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Spectral Approaches to Natural Mesh Processing

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Spectral Approaches to Natural Mesh Processing

Takamitsu Kawai

Dissertation submitted to the
College of Engineering and Mineral Resources
at West Virginia University
in partial fulfillment of the requirements
for the degree of

Doctor of Philosophy
in
Computer Science

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Allometric Scaling, Nonlocal Mesh Editing, Mesh Skeleton Generation
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Abstract

Spectral Approaches to Natural Mesh Processing

Takamitsu Kawai

Mesh design is a major bottleneck in the creation of computer games and animation. Therefore simplifying the process of mesh editing is an important problem. Natural mesh processing is generally difficult to perform since natural meshes often have nontrivial surface shapes and high degrees of freedom. In this study I present novel approaches to natural mesh processing utilizing spectral methods based on the manifold harmonic basis.

Geometric scaling transformations do not respect the biological processes which govern the size and shape of living creatures. I describe an approach to scaling which can be related to biological function. Known biological laws of allometry are used which are expressed as power laws to control the mesh deformation in the frequency domain. This approach is motivated by the relation between fractal biological systems and their underlying power-law spectra. I demonstrate my approach to biology-aware character scaling on triangle meshes representing quadrupedal mammals.

Mesh editing is a time-consuming and error-prone process when changes must be manually applied to repeated structures in the mesh. I propose a fast and accurate method for performing region matching which is based on the manifold harmonic transform. Then this matching method is demonstrated in the context of *nonlocal mesh editing* - propagating mesh editing operations from a single source region to multiple target regions which may be arbitrarily far away. Finally, I show how mesh skeleton generation can be simplified using spectral approaches. These contributions will lead to more efficient methods of mesh editing and character design.

*To my parents Sumiaki Kawai and Kumiko Kawai,
and all of my families and ancestors*

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Chapter 1

Introduction

1.1 Goal of this study

Modeling triangular meshes is one of the common yet challenging tasks among various creation processes in computer graphics. Particularly, modeling *natural meshes*¹ such as animal characters and natural scenes is difficult since the shape of natural meshes is often complex and the number of vertices tends to be high. In a typical mesh modeling scenario, artists start with creating a primitive polygon model or a spline model to roughly model the entire shape. Then they incrementally subdivide the polygons or splines and apply deformations to the mesh by properly moving the vertices or control points to obtain a desired shape. One of the problems in this process is that the shape of the resultant mesh is manually controlled by the artists and it is often difficult for them to incorporate plausible anatomical and biological influences into the shape of the mesh.

Another common problem arising in mesh modeling is to apply similar deformation operations to multiple similar regions within a mesh. Repeating similar operations including

¹Drawing on the notion of *natural images* [88, 31], in this study 'natural meshes' are defined as meshes observed in nature exhibiting power-law spectra typically resulting from fractal structures.

selecting relevant vertices and applying deformation operations to multiple similar regions is a daunting and error-prone task for artists.

Once modeling of the mesh is completed, *bones* are often inserted into the mesh to create an animation. For each bone segment the corresponding nearby mesh vertices are associated. This process allows artists to indirectly deform the mesh by means of the motion of the bones. In this process one of the difficult issues is to identify the proper number and position of the bones and joints.

The goal of this study is to develop methods to address the issues mentioned above. Therefore, this study is comprised of the following 3 parts:

- Mesh deformation with allometric scaling laws (Chapter 3)
- Nonlocal mesh editing based on spectral methods (Chapter 4)
- Mesh skeleton generation based on spectral methods (Chapter 5)

As I will present in the following chapters, it turns out that the use of spectral methods is quite effective in addressing all the problems mentioned above. This study makes extensive use of the *manifold harmonics* that plays an important role in spectral mesh processing. In the following sections, I describe the scope of each study.

1.1.1 Mesh deformation with allometric scaling laws

The design of virtual living characters for movies, games and other computer graphics applications is largely an artistic endeavor. As a result, biological issues may be overlooked during character design. By incorporating known relations between scale and biological function into the character design process one can force the resulting data to be bio-

logically plausible. This can simplify the process of character design by permitting the designer to manipulate the geometric form of a character by setting a few scale parameters, and to generate a spectrum of characters at different scales from a single mesh. This process can also provide insight into the relations between form and function of living creatures by allowing the user to explore the space of plausible creatures. In this study, I present a method of incorporating known correspondences between biological function and geometric form in the character editing process using spectral mesh processing techniques.

Characters are typically modeled as triangle meshes consisting of thousands or more vertices. Editing these triangle meshes can be time consuming due to the large number of vertices. The number of variables needed to specify a mesh can be reduced by using modeling techniques such as splines or subdivision surfaces. Another approach, spectral mesh processing, allows us to represent the mesh as a combination of manifold harmonic basis functions. This permits meshes with hundreds of thousands of vertices to be manipulated in terms of about a thousand variables, and simplifies many processes such as mesh filtering, segmentation, and computation of the mesh skeleton. The number of variables is further reduced to fewer than 10 by finding the combinations of coefficients with anatomical and biological meaning.

In this study 3 types of relations are incorporated into the manifold harmonic mesh representation to simplify the character design process: biomechanical, cardiopulmonary, and metabolic.

Biomechanical relations allow us to impose constraints which guarantee that the character has a musculoskeletal system which can resist internal stresses. In terms of visual properties, these constraints will influence the cross-sectional area of the load-bearing

extremities of the character.

Cardiopulmonary relations can be used to guarantee that the character has a cardiovascular system which can supply blood throughout the body, and a respiratory system capable of oxygenating the blood stream. The size of the heart and lung has a large influence on the size of the chest. Systolic blood pressure can limit the maximum height to which blood can be pumped.

Metabolic relations enforce the character to have a digestive system capable of generating enough energy for activity by metabolism. The energy requirements dictate the mass of the digestive system which can influence the size of the lower abdomen.

Character modeling using such biological relations will simplify editing of meshes representing living creatures. This can lead to more efficient generation of biologically plausible character designs.

1.1.2 Nonlocal mesh editing based on spectral methods

Mesh editing can be a time-consuming task when similar changes must be made to multiple regions of the mesh. Consider the problem of editing the limbs of an animal, for example the hooves of horse. If an artist wishes to change the shape of the hooves, the editing procedure must be manually applied to all four hooves. This process is time-consuming and prone to error. In the case of meshes representing inorganic structures, such as buildings, there may be dozens of repeated structures, such as windows, making the problem even more complex. I present a framework for nonlocal mesh editing and a method for quickly identifying similar substructures in a mesh. The presented technique is used on several meshes representing organic characters and inorganic structures.

1.1.3 Mesh skeleton generation based on spectral methods

In shape analysis, skeleton generation has been done for 2D/3D images in many applications such as object recognition, optical character recognition, fingerprint recognition, visual inspection, binary image compression, and protein database retrieval. In the context of computer graphics, skeleton generation for 3D meshes is essential in character animation and is an important task. This common process is also known as character rigging. It requires artists to insert proper number of skeletons (or bones) at a proper position of a given mesh and associate the corresponding subset of mesh vertices to each bone. This allows the artists to indirectly deform the given mesh by manipulating the bones. Identifying the proper number of bones and their position is a manual process and is time-consuming. I propose a novel automatic mesh skeleton generation method based on spectral methods. The proposed method utilizes the Fiedler vector and the Reeb graph. This method is effective when skeleton generation is performed in conjunction with allometric scaling since the Fiedler vector is already computed in the allometric scaling algorithm.

1.2 Dissertation outline

Chapter 2 will present the background of this study. Historical perspective of allometry, allometric laws in biology and other sciences, biological approaches to graphics, and spectral mesh processing will be discussed. The implementation and experimental results of mesh deformation with allometric scaling laws will be shown in Chapter 3. The results for global allometric scaling, local allometric scaling, and biologically-aware allometric scaling will be shown. The implementation and experimental results of nonlocal mesh

editing based on spectral methods will be shown in Chapter 4. The algorithmic sketch of the mesh skeleton generation method based on spectral methods and its experimental results will be shown in Chapter 5. In Chapter 6 conclusions and future work will be presented.

Chapter 2

Background

The study of the connection between form and function is an old one. One of the earliest discussions on the topic was by Galileo [27] who was especially interested in how changes in scale affected the shape of certain mechanisms and animals. This line of questioning was also pursued in the early 1900s by Haldane [32] and more recently by Bonner [8, 9]. The relations between biological function and anatomical form can be expressed as mathematical models which are theoretical in nature, or they can be based on observations and measurements of many species (such as the allometric laws discussed later).

The “square-cube law” refers to the relation between volume and cross-sectional area as objects undergo dramatic scaling, and it can have biomechanical consequences. These consequences are often described in the context of the extreme scaling transformations depicted in 1950’s horror movies such as “Attack of the 50 Foot Woman” or “Them,” which is about giant mutated ants. Examples of these fantastic characters are shown in Figure 2.1. The enormous creatures featured in these films are unrealistic, in part, due to changes in proportionality between volume and area that are required when objects undergo scaling transformations. The square-cube law states that applying a uniform

Figure 2.1: 1950s Sci-Fi and Horror movies featured many characters scaled to fantastic degrees. The isometric scaling performed to create these characters is implausible for physical and biological reasons.

scaling factor, s , to each dimension of an object causes the volume to increase by a factor of s^3 , but the cross-sectional area only increases by a factor of s^2 . Assuming that material properties are unchanged by the scaling, the weight of the object will scale by s^3 , but the structural ability of the object to resist tensile and shear stresses will only scale by s^2 . What this means for the 50 foot woman is that she would collapse under her own weight. The method of character design proposed in this study permits artists to easily generate plausible character designs with respect to such scaling.

