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ORIGINAL ARTICLE

Human dental age estimation using third molar developmental stages: does a Bayesian approach outperform regression models to discriminate between juveniles and adults?

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Abstract Dental age estimation methods based on the radiologically detected third molar developmental stages are implemented in forensic age assessments to discriminate between juveniles and adults considering the judgment of young unaccompanied asylum seekers. Accurate and unbiased age estimates combined with appropriate quantified uncertainties are the required properties for accurate forensic reporting. In this study, a subset of 910 individuals uniformly distributed in age between 16 and 22 years was selected from an existing dataset collected by Gunst et al. containing 2,513 panoramic radiographs with known third molar developmental stages of Belgian Caucasian men and women. This subset was randomly split in a training set to develop a classical regression analysis and a Bayesian model for the multivariate distribution of the third molar developmental stages conditional on age and in a test set to assess the performance of both models. The aim of this study was to verify if the Bayesian approach differentiates the age of maturity more precisely and removes the bias, which disadvantages the systematically overestimated young individuals. The Bayesian model offers the discrimination of subjects being older than 18 years more appropriate and produces more meaningful prediction intervals but does not strongly outperform the classical approaches.

Keywords Forensic science · Forensic odontology · Age estimation · Third molar development · Linear regression · Polynomial regression · Bayesian model

Introduction

Forensic age estimation methods based on the correlation between the radiologically detected developmental stage of third molars and chronological age are among the few approaches affording information about age in the transition zone between juvenile and adult status [1–5]. They are therefore one of the major forensic age investigations in judging young unaccompanied asylum seekers [6–8]. In these retrospective studies, orthopantomograms of individuals with known chronological age at the time of radiologic exposure, gender, and preferably including origin were collected. Only individuals with no medical history, no visible dental pathology on the radiographs, and usually with at least one upper and one lower third molar present were included. All present third molars were classified by a scoring system proposed by diverse authors [9–12] and can be imported in an image manipulating program to obtain more accurate scoring [13].

Based on the gathered information, a prediction model was constructed, yielding an age estimate as a function of the third molar information and also a quantification of the uncertainty of this prediction. For unaccompanied young asylum seekers, specific interest lies in an adequate discrimination between juvenile and adult age. Legal

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systems around the world either based on civil jurisdiction or on common law and equity give suspects the benefit of doubt during judgment. Therefore, not only should the age estimates be accurate and unbiased but also the uncertainty should be quantified appropriately.

The classical approach for age estimation based on third molar developmental stages is the use of a regression model, where the age of the *i*-th subject is predicted using the information of one or more developmental stages:

$$\mathrm{Age}_i = h(x_{i1}, \ldots, x_{i4}) + \varepsilon_i, \tag{1}$$

where x_{i1}, …, x_{i4} denote the developmental stages of the four molars. When only one stage is used, Eq. 1 reduces to a simple regression model. Typically, $h(.)$ is a linear function, i.e., $\mathrm{Age}_i = \alpha + \beta x_i + \varepsilon_i$, and the number of used stages is restricted due to the high correlation between the stages as proposed by, e.g., Gunst et al. [5]. Within the linear regression modeling framework, the assumption of linearity can be relaxed using a spline or a polynomial function as $h(.)$. Chaillet and Dermirjian [14–16] considered regression models with a cubic function for one or two stages. For example, with only one molar stage Eq. 1 then becomes $\mathrm{Age}_i = \alpha + \beta_1 x_i + \beta_2 x_i^2 + \beta_3 x_i^3 + \varepsilon_i$. Note that these extensions still fit within the linear regression framework since age is still modeled as a linear function of a set of terms (e.g., linear, quadratic, cubic). A crucial feature of the discussed regression model is that the residuals ε_i (i.e., the difference between an observed value of the response variable and the value predicted by the model [17]) are assumed to be normally distributed around the regression line with a variance which remains constant. As such, the use of the regression approach implies a strict assumption about the shape (i.e., normal) and the variance (i.e., constant) of the age distribution. It should be emphasized that it is exactly this distribution which is used to quantify the uncertainty about the predicted age (i.e., by constructing a 95% prediction interval) and to calculate specific probabilities such as the probability of being a juvenile (Fig. 1). This reveals a first drawback of the linear regression model for age since the assumption about the age distribution might often be too restrictive in practice. Another practical limitation pertains to the high correlation between the independent variables in the regression model and to the presence of missing values for them. To circumvent this so-called multicollinearity problem, in practice, regression models are restricted to a limited set of the available stages. To handle the missing values, separate models are constructed for the various patterns of observed information. As such, the regression model approach results in an extended set of regression equations, each of them designed for a specific situation. A more serious concern, discussed in depth by Aykroyd et al. [18, 19], pertains to the systematic bias in age estimation when using the classical regression approach: The weaker the relation between the stages and age, the more the residuals ε_i in Eq. 1 will be related to age. As such, estimated ages are too old for young individuals and too young for old individuals. The direction of this bias is exactly what is not tolerable in the current legal context, as opposed to a bias pattern where the age of juveniles would be underestimated. To remove the bias induced by the use of a regression model for age, Lucy et al. [20] proposed to use a Bayesian approach. Recent examples can be found in Prince et al. [21, 22]. Following the notation in Eq. 1, the age distribution given a specific pattern of stages would in the current context be obtained as:

