

— Metamorphers —

A Formalization of Transitions in Illustrative Molecular Visualization

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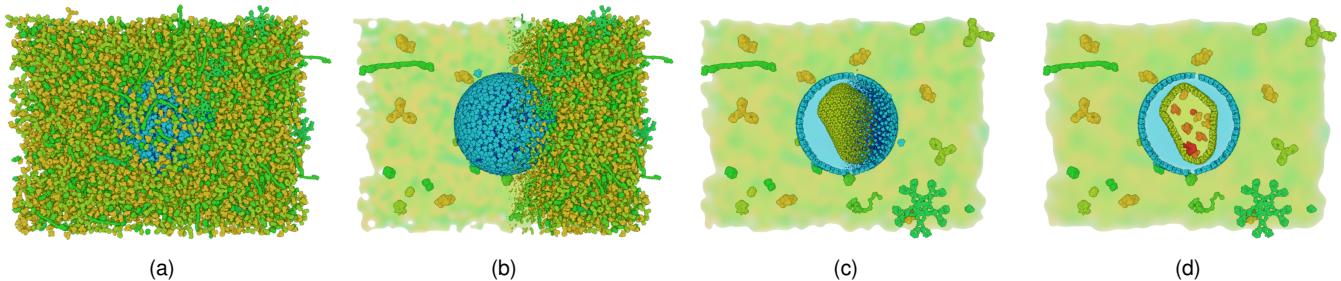


Fig. 1: Metamorphosis to a schematic representation of an HIV particle in blood serum. Protein types are shown in a reduced quantity that represents their number within a compartment. Each representative is enlarged for better readability of its atomic composition.

Abstract— Illustrators in molecular biology often use animated transitions as a means to communicate complex phenomena. While these animations are popular, they still have to be created manually in 3D modeling software. We therefore provide illustrators with a streamlined way for creating such transitions between various representations of molecular data. We propose a formalization of the process of specifying transitions to arbitrary representations in the form of a conceptual pipeline. Data representations are specified in such a way that they form a continuous space. The first three stages of the pipeline are responsible for creating this continuum. The final four stages of the pipeline are responsible for presenting the continuum. This continuum can be arbitrarily sampled in order to create a transition between two representations, e.g., densely, in the form of animation, or sparsely, in the form of small multiples. We demonstrate our concept on exemplary use cases by creating multiple operators, so called metamorphers, for each pipeline stage. These metamorphers can be combined to achieve different types of transitions for arbitrary molecular data sets. We present three transitions that we designed in collaboration with illustrators, based on the data set of HIV: the explosion of inner and outer cellular compartments, a novel illustrative rendering approach for automatic schematization of mesoscopic data, and a transition to an infographic view, conveying quantitative relationships. In a qualitative discussion of our results, we received positive feedback from domain experts in illustration.

Index Terms—Molecular Visualization, Illustrative Rendering, Animation.

1 INTRODUCTION

The traditional approach for the visual communication of scientific insights is handled by illustrators and animators. Their goal is to convey complex phenomena in an accessible way, and to attract the interest of broad audiences. In recent years, we have seen a rapid increase in the communication of topics from molecular biology [cite], [drew berry, gj, david bolinsky, Gal McGill, janett iwasa], such as the splitting of DNA, the transport of oxygen in the blood stream, or the comparison of molecular structures within a cell. Such animations are used in teaching undergraduate level biology worldwide.

When illustrators want to convey, for instance, the inner and outer structures of a cell, they face the challenge that the structures of their data are very densely packed. The dense data makes it very difficult to convey inner and outer structures at the same time. Therefore they employ means for occlusion handling, such as exploded views, in order to make all important aspects of the data visible. Illustrators often want to convey the entire variety of different molecules within a cell in form of an atlas-based view [cite some atlas]. However, a cell contains

in reality many thousand instances of the same molecular structures. To achieve such an atlas based view, an illustrator does not want to display every single molecule but would rather draw various structures at sufficiently large scale so that the viewer can understand the structural details. In these examples, the illustrator represents abstracted spatial information within same spatial frame of reference. We denote this as a transformation *within* the same visualization space (Figure 2a). In other cases, illustrators want to convey quantitative instead of spatial information, e.g., how many different molecules of each type a biological entity contains, or how a functional relationship between these molecules would look like. In the former case, a bar chart could be used as representation of the quantities. A node-link diagram could be chosen in the latter case to convey the relationships. In such cases, the illustrator would abstract the biological structure from a spatial representation to a quantitative or relational one, which we denote as a transformation *across* visualization spaces (Figure 2b).