2.1 Historical perspective of allometry

Galileo published many observations regarding the scale of mechanisms and structures [27]. Included in this work is some discussion of scale of living creatures accompanied by a sketch in Figure 2.2 which shows the changing proportions of a bone which scales to 3 times its original length. His observation was that the bone does not simply scale uniformly - it must change shape. Specifically, the larger bone must be thicker in order

Figure 2.2: *Galileo’s sketch of two bones. One is three times as long, but the shape must change if the larger bone is to perform the same function as the smaller bone.*

to support the increased weight it must bear. This can be seen as a biological example of the design principle “form follows function.”

Galileo admits that changes in material may mitigate the effects of scale, as will buoyancy as demonstrated by large fish and whales whose skeleton cannot support their weight outside of the water. In this work, I concentrate on terrestrial animals to avoid such concerns.

Haldane [32] also described the relation between structure and scale in his essay “On Being the Right Size,” though he did not explicitly reference Galileo’s work. *Haldane’s principle* states that the structure and complexity of living organisms are dictated by their size as well as function. He gives examples of possible changes in structure which may compensate for changes in scale:

“...suppose that a gazelle, a graceful little creature with long thin legs, is to become large, it will break its bones unless it does one of two things. It may make its legs short and thick, like the rhinoceros, so that every pound of weight has still about the same area of bone to support it. Or it can compress its body and stretch out its legs obliquely to gain stability, like the giraffe.”

These are exactly the types of transformations of shape I propose to model in response

to changes in scale.

2.2 Allometric laws in biology and other sciences

The term “allometric” means “by a different measure,” and comes from the Greek word “allois” for “different.” This is in contrast to “isometric” which literally means “by the same measure.” “Allometric change” or “differential scaling” occurs when the proportions of an organism adjust in response to changes in size or other parameters. The term was coined by Julian Huxley [33] who presented the first allometric laws relating body weight to quantitative biological properties.

Allometric laws relate two biological characteristics, and commonly take the form of a power law, $X = aY^b$. Laws of this form may be linearized by taking the logarithm of both sides, $\log X = \log a + b \log Y$. For example Kleiber’s law, $B = aM^{3/4}$, relates metabolic rate, B , and body mass, M . Although many of these laws are based on empirical observations they often hold true over a large number of species. A log-log plot of Kleiber’s law over 391 species is shown in Figure 2.3. Allometric laws can be roughly classified in terms of the value of the exponent, b . If $b = 1$ the relation is linear, and the mass scaling is a linear function of the biological variable (isometric scaling). If $b < 1$ the relation is a ‘negative allometry’, and X increases relatively slowly as Y increases. The case of $b > 1$, ‘positive allometry’ implies that X increases quickly relative to Y . If $b = 0$ then X is invariant with respect to Y . A familiar example of negative allometry is the relation between head size and body mass. Juvenile animals typically have large heads relative to their body weight. As the creature grows older the body weight increases more quickly than the head size, so that in the adult the head is proportionally smaller relative to the

body.

The influential biologist Stephen J. Gould [30] suggested that allometry was more than the mere study of such power laws, but that it was "the study of size and its consequences." Since many of these laws are expressed with mass, length or area as one of the characteristics they are useful in developing plausible scaling transformations. Allometric laws involving many physiological systems have been proposed, including circulatory models [50] and cardiovascular models [87]. As a statistical tool, allometry has proved to be useful for comparative physiology.

Jerison [38] proposed the concept of Encephalization Quotient (EQ) as a measure of animal's intelligence. It is defined as the ratio of the expected brain weight of the animal to the weight of a typical animal of the same body weight. The expected brain weight can be described as an exponential function of body weight and thus the EQ is another example of power law.

West [98] established a connection between allometric laws and the fractal structure of biological systems, such as the branching networks of tubes forming vascular and respiratory systems. In fact, allometric relations often arise in the study of non-biological systems with self-similar or self-affine structure at many scales. Kolmogorov's 5/3 law governs turbulence at multiple scales in fluids and can be exploited in fluid simulation and animation [81, 10]. The law was derived by Kolmogorov from theoretical principles, not empirical observations, and relates the energy contained in each wavenumber (or spatial frequency) to the wavenumber itself through the power law $E(k) = Ck^{5/3}$. The connection between natural systems exhibiting fractal geometry and power laws in the spectral domain shows up in many other areas.

Figure 2.3: Allometric relation between metabolism and mass for 391 species of mammal. The relation is linear when plotted on a log-log scale.

Mandelbrot and Van Ness [57] first established that self-affine processes have a power spectrum in the form of a power law. Furthermore, the power law exponent is directly related to fractal dimension. One particular process, fractional Brownian motion has been used in computer graphics to generate fractional Brownian surfaces which are useful as terrain models [56]. Power-law filtering of Fourier coefficients is used in studies of geology [46], to describe rain and clouds [76], and in analyzing images of sea ice [25].

'Pink noise' or ' $1/f$ noise' with a spectral density $S(f) = C/f^\alpha$ occurs in many natural phenomena. Some approaches to procedural texture generation are based on controlling image spectra to impose the ' $1/f$ ' structure [23]. A well-known example is the *turbulence* function described by Perlin [65]. In fact, the power spectrum of natural images is known to obey a power law relation [71].

In this study I explore the extension of these concepts to mesh processing. The manifold harmonic transform provides us with a frequency domain representation of the mesh, and a means of directly manipulating the power spectrum. It is observed that the power spectrum of character meshes obeys a power law, just as natural images do. I will show that power-law filtering of the mesh spectrum results in allometric scaling of the mesh. Then, using known biological allometric relations we can control local scaling to generate biologically plausible changes in shape.

2.3 Biological approaches to graphics

Models of biological processes have been exploited to improve the realism of graphics applications. Previous examples of biologically inspired graphics include the 'artificial life' proposed by Terzopoulos [84, 85]. Much work in this area has concentrated on modeling

of behaviors, such as flocking and herding of groups [73].

Lee [47] used biomechanical modeling for simulation and animation. Tu [89] developed models based on the biomechanics and locomotion of fish. Terzopoulos [86] utilized biomechanical models of the head for facial animation. Ijiri et al. [34] developed a system for realistic animation of opening flowers. The reaction-diffusion process proposed by Turing [90] as an explanation for patterns on animal skins has been used to generate texture maps with an organic appearance [99, 91].

Unlike this previous work, I do not propose to generate any animation or to numerically simulate any process. Instead the goal of this study is to model how biological processes influence changes in shape. Along those lines, there have been several other approaches taken for structural generation of plants [68, 69, 63]. Unlike this work, I do not generate a mesh but modify an existing mesh. Anguelov et al. [2] proposed the SCAPE method, a data-driven method for building a human shape model that spans variation in both subject shape and pose. Their method is based on learning pose deformation from data. Allen et al. [1] developed a method for fitting high-resolution template meshes to detailed human body range scan data with sparse 3D markers. An optimization problem is formulated where the degrees of freedom are an affine transformation at each template vertex. The technique I developed is not based on an evolution of curvature, i.e., the geodesic heat equation. As pointed out in [22], the issue of choosing a correct exponent (e.g. $2/3$ versus $3/4$) in power laws for a specific type of organism still remains controversial and the coefficients in power law formula vary depending on the problem domain. However, the framework proposed in this study can incorporate any allometric laws that are described in a form of power law.

2.4 Spectral mesh processing

The manifold harmonic transform which is used in this study for processing character meshes is a product of the active research area of spectral mesh processing. Spectral methods, in general, involve analysis of the eigenvalues and eigenfunctions of appropriate differential operators defined over a continuous domain. In the mesh processing context, the differential operators are represented by appropriately defined matrices and the eigenfunctions are discretized as the eigenvectors. The set of eigenvalue-eigenvector pairs is numerically computed by an efficient algorithm utilizing a sparse eigensolver (see Appendix).

Spectral methods are mainly derived from a great deal of research in the field of *spectral graph theory* as found in the book by Chung [16], *signal processing* related to the classical Fourier analysis, and *machine learning*. These methods have been applied to many topics in the computer graphics and shape analysis fields. In the following subsections I review the spectral methods from these perspectives and present their relations to my study.

2.4.1 Spectral graph theory perspective

The main focus on spectral graph theory has been analysis of relationships between the eigensystems derived from the Laplacian or adjacency matrices of a graph and fundamental graph-theoretic properties for graphs. Another important aspect derived from spectral graph theory is the Fiedler vector. The Fiedler vector is the eigenvector corresponding to the smallest nonzero eigenvalue of the Laplacian matrix. It turns out that there are many applications to graphics. One of the typical applications of the Fiedler vector is graph partitioning as described in Spielman and Teng’s work [80] and Shi and Malik’s

work [77]. Graph reordering is closely related to graph partitioning. Isenburg and Lindstrom [35] developed a streaming format for polygon meshes based on the Fiedler vector that is simple enough to replace current offline mesh formats. Liu et al. [55] discussed linear sequence generation as a problem of preserving graph distances. These studies make sense considering a physical analogy of vibrational objects, i.e. the Fiedler vector has favorable characteristics that the transition of the values of the vector components naturally follows the overall mesh shape as shown in Figure 2.6. Also the Fiedler vector roughly corresponds to the vibrational mode of the lowest resonance frequency and its nodal set that represents the zero-amplitude points provides good heuristics for graph partitioning. Another usefulness of the fact that Fiedler vector has natural transition of its values is that it allows one to extract the skeleton of a mesh by computing isocontours of the Fiedler vector as shown in Figure 3.3.

