

Approximating fragmented functional data by segments of Markov chains

BY A. DELAIGLE AND P. HALL

School of Mathematics and Statistics, University of Melbourne, Parkville, Victoria 3010, Australia

A.Delaigle@ms.unimelb.edu.au

SUMMARY

We consider curve extension and linear prediction for functional data observed only on a part of their domain, in the form of fragments. We suggest an approach based on a combination of Markov chains and nonparametric smoothing techniques, which enables us to extend the observed fragments and construct approximated prediction intervals around them, construct mean and covariance function estimators, and derive a linear predictor. The procedure is illustrated on real and simulated data.

Some key words: Crossvalidation; Functional principal component; Incomplete curve; Markov chain.

1. INTRODUCTION

We consider functional data X_1, \dots, X_n , where each X_i is a random curve defined on an interval \mathcal{I}_0 . It is common to assume that the curves are completely observed, or that they are observed on a grid of points that are closely spaced within \mathcal{I}_0 . However, in some problems we can observe each curve X_i on only one or a few small subsets of \mathcal{I}_0 .

One can distinguish principally two types of partially-observed functional data. The first type, often referred to as the sparse functional case, corresponds to the situation where each curve is observed at a small number of points that are distributed randomly over \mathcal{I}_0 . For the second type, which we refer to as the fragmentary functional case, each curve is observed at points that cover a subset of \mathcal{I}_0 in such a way that the observations can reasonably be treated as fragments of curves; see the Supplementary Material.

As demonstrated by [Delaigle & Hall \(2013\)](#), the methods appropriate for analysing these two types of incomplete data are different. In the sparse functional case, because the points where each curve is observed are randomly distributed over the whole interval \mathcal{I}_0 , one can use relatively standard smoothing techniques to estimate the mean and covariance functions. See, for example, [James et al. \(2000\)](#) and [Yao et al. \(2005\)](#), who also suggest a way of reconstructing the functions on \mathcal{I}_0 using a predictor based on the assumption that the data are normally distributed. Those methods are usually inappropriate for the fragmentary case, where each curve is observed on only one or two small subsets of \mathcal{I}_0 . [Delaigle & Hall \(2013\)](#) suggested a method for reconstructing the functions by adjoining, to each fragment, shifted versions of other observed fragments. However, their method is designed specifically for situations where only one fragment per curve is observed, and it forces each of the reconstructions to have exactly the shape of an observed fragment. [Kraus \(2015\)](#) considered a related problem, but his setting is closer to that of [Yao et al. \(2005\)](#) since, like there, his fully nonparametric approach requires fragments to cover the whole interval \mathcal{I} . There

has also been interest in forecasting future observations, but not in our setting of fragmentary data; see, for example, [Liebl \(2013\)](#) and [Goldberg et al. \(2014\)](#).

In this paper we propose a new approach to reconstructing curves from a sample of fragments, with a particular focus on small fragments. In a first step, we discretize the problem in both time and space. For a curve $X(t)$, $t \in \mathcal{I}_0$, we refer to t as time and to $X(t)$ as space. At each discrete point t we model the transition of X from that point to the next by a Markov chain. To estimate the transition probabilities at each discrete t , we borrow information from neighbouring data values using a smoother that takes into account the shapes of the fragments. Most of our attention is focused on short and sparse fragments. There, limited by the poor quality of the data, we use low-order Markov chains. In § 5.2 we extend our approach to higher-order chains, which are able to capture more complex structures but can be employed only when the fragments are longer and less sparse.

Markov modelling enjoys a remarkable diversity of applications, including climate science and fluid dynamics ([Franzke et al., 2008](#)), medicine ([Strachan et al., 2009](#)), genomics ([Yau et al., 2010](#)) and many other fields. In these settings, Markov modelling leads to computationally feasible solutions where other approaches often fail. Sometimes this entails compromises. For example, in fluid dynamics, Markov models are attractive even though they require compromises relating to theoretical issues. In particular, when developing continuous-time Markov process models of the atmosphere as a fluid, it may be necessary to consider instantaneous, infinite accelerations at various points; see, for example, [Legg & Raupach \(1982\)](#).

The potential of Markov modelling to supply solutions that might otherwise be out of reach is also useful in applications to functional data. For example, the covariance function, Γ , can be particularly difficult to estimate from fragmented functional data if we use conventional methods, such as the approach of [Yao et al. \(2005\)](#). Indeed, their curve extension method relies on the construction of a kernel estimator of Γ , which itself requires observing at least several individual curves at each pair of time-points $(s, t) \in \mathcal{I}_0 \times \mathcal{I}_0$. While this is possible in their sparse data setting, it is not possible in the fragmentary context. The Markov modelling approach introduced in this paper enables us to estimate Γ by a relatively simple, explicit estimator. Another attractive property of our approach compared to related methods developed in the sparse setting is that it produces an estimator of the conditional distribution of the missing function values, which makes possible further analysis of conditional characteristics. For example, it enables us to construct approximate prediction intervals around the reconstructed curves, as we discuss in § 3.2.

[Legg & Raupach \(1982\)](#), among other authors, have pointed to the advantages of using Markov chain rather than Markov process models. A Markov chain is a discrete-time random process, whereas a Markov process, if it does not have jump discontinuities, is a diffusion, and in particular is a continuous process without a first derivative ([Ghosh, 2011](#)). Therefore, the discretization that we shall introduce in the second paragraph of § 2 should not be seen as producing grids that will become infinitesimally fine as the sample size increases. On the other hand, although it is required in practice, in theory the space discretization is not really needed, and we discuss this in § 5.3. Markov models can be used widely in functional data analysis, for example as an aid to building classifiers, but we shall restrict our attention here to their application to covariance estimation, and to solving prediction problems, in the case of fragmented data.

2. MODELS AND DATA

We record independent and identically distributed data (X_i, Y_i) , where X_i , an explanatory variable, is a function supported on a compact interval $\mathcal{I}_0 = [a, b]$, and Y_i is a scalar response.

However, while the Y_i ($i = 1, \dots, n$) are all known, we observe each X_i only on the interval $\mathcal{I}_i = [A_i, B_i] \subseteq \mathcal{I}_0$, for $i = 1, \dots, n$; the case of several disjoint intervals will be discussed in § 5.1. Our goal is to reconstruct the unobserved parts of the curves X_i , predict the value of Y given that a newly observed X takes the value x , observed on $\mathcal{I} = [A, B] \subseteq \mathcal{I}_0$, and estimate the mean and covariance functions of X . We assume throughout that the fragments of the functions X_i are observed without noise. The procedures we suggest can be adapted to the case where the X_i are observed with additive noise by using deconvolution techniques employed in nonparametric errors-in-variables problems, as in Carroll & Hall (1988) and Delaigle et al. (2008). This problem will be dealt with elsewhere.

We propose to employ Markov chain models for inference based on a discretized version of the process X . Our discretization is effected in both time and space. We start by constructing a grid of points t_j on the time, or horizontal, axis, $\mathcal{I}_0^{\text{disc}} = \{t_1, \dots, t_{m_1}\} \subseteq \mathcal{I}_0$, where $a \leq t_1 < \dots < t_{m_1} \leq b$. The superscript disc denotes discrete. It will simplify notation if the endpoints a and b of \mathcal{I}_0 are elements of $\mathcal{I}_0^{\text{disc}}$, and so we make that assumption. Throughout this work, writing \mathcal{J} for a general subinterval of \mathcal{I}_0 , we let $\mathcal{J}^{\text{disc}} = \mathcal{J} \cap \mathcal{I}_0^{\text{disc}}$.

Next, we construct a grid of points z_1, \dots, z_{m_2} on the state space, or vertical, axis, and reduce the data function $X_i(t)$, $t \in \mathcal{I}_i$, to the set of point pairs $\{t_j, Z_i(t_j)\}$, $t_j \in \mathcal{I}_i^{\text{disc}}$, where $Z_i(t_j)$ takes the value z_k if $(z_{k-1} + z_k)/2 < X(t_j) \leq (z_k + z_{k+1})/2$ and we define $z_0 = -\infty$ and $z_{m_2+1} = \infty$; see the Supplementary Material. If $Z_i(t_j) = z_k$, then we say that the chain Z_i is in state z_k at time t_j . The points t_j and z_k need not be regularly spaced, but often they will be, and to simplify our discussion we shall assume from now on that they are. We denote the distance between two consecutive t_k by Δt and the distance between two consecutive z_k by Δz . The estimators we shall propose in § 3.1 involve smoothing, so we can take our discrete grids to be relatively fine. See § 6.1 for details of the practical implementation.

In our notation, for simplicity, the time-points t_j at which we discretize the function X_i are assumed not to depend on i . We anticipate this to be the case in practice, not least because we can interpolate between times at which X_i is actually measured. Only minor complications arise if we take the t_j to depend on i , as long as the numbers and spacings do not vary widely.

We first focus on the case where the fragments are sparse and short. There, the data are so poor that progress can only be made if the data vary in a simple way. In this setting, we propose modelling the discretized data using first-order Markov chains. Specifically, we assume that the random process $Z(t)$, $t \in \mathcal{I}_0^{\text{disc}}$, is a first-order Markov chain, which is true if and only if whenever $s, t \in \mathcal{I}_0^{\text{disc}}$ with $s < t$, for all subsets \mathcal{B} of the countable set of states we have

$$\text{pr}\{Z(t) \in \mathcal{B} \mid \mathcal{F}_s\} = \text{pr}\{Z(t) \in \mathcal{B} \mid Z(s)\}, \quad (1)$$

where \mathcal{F}_s denotes the sigma-field generated by $Z(u)$ for all $u \in [a, s]^{\text{disc}}$.

The fact that we use this simple model does not imply that we believe all discretized functional data can be approximated reasonably well by first-order Markov chains. Rather, our solution provides a reasonable approximation in cases where the population consists mostly of curves whose value at a time t is roughly dictated by values in the very recent past. If the observed fragments are longer and less sparse, we can model data with more complex structures by using higher-order Markov chains; see § 5.2.

Equivalently to (1), the random process $Z(t)$, $t \in \mathcal{I}_0^{\text{disc}}$, is a first-order Markov chain if and only if the past and the future are independent, conditional on the present. Since this statement is symmetric in the notions of past and future, property (1) holding whenever $a \leq s < t \leq b$ is

equivalent to the following: whenever $a \leq t < s \leq b$ with $s, t \in \mathcal{I}_0^{\text{disc}}$,

$$\text{pr}\{Z(t) \in \mathcal{B} \mid \mathcal{G}_s\} = \text{pr}\{Z(t) \in \mathcal{B} \mid Z(s)\}, \quad (2)$$

where \mathcal{G}_s is the sigma-field generated by $Z(u)$ for $u \in [s, b]^{\text{disc}}$.

Similarly, if \mathcal{B}_1 and \mathcal{B}_2 are subsets of the set of states, if $\mathcal{H}_{s_1 s_2}$ denotes the sigma-field generated by $Z(u)$ for $u \in [s_1, s_2]^{\text{disc}}$, and if $s_1, s_2, u_1, u_2 \in \mathcal{I}_0^{\text{disc}}$, then

$$\text{pr}\{Z(u_1) \in \mathcal{B}_1, Z(u_2) \in \mathcal{B}_2 \mid \mathcal{H}_{s_1 s_2}\} = \prod_{j=1}^2 \text{pr}\{Z(u_j) \in \mathcal{B}_j \mid Z(s_j)\} \quad (3)$$

when $a < u_1 < s_1 \leq s_2 < u_2 < b$. Moreover, the left-hand side of (3) equals $\text{pr}\{Z(u_1) \in \mathcal{B}_1, Z(u_2) \in \mathcal{B}_2 \mid Z(s_1)\}$ when $a \leq u_1, u_2 < s_1 \leq s_2 \leq b$ and equals $\text{pr}\{Z(u_1) \in \mathcal{B}_1, Z(u_2) \in \mathcal{B}_2 \mid Z(s_2)\}$ when $a \leq s_1 \leq s_2 < u_1, u_2 \leq b$.

