

# Interactive Coordinated Multiple-View Visualization of Biomechanical Motion Data

Daniel F. Keefe, *Member, IEEE*, Marcus Ewert, *Student Member, IEEE*,  
William Ribarsky, *Senior Member, IEEE*, and Remco Chang, *Member, IEEE*

**Abstract**— We present an interactive framework for exploring space-time relationships in databases of experimentally collected high-resolution biomechanical data. These data describe complex 3D motions (chewing, walking, flying, etc.) performed by animals and humans and captured via high-speed imaging technologies, such as biplane fluoroscopy. In analyzing these 3D biomechanical motions, interactive 3D visualizations are important, in particular, for supporting spatial analysis. However, as researchers in information visualization have pointed out, 2D visual representations of motion are also effective for trend analysis, especially for long and complex animation sequences. Our approach, therefore, combines techniques from both 3D and 2D visualizations. Specifically, it utilizes a multi-view visualization strategy including a small multiples view of motion sequences, a parallel coordinates view, and detailed 3D inspection views. The resulting framework follows an overview first, zoom and filter, then details-on-demand style of analysis, and it explicitly targets a limitation of current tools, namely, supporting analysis and comparison at the level of a collection of motions rather than sequential analysis of a single or small number of motions. Scientific motion collections appropriate for this style of analysis exist in clinical work in orthopedics and physical rehabilitation, in the study of functional morphology within evolutionary biology, and other contexts. An application is described based on a collaboration with evolutionary biologists studying the mechanics of chewing motions in pigs. Interactive exploration of data describing a collection of more than one hundred experimentally captured pig chewing cycles is described.

**Index Terms**—Scientific visualization, information visualization, coordinated multiple views, biomechanics.

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## 1 INTRODUCTION

Effective visualization of 3D motion is a complex problem, especially as it relates to experimentally collected data in biomechanics. Imaging modalities, such as biplane fluoroscopy combined with CT, are now able to capture high-speed motion of the bones of a joint at rates of 250 to 500 frames per second with sub-millimeter accuracy [1, 22]. These data allow for far more detailed study of a variety of complex motions in animals and humans than was previously possible. Several important visualization challenges arise from working with motion data sets collected with these technologies.

The first challenge in visualization and analysis of these data is understanding the complex spatial relationships that are present. This is a 3D problem, in the sense that the bones exist in a 3D space and, in many cases, the relationship between the 3D shape of the bones and their function (functional morphology) is one of the primary scientific research questions. Thus, effective 3D spatial understanding is an important feature of visualization systems appropriate for use with these data.

The second challenge in analysis of these motion data is that, in both clinical and experimental work, these data typically exist as part of a large database. For example, when a scientist designs an experiment to study chewing motions (the primary example used in this paper) she will typically collect data on tens to hundreds of chewing cycles. Questions posed during analysis may be of the form, what is a typical chewing motion as exhibited across the data? Or, they may be of the form, how does chewing change based upon the amount of food in the mouth, the type of food, or other variables? This style of analysis requires understanding the time-varying spatial data that describes a single chewing motion, and, beyond that, it requires understanding

trends and anomalies in this time-varying spatial data across databases of numerous repeated motions.

Previous approaches to visualization of biomechanical motion data have benefited from animated and interactively controlled 3D graphics [8, 10, 21]. Our collaborators in evolutionary biology have also had positive experiences with 3D visualization of their data. In fact, several of them have found 3D views to be so useful that they have taught themselves how to use a combination of Maya and Matlab to produce their own 3D visualizations. In general, previous 3D visualizations presented in the literature have provided useful capabilities for investigating individual motions, but provided only limited capabilities for analysis and comparison of a set of motions. We present a framework that explicitly supports visualization of multiple related motion sequences, an important scientific task in this context.

Visualization of trends in time-varying and multi-variate data has a rich history of study within the *information visualization* community [16]. Our work is motivated by a desire to leverage the theories and techniques resulting from this work and bring these to bear within a system that targets time-varying 3D data. Since spatial relationships in these data are so important, they have tended to be visualized in the past with what have traditionally been termed *scientific visualization* techniques, or 3D spatial layouts where the spatial arrangement is pre-determined by the true 3D arrangement of bones in space. To observe motion over time, these 3D views have been animated, and often additional data attributes are visualized via color, texture, streamlines, and 3D data glyphs [8, 10, 21]. While these sophisticated 3D views are clearly valuable, evidence in the information visualization literature suggests that, in general, understanding trends over time through animation may not be the most effective strategy [16]. Based on this insight and other promising results in information visualization [3, 11, 15], we have been motivated to explore a new visualization framework that combines the strengths of both information and scientific visualization approaches and targets understanding of spatially complex, time-varying motion data.

The idea of bringing information and scientific visualization together is not new [7, 14], and several compelling examples tied to real scientific analysis now exist in the literature [12, 13, 19]. However, many challenges remain in this line of research, especially as it relates to specific forms of data. Analysis of detailed 3D motion, for example, raises the question of the most appropriate roles for animation,

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• Daniel F. Keefe and Marcus Ewert are with the Department of Computer Science and Engineering at the University of Minnesota. E-mails: keefe@cs.umn.edu, ewert@cs.umn.edu.

• William Ribarsky and Remco Chang are with The Charlotte Visualization Center, UNC Charlotte, E-mails: ribarsky@uncc.edu, rchang@uncc.edu.