Many attempts have been made to apply spectral graph theory to mesh segmentation. Katz and Leifman [43] presented an algorithm for segmenting a mesh into visually meaningful sub-meshes. Zhang and Liu [103] presented a mesh segmentation algorithm via recursive spectral 2-way cut and Nyström approximation. Liu and Zhang [54] also applied spectral clustering to 3D mesh segmentation. The selected eigenvectors of the affinity matrix or its closely related graph Laplacian are used. My local allometric scaling algorithm presented in Chapter 3 requires the segmentation of the entire body into multiple anatomical regions. Liu and Zhang’s method is used as a part of my algorithm since it allows one to reuse the precomputed manifold harmonic basis. De Goes et al. [20] presented a segmentation method to assist the rigging of articulated bodies. The method computes a coarse-to-fine hierarchy of segments ordered by the level of detail. This work is closely related to the mesh skeleton generation algorithm presented in Chapter 5.

2.4.2 Signal processing perspective

In conventional audio and image signal processing, input signals are defined over a time or spatial domain. These input signals are transformed into the frequency domain by standard transform algorithms such as the fast Fourier transform and discrete wavelet transform. Then the frequency components of the signals are modified by filtering process to enhance and/or suppress specific frequency bands. The filter coefficients are appropriately controlled to obtain desired frequency characteristics. Finally, the modified frequency coefficients are transformed back into the time or spatial domain. Interestingly, one can come up with a similar signal processing framework for triangular meshes considering this analogy by using the notion of *manifold harmonics* as described in Section 2.5.

Application of signal processing concepts for meshes was first introduced by the work by Taubin [82, 83]. He introduced the use of mesh Laplacian operators to filter spatial vertex coordinates of meshes. His filtering scheme directly operates on the spatial domain and the frequency characteristics of the signal are implicitly modified. Vallet and Lévy [92] presented a method to convert the spatial geometry of a mesh into the frequency domain. The eigenfunctions of the Laplace-Beltrami operator are used to define Fourier-like function basis functions (manifold harmonics) and transform. This method can be considered as the extension of the conventional Fourier analysis to manifolds. The eigenanalysis method used in my study is based on their work.

The realization of computing the manifold harmonic basis and transforming spatial signals of mesh vertices into the frequency domain has led to many applications. Karni and Gotsman [41] applied spectral methods to obtain compact representations of 3D mesh data. The algorithm projects the mesh geometry onto an orthonormal basis derived from

the mesh topology. The mesh is partitioned into a number of balanced submeshes with minimal interaction and each mesh is compressed independently. They also introduced a spectral compression method of 3D meshes [42]. It provides mesh augmentation and generation of a neighborhood-preserving mapping between the vertices of a 3D mesh. Zhang and Blok [102] described a simple autoregressive model for 3D mesh geometry based on linear prediction. Zhang [101] discussed digital geometry processing (DGP) using signal processing style algorithms for surface geometry. The relations between spectral decomposition and traditional statistical analysis methods have also been studied. Ben-Chen and Gotsman [4] showed that, for certain classes of geometric mesh models, spectral decomposition using the eigenvectors of the symmetric Laplacian of the connectivity graph is equivalent to principal component analysis on that class, when equipped with a natural probability distribution.

As shown above, various applications of spectral methods are possible utilizing the signal processing concepts. In my allometric scaling algorithm presented in Chapter 3 the signal processing concept is applied to deform the input mesh in the frequency domain. The frequency characteristics of the input mesh are modified by a set of power laws derived from biological and physiological constraints on shapes.

2.4.3 Machine learning perspective

From the machine learning perspective, many topics have been addressed by means of spectral methods such as spectral clustering, mesh processing, surface reconstruction, spectral embeddings, shape correspondence and retrieval, symmetry detection, Isomaps, Laplacian eigenmaps, kernel PCA, and dimensionality reduction on manifolds. The spec-

tral characteristics of graphs are often used to identify the similarity and correspondence among different shapes. In the field of shape correspondence research, Leordeanu and Hebert [49] presented a spectral method for finding consistent correspondences between two sets of features. Jain and Zhang [36] presented an algorithm for finding a meaningful vertex-to-vertex correspondence between two 3D shapes given as triangle meshes. Jain and Zhang [37] presented a method for robust shape retrieval from databases containing articulated 3D models. Each shape is represented by the eigenvectors of an affinity matrix and retrieval is performed in the spectral domain using global shape descriptors. Mateus et al. [58] proposed a general framework to solve the articulated shape matching problem formulated as finding point-to-point correspondences between two shapes represented by point clouds. The original point sets are embedded in a spectral representation and the matching is performed in the embedded space. In the field of shape indexing research, Elad and Kimmel [24] presented a method to construct a bending invariant signature for isometric surfaces. The bending invariant representation is constructed by first measuring the intergeodesic distances between uniformly distributed points on the surface. Next, a multidimensional scaling technique is used to extract coordinates in a finite dimensional Euclidean space where geodesic distances are replaced by Euclidean ones. Reuter et al. [72] introduced a method to extract “Shape-DNA,” a numerical fingerprint of any 2D or 3D manifold by taking the eigenvalues of its Laplace-Beltrami operator. Jain and Zhang [37] presented an approach for robust shape retrieval from databases containing articulated 3D models using spectral methods. Rustamov [75] introduced a deformation invariant representation of surfaces called the GPS embedding using the eigenvalues and eigenfunctions of the Laplace-Beltrami differential operator. This line of work will be useful for constructing a large database of 3D models and retrieve a specific model from

those databases using spectral similarities.

Symmetry detection is one of the useful concepts in shape processing. Ovsjanikov [62] presented an approach for computing symmetries of a shape which are invariant up to isometry preserving transformations. It shows that the intrinsic symmetries of a shape are transformed into the Euclidean symmetries in the signature space defined by the eigenfunctions of the Laplace-Beltrami operator. In my nonlocal mesh editing algorithm presented in Chapter 4 regions with similar shapes within an input mesh are automatically identified. The similarity is efficiently computed using spectral matching based on a metric derived from a combination of the Euclidean distance and cross correlation.

Clustering is a method of assigning a set of data into subsets such that the data in the same cluster are similar with respect to a certain metric. In the computer graphics and shape analysis context the concept of clustering is useful for mesh segmentation and object recognition. Ng et al. [60] introduced a simple spectral clustering algorithm and presented successful examples of clustering that could not be handled by the k -means algorithm. Belkin and Niyogi [3] introduced the Laplacian eigenmaps. This algorithm provides nonlinear dimensionality reduction that has locality preserving property. Kannan et al. [40] gave a natural bicriteria measure for assessing the quality of clustering. Von Luxburg et al. [96] investigated the question whether the partitions constructed on finite samples converges to a useful clustering of the whole data space as the data size increases. As discussed in Section 2.4.1, the spectral clustering technique based on Liu and Zhang's work [54] is used in my study since it allows one to reuse the precomputed manifold hamonic basis.

2.5 Manifold harmonics

In the late 18th century, a physicist Ernst Chladni published a book entitled “Entdeckungen über die Theorie des Klanges (Discoveries in the Theory of Sound) [15].” In his book, he presented the vibrational pattern (modes) of a square-shaped thin metal plate. He put sand over the thin metal plate and applied vibrations by scratching the edge of the plate using a violin bow. The sand is excited by the vibration caused by the bow, accumulates in certain zones, and creates surprisingly complex patterns. These zones are known as a *node* where the amplitude of the vibration is zero. Figure 2.4 shows some of the vibrational patterns of a square thin plate observed by Chladni. Physically this phenomenon is explained by the theory of stationary waves. Wave phenomena on a continuum body are generally described by the PDE called the wave equation

$$\frac{\partial^2 u}{\partial t^2} = c^2 \Delta u, \quad (2.1)$$

where Δ is the Laplace operator, u is the displacement, and c is the propagation speed of the wave. The standing waves on the continuum body can be described by the Helmholtz equation

$$-\Delta u = \lambda u, \quad (2.2)$$

where $\lambda = \omega^2$ characterizes the resonance frequency, ω . The vibrational modes of the continuum body can be computed by solving the eigenvalue problem for the Helmholtz equation.

The set of sinusoidal basis functions that appears in the Fourier analysis can be obtained by computing eigenfunctions of the Laplacian matrix derived from a vibrating circle or a circle graph (Figure 2.5).

Figure 2.4: *Vibrational modes of Chladni's plates.*

Figure 2.5: Sinusoidal basis functions and their corresponding eigenvalues numerically computed as eigenvectors and eigenvalues of the Laplacian matrix derived from a 1D circle graph.

The manifold harmonic basis (MHB) is analogous to the sinusoidal basis implied by the Fourier transform - both are eigenfunctions of Laplacian operators defined on their respective spaces. The Fourier transform operates on functions of real variables, but the manifold harmonic transform (MHT) operates on functions whose domain is a discrete graph representing the connectivity of the mesh.

Given a triangulated mesh with n vertices one can compute basis functions H^k , $k = 1, \dots, m$, $1 \leq m \leq n$, called the manifold harmonic basis. Each basis function is assumed to be a piecewise linear function represented by its value H_i^k at each vertex, i . These basis functions, in matrix form, can be used to transform the vertices back and forth between their native geometric space and the frequency domain. Let $x = [x_1, x_2, \dots, x_n]$, $y = [y_1, y_2, \dots, y_n]$, and $z = [z_1, z_2, \dots, z_n]$ be the geometric coordinates and $\tilde{x} = [\tilde{x}_1, \tilde{x}_2, \dots, \tilde{x}_m]$, $\tilde{y} = [\tilde{y}_1, \tilde{y}_2, \dots, \tilde{y}_m]$, $\tilde{z} = [\tilde{z}_1, \tilde{z}_2, \dots, \tilde{z}_m]$ be the frequency coordinates.

The frequency domain vertices can be computed using the manifold harmonic transform

$$\tilde{x} = xDH, \quad (2.3)$$

where D is a lumped mass matrix which depends on triangle areas within the mesh. Similar expressions hold for $\tilde{y}, \tilde{z}$.