3. ESTIMATORS AND LINEAR PREDICTORS

3.1. Transition probabilities and their estimators

In order to estimate the quantities that interest us, we need to start by estimating the transition probabilities that govern the discrete-time process $Z(t)$ for $t \in \mathcal{I}_0^{\text{disc}}$. These probabilities are defined by $p(t_j, z_{k_1}, z_{k_2}) = \text{pr}\{Z(t_{j+1}) = z_{k_2} \mid Z(t_j) = z_{k_1}\}$ and $q(t_{j+1}, z_{k_1}, z_{k_2}) = \text{pr}\{Z(t_j) = z_{k_2} \mid Z(t_{j+1}) = z_{k_1}\}$ for each j, k_1 and k_2 . In particular, the quantities $p(t_j, z_{k_1}, z_{k_2})$ represent transitions forward in time, whereas the quantities $q(t_{j+1}, z_{k_1}, z_{k_2})$ represent backward transitions.

A naive approach to estimating these probabilities would be to use maximum likelihood estimators. Let $N(t_j, z, z') = \sum_{i=1}^n I\{Z_i(t_j) = z, Z_i(t_{j+1}) = z', A_i \leq t_j < B_i\}$ and $N(t_j, z) = \sum_{z'} N(t_j, z, z')$. We show in the Supplementary Material that the maximum likelihood estimators of the $p(t_j, z, z')$ are given by

$$\hat{p}_{\text{ML}}(t_j, z, z') = N(t_j, z, z') / N(t_j, z), \quad (4)$$

where the right-hand side of (4) is interpreted as zero when $N(t_j, z) = 0$.

While this approach is simple, our data are sparse, and in practice the quantities $\hat{p}_{\text{ML}}(t_j, z, z')$ are each generally computed from too few observations. To illustrate this, we consider partially observed growth curves for 153 females from four ethnic groups, referred to as Asians, Blacks, Hispanics and Caucasians, from a dataset described in [Bachrach et al. \(1999\)](#), where growth was measured by the spine bone mineral density. In the study, each woman was typically followed for only a few years, whence the fragmentary nature of the data, depicted in Fig. 1 for the Hispanic and Black ethnic groups. In each group, the fragments are so sparse that for most values of (t_j, z, z') , $\hat{p}_{\text{ML}}(t_j, z, z')$ is equal to zero, whereas the remaining few equal unity.

Fortunately, in a functional data context it is reasonable to assume that if two points (t_j, z, z') and (t_k, u, u') are close, then $|p(t_j, z, z') - p(t_k, u, u')|$ is small. This motivates us to introduce smoothing in time and space and estimate $p(t_j, z, z')$ by

$$\hat{p}(t_j, z, z') = \hat{A}(t_j, z, z') / \sum_{z'} \hat{A}(t_j, z, z'), \quad (5)$$

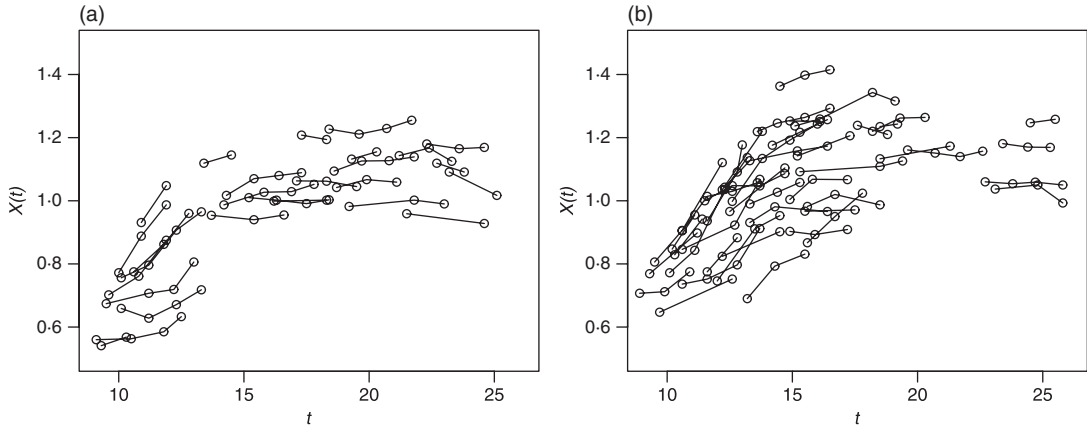


Fig. 1. Curve fragments of growth, measured by the spine bone mineral density, in g cm^{-2} , for females from the (a) Hispanic and (b) Black ethnic groups described in [Bachrach et al. \(1999\)](#).

where $\hat{A}(t_j, z, z')$ denotes a smoothed version of the numbers $N(t_k, z, z')$ and the right-hand side of (5) is interpreted as zero when $\sum_{z'} \hat{A}(t_j, z, z') = 0$.

To define $\hat{A}(t_j, z, z')$, we note that the numbers $N(t_k, z, z')$ will tend to be unduly large or small, depending on whether the interval \mathcal{I}_i often covers the pair (t_k, t_{k+1}) or covers it infrequently, respectively. To counter the effect of this source of bias, we replace $N(t_k, z, z')$ by

$$\tilde{N}(t_k, z, z') = \frac{\sum_{i=1}^n I\{Z_i(t_k) = z, Z_i(t_{k+1}) = z', A_i \leq t_k < B_i\}}{\sum_{i=1}^n I(A_i \leq t_k < B_i)} \quad (6)$$

and take

$$\hat{A}(t_j, z, z') = \sum_{u, u'} \sum_{k=1}^{m_1-1} \tilde{N}(t_k, u, u') w(t_j, t_k) \omega\{(z, z'), (u, u')\}, \quad (7)$$

where the weights w and ω are defined below. We take the contribution to the right-hand side of (7), for index k , to equal zero if $\sum_{i=1}^n I(A_i \leq t_k < B_i) = 0$.

Let K be a symmetric, positive and continuous kernel function, and let $h \geq 0$ and $g \geq 0$ be two bandwidths. For $h > 0$ put $K_h(u) = h^{-1}K(u/h)$, and for $h = 0$ let $K_0(u) = 1\{u = 0\}$; define K_g analogously. We define our weights w and ω by $w(t_j, t_k) = K_h(|t_j - t_k|)$ and

$$\omega\{(z, z'), (u, u')\} = K_g\{\alpha(|z - u| + |z' - u'|) + (1 - \alpha)|z - z' - (u - u')|\},$$

where $\alpha \in [0, 1]$ is a parameter used to control the spatial direction in which smoothing is applied. In particular, the smaller α is, the more smoothing will focus on data fragments for which the difference quotient $(u' - u)/\Delta t$ is similar to $(z' - z)/\Delta t$.

Probabilities $q(t_j, z, z')$ of backward transitions are estimated similarly, producing estimators $\hat{q}(t_j, z, z')$. Our estimators can easily be adapted to satisfy some constraints. For example, to reconstruct functions that are monotone increasing, we can set $\hat{p}(t_j, z, z')$ to zero for all $z' < z$ and rescale the probabilities so that their sum over z' equals unity, with similar changes for \hat{q} .

3.2. Imputing the missing parts of curves

Let X denote a curve observed on $\mathcal{I} = [A, B] \subset \mathcal{I}_0 = [a, b]$, where it takes the value x ; that is, for $s \in \mathcal{I} \subset \mathcal{I}_0$, $X(s) = x(s)$. We propose estimating the unobserved parts $X(t)$ for $t \in \mathcal{I}_0 \setminus \mathcal{I}$ by an estimator of the predictor $E\{X(t) \mid X(s), s \in \mathcal{I}\}$ constructed from the discretized process $Z(t)$, $t \in \mathcal{I}_0^{\text{disc}}$. As before, assume for simplicity that $a, b, A, B \in \mathcal{I}_0^{\text{disc}}$ and define, for $t \in \mathcal{I}_0^{\text{disc}}$,

$$v_1(t \mid Z, \mathcal{I}) = E\{Z(t) \mid Z(s), s \in \mathcal{I}^{\text{disc}}\} = \begin{cases} Z(t), & t \in \mathcal{I}^{\text{disc}}, \\ E\{Z(t) \mid Z(A)\}, & a \leq t < A, \\ E\{Z(t) \mid Z(B)\}, & B < t \leq b, \end{cases} \quad (8)$$

where we have used (1) and (2) to obtain the last equality. For $t \in \mathcal{I}_0^{\text{disc}} \setminus \mathcal{I}^{\text{disc}}$, we predict the unobserved $X(t)$ by an estimator $\hat{v}_1(t \mid Z, \mathcal{I})$ of $v_1(t \mid Z, \mathcal{I})$. For $t \in \mathcal{I}_0 \setminus \mathcal{I}_0^{\text{disc}}$ we can use, for example, linear interpolation.

To construct \hat{v}_1 , we derive explicit formulae for $E\{Z(t) \mid Z(A)\}$ and $E\{Z(t) \mid Z(B)\}$. Assuming that $A = t_j$ and $t = t_{j-r+1}$, or $B = t_j$ and $t = t_{j+r-1}$, for some j and r , we have

$$E\{Z(t) \mid Z(A)\} = \sum_{\ell=1}^{m_2} \left\{ \sum_{\text{paths to } z_\ell} \prod_{k=1}^{r-1} q(t_{j-k+1}, z_{j_k}, z_{j_{k+1}}) \right\} z_\ell \quad (a \leq t < A), \quad (9)$$

$$E\{Z(t) \mid Z(B)\} = \sum_{\ell=1}^{m_2} \left\{ \sum_{\text{paths to } z_\ell} \prod_{k=1}^{r-1} p(t_{j+k-1}, z_{j_k}, z_{j_{k+1}}) \right\} z_\ell \quad (B < t \leq b), \quad (10)$$

where the summation $\sum_{\text{paths to } z_\ell}$ is over all paths $z^0 = z_{j_1} \mapsto z_{j_2} \mapsto \dots \mapsto z_{j_r} = z_\ell$ that lead from state z^0 to z_ℓ in just $r-1$ steps, with z^0 denoting $Z(A)$ or $Z(B)$ in the cases of (9) and (10), respectively. Our estimator $\hat{v}_1(t \mid Z, \mathcal{I})$ of $v_1(t \mid Z, \mathcal{I})$ is obtained by replacing each p and q in (9) and (10) with the estimators \hat{p} and \hat{q} derived in § 3.1. While it may seem complex to find all the paths that lead to z_ℓ , and thus to compute (9) and (10), we show in the Supplementary Material that these can be calculated very simply via sums and products of matrices.