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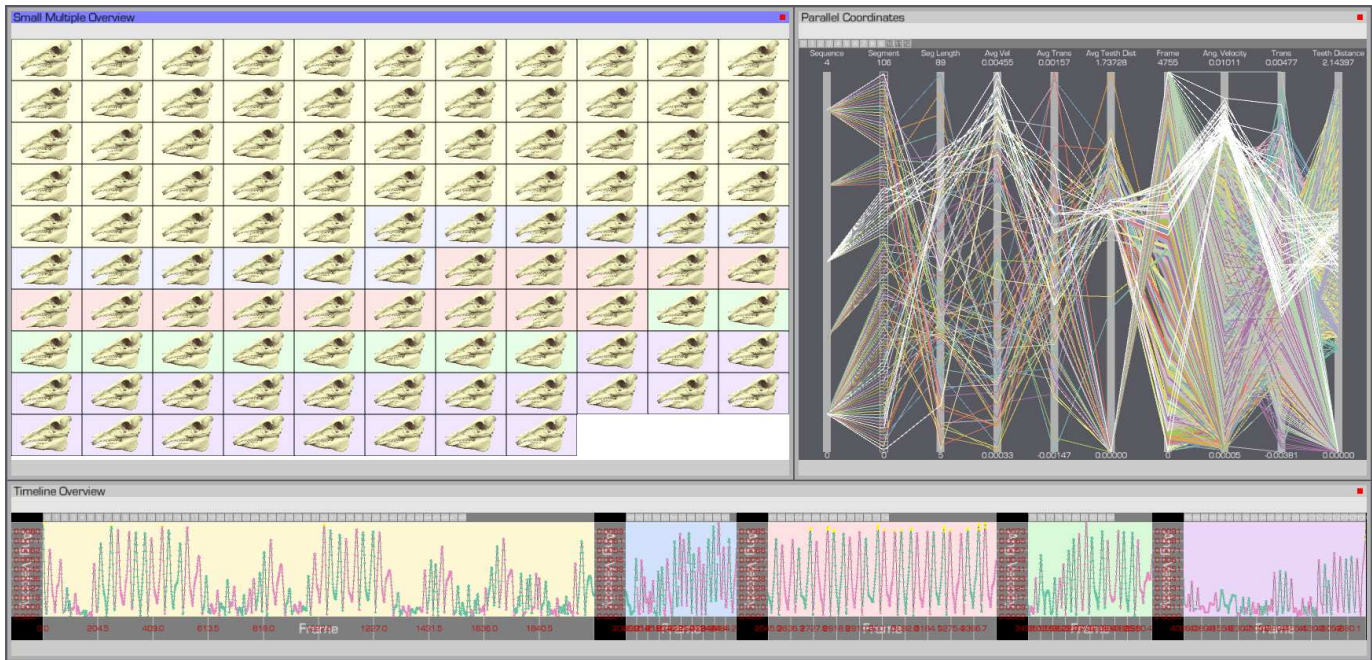


Fig. 1. When data are first loaded into the visualization framework, an overview of the motion database is presented using three coordinated data views: 1. A small multiples view generated from snapshots of 3D renderings (top-left window in the figure). 2. A parallel coordinates view (top-right), data dimensions plotted in this example are: trial number, chew cycle number, cycle duration, average angular velocity for the cycle, average translational velocity for the cycle, average distance of separation of the teeth for the cycle, then frame number and the same set of descriptive statistics but calculated at the single frame level rather than as averages over a cycle. 3. A 2D plot of data values over time (bottom), here angular velocity over time. All views are linked through both visual and interactive strategies. In this case, 108 chewing motions cycles from five different trials are displayed in this overview.

comparison views, and techniques such as parallel coordinates, which have been widely applied in general, but less so within the context of biomechanical analysis.

Specific to analysis of 3D biomechanical motion data, integrating 3D and 2D visualization techniques, as in the overview visualization of Figure 1, is particularly appealing because each brings a unique strength that compensates for the other’s weakness. Analyzing motion trends using only 3D visualization tools imposes a high cognitive load on the user, since analysis often requires comparisons between multiple detailed motions that the user must keep in his working memory [9, 16]. On the other hand, when analyzing motion using only 2D visualizations, the abstract representations of the motion data do not provide the necessary context for the user to understand the 3D structure of the object or its movement in space. We propose that when the two are integrated together in a tightly-coupled manner, the user gains the benefit of both perspectives and can perform analysis of the motion in both space and time.

The high-level contribution of our work is presenting an integrated framework for 2D and 3D interactive visualization of experimentally collected biomechanical motion data sets. To this end, specific contributions of the work are: 1. The design of an overview technique for visualization of hundreds of repeated cyclic motions. 2. Methods for zooming, filtering, and exploring motion data via linked 2D and 3D views, including the ability to pass data generated through interaction with 3D views on to linked 2D visualizations, and vice versa. 3. The design of side-by-side and overlay-style coordinated views for comparison of the motion of bones in space and the resulting interaction between multiple bone surfaces. 4. A discussion of lessons learned, current limitations, and future directions as motivated by a driving real-world application.

In the following section, we provide some background on the data and scientific application (analysis of pig chewing behavior) discussed in this paper. This is followed by a discussion of related work in visualization. Then we present the motion visualization framework in detail, followed by more specifics of the driving application and ini-

tial feedback from domain scientists. Finally, we present a discussion of lessons learned in developing this system, including limitations and future directions.

## 2 BACKGROUND IN APPLICATION AREA AND DATA

The framework presented here is likely to apply to analysis of a number of experimentally-captured motions of interest to orthopedists, physical therapists, and evolutionary biologists. The example application driving the work in this paper comes from the field of evolutionary biology, where our collaborators are studying mastication in minipigs (Sinclair strain).

In general, the mechanics of the mandible, skull, and teeth working together in chewing motions are an interesting area of study, both in humans [6], and in animals [8]. Pigs, in particular, follow an unusual chewing pattern, called bilateral chewing, that is characterized by motion of the jaw up, then a food grinding motion to one side, then down, then up again, then sideways food grinding motion to the other side, then down again. This pattern repeats over several chewing cycles. (The alternating grinding from side-to-side pattern can be seen in the tracer paths in adjacent small multiples views in Figure 2.) This characteristic motion has been visualized previously [8], but only for investigating a single chewing motion at a time. Research questions require analysis of multiple instances of this motion (an important goal of this framework). For example: Can we catalog a “typical” chewing behavior? How does the movement of bones change over time based upon the amount of food in the mouth or the type of food?

