Kinematics of Cranial Ontogeny: Heterotopy, Heterochrony, and Geometric Morphometric Analysis of Growth Models

CHRISTOPH PETER EDUARD ZOLLIKOFER AND MARCIA SILVIA PONCE DE LEÓN
Anthropological Institute, University of Zurich, CH-8057 Zürich, Switzerland

ABSTRACT In this paper, we examine the relationship between the classical concepts of heterotopy, heterochrony and ontogenetic allometry as descriptive and as explanatory categories in the investigation of evolutionary developmental novelty in the hominid skull. We use concepts of kinematic analysis of locomotion to propose a methodological framework for the kinematic analysis of cranial form change during ontogeny. We argue that a combination of geometric-morphometric methods with graphics visualization tools currently represents the most adequate means to analyze the kinematics of ontogeny. Using cranial growth models, we simulate how evolutionary modifications of developmental processes impinge on morphological patterns of ontogeny, and explore how differences in ontogenetic patterns can tentatively be traced back to underlying process differences. Our analyses indicate that minor alterations in growth parameters elicit complex patterns of ontogenetic modification that are difficult to describe with the standard repertoire of heterochronic terminology. The proposed kinematic and model-based approach is used in a comparative analysis of cranial ontogeny in Neanderthals and anatomically modern humans, indicating that early ontogenetic modification of a small set of growth parameters is a major source of evolutionary novelty during hominid evolution. J. Exp. Zool. (Mol. Dev. Evol.) 302B:322–340, 2004.

INTRODUCTION Since the early days of evolutionary thinking it has been recognized that a prime source of phylogenetic novelty lies in the modification of ontogeny. Haeckel’s initial definition of heterochrony and heterotopy as the temporal and spatial agents of evolutionary change of ontogenetic pathways (Haeckel, 1866) still represents an important conceptual framework to explore, measure, and explain how new morphologies are brought about during evolution. How can, in an evolutionary-developmental research setting, heterochrony and heterotopy be studied as agents of biological change? Researchers investigating animal models or clinical instances of cranial developmental modification face the challenge of disentangling the tremendously complex network of cause and effect that links genes via epigenetic interactions at various levels of organization to spatiotemporal patterns of change in cranial morphology. Nevertheless, developmental geneticists find themselves in a relatively comfortable situation compared with paleoanthropologists who study evolutionary developmental diversification of the hominid cranium. In addition to the notorious material scarcity of the fossil record, fossil hominid ontogenies are no longer accessible to direct observation and/or experimental interaction such that patterns of morphological diversity observed in the fossil record must be linked with experimental evidence from extant species to infer potential mechanisms of evolutionary novelty via developmental modification.

In this paper, we discuss two closely related questions that arise in comparative morphometric studies of fossil hominids from an evolutionary development perspective: 1) How can spatiotemporal patterns of morphological change in the growing skull be optimally measured to establish and test hypotheses about underlying developmental processes? 2) How does evolutionary...
modification of a developmental process impinge on spatiotemporal morphological patterns of ontogeny? We study these issues using growth models, computer simulations and empirical evidence. Growth models are exploratory tools that assume a middle position between experiment and analysis. They combine the bottom-up approach of “in silico” (i.e., computer-based) simulation of developmental processes with top-down analysis of the resulting morphological patterns of shape change, while giving full control over all growth parameters. This approach provides general insights into potential correlations between developmental process modification and pattern modification that can later be used to assess empirical data of spatiotemporal morphological change.

The language of ontogenetic modification, from molecules to morphology

Heterochrony sensu Gould (’77) can be understood as a dissociation of the velocities of change in size versus change in shape between ancestor and descendant taxa. Building upon Gould’s arguments, Alberch et al. (’79) proposed an operational framework for quantitative analysis of heterochronic dissociation, using the concept of ontogenetic trajectories that can be followed through age-size-shape space. Over past decades, concepts and terminology of heterochronic analysis have undergone considerable diversification and modification (e.g., Shea, ’84, ’88; Raff and Wray, ’89; McKinney and McNamara, ’91; McNamara, ’97). Gould’s terminology, which was originally confined to comparative description of modifications of shape-age trajectories, was expanded to include heterochronic dissociation of size-age trajectories (Godfrey and Sutherland, ’96; Godfrey and Sutherland, ’96; McNamara, ’97; Rice, ’97; Klingenberg, ’98). In parallel to the expansion of terminology, the scope of heterochronic analysis was widened considerably and now comprises studies of almost any phenomenon of temporal modification of ontogeny, from genes and morphogenetic processes (e.g., Wilson, ’88; Slack and Ruvkun, ’97) to phenes and morphological pattern (e.g., Zelditch et al., 2003). With growing empirical evidence from molecular developmental genetics, it was recognized that the relationships between process heterochrony and pattern heterochrony are intricate and difficult to disentangle. Within the complex network of spatiotemporal interactions that connects genes with phenes, “process” and “pattern” can be defined at various levels of scale in both space and time. For example, it was shown that a heterochronic pattern may be caused by a heterotopic process (Raff and Wray, ’89; Cubo et al., 2000). Conversely, heterochronic dissociation between developmental modules may result in heterotopic dissociation in the structure as a whole (McNamara, 2002a). Terminology thus appears as a matter of perspective.

These issues can be exemplified with a clinical example (a perspective already adopted by Wilson et al., ’88). Crouzon syndrome is a congenital malformation characterized by craniosynostosis (early closure of one or more cranial sutures), a hypoplastic maxilla causing upper airway obstruction and pseudoprognathism, and other congenital cranial and postcranial defects (Jones, ’88) (Fig. 1). It has been shown that premature suture closure, which is prevalent in both Crouzon and Apert syndrome, is related to three different types of gain-of-function mutants of FGFR (fibroblast growth factor receptors) genes 1 to 3 (Reardon et al., ’94; Neilson, ’95; Wilkie et al., ’95; Yu et al., 2000). These mutations affect temporal patterns of differentiation, and probably also spatial migration patterns, of neural crest cells (Sarkar et al., 2001; Abzhanov et al., 2003; Santagati and Rijli, 2003).

How can Crouzon syndrome be described in terms of spatiotemporal process modification? A gain-of-function mutant in an FGF receptor gene represents molecular process heterochrony, as it leads to increased rates of signal transduction, differentiation and bone deposition in neural crest cell derivatives. At the same time, potential effects on migratory patterns must be referred to as heterotopic. From a phenotypic perspective

Fig. 1. Crouzon syndrome in an adolescent. Note maxillary hypoplasia, and re-ossification of coronal suture following surgery (arrows).
which is important regarding timing and strategies of surgical correction (Richtsmeier et al., '98; Sailer et al., '98)—suture closure is a peramorphic effect, thus representing an adult feature, but reduced midfacial growth is paedomorphic. Finally, considering the skull as a whole, functional pseudoprognathism resulting from dissociation between normal mandibular (Andresen et al., 2000) and retarded midfacial growth results in cranial heterotopy in comparison to unaffected subjects.