An attractive aspect of our approach is that it also provides an estimator of the conditional distribution of $Z(t) \mid Z(A)$ for $t < A$ and of $Z(t) \mid Z(B)$ for $t > B$. In particular, using the same notation as above, we have

$$\begin{aligned} \hat{\text{pr}}\{Z(t) = z_\ell \mid Z(A)\} &= \sum_{\text{paths to } z_\ell} \prod_{k=1}^{r-1} \hat{q}(t_{j-k+1}, z_{j_k}, z_{j_{k+1}}) \quad (a \leq t < A), \\ \hat{\text{pr}}\{Z(t) = z_\ell \mid Z(B)\} &= \sum_{\text{paths to } z_\ell} \prod_{k=1}^{r-1} \hat{p}(t_{j+k-1}, z_{j_k}, z_{j_{k+1}}) \quad (B < t \leq b). \end{aligned}$$

We deduce estimators of the conditional cumulative distribution function by taking, for each $z \in \mathbb{R}$, $\hat{\text{pr}}\{Z(t) \leq z \mid Z(A)\} = \sum_{\ell=1}^{m_1} I(z_\ell \leq z) \hat{\text{pr}}\{Z(t) = z_\ell \mid Z(A)\}$ and $\hat{\text{pr}}\{Z(t) \leq z \mid Z(B)\} = \sum_{\ell=1}^{m_1} I(z_\ell \leq z) \hat{\text{pr}}\{Z(t) = z_\ell \mid Z(B)\}$. For any $\beta \in (0, 1)$, let $\hat{q}_\beta\{Z(t) \mid Z(A)\}$ and $\hat{q}_\beta\{Z(t) \mid Z(B)\}$ denote the estimators of the conditional quantiles of level β found by inverting these estimators of the conditional cumulative distribution functions. We can construct approximate pointwise prediction intervals of level β for $Z(t)$ by taking $[\hat{q}_{\beta/2}\{Z(t) \mid Z(A)\}, \hat{q}_{1-\beta/2}\{Z(t) \mid Z(A)\}]$ if $t < A$ and $[\hat{q}_{\beta/2}\{Z(t) \mid Z(B)\}, \hat{q}_{1-\beta/2}\{Z(t) \mid Z(B)\}]$ if $t > B$.

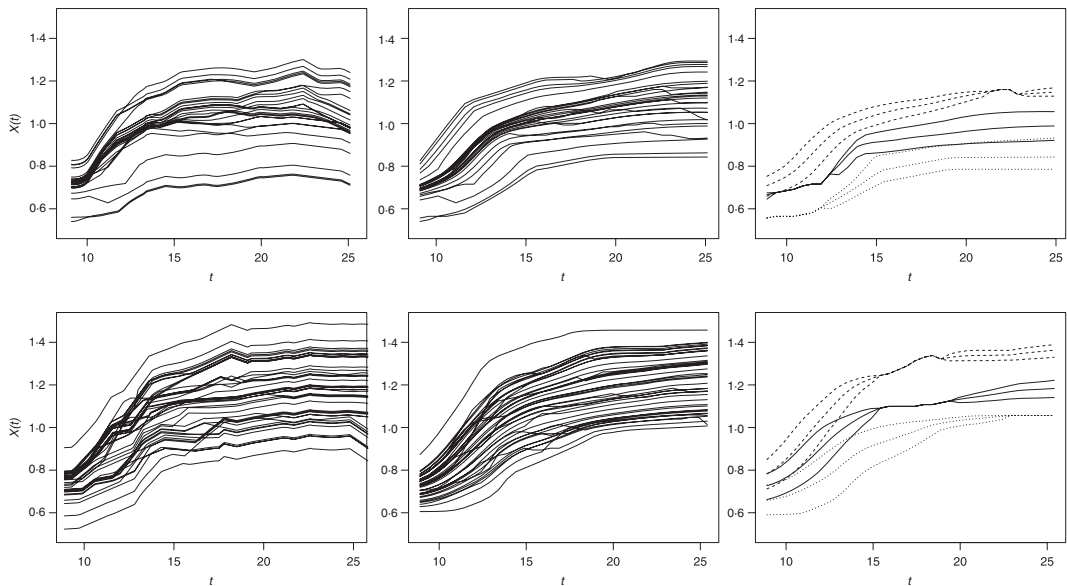


Fig. 2. Reconstruction of growth curves, measured by spine bone mineral density, in g cm^{-2} , from the incomplete data depicted in Fig. 1 for females from the Hispanic (top) and Black (bottom) ethnic groups described in [Bachrach et al. \(1999\)](#), using the method of [Delaigle & Hall \(2013\)](#) (left) or our new approach (middle). The right panels show approximate 95% prediction intervals and reconstructed curves using our new approach, for three individuals each from the Hispanic group (top) and the Black group (bottom); each individual is represented by a different line type.

To illustrate how effective our method can be, we apply it to the growth data introduced in § 3.1. For each ethnic group, using only the data from that group, we imputed the missing parts of the curves by $\hat{v}_1(t \mid Z, \mathcal{I})$, where, to compute \hat{p} and \hat{q} , we chose the parameters as described in § 6.1. Since, despite small fluctuations, bone mineral density does not usually start decreasing until after 25 years of age, we imposed the monotonicity constraint on \hat{p} and \hat{q} discussed at the end of § 3.1, but did not alter the few observed nonmonotone fragments. To highlight the attractiveness of our method compared to that of [Delaigle & Hall \(2013\)](#), in Fig. 2 we display, for both methods, the reconstructed curves for the Hispanic and Black ethnic groups. As shown by the graphs, a drawback of the approach of [Delaigle & Hall \(2013\)](#) is that their reconstructed curves are composed of observed fragments, shifted up and down. As a result, if atypical fragments are observed in sparse regions, many of their reconstructed curves inherit this atypicality, whereas the present approach is more flexible.

As discussed above, another advantage of our approach is that it enables us to construct approximate prediction intervals. To illustrate this, in the right panels of Fig. 2 we plot reconstructed curves and the approximate 95% pointwise prediction intervals for three individuals from each of the Hispanic and Black groups. Each individual is represented by a different line type, with no ambiguity between the reconstructed curves and the upper and lower limits of their prediction intervals, as the former always lies between the latter two. Of course, at points t where the curve was observed, there is no prediction interval to construct and we show only the curve itself. We can see that, quite naturally, the length of each prediction interval at a time t increases as t gets further away from the interval where the fragment was observed.

As already highlighted by [Delaigle & Hall \(2013\)](#), methods dedicated to the sparse setting rather than the fragmentary setting, such as those of [James et al. \(2000\)](#) and [Yao et al. \(2005\)](#), do not manage to reconstruct the curves in an attractive way and so are not discussed here.

3.3. Estimating the mean and covariance functions

Our approach can also be used to estimate the mean function $\alpha_1(t) = E\{X(t)\}$ and the covariance function

$$\Gamma(t, u) = E\{[X(t) - \alpha_1(t)][X(u) - \alpha_1(u)]\} = \alpha_2(t, u) - \alpha_1(t)\alpha_1(u), \quad (11)$$

where $\alpha_2(t, u) = E\{X(t)X(u)\}$. We can estimate readily the function α_1 from the data X_i using the empirical mean $\hat{\alpha}_1(t) = n^{-1}(t) \sum_{i=1}^n X_i(t)I(t \in \mathcal{I}_i)$, where $n(t) = \sum_i I(t \in \mathcal{I}_i)$ and it is understood that we regularize the estimator $\hat{\alpha}_1(t)$ for values of t for which $n(t)$ is too small. However, in the most interesting case where the data fragments are relatively sparse, at each t , $\hat{\alpha}_1(t)$ defined as above is typically computed from just a few fragments and is not a very good estimator of α_1 . We propose the following Markov-based estimator of α_1 , for $t \in \mathcal{I}_0^{\text{disc}}$:

$$\hat{\alpha}_1(t) = \frac{1}{n} \sum_{i=1}^n \hat{v}_1(t \mid Z_i, \mathcal{I}_i), \quad (12)$$

where \hat{v}_1 is the estimator of v_1 in (8) derived in § 3.2.

Estimating α_2 is more complex. Let $\mathcal{I} = [A, B]$ and Z denote generic values of \mathcal{I}_i and Z_i , and assume for simplicity that $a, b, A, B \in \mathcal{I}_0^{\text{disc}}$. For $t, u \in \mathcal{I}_0^{\text{disc}}$, define

$$v_2(t, u \mid Z, \mathcal{I}) = \begin{cases} Z(t)Z(u), & t, u \in \mathcal{I}^{\text{disc}}, \\ Z(t) v_1(u \mid Z, \mathcal{I}^{\text{disc}}), & t \in \mathcal{I}^{\text{disc}}, u \notin \mathcal{I}^{\text{disc}}, \\ Z(u) v_1(t \mid Z, \mathcal{I}^{\text{disc}}), & u \in \mathcal{I}^{\text{disc}}, t \notin \mathcal{I}^{\text{disc}}, \\ E\{Z(t)Z(u) \mid Z(A)\}, & a \leq t, u < A, \\ E\{Z(t)Z(u) \mid Z(B)\}, & B < t, u \leq b, \\ E\{Z(t) \mid Z(A)\}E\{Z(u) \mid Z(B)\}, & a \leq t < A \leq B < u \leq b. \end{cases} \quad (13)$$

In the first case and the last three cases of (13), we permit t and u to be identical. Much in the same way as we derived formulae (9) and (10), if $a \leq t \leq u < A$, and assuming that $A = t_j$, $u = t_{j-r_1}$ and $t = t_{j-r_1-r_2}$ for some j, r_1 and r_2 , we have

$$E\{Z(t)Z(u) \mid Z(A)\} = \sum_{\ell_1=1}^{m_2} \sum_{\ell_2=1}^{m_2} \left\{ \sum_{\text{paths to } z_{\ell_1}, z_{\ell_2}} \prod_{k=1}^r q(t_{j-k+1}, z_{i_k}, z_{i_{k+1}}) \right\} z_{\ell_1} z_{\ell_2}, \quad (14)$$

where $r = r_1 + r_2$ and the summation $\sum_{\text{paths to } z_{\ell_1}, z_{\ell_2}}$ is over all paths $z^0 = z_{i_1} \mapsto z_{i_2} \mapsto \dots \mapsto z_{i_{r+1}} = z_{\ell_2}$ that lead from state z^0 , representing $z(A)$, to state z_{ℓ_1} after r_1 steps, and thence to z_{ℓ_2} after another r_2 steps. The case $B < t \leq u \leq b$ is similar, and the other components of the formula in (13) are trivial. As with equations (9) and (10), (14) can be computed very simply via sums and products of matrices; see the Supplementary Material.

Upon replacing each p and q , in (14) and its analogues, by the estimators \hat{p} and \hat{q} derived in § 3.1, we obtain an estimator \hat{v}_2 of v_2 and can compute $\hat{\alpha}_2(t, u) = n^{-1} \sum_{i=1}^n \hat{v}_2(t, u \mid Z_i, \mathcal{I}_i)$. For $t, u \in \mathcal{I}_0^{\text{disc}}$, we estimate the covariance $\Gamma(t, u)$ in (11) by

$$\hat{\Gamma}(t, u) = \hat{\alpha}_2(t, u) - \hat{\alpha}_1(t) \hat{\alpha}_1(u). \quad (15)$$

Remark 1. Estimating the mean is much easier than estimating the covariance, and, unlike the latter, the former does not necessarily require methods designed specifically for the fragmentary setting. In particular, even though it was designed for the sparse setting, the smooth mean estimator of Yao et al. (2005) can work also in the fragmentary setting. However, as pointed out by Delaigle & Hall (2013), even when the mean estimator of Yao et al. (2005) works well, their covariance estimator, also designed for the sparse setting, cannot give reasonable results in our fragmentary context. Since our covariance estimator exploits our Markov assumption, to avoid the awkwardness of estimating the mean and covariance functions with incompatible approaches we suggest estimating the mean by the estimator in (12). Delaigle & Hall (2013) also proposed estimators of the mean and covariance functions designed specifically for the fragmentary setting. However, their approach works only in the case of a single fragment per curve and suffers from problems similar to those of their curve reconstruction algorithm.

