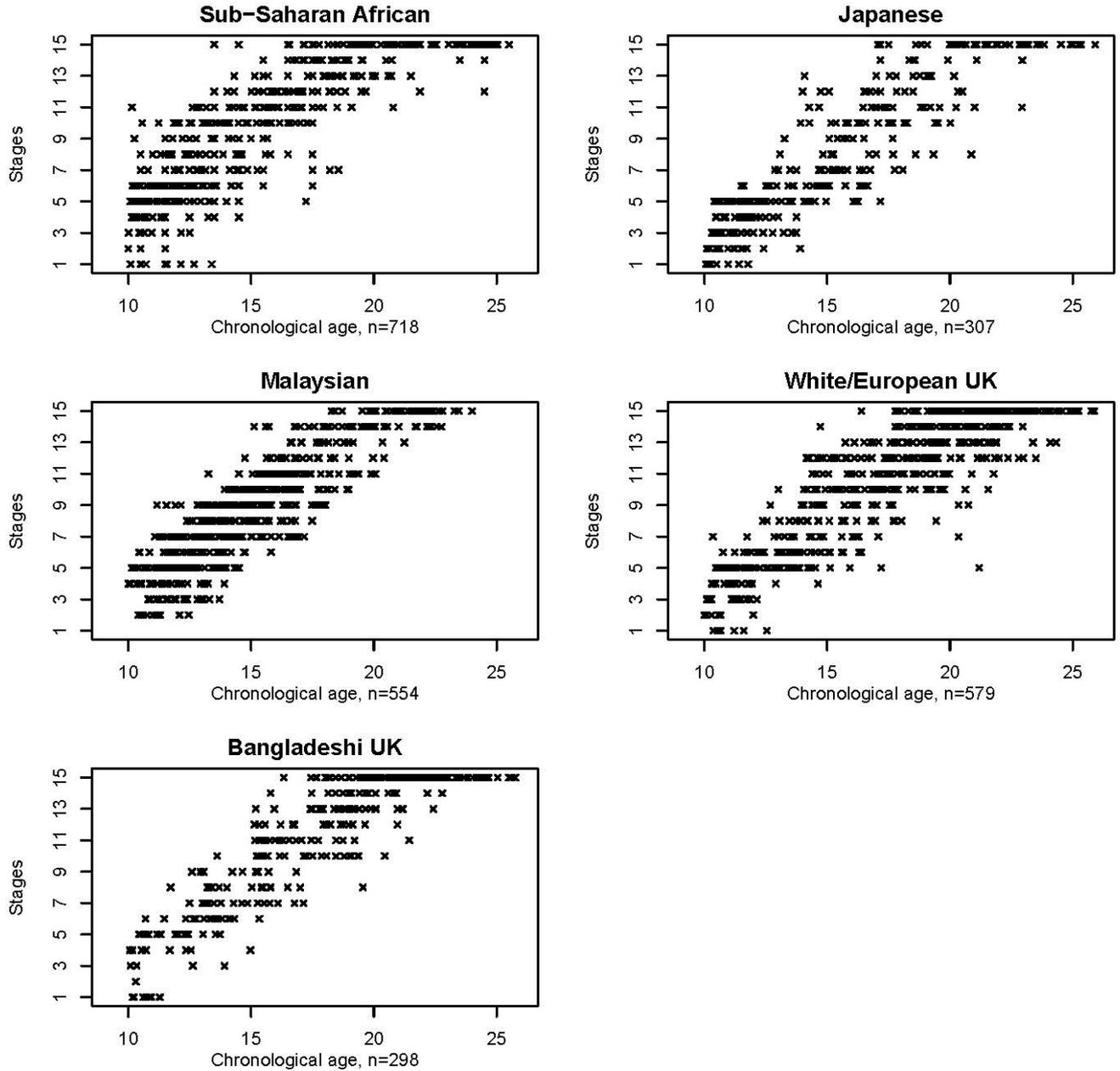
Figure 2. The chronological age versus developmental stage for the third molar for females (clusters of data points indicate several observations).

2.2 The second molar data

Table 2 displays the number of males and females in each of the five ethnic groups.

Table 2. Number of records for males and females for the five different ethnicities for the second molar.					
Ethnic group					
	Sub-Saharan African	Japanese	Malaysian	White/ European UK	Bangladeshi UK
Males	642	219	402	430	311
Females	700	336	554	606	288

Figure 3 and 4 display the age versus molar stage for the ethnic groups for males and females respectively.

Molar 2, males
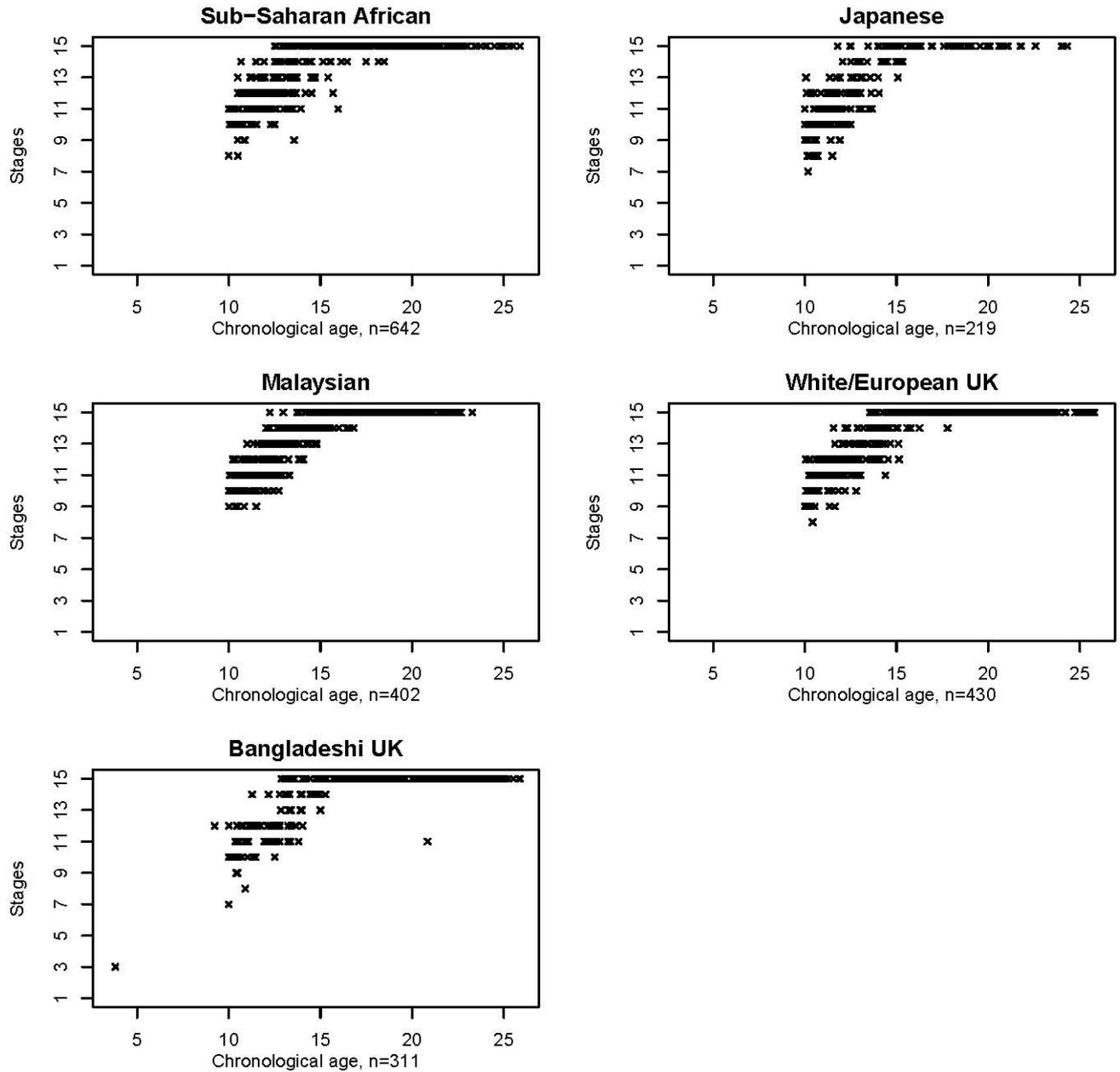
Figure 3. The chronological age versus molar stage for the second molar for males (clusters of data points indicate several observations).

Molar 2, females
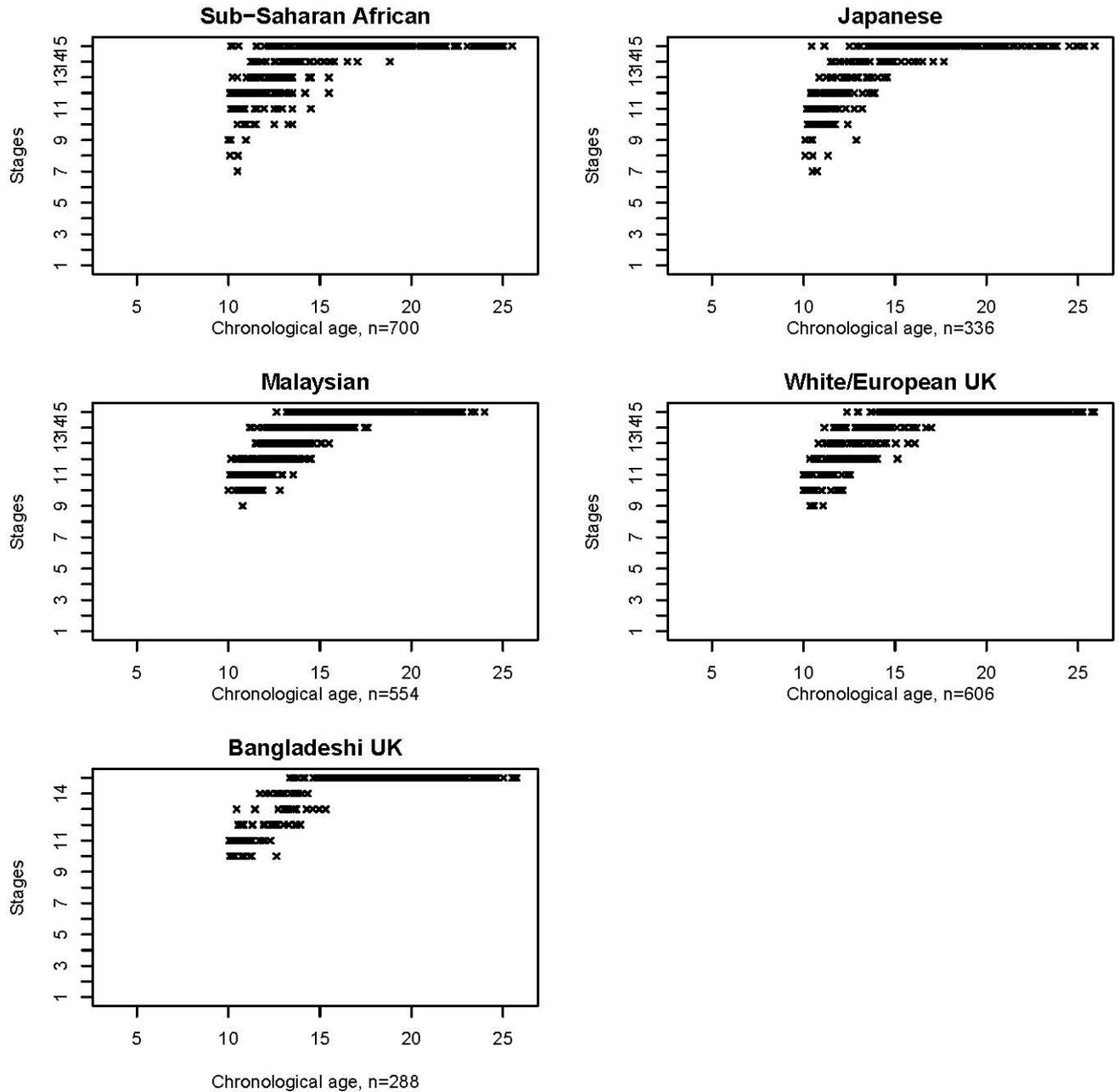
Figure 4. The chronological age versus developmental stage for the second molar for females (clusters of data points indicate several observations).