The Crouzon example shows that heterochronic and heterotopic terminology is indeed a matter of perspective. However, “perspective” does not signify here personal taste but expresses that fact that cause and effect, or process and pattern, of spatiotemporal variants of developmental pathways must be investigated and compared at different levels of organization and integration.

Similar arguments can be applied to questions of evolutionary modification of cranial ontogeny. Reconstructing phylogenies with evolutionary developmental data means that we must examine spatiotemporal homology relations between ontogenetic processes at various levels of scale, both in time and space (Lieberman, 2002). The definition of homology relations between developmental units and processes is a complex task, since cranial development is governed by a web of genetic and epigenetic interactions rather than by a temporal sequence and/or spatial hierarchy of cause and effect connecting genes to phenes (Lieberman, '99). Nevertheless, establishing and testing hypotheses about ontogenetic homology relationships—at least at the pattern level—is an essential prerequisite for measuring ontogenetic modification at the phenotypic level.

Various researchers have tackled these issues and contributed to the foundations of a quantitative framework for comparative analysis of heterochronic and heterotopic dissociation in two- and three-dimensional morphologies (Fink and Zelditch, '95; Godfrey and Sutherland, '96; Zelditch and Fink, '96; Godfrey et al., '98; O’Higgins, 2000; Zelditch et al., 2000; Roopnarine, 2001; Zelditch et al., 2003), and there is a growing number of studies investigating the modular temporal aspects of ontogeny and their dissociation (Rice, '97; Vrba, '98; Cubo, 2000; Cubo et al., 2002; McNamara, 2002b; Vinicius and Lahr, 2003). Here, we build upon these achievements and complement them with model considerations to devise an explicit operational framework for the comparative morphometric analysis of developmental modifications during the course of the hominid skull.

The kinematics of morphology

In physics, during the analysis of movement a clear difference is made between kinetics and kinematics. While the former discipline studies forces, energy and moments, the latter describes the movement of bodies in space and time, without explicit reference to the underlying processes. Analogously, ontogenetic analysis has a kinetic and a kinematic aspect: we may study processes of growth and development (kinetics), or the resulting spatiotemporal patterns of morphological change (kinematics). In this section, we formulate a kinematic approach to the classic notions of heterochrony, heterotopy and allometry.

To illustrate the logical issues that have to be taken into consideration during such analyses, we use the analysis of human locomotion (Winter, '90) as an example (Fig. 2A). In kinematic studies, one measures temporal changes in morphology by tracking the position of reference points on the human body (so-called landmarks) that were chosen to denote relevant anatomical locations on limbs (notably joints), trunk and head. It is most reasonable and efficient to sample spatial positions $p_i(x_i, y_i, z_i)$ of the reference points in an...
external system of coordinates (e.g. that of a video tracking system) at various points in time \( t \). The resulting spatiotemporal trajectories \( P(t) \)

\[
P(t) = \begin{pmatrix}
    p_1(t) \\
p_2(t) \\
    \vdots \\
p_K(t)
\end{pmatrix} = \begin{pmatrix}
    x_1(t) & y_1(t) & z_1(t) \\
x_2(t) & y_2(t) & z_2(t) \\
\vdots & \vdots & \vdots \\
x_K(t) & y_K(t) & z_K(t)
\end{pmatrix}
\]

of all points \( p_i \ (i=1\ldots K) \) describe the individual’s trajectory through space. Kinematic trajectories can be used to derive a variety of additional measurements; for example, it is possible to calculate velocity vectors

\[
v_i(t) = \left( \Delta x_i \Delta y_i \Delta z_i \over \Delta t \Delta t \Delta t \right) = (v_{xi} v_{yi} v_{zi})
\]

that indicate the speed and direction of movement of each landmark in space and time (\( \Delta t \) can be thought of as the frame rate of the video system). The set of all velocity vectors defines a vector field, or **displacement field**

\[
D(t) = \{ v_i \}
\]

that indicates, for each landmark, how its position will change from time \( t \) to time \( t + \Delta t \).

Taking into account that the human body has a modular organization, \( D(t) \) can be analyzed in various ways. For example, we may investigate how the subject is displaced as a whole relative to the outside world, or we may study how body segments move, accelerate and decelerate relative to each other. As a further strategy, we may explore the structure of \( D(t) \) with statistical methods to decompose locomotion into yet unrecognized modules exhibiting localized kinematic properties. In a subsequent step, we compare trajectories between individuals. To perform these comparisons in a biologically meaningful way, the following conditions must be met:

- **Correspondence of measurement points**: Data sampling must be based on homologous landmarks in all individuals.
- **Correspondence of locomotor conditions**: Comparisons of running performance (e.g. speed) presuppose that all individuals in the sample run into the same direction, under the same general conditions (e.g. level run OR slope run), and use the same stepping pattern (e.g. bipedal running OR bipedal hopping OR quadrupedal locomotion). In other words: comparisons between magnitudes \( |v_i| \) of velocity vectors presuppose that the vectors \( v_i \) are collinear.

- In a final step, we may complement kinematic analyses with data from force platforms, strain gauges and electromyograms in an attempt to reconstruct the kinetics behind the observed kinematic patterns.

Let us return to the analysis of ontogenetic kinematics. To tackle questions of heterochronic and heterotopic modification, morphometric studies must follow similar aims and strategies (Fig. 2B). In ontogenetic kinematics, the term “movement” (which signifies change in spatial position over time) is substituted with “morphological change” or “change in form,” while “speed” is substituted with “developmental rate” or “growth rate.” The basic analytical strategy consists in tracking spatial morphological change over time, analyzing and comparing developmental trajectories through morphospace, and complementing these data with results from experimental developmental biology in order to infer the processes that generate the observed patterns of morphological change.

A central issue of ontogenetic kinematic analysis is data sampling. As in a kinematic study of human locomotion, in a kinematic study of cranial development it is most reasonable and efficient to sample the spatial position of anatomical landmarks, which denote locations of homology between the specimens in a sample. Ontogenetic kinematic data can be obtained in two ways, by sampling landmark positions \( p_i(x_i,y_i,z_i) \) from the same individual at subsequent points in time (longitudinal data) or, alternatively, by sampling homologous data from individuals belonging to the same population or taxon, but representing different ages (cross-sectional data).

In both cases, the resulting data set can be imagined as an ontogenetic trajectory \( P(t) \) (see Eq. 1) through shape space (a precise definition of shape space is provided in Appendix I). Following the formalism proposed in Equations (1-3), it is possible to derive developmental velocity vectors \( v_i(t) \) that indicate the rate (temporal component; vector magnitude) and direction (spatial component) of positional change of \( p_i \) at a given time \( t \). Further, we calculate displacement fields \( D(t) \) that indicate how the skull as a whole changes its shape during ontogeny, and how position and orientation of different cranial regions are modified relative to each other.

