

Visualising Organisms with Hydraulic Body Parts: A Case Study in Integrating Simulation and Visualisation Models

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Abstract

The physical structure of organisms can be modelled as a set of coupled hydraulic entities. The hydropneumatic biosimulation is a methodology that is able to simulate the behavior (like movements) of such organisms on the physical level in a biological correct way. Hydropneumatic simulation heavily relies on visualisation: the simulation model is visually constructed and the simulation results are presented visually to the user. This case study presents an approach, how a visualisation of the results of a hydropneumatic biosimulation can be obtained by integrating the biological simulation model with a Computer Graphics geometry model.

1. Introduction

Hydraulic body parts (e.g. fluid filled body cavities (=coeloms) or fluid filled appendages (=legs of spiders)) play an important role in the functional design of almost all organisms. A hydraulic conceptualisation of organisms as structural-functional entities provides a fruitful approach for quasi-engineering investigations. In contrast to investigations on a genome level, these investigations can provide valuable insight and explanations how and why certain functional concepts were developed and selected in the course of evolution. This paper shows how visualisation can play a key role in exploring, understanding and forming theories about the functional design of organisms with hydraulic body parts.

From a visualisation point of view, conceiving and implementing useful visualisations in this context is a challenging task. As we will see in this paper, traditional information visualisation models or static 2D drawings are only of limited value. Facilitating animated 3D graphics seems to be the best solution, however, modelling hydraulic body parts of organisms with existing 3D object models used in computer graphics is not straightforward. These models are meant for rendering 3D graphics and not for biological investigations. Thus, these models lack essential properties and these models are difficult to use for a biologist. The un-

derlying problem is that a simulation model from the application area (here: to simulate the behavior of hydraulic body parts) needs to be integrated with a computer graphics model (here: how 3D geometries can be animated and rendered). This is in contrast to the common practice to generate data with a simulation of the application area and to visualise the data with computer graphics models independent from the original simulation. In this case study, we will show how we accomplished the integration of the two models.

The paper is organised as follows. In the next section, we will give more details about the application background and state the visualisation goals. We will show why it is difficult to meet these goals with traditional visualisation techniques. In section 3, we will present our approach of integrating a simulation model with a computer graphics model. Before we conclude the lessons learned in our case study and give an outlook on future work in section 5, section 4 reports results and experiences with our approach.

2. Visualisation Task Analysis

2.1. Application Background

A hydraulic organisation of the body plan can obviously be found in many wormlike invertebrates, such as bristle worms, earthworms, leeches. Also in arthropods (crabs, insects, spiders) hydraulics have been identified as in impor-

tant aspect in form determination. During their individual growth the arthropods have a phase in which they have no rigid skeleton, so that their body shape has to be preserved by interaction of muscles and the hydraulic body fluid, until the new exoskeleton becomes hardened [TK03]. Even in vertebrates hydraulic cavities play an important role during embryological development and in overall activity of an organism. Since hydraulic cavities can be found in almost all organisms, the hydraulic conceptualisation of organisms as structural-functional entities provides a far-reaching approach for a theoretical analysis of underlying concepts in organisms. If organisms are modelled as hydraulic entities, the various anatomical structures and their arrangement have significant relevance in the process of shape generation, locomotion and propagation (activity of an organism and reproduction). The fluid filled body cavities as well as internal organs which behave in a functional sense as fluid fillings are hydraulic systems and therefore they work as skeletons (=hydroskeleton) which transmit forces generated by the contractile (muscles) or elastic (tensiles) elements. The particular shape of an organism is generated by the activity and the arrangement of contractile and tensile structures. Also rigid skeletal elements such as internal bones, sclerites or outer exoskeletons as the arthropoda, play a particular role in shape generation and preservation of organisms [Gut85, Gut88, Gut93]. With the development of a simulation model of these hydraulic arrangements, the hydropneumatic biosimulation, new fields of research are opened. For example, in evolutionary biology, the hydraulic conceptualisation can be used for evolutionary reconstructions. If an organism is understood as a hydraulic entity, it is necessary to understand evolutionary changes as gradual transformation of the entire hydraulic system. Therefore, the hydropneum provides functional restraints (=limitation of the possible changes which always have to be functional since all "in-between organisms" need to be viable - this is far more constrained than a simple morphing operation) for the possible evolutionary transformations and this allows for the reconstruction of the evolutionary history of particular organisms by applying the hydraulic conceptualisation to understand their body structure. Another research goal is to find and to understand basic stimulus pattern for muscles and other basic behavioral structures. This is not only interesting in the field of biology, but could provide a novel tool to visualise organisms and organic functions in a way that is correct from a biological point of view.