The mesh may be reconstructed from the frequency domain vertices by

$$x = \tilde{x}H', \quad (2.4)$$

and similar expressions can be written for y, z .

Spatial frequencies, ω_i , of the basis functions are related to the eigenvalues, λ_i , associated with each eigenvector by $\omega_i = \sqrt{\lambda_i}$. Plots of several MHB functions for a horse mesh are

shown in Figure 2.6.

A frequency-space filter can be implemented by multiplying the frequency coordinates with filter weights, f during reconstruction

$$x = \tilde{x}FH', \quad (2.5)$$

where F is a diagonal matrix whose entries are given by f . The filtering achieved by this process is similar to filtering spatial or time domain signals using the Fourier transform: low pass filtering can be implemented by attenuating the coefficients of high frequency basis functions. Details may be enhanced by boosting the same coefficients. When filter coefficients are all equal, $f = [a, a, \dots, a]$ the filter performs an isometric scaling by factor a .

Allometric mesh scaling is performed in terms of these filter coefficients by giving anatomical and functional meaning to certain combinations of coefficients. Usually, directly manipulating filter coefficients is not an intuitive way to edit a mesh. In general terms f_i controls low-frequency shape when λ_i is low, and high frequency detail when λ_i is high, but it is difficult to achieve desirable results when manually changing these coefficients. Mesh editing in terms of these filter coefficients has potential to be a powerful tool if they can be controlled in a meaningful way. For example, Rong et al. [74] performed mesh deformation in terms of manifold harmonics, but the deformations described were changes in pose, not shape. My work will connect biological and physiological function to mesh shape through these filter coefficients.

(a) 2

(b) 3

(c) 20

(d) 100

(e) 500

(f) 1000

Figure 2.6: Selected manifold harmonic basis functions computed for the horse mesh. The number below each figure indicates the index of the eigenfunction.

2.6 Nonlocal image processing

The nonlocal mesh editing presented in this study is inspired by some of the notions in nonlocal image processing. Nonlocal image denoising was introduced by Buades et al. [11] in 2005. Many previous approaches to image denoising were based on local processing (such as local averaging). Nonlocal methods are based on the observation that due to texture and repetition, there may be nonlocal redundancy in an image which can be exploited for denoising. The idea was extended to denoising of video sequences [12], and also applied to other image processing problems, such as image demosaicing [13]. Nonlocal redundancy can be used as a regularizer for inverse problems, such as super-resolution [66] which has commonly used local smoothness as a standard constraint.

Searching over the entire image domain for similar regions can make these algorithms slow. Much recent work has focused on improving the efficiency of nonlocal methods. One approach is to restrict the search to large neighborhoods rather than the entire image. Nonlocal approaches to image processing address the redundant nature of many natural images due to periodicity and symmetry. This redundancy occurs, for example, when the texture of a wall contains many similar bricks, or two eyes are visible on the same face. The drawback of these methods is the search time required to find similar regions. The classical image processing assumption of smoothness is a local property, and may be assessed using differential operators or local neighborhood searches. Nonlocal methods typically involve searches for similarity over the entire image domain, and typically show improved results over local methods at the expense of speed.

Many meshes also have the property of nonlocal self-similarity. The structure of many living creatures is characterized by bilateral (left-right) symmetry. There is geometric

similarity between pairs of arms, legs, and facial features. Many non-living objects are also characterized by repetition: a car may have multiple wheels, a building may have periodic architectural details, such as windows and doors.

In Chapter 4 I propose to simplify mesh editing by identifying such redundancies and automatically propagating mesh editing operations on one structure to other similar structures. Similarity of mesh regions is quantified and quickly identified by using a region spectrum determined from a frequency domain decomposition of the mesh.

2.7 Mesh skeleton generation

Early work was done by Bloomenthal and Lim [7] to apply skeleton generation to computer animation. They derived the geometric skeleton from a static object using an implicit 'directions' method. An IK (Inverse Kinematics) skeleton (or bone) is derived from and used to manipulate the geometric skeleton. The model may be reconstructed from the modified skeleton using implicit distance and convolution methods. Katz and Tal [44] proposed a hierarchical mesh decomposition algorithm. It computes a decomposition into the meaningful components of a given mesh, which generally refers to segmentation at regions of deep concavities. The algorithm also avoids over-segmentation and jaggy boundaries between the components.

Liu et al. [53] proposed a method to construct a skeleton by finding skeleton joints, connecting the joints to form an animation skeleton, and binding skin vertices to the skeleton. Initially, a repulsive force field is constructed inside a given model, and a set of points with local minimal force magnitude are found based on the force field. Then, a modified thinning algorithm is applied to generate an initial skeleton, which is

further refined to become the final result. Dey and Sun [21] proposed a function called medial geodesic on the medial axis which leads to a mathematical definition and an approximation algorithm for curve-skeletons. Empirical study shows that the algorithm is robust against noise, operates well with a single user parameter, and produces curve-skeletons with the desirable properties. Lien et al. [51] proposed an iterative approach that simultaneously generates a hierarchical shape decomposition and a corresponding set of multi-resolution skeletons. In their method, a skeleton of a model is extracted from the components of its decomposition - that is, both processes and the qualities of their results are interdependent. In particular, if the quality of the extracted skeleton does not meet some user specified criteria, then the model is decomposed into finer components and a new skeleton is extracted from these components. The process of simultaneous shape decomposition and skeletonization iterates until the quality of the skeleton becomes satisfactory. Lien et al. [97] presented two solutions for skeletonization, one general and one specific. The general solution involves several steps including discretizing the figure, approximating its medial surface, and using that surface to construct a control skeleton. The specific solution builds upon the general one but is geared toward producing more desirable skeletons for the very common case involving human-like and animal-like figures. Certain assumptions are made about the figure and about the type of control skeleton desired. In addition, heuristics based upon human and animal anatomy are invoked to adjust the control skeleton so that it is more anatomically appropriate. Cornea et al. [19] introduced the concept of hierarchical curve-skeletons and describe a general and robust methodology that computes a family of increasingly detailed curve-skeletons. The algorithm is based upon computing a repulsive force field over a discretization of the 3D object and using topological characteristics of the resulting vector field, such as critical

points and critical curves, to extract the curve-skeleton. Shinagawa et al. [78] proposed a method to interpret 3D objects' cross sections and encode 3D surfaces based on an extended Morse theory. Their method can encode objects that have branches, handles, and internal structures with multilayered surfaces.

In Chapter 5 an overview of my skeleton generation algorithm will be described. The advantages of this method is that it makes extensive use of the manifold harmonic basis that has been computed in previous computational stages in allometric scaling. It utilizes the Fiedler vector to compute a reasonable Reeb graph of the mesh. This leads to generating natural skeletons since the transition of the Fiedler vector values tends to follow naturally over the entire mesh. The proposed algorithm also performs *symmetrization* that detects existing symmetry using a structural similarity detection algorithm similar to the one in the nonlocal mesh editing. Finally, the algorithm also allows to compute bone weights using the projection of indicator vectors onto manifold harmonic basis, eliminating the need for solving the heat equation that is used in conventional bone weight computation methods.

Chapter 3

Mesh deformation with allometric scaling laws

3.1 Implementation

The manifold harmonic decomposition was implemented as described by Vallet and Lévy [92, 93] and applied it to mesh data from public mesh repositories. Results for a horse mesh (58485 vertices, 96966 faces) are shown in this section.

A plot of the absolute value of manifold harmonic coefficients for the horse mesh is shown in Figure 4.1. The coefficients roughly obey a power law with respect to eigenvalue, and therefore also frequency. This behavior is observed over all of the input meshes used in this study and the similarity with natural images is found which are also characterized by power law spectra. Qualitatively, this behavior is also apparent in Figure 3.2 which shows a mesh reconstructed from various numbers of basis functions. Using only the 20 lowest frequency basis functions the quadrupedal structure of the character is apparent, and much of the volume of the torso is filled. As the number of basis functions increases, progressively finer details are added.

Figure 3.1: Absolute value of manifold harmonic coefficients plotted on a semilog scale. Red, green, and blue crosses are $\tilde{x}$, $\tilde{y}$, and $\tilde{z}$ coordinate coefficients respectively. The black line shown for reference is the power law $1/\lambda^{1.25}$.

Figure 3.2: *Horse reconstructed from varying numbers of manifold harmonic basis functions. Low frequency components describe the shape of the horse, and high frequency components represent detail.*

Some known allometric relations involve global geometric properties of the body, such as volume, surface area or length. Other relations are specific to anatomical regions. To accommodate both types of relations I present separate global and local allometric scaling techniques in the following sections. In both algorithms I presume that the input mesh is plausible, and generate new meshes which are also plausible.

3.1.1 Global allometric scaling

Figure 3.4 shows the global allometric scaling algorithm described in this section. The global allometric scaling is determined by one parameter, and only biomechanical considerations are taken into account. The overall algorithm works as follows: Given an input mesh, the manifold harmonic basis is computed. The manifold harmonic transform is performed to produce the manifold harmonic coefficients by projecting the spatial vertex coordinates onto the manifold harmonic basis. The Fiedler vector is passed to the skeleton computation and cross-sectional area computation module. The cross sectional area of one of limbs is used to control the allometric scaling law. This allometric scaling law controls the amplitude of the manifold harmonic coefficients. Finally, the inverse manifold harmonic transform is applied to the scaled manifold harmonic coefficients to produce the final output mesh.

Biewener [6] reports that “mammalian skeletons experience peak locomotor stresses (force per area) that are 25 to 50% of their failure strength, indicating a safety factor of between two and four.” This provides valuable information about how the biomechanics of terrestrial locomotion influence the size of the limbs. In particular it places bounds on the cross-sectional area of the limbs.