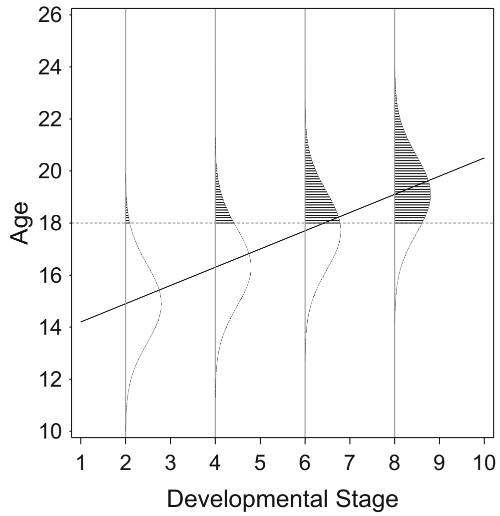

Fig. 1 Illustration of the assumption of constant variance and normality in the regression model. Given is a hypothetical example where the age is modeled as a linear function of one developmental stage. The *shaded part* pertains to the probability of being mature given a specific stage

$$f(\mathrm{age}_i | x_{i1}, \ldots, x_{i4}) = \frac{f(x_{i1}, \ldots, x_{i4} | \mathrm{age}_i) f(\mathrm{age}_i)}{\int\limits_i \left(x_{i1}, \ldots, x_{i4} | \mathrm{age}_i\right) f(\mathrm{age}_i)}. \tag{2}$$

Equation 2 consists of three parts. The left-hand side of the equation, i.e., the age distribution given an observed pattern of stages, is referred to as the *posterior distribution*. Note that its equivalent in the regression approach is the normal distribution with constant variance. However, the age distribution conditional on the observed stages is not a priori assumed to have a specific shape and variability in the Bayesian framework. Indeed, both features will depend on the *likelihood* $f\left(x_{i1}, \ldots, x_{i4} | \mathrm{age}_i\right)$and the *prior distribution* $f(\mathrm{age}_i)$. The likelihood function reflects the probability of the observed pattern of stages given that a subject has a specific age. The denominator in Eq. 2, which represents the probability of the observed pattern of developmental stages, is only used for normalization purposes such that the total surface of the posterior distribution equals one and surfaces under the posterior distribution can be interpreted as probabilities. Indices of location (e.g., median, modus) of the posterior distribution can be used as point predictions for age, but more informative is the prediction interval which can be obtained from its percentiles (e.g., 2.5th and 97.5th percentiles to represent a 95% prediction interval). Moreover, the calculation of a specific surface under the posterior distribution, i.e., the probability that age exceeds 18 years, will be crucial in the current context. The prior distribution of age $f(y)$ will often be a uniform distribution over a particular age range and can be changed if there is more specific prior knowledge about the age.

The aim of this paper is to compare the human age estimation based on third molar information using classical regression models and a Bayesian framework. More specifically, the aim is to verify if a Bayesian approach discriminates more accurately between adults and juveniles and removes the bias which disadvantages the latter group.

