The past and future of growth rate estimation in demographic temporal frequency analysis:
Biodemographic interpretability and the ascendance of dynamic growth models

William A. Brown

Abstract

Population growth rate estimators have recently emerged in demographic temporal frequency analysis (dTFA) as further tools to monitor pre-census population dynamics. The information that such estimators supply affords considerable heuristic potential for population-ecological research both because they implicate the environmental, behavioral, and physiological mechanisms that condition population growth, and because they impose much-needed empirical constraints on our efforts to build theory addressing long-run human population dynamics. However, the earnestness with which these estimators have been applied warrants caution. First, several nonidentical measures of population growth are current in both formal demography and dTFA, creating an opportunity for their equivocation. Second, our ability to insightfully interrogate growth estimates for population-ecological information has been checked by a tendency to interpret them in the framework of off-the-shelf parametric growth models ill-suited to long-run population dynamics. This paper evaluates the biodemographic merit of three estimators recently applied in dTFA. It also advocates a transition away from parametric and toward dynamic growth models and introduces an inductive, regression-based approach to the latter. A Monte Carlo simulation study indicates that this inductive approach can successfully recapture information about environmental influences on population growth from archaeological summed probability distributions, less so from kernel density estimates.

Key words: archaeological demography; demographic temporal frequency analysis; population growth measurement; dynamic population modeling; taphonomic bias; composite kernel density estimation

1. Introduction

Population growth rate estimation offers considerable heuristic potential for population-ecological and biodemographic research in archaeology. Because spatiotemporal variability in the tempo of population growth is driven by variability both in distal factors – including both exogenous or natural and endogenous or human-systemic components – and in proximate (behavioral and physiological) factors, the empirical demonstration of paleopopulation growth rate variability therefore implicates variability in one or more of these driving factors and pulls us into the domain of explanatory demographic work, in-line with Billari’s (2015) two-stage, discovery-and-explanation framework for population research. Additionally, because demography’s standard measures of population growth are expressed as per capita rates, they bridge the gap separating micro-demographic research focusing on the fertility, mortality, and migration experiences of individuals and macro-demographic research focusing on the behaviors of whole populations (Billari, 2015; Coleman et al., 2015).

As mainstream population research returns to an interest in exploring “large-scale, long-term, interdisciplinary population problems” (Coleman et al., 2015: S1), archaeological demography is uniquely positioned to provide one of the longest views on human population available (Binford, 1962: 224; Plog, 1973: 194), vastly exceeding the temporal scope even of historical demography (van de Walle, 2006). It is therefore timely that a handful of recent studies in demographic temporal frequency analysis (dTFA) – archaeological research aimed at the recovery of paleopopulation abundance information from temporal frequency distributions (*tfd*s) of archaeological deposits (e.g., sites) – have included efforts to estimate paleopopulation growth rates based on *tfd*s from study regions spanning the globe (Bandy, 2005; Rallu, 2007: 20; Collard et al., 2010; Peros et al., 2010; Kelly et al., 2013; Williams, 2013; Downey et al., 2014, 2016; Zahid et al., 2016; Fitzhugh et al., 2016; Goldberg et al., 2016; for an early example, see Hommon, 1976:181, 217; see Supplementary Material for an extensive list of archaeological and paleontological publications featuring *tfd*s). The papers by Collard et al. (2010), Downey et al. (2014, 2016), and Zahid et al. (2016) stand out among these for their tacitly biodemographic interrogations of such growth rate estimates – Collard et al. (2010) focusing on the upper limits of biologically plausible growth and thus the implications of high growth rates for immigration inputs; Downey et al. (2014, 2016) focusing first on the fertility, mortality, and growth implications of Neolithization (2014) and the growth rate signals of adaptive resilience and vulnerability (2016); and Zahid et al. (2016) focusing on the fertility and mortality experiences of individuals that may be inferred from particular growth rates (under the strong assumptions of Lotka’s stable population model [Lotka, 1925, 1939; cf. Cole, 1954; Preston et al., 2001: 138-170; Skalski et al., 2005: 29, 330-335], Brass’s and colleagues’ polynomial fertility model [1975; cf. Preston et al., 2001: 204-208], and Gurven and Kaplan’s fitting of Siler’s survival model to hunter-gather mortality data [Siler, 1979; Gurven and Kaplan, 2007; cf. Preston et al., 2001: 192-201; Wood et al., 2002; Skalski et al., 2005: 141-150]).

While growth rate estimation in dTFA is ripe with potential for long-view biodemography and population ecology, the issue of apples-to-apples comparison must be raised,

because several growth rate measures are available in formal demography, and likewise several estimators have already been applied in dTFA. This paper reviews these measures (Section 2) and estimators (Section 3) in explicit formal detail, motivated by a need to cultivate greater formal demographic literacy and care in *tfd*-based growth rate estimation. In addition, our ability to interrogate paleopopulation growth rate estimates for the population-ecological and biodemographic information they bear on past individuals and populations has been limited by a continuing reliance on textbook parametric growth models, namely the exponential and logistic growth models. Section 4 briefly reviews the biodemographic and population-ecological content of these models; their theoretical and empirical limitations when applied to human population dynamics particularly over vast tracts of time; and the present transition from these to dynamic growth models, which are better able to capture moment-to-moment population responses to ecological contingencies. Section 4 also presents an inductive approach to dynamic population growth modeling in dTFA and provides formal support for it rooted in causal modeling and time series autoregressive (AR) modeling with covariates. A simulation experiment emulating the *tfd* data generating process is presented which demonstrates the application, potential, and best practices of such an approach to dynamic growth modeling.

2. Standard population growth rates in formal demography

Three related growth rate measures have currency in demography:

- the annualized growth rate (with both instantaneous and interval-averaged counterparts), here denoted r with prefixes;
- the annual factor of change in population abundance, denoted λ by Skalski and colleagues (2005: 290) and by Lee and colleagues (Lee and Tuljapurkar, 2008, 2010; Lee et al., 2009; Puleston and Tuljapurkar, 2009), here denoted using interval notation as $\lambda[t, t - 1]$ ¹
- “the fractional increase or decrease in abundance from one year to the next” (Skalski et al., 2005: 290; cf. Chamberlain, 2006: 20; Crema, 2012: Footnote 4), denoted R by Skalski and colleagues (2005: 290), here denoted using interval notation as $R[t, t - 1]$.

$\lambda[t, t - 1]$ is formally defined as the ratio of the closing to principal population abundance, denoted $N(t - 1)$ and $N(t)$, respectively:

$$\lambda[t, t - 1] \stackrel{\text{def}}{=} \frac{N(t - 1)}{N(t)} \quad (1).$$

¹ Note that placement of t before the numerically smaller $t - 1$ in the seemingly right-open interval defies standard practice in interval notation. While the left-open expression $(t - 1, t]$ may be more conventionally acceptable, the unconventional expression used in this case is also used throughout the paper to reflect the contrary nature of the cal BP timeline, which decreases in value as time elapses.

Conversely, $R[t, t - 1]$ is formally defined as the ratio of annual change in population abundance to the principal and is related to $\lambda[t, t - 1]$ as

$$R[t, t - 1] \stackrel{\text{def}}{=} \frac{N(t - 1) - N(t)}{N(t)} = \frac{N(t - 1)}{N(t)} - 1 = \lambda[t, t - 1] - 1 \quad (2).$$

The instantaneous case of the annualized growth rate, denoted $r(t)$, is defined as the ratio of the first derivative of the population abundance function at time t to the population abundance function at time t :

$$r(t) \stackrel{\text{def}}{=} \frac{N'(t)}{N(t)} = \lim_{dt \rightarrow 0^+} \frac{\left[\frac{N(t - dt) - N(t)}{dt} \right]}{N(t)} \quad (3)$$