2.2. Visualisation Goals

Visualisation is not only necessary to interpret the results of the hydropneumatic biosimulation but also to conduct the simulation itself. The visualisation goals are

- to support interactive exploration in the context of the hydropneumatic biosimulation and to support the formulation of explanations about causal relationships (e.g. to explore how different arrangements of muscles and tensiles

could lead to sensible functions or to formulate hypotheses how certain functions were developed in the course of evolution)

- to validate the hypotheses formed (e.g. by judging whether the functional designs are sensible or not and whether the designed organisms would be viable or not)
- to communicate the explanations found (e.g. to explain how certain methods of movement were developed in the course of evolution).

Traditional information visualisation techniques are not suitable to meet these goals since the viewer is not able to properly interpret the information presented in an abstract fashion: the viewer likes to visually compare functions (like movements) of a simulated organism with the functions of existing organisms (e.g. in order to judge whether the movement is useful for the organism or not). Therefore, a realistic visualisation of the behavior of the organism is preferred. Thus, two-dimensional drawings were used so far, however, up to now it is not possible to visualise the interactions of the structural-functional elements (e.g. it is not possible to test the functional designs which have been reconstructed). This could be achieved by employing 3D animation techniques. Here functional defects become obvious in the visual representation of the simulation results.

2.3. Biosimulation Models vs. Computer Graphics Models

Since hydropneumatic biosimulation inherently deals with geometrical entities like muscles or tensils, geometrical models developed in Computer Graphics (like polygon meshes, volume models, constructive solid geometry, soft objects) might be used to visualise the simulation results or even serve as a basis for the biosimulation model. However, the Computer Graphics models lack important properties essential for the biosimulation (e.g. they do not guarantee volume constancy nor do they allow for modelling hydraulic deformations, complex interdependencies between layers of different tissues in an organism cannot be expressed). Moreover, the geometric models are designed to serve Computer Graphics users who want to render an image and for non biologists. For instance, biologists are overemployed with using geometric modelling tools in order to describe complex and nested 3D geometrical structures (like they occur even in simple organisms, e.g. starfish). Here, the biologists need more abstract means of specifying geometrical models - and modifying them in the course of an exploratory interactive analysis. Another solution considered was to use Computer Graphics models that build upon or imitate biological functions. In the literature, one can find several geometry models of organisms that are based on basic models (like finite elements or implicit surfaces) and mimic anatomical structures, like muscles, skin or bones [CHP89, JTN02, SR02]. In our context, those models are not usable since they either do not model deformations or other biological functions correctly

(the goal is just imitation) or they are not usable for a real-time application. Moreover, they do not provide a suitable level of description for biologists. An alternative to using Computer Graphics models directly is to map the biosimulation model to a Computer Graphics model. However, this approach turns out to be very cumbersome and labour intensive.

As a result, we encountered a situation in our application case where we need to augment a Computer Graphics model and provide multiple abstraction layers - useful for specifying the biosimulation model (e.g. allowing the user to introduce application motivated constraints) as well as the Computer Graphics model needed to render the imagery needed for visualisation. A major requirement for this model is that it allows for interactive visualisation and that it is feasible to meet according real-time constraints.

