**Supporting Information**

**Method S2. Bayesian Model Description**

The OsteoBioR model considers a matrix with entries representing a remodelling percentage x. Matrix rows represent the selected time intervals (t) and each column (n) an isotopic measurement made on a certain skeletal material. In the case of tooth dentine sections, we assumed a constant remodelling rate (*c.* 6 μm/day for ancient populations, Dean & Scandrett 1995) and that once dentine is formed no further remodelling is possible. Since the length of a tooth section does not necessarily match univocally a six-month interval each measured section is divided into a number of columns corresponding to the number of six-month intervals that it spans and the entries for the remodelling values x in each column and time row combination correspond to the percentage of the tooth section contained within a certain time interval.

     To estimate the vector of isotopic values (i) across the t time points we consider that the isotopic measurements made on tooth sections (y) with a certain uncertainty (σy) and represented across different columns follow:

y ~ N(x \* i, σy)

with

i ~ N(μ, K(α, ρ)) as a Gaussian process with covariance matrix K following the exponentiated quadratic covariance function k(t, t') = Cov(it, it') = α^2 \* exp(1 / (-2 ρ^2) \* ( it -  it')^2)

      The following prior distributions were specified: μ ~ t(0, 10, df = 1); ρ ~ N(1, 0.25); α ~ N(2, 0.5). Computation was done using Hamiltonian Monte Carlo (HMC, Carpenter *et al.* 2017), a Markov chain Monte Carlo algorithm, to draw observations from the posteriors. This was done using (R)Stan (Stan Development Team 2018) within R (Development Core Team 2020) Absolute time shifts in isotopic values larger than a user defined percentage were automatically detected.

The Bayesian approach allows us to provide results on a common temporal scale which is independent of intra- and inter-individual differences. This issue arises since the tooth sections did not always have the same exact length. Furthermore, in some cases the amount of collagen from a single segment was insufficient for measurement, a common occurrence in this type of work. For these we combined for measurement multiple increments. This is described in sections’ text labels by concatenating the letter codes corresponding to single increments (e.g. BN124-M1-A+B). In raw plots, combined measurements refer to extended time periods. By using the Bayesian model we generate estimates for shorter temporal resolutions and with an uncertainty larger than analytical uncertainty. It should also be noted that there is also uncertainty when matching isotopic measurements for each section to a specific lifetime period of an individual. Under the Bayesian modelling approach estimates are generated for time intervals within the lifetime of an individual rather than to a specific time point. This is pertinent as the sections have a thickness and so represent a temporal average of c. 6 months. Furthermore, this issue is compounded when multiple sections are combined.

**References**

Carpenter B, Gelman A, Hoffman MD, Lee D, Goodrich B, Betancourt M, Brubaker M, Guo J, Li P, Riddell A 2017. *Stan: A probabilistic programming language*. Journal of Statistical Software **76**. DOI: 10.18637/jss.v076.i01

Dean MC, Scandrett AE. 1995. Rates of dentine mineralization in permanent human teeth. *International Journal of Osteoarchaeology* **5**: 349-358. DOI: 10.1002/oa.1390050405