Evolutionary biologists began their study by collecting data from multiple experimental trials in the lab. The trials captured motion from a number of different chewing-related behaviors, including food gathering, feeding on pig chow, and feeding on hard nuts (in the shell). Data were captured and processed using the X-Ray Reconstruction of Moving Morphology (XROMM) methodology [1], in which high-speed biplane fluoroscopy is used to capture motion data during the experiment and a CT scan captured separately is used to reconstruct

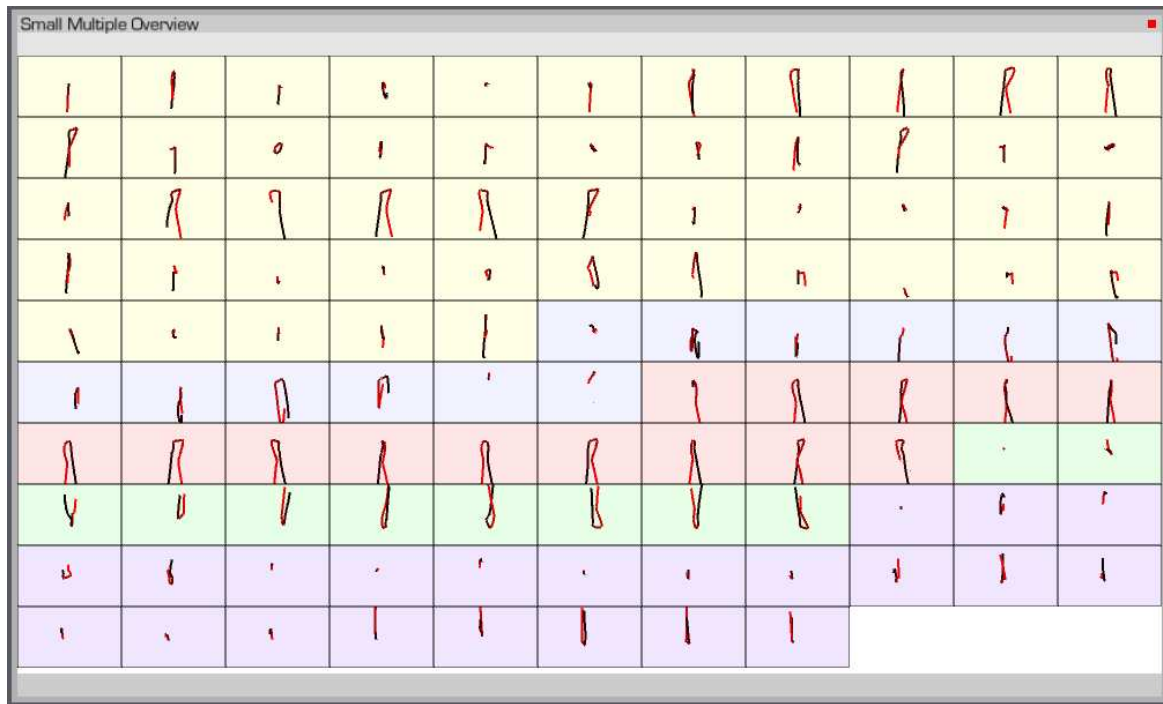


Fig. 2. A small multiples display setup interactively by a user. To tune the display, the user zooms in to one of the small views, making an interactive 3D rendering of it fill the window. Then, he adjusts visualization and camera settings in the zoomed in view. When he returns to the small multiples view, each of the multiples is re-rendered using the new visualization settings. In this case, the user added a tracer curve to the visualization to trace out the path of the pig's front tooth. Then, he zoomed in on the location of the tooth and made the bones invisible. The characteristic bilateral chewing motion of the pig may be seen in many of the adjacent images. Look for a tracer that begins (black end of the curve) on one side, moves up, then comes down on the other side. In the image immediately to the left or right of this one, you are likely to find a tracer exhibits a similar pattern, but moving in the opposite direction. Cycles that capture food gathering behavior can also be identified in the display, characterized by tracers that are more compact than the elongated chewing motions. The background color for each multiple is set to encode the trial from which the data are drawn; the colors correspond to those used in the 2D time plot at the bottom of the screen (see Figure 1). Note: to better understand how the tracers were created, see the 3D view in Figure 3, which shows the bones together with a tracer placed in the same position as was used to generate these small multiples renderings.

the 3D geometry of the bones and teeth. Computational tools are utilized to register the two sources together to reconstruct high-speed 3D motion data. These data are the source for the visualizations presented here. For this study, they include more than one hundred chewing motions (up-down motions of the jaw) collected during five experimental trials.

### 3 RELATED WORK

In this section, we relate our work to relevant research in evaluating animated visualization as a tool for trend analysis, visualizing 3D biomechanics, designing coordinated multi-view visualizations, and combining scientific and information visualization strategies.

#### 3.1 Trend Analysis and Animated Visualization

In recent work, Robertson et al. examined the effectiveness of animation for visualizing trends in data [16]. While animation is often attractive for presentation purposes, the results of this work suggest that static small multiples views and static traces of trend lines over time may be more effective than animation in analysis of trends over time.

These findings have far reaching implications for visualizations of motion data, which are, nearly by default, viewed as animations. While viewing an animated visualization of the motion of an animal does seem natural and intuitive (after all the data are collected over time) the question is raised, are animated visualizations the right tool for *analyzing* these motion data?

Based upon our experience with collaborators and the results of previous animated 3D visualizations in biomechanics, we believe interactive/animated 3D visualizations do play some important role in

analysis. However, the findings of Robertson et al. highlight the potential importance of alternative complimentary techniques and raise the issue of identifying the right mix of animated and static views for motion visualization. Our framework explores these issues and builds upon the static representations demonstrated by Robertson et al. A key component of our initial motion overview visualization is a small multiples visualization [20], which we have often found useful to construct as a set of tracer lines (See Figure 2), following in the style of the small multiples traces presented in [16].