A central task of the evolutionary analysis of ontogenetic kinematics is to compare ontogenetic trajectories between taxa. In analogy to the
kinematic analysis of locomotion, during such analyses, the following preconditions must be met:

- **Homology of structure**: Data sampling must be based on homologous landmarks.
- **Homology of pattern**: If we compare ontogenetic trajectories with respect to their temporal properties (heterochrony), we must verify that they represent spatially homologous patterns (and, ultimately, homologous underlying processes) (Nehm, 2001; Roopnarine, 2001). In operational terms: magnitudes \( |v_i| \) along ontogenetic trajectories can only be compared if vectors \( v_i \) are collinear (Fig. 3). Accordingly, the postulate from locomotion analysis ("running into the same direction under the same conditions") translates into "moving along the same ontogenetic trajectory" (Zelditch and Fink, '96; Godfrey et al., '98) or, equivalently, "exhibiting similar ontogenetic displacement fields \( D(t) \)."

Landmark-based geometric morphometric (GM) methods provide an ideal mathematical framework that analyzes the issues discussed up to this point in quantitative terms (see Appendix I). GM integrates real-space properties into multivariate analyses (Bookstein, '91), such that a point in shape space corresponds to a specific landmark configuration \( P(t) \) in physical space, and a direction through shape space corresponds to one specific pattern of correlated shape change in the landmark configuration, i.e., a displacement field \( D(t) \) in physical space (Zollikofer and Ponce de León, 2002). Accordingly, heterotopy manifests itself by divergence of ontogenetic trajectories through shape space, and heterochrony in translation and scaling of a descendant relative to an ancestral trajectory (Fig. 3B). Note that we relax the collinearity condition of "pure" heterochrony (Fig. 3A) in favor of parallel trajectories (Fig. 3B), implying that ancestor and descendant may be dissimilar in shape but still follow similar growth trajectories (ontogenetic pattern homology).

Heterotopic and heterochronic pattern analysis can be extended to more complex ontogenetic trajectories through shape space (Fig. 3C). In GM

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Fig. 3. A geometric-morphometric perspective on the kinematics of ontogeny (letters A and D indicate ancestral and descendant trajectories, respectively). **A**: "Pure" heterochrony sensu Gould. All classical categories of heterochronic variation can be imagined as variations resulting from shift/scaling along an ancestral trajectory through shape space. **B**: Generalized heterochrony. Segments of ontogenetic trajectories of an ancestral (A) and a descendant (D) species run along parallel lines through shape space (PC1, PC2) and are separated by distance \( \Delta v \). Under these conditions, it is possible to establish a coordinate system \((u,v)\), whose axis \( u \) captures the age-related component of shape change, independent of the species-specific component \( v \). Trajectories projected onto \( u \) can be analyzed in heterochronic terms. **C**: Heterotopy. Divergent ancestral (A1) and descendant (D1) trajectories indicate heterotopic developmental patterns in the two species. Heterochronic analysis is not feasible under these circumstances. However, as long as trajectories can be superimposed by translation (A2 and D2), a common parameter \( u' \) can be defined which describes the time course of development as in A.
size-shape space, each temporally confined phase appears as a line segment, whose characteristic direction corresponds to a specific spatial pattern of shape change.

**Modeling cranial ontogeny**

Having established an operational framework for quantitative kinematic analysis of patterns of ontogenetic shape change, we use model simulations to investigate the relationship between ontogenetic kinetics (process) and kinematics (pattern). Specifically, we explore how modifications of cranial growth processes impinge on the resulting ontogenetic trajectories through age-size-shape space, and vice versa, how process information may be inferred from morphometric patterns of cranial ontogeny. The modeling procedure is as follows:

1. A minimal cranial ontogenetic model is devised, which specifies spatial and temporal growth parameters of a morphological structure.
2. Modification of process parameters in the model simulates evolutionary change.
3. Form change in the resulting virtual ontogenetic series is analyzed with GM methods.
4. Alterations in the course of descendant versus ancestral ontogenetic trajectories through shape space are correlated with alterations in process parameters.

**A minimal model of cranial ontogeny**

In Equation (1), we stated that the spatiotemporal trajectory of a moving body can be described with a matrix $P(t)$ summarizing positional change of measurement points over time. The same formalism can be applied to describe positional change in $K$ cranial landmarks $p_i$ over ontogenetic time $t$:

$$P(t) = \begin{pmatrix} p_1(t) \\ p_2(t) \\ \vdots \\ p_i(t) \\ \vdots \\ p_k(t) \end{pmatrix} = \begin{pmatrix} x_1(t) & y_1(t) & z_1(t) \\ x_2(t) & y_2(t) & z_2(t) \\ \vdots & \vdots & \vdots \\ x_i(t) & y_i(t) & z_i(t) \\ \vdots & \vdots & \vdots \\ x_k(t) & y_k(t) & z_k(t) \end{pmatrix}$$

(4)

In a growth model, we need to specify explicitly how each landmark position $p_i(t)$ changes over time under the influence of various growth processes. We introduce $L$ growth processes $u_j(t)$, which are summarized in a vector $U(t)$

$$U(t) = \begin{pmatrix} u_1(t) \\ u_2(t) \\ \vdots \\ u_j(t) \\ \vdots \\ u_L(t) \end{pmatrix}$$

(5)

These model processes assume the role of the “true” units of cranial growth (in empirical studies, they represent the hidden units of development that we try to infer from kinematic data). Processes $u_j(t)$ are defined as Gompertz (sigmoid) growth functions (Zeger and Harlow, ’87)

$$U(t) = \begin{pmatrix} u_1(t) \\ \vdots \\ u_j(t) \\ \vdots \\ u_L(t) \end{pmatrix} = \begin{pmatrix} u_1(t) = u_{01} \cdot e^{b_1(1-e^{-a_1(t-u_0)})} \\ \vdots \\ u_j(t) = u_{0j} \cdot e^{b_j(1-e^{-a_j(t-u_0)})} \\ \vdots \\ u_L(t) = u_{0L} \cdot e^{b_L(1-e^{-a_L(t-u_0)})} \end{pmatrix}$$

(6)

that approach a finite upper limit at $u_{\infty} = u_{0j}e^{b_j}$ (details are given in Appendix II, Model A). It is convenient to summarize the growth parameters of all functions $u_j(t)$ in matrix $G$

$$G = \begin{pmatrix} u_{01} & a_1 & b_1 & \Delta t_1 \\ \vdots & \vdots & \vdots & \vdots \\ u_{0j} & a_j & b_j & \Delta t_j \\ \vdots & \vdots & \vdots & \vdots \\ u_{0L} & a_L & b_L & \Delta t_L \end{pmatrix}$$

(7)

In a next step, we specify how processes $u_j(t)$ determine landmark positions. For each landmark, positional change over time $p_i(t)$ is modeled as a function $F_i$ of growth processes $U(t)$:

$$p_i(t) = F_i(U(t)) = (F_{i1}(U(t))F_{i2}(U(t))F_{i3}(U(t)))$$

(8)

Assuming generalized epigenetic interactions, each process $u_j$ may potentially contribute to the position of each anatomical landmark $p_i$:

$$P(t) = \begin{pmatrix} p_1(t) \\ p_2(t) \\ \vdots \\ p_i(t) \\ \vdots \\ p_k(t) \end{pmatrix}$$
In real biological systems, we expect less connectivity, such that several, but not all, processes contribute to a landmark position \( p_i(t) \).