Figure 3.3: *Isocontours of the second manifold harmonic basis function (left) and mesh skeleton computed from centroids of isocontours (right). The isocontours provide us with a measure of local cross-sectional area, and the skeleton allows us to estimate bone lengths.*

Figure 3.4: Block diagram of global allometric scaling algorithm.

Furthermore, forces generated during motion are generally proportional to body weight, and the highest forces experienced are usually impact forces due to falling or jumping. These can be 5 to 10 times body weight. By comparison, running may result in forces approximately 2 to 3 times body weight. Rather than requiring the user to estimate safety factors, I assume that the safety factor in the scaled mesh will be equally to the safety factor in the original mesh. However, it would be trivial to incorporate variable safety factors, or activity levels into the proposed system.

Since shear stresses, τ , and compressive stresses, σ , are both given by F/A where F is the applied force and A is the cross-sectional area one can see that increased forces due to higher body weight can be mitigated by increased cross-sectional area. Bending stresses are more complicated since they depend on the cross-sectional shape (through the area moment of inertia). However, the stress can be reduced by decreasing the bending moment. This can be achieved by shortening the limb or decreasing the applied force. It can also be achieved by increasing the area moment of inertia, which I do not explicitly address.

To estimate the body mass of a character I assume a constant material density, ρ , and then compute mass from the volume, $M = \rho V$. I use the method described by Mirtich [59] for computing the volume of triangle meshes. Since the scaling calculations are done in terms of ratios the algorithm does not require the user to input a value for ρ , and weight, mass, and volume can be considered to be equivalent.

To estimate cross-sectional area I again make use of the manifold harmonic decomposition. In particular the Fiedler vector is used. The Fiedler vector and corresponding eigenvalue figure prominently in spectral graph partitioning and the study of graph topology. The

property of the Fiedler vector that makes it so useful for segmentation problems is that nearby vertices have similar values in the Fiedler vector. This implies that isocontours of the Fiedler vector should form short closed paths on the mesh. Critical points, where the isocontour length becomes zero, occur at mesh extremities. These properties make the area of the isocontours useful for characterizing peak stresses in the mesh. From these contours I also compute the mesh skeleton which I make use of in the next section. The centroid of each contour is a point on the skeleton of the mesh. The isocontours of the Fiedler vector are shown in Figure 3.3 along with the computed skeleton. Additional skeleton results are shown in Figure 3.5. The skeleton computed in this study is a geometric medial axis rather than a true approximation of the anatomical skeleton. Therefore, for example, the skeleton lacks features such as a skull and ribs. However, it is useful for approximating lengths.

The relationships between allometry, fractal systems and frequency domain power laws motivate the implementation of allometric scaling in terms of manifold harmonic coefficients. Consider the function

$$\tilde{x}'_i(s, \alpha) = s \tilde{x}_i \lambda_i^\alpha. \quad (3.1)$$

After applying this transformation to the coefficients they still obey a power law, but with a different exponent, so the underlying mesh still falls within the class of 'natural meshes'. The expected results of this function can be explained in terms of Figure 3.2. Note that the reconstruction using a few basis function reveals the skeletal shape and the torso. As higher frequencies are added the neck and then legs appear. High spatial frequencies correlate with small cross-sectional area. When $\alpha > 0$ the coefficients corresponding to small area shrink faster than those corresponding to high area. The expectation is that the limbs in these meshes will become thinner compared to the torso, for example.

Figure 3.5: *Skeleton results for several quadrupedal mammals.*

This corresponds to scale reduction in that the smaller creature can be supported by relatively thin legs. For $\alpha < 0$ the situation is reversed, and for $\alpha = 0$ the scaling is isometric.

Not all of the cross-sectional areas computed from isocontours are load-bearing, for example, it is not expected that the ears or tail of an animal supports the full body weight. With this in mind I pick an isocontour with small cross-section in one of the limbs to characterize the peak stresses expected in the character. Then the peak stresses in the original mesh $\sigma_0 = M_0/A_0$. After scaling with isometric factor, s and allometric factor, α , one wants the peak stresses to be equal, $\sigma_1(s, \alpha) = \sigma_0$. Since isometric scaling affects stress in a linear manner $\sigma_1(s, 0) = \frac{s^3 V_0}{s^2 A_0} = s\sigma_0$, the isometric scale factor can be computed as $s = \sigma_1(1, \alpha)/\sigma_0$ given α .

The global allometric scaling results in Figure 3.6 and 3.7 do demonstrate the nonuniform scaling as one would expect when trying to compensate for the square-cube law. The bone becomes proportionally thicker as it becomes larger, as predicted by Galileo in the sketch in Figure 2.2. The smaller chair can be supported by longer, thinner legs, and the larger chair has thicker, and proportionally shorter legs to support a higher weight. These results also demonstrate the generality of the scaling method with respect to topological genus.

Figure 3.6: *Original bone (left), allometrically scaled bone (middle), isometrically scale bone (right). The proportions have changed in a way similar to the prediction of Galileo.*

Figure 3.7: *Original chair (middle), and allometrically scaled chair (left, right). Note that the scaling is effective when the topological genus is greater than 0.*

3.1.2 Local allometric scaling

Figure 3.8 shows the block diagram of the local allometric scaling algorithm. Like in the global allometric scaling algorithm presented in Section 3.1.1, the MHB is computed for the input mesh and the Fiedler vector is passed to the skeleton computation and then the cross-sectional area and length are computed. The significant difference from the global allometric scaling algorithm is that the local allometric scaling algorithm performs segmentation of the input mesh into multiple anatomical regions and applies different scaling laws to each region. The set of MHBs is passed to the spectral clustering module to perform the clustering. For each anatomical region the MHT is individually performed and the corresponding set of coefficients are obtained. Each set of coefficients is modified by allometric scaling laws associated with the respective anatomical regions. The variation of the size of each anatomical region is associated with the body weight. This allows the allometric scaling laws to be controlled ultimately only by one parameter.

As mentioned above, local scaling requires a segmentation of the mesh which defines the local regions. I developed a user-assisted technique based on the method presented by Zhang and Liu [54]. An automatic segmentation into 24 regions is first performed, then the user merges selected regions to obtain the 6 desired regions: head, neck, upper torso, lower torso, forelimbs, and hindlimbs. For each segmented region I apply power-law scaling on only the coefficients of basis functions which contribute most to the segmented region. Thus, the mesh is manipulated in the frequency domain rather than in spatial domain. The continuity at the boundaries between the segmented regions is naturally preserved. Therefore an exact segmentation is not needed.

From the segmentation one can obtain an indicator function for each region, I_{seg} such

Figure 3.8: Block diagram of local allometric scaling algorithm.

that $I_{seg}(x_i) = 1$ when vertex x_i is part of the specified region, and $I_{seg}(x_i) = 0$ otherwise. Then the vertex set $x_{seg} = I_{seg}x$ is defined.

The MHT of the segmented vertex set is performed in terms of basis functions, H , and lumped-mass matrix, D , of the original mesh

$$\tilde{x}_{seg} = x_{seg}DH. \quad (3.2)$$

The proposed approach to local allometric scaling is to perform power-law scaling on only the coefficients of basis functions which contribute most to the segmented vertex set. Since the basis functions are global it is not possible to guarantee that this transformation will only change vertices in the segmented set, but I aim to minimize the distortions in other areas.

In formulating local allometric scaling I make use of the fact that if $|\tilde{x}|$ has power law form then $|\tilde{x}|^{1+\alpha}$ also has a power law form with similar exponent when α is small. The transformation of frequency coordinates is given by

$$\tilde{x}'_i = \text{sgn}(\tilde{x}_i)|\tilde{x}_i|^{1+\alpha G(\tilde{x}_i, \tilde{x}_{seg,i})}, \quad (3.3)$$

where G is the geometric mean defined as

$$G(a, b) = \begin{cases} \sqrt{ab} & \text{if } ab > 0 \\ 0 & \text{otherwise.} \end{cases} \quad (3.4)$$

The transformation in Equation 3.3 preserves the sign of the frequency coordinates, which prevents spurious reflections from occurring, and also avoids the generation of complex coordinates. The geometric mean of two numbers tends to be close to the lower number, which makes it useful for isolating the coefficients which contribute most to the segmented region. When $\tilde{x}_i$ and $\tilde{x}_{seg,i}$ are large, the geometric mean will be large, but when either of

the coefficients (or both coefficients) are small the geometric mean is small. The geometric mean of two numbers is always less than or equal to the arithmetic mean of two numbers. Therefore, when a coefficient contributes very little to segmented region the exponent computed by Equation 3.3 will be close to one. The more a coefficient contributes to the region, the more the exponent may differ from the value one.

The naive approach, arithmetically scaling the coefficients of the vertex set, has predictably bad results as shown in Figure 3.10. That is because this method is equivalent to simply scaling the segmented vertex set, which leads to discontinuities at the segmentation boundary. The approach to local allometric scaling proposed in this study does not suffer from this consequence. Simply following arithmetic scaling with low-pass filter would also be unsatisfactory since some of the desired high frequency detail would be blurred as well.

The local allometric scaling is a useful mesh editing tool by itself since it gives anatomical meaning to combinations of frequency coordinates for a mesh. I extend this idea even further by using allometric laws to connect relative rates of change of different regions to obtain biologically plausible results.

Results of local allometric scaling are shown in Figure 3.11. In this case local anatomical changes were made by explicitly specifying values of α_j in Equation 3.3. As expected, the scaling results in minor changes in pose and other non-local deformations, but no discontinuities are observed.