Materials and methods

Sample and measurements

A database of 2,513 orthopantomograms of Belgian Caucasian patients between 15.7 and 23.3 years of age, collected by Gunst et al. [5] and scored by the same authors on third molar developmental stages according to a modified technique of Gleiser and Hunt [9], was used. Since the performance of an approach might be related to age, for its comparison between both approaches, a subset of patients between 16 and 22 years has been used. This subset has a uniform age distribution and contains for each age interval of 1 year, between 16 and 22 years, the biggest overall found amount of women (n = 75) and men (n = 55) out of the main dataset. The subset is split at random into a training and test set of comparable size. The models were developed on the training set, and the performance of both approaches is assessed using the test set.

Classical regression model

Initially, Gunst et al. [4, 5] calculated 30 linear regression and multiple linear regression formulae (for females 17 and males 13) allowing to determine age based on the developmental stages of the third molars. This assortment of formulae was proposed because many subjects had one or more third molars missing and due to the high correlation between the different third molar stages a maximal of two stages could be used as predictors. Instead, we propose a more parsimonious strategy. Since there was no evidence for a left–right asymmetry in this study, the stages of the left molars, unless they were missing, are arbitrarily chosen as predictors. As such, three regression models are designed for males and females separately. One model pertains to the situation where information is available in both jaws, and two other models apply when there is only information on one jaw (upper or lower). Following Chaillet and Demirjian [14–16], the inappropriate assumption of the linear relationship between stages and age is relaxed using a cubic function for the upper and/or the lower stage. The models are fitted using the procedure PROC REG in the statistical package SAS, version 9.1 (SAS Institute, Cary NC, USA).

Bayesian approach

In the classical regression model, the molar stages serve as predictors to model the variability in age. The distribution and variability of the molar stages and the correlation between them are not modeled. The distribution of the molar stages is even irrelevant, except for the correlation which, as we have indicated, can induce multicollinearity problems. As such, the approach is straightforward from a computational point of view since the response in the model (i.e., age) remains univariate, irrespective of the number of stages used as predictors. In the Bayesian approach, the most important factors are the likelihoods $f\left(x_{i1},\ldots,x_{i4}|\mathrm{age}_i\right)$, which, combined with prior information about age, yield a (posterior) age distribution. To obtain these likelihoods, a model is needed for $(x_{i1},\ldots,x_{i4i})$, and we are faced with a multivariate instead of a univariate response. The challenge of the Bayesian approach in this setting is the construction of a model for the multivariate distribution of the stages conditional on age, i.e., the likelihood function. Note that each stage represents an ordinal variable. Therefore, we propose the use of a multivariate ordinal regression model with a random subject effect [23] to incorporate the correlation between the third molar developmental stages of the subject. Fitting the multivariate ordinal regression model such that the likelihoods can be obtained is computationally intensive. Details on this model and on the calculation of the posterior probabilities can be found in the Appendix.

Various quantifications have been used to compare the performance of the classical regression and the Bayesian approach. First, the difference between predicted and true age is calculated. The smaller this difference, the more accurate the model. Second, the precision of the prediction is reflected by the width of the 95% confidence intervals (CI). Obviously, the precision should be realistic, meaning that using 95% CIs, only 5% of the observed ages should fall outside the CI. If this percentage is higher, this might reflect either a systematic bias in the point prediction or a prediction interval which is too optimistic (too narrow). This property is referred to as *coverage.* Third, the Pearson correlation between age and the difference between true and predicted age is used to quantify the degree of bias. The stronger the correlation, the higher the age of young individuals will be overestimated. Finally, the posterior probabilities to be a mature and their corresponding diagnostic indices (sensitivity, specificity) are compared.

In the classical approach, a regression model with only linear terms as well as a model considering a polynomial function of the third degree has been used. In the remainder, we will refer to the latter regression model as the polynomial model

Results

Unless otherwise stated, reported results from the classical approach are based on the polynomial model.

Figure 2 shows the age distribution observed at different developmental stages. Clearly, the shape of the age distribution differs for the various stages. Whereas the variability (e.g., height of the boxes) does not strongly differ, the skewness does: For early stages, the age distribution is right-skewed (i.e., a tail toward higher age values); for late stages the opposite holds. The line representing the trend in the relation between the stages and age illustrates the inappropriate assumption of linearity (Fig. 2).