From figures 3 and 4 we see that the recorded stages are in the range 7-15, 8-15 or 9-15. For analysis we will omit the single stage three recording for the male Bangladeshi UK group and further merge seven, eight and nine stages together into stage nine.

2.3 Summary: stages for analysis

Table 3 sums up the data preparation procedure and the molar stages to be considered for analysis.

Table 3. Summary; data preparation procedure and the molar stages to be considered.		
Preparation steps	Third molar	Second molar
0. Initially	4 561	4 561
1. Minus stage 0-records	119	0
2. Minus missing records (molar)	9	69
3. Minus missing records (gender)	3	3
4. Minus outlier	0	1*
Records for analysis	4 430	4 488
Stage merging	Merge stage 1 and 2 into stage 2	Merge stage 7-9 into stage 9
Stages for analysis	2-15	9-15
* Omitting stage 3 Bangladeshi UK record		

3   Age estimation procedure

Boldsen et al (2002) describe what they term "transition analysis", which is "a parametric method for modelling the passage of individuals from a given developmental stage to the next stage in an ordered sequence" (Konigsberg et al., 2008). The dental maturity process is a continuous one, and it is arbitrarily divided into discrete stages (Liversidge, 2015). It is difficult to say at which time a tooth "switched" from one stage to the next stage as there is typically only one observation of an individual's dental stage. Therefore, a modelling approach seems reasonable, implying assumptions of a distributional form for the transitions, where such a model can be fitted by maximum likelihood estimation (Konigsberg et al., 2008). We take such an approach. Based on the results of this fitted transition analysis we can derive the age distribution conditional on stage through a Bayesian estimation procedure.

The age given stage distributions are hence obtained in a two-step procedure. In the first step we fit a probit model for categorical data. We let the molar stages depend upon ln(age), where ln is the natural logarithm. From this probit model analysis we obtain the mean transition ages between stages and the (common) standard age deviation for transitions. In the second step we fit a model for the molar stages, as dependent upon age. This gives the age distribution for each stage. This two-step procedure is given by Lyle Konigsberg, and in lines with the work in Konigsberg et al (2008). The first step is carried out using the statistical software R and the second step is carried out using WinBUGS (run from R). WinBUGS is a statistical software for Bayesian analysis using Markov chain Monte Carlo (MCMC) methods. Hence, in the last step

we take a Bayesian approach; see Konigsberg and Frankenberg (2013) for an introduction in the Bayesian way of thinking in biological anthropology.

3.1 Step 1: Categorical data analysis

The purpose of the first step is to obtain the mean age for transition between stages and the (common) standard age deviation for transitions. For each molar for each ethnic group and gender we consider a data matrix containing two columns; the first contains the individual's actual age and the second the recorded molar stage (stages j=1, …, J).

A probit model is a regression model where the dependent variable can only take a known set of discrete values, such as molar stages (in a bivariate probit model there are only two discrete outcomes, in a multivariate model there are several outcomes). The probit model can be written as

$$probit(stage_j) \sim f(\ln(age_i)) = \alpha_j + \beta \ln(age_i),$$

$$j = stage\ 1, …, J - 1, i = individual\ 1, …, I.$$

Fitting this model in R is done by the following command:

fit2<-vglm(stage~log(age), cumulative(link='probit',parallel = T, reverse = F)).

This gives J-1 intercept estimates (α_j) and one slope parameter (β). From this we obtain the estimated mean age of transition between the stages j and (j+1) (on the natural logarithmic scale), given by $\hat{\mu}_j = \hat{\alpha}_j / -\hat{\beta}$, j=1,…, J-1, and the estimated common standard deviation for transitions (on the natural logarithmic scale), $\hat{\sigma} = 1/-\hat{\beta}$. Hence, the estimated mean age for transition between stage one and two, on the natural logarithmic scale, is given by $\hat{\alpha}_1 / -\hat{\beta}$.

3.2 Step 2: Conditional age distribution

The purpose of this step is to obtain the age distribution for each stage. We assume the stages to be multinomial distributed given age. We let p_{ij} denote the probability for the tooth to be in stage j given age_i. The p_{ij}'s are given by

$$p_{i1} = 1 - \Phi\left(\frac{\ln(age_i) - \hat{\mu}_1}{\hat{\sigma}}\right), for\ stage\ j = 1$$

$$p_{ij} = \Phi\left(\frac{\ln(age_i) - \hat{\mu}_{j-1}}{\hat{\sigma}}\right) - \Phi\left(\frac{\ln(age_i) - \hat{\mu}_j}{\hat{\sigma}}\right), for\ j = 2, …, J - 1$$

$$p_{iJ} = \Phi\left(\frac{\ln(age_i) - \hat{\mu}_{J-1}}{\hat{\sigma}}\right), for\ stage\ J.$$

The estimated parameters $\hat{\mu}_1, …, \hat{\mu}_{J-1}$ and $\hat{\sigma}$ were obtained in the first step, so the only unknown in these equations are the ages. The age for a given stage is uncertain, and we

choose to express this uncertainty a priori by letting age_i be uniformly distributed between 0 and 110. Fitting this model in WinBUGS gives the posterior distribution for age given stage. In this procedure the age estimates for the lowest and highest stage will be bounded (the lowest by 0 and the highest by 110). What should a priori be set as boundaries for age is debatable, and a general idea is that 0 and 110 are "sufficiently large". From the model it is clear that the estimate of the lowest and highest stage will be influenced by the lower and upper bound in the prior distribution. As a consequence the estimated age distributions for the lowest and highest stages should be disregarded as they are clearly affected by these boundary choices. For a further discussion see section 4.3.

3.3 Bayesian analysis using Markov chain Monte Carlo (MCMC) methods

We fitted our model using WinBUGS by performing initial 250 000 simulations (so-called burn-ins and hence disregarded) and then another 250 000 iterations, where we retain every 100 iteration. This gave 2 500 age samples for each molar and stage. The Bayesian equivalence of a confidence interval is a credibility interval, and these intervals are given by the 2.5 and 97.5 percentiles in the distribution of the 2 500 samples.

The two-step approach presented in section 3.1 – 3.2 fits a probit model for estimating the mean age of transition between the stages and the estimated common standard deviation for transitions (on log scale), one fitted model for each ethnic group, gender and molar. It thereafter uses these estimates to derive the age distributions for each stage (for each ethnic group, gender and molar considered separately). Hence, in the second step the estimates from the probit model are considered known, and it does not take into consideration the uncertainty in the estimates. If these uncertainties had been taken into consideration the second step (incorporating the co-variance matrix for the alpha and beta estimates and translating these to mu and sigma) the estimated age distributions could be somewhat different.

Hence, these age distributions given molar stage represent the age distribution arriving from the fitted probit model, given that we believe in the estimated mean age of transition between the stages and the estimated common standard deviation for transitions (without thinking about uncertainty in the fitted probit model), that is what we could call the most likely age distribution.

4 Results

We have analysed the second and third molar data separately, and the estimated mean ages for each developmental stage for the second and third molar for males and females are displayed in figure 5. The analysis results are presented in detail in section 4.1 and 4.2. We first present the third molar data results and then the second molar data results.
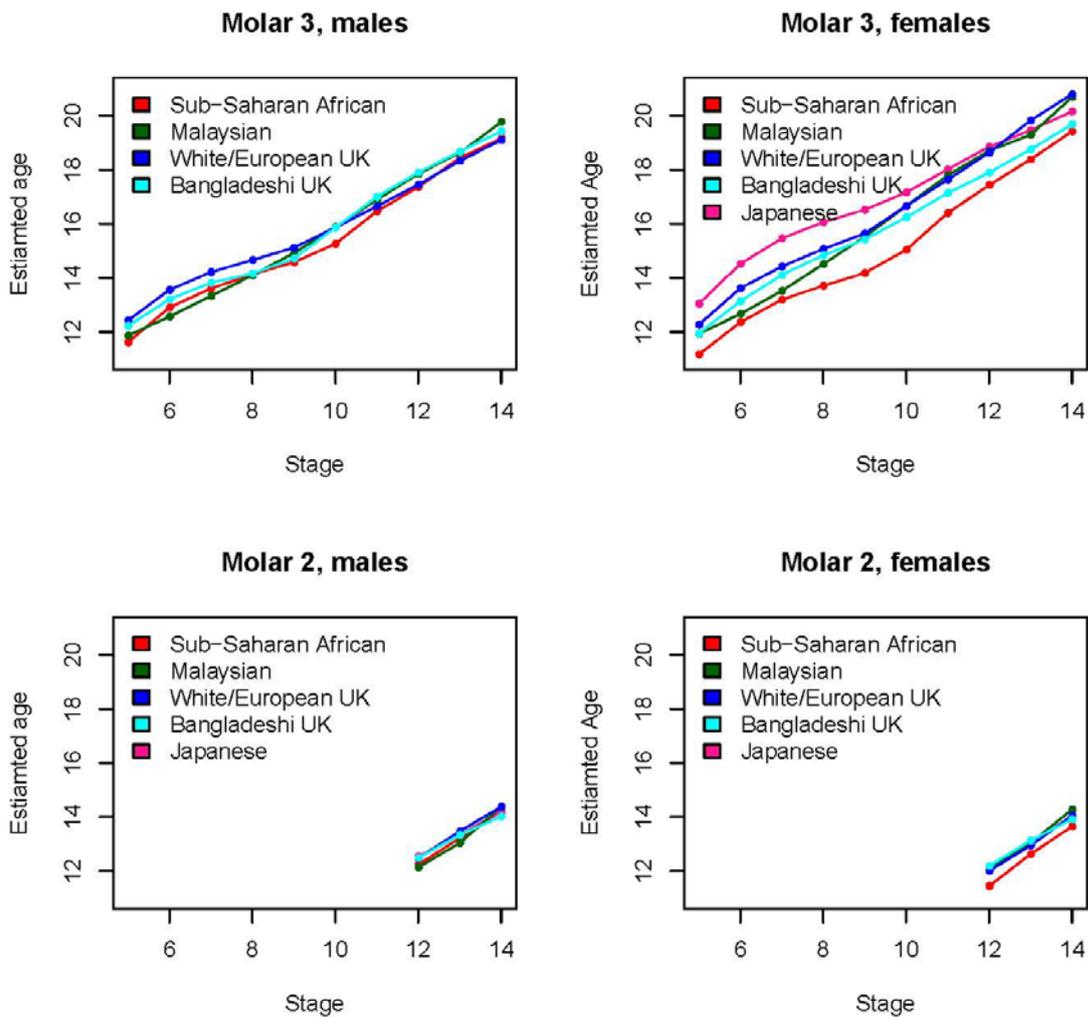
Figure 5. The estimated mean age for each molar stage for the second and third molar for males and females.