#### 3.2 3D Biomechanics Visualization

Several systems for 3D visualization of biomechanics data exist in the literature [2, 8, 10, 21]. A primary function of these tools is providing a view of anatomical features (bones, ligaments, etc.) positioned appropriately in 3D space. Almost all of these systems also support some form of motion playback, often with some interactive support for adjusting camera parameters and playback speed.

Beyond simply replaying experimentally captured data, 3D visualization systems also provide for visualization of derived data. For example, computing helical (or screw) axes to describe the motion of one bone relative to another is a technique that is gaining popularity within the biomechanics community [4, 6]. Viewing the position of this axis in space relative to anatomical landmarks in a 3D visualization can provide insight into the rotation and translational components of a complex motion [8, 21]. Other examples of 3D visualization of these data include applying color maps to bone surfaces to indicate the distance from one bone to another [10], and drawing 3D tracer curves to indicate the path some anatomical feature takes through space over time [2]. Our 3D visualizations employ each of these techniques. The

focus of our investigation is not on the introduction of novel 3D visualization techniques, but rather on how a state-of-the-art 3D visualization of biomechanics may be leveraged within a system that interactively links it with complimentary 2D visualizations.

### 3.3 Multi-View and “Scientific-Information” Visualization

The benefits of using multiple coordinated 2D visualizations for data analysis have been well documented [3, 11, 15].

Our approach relates most closely to multi-view techniques that employ a combination of 2D and 3D views to investigate data that follow a pre-defined spatial distribution, thereby combining scientific and information visualization techniques. Several visualization and interaction techniques fitting this description have been documented previously, for example, linking 2D and 3D scatterplots [13], brushing over multiple dimensions in 2D views to identify 3D features [12], and using parallel coordinates as an interface for exploratory volume visualization [19]. Our work follows closely in the spirit of these techniques, however, our overview visualization, coordinated views, and use of animation and interaction are designed specifically to target analysis of high-precision motion data sets. As such, we have a special emphasis on the role of animation within our framework, and we have utilized specific properties of the data, such as its cyclic nature, in designing several components of the framework, such as the small multiples overview.

## 4 MOTION VISUALIZATION FRAMEWORK

In this section, we describe a novel framework for visualization of scientific 3D motion data. Through a series of visual tools, the framework supports the typical visual information seeking mantra: “Overview first, zoom and filter, then details-on-demand” [17].

### 4.1 Small Multiples and Coordinated Views for a Motion Database Overview

When a data set is first loaded, an overview of the data is displayed using the three coordinated view windows seen in Figure 1: a small multiples view, a parallel coordinates view, and a 2D plot of descriptive statistics computed for each frame of the motion over time. These three views have been carefully chosen for their analytical capabilities in analyzing different aspects of a 3D motion sequence. The small multiples view displays a representative motion snapshot for each motion sequence. The 2D xy-plot is chosen for its intuitive nature in representing time, described by Ericson during his keynote address in the 2007 InfoVis conference [5]. Lastly, the parallel coordinates view is used to reveal relationships between data dimensions based motion statistics and derived quantities. Together, these views allow the user to explore the 3D motion sequence in space, time, and at a dimensional level.

#### 4.1.1 3D Snapshot Small Multiples

The utility of small multiples displays for analysis of trends over time has been demonstrated in a 2D data context [16], but several open questions remain in developing a small multiples strategy for 3D motion data. Relevant full-scale 3D visualizations are typically interactive and detailed. How do these translate to small scales? If the individual multiples are to support the same style of interaction as in normal visualization, then how do the interaction strategies change to work within a much smaller window? Several questions that are specific to motion visualization also arise, including, how are motions assigned to a small multiple? One small multiple per frame of the motion data will result in far too many views to be useful. On the other hand, if a single multiple stands in for a sequence of frames in the data, then how does that single image best visually represent motion over time?

Our approach to assigning motion to a particular small multiples image is based upon a characteristic of our target data. The biological motions we examine (chewing, walking, flying, etc.) are almost always cyclic. It is quite common to segment motions such as these into cycles as a part of the analysis. In walking, the moment the foot first touches the floor can be used as an indicator of the beginning and

end of a single stride. In the chewing examples presented here, the motions are divided into segments of chewing patterns (a single up and down motion of the jaw bone). One motion segment is assigned to each small multiple image.

The image displayed for each small multiple is a snapshot of a 3D visualization generated using our typical 3D rendering engine and then texture mapped onto a small rectangle to produce the array of multiples. The default view when data are first loaded into the system is shown in Figure 1. Here, each multiple is a snapshot of a 3D rendering of the bones posed during the initial frame of each motion segment. The user may change the frame that represents this view by mousing-over a frame number along the x-axis of the 2D plot, or highlighting a specific marker in the same 2D plot, or he may change the 3D view by clicking on a particular small multiple, which enlarges the rendering to fill its parent window, hiding the other small multiples. At a larger size, the 3D view is now easier to manipulate. The display now switches into an interactive 3D rendering mode and activates typical mouse and keyboard-based interaction widgets for camera manipulation, showing and hiding particular bones within the view, and adding visualization glyphs such as axes of rotation and tracer lines to the view. After some manipulation of these viewing parameters, the user escapes from this interactive view and is returned to the small multiples display, which is then re-rendered so that all of the views match the camera and visualization settings set by the user in the interactive mode. The background color of each multiple is set to encode the trail from which the data come; the colors correspond to those in the 2D time plot (see bottom of Figure 1).

Figure 2 shows a small multiples display generated in this way. In the interactive mode, the user attached a tracer to the front tooth on the jaw, zoomed the camera in to focus on the tooth, turned off the rendering of the bones, and then returned to the small multiples display.

#### 4.1.2 Integrated Time-Plots and Parallel Coordinates Views

Accompanying the small multiples display in the overview visualization are two 2D views: a parallel coordinates visualization and a 2D plot of motion data over time. The three views are linked together via interactive brushing and highlighting. For example, as the mouse moves over the time plot the corresponding small multiple view highlights. Conversely, moving the mouse over a small multiple image highlights the corresponding section of the time plot. Each line in the parallel coordinates view corresponds to a frame of motion data. Brushing over data in the parallel coordinates view highlights the corresponding frames and data values in the time plot. The value plotted on the Y axis of the time plot may be changed interactively to map to any data attribute that may be calculated for each frame of the data. In practice, values such as angular or translational velocity for a particular bone are useful. The angular velocity of the rotation of the mandible is plotted over time in the view shown in Figure 1.