In more than 98.5%, the difference between the developmental stage of the left and the corresponding right third molar was less than or equal to 1. A paired Wilcoxon test did not reveal a systematic difference between the stages at the left and at the right side ($p = 0.22$).

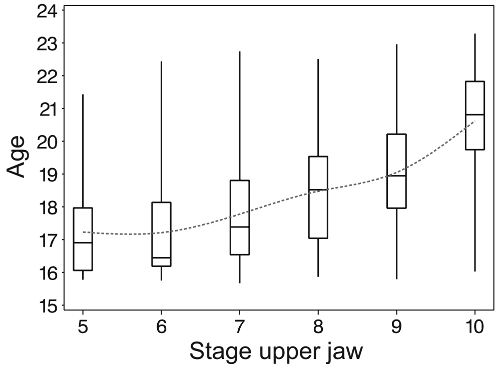

Fig. 2 Relation between the stage and age for male subjects. Boxplots (whiskers pertain to minimum and maximum value) for the age distribution observed at each of the possible stages. Stages in the upper jaw (right stage if left one is not available) from 991 male subjects are chosen for illustrative purposes. Stages ≤5 are considered as one category. The *trend line* illustrates the inappropriate assumption of linearity for the relation between the stage and age

The polynomial model as well as the multivariate ordinal model offers evidence for a difference between males and females ($p < 0.0001$ for both models). Note that the gender difference is assessed by comparison of a model with all parameters gender specific and a model with all parameters shared between males and females ($p < 0.0001$ for both models).

In the polynomial model, an interval of likely ages given the third molar developmental stage(s) of new subjects is given by the percentiles of the normal distribution with the mean a function of the stage(s) and the variance independent of the stages. In the Bayesian approach, the interval of likely ages is obtained from the percentiles of the posterior distribution where the shape can vary as a function of the (pattern) stage(s). Figure 3a and b presents some posterior distributions for specific stage patterns, clearly having different shapes, obtained for male subjects. The probability of being mature corresponds to the surface to the right of 18 years under the posterior distribution. For example, if a male subject has a stage 6 for all four molars, the 95% range of likely ages is (≤15;19.8) and the probability of being mature is 16.5%. Note that the polynomial model yields a 95% prediction interval of (14.5;20.1), which is similar to the Bayesian approach. However, the probability of being mature is increased to 30.3%. The next paragraphs contain the results of the systematic comparison of both approaches based on the mentioned subset of patients between 16 and 22 years with a uniform age distribution.

Using the polynomial model, the mean absolute difference between the observed and the predicted age equals 1.13 years (median (Me)=0.97, interquartile range (IQR) 0.49–1.57). Using the median of the posterior distribution as a point prediction for the age, the Bayesian approach yields a comparable distribution for the mean absolute differences (Mann–Whitney *U* test, $p = 0.40$) of 1.13 years (Me = 0.89, IQR 0.44–1.62).

If the 95% range of likely age values obtained with both approaches is realistic, then ideally, 95% of the ages in the test dataset should fall within this range. The same should hold for other ranges of likely values (e.g., 90% range). With the polynomial model, 93.2% and 97.2% of the observed ages fall within the 90% and 95% prediction intervals, respectively. Also, with the Bayesian approach, the obtained ranges of likely age values are slightly too wide: 96% and 98.6% of the observed ages fall in the 90% and 95% prediction intervals. However, within the Bayesian approach, the width of the range of likely values will not only depend on the amount of information used (the more stages available, the narrower the prediction interval) but also on the degree of agreement between the various stages. More specifically, it is expected that with the Bayesian approach, the range of likely ages will be more narrow if the stages within a jaw correspond with each other. To illustrate this, the mean width of the 95% prediction interval is 6.34 years (Me = 6.60, IQR 6.0–7.0) if the left and right stages are not equal in either the lower or the upper jaw (N = 169). The width of the 95% prediction interval is significantly (p = 0.0002) reduced when the left and right stages agree in both jaws: The mean width of the 95% prediction interval equals 5.95 years (Me = 6.0, IQR 5.3–6.8).