(Preston et al. 2001: Eq. 1.3), i.e. as the average per capita change in population abundance over the infinitesimally small interval $[t, t - dt]$. Conversely, the discrete case – the mean annualized growth rate – is formally defined and empirically tractable as

$$\begin{aligned} \bar{r}[t, t - \Delta t] &\stackrel{\text{def}}{=} \frac{\int_t^{t-\Delta t} r(\tau) d\tau}{\Delta t} = \frac{\int_t^{t-\Delta t} \frac{N'(\tau)}{N(\tau)} d\tau}{\Delta t} \\ &= \frac{\ln \left[\frac{N(t - \Delta t)}{N(t)} \right]}{\Delta t} = \frac{\ln[N(t - \Delta t)] - \ln[N(t)]}{\Delta t} \quad (4), \end{aligned}$$

where Δt is the length of time over which the instantaneous growth rate is averaged (Preston et al., 2001: Eq. 1.8; Skalski et al., 2005: Eq. 7.16; cf. Chamberlain, 2006: 20).² For one-year intervals, $\bar{r}[t, t - \Delta t]$ is related to $R[t, t - 1]$ and $\lambda[t, t - 1]$ as

$$\bar{r}[t, t - 1] = \ln[\lambda[t, t - 1]] = \ln[1 + R[t, t - 1]] \quad (5).$$

If we Invert the formal relationship between population abundance and population growth rates, the annually discretized rates $\lambda[t, t - 1]$ and $R[t, t - 1]$ may be used to describe extended periods of past growth or projections of extended periods of future growth per the following equations

² As with interval notation, integrals throughout this paper are written such that the lower, inclusive boundary is the numerically larger t and the upper, exclusive boundary is the smaller $t - 1$, to reflect the contrary nature of the cal BP timeline.

$$N(t - \Delta t) = N(t) \times \prod_{\tau=t}^{(t-\Delta t)+1} \lambda[\tau, \tau - 1] \quad (6);$$

$$N(t - \Delta t) = N(t) \times \prod_{\tau=t}^{(t-\Delta t)+1} [1 + R[\tau, \tau - 1]] \quad (7)^3$$

(where Δt in Eqs. 6-7 is limited to positive integers). Eqs. 6-7 include geometric growth as a special case (i.e. assuming that the growth rate holds constant between sub-intervals, denoted with asterisks in the following):

$$N(t - \Delta t) = N(t) \times [\lambda^*]^{\Delta t} \quad (8);$$

$$N(t - \Delta t) = N(t) \times [1 + R^*]^{\Delta t} \quad (9).$$

The vastly more flexible, continuous-time counterpart to Eqs. 6-7 based on the mean annualized growth rate is

$$N(t - \Delta t) = N(t) \times e^{\bar{r}[t,t-\Delta t] \times \Delta t} = N(t) \times e^{\int_t^{t-\Delta t} r(\tau) d\tau} \quad (10)$$

(noting that Δt is no longer restricted to integer values but may take any positive real value). This projection includes exponential growth as a special case, i.e. assuming a constant annualized growth rate denoted r^* :

$$N(t - \Delta t) = N(t) \times e^{r^* \times \Delta t} \quad (11)$$

(Preston et al., 2001: 11; Skalski et al., 2005: 12-13).

While all three measures are imminently biodemographically interpretable – all three express realized reproductive effort as an average individual effort across population membership – the discrete rates $\lambda[t, t - 1]$ and $R[t, t - 1]$ are less flexible than are either $r(t)$ or $r[t, t - \Delta t]$ in that the first two

- attribute growth over an annual interval solely to the population's principal members;
- suppress the recognition that principal members' realized reproductive efforts may have been greater than is reflected in the end-of-year count, since individuals recruited into the population during a given interval who also perish during that interval are not reflected in the closing balance.

³ Once again, the boundaries of the large product operator in Eqs. 6-7 are reversed to reflect the contrary nature of the cal BP timeline.

Conversely, the growth rate $r(t)$ (Eq. 3) distributes realized reproductive effort across all members of the population at a single instant in time, whereas its interval-averaged counterpart (Eq. 4) distributes such effort not only across the interval's principal membership but rather across all individuals who held membership in the population at any point during the interval, weighted by the degree to which they held this status over the interval. In short, while the discretized rates are reasonably well-suited to species exhibiting annual reproductive cycles (Skalski et al. 2005: 292), the instantaneous growth rate and its interval-averaged counterpart are broadly applicable to species showing any reproductive cycle, including those with no strongly pronounced reproductive cycle at all (e.g., *Homo sapiens*).

3. Growth rate estimators used in dTFA

At least three *tfd*-based growth rate estimators have been employed in dTFA, only two of which are generally analogous to two of the above measures in formal demography.

The first (employed by Bandy, 2005; Collard et al., 2010; Downey et al., 2014; Zahid et al., 2016; Fitzhugh et al., 2016) is an estimator of the mean annualized growth rate, here denoted $\hat{r}[t, t - \Delta t]$:

$$\hat{r}[t, t - \Delta t] \stackrel{\text{def}}{=} \frac{\ln \left[\frac{u(t - \Delta t)}{u(t)} \right]}{\Delta t} = \frac{\ln[u(t - \Delta t)] - \ln[u(t)]}{\Delta t} \quad (12),$$

where the *tfd* functions $u(t)$ and $u(t - \Delta t)$ are the principal and closing abundances of archaeological deposits for a given interval, respectively.

The second is a measure labeled the “rate of annual increase” by Hommon (1976: 181, from Groube, 1970: 137), here denoted $\bar{R}[t, t + \Delta t]$ and calculated as

$$\hat{\bar{R}}[t, t - \Delta t] \stackrel{\text{def}}{=} e^{\frac{\ln[u(t - \Delta t)] - \ln[u(t)]}{\Delta t}} - 1 = \left[\frac{u(t - \Delta t)}{u(t)} \right]^{\frac{1}{\Delta t}} - 1 \quad (13),$$

which is analogous to the geometric growth model's R^* reflected in Eq. 9. This estimator is one of the earliest used in dTFA (Hommon 1976). Its one-year counterpart, which simplifies to the archaeological equivalent of Eq. 2, has also recently been recommended by Crema (2012: footnote 4) and employed by Goldberg and colleagues (2016).

The third is a measure labeled the “average annual growth rate” by Peros and colleagues (2010: Eq. 2; cf. Williams, 2013: Eq. 4.2), here denoted $GR_{Ann}[t, t - \Delta t]$:

$$\begin{aligned}
GR_{Ann}[t, t - \Delta t] &\stackrel{\text{def}}{=} \frac{\left[\frac{u(t - \Delta t) - u(t)}{\Delta t} \right]}{u(t)} = \frac{\left[\frac{u(t - \Delta t) - u(t)}{u(t)} \right]}{\Delta t} \\
&= \frac{\left[\frac{u(t - \Delta t)}{u(t)} - 1 \right]}{\Delta t} \quad (14).
\end{aligned}$$

Note that Eq. 14 differs from the expression originally introduced by Peros and colleagues in two respects: Eq. 14 expresses the rate as a proportion rather than as a percentage, and it generalizes the bicentennial estimation span employed by Peros and colleagues to a duration variable Δt which may be set at will to any empirically tractable size favored by the researcher. The bicentennially assessed $GR_{Ann}[t, t - \Delta t]$ employed both by Peros and colleagues (2010) and by Williams and colleagues (Williams, 2013; Williams et al., 2013, 2015) eludes any well-known analogue among formal demography's standard growth measures, though the generalized form of the rate given in Eq. 14 converges on the rate of annual increase given in Eq. 13 when $\Delta t = 1$. Similarly, $\hat{r}(t)$ (the *tfd*-based analogue of the instantaneous growth rate) is the limiting case of $GR_{Ann}[t, t - \Delta t]$ as Δt approaches 0 (per Eq. 3). All three rates also converge when the principal and closing abundances are equal, $u(t) = u(t - \Delta t)$. In every other case, the three estimators diverge from one another, requiring conversion prior to any valid comparison between them. It is on this point that Zahid and colleagues err, comparing Peros and colleagues' estimates to their own and others' based on the mean annualized growth rate (Zahid et al., 2015; Fig. 3).

Perhaps more importantly, Peros and colleagues' measure suffers a limitation of biodemographic interpretability as Δt increases beyond 1. As has already been noted for $R[t, t - 1]$ above, Peros and colleagues' measure attributes realized reproductive effort strictly to the principal membership of the population at the start of the estimation interval. Consequently, this measure would be most ideally suited for the study of species that reproduce at Δt -length cycles. Conversely, when calculate over a bicentennial interval, it defies biodemographic interpretation when applied to our species, given our sub-centennial reproductive career and life expectancy at birth.