4.1 Third molar analysis

Tables 4 and 5 contain the estimated mean age, standard deviation and uncertainty intervals for stages 5 - 14 for males and females respectively.

Table 4. Estimated mean age, standard deviation (SD) and 95% credibility intervals in years for third molar, for males.								
Sub-Saharan African					Malaysian			
Stage	Mean	SD	95% CI		Stage	Mean	SD	95% CI
5	11.62	1.44	(9.01,14.58)		5	11.87	1.14	(9.84,14.27)
6	12.91	1.56	(10.10,16.23)		6	12.57	1.19	(10.46,14.97)
7	13.61	1.63	(10.73,16.99)		7	13.33	1.26	(11.02,15.99)
8	14.13	1.70	(11.11,17.74)		8	14.10	1.33	(11.74,16.92)
9	14.58	1.80	(11.44,18.39)		9	14.92	1.43	(12.37,17.90)
10	15.26	1.86	(11.95,19.25)		10	15.88	1.50	(13.10,19.10)
11	16.46	2.00	(12.81,20.61)		11	16.89	1.64	(13.91,20.34)
12	17.36	2.15	(13.39,21.89)		12	17.85	1.68	(14.82,21.52)
13	18.43	2.23	(14.37,23.18)		13	18.62	1.74	(15.46,22.27)
14	19.16	2.25	(15.17,23.98)		14	19.76	1.88	(16.36,23.65)
White/ European UK					Bangladeshi UK			
Stage	Mean	SD	95% CI		Stage	Mean	SD	95% CI
5	12.43	1.28	(10.21,15.11)		5	12.23	1.48	(9.57,15.46)
6	13.56	1.37	(11.01,16.48)		6	13.21	1.55	(10.41,16.48)
7	14.21	1.40	(11.63,17.15)		7	13.82	1.61	(10.92,17.18)
8	14.66	1.44	(12.04,17.64)		8	14.16	1.68	(11.12,17.70)
9	15.12	1.47	(12.37,18.33)		9	14.72	1.74	(11.54,18.39)
10	15.86	1.60	(12.93,19.04)		10	15.86	1.90	(12.53,19.94)
11	16.65	1.66	(13.67,19.93)		11	17.00	1.98	(13.57,21.25)
12	17.45	1.73	(14.29,20.95)		12	17.90	2.15	(14.04,22.43)
13	18.32	1.84	(15.04,22.29)		13	18.67	2.20	(14.67,23.46)
14	19.10	1.90	(15.62,23.08)		14	19.42	2.26	(15.45,24.20)

Table 5. Estimated mean age, standard deviation (SD) and 95% credibility intervals in years for third molar, for females.								
Sub-Saharan African					Malaysian			
Stage	Mean	SD	95% CI		Stage	Mean	SD	95% CI
5	11.17	1.45	(8.69,14.19)		5	11.93	1.36	(9.52,14.86)
6	12.36	1.65	(9.47,15.87)		6	12.67	1.36	(10.30,15.66)
7	13.20	1.68	(10.21,16.79)		7	13.52	1.51	(10.85,16.68)
8	13.71	1.74	(10.59,17.51)		8	14.51	1.60	(11.62,17.88)
9	14.18	1.76	(11.06,17.91)		9	15.52	1.73	(12.46,19.16)
10	15.04	1.96	(11.62,19.25)		10	16.66	1.86	(13.19,20.64)
11	16.40	2.10	(12.66,20.88)		11	17.79	1.99	(14.39,22.12)
12	17.43	2.23	(13.41,22.00)		12	18.70	2.07	(14.95,23.10)
13	18.38	2.32	(14.43,23.29)		13	19.29	2.10	(15.44,23.75)
14	19.42	2.41	(15.02,24.67)		14	20.68	2.39	(16.41,25.73)

White/ European UK					Bangladeshi UK			
Stage	Mean	SD	95% CI		Stage	Mean	SD	95% CI
5	12.27	1.55	(9.56,15.53)		5	11.95	1.31	(9.58,14.63)
6	13.62	1.68	(10.62,17.23)		6	13.14	1.46	(10.53,16.12)
7	14.42	1.79	(11.23,18.38)		7	14.11	1.52	(11.39,17.30)
8	15.07	1.88	(11.65,19.15)		8	14.84	1.58	(11.96,18.21)
9	15.64	1.86	(12.26,19.52)		9	15.42	1.66	(12.43,18.87)
10	16.66	2.04	(12.99,21.00)		10	16.24	1.67	(13.13,19.71)
11	17.63	2.15	(13.77,22.17)		11	17.14	1.81	(13.96,20.91)
12	18.63	2.34	(14.35,23.66)		12	17.89	1.82	(14.68,21.63)
13	19.82	2.40	(15.57,24.95)		13	18.75	1.97	(15.17,22.80)
14	20.79	2.54	(16.24,26.12)		14	19.68	1.99	(15.99,23.77)
Japanese								
Stage	Mean	SD	95% CI					
5	13.05	1.55	(10.38,16.31)					
6	14.52	1.73	(11.36,18.15)					
7	15.46	1.76	(12.11,19.21)					
8	16.06	1.84	(12.78,20.11)					
9	16.52	1.86	(13.19,20.49)					
10	17.16	1.97	(13.72,21.43)					
11	18.01	1.99	(14.43,22.20)					
12	18.85	2.15	(15.09,23.39)					
13	19.46	2.28	(15.34,24.18)					
14	20.15	2.33	(16.01,25.04)					

The estimated age distributions for males and females for stages 5-9 and 10-14 are displayed in figures 6 through 9, respectively. All distributions have been drawn using the sm.density.compare-function in the sm-package in R (Smoothing methods for nonparametric regression and density).

Molar 3, males

Stage 5

Stage 6

Stage 7
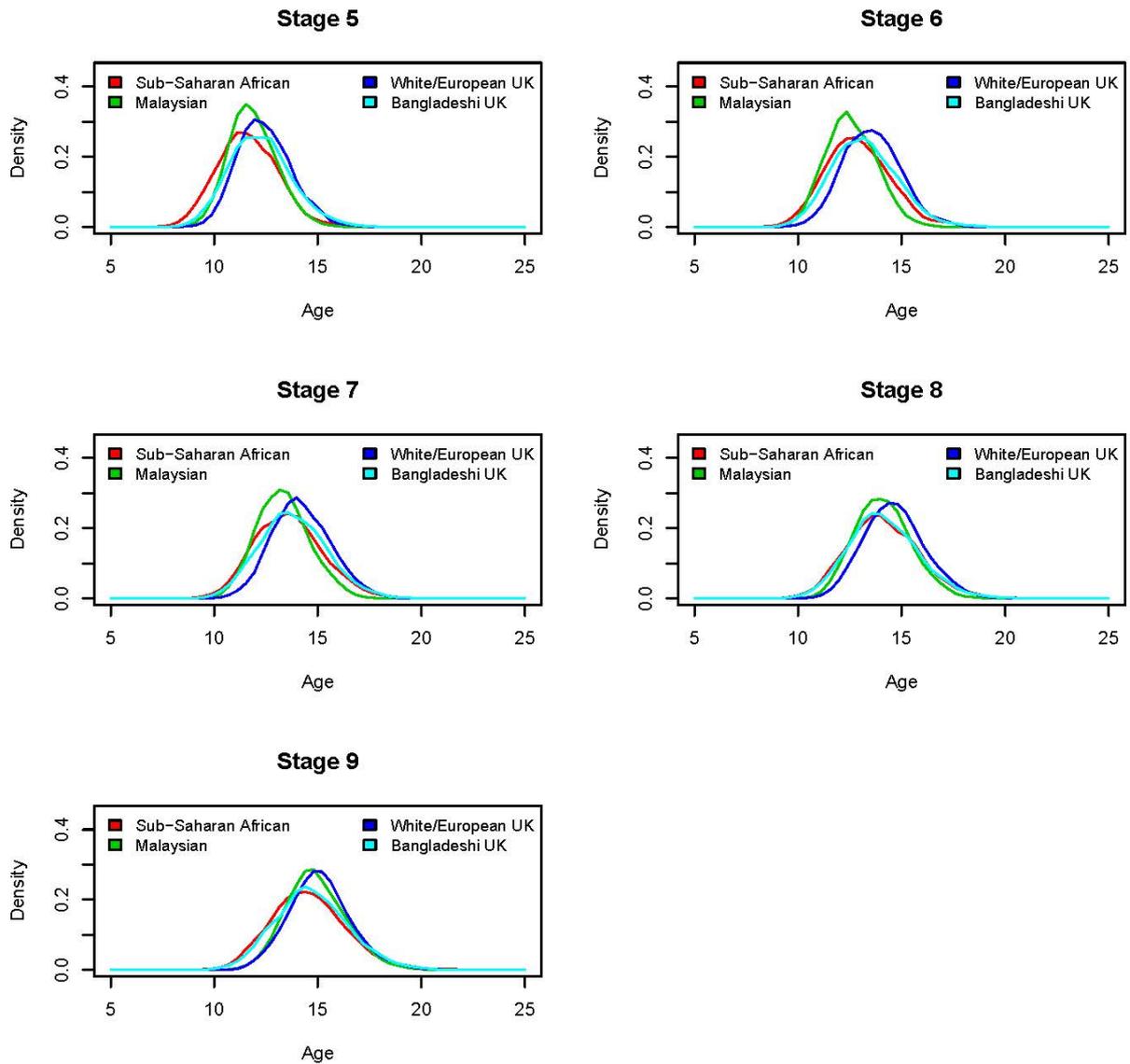
Stage 8

Stage 9

Figure 6. Estimated age density plots for stages 5 through 9 for males, third molar data.