### 4.2 Filtering to Generate Zoomed-In Coordinated Views

Following Shneiderman’s mantra “overview first, zoom and filter, then details-on-demand,” the system supports filtering down to specific segments or time ranges of the motion sequence. In the small multiples overview, a right mouse click on an image activates a menu, which is used to create a new coordinated view filtered to display just the segment of the motion that corresponds to the small multiple. Similarly, after brushing with the mouse to select a portion of the data in the time plot view, a right click and menu selection sends the selected data to a new multi-view zoomed-in window. Figure 3 shows this new zoomed-in window.

#### 4.2.1 Interaction Between Views

The zoomed-in window contains three data views: the parallel coordinates plot, 2D time plot, and a new interactive 3D view. Both 2D views are similar to the overview versions with the exception that the data visualized is a subset of the original data. The 3D view is different from the overview. Rather than a small multiples representation, spatial trends are now depicted via a real-time 3D rendering of the data that is responsive to mouse and keyboard controls for adjusting

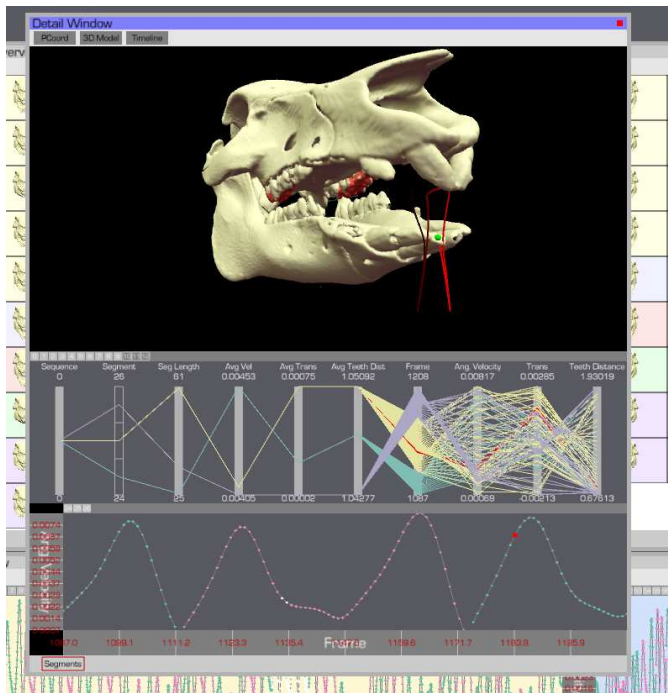


Fig. 3. A coordinated multiple view window created by zooming in on a portion of the larger data set.

viewing and visualization parameters. All views are linked visually and interactively. For example, the 3D view may be animated either through interaction in the 3D view or by mousing over the 2D time plot. In either case, the views advance together to display the active data frame as the animation plays. The 2D plot is not restricted to depicting time on the X axis. Other plots, for example, angular velocity vs. distance between bones, are also useful.

#### 4.2.2 Generating and Visualizing Data through Exploration

A more interesting example of the tight linkage between these multiple views is the ability to seed new visualizations from data generated during analysis. Figure 4 illustrates an example of this. The user first filtered the data from the original overview to zoom in to a sequence of four main chewing patterns. Then, while interacting with the 3D view window, a tracer was created to mark the path of a point on the left condyle of the mandible. The path that this point travels through space is calculated and stored in a coordinate system relative to the pig's skull. The 3D points that make up the path then become available as a data source for the linked 2D views. In this example, the user brushed over high positive values for the vertical position (relative to the pig's skull) of the tracer using the parallel coordinates view. The white lines in this view show the highlighted data points. Since the views are linked, these values also highlight in yellow within the plot below of average distance between the teeth over time. The visualization shows that during jaw closing, the selected point on the condyle rotates backward and downward. At its low point, there is some side-to-side motion of the jaw as the teeth come together to grind food. The sideways motion is visible in the in the tracer shown in the 3D view.

Other 3D visualization systems have exported data generated during exploration to tools that may then be used to generate related 2D plots [8]. Important differences in the strategy described here are the tight coupling of the multiple views and the ability to build new views based upon data generated during exploration. A tracer placed in one view may generate data that are then used for exploration via interactive brushing and ultimately for a new filtering strategy. Then, based on this new filtering, a second zoomed-in coordinated view may be created.

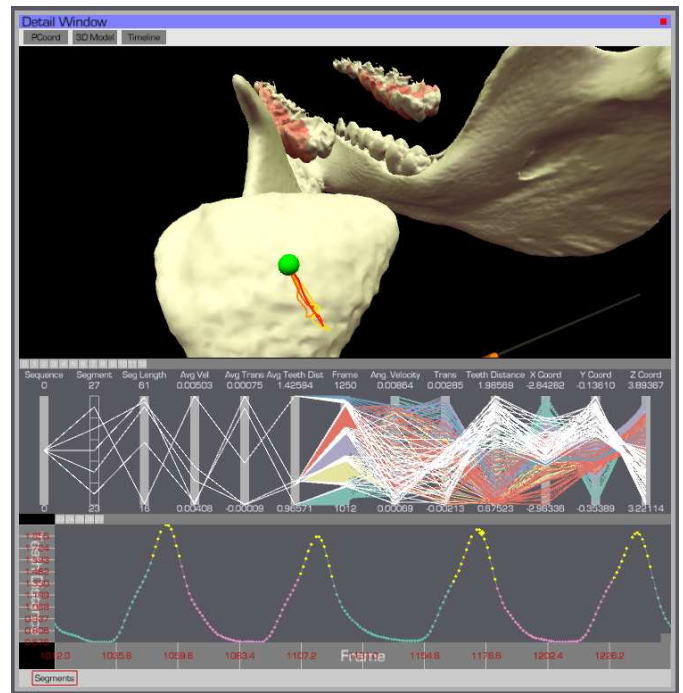


Fig. 4. The tracer created in the 3D view window generates new data (x,y,z points over time) that become available for display in the other linked views.