By consequence, $GR_{Ann}[t, t - \Delta t]$ is always greater than $\hat{r}[t, t - \Delta t]$, save in the special case that $u(t - \Delta t) = u(t)$. For example, the already-impressive mean annualized growth rates 1%, 2%, and 3% inflate to average annual growth rates of 3.19%, 26.80%, and 201.21%, respectively, conditional on $\Delta t = 200$. By the same token, negative mean annualized growth rates of -1%, -2%, and -3% inflate to the considerably less negative average annual growth rates of -0.43%, -0.49%; and -0.50%, respectively, under the same condition. Applied to real-world population estimates, the global population increase from approximately 1 billion in AD 1800 to 6 billion in AD 2000 implies a mean annualized growth rate of approximately 0.8959% but an average annual growth rate of 2.5%!

Comparison between these two estimators thus warrants either a downward conversion of $GR_{Ann}[t, t - \Delta t]$ following the curvilinear relationship

$$\hat{r}[t, t - \Delta t) = \frac{\ln\{1 + GR_{Ann}[t, t - \Delta t) \times \Delta t\}}{\Delta t} \quad (15),$$

or inversely the upward conversion of $\hat{r}[t, t - \Delta t)$

$$GR_{Ann}[t, t - \Delta t) = \frac{1}{\Delta t} \times [e^{\hat{r}[t, t - \Delta t) \times \Delta t} - 1] \quad (16).$$

It is perhaps a minor consolation for Zahid and colleagues' analysis that such conversion mandates only small adjustments when $GR_{Ann}[t, t + \Delta t)$ falls very close to zero. For example, the time series of estimates reported at 200-year spans by Peros and colleagues (2010) for the North American population over the last 12,000 years ranges between approximately -0.05% and 0.08%, requiring only a slight downward adjustment to between -0.0527% and 0.0742% for their valid comparison against mean annualized growth rate estimates. Rounding or visual approximation alone may be sufficient to neutralize such small differences, leaving Zahid and colleagues' interpretation essentially intact on this point. Nevertheless, the two measures remain algebraically and biodemographically disparate, and we would be well-served to decisively favor a single growth rate estimator – presumably the mean annualized growth rate – for the sake of future comparative studies.

4. Growth rate measures and population growth models

4.1. Overview of growth rate models in dTFA

Presently, two well-known parametric population growth models continue to enjoy frequent application in dTFA:

- the exponential growth model employed both by Zahid and colleagues (2016) and by EUROEVOL Project participants (following Shennan et al. 2013);
- the logistic growth model, long advocated by Bettinger and Young (Young and Bettinger, 1995; Bettinger and Young, 2004; Bettinger, 2016) and most recently applied in dTFA by Goldberg and colleagues (2016) alongside the exponential model.

Elsewhere in the anthropological and demographic literatures, other parametric growth models have also been discussed (Skalski et al., 2005: Table 2.1), particularly the Doomsday model (Cohen, 1995: 88-90; Johnson and Earle, 2000: 9-14).

The exponential and logistic growth models are often regarded as convenient off-the-shelf tools for tracking short-term population growth dynamics insofar as they are derived from or at least are coherent with fundamental principles of population ecology and biodemography:

- Lotka's stable population model (Lotka, 1925, 1939; Cole, 1954; Preston et al., 2001: 141-144; Skalski et al., 2005: 29, 330-335), which decomposes the rate of natural

increase into age-patterned fertility and mortality rates, is a sufficient (but not a necessary) condition for the exponential growth model.

- Verhulst's logistic growth model (Verhulst, 1838; Pearl and Reed, 1920; Skalski et al., 2005: 15-25, 290-291, 314-322) is coherent with the Malthusian notion that population growth leads to increasing resource competition and subsistence stress, in turn depressing population growth (negative density-dependence) until the population has reached the upper limits of sustainable abundance ('carrying capacity' or 'equilibrium size'). Generalizations of the logistic model are available that improve its flexibility in empirical applications (Skalski et al., 2005: 21-22). Likewise, several alternative models are available that are coherent not only with negative density-dependent effects in growth (Skalski et al., 2005: 22-23) but with positive density-dependent (or 'Allee') effects as well (Skalski et al., 2005: 24-26; cf. Taylor and Hastings, 2005; Steele, 2009: 126-127).

Both the exponential and logistic growth model also afford closed-form expressions for their respective instantaneous growth rates, as well as their counterpart first derivatives (per Eq. 3):

- The exponential growth model exhibits a constant growth rate as discussed in Section 2, r^* , whose first derivative is thus

$$N'(t|r^*) = r^* \times N(t|r^*) \quad (17).$$

- The logistic growth model is often defined as the first derivative of the population abundance curve it implies:

$$N'(t|\rho, K) = \rho \times N(t|\rho, K) \times \left[1 - \frac{N(t|\rho, K)}{K} \right] \quad (18)$$

(Skalski et al., 2005: 17), where ρ is the "intrinsic" growth rate for a given species or population (i.e., the rate at which that population would grow if uninhibited by exogenous factors; Skalski et al. 2005: 290) and K is the asymptote of population abundance (coherent with the population-ecological concept of "carrying capacity" or "equilibrium population size"). Rearranging Eq. 18 per Eq. 3, the mean annualized growth rate corresponding with this differential equation is

$$r(t|\rho, K) = \frac{N'(t|\rho, K)}{N(t|\rho, K)} = \rho \times \left[1 - \frac{N(t|\rho, K)}{K} \right] \quad (19)$$

(Skalski et al., 2005: 13), implying one of two monotonic trajectories over time: when $N(t) < K$, this instantaneous growth rate decreases asymptotically toward 0 over time,

while it increases asymptotically toward 0 over time when $N(t) > K$. (The latter behavior undermines the coherence of K with density-dependent constraints on growth).

Despite the mathematical parsimony of these models, their mechanistic transparency, realism, and long-run applicability to human population growth dynamics have all been increasingly challenged on theoretical grounds (Rogers 1992: 378-380; Kelly 1995: 228-229; Surovell and Brantingham, 2007: 1869; Riede et al., 2009: 178-179; Lee and Tuljapurkar, 2008; 2010: 115). Likewise, their goodness of fit with population data has been challenged on empirical grounds (Cohen 1995: 76-95; Johnson and Earle, 2001: 7-14; Shennan et al., 2013; Timpson et al., 2014; Zahid et al., 2016: 932). In response, these textbook models have begun to recede in favor of more realistic if complex dynamic growth models, wherein population growth rates respond moment by moment to changing environmental exigencies and historical happenstance rather than rigidly conforming to the deterministic, almost teleological, rates stipulated by the exponential, logistic, or other parametric growth models.

While in theory population growth dynamics are a continuous process, in practice efforts to model them are often pursued in a discrete-time framework: temporal variability in the observed or projected pace of population growth is reported as a time series of finite-interval rates such as the annual factor of change $\lambda[t, t - 1]$ (Skalski et al., 2005: 306-314; Lee and Tuljapurkar, 2008, 2010; Lee et al., 2009; Puleston and Tuljapurkar, 2009) or the mean annualized growth rate $\bar{r}[t, t - \Delta t]$. Taking such a discrete-time approach is undeniably limiting, insofar as finite-interval growth rates obscure the instant-to-instant change in the pace of growth within such intervals (Eqs. 4 and 10); instead, our ability to move from $\bar{r}[t, t - \Delta t]$ or $\lambda[t, t - 1]$ to $r(\tau)$ (where τ denotes any point in time within the reference interval) requires the acceptance of additional helping assumptions, for example the assumption of constant intra-interval growth that reduces Eq. 10 into the special case expressed in Eq. 11. By extension, when time series of period growth rates are linked to similarly granular time series of environmental covariates, a degree of mechanistic opacity regarding their relationship results, since the influence of such covariates on the intra-interval instantaneous growth rates is obscured by the latter's elusiveness.