The bias as a function of age is clearly present when using the polynomial model. There is a strong (Pearson r = 0.66) positive correlation between age and the difference between predicted and observed age, implying that the age of younger subjects is systematically overestimated. This bias is reduced with Bayesian framework using the median (r = 0.38) and the modus (r = 0.01) from the posterior distribution as point prediction.

Using the posterior probabilities to be mature (P(m)) to discriminate between juveniles and mature subjects, both approaches yield a similar overall performance: The area under the ROC curve equals 0.847 for the polynomial model and 0.853 for the Bayesian approach. However, for the 260 subjects in the test dataset that are younger than 18 years, the median P(m) is 0.51 (IQR 0.40–0.72) with the polynomial model and 0.31 (IQR 0.17–0.61) with the Bayesian approach, resulting in a stronger tendency for the polynomial model to classify younger subjects to soon as mature.

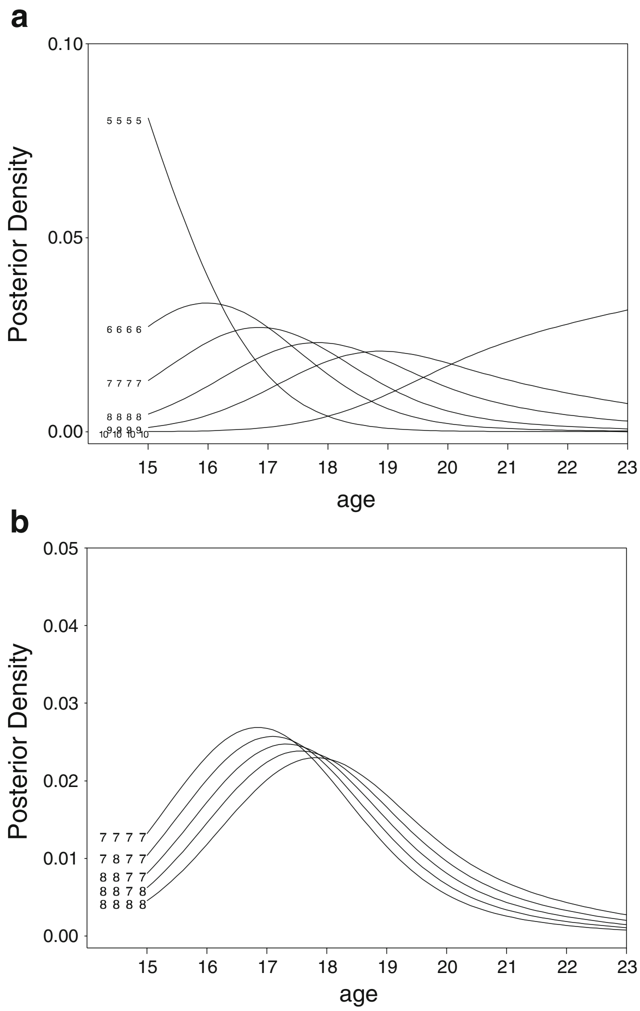

Fig. 3 Posterior distribution of male subjects for different stage patterns. **a** All possible homogeneous stage patterns (four times the same stage). The right-skewed distribution of age for teeth in the lowest developmental stage with all four stages equal to five or lower (5555) smoothly evolves to a left-skewed age distribution when all third molars are fully developped (10101010). **b** The subtle differences in age distribution when the stage of one third molar changes one unit

Discussion

Linear regression models constitute the classical approach to estimate age and discriminate between juveniles and adults using third molar developmental stages. These models are easy to apply and can be adapted such that non-linear relations between a stage and age are allowed. However, various criticisms have been raised against the use of these models for age estimation. A first shortcoming of the approach pertains to the unrealistic assumption that at every combination of stages age has the same distribution with respect to shape and variance, possibly yielding inappropriate prediction intervals. Secondly, arbitrary strategies are needed to handle the correlations between the stages. Typically, at most two stages will be used leading to some loss of information. Finally, the age of juveniles will systematically be overestimated, which is unacceptable for young asylum seekers. To overcome these disadvantages, the use of a Bayesian framework has been advocated (see for example Prince et al. [21, 22]). In this paper, Bayes' rule was used to derive the distribution of age given the four third molar stages. For the conditional distribution of the molar stages, i.e., the challenging part of the rule, we proposed the use of a generalized linear mixed model for ordinal data. We clearly obtained a higher degree of flexibility with the Bayesian approach. The obtained posterior distributions varied in shape and variability as a function of the various stage patterns. The assumption of one common normal distribution was clearly not appropriate. Also, the presence of multicolinearity is dealt with in a natural way since the stages are not considered as predictors, but as a set of repeated responses. A random subject effect is used in the generalized linear mixed model to capture the correlation between these responses (i.e., stages). An additional advantage of considering the stages as responses is that the presence of missing stages does not induce any problem. Note that in the classical approach, a separate regression model needs to be built for each possible pattern of missing information. Further, the Bayesian approach yields confidence intervals whose width varies as a function of the amount of available information and as a function of the degree of agreement between the information.