Figure 3.9: *Mesh segmentation used for local allometric scaling. The various regions will be allometrically scaled independently.*

Figure 3.10: *Local allometric scaling of the torso of the horse mesh. Arithmetic manipulation of the spectrum results in discontinuities (left). Power-law manipulation of the spectrum gives a smoother result (right).*

Figure 3.11: Local allometric scaling permits specific anatomical regions to be targeted for scaling. Top row: Torso smaller (left) and larger (right), Center row: legs shorter (left) longer (right), Bottom row: neck shorter (left) and longer (right).

3.1.3 Biology-aware allometric scaling

Prothero [67] tabulated allometric relations between different local variables for many species. The variables included length and diameter of forelimbs, hindlimbs and torso as a means of describing a simplified model composed of cylinders. I draw on this work, but segment the mesh further. I decompose the torso into chest and abdominal segments, and also add head and neck segments.

The abdominal region contains organs vital to the digestive system - small and large intestines, and so its shape is controlled by metabolic parameters. Prothero presents the relation $M_{ab} \propto M_{body}^{0.74}$. This is thought to be a direct consequence of Kleiber's law relating metabolic rate to body mass with an exponent of 0.75.

There is no general relation between head size and body mass which holds over a large number of species. For the families in which allometric relations have been observed the relation is negative, such as the relation in primates $M_{brain} \propto M_{body}^{0.78}$. Also, within a single species there is a negative allometry associated with maturation $M_{brain} \propto M_{body}^{0.70}$.

The anatomical measurements and the allometric relations I use in the biology-aware scaling algorithm are

$$\begin{aligned}
 (\text{foreleg length}) \ L_{fl} &\propto M_{body}^{0.360} \\
 (\text{hindleg length}) \ L_{hl} &\propto M_{body}^{0.336} \\
 (\text{chest girth}) \ G_{chest} &\propto M_{body}^{0.365} \\
 (\text{head mass}) \ M_{head} &\propto M_{body}^{0.700} \\
 (\text{abdominal mass}) \ M_{ab} &\propto M_{body}^{0.740} .
 \end{aligned} \tag{3.5}$$

The segment I have not addressed yet is the neck. Like the head, no general observations are found, except among creatures characterized by exceedingly long necks. Animals such as the giraffe and flamingo with very long necks must have high blood pressures in order to push blood up to the brain. I provide the user with a control for separately controlling this attributes.

I perform scaling which takes all of the above relations into account using the following extension of Equation 3.3

$$\tilde{x}'_i(s, \alpha) = s \operatorname{sgn}(\tilde{x}_i) |\tilde{x}_i|^{1+\alpha_0+\sum_{j=1}^6 \alpha_j G(\tilde{x}_i, \tilde{x}_{j,i})}, \quad (3.6)$$

where α_0 is the global allometric scale, and j indexes the 6 segmented regions. As in the global scaling case, I compute the isometric scale factor, s , which will make the mesh biomechanically plausible.

I use an energy minimization approach to perform local allometric scaling subject to the constraints in Equation 3.5. To limit the amount of mesh deformation performed, I set a target mass $M_{body,1} = 1.1M_{body,0}$ when scaling up, and $M_{body,1} = 0.9M_{body,0}$ when scaling down, where $M_{body,0}$ is the initial volume of the mesh. Given this target mass, target values can be set for the variables on the left-hand side of Equation 3.5,

$$\begin{aligned} L_{fl,1} &= r^{0.360} L_{fl,0} \\ L_{hl,1} &= r^{0.336} L_{hl,0} \\ G_{chest,1} &= r^{0.365} G_{chest,0} \\ M_{head,1} &= r^{0.700} M_{head,0} \\ M_{ab,1} &= r^{0.740} M_{ab,0}, \end{aligned} \quad (3.7)$$

where r is the ratio of target mass to initial mass $M_{body,1}/M_{body,0}$, which is 1.1 or 0.9 in

the presented experiments. Larger or smaller mass ratios can be achieved by repeated applications of the optimization procedure with recomputation of the MHB and MHT between iterations. The energy to be minimized is given by

$$\begin{aligned}
 E(\tilde{x}') = & (M_{body}(\tilde{x}') - M_{body,1})^2 + (L_{fl}(\tilde{x}') - L_{fl,1})^2 + \dots \\
 & (L_{hl}(\tilde{x}') - L_{hl,1})^2 + (G_{chest}(\tilde{x}') - G_{chest,1})^2 + \dots \\
 & (M_{head}(\tilde{x}') - M_{head,1})^2 + (M_{ab}(\tilde{x}') - M_{ab,1})^2 + \dots \\
 & (\sigma(\tilde{x}') - \sigma_1)^2,
 \end{aligned} \tag{3.8}$$

where σ is the biomechanical stress described in Section 3.1.1.

I find the values of $s, \{\alpha\}$ which minimize Equation 3.8 using a nonlinear least-squares solver [61] based on the trust-region Newton-CG method. In practice it is not necessary to find the exact minimizer of the energy function since allometric relations describe general trends observed over large samples sizes. Natural anatomic variation allows for some variance in individual measurements. When $E(\tilde{x}')$ falls to 10% of its initial value the optimization is halted whether or not convergence has occurred.

3.2 Results

12 triangle meshes representing quadrupedal terrestrial animals were processed. The meshes were preprocessed to remove unreferenced vertices and non-manifold faces, then simplified to contain fewer than 100,000 vertices. The simplification process reduces the memory requirements for storing the MHB which may not fit into main memory for large meshes. The MHB and MHT of each mesh were computed, then a skeleton was automatically extracted and a user-assisted segmentation was produced. The data were

processed on desktop computer with Intel Quad Core QX6700 2.66 GHz CPU and 4 GB RAM.

3.2.1 Global allometric scaling

Global allometric scaling applied to the horse mesh is shown in Figure 3.13 along with images of actual horse breeds for reference. Horse breeds vary over a wide range of scales, which leads to much variation in shape. In Figure 3.13 the Breton corresponds to the large scale and the miniature stallion the small scale. Since there are many feasible horse shapes I do not expect an exact match, but there are many similarities between the meshes and the photographs. The Breton is a large draft horse characterized by stocky, powerful legs, a short neck, and a wide chest. The corresponding mesh has matching characteristics, however the length of the torso of the actual horse is longer. The miniature stallion in the reference photo has spindly legs, a narrow torso and a long thin neck, much like the corresponding mesh.

3.2.2 Local allometric scaling

Figures 3.15 and 3.16 show the local allometric scaling of a horse mesh and a pig mesh, respectively. In each figure, two parameters are manually varied: the row corresponds to the leg length and the column corresponds to the torso size. Based on the original input mesh (located at the center of the figure) it can be seen that the meshes are plausibly deformed according to the controlling parameters.

3.2.3 Biology-aware allometric scaling

Additional results for global allometric scaling are shown in Figure 3.14 for camel, pig, elephant, cow, and giraffe meshes. The anatomical features scale in the same way as the horse mesh - the enlarged creatures tend to have shorter and thicker body parts and the shrunken meshes are longer and thinner. When performing large deformations, as in Figure 3.12, the transformed spectrum of the input mesh may not correspond to the spectrum of resulting mesh. This is because the new mesh does not necessarily have the same manifold harmonic basis as the input mesh. For this reason, large scale changes are performed iteratively - applying a small scale change, recomputing the MHB and repeating, as in the biology-aware allometric scaling shown in Figures 3.17 and 3.18.

The allometric scaling process I have described does not perform any collision detection, and so some self-intersections may be generated. This can be seen in the tail of the cow in Figure 3.14. Another visible artifact is high frequency rippling, as seen in Figures 3.6 and 3.7, and smoothing of some fine details. Some sharp corners and points degenerate into line-like features, such as the tail of the elephant, and the horns of the cow. These issues have been mitigated in the character mesh results by a combination of low-pass filtering of the input to the scaling algorithm, and detail enhancement of the output [93].

Figure 3.12: *Allometric scaling of a horse mesh. The original mesh is in the middle, and it has been scaled larger and smaller such that biomechanical constraints are satisfied.*

Figure 3.13: Visual comparison of global allometric scaling results (left) and photographs of horse breeds (right).

Figure 3.14: Global allometric scaling results. Allometric minification with $\alpha = +0.1$ (left), the input mesh (middle) and allometric magnification with $\alpha = -0.1$ (right) for several meshes.

Figure 3.15: *Local allometric scaling of a horse mesh. The original mesh is in the center. The torso grows larger/smaller to the left/right. The legs grow longer/shorter to top/bottom.*

Figure 3.16: *Local allometric scaling of a pig mesh. The original mesh is in the center. The torso grows larger/smaller to the left/right. The legs grow longer/shorter to top/bottom.*

Figure 3.17: *Biology-aware allometric scaling results. Relative scales of anatomical regions have been linked to make the scaling match observed allometric relations which are governed by biological function. The overall scale of each mesh has been normalized in this figure.*

Figure 3.18: *Biology-aware allometric scaling results. Relative scales of anatomical regions have been linked to make the scaling match observed allometric relations which are governed by biological function. The overall scale of each mesh has been normalized in this figure.*

Chapter 4

Nonlocal mesh editing based on spectral methods

4.1 Implementation

Spectral methods have been useful in many area of mesh processing, including segmentation [54] and deformation [74]. The mesh spectrum has previously been applied to matching and correspondence problems [72, 36]. In contrast to earlier work, I am not considering the problem of comparing multiple meshes, but comparing different parts of the same mesh. This permits us to quickly compute an approximation of the spectrum, as I will demonstrate.

I utilize the MHT to estimate the frequency spectrum for the region being edited. The spectrum has several properties which make it efficient for region comparison:

- **Location invariance:** The spectrum is unchanged by translating the region.
- **Rotation invariance:** The spectrum is unchanged by changing the orientation of the region. This is important because similar regions may be rotated due to the

pose of the mesh.