Even so, the acceptance of analytical granularity is justified for two reasons: First, our capacity to measure and record the theoretically continuous stream of population growth in empirical contexts is limited by the instruments we apply to these tasks, as is true of dynamic phenomena in general (Shumway and Stoffer, 2011: 11). Second, in contexts of purely hypothetical population projection (Preston et al. 2001: 117-118), the successful identification of analytically tractable, closed-form expressions for the $r(t)$ function becomes increasingly unlikely as time-varying population structures or environmental covariates are added to the model, especially when these are stochastic or include lag, feedback, or autoregressive effects. Consequently, it is often more computationally efficient in population projection contexts to accept the granularity entailed by discrete-time models (Mangel and Clark, 1988: 4, 45, 210-212; Preston et al., 2001: 119-120; Lee and Tuljapurkar, 2008, 2010; Lee et al., 2009; Puleston and Tuljapurkar, 2009).

For the most part, dynamic growth models pursued in dTFA have taken the form of deductive models (Belovsky, 1988; Lee and Tuljapurkar, 2008; Puleston and Tuljapurkar, 2008; Lee et al., 2009; Lee and Tuljapurkar, 2010; Kirch et al., 2012; Tallavaara et al., 2015), in which case temporal frequency data may be formally or informally enlisted to evaluate the goodness of fit of such models to reality. However, the potential utility of dynamic growth models derived inductively through time series regression has also recently been demonstrated by Kelly et al. (2013: 444-445). While the prospects and limitation of the deductive approach are worthy of consideration in their own right, the focus of the remainder of this paper is on those of the inductive approach.

Kelly et al.'s (2013) examination of climatic impacts on Rocky Mountains hunter-gatherer population dynamics provides a useful prototype for the pursuit of inductive dynamic population modeling. Their approach involved regressing temporal frequency data on reconstructed moisture and temperature time series data, taking the general, multiple log-linear form

$$\ln[u(t)] = \left[\beta_0 + \sum_{j=1}^k \beta_j x_j(t) \right] + \varepsilon(t) \quad (20a);$$

$$u(t) = \left[e^{\beta_0} \times \prod_{j=1}^k (e^{\beta_j})^{x_j(t)} \right] \times e^{\varepsilon(t)} \quad (20b),$$

where β_0 denotes the model's y -intercept; β_j is the slope corresponding with the j th climatic covariate out of k covariates; $x_j(t)$ is the value of the j th covariate at time t ; the component in brackets contains the expected value of the log-*tfd* (Eq. 20a) or *tfd* (Eq. 20b) at time t ; and $\varepsilon(t)$ is the residual error separating the observed from the expected log-*tfd* at time t .

A revision to this approach is advocated here, in which time series of mean annualized growth rates estimated from *tfd*s at uniform temporal intervals are regressed on covariates of interest:

$$\hat{r}[t, t - \Delta t] = \left[\beta_0 + \sum_{j=1}^k \beta_j x_j(t) \right] + \varepsilon[t, t - \Delta t] \quad (21)$$

(compare Eq. 20a). Ostensibly, this approach differs from Kelly and colleagues' in its treatment of the *tfd*-based growth rate rather than the *tfd* function as the model's dependent variable, but in fact Eq. 21 implies a model closely resembling Eqs. 20a-20b, if we substitute $u(t)$ for $N(t)$ and Eq. 21 for $\bar{r}[t, t - \Delta t]$ in Eq. 10:

$$\begin{aligned}
u(t - \Delta t) &= u(t) \times e^{\hat{r}[t, t - \Delta t] \times \Delta t} = u(t) \times e^{\left[\beta_0 + \sum_{j=1}^k \beta_j x_j(t) \right] + \varepsilon[t, t - \Delta t]} \times \Delta t \\
&= \left[u(t) \times e^{\gamma_0} \times \prod_{j=1}^k (e^{\gamma_j})^{x_j(t)} \right] \times e^{\varepsilon[t, t - \Delta t]} \quad (22a); \\
\ln[u(t - \Delta t)] &= \left[\ln[u(t)] + \beta_0 \times \Delta t + \sum_{j=1}^k \beta_j \times \Delta t \times x_j(t) \right] + \varepsilon[t, t - \Delta t] \times \Delta t \\
&= \left[\ln[u(t)] + \gamma_0 + \sum_{j=1}^k \gamma_j x_j(t) \right] + \varepsilon[t, t - \Delta t] \quad (22b),
\end{aligned}$$

where $\gamma_j = \beta_j \times \Delta t$ and $\varepsilon(t) = \varepsilon(t) \times \Delta t$. The one feature that distinguishes the models expressed in Eqs. 20a and 22b is the presence of the term $\ln[u(t)]$ in the latter, qualifying it as a first-order autoregressive (AR) model with covariates (Shumway and Stoffer, 2011: 84-84), vis-à-vis Eq. 20a's classic regression of one time series upon others (Shumway and Stoffer 2011: 48). Eq. 22b is thus in-line with Kelly and colleagues' proposition that "later population size is undoubtedly affected by earlier population size" (2013: Supporting Information) but eludes their concern that "the use of summed probability distributions [*spds*] and further smoothing artificially inflates the strength of this relationship" (2013: Supporting Information), insofar as this term lacks any free parameter to estimate and is axiomatically necessary.

An additional, indirect effect of present population abundance on future abundance via the growth rate is also considered, specifically revising Eq. 21 to

$$\hat{r}[t, t - \Delta t] = \left[\beta_0 + \beta_1 u^2(t) + \sum_{j=2}^k \beta_j x_j(t) \right] + \varepsilon[t, t - \Delta t] \quad (23)$$

implying

$$\begin{aligned}
u(t - \Delta t) &= \left[u(t) \times e^{\gamma_0} \times (e^{\gamma_1})^{u^2(t)} \times \prod_{j=2}^k (e^{\gamma_j})^{x_j(t)} \right] \times e^{\varepsilon[t, t - \Delta t]} \quad (24a); \\
\ln[u(t - \Delta t)] &= \left[\ln[u(t)] + \gamma_0 + \gamma_1 u^2(t) + \sum_{j=2}^k \gamma_j x_j(t) \right] + \varepsilon[t, t - \Delta t] \quad (24b),
\end{aligned}$$

This formulation is once again a first-order AR model with covariates, this time involving one fixed and one free autoregressive term, $\ln[u(t)]$ and $\gamma_1 u^2(t)$ respectively. As before, the first of

these terms captures the direct, deterministic, and axiomatically necessary effect of present on future abundance. Conversely, the second term captures an indirect, probabilistic influence of present on future abundance, mediated through the population growth rate. (See Appendix A in Supplementary Material for an argument against the application of second- or higher-order AR models to population abundance time series; see also Shumway and Stoffer, 2011: 135.) In the case that $\beta_1 < 0$ in Eq. 23 (or equivalently that $\gamma_1 < 0$ in Eqs. 24a-24b), population abundance exerts a negative and specifically downward-parabolic influence on the mean annualized growth rate coherent with negative density-dependent constraints on growth (cf. Taylor and Hastings, 2005: Fig. 1). This parabolic influence necessarily implies an upper intercept along the $u(t)$ axis above which the expected growth rate takes on increasingly negative values, hereafter labeled the “growability threshold,” coherent with the population-ecological concept of carrying capacity or equilibrium size,

$$u^*(t|\beta_1, c(t)) = |\beta_1|^{-0.5} \times c(t)^{0.5} \quad (25),$$

where

$$c(t) = \beta_0 + \sum_{j=2}^k \beta_j x_j(t) \quad (26).$$

The dependence of this threshold on the model’s other time-varying covariates, captured by the function $c(t)$, is coherent with the influence of temporally heterogeneous environmental and/or cultural variables on equilibrium size (cf. Steele, 2009: 129-130). We may also note that a special case of the model exists in which the growability threshold is undefined in the mathematical sense, specifically when $c(t) < 0$ per Eq. 25. In this case, no value of $u(t)$ is sufficient to induce positive expected growth (the maximum of the parabola falling below 0), coherent with Stein Mandryk’s (1993) concept of submarginal environments. Consequently, the model implies the possibility of three alternative scenarios for population decline: those that obtain when population increase has led the population to overshoot the growability threshold; those that obtain when the threshold has lowered below current population abundance; and those that obtain when the threshold has fallen out of definition. The first two cases are expected to induce compensatory downward adjustments in population abundance to the threshold, while the third is expected to lead to sustained decline, which may become terminal if allowed to persist for long enough.