In the following simulations, we consider how “evolutionary” modifications of growth parameters \( G \) and of functions \( F_j(U) \) impinge on the resulting spatiotemporal pattern of shape change \( P(t) \). In a 2-dimensional implementation, we use \( K=5 \) landmarks and \( L=3 \) processes to simulate growth in the midplane of a model skull (Fig. 4). In a 3-dimensional implementation, we use \( K=9 \) landmarks (2 bilateral pairs, 5 midsagittal) and \( L=4 \) growth processes (Fig. 4; detailed model specifications are given in Appendix III). It may be anticipated here that inclusion of the third spatial dimension does not alter the general findings obtained with the 2D model. For ease of argument, we therefore focus on the 2D model and use the 3D model to generalize our findings.

**Simulations**

To explore how modifications of temporal and spatial properties of model growth processes impinge on resulting patterns of shape change, we proceed as follows:

1) The ontogeny of “ancestral” and “descendant” populations is simulated according to ancestral parameter sets \( G_0 \) and \( P_0 \), and modified descendant parameter sets \( G_i \) and \( P_i \), respectively.

2) The landmark configurations of the resulting cranial forms are “sampled” at various ages, i.e., at various points along time \( t \), and form variability of the pooled sample is analyzed with principal components analysis (PCA) of shape (Dryden and Mardia, ’98; see Appendix I).

“Evolutionary” modifications of the model system may affect any number and combination of parameters in matrices \( G \) and \( P \). In the following simulations, our principal aim is to explore contrasts between two extreme types of modification, correlated modification of entire sets of process parameters, and modification of single parameters. In the first case (Fig. 5), all elements in a column of matrix \( G \) are modified in the same way (for example, all \( u_{ij} \) are multiplied by the same factor). In the second case, single elements of matrices \( G \) or \( P \) are modified.

The results of computer simulations are graphed in Figures 5–8. To interpret these Figures, recall that in GM analysis, a point in shape space corresponds to one specific cranial shape in physical space, and a linear trajectory corresponds to a constant displacement field \( D(t) \) in physical space. PCA typically yields two shape factors, PC1 and PC2. Together with size and age (i.e., time \( t \), PC1 and PC2 constitute a 4-dimensional morphospace. For ease of visualization, we graph 2-dimensional projections of that space; PC2 versus PC1, and PC1 versus log-size (ontogenetic allometry). Time is represented implicitly by the spacing between the data points along trajectories. In all analyses, the temporal direction of trajectories is from left to right.

**RESULTS**

All ontogenetic trajectories through shape space have several characteristics in common (see PC1-PC2 graphs in Figs. 5 to 7). First, they approach adult cranial shapes as an “attractor point” in shape space, which reflects the basic property of the growth functions to asymptotically approach a finite value (see Eq. 6). Further, growth trajectories through shape space are typically slightly curved. This indicates that the associated physical displacement fields change over time to some extent, although the underlying growth processes remain constant. Exploration of the parameter space of \( G \) and \( P \) indicates that an increase in temporal and spatial disparity between processes \( u_i(t) \) results in increased curvature of the

\[
\begin{pmatrix}
F_1(u_1, \ldots, u_j, \ldots, u_L) \\
F_2(u_1, \ldots, u_j, \ldots, u_L) \\
\vdots \\
F_i(u_1, \ldots, u_j, \ldots, u_L) \\
\vdots \\
F_K(u_1, \ldots, u_j, \ldots, u_L)
\end{pmatrix}
\]

Fig. 4. A minimal model of cranial growth. Cranial growth in the midsagittal plane is determined by three processes \( u_1 \), \( u_2 \), \( u_3 \) governing growth of the braincase, the face and the cranial base, respectively; mediolateral growth is governed by process \( u_4 \). Cranial shape is determined by a 5-landmark configuration in two dimensions (circles 1-5), and by a 9-landmark configuration in three dimensions (landmarks 6a,b and 7a,b lie on right and left cranial sides, respectively).
trajectories (data not shown). Visualization of the actual spatial shape change associated with the simulated growth trajectories (Fig. 5, bottom) shows that, given the considerable physical nonlinearities of shape transformation, deviation from linearity of trajectories through shape space is moderate.

Fig. 5. Modeling pure heterochrony and ontogenetic allometry. Simulation of ontogenetic modifications in a 2-dimensional cranial growth model (see Fig. 4 and Appendix III for model specifications). Left graphs: ontogenetic trajectories through shape space (PC1 and PC2 represent the first two principal components from PCA of shape). Correlated modification of parameter sets \(\{u_0\}, \{a_j\}, \{b_j\}, \text{ and } \{\Delta t_j\}\) of growth equations \(u_j(t) (j=1..3)\) results in characteristic shift and/or scaling of the descendant trajectory (open circles) relative to the ancestral trajectory (filled circles). Right graphs: ontogenetic allometry. The TPS deformation grid at the bottom visualizes shape change corresponding to advancement along the ancestral trajectory (gray arrow in the top left graph).

**Effects of correlated parameter modifications**

In a first set of simulations, we examine the effects of modification of each parameter set \(\{u_0\}, \{a_j\}, \{b_j\}, \text{ and } \{\Delta t_j\} (j=1...L)\). In all analyses,
shape component PC1 captures \( \approx 99.5\% \) of the total shape variability in the sample, while component PC2 captures the remaining \( \approx 0.5\% \). The effects of parameter modification on ontogenetic trajectories are shown in Figure 5 (graphs in the left column). A conspicuous common feature of these simulations is the coincidence of ancestral and descendant trajectories. This corresponds to “pure” heterochrony (Fig. 3A), where descendant trajectories represent variations along the ancestral trajectory. Correlated changes in \( a_j \) extend or shorten the ontogenetic trajectory with respect to a common onset point in shape space, and changes in \( b_j \) have similar effects. Correlated changes in \( \Delta t_j \) extend or shorten the ontogenetic trajectory, while its adult end acts as a fixed point. Note that correlated changes in \( u_{0j} \) have no effect on the trajectory through shape space, as they only affect size, not shape.