For biological entities, a "canonical" representation, especially for non-experts, is the one closest to their mental model that is formed by images from photography, microscopy, and crystallography. The mental model is therefore anchored within the same visualization space as the actual biological entity. If no obvious relation between a mental model and a particular representation exists, the viewer needs guidance on how to relate their mental model to this transformed representation, in order to comprehend the other (transformed) representation form.

In scenarios where interaction is possible or desired, e.g., in an in-

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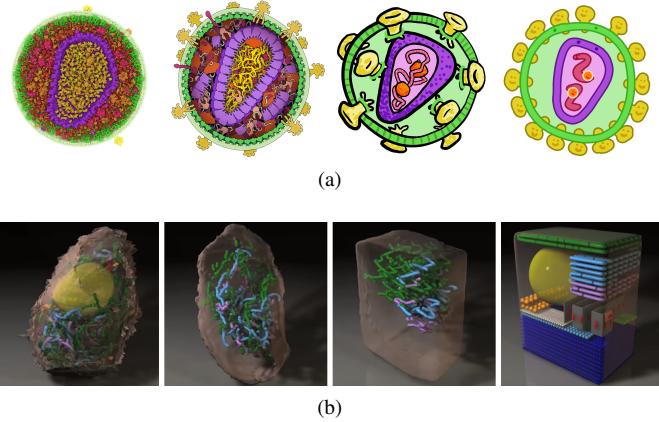


Fig. 2: (a) Examples of transitions within the same visualization space and (b) across different visualization spaces.

teractive analysis scenario, approaches such as coordinated multiple view (CMV) visualizations can be used for conveying the relations between two representations, e.g., via brushing and linking.

In cases, where interaction is not feasible or very limited, such as in presentation scenarios, this guidance is often realized by depicting a transition from a representation A to a representation B, e.g., in the form of static sequence of snapshots/small multiples, or an animation/animated transition. We denote such a transition as a metamorphosis and the individual building blocks of the metamorphosis as metamorphers.

Animations are a powerful tool for conveying these metamorphoses, since they are capable of displaying such a transition between two representations in a continuous way. The continuous presentation supports an intuitive understanding of the relationship between representation states. The presentation is both self-explanatory, and enjoyable to audiences [15]. Despite their immense popularity in the visual communication crafts, animations are also critically regarded by the visualization community. Tversky describes the fleetingness of the displayed information and the potential sensory overload and distracting nature of badly designed animations.

Alternative solutions for conveying transitions alleviate the fleetingness of the displayed information by sacrificing the continuous aspect of the representation. Examples are narrative sequences of small multiples or static images that supplement the missing information of the continuity with glyphs. While solving the problem of fleetingness, they have to be well designed to be understandable.

Once a transition from one representation to another one is planned/conceptualized, there is little aid in modelling tools to realize it. Animators employ key frame animation and create these keyframes manually which is a laborious and time-consuming task. Considering that new discoveries are made frequently in molecular biology, these representations and their transitions have to be re-modeled when new insights are found, which makes the effort for maintaining them even higher.

We therefore set our goal to assist illustrators by eliminating the need to manually author their target representations and the transitions to them. We supply illustrators with a pipeline for creating continuous target representation as well presenting the transitions to them.

Our primary contribution is a formal description of a uniform method for creating continuous target representations for spatial biological data sets, as well as presenting the transitions to these representations - describing the complete metamorphosis of the data representation, so to say.

Data representations are specified in such a way that they form a continuous space. The first three stages of the pipeline are responsible for creating this continuum. The final four stages of the pipeline are responsible for presenting the continuum. This continuum can be arbitrarily sampled in order to create a transition between two representations,

e.g., densely, in the form of animation, or sparsely, in the form of small multiples. Each stage supports operators, so called metamorphers, that are responsible for one aspect of the metamorphosis.

As our secondary contribution, we demonstrate a proof-of-concept implementation of this pipeline based on three use cases that we developed in collaboration with illustrators. One of these results, a novel illustrative rendering approach for automatic schematization of mesoscopic data, is our third and final contribution.

2 RELATED WORK

Animation and transitions between visual and data representations have been employed in many contexts. They serve as powerful tools for the dissemination of complex relations in space, time and abstract dimensions. They are frequently used in visual story telling and for the depiction of correspondences between data representations as well as visual representations.

2.1 Visual story telling

Kosara and Mackinlay [10] note that for a long time the focus of visualization research was on exploration and analysis but that presentation of findings especially using elements of story telling should be a research focus of equal importance. They list prominent examples of story telling that include animated transitions for trend analysis and dissemination.