Population-ecological realism notwithstanding, the question remains open as to how successful these models can be in reliably recovering information about the drivers of paleopopulation growth when fitted to growth rate time series estimated from archaeological temporal frequency data rather than those derived directly from population abundance records. Inevitably, the intervening transformations that characterize the *tfd* data generating process

(DGP) – including both random and systematic varieties of creation, preservation, and investigation error (Rick, 1987) – introduce additional error into the system beyond that which characterizes the population growth processes of interest. The nature in which such error expresses itself in the archaeologically fitted model depends largely on whether such error is random or systematic. Random error is expected primarily to inflate the dispersion of residuals around the fitted model’s expectation. Conversely, the influence of systematic error on the fitted model may behave differently between contexts. In many cases, it may obscure the relationship (i.e., forcing the confidence interval around the estimated regression coefficient to include 0). Conversely, it may lead to spurious estimates of effect size, i.e. to regression coefficient estimates that do not include the true value in their confidence intervals. This latter possibility includes Kelly and colleagues’ caution that *spds* or especially smoothed *tfd*s will artificially inflate the strength of influence of present on future population abundance (2013: Supporting Information).

The following subsection thus explores the potential successes and limitations of fitting such regression models to archaeological *tfd*s, in the context of a well-controlled Monte Carlo (MC) simulation experiment. Such an approach affords several benefits:

- It allows the analyst to specify (and thus to know) the nature of various covariates’ influences on population growth dynamics as inputs of the simulation.
- It allows the analyst to inspect (and thus to know) the population growth output of this initial step in the simulation.
- It allows the analyst to realistically simulate the *tfd* DGP and thus the potentially confounding influences of creation, preservation, and/or investigation error on regression models fitted to the simulated archaeological output vis-à-vis the known input.

4.2. Exploring the efficacy of regression-based dynamic growth rate modeling through Monte Carlo simulation

The simulation begins with a dynamic model in which mean annualized growth rates over five-year intervals respond to present population abundance and one climatic covariate – temperature – according to the following equation:

$$\bar{r}[t, t - 5) = [\beta_0 + \beta_1 N^2(t) + \beta_2 D^2(t)] + \varepsilon[t, t - 5) \quad (27),$$

where $D(t)$ denotes the temperature deviation from the Holocene mean as estimated from the GISP2 ice core (in degrees C; Alley, 2004); β_j denote the model’s regression coefficients as before; and $\varepsilon[t, t - 5)$ denotes residual deviation in realized growth relative to the expected growth rate (bracketed component).

As was true for the *tfd*-focused regression model given in Eq. 23, negative values of β_1 in this model will impose a negative, downward-parabolic influence of present population abundance on future growth. A similar situation holds for β_2 , which if negative will induce a

downward-parabolic influence on growth at extreme temperature departures from $D(t) = 0$. The combination of the $N(t)$ and $D(t)$ terms in Eq. 27 therefore implies that expected growth rates will fall along a downward-opening (elliptic) paraboloid surface. The maximum of this surface is located at the origin of the covariate space, $(N(t) = 0, D(t) = 0)$ where it equals β_0 at this point, decreasing monotonically toward $-\infty$ either as $N(t)$ increases toward ∞ or as $D(t)$ deviates in either direction from the Holocene average (or both). The β_0 term is therefore coherent with the intrinsic growth rate concept: the “population growth rate under the most favorable conditions for maximal growth” (Skalski et al., 2005: 290). Similarly, the $D(t)$ term is coherent with the intuition that severe temperatures in either direction are bad for survival, fertility, and thus growth. The growability threshold in this case resembles that given in Eq. 25, noting however that this time it applies to the population abundance function $N(t)$ rather than its archaeological proxy $u(t)$:

$$N^*(t|\beta_1, c(t)) = |\beta_1|^{-0.5} \times c(t)^{0.5} \quad (28),$$

where

$$c(t) = \beta_0 + \beta_2 D^2(t) \quad (29).$$

(The relationship between the growability threshold $N^*(t|\beta_1, c(t))$ and its archaeological counterpart $u^*(t|\beta_1, c(t))$ is discussed further in Appendix F in Supplementary Material. Also see Appendix B in Supplementary Material for discussion of potential refinements on Eqs. 21, 23, or 27 that accommodate both Allee effects and the influence of natural disasters and cultural change on expected growth.)

Finally, the residual deviation term in Eq. 27 introduces white noise around model expectation, being normally distributed around 0 and having a standard deviation σ_r :

$$\varepsilon[t, t-5] \sim \mathcal{N}(0, \sigma_r) \quad (30).$$

As a result of this noise, substitution of Eqs. 27 and 30 into Eq. 10 and rearrangement reveals a population abundance time series following a lognormally distributed random walk with covariate-conditioned drift (Shumway and Stoffer, 2011: 14-15),

$$N(t-5) = \left[N(t) \times e^{5 \times \beta_0} \times (e^{5 \times \beta_1})^{N^2(t)} \times (e^{5 \times \beta_2})^{D^2(t)} \right] \times e^{5 \times \varepsilon[t, t-5]} \quad (31),$$

where the first factor captures the deterministic influence of present on future abundance; the second factor captures the influence of the intrinsic growth rate on future abundance; the third factor captures the indirect, negative influence of present on future abundance; the fourth factor

discounts future abundance depending on present temperature deviation; and the fifth factor captures the influence of lognormal noise around expected future abundance (compare Eq. 24a).

Operationalization of the simulation involves the parameterization of Eq. 27 with the following values –

$$\beta_0 = 0.003 \quad (32a)$$

$$\beta_1 = -3.3 \times 10^{-12} \quad (32b)$$

$$\beta_2 = -0.003 \quad (32c)$$

$$\sigma_r = 0.0005 \quad (32d).$$

– implying an intrinsic growth rate of 0.3% (β_0) and a growability threshold of 30,000 at $D(t) = 0$ (per Eqs. 28-29). Approximately 95% of observed growth rates should fall within a $\pm 0.098\%$ span around the expected growth rate.

The simulation begins with the colonization of a hypothetical study region at 10,000 cal BP by a founding population of 600 individuals. Subsequently, this population is exposed to a time series of temperature fluctuations equivalent to those inferred from GISP2 ice core data, interpolated at five-year intervals. The upper panel of Fig. 1 describes both this temperature time series (black line) and its squared transformation upon which expected growth is based per Eq. 27 (gray line). The middle panel presents a population abundance time series simulated from the preceding parameterization (solid black line), while the lower panel presents the corresponding growth rate time series (gray line). The dashed line in the middle panel presents temporal variation in the growability threshold per Eqs. 28-29, while vertical blue bars indicate those temporal intervals over which the growability threshold is undefined. The black line in the lower panel describes temporal variation in expected growth, around which the realized growth rate fluctuates.

Fig. 1. [1.5-column figure] Dynamic population growth simulation model. *Upper panel:* Greenland paleotemperature reconstruction derived from the GISP2 data (Alley, 2004), reported as the deviation from the average temperature over the last 10,000 years cal BP (in degrees C; black curve). The gray curve describes the square of this record, upon which the dynamic population model is based. *Middle panel:* simulated population

abundance time series (solid curve); the temperature-modulated growability threshold (dashed curve); and temporal intervals over which this threshold is undefined (blue/gray bars). *Lower panel:* Expected population growth rate time series (black curve) and simulated growth rate time series (gray curve). Blue/gray bars are as in middle panel.

This figure concretely illustrates several of the points made above regarding the model. First, the growability threshold tops off at just 30,000 as temperature deviation from the Holocene mean approaches 0 (Fig. 1, upper panel). Conversely, this threshold exhibits sharp dips corresponding with moderate temperature deviations in either direction, while it falls out of definition when temperature deviates to an extreme degree. Second, growth continues uninterrupted when population falls below the growability threshold even when this threshold ticks down. Conversely, population declines when realized abundance exceeds the threshold, all the more so when the threshold is undefined. Third, growth levels off to near zero values when population reaches the threshold, for example over the relatively stable intervals 7000-5000 cal BP and 3100-1500 cal BP.