3.4. Linear prediction of Y given a new fragment

Our next goal is to construct a predictor of Y for a new fragment $\{X(t), t \in \mathcal{I} \subset \mathcal{I}_0\}$ whose Y is unknown, using a sample of fragmentary data $(\{X_i(t), t \in \mathcal{I}_i \subset \mathcal{I}_0\}, Y_i)$ for $i = 1, \dots, n$. The pair (X, Y) has the distribution of the pairs (X_i, Y_i) , where X and X_i refer to the unobserved complete curves. As usual, the form of our predictor depends on the way in which we model the relationship between Y and X . A variety of models, parametric or nonparametric, could be considered, but given the sparse nature of our data, we cannot reasonably contemplate using sophisticated models. If we were able to observe the curves X_1, \dots, X_n on the whole interval \mathcal{I}_0 , one of the simplest models we could consider would be the functional linear model,

$$Y = \theta_0 + \int_{\mathcal{I}_0} \theta X + \epsilon, \quad E\{\epsilon \mid X(t), t \in \mathcal{I}_0\} = 0, \quad (16)$$

where θ_0 is a scalar and θ is a function; see, for example, Cai & Hall (2006), Apanasovich & Goldstein (2008), Crambes et al. (2009), Delaigle et al. (2009) and Lee & Park (2012).

Since we observe only fragments $X_i(t)$, $t \in \mathcal{I}_i \subset \mathcal{I}_0$, we suggest using an approach similar to those employed in the previous sections. Specifically, we use the model

$$Y = \theta_0 + \sum_{j=1}^{m_1} \theta_j Z(t_j) + \epsilon, \quad E\{\epsilon \mid Z(t), t \in \mathcal{I}_0^{\text{disc}}\} = 0, \quad (17)$$

where Z is the discrete process introduced in § 2 and $\theta_0, \dots, \theta_{m_1}$ are unknown scalars. Then, we predict Y by $\hat{Y} = \hat{\mu}_{\mathcal{I}}(Z)$, where $\hat{\mu}_{\mathcal{I}}(Z)$ is an estimator of

$$\mu_{\mathcal{I}}(Z) = E\{Y \mid Z(t), t \in \mathcal{I}^{\text{disc}}\}. \quad (18)$$

Note the distinction between $\mathcal{I}^{\text{disc}}$ in (18) and $\mathcal{I}_0^{\text{disc}}$ in (17).

Using (17), and recalling the definition of v_1 in (8), we can write $\mu_{\mathcal{I}}(Z) = E\{Y \mid Z(t), t \in \mathcal{I}^{\text{disc}}\} = \theta_0 + \sum_{j=1}^{m_1} \theta_j v_1(t_j \mid Z, \mathcal{I})$. An estimator \hat{v}_1 of v_1 was derived in § 3.2, and to estimate $\hat{\mu}_{\mathcal{I}}$ it suffices to construct estimators of $\theta_0, \dots, \theta_{m_1}$. While we could estimate these parameters by minimizing the sum of squares

$$\sum_{i=1}^n \left\{ Y_i - \theta_0 - \sum_{j=1}^{m_1} \theta_j \hat{v}_1(t_j \mid Z_i, \mathcal{I}_i) \right\}^2 \quad (19)$$

with \hat{v}_1 as in § 3.2, often m_1 is large, and better results can be obtained if we reduce the dimension. This can be done in a standard way, as follows. Let $\theta = (\theta_1, \dots, \theta_{m_1})^T$ and $v_{1i} = \{\hat{v}_1(t_1 | Z_i, \mathcal{I}_i), \dots, \hat{v}_1(t_{m_1} | Z_i, \mathcal{I}_i)\}^T$, let $\psi_1, \psi_2, \dots, \psi_{m_1}$ be an orthonormal basis of \mathbb{R}^{m_1} , and write $\theta = \sum_{k=1}^{m_1} \beta_k \psi_k$ and $v_{1i} = \sum_{k=1}^{m_1} \gamma_{ik} \psi_k$, where $\beta_k = \theta^T \psi_k$ and $\gamma_{ik} = v_{1i}^T \psi_k$. Keeping only the first m terms of these two series, where the choice of m will be discussed in § 6.1, we replace the objective function in (19) by

$$S_m(\theta_0; \beta_1, \dots, \beta_m) = \sum_{i=1}^n \left\{ Y_i - \theta_0 - \sum_{k=1}^m \beta_k \gamma_{ik} \right\}^2. \quad (20)$$

For a given m we compute estimators $\hat{\theta}_0, \hat{\beta}_1, \dots, \hat{\beta}_m$ of $\theta_0, \beta_1, \dots, \beta_m$ by minimizing (20). Finally, we estimate $\mu_{\mathcal{I}}(Z)$ by $\hat{\mu}_{\mathcal{I}}(Z) = \hat{\theta}_0 + \sum_{k=1}^m \hat{\beta}_k \gamma_k$, where $\gamma_k = \{\hat{v}_1(t_1 | Z, \mathcal{I}), \dots, \hat{v}_1(t_{m_1} | Z, \mathcal{I})\} \psi_k$.

3.5. Principal component basis

One possible choice for the orthonormal basis $\psi_1, \dots, \psi_{m_1}$ used in § 3.4 is the sequence $\hat{\phi}_1, \dots, \hat{\phi}_{m_1}$ obtained through empirical spectral decomposition of the covariance, as follows. For estimation of this basis in the fully observed functional context, see Hall & Hosseini-Nasab (2006), for example. For $t_k, t_\ell \in \mathcal{I}_0^{\text{disc}}$, the kernels Γ and $\hat{\Gamma}$ introduced in § 3.3 can be expressed via singular value decompositions as

$$\Gamma(t_k, t_\ell) = \sum_{j=1}^{\infty} \lambda_j \phi_j(t_k) \phi_j(t_\ell), \quad \hat{\Gamma}(t_k, t_\ell) = \sum_{j=1}^{m_1} \hat{\lambda}_j \hat{\phi}_j(t_k) \hat{\phi}_j(t_\ell), \quad (21)$$

where (λ_j, ϕ_j) are (eigenvalue, eigenfunction) pairs, $(\hat{\lambda}_j, \hat{\phi}_j)$ are (eigenvalue, eigenvector) pairs, and the eigenvalues are ordered so that $\lambda_1 \geq \lambda_2 \geq \dots$ and $\hat{\lambda}_1 \geq \hat{\lambda}_2 \geq \dots$. In the case of Γ , the eigenvalues are all nonnegative, but this is not necessarily true for $\hat{\Gamma}$, and the second expansion in (21) should be interpreted as including terms that correspond to negative eigenvalues. Comparing the two expansions in (21), we view $\hat{\theta}_j$ and $\hat{\phi}_j$ as approximations to θ_j and ϕ_j , respectively. Of course, $\hat{\phi}_j$, a vector, is interpreted as a discrete approximation to the function ϕ_j .

4. THEORETICAL PROPERTIES

4.1. Setting and conditions

Recall that we have discretized time as $\mathcal{I}_0^{\text{disc}} = \{t_1, \dots, t_{m_1}\} \subseteq \mathcal{I}_0$, where $a \leq t_1 < \dots < t_{m_1} \leq b$, and discretized space as $z_0 < \dots < z_{m_2+1}$, where $z_0 = -\infty$ and $z_{m_2+1} = \infty$ but z_1 and z_{m_2} are finite. Recall too that $Z(t_j) = z_k$ if $(z_{k-1} + z_k)/2 < X(t_j) \leq (z_k + z_{k+1})/2$, and that we consider the functions X_i to have been recorded originally on \mathcal{I}_0 , but that we are able to observe X_i only on $\mathcal{I}_i = [A_i, B_i] \subseteq \mathcal{I}_0$. We make the following assumptions.

Condition 1. The random functions X_i are identically distributed.

Condition 2. The pairs (A_i, B_i) are identically distributed.

Condition 3. For each pair of consecutive points (t_j, t_{j+1}) in the time grid, $\text{pr}([t_j, t_{j+1}] \in [A, B]) > 0$, where (A, B) has the common distribution of the pairs (A_i, B_i) .

Conditions 1 and 2 are conventional, and it is straightforward to see that if Condition 3 fails to hold then it is not possible to estimate the probabilities of transitioning from any given time-point t_j to an adjacent one, in either direction. We also assume the following.

Condition 4. The random functions X_i and the random intervals $\mathcal{I}_i = [A_i, B_i]$ are completely independent.

The implications of the assumed independence in Condition 4 are subtle. If (A, B) denotes a generic pair (A_i, B_i) and is not independent of X , then estimators of transition probabilities can be seriously biased, as the following example shows. Suppose Condition 3 is satisfied and that the following property holds for particular values of j and k : $[t_j, t_{j+1}] \subseteq [A, B]$ only when the event

$$\mathcal{E} = \left\{ X(t_j) \in \left(\frac{z_{k-1} + z_k}{2}, \frac{z_k + z_{k+1}}{2} \right] \right\} \cap \left\{ X(t_{j+1}) \in \left(\frac{z_k + z_{k+1}}{2}, \frac{z_{k+1} + z_{k+2}}{2} \right] \right\},$$

or equivalently $\mathcal{E} = \{Z(t_j) = z_k\} \cap \{Z(t_{j+1}) = z_{k+1}\}$, holds. We shall call this property (P). Except in the pathological case where $\text{pr}(\mathcal{E}) = 1$, (P) requires that the quantities (A, B) and X not be independent. If (P) holds, and if the process is in fact a first-order Markov chain, then our estimator of $p(t_j, z_k, z_{k+1})$ will typically converge to too large a value. A consequence of this example, and others like it, is that if Condition 4, or a similar condition, does not hold, then no approach to estimating the transition probabilities can be guaranteed to produce consistent estimators, even if the stochastic process Z is a true Markov chain.

4.2. Theoretical results

Our method uses statistical smoothing to extract as much information as possible from the data. A conventional theoretical account of the performance of that technique would involve so-called infill asymptotics, where the number of data points per unit interval of time is permitted to diverge, retaining the Markov property at each step and also in the asymptotic limit. However, the latter argument is not appealing here, since the continuous process to which a Markov chain converges is a diffusion process, and has only half a derivative. Consequently, theoretical large-sample convergence rates are extremely slow, suggesting a level of performance that is much lower than we find in practice. Therefore, we keep the grid sizes m_1 and m_2 fixed, which implies that our process Z remains discrete in the limit as $n \rightarrow \infty$.

Our Markov assumption implies that the discretized process $Z(t)$ for $t \in \mathcal{I}_0^{\text{disc}}$ is modelled parametrically; with this model, only a finite number of transition probabilities needs to be estimated. In particular, although smoothing is needed for small samples due to the sparsity of the data, asymptotically our estimator with $h = g = 0$ and $\alpha = 1$ enjoys the optimal $n^{-1/2}$ convergence rate. This result, which will be established in Theorem 1, contrasts with standard smoothing results for continuous random variables, where a bandwidth is not usually allowed to equal zero. Thus, unlike more conventional problems, the most interesting and challenging aspects of the fragmentary data, which require us to use smoothing techniques, arise only in small samples. As sample size increases, these difficulties disappear and the asymptotic theory becomes that of a standard parametric problem. In § 5.3, we shall discuss an alternative approach based on a continuous-space model, which has theoretical properties similar to those of standard kernel estimators.