#### 4.3 Overlays and Side-by-Sides for Detailed Comparisons

Visual comparison of motion sequences occurs at all levels of the framework, and as the focus narrows, the method of visual comparison changes. As noted by Robertson et al. [16], small multiples (or side-by-side windows) and overlays each have advantages in comparing motion. The advantage in using overlays is that “counter trends” are easily detectable, but overlays often suffer from visual clutter. On the other hand, side-by-side comparisons are less sensitive to visual clutter, but require more visual real estate to represent the same amount of information and require more time in visual scanning of all the windows. In this framework, the choice of the most appropriate mix of these styles of comparison is left to the user.

In motion overlay views, data for multiple sequences are plotted and rendered together. Figure 5 shows an example. Note that, even in the 3D view, the pig is rendered with two overlaid jaw bones, one corresponding to each of the motion sequences that is being visualized.

Side-by-side comparisons may be established informally by simply arranging zoomed-in coordinated views side-by-side on the screen. Alternatively, data selected in a time plot within the motion overview or any zoomed-in window may also be sent to an existing window, which then resizes to arrange the views appropriately for a side-by-side comparison, as in Figure 7.

### 5 APPLICATION TO EXPERIMENTALLY COLLECTED BIOMECHANICS DATA

This section describes application-specific implementation details, initial findings, and feedback from domain scientists for the study of pig chewing behavior introduced in section 2.

#### 5.1 Processing Motion Data

Before loading the pig chewing motion data into the visualization framework, a simple Matlab script was prepared to segment the motion into cycles. While, more advanced time series analysis could certainly be utilized in this step, the approach taken here is quite simple. The angular velocity of the jaw bone is already calculated for these data in a preprocessing step. Using this information, a sign change from negative to positive in the angular velocity is detected. This occurs

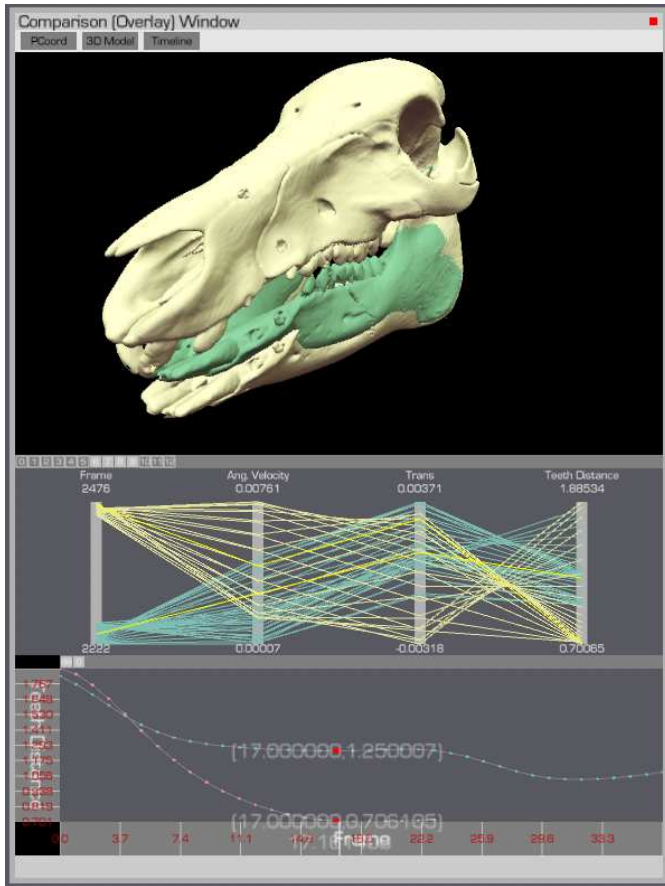


Fig. 5. Detailed motion comparisons are supported via overlay-style visualization applied to each of the coordinated views. Data from multiple motion segments are plotted on the same axes and in the same registered 3D space to produce these visualizations.

regularly at the bottom of a chewing motion when the jaw stops opening and begins to close. The data frames where this occurs are saved to a file and loaded into the visualization system to seed the techniques, such as the small multiples display, that work based on segments of the motion data. In all, data from five different trials are loaded into the system resulting in 108 motion segments identified in this manner. All this data can be seen in the motion overview in Figure 1. Note that not all of the sequences correspond to a chewing cycle, some refer to food gathering. The small multiples traces view in Figure 2 provide a visual means for distinguishing chewing and food gathering patterns.

## 5.2 Identifying Spatial Relationships and Surface Interactions

Many biomechanical analyses require investigation of patterns in the interaction of surfaces, particularly bone-to-bone surface interaction within joints [10]. Chewing motions are interesting in this regard in that there are three areas of surface-to-surface interaction: the attachment of the jaw to the skull on the left and on the right, and the teeth. The occlusion and grinding patterns of the teeth are of particular interest. Figure 6 shows a series of zoomed-in data views setup as a side-by-side comparison. The vertical distance between the teeth has been calculated and plotted directly on the 3D view as a color map textured to the tooth geometry. These distance data are calculated for each frame of the motion in a preprocessing step and are rendered interactively in the 3D views using a texture-based color map implementation. Within this framework, these data may be viewed both in the 3D visualization and in 2D plots, where the average distance between the two sets of teeth is a useful variable to explore.

## 5.3 Identifying Clusters of Related Motion Sequences

Figure 7 demonstrates the use of multiple linked views for identifying and characterizing related motion sequences. The user has filtered down to a subset of the data (eleven chew sequences) that are visible in the parallel coordinates view and the 2D plot of average distance between teeth vs. frame number. The 2D plot has been arranged to overlay the chewing sequences, starting each at frame zero on the left side of the plot. In this arrangement, two similar clusters of motions are easily distinguishable, with an outlier that does not clearly fit into either pattern. Each cluster is likely to correspond to a different chewing behavior, for example, chewing and food gathering. Using the 2D views, we can clearly identify the two clusters and also explore the amount of variance within each cluster for different data variables.