Following the generation of this population history, the simulated DGP shifts to archaeological record formation (i.e., from the sphere of general to middle-range and low-level theory). First, the population inhabiting our hypothetical study region generates some archaeologically tractable unit of observation at a constant per capita rate per unit time, implying that the record of such units prior to any further transformation is proportional to the population abundance curve, i.e. such that the timestamp anchoring each (κ th) created unit to the timeline, t_κ , follows a proportionate population abundance function $f_N(t)$:

$$t_\kappa \sim f_N(t) \quad (33).$$

Second, not all units thus created survive to present. Specifically the attrition of such units is simulated to probabilistically follow the Lomax (1954) survival model tacitly adopted by Surovell and colleagues (Surovell et al., 2009; Surovell and Pelton, 2016):

$$S(t_\kappa) = \left(1 + \frac{t_\kappa}{b}\right)^{-c} \quad (34),$$

where $S(t_\kappa)$ is the survival function for deposits of age t_κ , i.e. the probability that deposits of such age will survive to the present; and b and c are the Lomax model's scale and shape parameters (respectively set to 2176.4 and 1.3925309 by Surovell and colleagues [2009]; see Appendix C in Supplementary Material for further exposition of the relationship between Lomax's and Surovell and colleagues' models). The simulation determines whether each (κ th) created unit survives to the present by parameterizing the Bernoulli distribution with this survival function.

Third follows the simulated detection of preserved units during fieldwork and ascertainment into the working dTFA database. The probability of detection and ascertainment of a preserved unit of a given age is denoted $p_I(t)$ (where the subscripted I denotes

‘investigation’, in-line with Rick’s [1987] investigation error). For the sake of argument, the simulation assumes the ideal case in which inclusion is unbiased (i.e., assumes that $p_I(t)$ holds constant across the timeline) such that the overall probability that a unit will be created at time t , preserved to the present, and detected and ascertained into the sample is:

$$f_I(t) \propto f_N(t) \times S(t) \times p_I(t) \propto f_N(t) \times S(t) \quad (35).$$

To simulate a working dataset including n cases from such a distribution, the simulation thus implements the following procedure:

1. Calendric timestamps for $100n$ units are randomly drawn from a temporal frequency distribution proportional to the abundance distribution depicted in Fig. 1 (middle panel), per Eq. 33.
2. To simulate deposit preservation, each of these cases is then subjected to a Bernoulli trial with probability of survival $S(t_k)$ calculated per Eq. 34 and parameterized per Surovell and colleagues (2009).
3. Out of the subset of surviving deposits, the first n are selected to simulate unbiased archaeological sampling.

The simulation then “obscures” the true calendric age of each case included in the working database (t_i) by probabilistically mapping it onto the ^{14}C timeline (Brown, 2015: Eq. 3; a procedure sometimes labeled “uncalibration” [Shennan et al., 2013: 6] or “back-calibration” [Timpson et al., 2014: 446]) using the IntCal13 model (Reimer et al., 2013) as a forward map. For each true ^{14}C age thus generated, an accompanying measurement error s_i is randomly selected following a lognormal distribution parameterized as

$$s_i \sim \ln \mathcal{N}(\mu = 4.10, \sigma = 0.16) \quad (36),$$

which approximates the distribution of measurement errors characterizing Kelly and colleagues’ Wyoming sample (2013: Supporting Information). To simulate measurement error, the measured ^{14}C age (r_i) is then displaced from the true ^{14}C age with s_i per Brown (2015: Eq. 4-5; cf. Bronk Ramsey 2009: Eqs. 7-9).

The challenges confronting the hypothetical archaeologist, naïve of the true calendric ages of the cases that their database comprises, are first of all to generate a *tfd* on the calendric timeline using this information and second of all to transform this *tfd* with the goal of accurately inverting the multi-step DGP underlying its existence (Santosa and Symes, 2015). It is against such inverted *tfd*s that the model expressed in Eq. 23 is most appropriately fitted, if the goal is to recover the “correct” parameterization of Eq. 27 (i.e., to recover the parameter values given in Eqs. 32a-d).

The ascendant standard practice in dTFA to control for uncertainty in radiocarbon-based age estimation is to construct *tfd*s in the form of summed probability distributions (*spds*;

technical details provided in Appendix D in Supplementary Material). In effect, *spds* provide our best guess at the temporal distribution of data points included in a sample given our uncertainty regarding each's true calendric age (Bronk Ramsey, 2001: 361). Conversely, they do not control for further uncertainty regarding which out of all possible cases have eluded detection or inclusion in the sample through random sampling error. The structures evident in any given *spd* may thus be driven in part by random sampling error, whose magnitude is modulated by sample size as usual, and in part by systematic interference entailed by the variable slope of the forward map model used to calibrate the timestamps included in the sample (Brown, 2015).

More recently, archaeologists have begun applying a new procedure for *tfd* construction – smoothing them – either to mitigate sampling error (Louderback et al., Tallavaara, 2015; Weitzel and Coddling, 2016) or calibration interference (mainly in the form of weighted moving averages on the *spd* – Weninger, 1986; Williams, 2012; Kelly et al., 2013; Shennan et al., 2013 – though loess regression has also recently been implemented in this capacity by Downey et al., 2014; cf. Shumway and Stoffer, 2011: 74-75). Fitzhugh and colleagues (2016, present author included) have recently applied an experimental, data-driven kernel-smoothing procedure to an *spd* from the Kuril Islands along the Northwest Pacific Rim with the intention of mitigating both problems. Once again, it should be noted that *spds* and kernel density estimates (*KDEs*) fundamentally differ in motivation, despite their algebraic likeness as noted by Grove (2011) and Baxter and Cool (2016), thus warning against their operational conflation; on the contrary, it would be entirely appropriate to apply both methods, despite the undesirable propagation of error that doing so entails (or rather illuminates).

Here, a new approach to *tfd* calculation is introduced and implemented in the context of the simulation experiment – composite kernel density estimation – which takes advantage of decades of research on the optimization of kernel density estimation techniques while also incorporating full information on the uncertainty that accompanies ^{14}C -based age estimates, thus improving upon similar, recent approaches based on fixed single-point estimates (Tallavaara, 2015; Weitzel and Coddling, 2016). Specifically, the distribution that this procedure generates – a composite kernel density estimate (*CKDE*) – is an averaged model across multiple individually generated *KDEs*, each calculated from a sample of possible single-point timestamps for the ^{14}C -dated dataset. (Technical details of composite kernel density estimation are presented in Appendix D in Supplementary Material.)

To evaluate Kelly and colleagues' proposition that *spds* and especially smoothed *tfd*s artificially inflate the strength of autoregressive relationships across these time series, both an *spd* and *CKDE* are calculated for the simulated dataset.

Next, to correct for taphonomic bias, both of these *tfd*s are multiplied by the reciprocal of the survival function given in Eq. 34, once again assuming Surovell and colleagues' (2009) parameterization:

$$u_{taph}(t) \propto u(t) \times S^{-1}(t) \quad (37),$$

where $u(t)$ denotes a generic *tfd* function and $u_{taph}(t)$ denotes its taphonomically corrected counterpart.

Fig. 2 illustrates the results of the preceding simulated archaeological operations. The dark blue curve in the upper panel (labeled 1) is the proportionate population abundance function governing the creation of archaeologically observable units (per Eq. 33). The dark blue curve in the lower panel (labeled 2) describes the corresponding distribution of units expected to be preserved and recovered following their creation (per Eq. 35), while the rug plot and gray curve (2') describe the distribution of true calendric ages of the first 1000 units generated following the three-step procedure outlined above. The light blue curve in the lower panel (3a) describes the *spd* generated from ^{14}C age estimates assigned to these 1000 units, while the black curve in the lower panel (3b) describes the *CKDE* generated from the same. Finally, the light blue curve in the upper panel (labeled 4a) describes the taphonomic correction of the lower panel's *spd*, while the black curve in the upper panel (4b) describes the taphonomic correction of the corresponding *CKDE*.

Fig. 2. [1.5-column figure] Simulated archaeological temporal frequency distributions (*spd* and *CKDE*), including the simulated proportionate population abundance function for comparison. The upper panel presents *tfd*s free of taphonomic influence, while the lower panel illustrates the marked difference in *tfd* shape resulting from taphonomic

bias. The grey curve in the lower panel denotes a KDE of the archaeological sample if the true ages of this sample could be known.