3. Approach

In this section we describe our basic approach how we conceptually combined a biosimulation model with a computer graphics model in order to obtain a *hydropneumatic biosimulation*. Then, we describe how a simulation model is specified from a user's point of view. Finally, we describe how we realized the Computer Graphics part of the hydropneumatic biosimulation.

3.1. Basic Idea

The basic idea is that the user constructs the simulation model and the graphical model simultaneously. In order to accomplish this tasks, the model provides basic object types that offer a certain behavior and a set of actions.

We distinguish three different basic **object** types that encapsulate a behaviour simulation model as well as a graphical representation. These object types are pneumatic objects, deformation objects and modification objects.

The pneumatic objects identified in our concept are:

- Main, which is the basic pneu (and may be used at the root of an object hierarchy).
- Bulge, which is a pneu made for the ramification of another pneu. A bulge has always a parent pneu to which it is attached. A smooth transition at the junction between bulge and parent pneu is calculated automatically.
- Organ, which is a pneu, which is positioned interior to another pneu.
- Canal, which is a pneu, which interpenetrates another pneu and thus has an ingoing and an outgoing linkage to it.

The deformation objects are:

- Pinch, which represents an orthogonal strangling of a pneu. If we compare a pneu with a balloon, a pinch could be compared with a rubber band used to constrict the balloon.

- Squeeze, which represents a local deformation of a pneu. In order to specify a particular Squeeze, the volume which is taken by the Squeeze needs to be specified (see below). If we compare a pneu with a balloon, a squeeze describes a rigid object into which a balloon might be pressed leading to local deformations of the balloon that resembles the rigid object.
- Contractile, which represents an object able to execute an external force on the pneu (like a muscle that makes fingers squeeze a balloon). A contractile can be given a stimulus pattern that results into the execution of external forces to the pneu.

The modification objects available for the user are:

- Skin, which is a competitive texture field on the surface of the pneu, i.e. a texture that is adapted to the surface of a non-rigid object (like a rainbow texture can be put on a soap bubble - if two soap bubbles merge, the textures on both soap bubbles "compete" with each other).
- Sclerite, which is an ossification field for modification of the viscosity of the pneu surface.
- Medium, which represents the environment of the pneu (like water) with the according pneumatic properties (like water pressure).

The pneus are arranged in a hierarchical fashion. The different types of pneu indicate the spatial relationship (e.g. an Organ is *within* another pneu). The whole hierarchy of pneus is called the *dentropneu*. The dentropneu can be augmented by deformation and modification object. We call this hierarchy the object hierarchy.

There are six basic **actions**, which can be applied to a pneu, modification or deformation object: *Make* and *Kill* for constructing or disposing an object, *Add* and *Sub* for attaching or detaching an object to or from the object hierarchy, and *Stimulate* to make a Contractile execute a certain stimulus pattern and *Change* to alter particular parameters of the constructed objects. Each action has a varying number of parameters, e.g. the object it refers to or a stimulus pattern.

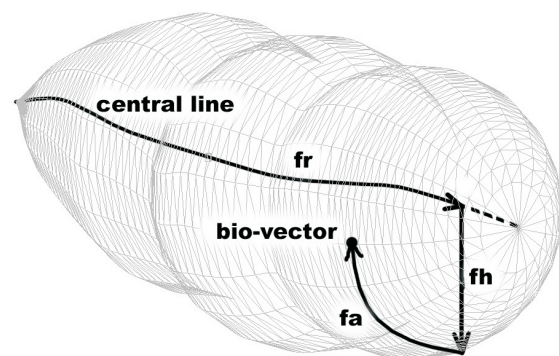


Figure 1: Specification of a Bio-Vector

3.2. Creation of a Simulation Model

Let us look at the standard procedure how a user builds a hydropneumatic biosimulation. The starting point is the ideal non-deformed pneumatic object, which is a sphere with a given volume. This sphere can then be deformed through several deformation objects, like Pinches (e.g. in order to model "compression rings" around the hydro-pneumatic sphere), Squeezes (e.g. in order to represent minor tractive or pressure forces) and Contractiles (e.g. in order to model interior tractive forces for lateral flexions). Moreover, the user may choose to use modification objects or pneumatic objects, which can be linked together to form a complex object hierarchy by using actions.