## 5.4 Feedback from Domain Scientists

While we have yet to perform an extended analysis of the use of this framework by domain scientists, we have collected some initial feedback from our collaborators based on our current implementation. Two high-level points of feedback are: first, there is widespread agreement that new analysis strategies are needed for working with these data, and second, the framework presented here is a drastic departure from current practice in fields such as evolutionary biology and orthopedics. A key point of departure is the notion that it may be possible to look at all of the data from an experiment at once via the overview visualization methods. During a feedback session with our collaborators, this point sparked considerable discussion, including discussion of the use of tracer lines within the small multiples views and the potential to extend this concept to more sophisticated “tracers” that also encode velocity, rotation angle, or other variables through color coding or other visual means. This feedback reinforces the importance of exploring the design space of potential small multiples views that are appropriate for motion visualization. During the same session, we also confirmed several characteristic features of pig chewing motions and investigated differences in the motion based upon the type of food (pig chow vs. nuts) through interactive exploration using this framework.

## 6 DISCUSSION

In this section we discuss current limitations and future research directions suggested by this work.

### 6.1 Scalability of Small Multiples

One question raised by the current framework is, how will the techniques scale to databases of various sizes? The initial overview visualization, including the small multiples view, is perhaps the most interesting aspect of the framework to discuss with scalability in mind. One answer to the question is that the utility of the small multiples visualization scales with the skill and creativity of the user in constructing a useful small multiples display. The display in Figure 2 is useful for discerning some trends across 108 related motion sequences. With fewer motion sequences, alternative views, including those that feature the bones prominently may be useful. With more motion sequences, this layout and others may still be useful, but certainly at some point, the utility of a small multiples display crafted from snapshots of 3D renderings will reach a limit.

A complimentary technique to address the scalability of this small multiples motion overview may be the use of filtering within the small multiples view or within new instances of it in separate windows. Currently this display functions as a complete overview of the entire database, however, such an overview may also be appropriate for a subset of the original data. We have discussed this idea, but have not yet developed an implementation of it. Several interesting user interface issues remain in developing an interactive display of this form that supports fluid, interactive exploration.

### 6.2 Scalability and Interactivity

Adding 3D renderings to a multi-window information visualization system requires special design to maintain interactive framerates. While the 2D graphics utilized in typical information visualization

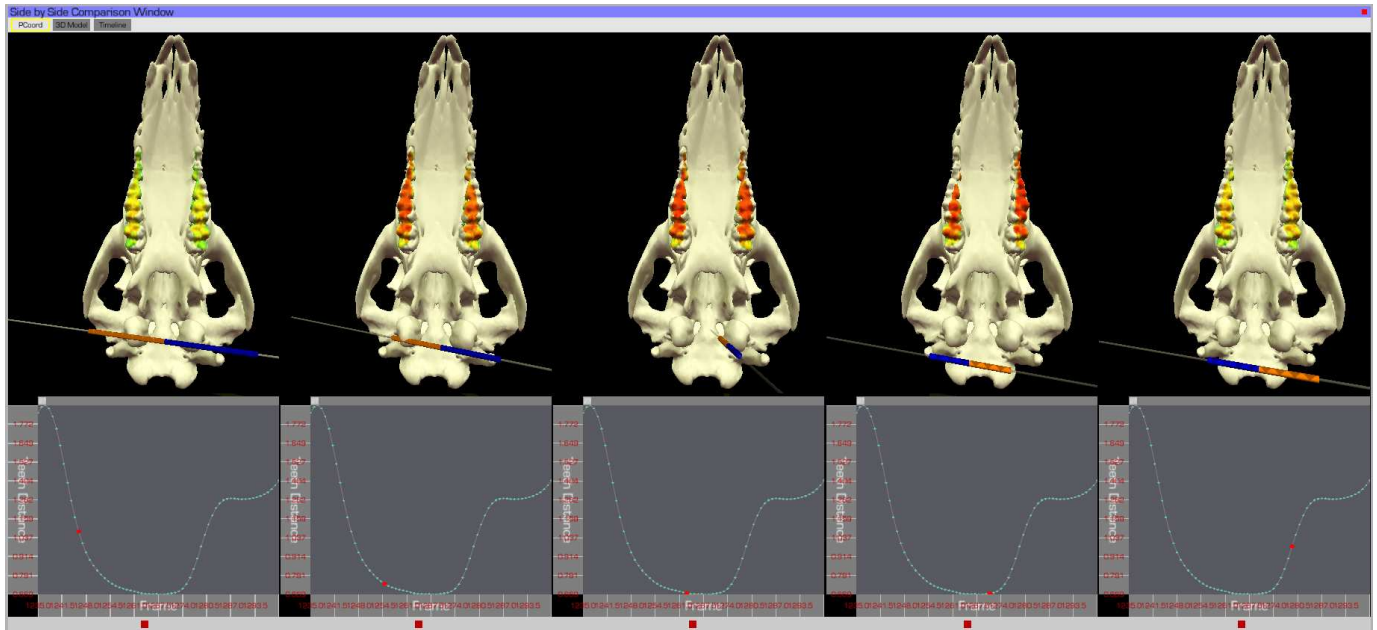


Fig. 6. A sequence of side-by-side visualizations that demonstrate how the teeth slide against each other. The 3D view has been rotated so that we are looking up at the top rows of teeth, and the mandible has been hidden from view. A color map has been texture mapped onto the forms of the teeth to encode the vertical distance (defined by the principle axes of the skull) separating the teeth. The chewing sequence advances in time across the views from left to right. A 3D instantaneous helical axis describing the motion of the mandible relative to the skull is also displayed.

techniques are relatively fast to render, 3D scientific visualizations often utilize the full extent of the rendering power provided by current graphics hardware, just to render a single view of the data.