For $j = 1, \dots, m_1 - 1$ and $k, \ell = 1, \dots, m_2$, define $p_0(t_j, z_k, z_\ell) = \text{pr}\{Z(t_{j+1}) = z_\ell \mid Z(t_j) = z_k\}$, where this probability is computed using the true probability measure for the random process

Z , i.e., without assuming a Markov model. Our theorem addresses the performance of the estimators \hat{p} and \hat{q} of the transition probabilities p and q , suggested in § 3.1. Its proof can be found in the Supplementary Material.

THEOREM 1. *Assume that Conditions 1–4 hold. Then for $j = 1, \dots, m_1 - 1$ and $k, \ell = 1, \dots, m_2$, where m_1 and m_2 are fixed, if we take $h = g = 0$ and $\alpha = 1$, our estimator in (5) satisfies $\hat{p}(t_j, z_k, z_\ell) = p_0(t_j, z_k, z_\ell) + O_p(n^{-1/2})$. Moreover, the analogues for transition probabilities $q(t_j, z_k, z_\ell)$ also hold.*

Recall the definition of the mean estimator $\hat{\alpha}_1(t)$ in (12), and assume that the conditions of Theorem 1 and the first-order Markov assumption hold. Then it follows from the theorem and the weak law of large numbers that for $t \in \mathcal{I}_0^{\text{disc}}$, $\hat{\alpha}_1(t) = \alpha_1(t) + O_p(n^{-1/2})$. Likewise, for $\hat{K}(s, t)$ defined in (15) and $s, t \in \mathcal{I}_0^{\text{disc}}$, we have $\hat{K}(s, t) = K(s, t) + O_p(n^{-1/2})$. Similarly, for all $1 \leq j, k \leq m_1$ such that $j \neq k$ and for $\ell = 1, \dots, m_2$, the estimator of $E\{Z(t_k) \mid Z(t_j) = z_\ell\}$ derived in § 3.2 is root- n consistent. In conventional linear prediction for functional linear regression, the linear model in (16) and its counterparts below that formula are infinite-dimensional quantities, a property that they inherit from the infinite-dimensional nature of the singular value decomposition of a covariance function. However, in the discrete context of a Markov chain model, discussed in § 3.4, the covariance is a finite covariance matrix, the model is finite-dimensional, and, as noted above, the covariance can be estimated root- n consistently. It comes as no surprise that, for the discrete Markov chain model discussed in § 3.4, the predictive model is also discrete, and in particular the function θ in (16) is replaced in (17) by a vector whose length does not diverge with sample size. In particular, $(\theta_1, \dots, \theta_{m_1})$ in (17) can also be estimated root- n consistently.

5. EXTENSIONS

5.1. Multiple disjoint fragments

Our method can be extended to cases where several disjoint fragments of each curve X_i are observed. Recall that we work with the discretized process $Z(t)$, $t \in \{t_1, \dots, t_{m_1}\}$. A fragment is a sequence of observations $Z(t_j), Z(t_{j+1}), \dots, Z(t_{j+r})$ for some j and r . Two disjoint fragments correspond to the case where the sequence of observations is of the type $Z(t_j), Z(t_{j+1}), \dots, Z(t_{j+r_1}), Z(t_{j+r_2}), Z(t_{j+r_2+1}), \dots, Z(t_{j+r_2+r_3})$, for some numbers j, r_1, r_2 and r_3 such that $r_2 > r_1 + 1$. Although we could construct smoothed versions of the maximum likelihood estimators of the forward and backward transition probabilities, this time taking into account all the possible paths that connect the various observed fragments of a given curve, this approach is rather complex. Instead, we propose estimating the transition probabilities using the smoothing approach introduced in § 3.1, treating all observed fragments as independent fragments.

On the other hand, when imputing the missing values of a curve X , in order to be able to join the fragments in a reasonable manner, we need to revise our estimator of v_1 . Likewise, in order to estimate the covariance functions K , we need to modify our estimator of v_2 , taking into account the fact that several fragments of the same curve have been observed. We describe in detail a modification for the case where two fragments of a given curve have been observed. This can be generalized to the case of more than two fragments per curve.

Suppose that we observe a curve X on two disjoint intervals $\mathcal{I} = [A, B] \subset \mathcal{I}_0 = [a, b]$ and $\mathcal{J} = [C, D] \subset \mathcal{I}_0$. As before, let Z denote the discretized version of X , defined on $\mathcal{I}_0^{\text{disc}}$, and assume that $a \leq A < B < C < D \leq b$ lie in $\mathcal{I}_0^{\text{disc}}$. To impute the missing values of $X(t)$ for

$t \in \mathcal{I}_0^{\text{disc}} \setminus (\mathcal{I}^{\text{disc}} \cup \mathcal{J}^{\text{disc}})$, we use the predictor

$$\begin{aligned} v_1(t | Z, \mathcal{I}) &= E\{Z(t) | Z(s), s \in \mathcal{I}^{\text{disc}} \cup \mathcal{J}^{\text{disc}}\} \\ &= \begin{cases} Z(t), & t \in \mathcal{I}^{\text{disc}} \cup \mathcal{J}^{\text{disc}}, \\ E\{Z(t) | Z(A)\}, & a \leq t < A, \\ E\{Z(t) | Z(D)\}, & D < t \leq b, \\ E\{Z(t) | Z(B), Z(C)\}, & B < t < C. \end{cases} \end{aligned} \quad (22)$$

The first three terms can be handled in the same way as in the case of one fragment, so here we focus on the last term on the right-hand side of (22).

Write $B = t_j$, $t = t_{j+r_1}$ and $C = t_{j+r}$ for some j , $r_1 \geq 1$ and $r > r_1$. We have

$$E\{Z(t_{j+r_1}) | Z(t_j) = z_{j_0}, Z(t_{j+r}) = z_{j_r}\} = \frac{\sum_{j_1, \dots, j_{r-1}=1}^{m_2} z_{j_{r_1}} \prod_{k=1}^r p(t_{j+k-1}, z_{j_{k-1}}, z_{j_k})}{\sum_{j_1, \dots, j_{r-1}=1}^{m_2} \prod_{k=1}^r p(t_{j+k-1}, z_{j_{k-1}}, z_{j_k})}.$$

Similarly, for the covariance function, the only difference from the case of one fragment per individual is the covariance between two points that are between the two fragments of the same individual. Specifically, for $1 \leq r_1 \leq r_2 < r_3$ we have

$$E\{Z(t_{j+r_1})Z(t_{j+r_2}) | Z(t_j) = z_{j_0}, Z(t_{j+r_3}) = z_{j_{r_3}}\} = \frac{\sum_{j_1, \dots, j_{r_3-1}=1}^{m_2} z_{j_{r_1}} z_{j_{r_2}} \prod_{k=1}^{r_3} p(t_{j+k-1}, z_{j_{k-1}}, z_{j_k})}{\sum_{j_1, \dots, j_{r_3-1}=1}^{m_2} \prod_{k=1}^{r_3} p(t_{j+k-1}, z_{j_{k-1}}, z_{j_k})}.$$

In practice, we compute all these quantities in matrix form; see the Supplementary Material.

5.2. Higher-order Markov chains

In the previous sections, we approximated the discretized process by first-order Markov chains, which can be fitted even if the data consist of a small number of very short fragments, as in the growth data example. On the other hand, this simple model is a reasonable approximation to the truth only if, at each time t_{k+1} , the main shape of the curves depends mostly on their shape at the previous time t_k . If not, for instance if the population consists of overlapping increasing and decreasing curves, so that given $Z(t_k) = z_j$, with high probability $Z(t_{k+1})$ can either increase or decrease, then the first-order Markov approximation will not work well in practice. In such instances, if we observe only a few very short fragments, sophisticated models cannot be fitted well from the data.

If the fragments are less sparse, more complex structures can be captured through higher-order Markov chains. Under an m th-order Markov assumption, using the notation $p(t_k, z_{j_0}, \dots, z_{j_m}) = \text{pr}\{Z(t_{k+m}) = z_{j_m} | Z(t_{k+m-1}) = z_{j_{m-1}}, \dots, Z(t_k) = z_{j_0}\}$, we have $\text{pr}\{Z(t_{k+m}) = z_{j_m} | Z(t_{k+m-1}) = z_{j_{m-1}}, \dots, Z(t_1) = z_{j_{1-k}}\} = p(t_k, z_{j_0}, \dots, z_{j_m})$. Let $\tilde{N}(t_\ell, u_0, \dots, u_m)$ equal

$$\frac{\sum_{i=1}^n I\{Z_i(t_\ell) = u_0, \dots, Z_i(t_{\ell+m}) = u_m, A_i \leq t_\ell < t_{\ell+m} \leq B_i\}}{\sum_{i=1}^n I\{A_i \leq t_\ell < t_{\ell+m} \leq B_i\}}$$

if $\sum_{i=1}^n I\{A_i \leq t_\ell < t_{\ell+m} \leq B_i\} \neq 0$ and equal zero otherwise. Generalizing our estimator in (5) to m th-order Markov chains, we take

$$\hat{p}(t_k, z_{j_0}, \dots, z_{j_m}) = \hat{A}(t_k, z_{j_0}, \dots, z_{j_m}) / \sum_{z_{j_m}} \hat{A}(t_k, z_{j_0}, \dots, z_{j_m}),$$

where

$$\begin{aligned} \hat{A}(t_k, z_{j_0}, \dots, z_{j_m}) &= \sum_{\ell=1}^{m_1-m} \sum_{u_0, \dots, u_m} \tilde{N}(t_\ell, u_0, \dots, u_m) \\ &\quad \times w(t_k, t_\ell) \omega\{(z_{j_0}, \dots, z_{j_m}), (u_0, \dots, u_m)\}, \end{aligned}$$

with w as in §3.1 and ω a generalization of the weight from §3.1, such as $\omega\{(z_{j_0}, \dots, z_{j_m}), (u_0, \dots, u_m)\} = K_g[\alpha\{|z_{j_0} - u_0| + \dots + |z_{j_m} - u_m|\} + (1 - \alpha)\{|u_m - u_{m-1} - (z_{j_m} - z_{j_{m-1}})| + \dots + |u_1 - u_0 - (z_{j_1} - z_{j_0})|\}/m]$.

As the order m increases, the Markov model becomes more sophisticated and can capture more complex structures, but more data are required to fit it, and the observed fragments need to be longer. However, second-order Markov chains can already be quite useful, since they enable us to distinguish curves with an upward trend from those with a downward trend. The techniques derived in §3.2–3.4 can be extended to higher-order Markov chains. Here we show how to extend to second-order chains the imputing algorithm from §3.2; similar ideas can be used for higher-order chains and for the methods developed in §3.3 and 3.4. Under the second-order Markov assumption, letting $\mathcal{I}^{\text{disc}} = [A, B] = [t_j, t_k]$ with $k > j$, (8) becomes

$$E\{Z(t) \mid Z(s), s \in \mathcal{I}^{\text{disc}}\} = \begin{cases} Z(t), & t \in \mathcal{I}^{\text{disc}}, \\ E\{Z(t) \mid Z(t_j), Z(t_{j+1})\}, & a \leq t < t_j, \\ E\{Z(t) \mid Z(t_{k-1}), Z(t_k)\}, & t_k < t \leq b, \end{cases}$$

where quantities such as those in the second and third lines can be estimated using approaches similar to the one in §3.2. For example, for the third line, letting $t = t_{k+r}$ with $r \geq 1$, we have $E\{Z(t) \mid Z(t_{k-1}) = z_{\ell_{-1}}, Z(t_k) = z_{\ell_0}\} = \sum_{\ell_1, \dots, \ell_r=1}^{m_2} z_{\ell_r} \prod_{i=1}^r \text{pr}\{Z(t_{k+i}) = z_{\ell_i} \mid Z(t_{k+i-1}) = z_{\ell_{i-1}}, Z(t_{k+i-2}) = z_{\ell_{i-2}}\}$, which can be estimated by replacing the probabilities with the estimators derived above.