As a possible implementation, the user specifies the construction of the model by writing a script in a specific XML-based scripting language. Each script can refer to another script and adds a *delta step*. Thus, the user is able to model an evolutionary process.

As a result, the user obtains a *hydropneumatic biosimulation* that ensures that the visual behavior is in accordance with hydropneumatic laws, e.g. the volume of a pneumatic object has to be invariant during its deformations and moving processes. In particular, the organism modelled moves after its construction stringent to its shape and structure without any further specifications by the user.

3.3. Implementation

In this section we will highlight the most important implementation aspects of our approach. The central concepts in our implementation are *Bio-coordinates* and *Pneus*.

Bio-coordinates serve as a derivate of cartesian coordinates which greatly facilitate the exact specification of locations on or within an object in the presence of deformation. Figure 1 depicts the general approach of the concept. In order to use bio-coordinates within our computer graphics environment, the bio-coordinates have to be translated into ordinary cartesian coordinates.

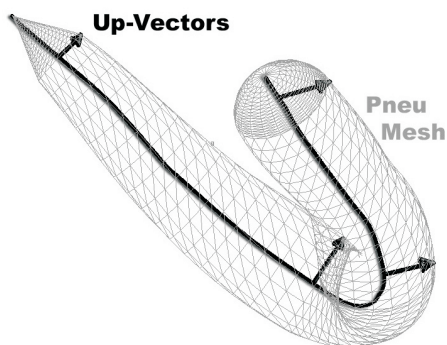


Figure 2: *Bio-Coordinates*

The implementation of the bio-coordinates relies on the definition of a *center line* which spans the object and defines the general orientation of the object. Figure 2 shows a center line in an undeformed state and after deformation. The center line is divided into line segments, the endpoints of which are subject to deformation. These endpoints are in fact derived from a NURB line which is modified by control points. The line segments are an approximation of this NURB. We store the cartesian coordinates of each endpoint along with a direction vector which is perpendicular to the slope of the original NURB line at that point.

These information are used to calculate the cartesian coordinates from a bio-coordinate point through the following algorithm:

- The fr value of the bio-coordinate (value range is $[0,1]$) describes a distance along the centerline as a fraction of the overall center line, counted from the frontside of the object (the start point of the center line).
- The fh value is an offset from the point on the center line identified by fr in the direction of the direction vector. The direction vector is interpolated from the direction vectors of the nearest line segment endpoints.
- The fa finally defines the cartesian coordinate of the point as being on a circle with radius fh and a midpoint defined by fr (see above). fa is the angle between the direction vector and the vector from the midpoint to the final point.

As the central line is deformed, the cartesian coordinates are recomputed from the bio-coordinates.

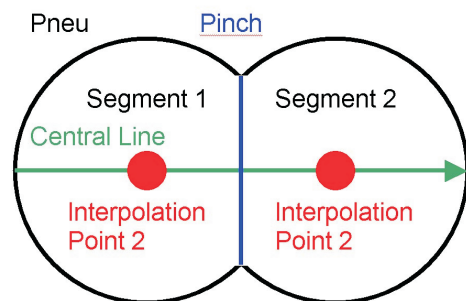


Figure 3: *Volume of Segments*

Pneus are the central building block of organisms. The ideal (hydro-) pneu is the representation of a liquid filled bag. The surface of the bag is to be minimal and is supposed to be of a flexible material. The geometry of an ideal pneu is a sphere. We make use of this feature to derive deformed pneus. While lateral deformation is trivially achieved through deformation of the pneu's center line, a spherical animal would not be able to move. The capability for form movements and other behaviours is introduced by segmentation of the main pneu (see Figure 3) In order to model the

segmentation of a pneu, we have to introduce a constriction in the spherical body, a *pinch*. To model the pinch in a physically correct way, we have to satisfy the following constraints:

- The resulting segments try to be as spherical as possible and
- the volume of the original pneu segment has to be preserved.