Age distribution estimation given molar stages for males and females for five ethnic groups

Molar 3, males

Stage 10

Stage 11

Stage 12

Stage 13

Stage 14
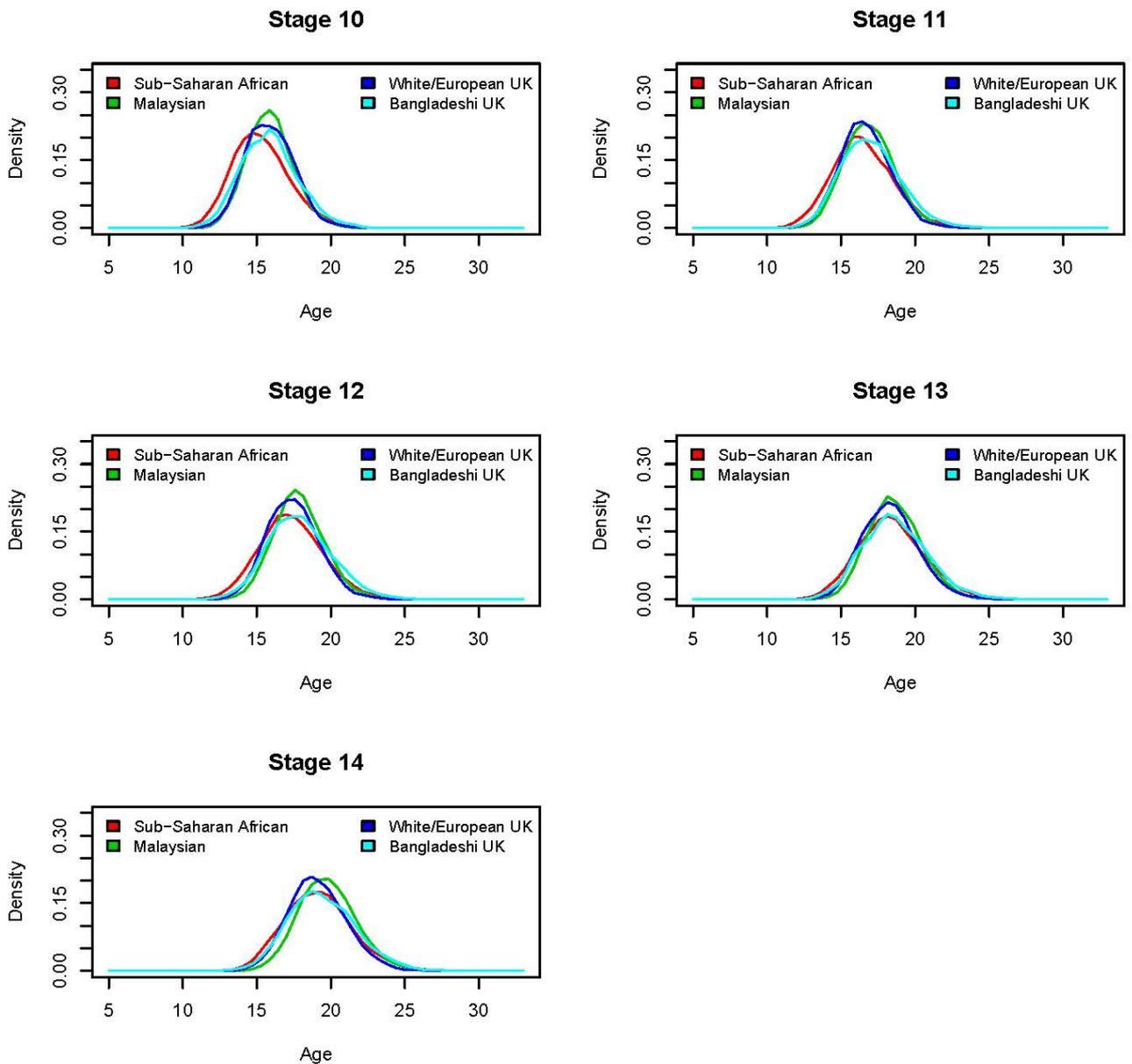
Figure 7. Estimated age density plots for stages 10 through 14 for males, third molar data.
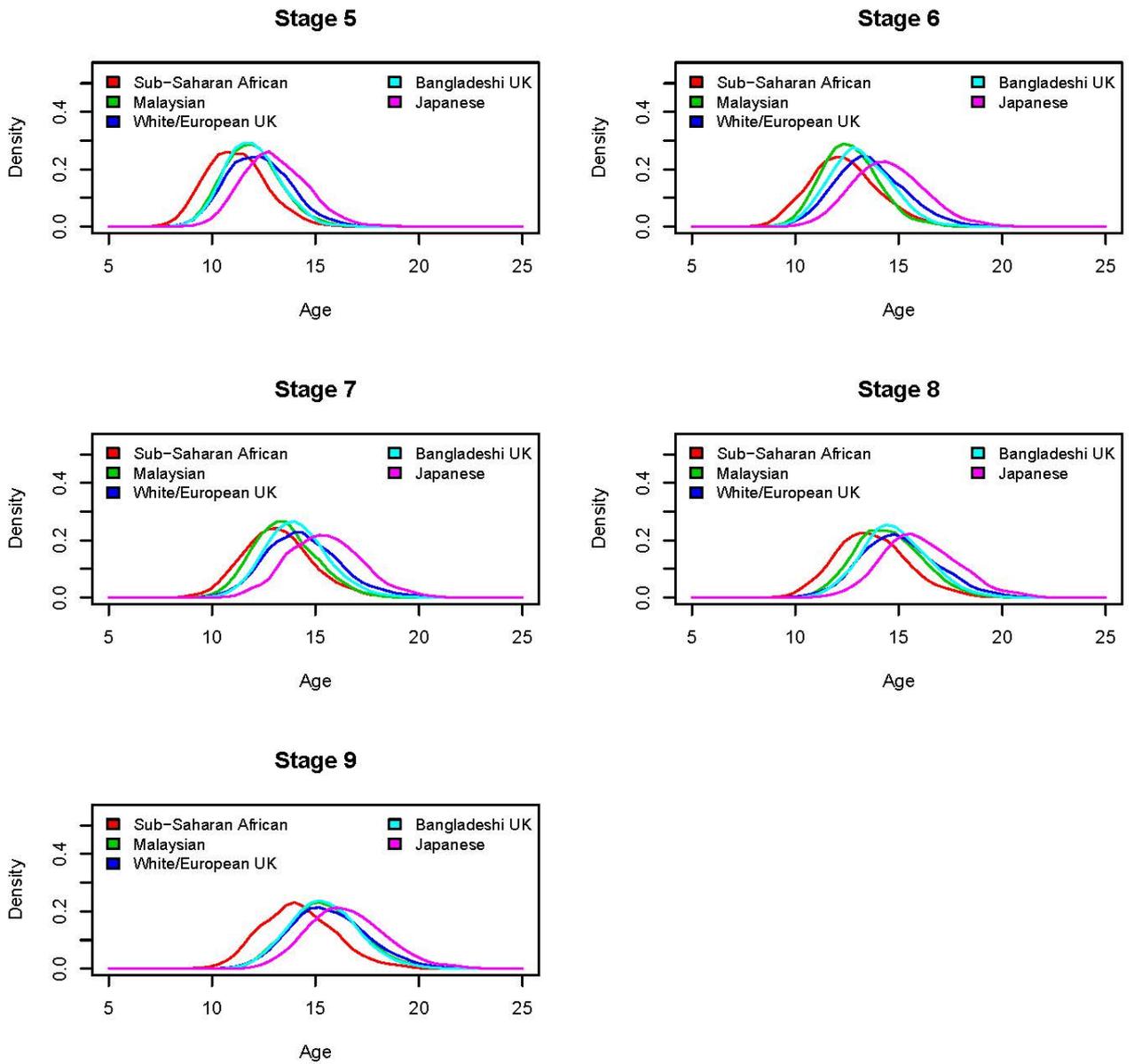
Molar 3, females

Figure 8. Estimated age density plots for stages 5 through 9 for females, third molar data.

Molar 3, females

Stage 10

Stage 11

Stage 12

Stage 13

Stage 14
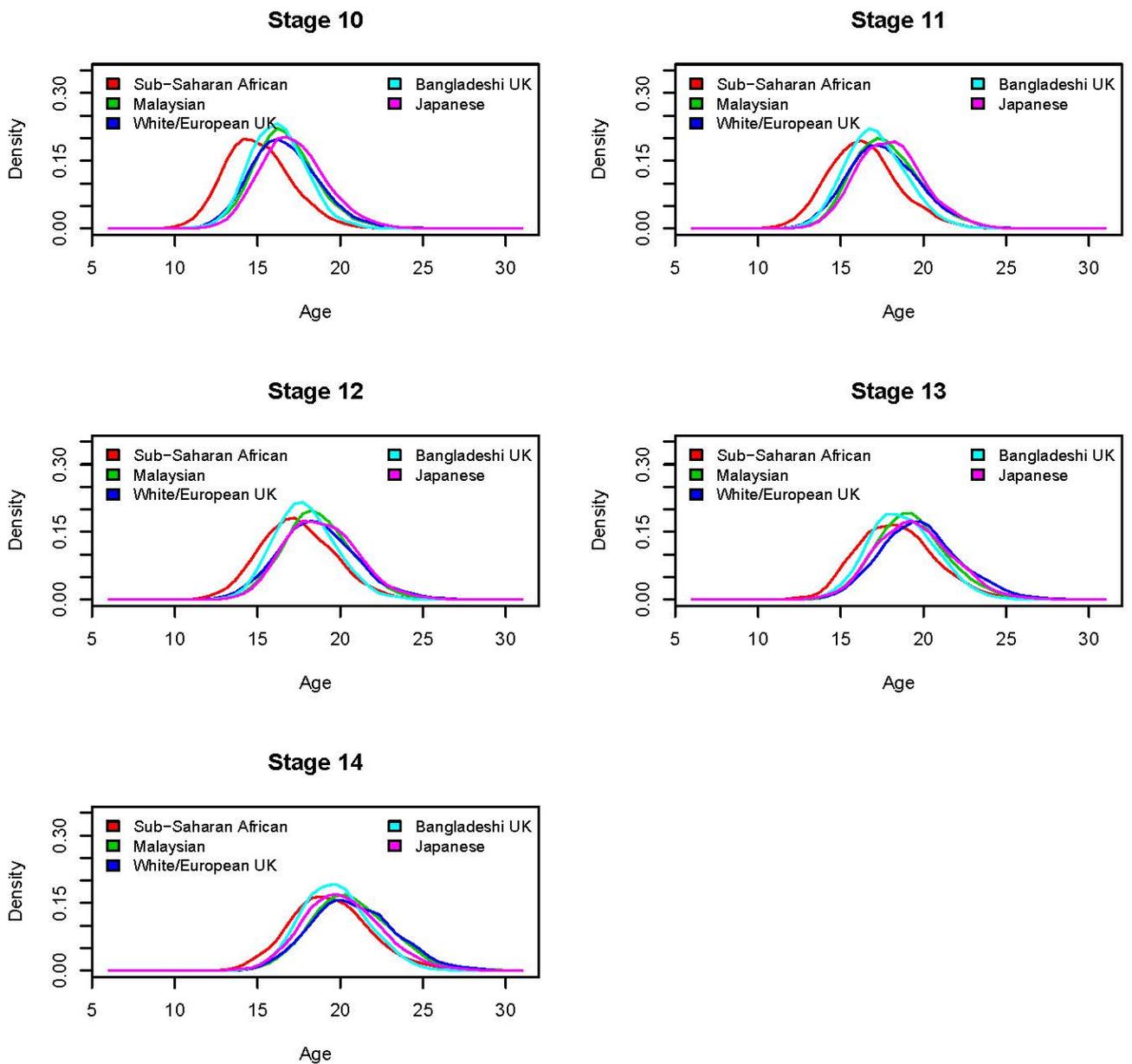
Figure 9. Estimated age density plots for stages 10 through 14 for females, third molar data.

4.2 Second molar analysis

Tables 6 and 7 contain the estimated mean age, standard deviation and uncertainty intervals for stages 12 through 14 for males and females respectively.