Changes in the relationship between size and shape are visualized by plotting shape component PC1 against log-centroid size (ontogenetic allometry, Fig. 5, graphs in the right column). The allometric shift in the graph for \( u_{0j} \) expresses the fact that the size-shape relationship of cranial form was changed by a general scaling factor \( (u_{0j} = 1.5) \).
Effects of single-parameter modifications

In a second series of simulations we explore the effects of modifications of single temporal and spatial process parameters. We consider 5 variants of descendant populations, representing modifications of temporal parameters $u_0, a_1, b_1, d_t$, as well as variations in the function $F_2 (U)$ defining the position of landmark #2 (see Appendix III for model specifications). The results are graphed in Figure 6. Overall, modification of single growth parameters results in more diversity of trajectories than correlated modification of parameter sets. Changes in $u_0$ result in positional shift of the ontogenetic trajectory while its direction and length remain almost unaffected. This corresponds to the definition of generalized heterochrony (Fig. 3B). Modification of $b_1$ or $a_1$ (data not shown) results in divergence of the descendant from the ancestral ontogenetic trajectory (heterotopy), and in alteration of trajectory length. Note that the onset of the ancestral trajectory acts as a fixed point of these alterations. Modification of $d_t$ leads to inverse effects, as the end of the ancestral trajectory assumes the role of a fixed point, towards which the shortened or extended trajectory of the descendant population converges. Finally, modification of the epigenetic interactions between processes influencing the position of landmark #2 has similar heterotopic effects as changes in growth parameters $a_1$ or $b_1$.

Graphs of PC1 versus centroid size (ontogenetic allometry; Fig. 6, right graphs) show various ways of decoupling the ancestral size-shape relationship. In the first case ($u_0$), decoupling is primarily effected via curve-shift. As an effect of modification of $a_1$ or $b_1$, the size-shape relationship diverges in a more complex way; the corresponding graphs in Figure 6 show that the shape trajectory is shortened, while the size trajectory is extended.

Exploration of the parameter space represented by $G$ and $P$ for 3-dimensional 4-process growth models yields essentially similar results. Figure 7 presents an example in which uncorrelated changes in all parameters $u_0$ result in parallel ancestral and descendant trajectories through shape space.

Model heterochrony and heterotopy

With regard to the concepts of heterochrony, heterotopy and ontogenetic allometry these results can be summarized as follows:

- **"Pure" heterochrony**: Correlated changes in growth processes yield pure heterochronic changes in ontogenetic patterns, i.e. extension or contraction of the ancestral trajectory through shape space (Fig. 5).
- **Generalized heterochrony**: Local changes in initial values $u_0$ of growth processes modify the initial shape and size of the structure under consideration, as evinced by displacement of the onset point of the descendant trajectory (which can be thought of as the end point of the preceding phase of ontogeny). With all other process parameters remaining unchanged, this results in parallel ontogenetic trajectories.
- **Heterotopy**: Changes in timing ($d_t$) and in the allometric growth characteristics ($a_j, b_j$) of single processes, or in the local spatial organization of developmental modules, lead to heterotopic changes, i.e., divergence between ancestral and descendant trajectories.
- **Process versus pattern heterochrony and heterotopy**: Modification of a single process parameter typically has a multi-pattern effect, leading to divergence and scaling of descendant relative to ancestral trajectories through shape space, as well as divergence of allometric trajectories.

Testing alterations in the model design

An important general issue that has to be addressed in simulations is to test the robustness
of results obtained with a given model system against changes in the premises of the model. To test robustness, we simulated ontogeny with alternative growth functions (see Appendix II, Models B and C). Model B implements exponential decay of absolute growth rates $du/dt$, while model C implements unlimited exponential growth. The results of simulations in analogy to Figures 5–7 yield largely similar results to those obtained with the Gompertz growth model (data not shown). In both cases, correlated parameter alteration yields pure heterochrony, single-parameter modification yields heterotopic dissociation, and changes in the initial conditions result in parallel ancestral and descendant trajectories through shape space.

Another test of robustness concerns landmark definitions. The shape of an object can be quantified with different sets and numbers of landmarks, such that alterations in measured ontogenetic trajectories can be expected. Figures 7A and B permit comparison between shape trajectories resulting from alternative landmark definitions applied to the same ontogenetic sample. It appears that even considerable changes in landmark definitions have relatively moderate effects on the outcome of shape analysis.
With a view on empirical studies, we may therefore conclude that the methods proposed to analyze ontogenetic trajectories are fairly robust in two respects; first, they are robust against considerable variation in the actual temporal characteristics of the underlying growth processes, second, they are robust against changes in landmark definitions.

**EMPIRICAL DATA: NEANDERTHAL VERSUS MODERN HUMAN ONTOGENY**

Model simulations are useful tools to explore the “behavior” of minimal cranial growth models under evolutionary variation. Here, we examine how insights gained from model systems can be applied to empirical data. We re-analyze a data set published earlier that shows that differences in cranial shape between Neanderthals and anatomically modern humans (AMH) arose very early during development and were maintained throughout postnatal ontogeny (Ponce de León and Zollikofer, 2001).

**METHODS**

The sample consists of 12 Neanderthal and 24 AMH crania (AMH range in individual age from late fetal stages to adulthood, Neanderthals from 2.5 years to adulthood; details see Ponce de León and Zollikofer, 2001). Cranial form was quantified with 43 landmarks (11 midsagittal; 16 bilateral pairs), and shape variability in symmetrized specimens (Zollikofer and Ponce de León, 2002) was analyzed with PCA of shape (Dryden and Mardia, ’98). Similar methods were applied to analyze landmark subsets representing facial and neurocranial form, respectively (face: 5 midsagittal landmarks, 8 bilateral pairs; neurocranium: 7 midsagittal landmark, 8 bilateral pairs). In each analysis, group mean differences in shape, divergence between group-specific ontogenetic trajectories through shape space, and divergence between allometric trajectories (obtained by multivariate regression of shape on size; Zelditch and Fink, ’96; Penin et al., 2002) were calculated, and the statistical significance of between-group differences was evaluated with permutation tests (Good, ’94; permutation tests generate empirical probability distributions by repeated randomization of group assignment in the pooled sample).

**RESULTS**

Figure 8A shows cranial shape variability in shape subspace formed by the first two principal components, PC1 and PC2. Neanderthals and AMH follow parallel ontogenetic trajectories along PC1 and are separated along PC2. Group mean shapes of Neanderthals and AMH are clearly distinct from each other (p < 0.01), while deviations between Neanderthal and AMH trajectories are not significant (p > 0.71). The apparent parallelism of trajectories suggests a shared postnatal pattern of shape change (unpublished data from neonate to 2-year old Neanderthal specimens suggest that trajectories started at similar neonate values of PC1). Visualization of the morphological displacement field corresponding to the trajectories through shape space reveals opposite growth characteristics of the face and the neurocranium (Fig. 8B); while the former grows with positive allometry, the latter grows with negative allometry.