5.3. Continuous-space model

In the last paragraph of the introduction, we discussed the advantages of using a discrete-time Markov chain instead of a continuous-time Markov process. On the other hand, in theory it is not necessary to discretize space, and in this section we discuss an alternative approach that uses a continuous-space model. As we shall see, it leads to estimators that are very similar to those derived using our discrete model.

In the continuous-space model, instead of assuming that the discretized process $Z(t)$ is a first-order Markov chain, we make the first-order Markov assumption on the process $X(t)$, where $t \in \{t_1, \dots, t_{m_1}\}$; that is, we assume that for each pair of positive integers j and r such that $j+r \leq m_1$, the conditional density of $X(t_{j+r})$ given $X(t_1), \dots, X(t_j)$ satisfies $f_{X(t_{j+r})|X(t_j), \dots, X(t_1)} = f_{X(t_{j+r})|X(t_j)}$. As in §3.2, let X denote a curve observed on $\mathcal{I} = [A, B] \subset \mathcal{I}_0 = [a, b]$, let $\mathcal{I}_0^{\text{disc}}$ and $\mathcal{I}^{\text{disc}}$ be as defined in that section, and assume for simplicity that $a, b, A, B \in \mathcal{I}_0^{\text{disc}}$.

Under the above continuous version of the Markov assumption, to estimate the unobserved parts $X(t)$ for $t \in \mathcal{I}_0^{\text{disc}} \setminus \mathcal{I}^{\text{disc}}$, we can directly construct an estimator of the predictor

$$E\{X(t) \mid X(s), s \in \mathcal{I}^{\text{disc}}\} = \begin{cases} X(t), & t \in \mathcal{I}^{\text{disc}}, \\ E\{X(t) \mid X(A)\}, & a \leq t < A, \\ E\{X(t) \mid X(B)\}, & B < t \leq b. \end{cases}$$

Similarly to our derivations in § 3.2, assuming that $B = t_j$ and $t = t_{j+r-1}$ for some j and r , we have $E\{X(t) \mid X(B) = x_j\} = \int \cdots \int x_{j+r-1} \prod_{k=1}^{r-1} [f_{X(t_{j+k})|X(t_{j+k-1})}(x_{j+k} \mid x_{j+k-1}) \times 1\{f_{X(t_{j+k-1})}(x_{j+k-1}) > 0\}] \prod_{k=1}^{r-1} dx_{j+k}$, and a similar expression holds for $E\{X(t) \mid X(A)\}$.

In practice, these integrals need to be approximated by sums involving the conditional densities, and then the conditional densities must be estimated from the data. No matter which approach we use, the error of the resulting predictor has two parts: a systematic error Err_{int} caused by the numerical integration, which does not tend to zero as n increases because of the limitations imposed by the computational feasibility, and the error caused by the estimation of the conditional densities, which tends to zero as n increases. We illustrate this below through the simple midpoint integral approximation, which is easy to explain and can be directly connected to our discretized approach from § 3.2. More sophisticated numerical integration rules can be applied, but the main ideas remain the same.

Reflecting most practical situations, assume that the $X(t_k)$ are bounded. Specifically, assume that for each k , $z_1 - \Delta z/2 \leq X(t_k) \leq z_{m_2} + \Delta z/2$, where the z_j and Δz are as in § 2. Letting $z_{\ell_j} = x_j$, the midpoint integration rule leads to

$$\begin{aligned} E\{X(t) \mid X(B) = x_j\} \\ = (\Delta z)^{r-1} \sum_{\ell_{j+1}=1}^{m_2} \cdots \sum_{\ell_{j+r-1}=1}^{m_2} z_{\ell_{j+r-1}} \prod_{k=1}^{r-1} \left[f_{X(t_{j+k})|X(t_{j+k-1})}(z_{\ell_{j+k}} \mid z_{\ell_{j+k-1}}) \right. \\ \left. \times 1\{f_{X(t_{j+k-1})}(z_{\ell_{j+k-1}}) > 0\} \right] + \text{Err}_{\text{int}}, \end{aligned} \quad (23)$$

where the integration error Err_{int} is bounded away from zero: while it decreases with Δz at a rate depending on the number of bounded derivatives of the conditional densities, Δz is always bounded away from zero because, for the sums to be computable, m_2 must be finite.

In practice, the conditional densities are unknown and need to be estimated from the data. Assuming that the densities $f_{X(t_{j+k})|X(t_{j+k-1})}$ and $f_{X(t_{j+k-1})}$ are all continuous at the boundary of their support, we can use relatively standard kernel density estimators, where, to overcome the sparsity of the observations at any given time-point, we smooth also in time, as we did in the previous sections for the discrete-space model. Specifically, for each k we can take

$$\begin{aligned} \hat{f}_{X(t_{k+1})|X(t_k)}(z_{\ell_{k+1}} \mid z_{\ell_k}) \\ = \frac{\sum_{\ell=1}^{m_1-1} \sum_{i=1}^n w(t_k, t_\ell) K_g\{z_{\ell_k} - X_i(t_\ell)\} K_g\{z_{\ell_{k+1}} - X_i(t_{\ell+1})\} I\{A_i \leq t_\ell < B_i\}}{\sum_{\ell=1}^{m_1-1} \sum_{i=1}^n w(t_k, t_\ell) I\{A_i \leq t_\ell < B_i\} K_g\{z_{\ell_k} - X_i(t_\ell)\}}, \end{aligned}$$

with w , which depends on a bandwidth h , K and g as in the previous sections. Substituting these conditional density estimators into (23), we get our estimator $\hat{E}\{X(t) \mid X(B)\}$ of $E\{X(t) \mid X(B)\}$. Comparing it with the estimator from § 3.2, we can see that the main difference is that the conditional transition probabilities are replaced by the conditional densities.

Using standard arguments as in [De Gooijer & Zerom \(2003\)](#), it can be proved that if Conditions 1–4 hold, if the conditional and marginal densities are bounded and twice continuously differentiable with all partial derivatives bounded, if K is such that $\int K(x) dx = 1$, $\int xK(x) dx = 0$, $0 < \int x^2 K(x) dx < \infty$ and $\int K^2(x) dx < \infty$, and if $h = 0$ and $g \asymp n^{-1/6}$, then we have

$$\hat{E}\{X(t) \mid X(B) = x\} = E\{X(t) \mid X(B) = x\} + \text{Err}_{\text{int}} + O_p(n^{-1/3}).$$

Recalling that Err_{int} is bounded away from zero even as $n \rightarrow \infty$, we deduce that, asymptotically, the prediction error is dominated by the numerical integration error Err_{int} .

6. NUMERICAL RESULTS

6.1. Details of implementation

Our procedure depends on several parameters that need to be selected in practice: the size of two grids $t_1 < \dots < t_{m_1}$ and $z_1 < \dots < z_{m_2}$, two bandwidths h and g , and a parameter α . While it would be possible to select all of them in a data-driven way by crossvalidation, the smoothing nature of our approach implies that provided m_1 and m_2 are relatively large, increasing them further typically has the same effect as reducing h and g . Therefore, we fix m_1 and m_2 at relatively large values, see below, and choose only h , g and α by crossvalidation.

We apply the same amount of smoothing in standardized time and space. Given the definition of our weights w and ω in § 3.1, we implement this by taking $h = g \hat{\sigma}_t / (2\hat{\sigma}_Z)$, where $\hat{\sigma}_t$ and $\hat{\sigma}_Z$ are the empirical standard deviations of, respectively, the time-points corresponding to all data fragments and the values $Z_i(t_j)$ corresponding to all data fragments. We choose g and α by crossvalidation. Specifically, if our goal is to reconstruct the missing parts of the curves as in § 3.2, see, e.g., Fig. 2, we choose g and α by minimizing $\sum_{i=1}^n \sum_{t \in \{A_i, B_i\}} |X_i(t) - \hat{v}_1^{(-i)}(t \mid Z_i, \mathcal{I}_i \setminus \{t\})|$, where $\hat{v}_1^{(-i)}$ denotes the estimator \hat{v}_1 computed without using X_i . If our goal is linear prediction, as in § 3.4, we choose g , α and m in (20) by minimizing $\sum_{\ell} \{Y_{\ell} - \hat{\mu}_{\ell, \mathcal{I}_{\ell}}(Z_{\ell})\}^2$, where, for $1 \leq \ell \leq n$, $\hat{\mu}_{\mathcal{I}_{\ell}}^{(-\ell)} = \hat{\theta}_0^{(-\ell)} + \sum_{k=1}^m \hat{\beta}_k^{(-\ell)} \gamma_k$, with $\hat{\theta}_0^{(-\ell)}$ and the $\hat{\beta}_k^{(-\ell)}$ obtained by minimizing the version of (20) with $\sum_{i=1}^n$ replaced with $\sum_{i \neq \ell}$.

Next, we discuss the choice of the discrete grids. As argued above, since we choose h , g and α in a data-driven way, the grids can be chosen quite flexibly. We suggest using the following default grids, which, in our experience, often contain enough points. Users who do not feel comfortable with this could choose the size of the grids by crossvalidation, but we argue that doing so would be unnecessarily complicated. Since the states usually differ more among individuals than do the times, by default we take more states than times. For the states, we use $m_2 = 100$ equally spaced points, and to cover a broad range of values we take 90% of those points in $[L, U]$, where $L = \min_{i,t \in \mathcal{I}_i} X_i(t)$ and $U = \max_{i,t \in \mathcal{I}_i} X_i(t)$; that is, we take $z_1 = L - (5\Delta_X/90)$ and $z_{m_2} = U + (5\Delta_X/90)$, where $\Delta_X = U - L$. We take the time-points t_j to be equally spaced in the interval $\mathcal{I}_0 = [a, b]$ and to satisfy two criteria that prevent us from using too small a grid. First, we use at least $m_1 = 35$ time-points. This value is chosen in much the same spirit as the recommendation of [Ruppert et al. \(2003\)](#) that 35 knots are usually enough for constructing splines in practice. Second, we want the \mathcal{I}_i to contain overall at least two or three consecutive points, although enforcing this constraint strictly could result in m_1 being too large. With this in mind, we take the distance Δt between two consecutive points to be no more than

one third of the median fragment length, $\text{med}(B_i - A_i)$. Combining these two criteria, we put $\Delta t = \min\{(b - a)/34, \text{med}(B_i - A_i)/3\}$.

Of course, for all $a \leq t_k < b$ our estimated transition probabilities should be such that if $\max_y p(t_k, y, z_j) > 0$, then $\max_z p(t_{k+1}, z_j, z) > 0$, which is not always satisfied for all values of the smoothing parameters; in such cases some of the probabilities need to be modified. We show how to do this in the Supplementary Material.