Table 6. Estimated mean age, standard deviation (SD) and 95% credibility intervals in years for second molar, for males.								
Sub-Saharan African					**Malaysian**			
Stage	Mean	Std	95% CI		Stage	Mean	Std	95% CI
12	12.24	1.36	(9.79,15.02)		12	12.14	1.04	(10.29,14.26)
13	13.22	1.43	(10.58,16.13)		13	13.04	1.09	(11.03,15.26)
14	14.22	1.56	(11.37,17.41)		14	14.38	1.25	(12.09,16.90)
White/ European UK					**Bangladeshi UK**			
Stage	Mean	Std	95% CI		Stage	Mean	Std	95% CI
12	12.47	1.15	(10.41,14.85)		12	12.49	1.42	(9.91,15.46)
13	13.47	1.19	(11.28,15.97)		13	13.34	1.44	(10.83,16.41)
14	14.38	1.28	(11.98,17.02)		14	14.02	1.57	(11.12,17.35)
Japanese								
12	12.54	1.21	(10.39,15.06)					
13	13.33	1.29	(11.03,16.00)					
14	14.21	1.41	(11.57,17.16)					

Table 7. Estimated mean age, standard deviation (SD) and 95% credibility intervals in years for second molar, for females.								
Sub-Saharan African					**Malaysian**			
Stage	Mean	Std	95% CI		Stage	Mean	Std	95% CI
12	11.45	1.40	(8.86,14.45)		12	12.08	1.13	(9.99,14.39)
13	12.63	1.50	(9.95,15.77)		13	13.03	1.23	(10.76,15.66)
14	13.65	1.59	(10.75,17.00)		14	14.28	1.44	(11.67,17.34)
White/ European UK					**Bangladeshi UK**			
Stage	Mean	Std	95% CI		Stage	Mean	Std	95% CI
12	12.01	1.14	(9.98,14.39)		12	12.19	1.08	(10.22,14.47)
13	12.95	1.17	(10.82,15.3)		13	13.13	1.14	(11.01,15.41)
14	14.05	1.29	(11.63,16.79)		14	13.92	1.19	(11.70,16.36)
Japanese								
Stage	Mean	Std	95% CI					
12	12.15	1.28	(9.82,15.00)					
13	13.06	1.36	(10.58,15.76)					
14	14.01	1.49	(11.34,17.27)					

The estimated age distributions for males and females for stages 12 through 14 are displayed in figures 10 and 11, respectively.

Molar 2, males

Stage 12
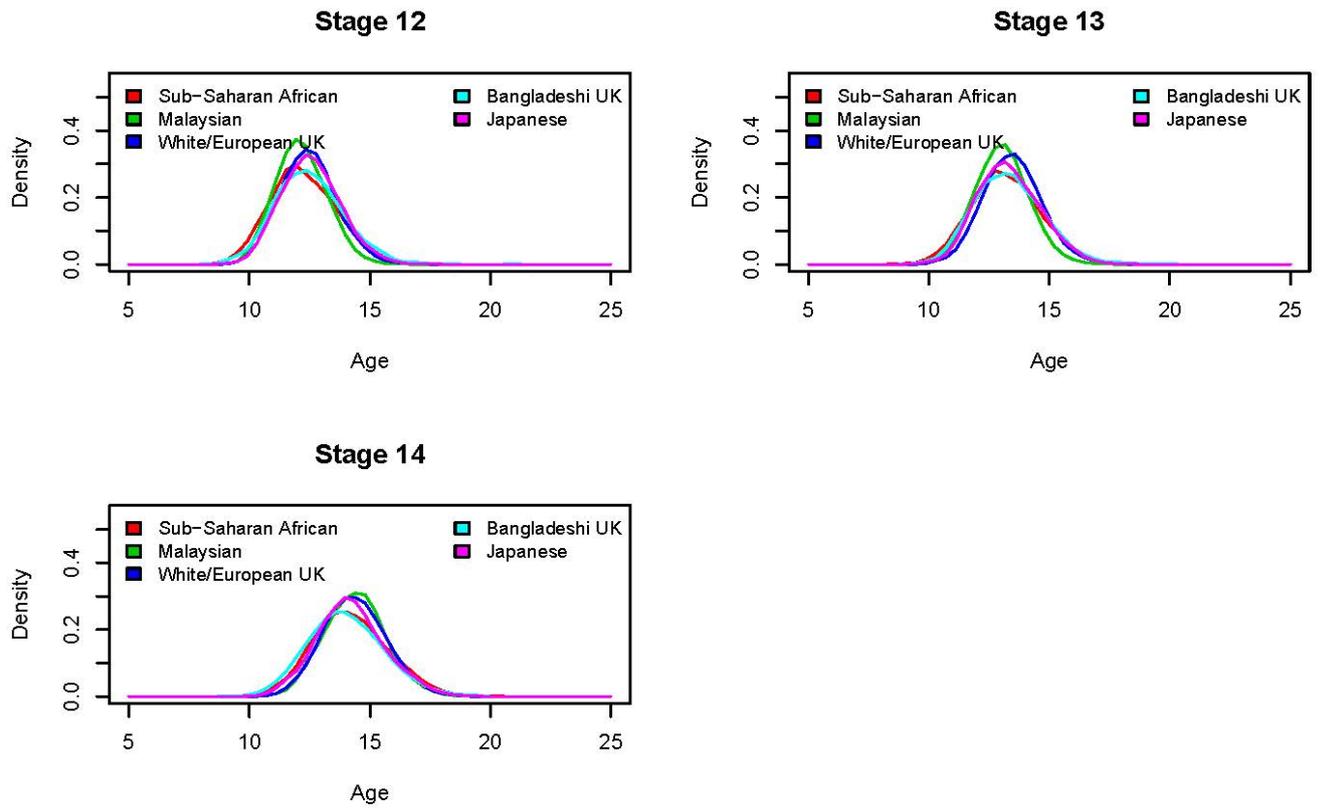
Stage 13

Stage 14

Figure10. Estimated age density plots for stages 12 through 14 for males, second molar data.

Molar 2, females

Stage 12
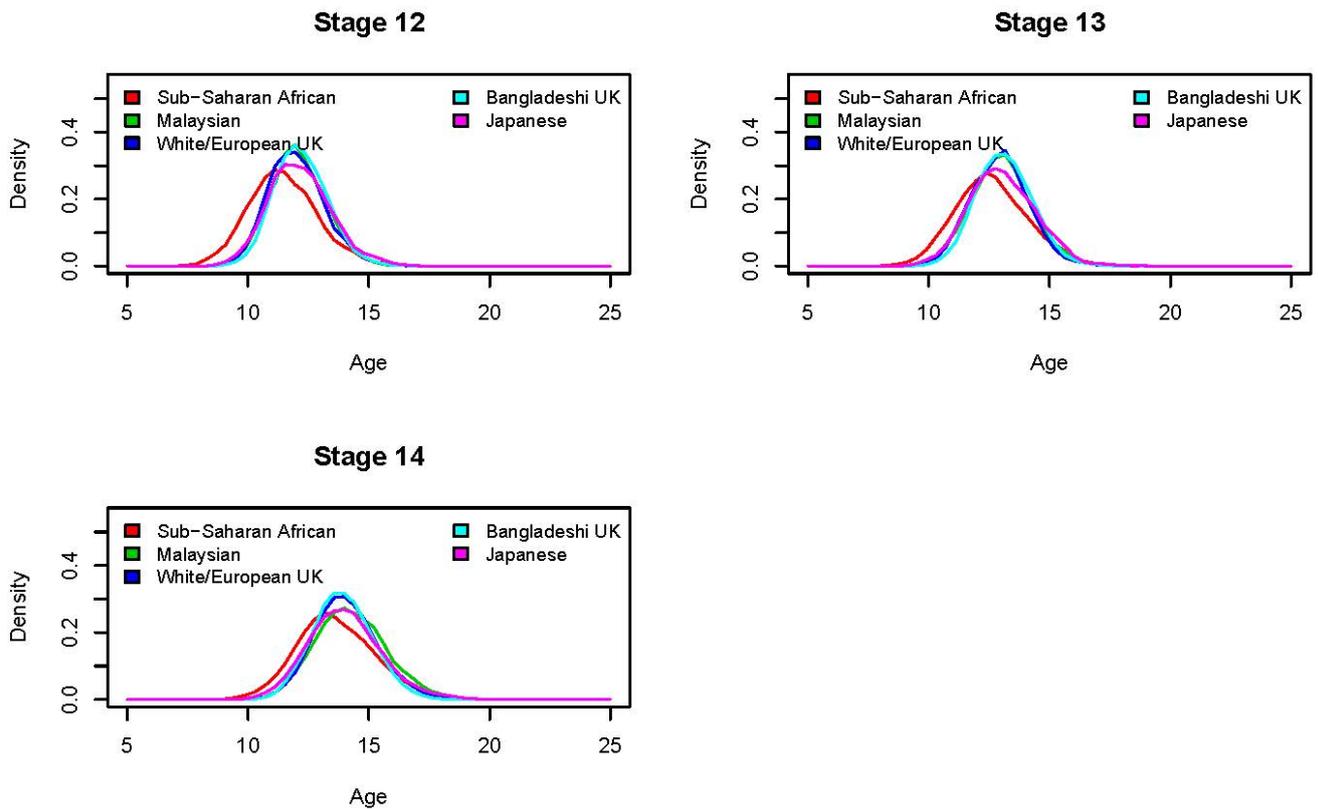
Stage 13

Stage 14

Figure 11. Estimated age density plots for stages 12 through 14 for females, second molar data.

4.3 Considering stage 15

As discussed in section 3, in estimating step 2 deriving the posterior age given stage distributions, the age for a given stage was a priori uncertain, and was expressed a priori by a uniform distribution, ranging between 0 and 110. Regarding the range in the uniform distribution, other choices could also be argued for. As a sensitivity analysis various upper limits (30, 60) was tried for the male African third molar data. As expected, the molar 15 stage age estimate is highly influenced by the upper limit choice. But most importantly, the age estimates for the other stages remain similar to the ones achieved in the analyses in section 4.1-4.2.

If one, for a specific purpose would argue for some a priori lower and upper limits, one might justify such choices, but the molar 15 stage age estimate will be influenced by the upper limit choice.

5 The probability of being 18 years or older

Based on the 2 500 age samples for each molar and stage achieved in the WinBUGS modelling figure 12 displays the percentage of individuals 18 years or older for third molar stages 5-14. In

general, there seems to be a greater degree of differences between ethnic groups among the females than the males.