Working with the data set described here, our current implementation maintains interactive framerates, depending on the view options set, while rendering on the order of five instances the 3D scene in the filtered and comparison views. This seems to be a minimum level of performance for reasonable analysis using the framework. To extend the framework to applications that involve more intensive 3D rendering, new strategies for addressing multi-view 3D rendering will be required. One potential direction for this research is to use a prioritized rendering scheme, directing more rendering resources to the views that are actively being manipulated. Since the viewer's attention is divided between several views in multi-view systems, artifacts in some views may be almost unnoticeable from a perceptual standpoint. An example would be the use of image warping [18] to support linked camera manipulation in several 3D windows. The view in the window that the user is actually manipulating might be rendered as a true 3D scene, while other (lower priority) views might update in an approximate fashion using a faster rendering technique.

### 6.3 Alternative Visual Representations for Motion

Previously demonstrated 3D animated small multiples displays have supported rendering just a handful of multiples [2], which give them a very different visual character than the display in Figure 2. With additional technical work to address rendering speed, it should be possible to develop animated 3D small multiples displays of tens to hundreds of animated 3D scenes. This raises the question of whether such a display would be useful in analysis of 3D motions. Our current work was motivated by the finding that static views may outperform animation in analysis of trends [16]. Based on this notion, adding even more animation seems to have more potential to distract than to clarify. Nevertheless, it would be interesting to investigate whether certain classes of 3D motion trends may be discernible through visualization in large-scale animated small multiples displays.

Currently, the most useful static small multiple representations for motion that we have discovered are of the form seen in Figure 2, simple geometric representations that describe motion from multiple

frames of data in a single image. In addition to tracers, other visuals commonly found in 3D motion visualization applications may also be useful as small multiple images. Examples beyond tracer particles that fit this description include the average axis of rotation or the ruled surface swept out by an instantaneous axis of rotation over a sequence of frames of motion.

### 6.4 New Data Sources

In applying this framework to other data sets, one of the important next issues to address is handling biomechanical systems containing more than two bones, such as the spine or the wrist. The skull and jaw system is a special, rather complicated, case for a two-bone system, in that the jaw has multiple attachment points to the skull (the TMJ on both sides), and the two bones also interact as the teeth come together. Thus, many of the strategies employed here (interacting with 3D views to establish spatial points of interest, using multiple windows to focus on multiple points of interest, etc.) are likely to be relevant to analysis in complex systems with more than two rigid bodies in motion.

## 7 CONCLUSION

As new high-speed, high-resolution imaging capabilities see increased use in fields such as orthopedics, physical therapy, and evolutionary biology; scientists will face considerable challenges in analyzing the wealth of complex, 3D, time-varying data that result from these systems. The framework presented here is specifically geared toward addressing many of the new challenges posed by these data. Comparative analysis across large sets of experimentally collected data is facilitated by integrating 2D and 3D interactive visualization tools to support an overview first, zoom and filter, then details-on-demand style of analysis. This work contributes a new interactive approach to constructing small multiples overview visualizations, which we demonstrate using a collection of more than one hundred repeated cyclic motions. Specific interactive links that may be made between 2D and 3D visualizations to facilitate zooming, filtering, and exploring motion data are also presented. These links include the use of data generated “on the fly” during analysis, as seen in Figure 4, where the path of a 3D tracer curve generated by the user acts as a filtering variable within coordinated 2D views. Two methods (overlays and side-by-sides) are presented for

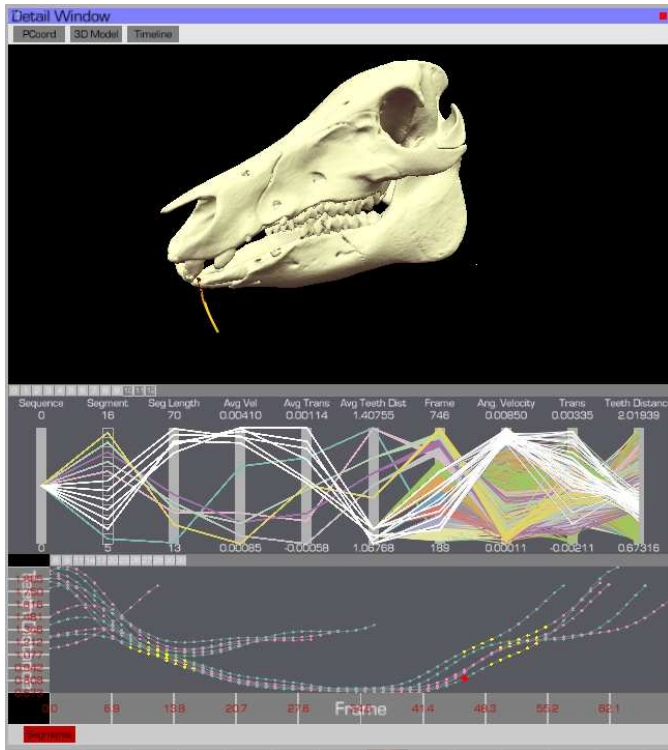


Fig. 7. Clusters of motion cycles can be identified using a combination of the 2D plot and the parallel coordinates.

detailed motion analysis using coordinated multi-view visualization. Each utilizes sophisticated 3D views that incorporate features, such as visualization of surface-to-surface distances via texture-mapped color coding, along with interactive 2D views, such as parallel coordinates plots that are non-traditional in this domain. Many challenges remain in this line of research, including scalability, refinement of visual representations, and extending this framework to new data sources. Our initial feedback from domain scientists confirms both the need for new analysis strategies, and the novelty of this framework compared to current practice in their fields. Our collaborators expressed considerable interest in the overview visualization component of the framework and in future work designed to extend the small multiples tracer views to depict additional data. These findings contribute to a growing body of knowledge of the topic of coordinated, multi-view visualization systems that reinterpret and recombine techniques from scientific and information visualization to address driving scientific analysis challenges.

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