We calculate the volume of segments:

$$V_{ges} = \frac{1}{3} \cdot (s_{End}^2 \cdot (3 \cdot r - s_{End}) - s_{Start}^2 \cdot (3 \cdot r - s_{Start})) \quad (1)$$

The points referred to as s_{Start} and s_{End} of the to segments are computed using the constraints that

- the start point of the left segment (see Figure 3) is identical to the startpoint of the original segment,
- the end point of the right segment (see Figure 3) is identical to the endpoint of the original segment and
- the volume of the original pneu distributed amongst the segments in the same ratio as pinch's division of the centerline.

Apart from the pneu segmentation, the addition of new pneus to an existing one is very important, i.e. the combination of several single pneumatic objects (main, bulges, organs and channels) to a complex dentropneu hierarchy, by means of interface junctions. In a first step in creating this interface junction, a hole is "milled" into the polygon mesh of the corresponding pneumatic object. The selection of the polygons which are a candidate for elimination is made using the bio-field defined above. If the bio-field scalars at the position of the bio-rays defined by the polygon vertices exceed a specified threshold, a Boolean elimination flag is switched on for the latter elimination process. The borderline vertices of the resulting hole are the *shard points* and serve as cyclic linked vertices for the latter binding process between two adjacent pneumatic objects. This binding process is the optical "glue" that conceals the fact, that there are two separate pneus linked to each other (see Figure 4).

4. Results

The concepts and workflow described above were implemented in the e-Voluzzer system and validated at the Naturkundemuseum Senckenberg in Frankfurt / Main, a museum for natural history. The implementation was done using C++ and the RealiMation Scene Graph API on a standard PC running WindowsXP. The figure 5 show example results of a quite sophisticated model of an animal. The system was used to model the evolution of several animals of the enteropneumatic domain. A fictive evolution obtained with our system is depicted in figure 6.

The e-Voluzzer system is used successfully to assess the validity of a constructed model in a fast and dynamic way. This is achieved through visual comparison of known movement and functional patterns. Furthermore, animated morphing between different stages of evolution allows for the

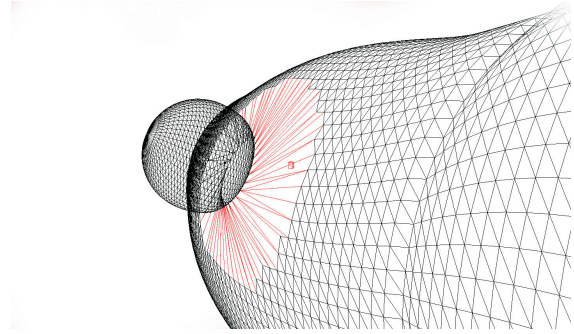


Figure 4: Interface Junctions (as wireframe and shaded)



Figure 5: An animal visualised by e-Voluzzer.

validation of in-between stages in the evolutionary path. This is especially important for the biological research, since dysfunctional stages cannot occur in natural evolution and would invalidate the evolution path, even if the resulting morphology would be valid.