Molar 3, estimated probability: 18 years or older
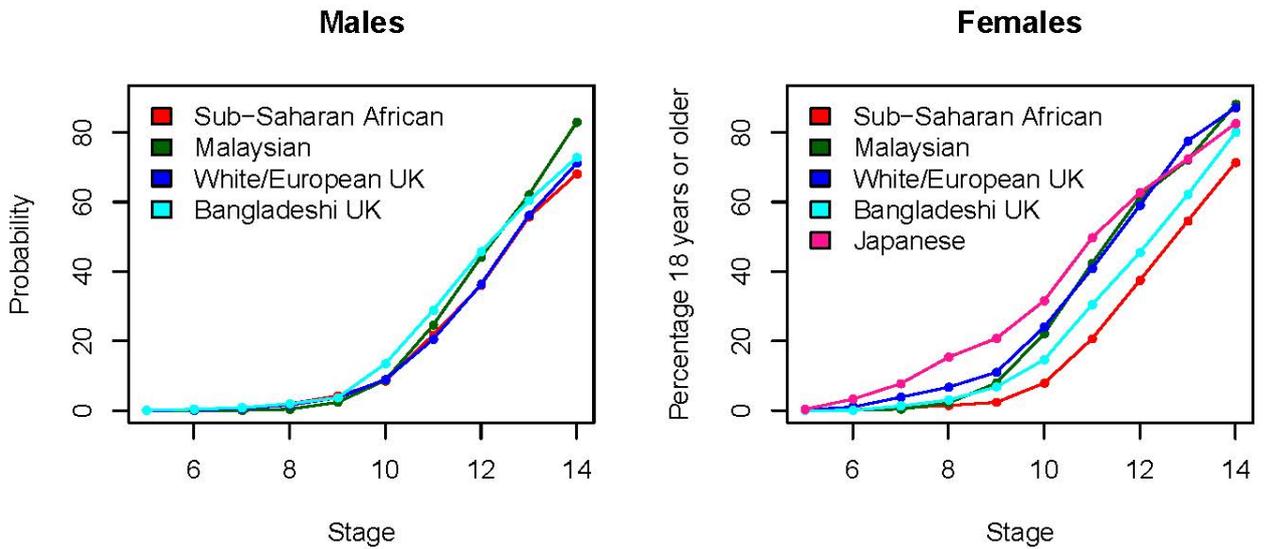
Figure 12. The estimated probability of being 18 years or older when in stages 5-14, for the third molar for the different ethnic groups.

Figure 13 displays the data, in terms of percentage of individuals 18 or older when in stages 5-14, for the third molar for the different ethnic groups.

Molar 3, percentage 18 years or older
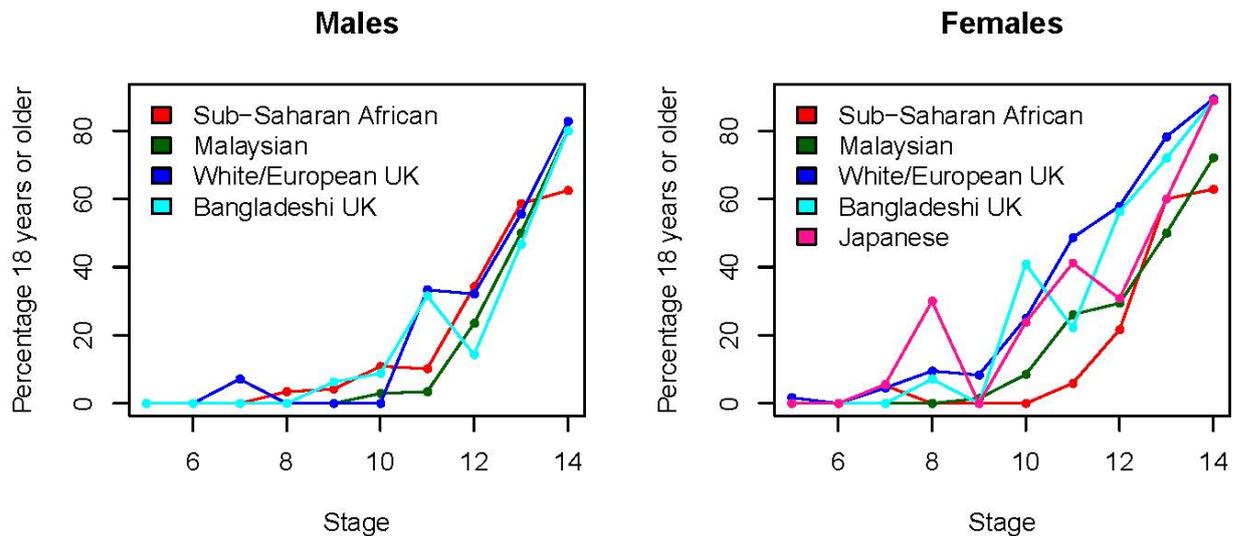
Figure 13. Percentage of individuals 18 years or older in stages 5-14, for the third molar for the different ethnic groups. Computed directly from the data in figures 1-4.

The estimated percentages of individuals 18 years or older in figure 12 represents a smoothed version of the actual percentages given in figure 13. Table 8 displays the estimated percentages of males and females 18 years or older when in stages 10-14, both the estimated percentages based on the statistical model and the actual percentages in parenthesis.

Table 8. The estimated and actual observed (in parenthesis) percent of individuals 18 or older for stages 10-14.								
	Males				Females			
Stage	Sub-Saharan African	Malaysian	White/European UK	Bangladeshi UK	Sub-Saharan African	Bangladeshi UK	Malaysian	White/European UK	Japanese
10	8.44 (10.87)	8.68 (2.94)	8.88 (0.00)	13.44 (8.82)	7.84 (0.00)	14.60 (40.91)	22.08 (8.47)	24.00 (25.00)	31.56 (23.81)
11	21.68 (10.20)	24.56 (3.45)	20.48 (33.33)	28.84 (31.58)	20.60 (5.88)	30.44 (22.22)	42.36 (26.09)	40.80 (48.65)	49.68 (41.18)
12	36.00 (34.29)	44.16 (23.53)	36.32 (32.14)	45.68 (14.29)	37.44 (21.62)	45.44 (56.25)	61.40 (29.41)	59.00 (57.89)	62.68 (30.77)
13	55.72 (58.62)	62.08 (50.00)	56.16 (55.56)	60.40 (46.67)	54.52 (60.00)	62.12 (72.00)	72.12 (50.00)	77.56 (78.26)	72.40 (60.00)
14	68.04 (62.50)	82.96 (80.00)	71.16 (82.76)	72.80 (80.00)	71.36 (62.86)	80.04 (88.89)	88.12 (72.09)	87.12 (89.36)	82.60 (88.89)

6 The third molar: detecting differences between ethnic groups and gender

Considering the probit models fitted in section 4 one can discuss whether separate models or a joint model should be fitted for the ethnic groups, and similar for gender. We examine this for the third molar data analyses.

6.1 Ethnic group differences

We consider three model approaches:

1. A separate model for each ethnic group
2. A joint model for all ethnic groups, same α and β parameter
3. A joint model for all ethnic groups, same α but different β parameter

We consider three model evaluation criteria:

1. Bayesian information criterion (BIC)
2. Akaikes information criterion (AIC)
3. Log likelihood ratio test

The BIC is computed as -2*log likelihood +log(n)*k, where n is the number of observations and k the number of parameters. The AIC is computed as -2*log likelihood + 2*k, where again k is the number of parameters. A lower BIC or AIC indicates a better model fit. A likelihood ratio test statistic T is given as twice the difference in log likelihood between two fitted models (the

alternative versus the "null" model), and this test statistic is compared to a chi squared distribution with k degrees of freedom where k is the difference in the number of parameters in the two models. Table 9 displays the results.

Table 9. Comparison of three model alternatives: 1) a separate model for each ethnic group, 2) a joint model for all ethnic groups, same α and β and 3) a joint model for all ethnic groups, same α but different β.

				Males, third molar		
Model	Log likelihood	Number of parameters	BIC	AIC	Log likelihood ratio test	
1	-2808.80	4*14	6036.75	5673.59		
2	-2895.04	14	5894.87	5818.08	Model 2 vs 1	T=172.49, compared with χ^2_{42}
3	-2880.65	17	5888.53	5795.29	Model 3 vs 1	T=143.70, compare with χ^2_{39}
				Females, third molar		
Model	Log likelihood	Number of parameters	BIC	AIC	Log likelihood ratio test	
1	-4143.91	5*14	8834.25	8427.81		
2	-4366.26	14	8841.80	8760.51	Model 2 vs 1	T=444.70, compared with χ^2_{56}
3	-4250.12	18	8640.75	8536.24	Model 3 vs 1	T=212.43, compare with χ^2_{52}

For both males and females we see that according to the BIC criteria model 3 performs best (lowest BIC), but according to the AIC criteria model 1 performs best (lowest AIC). Considering the log likelihood ratio test both tests (model 2 versus 1 and model 3 versus 1) conclude that model 1 is preferable.

As often is the case, different tests might result in different conclusions. Still, overall the findings in table 9 indicate differences between ethnic groups.

6.2 Gender differences

We consider 3 model approaches:

1. A separate model for males and females
2. A joint model for males and females, same α and β parameter
3. A joint model for males and females, same α but different β parameter

We consider the same three model evaluation criteria as in section 6.1. Table 10 displays the results.

Table 10. Comparison of three model alternatives: 1) a separate model for males and females, 2) a joint model for males and females, same α and β and 3) a joint model for males and females, same α but different β.

Model	Log likelihood	Number of parameters	BIC	AIC	Log likelihood ratio test	
Sub-Saharan African						
1	-2251.96	2*14	4706.09	4559.92		
2	-2268.68	14	4638.45	4565.37	Model 2 vs 1	T=33.45, compared with χ^2_{14}
3	-2265.69	15	4639.68	4561.37	Model 3 vs 1	T=27.46, compare with χ^2_{13}
Malaysian						
1	-1698.83	2*14	3589.81	3453.65		
2	-1714.02	14	3524.11	3456.04	Model 2 vs 1	T=30.38, compared with χ^2_{14}
3	-1708.10	15	3519.14	3446.20	Model 3 vs 1	T=18.54, compare with χ^2_{13}
White/ European UK						
1	-1583.32	2*14	3359.83	3222.64		
2	-1611.78	14	3320.15	3251.56	Model 2 vs 1	T=56.92, compared with χ^2_{14}
3	-1601.83	15	3307.15	3233.65	Model 3 vs 1	T=37.02, compare with χ^2_{13}
Bangladeshi UK						
1	-905.17	2*14	1990.14	1866.34		
2	-917.63	14	1925.15	1863.25	Model 2 vs 1	T=24.91, compared with χ^2_{14}
3	-916.57	15	1929.46	1863.14	Model 3 vs 1	T=22.8, compare with χ^2_{13}

Considering the comparisons of the models in table 10 the results are less uniform compared to the results in section 6.1. Different criteria indicate different results, although for the Malaysian group there seems to be agreement across the tests that model 3 is preferable. Still, overall the results in table 10 do indicate gender differences, although the results are not as strong as in the ethnic group case in section 6.1.

7 Some sensitivity analyses

Due to few observations for stage one and two we merge these two stages. How does this impact the results? Also, how sensitive are the results to limiting the number of observed stages? For examining this we estimate the age distribution for the third molar White/ European UK and Sub-Saharan African male populations for three different scenarios: 1) all data, 2) merge stage one and two (as in the analyses) and 3) only consider data for stages six through 15 for analysis (hence omit all age data for stages less than six). The results are displayed in figure 14 and 15. We see very small differences between the estimated age distributions in the three scenarios.