From the point of view of an omniscient observer, the close parallel between the *KDE* generated from the sample's true calendric ages (line 2') and the *CKDE* generated from its ^{14}C age estimates (line 3b) indicates that the composite kernel density estimation approach is nearly as successful in recovering information about the shape of line 2 as would be a simple *KDE* were we able to know the true calendric ages of all observations in the sample. At several points, the *CKDE* (line 3b) also out-performs the *spd* (line 3a) in approximating the expected distribution (line 2), smoothing away many of the extreme, fine-grained structures that idiosyncratically characterize *spds* as anticipated by Brown (2015: 143). Finally, taphonomic correction of both the *spd* and *CKDE* indicates a favorable degree of success, though of course the fine-grained structures characterizing the *spd* are increasingly exaggerated moving backward in time.

The upper and lower panels of Fig. 3 describe time series of growth rates calculated per Eq. 12 at five-year intervals, corresponding with Fig. 2's upper and lower panels (colors and labels are identical between figures). As is already evident in Peros and colleagues' previous study (2010: Fig. 5), the difference between growth rate time series calculated from corrected and uncorrected *tfd*s differ most sharply at the younger end of the timeline, though this difference is barely visually detectable (See Appendix E in Supplementary Material for the derivation of a closed-form expression for the difference between the uncorrected and corrected growth rate time series.) Visual comparison of the true growth rate time series (curve 1 in Fig. 3, upper panel) to both the estimated growth rate time series based on the *spd* on one hand (curve 4a) and that estimated from the *CKDE* on the other (curve 4b) indicates that the latter considerably reduces noise vis-à-vis the former. It also indicates that *CKDE*-based growth rates closely approximate true growth rates for relatively stable intervals but markedly underestimate them for those intervals showing catastrophic decline. Conversely, it is difficult to visually determine whether the central tendency of the *spd*-based growth rates approximate their corresponding true growth rates. However, we may at least conclude that both the high frequency and amplitude of variability in the *spd*-based growth rate time series are on the whole biologically implausible for human populations. Thus, as exploratory tools, *CKDE*-based estimators are preferable.

Fig. 3. [1.5-column figure] growth rate time series. Simulated true growth rates (dark blue line); estimated growth rates derived from the simulated *spd* (light blue line); estimated growth rates derived from the simulated *CKDE* (black line). Upper and lower panels refer to the taphonomically unaffected and affected *tlds*, as in Fig. 2. The

difference between them is visually slight (see Appendix E in Supplementary Material for a closed-form expression summarizing this difference), most noticeable near the younger end of the sequence.

However, a very different conclusion is recommended when we fit the regression model expressed in Eq. 27 to both *spd*- and *CKDE*-based growth rate time series. Table 1 compares the known parameters (Eqs. 32a-d) to parameter estimates derived from both of these archaeological time series. Note that estimates produced for the coefficient β_1 must be rescaled by a factor C^2 , where C is the normalizing constant by which the population abundance curve $N(t)$ is rescaled to yield the proportionate abundance curve $f_N(t)$. (see Appendix F in Supplementary Material for demonstration).

Table 1. Parameter estimates and accompanying standard errors for the dynamic growth regression model expressed in Eq. 27, including the known values used to parameterize the simulation (1st row) and values estimated from the *spd*- and *CKDE*-derived growth rate time series (2nd-3rd rows). The final column denotes the known standard deviation (1st row) and the standard deviation of fitted-model residuals (2nd-3rd rows). β_1 estimates for the fitted models are rescaled by the factor C^2 to adjust for the disparity of scale separating archaeological and demographic time series (described in detail in the text).

Growth rate time series	$\hat{\beta}_0$	$\hat{\beta}_1$	$\hat{\beta}_2$	$\hat{\sigma}_r$
Model parameter input	3×10^{-3}	-3.3×10^{-12}	-3×10^{-3}	5×10^{-4}
Model observed values	$3.04 \times 10^{-3} \pm 2.15 \times 10^{-5}$	$-3.40 \times 10^{-12} \pm 4.01 \times 10^{-14}$	$-3.02 \times 10^{-3} \pm 1.54 \times 10^{-5}$	5.01×10^{-4}
<i>spd</i> -based growth rate time series	$1.94 \times 10^{-3} \pm 9.18 \times 10^{-4}$	$C^2 \times (-5.20 \times 10^4 \pm 3.87 \times 10^4)$ $= -2.22 \times 10^{-12} \pm 1.65 \times 10^{-12}$	$-1.92 \times 10^{-3} \pm 6.71 \times 10^{-4}$	2.19×10^{-2}
<i>CKDE</i> -based growth rate time series	$1.04 \times 10^{-3} \pm 5.34 \times 10^{-5}$	$C^2 \times (-2.98 \times 10^4 \pm 2.42 \times 10^3)$ $= -1.27 \times 10^{-12} \pm 1.03 \times 10^{-13}$	$-0.87 \times 10^{-3} \pm 3.77 \times 10^{-5}$	1.23×10^{-3}

Two observations follow from these results. First, for all three of the model's β coefficients:

- parameter estimates derived from the *spd*-based growth rate time series fall closer to the known true values than do those from the *CKDE*-based time series;
- parameter estimates derived from the *CKDE*-based time series fall closer to 0 than do those derived from the *spd*-based time series, i.e. either

$$\beta_{j,true} < \hat{\beta}_{j,spd} < \hat{\beta}_{j,CKDE} < 0 \quad (38a)$$

or

$$\beta_{j,true} > \hat{\beta}_{j,spd} > \hat{\beta}_{j,CKDE} > 0 \quad (38b);$$

- 95% confidence intervals around all parameter estimates derived from the *spd*-based time series include the true value, while none of the confidence intervals derived from the *CKDE*-based time series do. By the same token, this is largely due to the fact that the confidence intervals surrounding the *spd*-based parameter estimates are considerably

wider than those surrounding the *CKDE*-based estimates, the former wholly engulfing the latter. Furthermore, the 95% confidence interval around the β_1 estimate for the *spd*-based time series is so wide that it includes 0.

Second, neither time series yields a useful estimate of the standard deviation characterizing residual variation around expectation ($\hat{\sigma}_r$), owing to the additional contributions of creation, preservation, and/or investigation error: while the known value σ_r is only 0.0005, the model fitted to the *CKDE*-based time series shows residuals with a standard deviation of 0.00123, and the *spd*-based time series, 0.0219. Overall, however, the fitted model performs better when fitted to the *spd*-based time series than to its *CKDE*-based counterpart.

Note that Kelly and colleagues' caution regarding the application of AR models to *spds* or especially to smoothed *tfd*s requires qualification in light of the preceding results. On one hand, the growth rate time series for the smoothed *tfd* – in this case the *CKDE* – suggests a negative but spuriously small autoregressive effect size: the 95% confidence interval around the corresponding regression coefficient is $-1.476 \times 10^{-12} \leq \beta_1 < -1.064 \times 10^{-12}$ ($t = -12.32$; $p = 1.14 \times 10^{-33}$), excluding the known true value $\beta_1 = -3.\bar{3}$. Consequently, rather than artificially inflating the influence of present on future population size (as measured by the effect size β_1), it artificially deflates it. On the other hand, the 95% confidence interval around the *spd*-based β_1 estimate is very imprecise, including not only values that overstate the negative influence of present on future size (in-line with Kelly and colleagues' warning) but also the true effect size, the null effect size, and positive effect sizes: $-5.52 \times 10^{-12} \leq \beta_1 < 1.08 \times 10^{-12}$ ($t = -1.346$; $p = 0.1785$). In short, in neither case does the range of possible estimates definitively overestimate the effect size of present on future abundance.

To more thoroughly evaluate Kelly and colleagues' caution, it would be necessary to conduct another simulation in which no autoregressive component is operative in the DGP, then to fit the regression model to the resulting archaeological time series. However, given that the central estimates of β_1 afforded by both archaeological time series underestimate the effect size of present on future abundance, it seems unlikely that a DGP lacking any autoregressive component would then lead to the spurious detection, and thus inflation, of autoregressive effects in archaeological growth rate time series.