In a next analytical step, the ontogenetic allometric characteristics of the skull and its subregions are studied in more detail (Figs. 8C-E). Allometric (i.e., size-shape) trajectories appear to be biphasic, indicating an early (perinatal) phase of near-isometric growth followed by a phase of constant allometric growth (in Figs. 8C-E isometry corresponds to slope=0). During the latter phase, Neanderthal and AMH ontogenetic trajectories do not differ significantly in slope (p > 0.89) but it appears that Neanderthal trajectories are shifted towards larger sizes at any given cranial shape. It may be noted here that the observed pattern of allometric ontogenetic disparity cannot be described with the classic heterochronic terminology of size hypomorphosis versus hypermorphosis, as these terms imply divergence and/or scaling of size-shape trajectories. Parallelism of trajectories, as evinced by Figures 8A-E, implies that species-specific differences between Neanderthals and AMH were already present at an early postnatal age. Note that Figure 8A exhibits close similarity to the simulation in Figure 7A, where model populations differ in initial conditions $u_0$, while all other growth parameters remain the same. Following a similar line of argument, one may hypothesize that the Neanderthal/AMH dichotomy mainly reflects distinct initial (i.e. perinatal) growth conditions. Given the wide spectrum of possible mechanisms of divergence between ontogenetic trajectories, the Neanderthal/AMH split thus appears as a
comparatively simple evolutionary ontogenetic modification. According to this hypothesis, postnatal ontogeny in both species represents evolutionary “conservatism” (similar growth parameters), while prenatal growth processes represent evolutionary novelty (generating distinct perinatal cranial morphologies).

Direct comparative investigation of prenatal growth patterns in Neanderthals is no longer feasible. However, it is possible to examine the available morphometric evidence in the light of developmental process data. Craniofacial growth is characterized by differential activities and/or distribution of depository/resorptive skeletal growth fields (Enlow, ’90). Accordingly, evolutionary modifications of growth fields can be described in terms of heterotopic and heterochronic alterations, i.e., changes in spatial patterning and temporal activity of growth fields.

To establish potential links between skeletal growth field activity and the Neanderthal/AMH morphological contrast, the quantitative morphological difference across Neanderthal and AMH trajectories is visualized. The resulting graph (Fig. 8F) reveals polarity between superior and inferior regions of the cranial vault (note that this graph does not convey an immediate picture of prenatal cranial growth fields; rather it visualizes the contrast between AMH and Neanderthal patterns of development before birth). The boundary between these regions probably coincides with the circumcranial reversal line that separates depository from resorptive growth fields on the internal surface of the braincase (Fig. 8G). Assuming that the spatial arrangement of cranial growth fields was largely similar in Neanderthals and AMH (i.e., no heterotopic modification), it suffices to postulate different temporal activity in spatially conservative growth fields, giving rise to species-specific perinatal morphologies. Hence, increased relative drift and displacement in the inferior vault may account for the low but posterolaterally-expanded braincase in Neanderthals relative to AMH.

As suggested by the model of Figure 7, similar growth processes acting on different initial conditions result in parallel ontogenetic trajectories, but also entail an array of subtle differences between trajectories, such as dissociation of the size-shape relationship (ontogenetic allometry). In view of these model findings, many postnatal developmental differences between AMH and Neanderthals, such as differences in ontogenetic allometric trajectories (Fig. 8C-E) and in various non-metric skeletal and dental developmental features (Dean et al., ’86; Tillier, ’86; Rak et al., ’94) probably have a single common cause in distinct perinatal cranial shapes. Overall, a phyletically “old” postnatal growth process acting on phyletically “new” perinatal cranial morphologies might suffice to explain a large array of postnatal developmental differences between Neanderthal and AMH skulls.

**DISCUSSION**

*Aspects of kinematics*

The proposed kinematic approach to cranial ontogeny analyzes patterns of three-dimensional morphological change in terms of velocity vector fields. In this approach, the differentiation between magnitude and direction of vectors is, at first instance, a technical procedure that facilitates comparative analysis of vector fields. However, this differentiation also relates to the biological meaning of size and shape. The many ways in which size and shape are defined in the literature are the principal cause of the often-cited inflation of heterochronic/heterotopic terminology and ensuing semantic confusion (McNamara, ’97; McKinney, ’99; Gould, 2000). For example, the “paradox of peramorphic paedomorphosis” of human development (Godfrey and Sutherland, ’96) essentially relates to questions as to how to define size, shape, rates of growth and development, and developmental sequences in time (Rice, ’97; McNamara, 2002b). As another example, consider spatial differences in velocity vector fields, termed “pattern heterotopy” in this paper. From a modular perspective, the same phenomenon is termed “dissociated heterochrony” (McNamara, 2002a). However, as pointed out by Zelditch and Fink (’96), and Zelditch et al. (2000), dissociated heterochrony may be a misinterpretation of actual process heterotopy, resulting from over-modularization of developmental data. Overall, detailed quantitative description of patterns of ontogenetic divergence is preferable over fitting observations to a complicated terminology, which often implies interpretation in terms of underlying processes. The kinematic approach proposed here offers a quantitative framework that permits clear distinction of measurement and analysis of form change from inference of process from pattern.
What can be learned from spatiotemporal growth models?

Evolving and analyzing cranial morphologies in silico showed that a minimal cranial growth model can replicate the wide variety of heterotopic and heterochronic phenomena proposed in theoretical considerations (e.g. Gould, '77; Alberch et al., '79; Godfrey and Sutherland, '96; Klingenberg, '98) and found in empirical studies (e.g. Shea, '88; Nehm, 2001; Roopnarine, 2001; Zelditch et al., 2003). Most notably, models show that modification of single process parameters typically results in complex alterations of ontogenetic trajectories through size-shape-age space (Fig. 6). From this perspective, unexpected effects such as convergence of ontogenetic trajectories towards adulthood, which were considered to represent functional/adaptive convergence (Roopnarine, 2001), can be understood as resulting from simple phase shifts between growth processes (see Fig. 6, graph representing modification of Δt).

On the other hand, the multiple and complex effects of process modification on pattern modification even in a simple growth model point to principal limits of inference of process from pattern. During evolutionary studies of cranial development, it is in fact notoriously difficult to establish such connections. First and foremost, in a spatially complex, modularly organized structure such as the hominid skull, no straightforward causal connection exists between actual growth processes and observable patterns of growth and development (Lieberman, '99). In addition, patterns of shape change reflect a combination of active local growth and passive displacement of cranial substructures, whose relative contributions to the observed displacement field cannot easily be distinguished (Enlow, '90).