Molar 3, Sub-Saharan African males
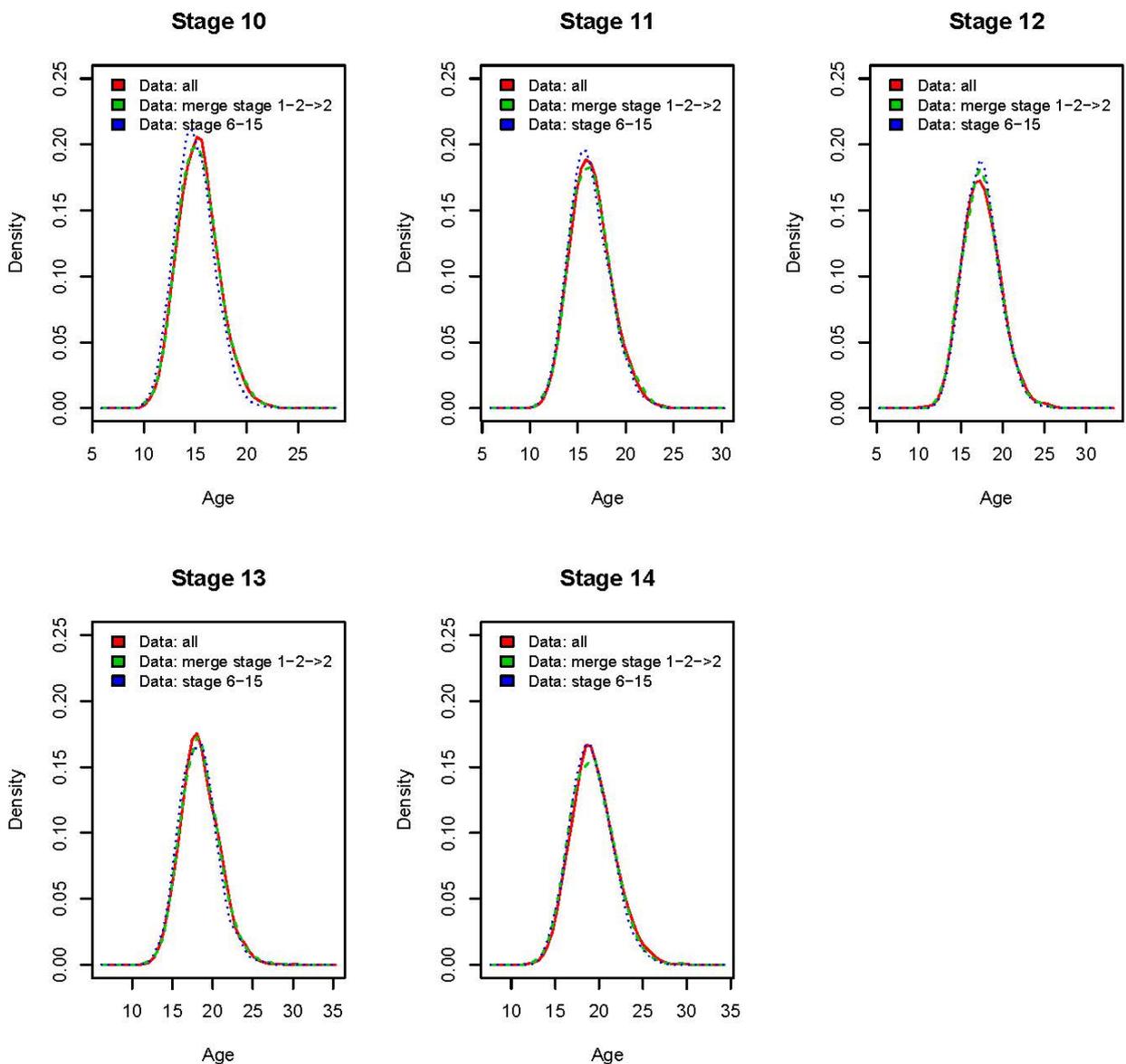
Figure 14. Sensitivity analysis: three scenarioes for Sub-Saharan African males.

Molar 3, White/European UK males

Stage 10

Stage 11

Stage 12

Stage 13

Stage 14
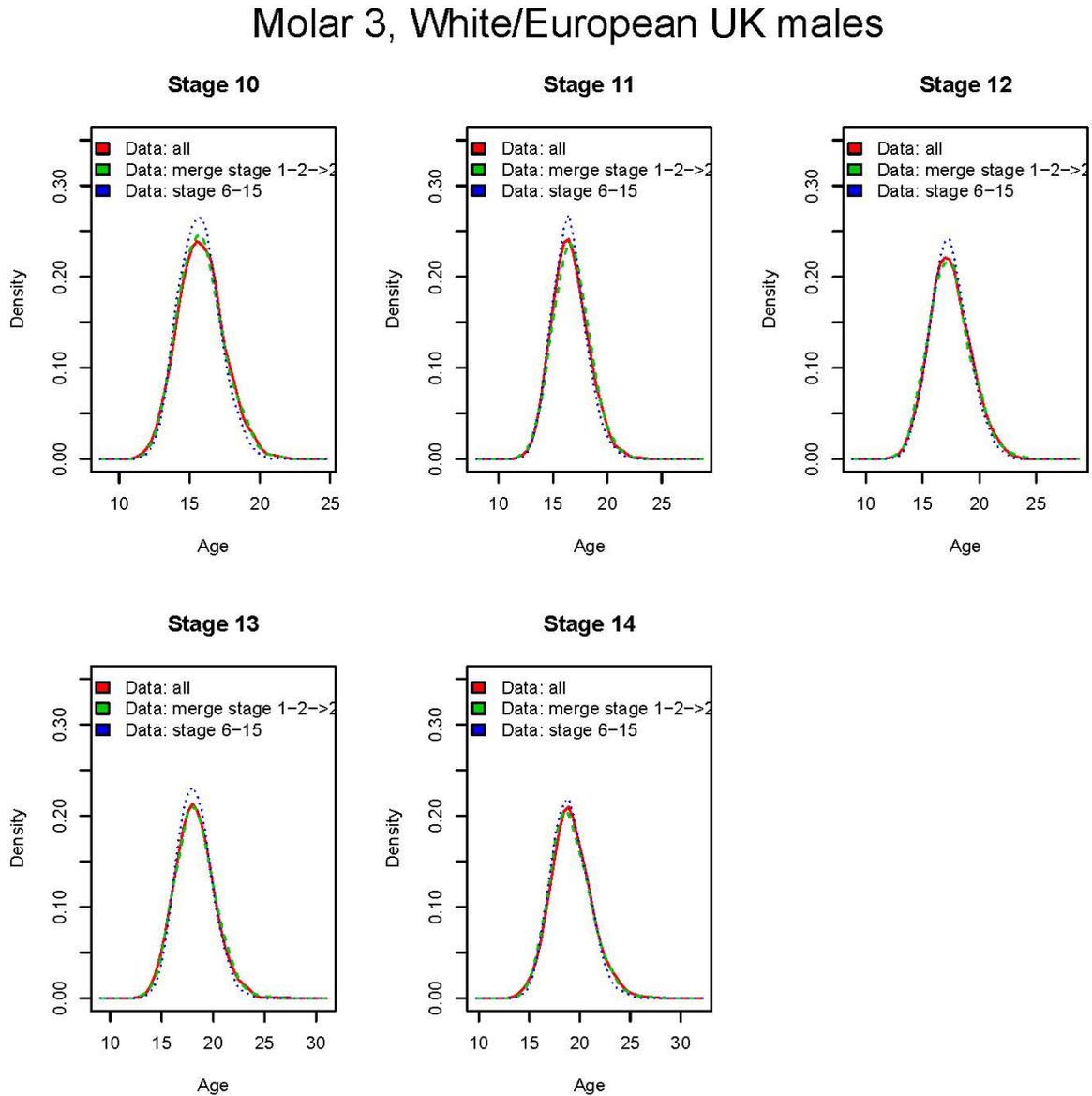
Figure 15. Sensitivity analysis: three scenarioes for White/European UK males.

8 Summary and discussion

We have in this note conducted a transition analysis, as introduced by Boldsen et al (2002), for modelling second and third molar teeth moving from one developmental stage to the following stage. This was done by fitting a probit model for molar developmental stages, giving the mean transition ages between stages and the (common) standard age deviation for transitions. With this as input into a Bayesian estimation procedure we obtained estimated age distributions for each developmental stage of second and third molars.

In the Bayesian estimation procedure a prior uniform distribution was assumed for age. This is a common prior to use in age estimation, as in e.g. Tangmose et al (2015) and Millard and Gowland (2002). Milner and Boldson (2012) compare the uniform prior to a so-called informative prior in estimating skeletal age, and detect little differences in age estimates up until 40 years. One could perhaps think of other prior assumptions, but as Konigsberg et al (2008) points out regarding skeletal age, the age distribution is not likely to be symmetric, such as e.g. the Gaussian distribution.

In section 6 we discussed whether separate models or a joint model should be fitted for the ethnic groups by comparing three model approaches using three model evaluation criteria. We did a similar comparison across genders. We concluded that there were differences across ethnic groups. All over, there here were also gender differences, although the results were not as strong as in the ethnic group case. In Liversidge (2008) head-to-head comparisons of ethnic groups were done, using much of the same data as used for the analyses in this note. Our approach to ethnicity and gender comparisons was in terms of an "overall model check", although we could also have done "head-to-head" ethnic group comparisons. Liversidge (2008) concludes in much the same way as in this note, that there are differences between ethnic groups, and also between genders for some stages and ethnic groups (although much weaker signs in the gender case).

9 References

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10 Appendix

10.1 Results, step 1, third molar stages

Tables A1 and A2 contain the estimated mean transition ages between stages and the (common) standard age deviation for transitions for males and females for the third molar stages, as obtained in step 1 of the model fitting procedure.

Table A1. Estimated mean transition ages between stages and the (common) standard age deviation for transitions, males, third molar, log scale (3 digits).														
							Stages							
		1,2→3	3→4	4→5	5→6	6→7	7→8	8→9	9→10	10→11	11→12	12→13	13→14	14→15
Sub-Saharan African	$\hat{\mu}$	2.178	2.269	2.37	2.499	2.577	2.607	2.643	2.674	2.739	2.811	2.867	2.913	2.952
	$\hat{\sigma}$							0.120						
Malaysian	$\hat{\mu}$	2.326	2.379	2.426	2.49	2.545	2.607	2.661	2.716	2.783	2.846	2.891	2.928	3.012
	$\hat{\sigma}$							0.093						
White/European UK	$\hat{\mu}$	2.317	2.402	2.451	2.561	2.623	2.659	2.687	2.717	2.78	2.815	2.873	2.909	2.964
	$\hat{\sigma}$							0.098						
Bangladeshi UK	$\hat{\mu}$	2.245	2.347	2.43	2.535	2.587	2.619	2.644	2.694	2.785	2.833	2.887	2.931	2.961
	$\hat{\sigma}$							0.117						

Table A2. Estimated mean transition ages between stages and the (common) standard age deviation for transitions, females, third molar, log scale (3 digits).														
							Stages							
		1,2→3	3→4	4→5	5→6	6→7	7→8	8→9	9→10	10→11	11→12	12→13	13→14	14→15
Sub-Saharan African	$\hat{\mu}$	2.222	2.263	2.336	2.442	2.535	2.575	2.614	2.643	2.733	2.803	2.859	2.912	2.967
	$\hat{\sigma}$							0.126						
Japanese	$\hat{\mu}$	2.343	2.428	2.48	2.609	2.692	2.744	2.771	2.794	2.851	2.895	2.933	2.967	3.001
	$\hat{\sigma}$							0.113						
Malaysian	$\hat{\mu}$	2.304	2.373	2.417	2.499	2.547	2.632	2.684	2.757	2.828	2.896	2.926	2.953	3.063
	$\hat{\sigma}$							0.11						
White/European UK	$\hat{\mu}$	2.279	2.346	2.398	2.552	2.625	2.669	2.708	2.748	2.822	2.868	2.936	2.989	3.043
	$\hat{\sigma}$							0.121						

Bangladeshi	$\hat{\mu}$	2.325	2.358	2.413	2.516	2.597	2.66	2.707	2.738	2.805	2.849	2.888	2.944	2.983
UK	$\hat{\sigma}$	0.104												

While table A1 and A2 display the mean transition ages between stages and the (common) standard age deviation for transitions on the (natural) log scale it could be interesting to have summary statistics for the transition ages between stages not on the (natural) log scale. The age's log-normal distribution is asymmetric on the raw scale (and normal on the (natural) log scale). We therefore choose to present the mode and the lower and upper limits for a 95% HPD rather than the typical mean and standard error. The mode is given by $e^{\hat{\mu}}/e^{\sigma^2}$. A HPD-interval is a highest posterior density interval (sometimes called minimum length confidence intervals) for a Bayesian posterior distribution. In the case of a symmetric distribution it is equivalent to common interval. Using the R library TeachingDemos with command hpd(qlnorm,conf=0.95,mean=2.151,sd=.127) we obtain limits (6.58,10.868), see table A3 and A4 for details.