- Can be made **scale invariant** : It is not addressed in this work, but the matching can be made scale invariant by normalization of the spectra.
- **Conciseness**: A spectrum of 1000 coefficients is sufficient to represent most meshes for reconstruction purposes. However, by smoothing and subsampling the spectrum we can represent each region with a few hundred scalar values for matching applications.

Regions with similar spectra are candidates for more accurate matching using mesh registration. This step yields an error metric and a transformation matrix which can be used to propagate mesh edits.

My mesh editing framework consists of the following steps:

- Compute the MHT for the entire mesh (precomputed offline)
- Select region of interest (ROI)
- Estimate the spectrum for the ROI
- Estimate the spectrum for all other regions
- Perform mesh registration on regions whose spectra match. This step yields a set of target regions, and transformation matrices.
- Transform editing operations from the ROI to all target regions.

In order to perform matching using the local spectra it is necessary to compute the MHB for the entire mesh. This involves computing the mesh Laplacian matrix, and the eigenvalue decomposition of this matrix. This computation can be performed once and

stored in a file rather than recomputing it for every editing operation. See Vallet and Lévy [92] for more details about the numerical methods.

4.1.1 Local spectrum estimation

The key to the proposed fast approach to local spectrum estimation is to not compute the MHT for the region around each vertex, but to reuse the global mesh harmonic basis functions to estimate the local MHT. Since the MHT involves computing eigenvalues of a large matrix, this approximation saves much computation time.

The local spectrum is estimated by restricting the basis functions to the selected region, R , by $G = H_j^k$ for $k \in [0, k_{max}]$ and $j \in R$. Let E denote a similar restriction of D that appears in Equation 3.2. Then the approximate MHT of the vertices in R , x_R , is given by

$$\tilde{x}_R = x_R E G. \quad (4.1)$$

Similar expressions hold for the y and z coordinates.

A rotationally invariant spectrum is obtained by combining the frequency domain coefficients

$$\tilde{r} = \sqrt{\tilde{x}_R^2 + \tilde{y}_R^2 + \tilde{z}_R^2}. \quad (4.2)$$

A plot of the rotationally invariant spectrum of the horse mesh is shown in Figure 4.1. The coefficients tend to decay exponentially with increasing frequency.

Figure 4.1: Rotationally invariant spectrum $\tilde{r} = \sqrt{\tilde{x}^2 + \tilde{y}^2 + \tilde{z}^2}$ computed for the horse mesh and plotted on a semilog scale against eigenvalue, λ .

4.1.2 Defining regions

I define mesh regions as sets of vertices within a threshold geodesic distance from a selected center point. Given the center point I use the fast marching method [45] to find all of the vertices belonging to the region of interest. It may not be the case that all of the vertices in the ROI will be edited, but defining the regions in this way allows the algorithm to exploit the rotation invariance of the region spectrum.

4.1.3 Spectrum similarity metric

There has been much previous work on matching frequency domain spectra in application areas such as content-based audio retrieval and image analysis. Some common spectrum similarity measures are based on L_1 (Manhattan) and L_2 (Euclidean) distances [17], cross correlation [95], and information theoretic approaches [14]. After experimenting with these approaches I determined that the most robust region matching was obtained with a combination of the Euclidean distance and cross correlation. Our measure, $d(a, b)$ is given by

$$\begin{aligned} d_E(a, b) &= \sqrt{\sum_{i=1}^n (a_i - b_i)^2} \\ d_{cc}(a, b) &= \frac{\sum_{i=1}^n (a_i - \bar{a})(b_i - \bar{b})}{(n-1)s_a s_b} \\ d(a, b) &= d_E(a, b) - d_{cc}(a, b), \end{aligned} \tag{4.3}$$

where $\bar{a}$ is the mean of spectrum a , and s_a is the sample standard deviation of a .

Plots of the spectral similarity given several meshes and selected vertex sets are shown in Figure 4.2. Darker colors indicate a better match. Note that the selected left ear of the

Figure 4.2: Matching function for 3 different meshes. The ROI vertices are marked with '+'. Darker colors indicate better match.

bunny matches the right ear, the selected finger of the hand matches the other 4 fingers, and the selected foot of the horse matches the other 3 feet. Also note that the matching function changes slowly. For large meshes the matching function is sparsely sampled over the mesh, then local maxima is found using hill-climbing. Then the local maxima is clustered using the mean-shift algorithm [18], and the vertex with best matching of the matching function in each cluster is taken as the center point of a target region. The results of clustering and center point determination are shown in Figure 4.3. The axes drawn in each region have their origin at the center point, and the axis directions correspond to the coordinate transformation determined by the mesh registration procedure described in the following section.

The hand and bunny results demonstrate the rotation invariance of the proposed spectral matching technique. Even though the fingers of the hand and the ears of the rabbit have different orientations we can still detect matches in these regions.

4.1.4 Mesh registration

It is known that meshes may be *cospectral* (i.e. share the same frequency spectrum) but not be identical [39, 29, 28, 94]. Due to this fact we must perform a geometrical comparison between regions whose spectra are similar. The iterative closest point (ICP) algorithm [5] is a method for mesh registration which minimizes an error metric. The error metric has value zero when two meshes are perfectly aligned. The ICP algorithm also yields a transformation matrix which allows us to transform coordinates from one region to another. I use a variant of ICP called *stochastic ICP* since it is less likely to become stuck in local minima of the energy functional during optimization. Mesh registration

(a) Clustering results

(b) Registration results

Figure 4.3: *Clustering of the matching function (top) reveals 4 regions of similarity. After ICP registration of the ROI with these 4 regions the bilateral symmetry of the mesh is revealed in the plots of the coordinate frames of each region.*

results are shown in Figure 4.3.

4.1.5 Propagating editing operations

Similar regions of the mesh may not be triangulated in the same way, so propagating changes in vertex location is problematic. One solution is to parameterize [26] the source and target regions to same domain. Then the target region may be retriangulated, or the vertex deformation may be interpolated.

In my experiments Laplacian mesh editing [79] is used to apply translations, rotations and scaling transformations to group of vertices with no need for exact vertex correspondence. Similar mesh editing techniques, such as differential coordinates [52] and Poisson mesh editing [100], would also work well in this framework.

4.2 Results

The proposed algorithm was applied to the horse, hand, and bunny meshes, and the resulting images are shown in Figures 4.4 and 4.5. The initial user-selected ROI is shown with a '+' at each vertex. The matching target regions are shown in white in the left column. The repeated hooves of the horse, fingers of the hand, and ears of the bunny were all successfully located. The right column of images shows the results after editing operations on the ROI have been propagated to all target regions.

In all cases the presented method was able to detect all relevant matches and accurately propagate the vertex displacements from the ROI to the target regions.

Figure 4.4: *Original meshes with ROI vertices plotted with '+', and automatically detected target regions in white (left). Results after ROI deformations have been automatically propagated to all target regions (right).*

Figure 4.5: *Original meshes with ROI vertices plotted with '+', and automatically detected target regions in white (left). Results after ROI deformations have been automatically propagated to all target regions (right).*

Chapter 5

Mesh skeleton generation based on spectral methods

In this chapter an overview of a novel skeleton generation algorithm and its preliminary results are presented. The purpose of this chapter is to show an algorithmic sketch of the method and its details are beyond the scope of this work.

5.1 Implementation

The advantage of the proposed method is that it makes extensive use of the manifold harmonic basis: the use of the Fiedler vector as an input for Reeb graph [70] computation, detecting similar parts in the mesh, and computing bone weights. The algorithm consists of the following steps:

- Computing the MHB
- Computing the Reeb graph
- Filtering the Reeb graph

- Embedding the Reeb graph nodes to Fiedler isocontour centers
- Symmetrization
- Computing the bone weights
- Selecting the root node

Computing the MHB Given an input triangle mesh, its manifold harmonic basis is computed. The Fiedler vector is computed as the basis (or eigenfunction) that corresponds to the smallest nonzero eigenvalue.

Computing the Reeb graph The Reeb graph is a fundamental data structure that encodes the topology of a shape. Using the vertices and faces of the input mesh and the Fiedler vector computed in the first step, the Reeb graph for the mesh is computed using the method by Pascucci, et al. [64].

Filtering the Reeb graph The generated Reeb graph is usually noisy and needs to be cleaned up. The graph filtering process eliminates those unwanted parts of the graph such as small branches and consolidates redundant nodes. This is done by the process of edge merge and edge collapse. The edge merge process merges two nodes that have a similar Fiedler vector value into one. The edge collapse process consolidates two nodes around a saddle point into one.

Embedding Reeb graph nodes to Fiedler isocontour centers In order to give the Reeb graph nodes the desired 3D vertex coordinates, the resulting Reeb graph is

embedded to the centroids of isocontours of the Fiedler vector.

Symmetrization The symmetrization process detects similar parts in the mesh using the similarity detection algorithm presented in Chapter 4. For example, in the horse mesh case, based on the shape of one of the legs other three legs are identified as its similar parts by the algorithm. After detecting the similar parts in the mesh the nodes in the Reeb graph associated with one of the mesh part are replicated into the corresponding parts of the Reeb graph associated with the other similar parts.

Computing the bone weights Once the skeleton (or bone) has been created, for each bone, the enclosing mesh vertices are identified and appropriate bone weights are assigned for each vertex in the mesh. The bone weights control which vertices in the mesh should be controlled by which bone. Typically 1 is assigned to all the enclosing vertices for the specific bone and decreasing weights are assigned to the vertices nearby the joints, and 0 to the vertices of all the other parts. The bone weights are interpolated at joints where multiple bone segments meet.