In any case, despite the fact that the *spd*-based time series exhibits greater noise and affords less precise confidence intervals around its parameter estimates than does the *CKDE*-based time series, the *spd*-fitted model may nevertheless be regarded as the more successful of the two in two main respects: first, the *CKDE*-fitted model shows spuriously small parameter estimates, and second, the *spd*-fitted model's parameter estimates fall closer to the true values than do the *CKDE*'s (Eqs. 38a-b). The superior performance of the *spd*-fitted model in these respects is perhaps most powerfully illustrated when the expected time series implied by each fitted model (Fig. 4, upper panels, black curves) is juxtaposed against the true growth rate time series (Fig. 4, upper panels, dark blue curves). On one hand, the expected growth dynamics implied by both fitted models match the true growth rate time series in terms of the location of

major transitions and disruptions in growth. Both also underestimate the amplitude of growth observed in the true time series. However, the expected time series implied by the *CKDE*-fitted model dampens the amplitude of growth to a much greater degree than does the *spd*-fitted time series. By extension, when each model's expected growth rate time series is used to re-project the *tfd* (black curves in Fig. 4, lower panels), the one generated from the *spd*-fitted model more closely approximates the true proportionate population distribution (dark blue curves in Fig. 4, lower panels) than does that generated from the *CKDE*-fitted model.

In short, while the *CKDE*-based growth rate time series may be regarded as a better exploratory estimator of the true growth rate dynamics underlying the archaeological data in the absence of population-ecological theory, the *spd*-based series serves as a more reliable source of information on the covariates of growth rate variability. Furthermore, the latter approach presents an alternative approach to data-smoothing as a byproduct based on the fitted models' expected growth rate time series, as illustrated in Fig. 4.

Fig. 4. [1.5-column figure] *Upper panels*: growth rate time series. Blue curve: simulated true growth rate time series. Gray curves: Estimated growth rate time series derived from the *CKDE* (upper left panel) and *spd* (upper

right panel). Black curves: Expected growth rate time series assuming the *CKDE*-fitted regression model (upper left panel) and the *spd*-fitted regression model (upper right panel). *Lower panels*: temporal frequency distributions. Blue curve: simulated proportionate abundance time series. Gray curves: simulated *CKDE* (lower left panel) and *spd* (lower right panel). Black curves: expected *tfd*s derived from the expected growth rate time series assuming the *CKDE*-fitted regression model (lower left panel) and the *spd*-fitted regression model (lower right panel).

Admittedly, it would be folly to mistake this simulation experiment for anything more than a heavily conditioned proof of concept for a regression-based approach to dynamic growth modeling in dTFA. On the contrary, the seeming success of this approach is due in no small part to the fact that several ideal research conditions have been baked into the simulation, few of which will always or even often hold in real-world dTFA contexts, particularly when no deliberate effort is made to insure them:

- *Minimal systematic creation error.* The simulated paleopopulation in this experiment has generated an archaeological record whose original temporal abundance is proportional to its own population abundance function ($f_N(t) \propto N(t)$). However, creation bias is widely recognized as a potential confounder on this proportionality. For example, when the archaeological unit of observation is the site, diachronic changes in regional settlement systems should likewise be expected to lead to fundamental changes in the rate of site formation, undermining the strong assumption of proportionality. This includes Allometric relationships between population size and spatial need (Hamilton et al., 2007); cyclical oscillations between concentrated and dispersed regional populations (Crema, 2014); and increasing sedentism corresponding with economic transitions such as the foraging-agriculture transition (Downey et al., 2014).
- *Correct survival model specification for systematic preservation error.* The Lomax survival function that our hypothetical archaeologist has inverted to correct for taphonomic bias is identical in form and parameterization to the taphonomic component of the simulated DGP.
- *Minimal systematic investigation error.* The simulated dataset has accumulated through the application of unbiased data recovery methods (i.e., no recovery bias has been included as a salient component of the simulated DGP). Conversely, real-world chronometric databases are typically generated through the application of field detection methods that are often unable to detect surviving deposits of different ages with equal probability and which are particularly unfavorable toward the recovery of older deposits. Furthermore, the compilation of large supra-regional databases is potentially affected by the sometimes eclectic but all too often shared research biases of generations of researchers.
- *Minimal random investigation error.* While a sample size of 1000 is increasingly achievable at a supra-regional level, particularly given the dedicated work of a handful of projects in amassing chronometric databases – for example the University of Wyoming’s “Populating a Radiocarbon Database of Western North America” project (cf. Zahid et al.,

2016); the EUROEVOL Project (cf. Shennan et al., 2013; Timpson et al., 2014); and the Canadian Archaeological Radiocarbon Database (cf. Chaput and Gajewski, 2016, and sources cited therein) – not all regions of the world have received equal chronometric attention. Likewise, the disaggregation of supra-regional databases into subsets for analyses at a smaller regional/sub-regional/local scale necessarily reduces sample size, often by a dramatic degree. As demonstrated by Williams (2012), Shennan and colleagues (Shennan et al., 2013; Timpson et al., 2014), Brown (2015), and others, such small samples are expected to introduce considerable noise into the *spd* that will not only amplify the residual error around the fitted model’s expectation but may also further decrease the precision (i.e. increase the standard errors associated with) the fitted parameter estimates.

- *Correct regression model specification for the population growth rate.* The regression model that our hypothetical archaeologist has fitted to his/her taphonomically corrected archaeological time series is identical in form to the population-ecological component of the simulated DGP.

An expansion of simulation work should therefore be pursued in the near future to more thoroughly evaluate the robustness of regression-based dynamic growth models such as the one considered here when these baked-in assumptions are relaxed. The results of such sensitivity analyses will undoubtedly deflate the degree of success characterizing the present simulation experiment, though probably not to such a degree that the enterprise as a whole is defeated. Nor should it be overlooked that archaeological researchers play an active role in resolving these and other potential confounders; rather than taking such strong assumptions for granted, many of dTFA’s most active recent contributors have dedicated considerable effort to the identification of best-practice protocols for the mitigation of the various sources of error that confront their paleopopulation research. With sufficient care and inferential constraint, the regression approach to dynamic population growth modeling recommended here will similarly benefit from such scrutiny.

5. Conclusions

The derivation of paleopopulation growth rate estimates from archaeological *tfd*s has recently emerged as a prominent activity in dTFA. While this move should be regarded as positive development ripe with biodemographic and population-ecological potential, care must be taken first of all to recognize the existence of multiple alternative growth rate measures in formal demography as well as multiple alternative estimators on offer in dTFA, and second of all to favor those that are most biodemographically interpretable. The mean annualized growth rate and its *tfd*-based equivalent stand out among these in this respect.

This emerging focus on paleopopulation growth rate estimation has begun to pull dTFA in the direction of long-run population growth modeling. While textbook parametric models drawn from population ecology have enjoyed wide currency in this capacity – namely the well-

known exponential and logistic growth models – mounting temporal frequency evidence has lent further empirical support to the perceived insufficiency of such models when applied to long-run human population dynamics, regardless of their elegance and computational ease. In their place, dynamic growth models – which allow population growth rates to articulate with variability in the states of natural and human systems and consequently to respond on a moment-to-moment basis to temporal fluctuations therein – have begun to take their place. These dynamic models have taken either of two general forms: deductive models, which are offered as null models against which to test the goodness of fit of temporal frequency data, and inductive models, e.g. regression models fitted to temporal frequency data and covariate time series.

As a proof of concept, this paper has explored a generic and relatively simple regression-based dynamic growth model. The model explored here asserts that the growth rate responds negatively both to present population abundance and to temperature extremes. The relative efficacy of such regression modeling when fitted to archaeological growth rate time series rather than directly to demographic time series is explored through a Monte Carlo simulation experiment, indicating that the model may be successfully fitted to simulated *spds* under certain conditions – namely that systematic creation and investigation error are minimal, the influence of systematic preservation error is correctly inverted, and sample size is large. Conversely, this experiment indicates that fitting the model to growth rate time series derived from a smoothed *tfd* yields spurious results, including deflated effect size estimates (contra Kelly et al., 2013: Supporting Information) and over-smoothed growth rate time series and *tfd*s as byproducts. Thus, *tfd* smoothing should be envisioned as an exploratory operation (Shumway and Stoffer, 2011: 70-78), most usefully applied when theory about the drivers of growth is underdeveloped. Future simulation work is warranted to more thoroughly evaluate the sensitivity of regression-based dynamic growth models to the various confounders that confront dTFA.

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