On the other hand, the Bayesian approach comes at the cost of a higher computational complexity. Nevertheless, it does not strongly outperform the classical approach in general. Indeed, there is no strong reduction of the differences between the observed and predicted age, no increase in precision, and the prediction intervals do not cover the observed age distributions more appropriately. However, using the Bayesian approach, there is a reduction in bias typically present in the regression model approach. The age of juveniles is less overestimated, yielding a better discrimination between subjects older and younger than 18 years such that subjects younger than 18 years will be classified correctly more often.

Lucy et al. [18] avoided the use of the computational intensive mixed model for multivariate ordinal data. They assumed that the observed correlation between the stages is accounted for by the age of a subject, meaning that given the age, the four stages are conditionally independent. The consequence of this assumption is that the conditional multivariate density $f(x/\text{age})$ can be written as a product of univariate densities, avoiding the computational complexity of fitting a multivariate ordinal model. Moreover a non-parametric approach for the conditional distribution is applied since the observed distribution of third molar stages as a function of pre-specified age categories is used. In a further extension, the same authors relaxed this strong conditional independence by the use of a weaker partial conditional independence [19, 20]. In further research, both the generalized linear mixed model proposed in this study and the multivariate model proposed by Lucy et al. should be evaluated to verify if the model with higher computational burden outperforms the model with the (partial) conditional independence assumptions.

Age groups lower than 15.7 years and according third molar developmental stages lower than 5 are not included in the original data and equally not in the test dataset. Collecting and importing a dataset including these subjects into the Bayesian model could ameliorate the prediction of the probability of a subject to be older than 18 years.

Regardless of the approach applied, the obtained knowledge of the third molar developmental stages of a subject does not strongly reduce the uncertainty about the age. Furthermore, alarmingly high prediction intervals (approximately 6 years) and far from optimal discrimination of maturity is obtained. Therefore, modern forensic age estimation protocols for unaccompanied asylum seekers take, apart from the clinical findings the evaluation of third molar developmental stages, the ossification stages of the medial clavicle epiphysis and the comparison of a radiograph from the subject's left hand with standard radiographs classified by age into consideration [24]. Incorporation of these additional sources of information into the Bayesian framework could be considered. Because of the expected correlation, this new information should be gathered simultaneously on each reference individual. In practice, it will be difficult to establish a large data set of subjects on which these three age evaluation systems are simultaneously applied. It means that within the same examined reference group, ten dental developmental stages [10–12], five clavicular ossification phases [25–27], and all the standard hand radiographs [28] have to be present, and for each subject, the evaluation of the different age indicators has to be carried out at the same chronological age. Ethically, it is not justified to submit test individuals to such a big amount of ionization [29], beside, in certain jurisdictions, it is legally prohibited. A way to diminish the quantity of the original data set could be established by reducing the amount of third molar developmental stages and restrict them to the clearly defined stages, simultaneously introducing better scoring reproducibility [30]. The introduction of other non-destructive and clinical detectable dental age estimation methods such as attrition [22, 31, 32] and attachment of the periodontal ligament [32, 33] into the model for the purpose of amelioration of the age estimation could be considered but are in the age group around majority difficult to differentiate and classify. The gentliest way to incorporate possible other age-related variables into a Bayesian framework would be achieved by taking into account their partial correlation and implementing them in the model presented by Lucy et al. [20].