How can heterochronic/heterotopic process and pattern analyses be brought together? Process and pattern analyses ask questions regarding proximate and ultimate causes of ontogenetic modification, respectively, and both perspectives are biologically relevant in their own right. Differences in developmental timing might have considerable functional and adaptive significance for the growing organism as a whole. On the other hand, identification of proximate developmental causes of ontogenetic diversity helps relax the rigors of the “adaptationist programme” (Gould and Lewontin, '79) and leads to a process-oriented understanding of species-specific morphologies.

A further implication from model data that is relevant for the empiricist concerns comparisons of cranial morphology in phyletic and cladistic analyses. Typically, such analyses are based on adult individuals, as one generally assumes that only adult specimens display the full range of taxon-specific features. While this might be the case for epigenetic traits and non-metric characters, it is likely not to be the case for overall cranial morphology as measured with GM methods. Considering Figures 5-7, it appears that comparisons between adults (i.e., offset points of ontogenetic trajectories), tend to mix various comparative criteria, such as shift, divergence and scaling of ontogenetic trajectories, in unknown proportions. Given the importance of identifying phyletically valid morphological characters representing the underlying genetics (Lieberman, '99), it is essential to compare trajectories through shape space rather than points in shape space.

Methods of data sampling and methods of inference

One issue of principal importance in ontogenetic kinematic analyses with GM methods relates to data acquisition. Whether stated explicitly or not, defining quantitative morphological units always implies hypotheses about the processes that generate the observed morphologies. Setting cranial landmarks, therefore, is equivalent to stating hypotheses about underlying growth processes, and it can be expected that the number and relative positioning of landmarks used to define cranial form influences the outcome of GM analyses. How can an optimum number and distribution of landmarks be found that establishes a balance between under- and over-determination of form? This issue is especially critical in the cranium, where the facial area is densely populated with easily identifiable landmarks (e.g., meeting points between sutures), while the cranial vault exhibits only few such landmarks. Various methods have been proposed to define additional reference points, so-called semilandmarks, in landmark-depleted regions of the skull (Bookstein, '97; Andresen and Nielsen, 2001). While these methods yield data points that are evenly distributed over entire regions of the skull, they tend to overdetermine geometric shape at the expense of growth-oriented shape. There is no definite solution to this problem, such that practical solutions must combine heuristics with
iterative refinement of landmark definitions. An important first step towards testing the biological (as opposed to the statistical) reliability of GM analysis is to study one and the same sample using different landmark sets, to analyze subsets of landmarks that represent subregions of the structure under investigation, and to use alternative methods of kinematic data analysis.

What can be learned from Neanderthals?

Morphometric evidence supports the view that early modification of cranial developmental patterns is a major source of hominid and hominoid evolutionary diversification, while variation in postnatal growth patterns contributes only a small part to the differentiation between species (Ponce de León and Zollikofer, 2001; Lieberman et al., 2002, Rogers Ackermann and Kroqvitz, 2002; Williams et al., 2002). Moreover, as evinced in a comparison between adult AMH and archaic humans (including Neanderthals), and between corresponding age classes of humans and chimps (Lieberman et al., 2002), it appears that the same small set of parameters is involved in generating evolutionary novelty by changing the relative size and position of the face, the neurocranium and the cranial base. These parameters influence cranial base flexion and length, relative proportions of the cranial fossae, and relative proportions of the face (Lieberman et al., 2000, 2002).

The Neanderthal data presented here fit into this general picture. Obviously, major contrasts between species-specific developmental patterns must be sought prenatally, while postnatally, Neanderthals and AMH develop along largely similar trajectories. The proximate developmental causes that generated dissociation between species can only tentatively be inferred. Evidence for the proposed hypothetical mechanism—differential growth activity in conserved cranial growth fields—comes from a comparative study of epigenetic traits in Neanderthal and AMH crania, indicating that relative thinning in the laterally-expanded cranial vault of Neanderthals might reflect differential activity in resorptive versus depository growth fields, which ultimately may reflect species-specific differences in cerebral and skeletal growth processes (Manzi et al., '96). Such hypotheses need further corroboration through comparative analysis of early developmental patterns in extant species (Lieberman and McCarthy, '99).

The results of this and an earlier study on Neanderthal and AMH ontogeny (Ponce de León and Zollikofer, 2001) largely converge with the results of a suite of studies dedicated to the same subject, but based on different methods. Kroqvitz (2000) investigated facial ontogeny with Euclidean Distance Matrix Analysis (EDMA; Lele and Richtsmeier, 2001), a geometric-morphometric method that defines form by the matrix of all interlandmark distances in a landmark configuration and uses Principal Coordinates Analysis (PCO, a variant of multidimensional scaling) to study shape variability. These studies, as well as a recent EDMA-based analysis of facial ontogeny in a sample comprising AMH, *Australopithecus africanus*, *Pan troglodytes* and *Pan paniscus*, suggest that evolution through ontogenetically early differentiation is an ancient pattern of hominoid phylogeny (Rogers Ackermann and Kroqvitz, 2002).

In another set of studies (Williams, 2000; Williams et al., 2002), Neanderthal versus human craniofacial ontogeny was analyzed with classical multivariate techniques applied to sets of craniometric distance measurements (Godfrey et al., '98). Interestingly, these authors converge in the conclusion that “modern humans and Neanderthals follow parallel shape changes from different points of origin” (Williams et al., 2002, p. 430). Altogether, these methodologically diverse studies point towards a basic pattern of ontogenetic kinematics—prenatal divergence versus postnatal homology of ontogenetic processes.

Direct investigation of early patterns of development is only beginning (Lieberman and McCarthy, '99; Jeffery and Spoor, 2002) and will help substantiate hypotheses about the role of ontogenetic divergence as a source of evolutionary novelty. Exploring the network of cause and effect that connects observed patterns of spatiotemporal shape change with underlying growth processes and processes of evolutionary modification is an iterative task. The endeavor of identifying developmental units, analyzing their ontogenetic kinematics, and studying their evolutionary variability must follow a multidisciplinary approach, combining kinematic morphometric analysis with model considerations and with insights from the “kinetic” disciplines of developmental biology.

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APPENDIX I: GEOMETRIC MORPHOMETRICS

In GM, the form of each specimen is quantified by the position of anatomical landmarks, which denote locations of biological homology between specimens in the sample. The two components of form, size (Centroid Size; Bookstein, '91) and shape are statistically independent of each other, which greatly facilitates tracking ontogenetic allometry along trajectories through age-size-shape space. A specimen’s shape is expressed as the multidimensional deviation of all landmarks from the corresponding landmarks of a reference configuration. The reference configuration is typically the sample mean and is evaluated with generalized-least-squares superimposition methods (Rohlf and Slice, '90). In contrast to size, which is a scalar, shape is a multivariate measure, i.e., a vector. Each specimen’s shape can be imagined as a location (i.e., a position vector) in multidimensional shape space (linearized Procrustes space; Dryden and Mardia, '98). To visualize patterns of shape variation in the sample, Principal Components Analysis (PCA) is used. This method permits extraction of statistically independent factors of shape variation that account for the largest, second largest and successively smaller proportions of shape variability in a sample. PCA is mainly used as a dimension reduction technique. A major strength of GM analysis is that it preserves a direct link between data in shape space and data in physical space. Most notably, vectors in shape space correspond to displacement fields in physical space. This permits visualization of ontogenetic trajectories in terms of cranial shape transformation (Zollikofer and Ponce de León, 2002; see Fig. 8B, F).