6.2. Simulation study: curve reconstruction

We applied our curve reconstruction algorithm from § 3.2 to simulated examples, and compared it with the method of [Delaigle & Hall \(2013\)](#). To the best of our knowledge, this is the only competing approach available that is designed for short fragments. As indicated earlier, methods for sparse functional data, such as those of [James et al. \(2000\)](#) and [Yao et al. \(2005\)](#), are not appropriate for fragments and in general do not work well when applied to fragments. A referee asked us to demonstrate this via simulations, which we have done; see the Supplementary Material.

We generated data from several settings, with either one fragment per curve observed on an interval $\mathcal{I}_i = [A_i, B_i] \in \mathcal{I}_0 = [1, 100]$, or two fragments observed on $\mathcal{I}_i = [A_i, B_i] \cap [C_i, D_i]$. Since the method of [Delaigle & Hall \(2013\)](#) can handle only one fragment per curve, we compare our approach with theirs only in the single-fragment cases considered below. In each setting we generated $M = 100$ samples of data (X_i, \mathcal{I}_i) for $i = 1, \dots, n$, where $n = 30$ or $n = 50$, from three models used by [Delaigle & Hall \(2013\)](#) and adapted to the single population setting.

To illustrate our approach with a single fragment per curve, we considered three cases. For each we took $\mathcal{I}_i = [A_i, B_i]$, where $A_i = [U_i]$ denoting the nearest integer and $B_i = \min(A_i + [V_i], 100)$, with $U_i \sim \text{Un}[1, 95]$ and with $V_i \sim \text{Un}[7, 15]$ in case (i) and $V_i \sim \text{Un}[5, 10]$ in cases (ii) and (iii). In cases (i) and (ii), $X_i(t) = m(t - W_{i1}) + \{W_{i2} + W_{i3} \sin(t/W_{i4})\}\{W_{i5} + \sin(t\pi/1000)\}$; for case (i), $m(t) = \exp\{0.1(t - 40)\}/[1 + \exp\{0.1(t - 40)\}]$, $W_{i1} \sim \text{Un}[-5, 10]$, $W_{i2} \sim \text{Un}[-0.75, 0.75]$, $W_{i3} \sim \text{Un}[0.02, 0.05]$, $W_{i4} \sim \text{Un}[2, 3]$ and $W_{i5} \sim \text{Un}[0.1, 0.5]$; and for case (ii), $m(t) = \sin(t/15)/\{0.1(t - 5)^2 + 1\}$, the W_{ik} for $k \neq 2$ are as in case (i), and $W_{i2} \sim \text{Un}[-1, 1]$. In case (iii), $X_i(t) = m(t) + W_{i1} + W_{i2} \sin(t/W_{i3}) + W_{i4}$, where $m(t) = \sin(t/15)/\{0.1(t - 5)^2 + 1\}$, $W_{i1} \sim \text{Un}[-1, 1]$, $W_{i2} \sim \text{Un}[0.02, 0.05]$, $W_{i3} \sim \text{Un}[2, 3]$ and $W_{i4} \sim N(0, 0.04)$. To illustrate our approach with two fragments per curve, we modified cases (i) and (ii) by replacing \mathcal{I}_i there with $\mathcal{I}_i = [A_i, B_i] \cup [C_i, D_i]$, where $A_i = [U_i]$ with $U_i \sim \text{Un}[1, 95]$, $B_i = \min([A_i + V_i], 100)$ with $V_i \sim \text{Un}[5, 10]$, and $[C_i, D_i] \sim [A_i, B_i]$.

For $i = 1, \dots, n$, let \hat{X}_i denote the curves reconstructed either by our method or by that of [Delaigle & Hall \(2013\)](#). To measure the performance of the reconstruction algorithm, we computed for both methods the average absolute error $\text{AAE} = n^{-1} \sum_{i=1}^n \int_{\mathcal{I}_0} |\hat{X}_i(t) - X_i(t)| dt$. In Table 1 we report, for both methods, the median and interquartile range of AAE computed over the M simulated samples. The results show that in all cases, our new method improves upon the method of [Delaigle & Hall \(2013\)](#), sometimes considerably. In particular, while their procedure can sometimes work almost as well as the new procedure for simple cases where the curves are monotone, as in model (i), it has more difficulties with curves whose shape is more complex, such as those from models (ii) and (iii), especially when the number of fragments is small.

To illustrate this graphically, in Figures 3 and 4 we show samples of $n = 30$ observed fragments from cases (i)–(iii), the corresponding true unobserved curves X_i , and the curves reconstructed by our new procedure and by that of [Delaigle & Hall \(2013\)](#). These samples were chosen to exemplify the properties discussed in the previous paragraph. In Fig. 3, both methods appear to provide good reconstructions of the simple monotone curves corresponding to samples of size

Table 1. Median and interquartile range (in parentheses) of M calculated AAE values for the curve reconstruction algorithm in models (i)–(iii), using our suggested approach in the cases of one and two fragments and the method of [Delaigle & Hall \(2013\)](#) for one fragment

n	Model (i)			Model (ii)			Model (iii)	
	One fragment		Two fragments	One fragment		Two fragments	One fragment	
	NEW	DH2013	NEW	NEW	DH2013	NEW	NEW	DH2013
30	5.7 (1.3)	7.3 (4.3)	4.8 (1.0)	12.7 (5.5)	19.4 (12.3)	8.6 (2.4)	9.8 (4.7)	27.1 (25.1)
50	5.3 (0.9)	5.6 (1.3)	4.0 (0.6)	10.9 (2.5)	14.6 (6.6)	7.8 (1.3)	7.2 (2.5)	10.5 (14.9)

NEW, the approach proposed in this paper; DH2013, the method of [Delaigle & Hall \(2013\)](#).

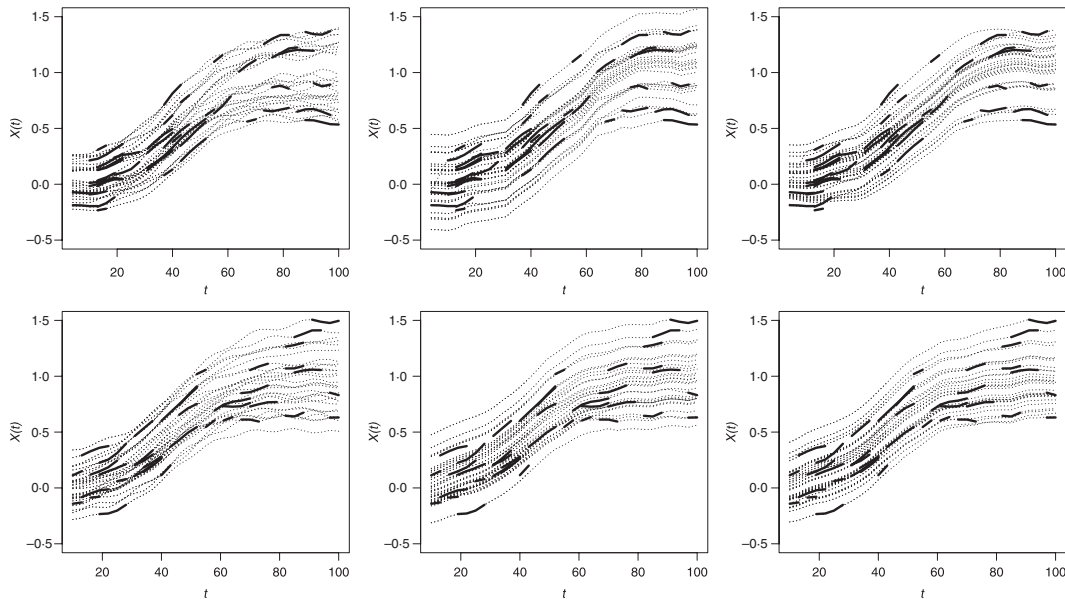


Fig. 3. Reconstruction of $n = 30$ curves for two samples, one in each row of panels, from model (i): true curves (left) and reconstructions using the method of [Delaigle & Hall \(2013\)](#) (middle) or our new approach (right); the observed fragments are shown in bold.

$n = 30$ generated by model (i). However, in Fig. 4 we can see that by the very nature of the algorithm in [Delaigle & Hall \(2013\)](#), which is based on copying shifted observed fragments, when the curves are more complex and the sample of fragments is sparse in some regions, the curves can be reconstructed poorly, whereas the smoothing nature of our new approach tends to guard against such dramatic problems. Both procedures improve as n increases, and the new method improves as the number of fragments per data curve increases. In addition to significantly improving upon the approach in [Delaigle & Hall \(2013\)](#), the new method has the advantage that it can be applied to the case where we observe multiple fragments per curve, unlike the method of [Delaigle & Hall \(2013\)](#).

6.3. Simulation study: prediction

To illustrate the linear prediction algorithm introduced in § 3.4, for each of the $M = 100$ samples of data (X_i, \mathcal{I}_i) for $i = 1, \dots, n$, where $n = 30, 50$ or 100 , generated from models (i) and (ii) in § 6.2, we also generated $Y_i = \theta_0 + \int_{\mathcal{I}_0} \theta X_i + \epsilon_i$ ($i = 1, \dots, n$), where $\theta_0 = 0.1$ and

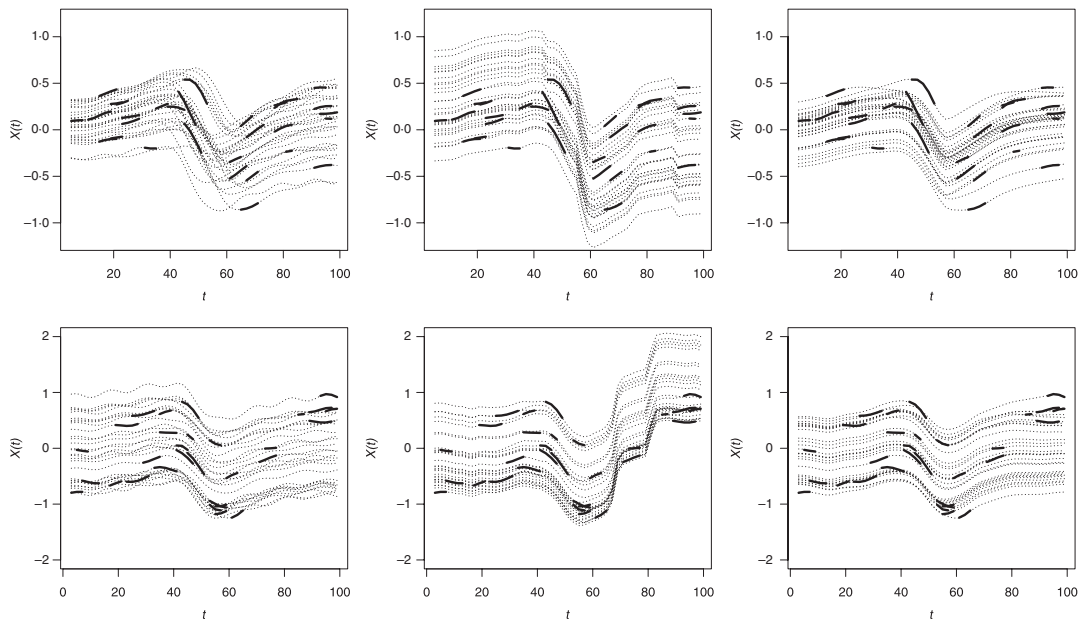


Fig. 4. Reconstruction of $n = 30$ curves for a sample from model (ii) (upper panels) or from model (iii) (lower panels): true curves (left) and reconstructions using the method of Delaigle & Hall (2013) (middle) or our new approach (right); the observed fragments are shown in bold.