While conventional visualisation tools, e.g. energy consumption charts or muscle tension charts, only permitted to have a partial view on the model organism, our system successfully provides for a comprehensive view on the animal. Such an approach alleviates the zoologists access to the simulation data, since it corresponds to the well established methods in this research domain. This application domain

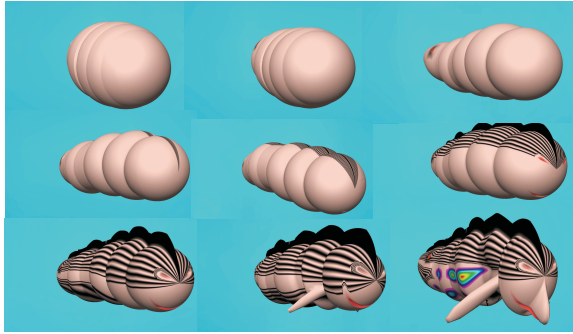


Figure 6: A biologically correct evolutionary morphing

centric approach is further advanced by letting the design of the scripting language reflect the evolutionary model of thought. This is achieved through a delta-encoding of the virtual scene, i.e. each stage in the evolution is modelled as the difference of the model in regard to the previous stage. In this way, even highly complex entities can evolve from fairly simple scripts. Using the e-Voluzzer system, the users were able to obtain novel insights. For instance, they were able to show that the three categories of objects (pneus, tensils and sclerites) defined in the visualisation model are indeed sufficient to describe the biological behaviour of the investigated species. Thus, the fusion of biological and Computer Graphics models at the conceptional level proved to be a valuable aid for the development of the biological models involved.

Besides the explorative visualisation in research, e-Voluzzer was successfully used for educational and didactical purposes. The Forschungsinstitut Senckenberg hosts an in house training course of approximately 20 summer students each year. Comparison between classes showed a qualitative increase in the students' understanding of peristaltic movements when the class had the opportunity to use the e-Voluzzer system interactively. In particular, the students proved to have a deeper understanding why certain muscle arrangements and stimulus patterns lead to certain basic types of movement.

5. Conclusions and Future Work

In order to meet the visualisation goals in our application case, it turned out that established visualisation techniques were not suitable. Moreover, we had to use sophisticated Computer Graphics models in order to provide a realistic, 3D animated visualisation which proved to be a beneficial visualisation method in our application scenario. Those Computer Graphics models offered the advantage that they could be used as a basis for the simulation model from the application domain, i.e. the biosimulation model. However, current Computer Graphics models are not easily extensible in the sense of application specific behavior and provide no ex-

PLICIT "hooks" for linking a simulation model. The Computer Graphics models are also more concerned with creating a satisfying visual appearance and it is difficult to extend them to obey application constraints (like volume constancy or biologically correct movements). This is even true for most biological motivated Computer Graphics models. In addition, the Computer Graphics models had the disadvantage that they are difficult to use for people from the application domain. While they allow interaction with the graphics, they prevent interaction with the model itself. Our visualisation goals, however, could only be met when the viewer is also able to change the underlying simulation model interactively.

As a consequence, we had to select appropriate (e.g. real-time capable) Computer Graphics models and had to integrate a simulation model from the application domain. No standard procedures or theoretically motivated guidelines are available today. Just best practice examples, like the one we provide in this case study. In addition, we had to add a higher level of abstraction that is suitable for biologists to access and modify the simulation model (and concurrently the Computer Graphics model). In our case study, we presented how we combined the biological and Computer Graphics models in a joined hydropneumatic simulation model and how we implemented them in the e-Voluzzer system, a tool designed to visualise functional validity of evolutionary animal morphologies. With this, we are able to model and visualise for the first time whole organisms with hydraulic body parts biologically correct in real-time.

While the original visualisation goals, the implementation of an evolution simulation tool for enteropneumatic animals and a didactical tool for the education of students, were met with our current system, we have plans to further enhance e-Voluzzer. The next stage will be the implementation of an visual authoring tool, which further facilitates the definition of animal models directly in the visual domain. Further on we plan to implement an interactive set of stimulus patterns, which allow for an in depth analysis of movement patterns and further validation of functionality. These tools will allow for a definition of behavioural models of even more complex animals in the evolutionary development. We plan to combine our novel visualisation tool with conventional information visualisation techniques, like the augmentation of 3D models with chart or icon based visualisation schemes.

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