APPENDIX II: GROWTH FUNCTIONS

Growth and static allometry

In the present context, Huxley’s allometric growth model represents a suitable starting point, as it postulates a process-oriented background of morphological patterns of allometry (Huxley, '32). In this model, growth processes $u_j(t)$ and $u_k(t)$ (as defined in Equation 5) exhibit proportionality of specific growth rates

$$\frac{du_j}{dt} = a \frac{du_k}{dt},$$

where the specific growth rate of $u$ is defined as the absolute growth rate ($du/dt$) in relation to the actual amount of $u$, and factor $a$ is a coefficient of epigenetic interaction between $u_j$ and $u_k$. Upon integration, Equation (A1) yields the static allometric equation

$$u_j = c \cdot u_k^a,$$

where $c$ is a scaling factor, and $a$ is the allometric coefficient. Note that upon integration of Huxley’s allometric process equation time $t$ vanishes, such that the resulting allometric pattern equation describes a time-independent correlation between units $u_j$ and $u_k$.

The time course of $u(t)$ follows from integration over the time course of its specific growth rate. Various functions describing this latter process have been proposed (Zeger and Harlow, '87). In computer simulations, we use the following models:

Model A: Gompertz growth

Integration of a function describing exponential decay of the specific growth rate over time

$$\frac{du}{dt} = b \cdot e^{-at}$$

yields the Gompertz growth function

$$u(t) = u_0 \cdot e^{b(1-e^{-at})},$$

which saturates at

$$u(t \rightarrow \infty) = u_0 \cdot e^b.$$

The point of inflexion is at $t=0$, where the slope reaches a maximum value of $ub$. The concept of allometry was expanded by Jolicoeur to a series of units $u_1, u_2, \ldots, u_j, \ldots, u_L$, such that we may think of sets of growth functions

$$\left\{ u_j(t) = u_{0j} \cdot e^{b_j(1-e^{-ajt})}; j = 1 \ldots L \right\},$$

where multivariate allometric exponents $a_j/a_k$ link any two variables $u_j$ and $u_k$ (Jolicoeur, '63). To allow “evolutionary” variability in the way growth processes interact with each other, we relax the condition of allometry and define individual processes $u_j(t)$ as

$$\left\{ u_j(t) = u_{0j} \cdot e^{b_j(1-e^{-ajt})} \right\},$$

where $a_j/a_k$...
where $o\Delta t_j$ accounts for temporal shifts between processes.

**Models B and C**

Two alternative models also satisfy allometric Equations (A1) and (A2). In model B, growth rates depend only on time, not on the actual amount of $x_i$. Assuming exponential decay of growth rates

$$\frac{du_j}{dt} = b_j \cdot e^{-at}, \quad (A8)$$

integration over time yields exponential saturation functions of the form

$$u_j(t) = u_{0j} + \frac{b_j}{a_j} \left(1 - e^{-a_j(t-\Delta t_j)}\right). \quad (A9)$$

Model C assumes time-dependent specific growth rates of the form

$$\frac{du_j}{dt} = b_j \cdot t. \quad (A10)$$

Integration yields a growth function exhibiting “allometry” in time:

$$u_j(t) = u_{0j} \cdot t^{b_j}. \quad (A11)$$

We may relax the allometric constraints and introduce a parameter for time shift, accounting for temporal modularity of ontogenetic processes

$$u_j(t) = u_{0j} \cdot (t - \Delta t_j)^{b_j}. \quad (A12)$$

Equation (A12) describes a single phase of the multiphase growth model proposed by Vrba (’98) and further studied by Vinicius and Lahr (2003). In our view, this model is biologically less realistic than models A and B, as it implies unbounded growth for $t \to \infty$.

**APPENDIX III: MODEL SPECIFICATIONS**

Growth in the midplane of a model skull is simulated with 3 processes $u_1(t)$, $u_2(t)$ and $u_3(t)$. The parameter set defining the “ancestral” condition for model A is summarized in matrix $G_0$:

$$G_0 = \begin{pmatrix} u_{01} & a_1 & b_1 & \Delta t_1 \\ u_{02} & a_2 & b_2 & \Delta t_2 \\ u_{03} & a_3 & b_3 & \Delta t_3 \end{pmatrix} = \begin{pmatrix} 1 & 1 & 1 & 0 \\ 1 & 1 & 2 & 0 \\ 1 & 1 & 1.5 & 0 \end{pmatrix}. \quad (A13)$$

In the “ancestor,” the spatial positions $P_0(t)$ of the 5 cranial landmarks are influenced by these processes in the following way (Fig. 4):

$$P_0(t) = \begin{pmatrix} x_1(t) & y_1(t) \\ x_2(t) & y_2(t) \\ x_3(t) & y_3(t) \\ x_4(t) & y_4(t) \\ x_5(t) & y_5(t) \end{pmatrix} = \begin{pmatrix} 0 & 0 \\ 0 & u_3(t) \\ -u_1(t) & 0 \\ -u_1(t) & u_1(t) \\ -u_2(t) & 0 \end{pmatrix}. \quad (A14)$$

This corresponds to a low-connectivity model (cf. Eq. 9). In evolutionary modifications of $P(t)$, function $y_2(t)$ contains process interaction

$$y_2(t) = \frac{u_2 + u_3}{2}. \quad (A15)$$

Growth of a 3-dimensional skull model is simulated with $L=4$ processes and $K=9$ landmarks. Matrix $G_0$ has the following ancestral form:

$$G_0 = \begin{pmatrix} 1 & 1 & 1 & 0 \\ 1 & 1 & 2 & 0 \\ 1 & 1 & 1.2 & 0 \\ 1 & 1 & 1.1 & 0 \end{pmatrix}. \quad (A16)$$

and landmark positions are determined as follows:

$$P_0 = \begin{pmatrix} 0 & 0 & 0 \\ 0 & \frac{u_2 + u_3}{2} & 0 \\ -u_1 & 0 & 0 \\ -u_1 & u_1 & 0 \\ \frac{-u_1}{2} & \frac{u_1 + u_2}{2} & \pm\frac{u_4}{3} \end{pmatrix}. \quad (A17)$$

**LITERATURE CITED**