Table 2. Median and interquartile range (in parentheses) of M calculated APE values for predicting values $Y_{\text{NEW},i}$ in models (i) and (ii), using our suggested approach in the cases of one and two fragments or using the full nonfragmented data

n	Model (i)			Model (ii)		
	Full	One fragment	Two fragments	Full	One fragment	Two fragments
30	0.09 (0.01)	0.29 (0.09)	0.22 (0.05)	0.09 (0.01)	0.63 (0.14)	0.52 (0.11)
50	0.08 (0.01)	0.26 (0.05)	0.20 (0.03)	0.08 (0.01)	0.58 (0.11)	0.46 (0.06)
100	0.08 (0.01)	0.22 (0.03)	0.17 (0.02)	0.08 (0.01)	0.51 (0.07)	0.41 (0.05)

$\theta(t) = 5\phi\{0.1(t - 50)\}$, with ϕ denoting the standard normal density and $\epsilon_i \sim N(0, 0.1^2)$. We then applied our predictor from § 3.4, with the basis chosen as in § 3.5, to $n_{\text{NEW}} = 100$ new fragmented data $(X_{\text{NEW},i}, \mathcal{I}_{\text{NEW},i})$ for $i = 1, \dots, n_{\text{NEW}}$. The value of Y , $Y_{\text{NEW},i}$, was not observed.

We compared our predictor with the standard linear functional predictor using the full unfragmented data curves, where the data are projected onto the standard functional principal component basis, with the number of basis functions chosen by crossvalidation. Let $\hat{Y}_{\text{NEW},i}$ denote the predicted $Y_{\text{NEW},i}$ computed using either predictor. To measure performance we computed, for each predictor, the average prediction error $\text{APE} = n_{\text{NEW}}^{-1} \sum_{i=1}^{n_{\text{NEW}}} |\hat{Y}_{\text{NEW},i} - Y_{\text{NEW},i}|$. The results are shown in Table 2, where we report, for the full data and the partial data observed on one or two fragments, the median and interquartile range of APE computed over the M simulated samples. Unsurprisingly, the predictor computed from the full data performs significantly better than that for fragmented data. The performance of our predictor improves as n increases and as the number of fragments per curve increases. Despite the difficulty of the fragmented case, our predictor works reasonably well; see Fig. 5, where we present scatterplots of pairs $(Y_{\text{NEW},i}, \hat{Y}_{\text{NEW},i})$ for $i = 1, \dots, 100$, when $\hat{Y}_{\text{NEW},i}$ is computed using our predictor.

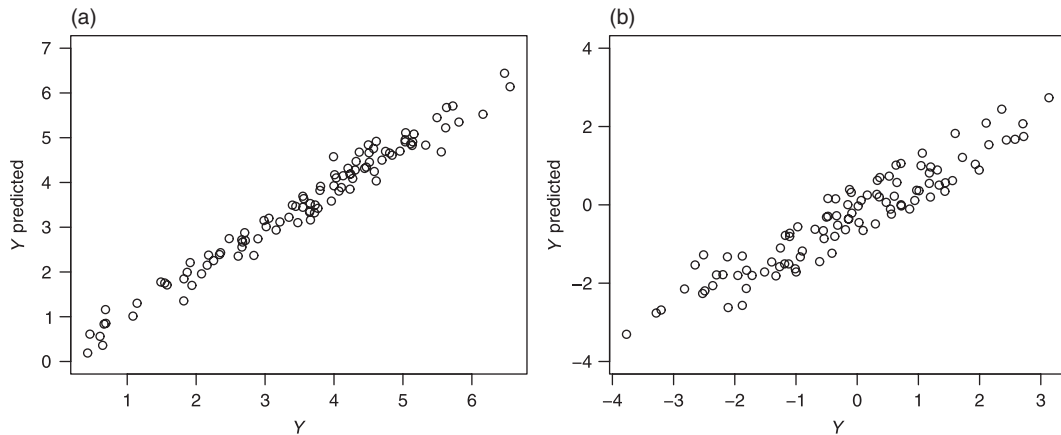


Fig. 5. Scatterplots of pairs $(Y_{\text{NEW},i}, \hat{Y}_{\text{NEW},i})$ for $i = 1, \dots, 100$, when $\hat{Y}_{\text{NEW},i}$ is the predictor proposed in this paper, computed from data observed on two fragments generated from (a) model (i) or (b) model (ii), with $n = 50$.

6.4. Real-data example

In addition to the bone mineral density growth dataset used in § 3.1 to illustrate the imputation of missing parts of curves, we applied our linear prediction algorithm to the Canadian weather stations data from Ramsay & Silverman (2005). This dataset consists of yearly average curves of temperature and precipitation at each of 35 weather stations. As in Chapter 15 of Ramsay & Silverman (2005), we let Y_i be the logarithm of total annual precipitation at the i th weather station, and we take X_i to be the yearly average temperature curve at that station. Like Ramsay & Silverman (2005), our predictor of Y is to be based on the linear model in (16), which we approximate through our discrete Markov process as in § 3.4.

Our goal is to compare the linear predictor based on the full data with our linear predictor applied to fragmented data. To do this, we extracted fragments of curves from the full curves by keeping, for the i th station, the values $X_i(t)$ for $t \in \mathcal{I}_i = [A_i, B_i]$, where $A_i = [U_i]$ with $U_i \sim \text{Un}[1, 350]$ and $B_i = \min([A_i + V_i], 365)$ with $V_i \sim \text{Un}[20, 60]$.

We generated $M = 100$ such fragmented samples of size $n = 35$. For each sample generated in this way, and for $i = 1, \dots, n$, we computed the predictor \hat{Y}_i of Y_i using the data pairs (X_j, Y_j) for $j \neq i$, where each X_j was either the full temperature curve of the j th weather station or the fragmented version we extracted from it; we used the predictors described in § 6.3. For each of the M samples, we measured the average prediction error $\text{APE} = n^{-1} \sum_{i=1}^n |\hat{Y}_i - Y_i|$. For the predictor based on the full data curves, the APE was equal to 7.81. For the predictor based on fragments, the median and interquartile range of the M values of APE were equal to 12 and 3.07, respectively. Given the much reduced data curves we generated by keeping only a fragment of each curve, the degradation in performance of the predictor based on fragments is rather small, suggesting that our predictor performs well.

ACKNOWLEDGEMENT

We downloaded the bone data from <http://fedc.wiwi.hu-berlin.de/quantnet/index.php?p=show&id=896>. This research was supported by the Australian Research Council. Delaigle is and Hall was a member of the Australian Research Council Centre of Excellence for Mathematical and Statistical Frontiers. Peter passed away on 9 January 2016 in Melbourne, Australia. He was a wonderful man and an extraordinary researcher. He will be sorely missed.

SUPPLEMENTARY MATERIAL

Supplementary material available at *Biometrika* online includes additional illustrations and calculations, an algorithm for practical implementation, and the proof of the theorem.

REFERENCES

- APANASOVICH, T. & GOLDSTEIN, E. (2008). On prediction error in functional linear regression. *Statist. Prob. Lett.* **78**, 1807–10.
- BACHRACH, L. K., HASTIE, T. J., WANG, M. C., NARASIMHAN, B. & MARCUS, R. (1999). Bone mineral acquisition in healthy Asian, Hispanic, Black and Caucasian youth: A longitudinal study. *J. Clin. Endocrin. Metab.* **84**, 4702–12.
- CAI, T. T. & HALL, P. (2006). Prediction in functional linear regression. *Ann. Statist.* **34**, 2159–79.
- CARROLL, R. J. & HALL, P. (1988). Optimal rates of convergence for deconvolving a density. *J. Am. Statist. Assoc.* **83**, 1184–6.
- CRAMBES, C., KNEIP, A. & SARDA, P. (2009). Smoothing splines estimators for functional linear regression. *Ann. Statist.* **37**, 35–72.
- DE GOOIJER, J. G. & ZEROM, D. (2003). On conditional density estimation. *Statist. Neer.* **57**, 159–76.
- DELAIGLE, A. & HALL, P. (2013). Classification using censored functional data. *J. Am. Statist. Assoc.* **108**, 1269–83.
- DELAIGLE, A., HALL, P. & APANASOVICH, T. V. (2009). Weighted least squares methods for prediction in the functional data linear model. *Electron. J. Statist.* **3**, 865–85.
- DELAIGLE, A., HALL, P. & MEISTER, A. (2008). On deconvolution with repeated measurements. *Ann. Statist.* **36**, 665–85.
- FRANZKE, C., CROMMELIN, D., FISCHER, A. & MAJDA, A. (2008). A hidden Markov model perspective on regimes and metastability in atmospheric flows. *J. Climate* **21**, 1740–57.
- GHOSH, A. P. (2011). Introduction to Diffusion Processes. *Wiley Encyclopedia of Operations Research and Management Science*, J. J. Cochran, L. A. Cox, Jr., P. Keskinocak, J. P. Kharoufeh & J. C. Smith, eds. New York: John Wiley & Sons.
- GOLDBERG, Y., RITOV, Y. & MANDELBAUM, A. (2014). Predicting the continuation of a function with applications to call center data. *J. Statist. Plan. Infer.* **147**, 53–65.
- HALL, P. & HOSSEINI-NASAB, M. (2006). On properties of functional principal components analysis. *J. R. Statist. Soc. B* **68**, 109–26.
- JAMES, G., HASTIE, T. J. & SUGAR, C. (2000). Principal component models for sparse functional data. *Biometrika* **87**, 587–602.
- KRAUS, D. (2015). Components and completion of partially observed functional data. *J. R. Statist. Soc. B* **77**, 777–801.
- LEE, E. R. & PARK, B. U. (2012). Sparse estimation in functional linear regression. *J. Mult. Anal.* **105**, 1–17.
- LEGG, B. J. & RAUPACH, M. R. (1982). Markov-chain simulation of particle dispersion in inhomogeneous flows: The mean drift velocity induced by a gradient in Eulerian velocity variance. *Boundary-Layer Meteorol.* **24**, 3–13.
- LIEBL, D. (2013). Modeling and forecasting electricity spot prices: A functional data perspective. *Ann. Appl. Statist.* **7**, 1562–92.
- RAMSAY, J. O. & SILVERMAN, B. W. (2005). *Functional Data Analysis*. New York: Springer, 2nd ed.
- RUPPERT, D., WAND, M. P. & CARROLL, R. J. (2003). *Semiparametric Regression*. Cambridge: Cambridge University Press.
- STRACHAN, I. G., HUGHES, N. P., POONAWALA, M. H., MASON, J. W. & TARASSENKO, L. (2009). Automated QT analysis that learns from cardiologist annotations. *Ann. Noninvasive Electrocardiol.* **14**, Supp. 1, S9–21.
- YAO, F., MÜLLER, H. G. & WANG, J. L. (2005). Functional data analysis for sparse longitudinal data. *J. Am. Statist. Assoc.* **100**, 577–90.
- YAU, C., PAPASPILLOPOULOS, O., ROBERTS, G. O. & HOLMES, C. (2010). Bayesian non-parametric hidden Markov models with applications in genomics. *J. R. Statist. Soc. B* **73**, 37–57.

[Received February 2015. Revised July 2016]