Table A3. Transition ages; the mode and the 95% HPD for males, third molar.							
	1,2→3	3→4	4→5	5→6	6→7	7→8	8→9
African	8.702 (6.867,11.028)	9.531 (7.521,12.079)	10.544 (8.32,13.363)	11.996 (9.466,15.203)	12.969 (10.234,16.436)	13.364 (10.546,16.937)	13.854 (10.932,17.557)
Malaysian	10.149 (8.451,12.188)	10.701 (8.911,12.851)	11.216 (9.34,13.469)	11.957 (9.957,14.36)	12.633 (10.52,15.171)	13.442 (11.193,16.142)	14.187 (11.814,17.037)
White/European UK	10.048 (8.285,12.187)	10.94 (9.02,13.268)	11.489 (9.473,13.935)	12.825 (10.574,15.555)	13.645 (11.25,16.55)	14.145 (11.663,17.157)	14.547 (11.994,17.644)
Bangladeshi UK	9.312 (7.392,11.73)	10.312 (8.186,12.99)	11.204 (8.895,14.114)	12.445 (9.879,15.677)	13.109 (10.407,16.514)	13.535 (10.745,17.051)	13.878 (11.017,17.482)
	9→10	10→11	11→12	12→13	13→14	14→15	
African	14.291 (11.276,18.11)	15.25 (12.034,19.327)	16.389 (12.932,20.769)	17.333 (13.677,21.966)	18.149 (14.321,23)	18.871 (14.89,23.914)	
Malaysian	14.990 (12.482,18.001)	16.028 (13.347,19.248)	17.070 (14.215,20.5)	17.856 (14.869,21.443)	18.529 (15.43,22.252)	20.153 (16.782,24.201)	
White/European UK	14.990 (12.359,18.181)	15.965 (13.163,19.364)	16.534 (13.632,20.053)	17.521 (14.446,21.251)	18.163 (14.975,22.03)	19.190 (15.822,23.275)	
Bangladeshi UK	14.59 (11.582,18.379)	15.98 (12.685,20.13)	16.765 (13.309,21.119)	17.696 (14.047,22.291)	18.491 (14.679,23.294)	19.055 (15.126,24.003)	

Table A4. Transition ages; the mode and the 95% HPD for females, third molar.							
	1,2→3	3→4	4→5	5→6	6→7	7→8	8→9
African	9.080 (7.08,11.647)	9.460 (7.376,12.134)	10.177 (7.935,13.053)	11.315 (8.822,14.513)	12.418 (9.682,15.927)	12.924 (10.077,16.577)	13.439 (10.477,17.236)
Japanese	10.280 (8.226,12.847)	11.192 (8.956,13.987)	11.790 (9.434,14.733)	13.413 (10.733,16.762)	14.574 (11.662,18.213)	15.352 (12.285,19.185)	15.772 (12.621,19.71)
Malaysian	9.894 (7.965,12.29)	10.600 (8.534,13.168)	11.077 (8.917,13.76)	12.024 (9.679,14.936)	12.615 (10.155,15.671)	13.734 (11.056,17.061)	14.467 (11.647,17.972)
White/European UK	9.625 (7.58,12.222)	10.292 (8.105,13.069)	10.841 (8.538,13.767)	12.646 (9.959,16.059)	13.604 (10.713,17.275)	14.216 (11.195,18.052)	14.781 (11.64,18.77)
Bangladeshi UK	10.117 (8.242,12.418)	10.456 (8.519,12.834)	11.047 (9,13.56)	12.246 (9.977,15.031)	13.279 (10.818,16.299)	14.142 (11.522,17.359)	14.823 (12.076,18.194)

	9→10	10→11	11→12	12→13	13→14	14→15	
African	13.834 (10.786,17.744)	15.137 (11.801,19.415)	16.234 (12.657,20.822)	17.169 (13.386,22.022)	18.104 (14.115,23.22)	19.127 (14.913,24.533)	
Japanese	16.139 (12.914,20.168)	17.086 (13.672,21.351)	17.854 (14.287,22.312)	18.546 (14.84,23.176)	19.187 (15.354,23.977)	19.851 (15.885,24.807)	
Malaysian	15.563 (12.528,19.333)	16.708 (13.45,20.755)	17.884 (14.397,22.216)	18.429 (14.835,22.892)	18.933 (15.241,23.519)	21.134 (17.013,26.253)	
White/European UK	15.384 (12.115,19.536)	16.566 (13.046,21.036)	17.346 (13.66,22.026)	18.567 (14.621,23.576)	19.577 (15.417,24.86)	20.663 (16.273,26.239)	
Bangladeshi UK	15.290 (12.457,18.767)	16.349 (13.32,20.068)	17.085 (13.919,20.971)	17.764 (14.472,21.805)	18.787 (15.306,23.06)	19.535 (15.915,23.978)	

10.2 Data summary, third molar, stages 14 and 15

Tables A5 – A8 give a short summary of the number of individuals within each of the two latest third molar stages in the data. The tables contain the number of males and females in molar stages 14 and 15 less than 15 years, 15.5 years etc. up until 19 years for the five ethnic groups.

It is important to note that these data cannot be used to compute e.g. the fraction of individuals under the age of 18 in stage 15 as a proxy to the risk of an individual in stage 15 being under the age of 18. Such a fraction is a function of the maximum age allowed to be included in the data, which in this case was 26 years. With higher ages included such a fraction would decrease and with a lower age cut-off this fraction would increase.

As stated in this note, it is in general difficult to say something about the age distribution for individuals in stage 15, and hence no results for stage 15 are reported. This is due to the nature of the data. Molar 15 is the last stage where one remains. Any attempt to say something about the age distribution, as e.g. represented by the fraction of individuals under a certain age, will be problematic as it depends upon the maximum age. As Liversidge and Marsden (2010) write: "Once the tooth is fully mature, age cannot be estimated by root development…». In their paper they consider molar stages 8 – 15 and report age distributions (represented by the mean and a 95% confidence interval) for molar stages 8 – 14.

Table A5. Males, third molar, stage 14; number of individuals being less than 15, …, 19 years of age and the total number of individuals recorded within each group.						
Years	Sub-Saharan African	Japanese	Malaysian	White/European UK	Bangladeshi UK	Sum over ethnic groups
<15	0	0	0	0	0	0
<15.5	0	0	0	0	0	0
<16	2	1	0	0	0	3
<16.5	3	1	0	0	1	5
<17	6	1	0	3	1	11
<17.5	7	1	3	4	1	16
<18	9	1	5	5	2	22
<18.5	10	1	7	11	3	32
<19	14	2	10	15	3	44
All*	24	3	25	29	10	91
*Hence, there were 10 individuals 19 years or older in the Sub-Saharan African group.						

Table A6. Females, third molar, stage 14; number of individuals being less than 15, …, 19 years of age and the total number of individuals recorded within each group.

Years	Sub-Saharan African	Japanese	Malaysian	White/European UK	Bangladeshi UK	Sum over ethnic groups
<15	0	0	0	1	0	1
<15.5	0	0	1	1	0	2
<16	2	0	3	1	1	7
<16.5	2	0	3	1	1	7
<17	7	0	6	1	1	15
<17.5	9	1	8	1	2	21
<18	13	1	12	5	2	33
<18.5	15	2	16	8	4	45
<19	24	5	19	14	6	68
All	35	9	43	47	18	152

Table A7. Males, third molar, stage 15; number of individuals being less than 15, …, 19 years of age and the total number of individuals recorded within each group.

Years	Sub-Saharan African	Japanese	Malaysian	White/European UK	Bangladeshi UK	Sum over ethnic groups
<15	1	0	0	0	0	1
<15.5	2	0	0	0	0	2
<16	5	0	0	0	0	5
<16.5	6	0	0	1	1	8
<17	7	0	0	1	4	12
<17.5	9	0	0	1	7	17
<18	15	0	0	5	8	28
<18.5	15	1	0	11	9	36
<19	20	3	0	15	14	52
All	152	24	46	119	107	448

Table A8. Females, third molar, stage 15; number of individuals being less than 15, …, 19 years of age and the total number of individuals recorded within each group.

Years	Sub-Saharan African	Japanese	Malaysian	White/European UK	Bangladeshi UK	Sum over ethnic groups
<15	2	0	0	0	0	2
<15.5	2	0	0	0	0	2
<16	2	0	0	0	0	2
<16.5	2	0	0	1	1	4
<17	6	0	0	1	1	8
<17.5	8	2	0	1	2	13
<18	13	4	0	4	4	25
<18.5	15	4	2	6	8	35

<19	26	8	3	10	11	58
All	162	51	38	140	100	491

10.3 Model WinBUGS program

Known input values (from step one) in the WinBUGS-model (in step two) are $\hat{\mu}_1, \dots, \hat{\mu}_{J-1}$ and $\hat{\sigma}$ (mtransage[1], … mtransage[J-1] and sigma). The model, as written in R is given as:

```
model
{
 for(i in 1:J){
 age[i] ~ dunif(0,110)
 ln.age[i] <- log(age[i])

# Likelihood from "transition analysis"
  p[i,1]<- 1 - phi((ln.age[i]-mtransage[1])/sigma)
  for(j in 2:(J-1)){
    p[i,j]<- phi((ln.age[i]-mtransage[j-1])/sigma) - phi((ln.age[i]-mtransage[j])/sigma)
  }
  p[i,J]<- phi((ln.age[i]-mtransage[J-1])/sigma)

# Phase has multinomial distribution
  stage[i] ~ dcat(p[i,1 : J])

 }
}
```

Sentences following # are comments. Here the stage is defined as a categorical variable with probability p. The model was run for 250 000 burn-ins and thereafter updated another 250 000 iterations (thinning every 100), giving 2 500 samples.