In my method, the bone weights are computed as follows:

- Setup the indicator vector (function) defined over the mesh vertices. The indicator vector is set to 1 for the enclosing mesh vertices for the bone under processing, 0 for all the other vertices.
- Apply the manifold harmonic transform to the indicator vector. That is, compute the projection of the indicator function onto the precomputed manifold harmonic basis. This produces the frequency spectrum of the indicator function.

- Apply low-pass filtering to the spectrum and apply the inverse manifold harmonic transform to create the final bone weights. The resulting bone weights are naturally smoothed out at the joint locations.

In a conventional bone weight assignment method, the heat equation is solved to compute the bone weights. My method is based on the projection of the indicator function onto the precomputed manifold harmonic basis. Therefore solving the heat equation is not required.

Selecting the root node Lastly, selecting the “root” node may be performed. This includes identifying which node in the Reeb graph corresponds to the head, and so on.

5.2 Results

Figure 5.1 shows the generated mesh skeleton for the horse mesh using the proposed method. It does not have redundant nodes and is a reasonable skeletal representation of the original mesh. Figure 5.2 shows the bone weights for one of the bones in the left hind leg computed by the presented method. The transition at the joints is naturally made by the low-pass filtering.

Figure 5.1: *Skeleton generation result.*

Figure 5.2: *Bone weights result.*

Chapter 6

Conclusions and Future Work

6.1 Mesh deformation with square-cube law computation

I have presented a novel character editing technique which respects biological and physiological principles. The resulting meshes are plausible in terms of biomechanical constraints and some biological processes which can be related to scale. In this work, I consider aspects of the cardiovascular system, metabolic system, and age. The presented system does not perform any time-consuming numerical simulation of biological processes, it merely relies on previously observed allometric relations between scale and function. The system does not require the user to input values for any parameters, but the input mesh is assumed to be plausible. Users interface with the presented system in a strictly qualitative way - simply choosing to increase or decrease mass. I have demonstrated that my methods give reasonable results by providing visual comparison with known horse breeds.

6.2 Nonlocal mesh editing based on spectral methods

I have presented a framework for nonlocal mesh editing and a fast method for performing mesh region matching. I demonstrated nonlocal mesh editing on several meshes, both organic and inorganic in nature. My approach is flexible enough to be used in conjunction with several mesh editing methods. The nonlocal mesh editing process relieves the user from performing repeated mesh editing operations.

6.3 Mesh skeleton generation based on spectral methods

I have presented an algorithmic sketch of a novel mesh skeleton generation method based on spectral methods. It is efficient due to the fact that it makes extensive use of the manifold harmonic basis in multiple steps in the entire algorithm: the use of the Fiedler vector as an input for Reeb graph computation, detecting similar parts in the mesh, and computing bone weights.

6.4 Future work

In the allometric mesh scaling of this study, I have focused on exploring intraspecies allometry. It would be interesting to implement additional rules and make a clearer distinction between interspecies and intraspecies allometry. Intraspecies allometric laws govern the development of animals of the same species as they mature, while interspecies laws govern differences among adults of different species. The user will then be able to pick a set of rules based on the biological class (e.g. mammal, reptile, insect) best

matching the mesh, and optionally include effects due to age.

There are other geometrical constraints to consider when scaling biological structures, including surface area-volume relations which govern how heat due to metabolism is dissipated. This typically becomes an issue at very small scales, such as with rodents and insects.

In this study the effectiveness of the proposed allometric scaling algorithm was verified by visual comparisons. It would be beneficial to perform a morphometrics-based analysis. The possible metrics include: principal component analysis of the shape of anatomical regions, regression using various dependent and independent variables regarding biological and physiological effects, linear discriminant analysis including cross-validation, and relations regarding fractal dimensions and allometric coefficients.

Regarding the nonlocal mesh editing, it would be interesting to implement scale invariance into the editing process and investigate the proposed spectral matching method in the context of mesh denoising.

Regarding the mesh skeleton generation, it would be beneficial to compare the quality of bones generated by other existing mesh skeleton generation algorithms that are not based on spectral methods. Another area of study is to analyze the computational cost for the bone weights computation. The presented method uses the manifold harmonic basis to compute bone weights. Computational cost analysis against the conventional bone weight computation methods using the heat equation solver would be interesting.

Besides the above ideas, I suggest the following possible relevant research ideas to explore as future work:

- *Crowd generation.* Generating large crowds or herds is a daunting task for animators. The presented technique can potentially provide an efficient way of automatically generating a wide variety of meshes based on a small number of original input meshes.
- *Medical imaging.* It would be useful if one can predict how an organ such as heart deforms as the body weight and age change by processing an input segmented organ image using the allometric deformation model of the organ.
- *Terrain rendering.* The spectrum of terrain obeys a power law as fractal structures generally do. Finding a way to manipulate a terrain mesh in frequency domain using a deformation model based on a power law would be an interesting research that would allow a plausible simulation of erosion of the terrain over time.
- *Mesh caricature.* A caricature is a portrait that exaggerates or distorts the essence of a person or thing. Generating caricatures for a given 3D mesh requires nonuniform deformation. It is expected that the ability of the presented technique to perform local deformation is applicable to implement an automated caricature generation system.

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Appendix

The manifold harmonic basis

In this appendix the formulation of the manifold harmonic basis is summarized. For more details the reader is referred to Vallet and Lévy's papers [92, 93]. In a Euclidean domain $\mathbb{R}^n$, the Laplace operator is defined as

$$\Delta = \operatorname{div} \operatorname{grad} = \nabla \cdot \nabla = \sum_i \frac{\partial^2}{\partial x_i^2}. \quad (1)$$

On a manifold $\mathcal{M}$ with metric g , the Laplacian is generalized to the Laplace-Beltrami operator

$$\Delta = \operatorname{div} \operatorname{grad} = \sum_i \frac{1}{\sqrt{|g|}} \frac{\partial}{\partial x_i} \left(\sqrt{|g|} \sum_j g^{ij} \frac{\partial}{\partial x_j} \right), \quad (2)$$

where $|g|$ is the determinant of g and g^{ij} is the components of the inverse of the metric tensor g . The eigenfunctions and eigenvalues of the Laplacian on $\mathcal{M}$ are defined as all the pairs (H^k, λ_k) that satisfy the Helmholtz equation

$$-\Delta H^k = \lambda_k H^k. \quad (3)$$

The eigenproblem can be discretized using the finite element method (FEM). A piecewise-linear function $\Phi^i (1 \leq i \leq n)$ is used for both the basis and test function. $\Phi^i (1 \leq i \leq n)$

is a piecewise-linear function on the triangles such that $\Phi^i(i) = 1$ and $\Phi^i(j) = 0$ for $i \neq j$.

The above eigenproblem is solved by finding $H^k = \sum_{i=1}^n H_i^k \Phi^i$ that satisfy

$$\forall j, \langle -\Delta H^k, \Phi^j \rangle = \lambda_k \langle H^k, \Phi^j \rangle. \quad (4)$$

This can be written in a matrix form

$$-Q\mathbf{h}^k = \lambda_k B\mathbf{h}^k, \quad (5)$$

where $Q_{i,j} = \langle \Delta \Phi^i, \Phi^j \rangle$, $B_{i,j} = \langle \Delta \Phi^i, \Phi^j \rangle$, $\mathbf{h} = [H_1^k, H_2^k, \dots, H_n^k]$,

$$\begin{cases} Q_{i,j} &= (\cot \beta_{i,j} + \cot \beta'_{i,j})/2, \\ Q_{i,j} &= -\sum_j Q_{i,j} \end{cases} \quad (6)$$

$$\begin{cases} B_{i,j} &= (|t| + |t'|)/12 \\ B_{i,j} &= (\sum_{t \in St(i)} |t|)/6, \end{cases} \quad (7)$$

t and t' are the two triangles that share the edge (i, j) , $|t|$ and $|t'|$ are their areas, $\beta_{i,j}$ and $\beta'_{i,j}$ are the two angles opposite to the edge (i, j) , and $St(i)$ is the set of triangle incident to vertex i . The above formulation can be simplified by approximating B by a diagonal matrix D as

$$-Q\mathbf{h}^k = \lambda_k D\mathbf{h}^k, \quad (8)$$

or

$$-D^{-1}Q\mathbf{h}^k = \mathbf{h}^k, \quad (9)$$

where

$$D_{i,i} = \sum_j B_{i,j} = \left(\sum_{t \in St(i)} |t| \right) / 3. \quad (10)$$

Numerically solving Equation 9 can be extremely computationally intensive when the number of vertices is large. I used the efficient algorithm that implements the band-by-band computation based on the factorization of the matrix [93] and ARPACK, an efficient sparse eigensolver library [48].

Contributions

Peer-Reviewed Journal Publications:

T. McGraw, T. Kawai, and J. Richards:

”Allometric Scaling for Character Design,”

Computer Graphics Forum (accepted in 2010, to appear).

T. McGraw, T. Kawai, I. Yassine, and L. Zhu:

”Visualizing High-Order Symmetric Tensor Field Structure with Differential Operators,”

Journal of Applied Mathematics (under review).

Peer-Reviewed Conference Publications:

T. McGraw, T. Kawai, I. Yassine, and L. Zhu:

”New Scalar Measures for Diffusion-Weighted MRI Visualization,”

International Symposium on Visual Computing (ISVC 2009),

Las Vegas, NV, Nov/Dec 2009, pp. 934–943.

Winner iCore Best Paper Award.

T. McGraw and T. Kawai:

”A Spectral Approach to Nonlocal Mesh Editing,”

International Symposium on Visual Computing (ISVC 2010),

Las Vegas, NV, Nov/Dec 2010, pp. 634–643.