It is recommended that the expert report of age assessment includes the most probable age of the investigated individual, the range of the scatter of the reference population, and possible observer error. Furthermore, the used methods and their reference studies should be cited [24]. In the context of the present study, “methods” refers to statistical analysis procedures of human dental age estimation on third molar developmental stages. With particular specifications, the classical approach as well as the Bayesian model provides information of the individual’s age and the probability of being mature. The results of both analyses should be reported, and simultaneously, a discussion of their correct and mutual weight preventing false interpretation of the provided information and avoiding the creation of fallacies similar as those described in forensic statistics, namely base rate fallacy, prosecutor's fallacy, and defense attorney's fallacy [34, 35], should be presented.

Conclusion

Classical linear and polynomial statistical regression analysis and a new developed Bayesian model were tested and compared on a large newly constructed test data set of developmental stages of third molars. Although the Bayesian model does not outperform the classical approaches, it allows a more appropriate discrimination of subjects being older than 18 years and produces more meaningful prediction intervals. In this way, the Bayesian model offers besides the linear and polynomial regression analysis useful additional tools in easing forensic decision making during determination of maturity ages. Using third molar developmental stages as the only variable in forensic discrimination between juvenile and adult provides overall poor results.

Appendix: Bayesian approach

A multivariate ordinal regression model to obtain the likelihoods $f\left(x_{i1},\ldots,x_{i4}|\mathrm{age}_i\right)$:Formally, let x_{ij} denote the j-th third molar stage, j = 1,…,4, for subject i, with K possible values, then

$$\log\left\{\frac{P\left(x_{ij}\leq k\right)}{1-P\left(x_{ij}\leq k\right)}\right\}=\alpha_{0k}+\alpha_{1k}U_{ij}+h\left(\mathrm{age}_i\right)+b_i, \quad (3)$$

where α_{0k} α_{0k} are the $K-1$ intercept terms to model the marginal frequencies in the K ordered categories of the stage. The left-hand side of the equation represents various logits, i.e., natural logarithms of a specific odds (the odds of observing a stage lower than a specific value k). Observe that if a developmental stage would only have two different values (say 1 and 2), the left-hand side would pertain to a single logit, yielding a binary regression model. A binary indicator U is valued 1 if the third molar is located in the upper jaw and 0 elsewhere. The α_{1k} quantify the difference in stage between upper and lower jaw. The subscript k indicates in the latter that the effect of jaw is allowed to be non-constant over the intercepts implicating that a proportional odds assumption is not made for this effect. A flexible function h(.) is used to relate age to the logit scale, more specifically, restricted cubic splines have been used [36]. The key idea is to allow non-linearity (on the logit scale) in a flexible way without over fitting the data. Finally, the b_i denotes the random subject effect, assumed to be normal distributed. By including this term in Eq. 3, each subject i is allowed to have its own stage level (on logit scale), hereby accounting for the correlation, which exists between the four repeated stage measures. The resulting model is a generalized linear *mixed* model, where the term *mixed* refers to the simultaneous presence of fixed effects (i.e., age and jaw) and a random effect (the b_i). See for example Molenberghs and Verbeke [37]. Due to the low incidence of stages lower than or equal to 5, those stages are combined into one category. Moreover, no distinction is made between the location (left/right) of a stage. As such, a stage pattern “8 8 6 7” pertains to two stages equal to 8 in the upper jaw and one stage 6 (left or right) and one stage 7 (left or right) in the lower jaw. The generalized linear mixed model is fitted with the procedure PROC NLMIXED in the SAS 9.1 statistical package (SAS Institute, Cary, NC, USA), using adaptive Gaussian quadrature.

Once model Eq. 3 is fitted on the data, the likelihood $f\left(x_{i1},\ldots,x_{i4}|\mathrm{age}_i\right)f\left(x_{i1},\ldots,x_{i4}|\mathrm{age}_i\right)$ can be calculated for all possible patterns (x_{i1},…,x_{i4}) given a specific age. This has been done in steps of 0.1 years, hence the integral in the denominator of Eq. 2 is replaced by a sum over age intervals of 0.1 years and the posterior distribution in Eq. 2 will also have steps of 0.1 years as support points. For the prior distribution, a uniform distribution has been used, implying that each age-category within the considered range (16–22 years for the comparison of the approaches) is given the same (prior) probability.

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