Robertson et al. [15] have looked at trend visualizations in depth. Three methods including animated transitions were analyzed. They found that animated transitions of data was reported to be more enjoyable and exciting to users. They also found that it was significantly faster when used for presentation but less exact and less effective for analyzing data. These results encouraged us to use animated transitions to facilitate presentation of complex molecular data.

Segel and Heer [16] analyze story telling with narrative visualization and point out different approaches. They distinguish between author- and reader-driven elements in a narrative and speculate that "exploration of transitions between them presents an exciting area for researchers and practitioners". Along these lines Wohlfart and Hauser [21] presented a guided interactive volume visualization approach. Their system enables authoring and editing of visualization stories that give the user partial control over the exploration.

Ma et al. [14] describe the need of new scientific visualization methods that can be used for scientific story telling. Among other issues they suggest that novel transitions between different coordinate systems are needed to address the overwhelming complexity involved in today's scientific story telling.

2.2 Animated transitions between visual representations

Kosara et al. [11] use 3D scatter plot matrices to establish a link between physical layout and the abstract dimensions of the data. Their work is an early attempt to connect information visualization and scientific visualization using points as data primitives. Elmqvist et al. [3] present an exploration technique for multi-dimensional data. They place scatter plots on the sides of a dice and animate the transitions when the dice is rotated.

Guilmaine et al. [4] compare different animated transitions of tree structures. They find that hierarchical animation is better suited for tracking of changes.

Basch [1] describes possibilities for animated transitions between volumetric rendering and abstract views like histograms and scatter plots. They use staggered animation to reduce occlusion. Hurter et al. [8] present a more general technique that interpolates data points between different views which are projections of the original data dimensions. They demonstrate applications for volume data as well as for images. Their approach addresses occlusion with interaction methods like brushing and locking of data points. Heer and Robertson [5] show animated transitions between different visual representations of statistical data. Their work makes extensive use of staging to reduce occlusion and clutter. Our approach is based on several findings of these previous works and formalizes animated transitions between spatial and abstract attributes.

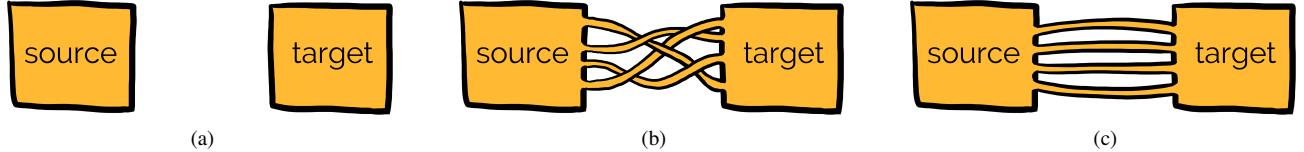


Fig. 3: The continuum between two representations describes the metamorphosis from one representation state to another: a) source and target representation. b) the continuum creation connects both representations. c) the continuum is restructured for presentation.

Huron et al. [7] present the visual sedimentation metaphor for the animation of data streams. This metaphor allows to transition from discrete visual elements to a continuous representation. We employ a similar metaphor for the transition of spatial objects to abstract charts.

Exploded views [2, 13, 9] have been used in different contexts as a technique for illustrating spatial or hierarchical relations of parts of an object. They are frequently used in animations or interactive systems and reported to be effective in the dissemination of complex layouts. Our approach is similar to exploded views, since it animates the decomposition of the object into its parts. However, the spatial displacement is not only driven by the visibility of the individual parts, but also by additional data attributes.

2.3 Alternatives to animated transitions

Small multiples [19], coordinated multiple views, and static images in conjunction with annotations, traces and glyphs are alternatives that are typically used to visualize transitions, trends, correspondences or sequences [15]. Hsu et al. [6] present an automated method for the illustrative visualization of multiscale phenomena. They generate an image that contains multiple levels of detail of one subject by blending the renderings of multiple pin hole cameras at different zoom levels together.

Tversky et al. [20] summarize cognitive studies on the benefits of animation. Although, they conclude that animation alone has not been convincingly demonstrated to be superior to static illustrations, other findings of their study suggest a direction for research on animations in visualization. They report that animation together with basic interaction methods like pausing, partial re-playing, zooming and change of perspective might be the key to enhance the effectiveness of animation. While techniques, such as CMV, require user interaction for establishing relationships between corresponding representations, Tversky et al. acknowledge that the non-interactive alternatives to animation (such as sequences of static illustration) are surprisingly hard to design and are therefore not an easy target for computer automation.

3 METAMORPHOSIS FORMALIZATION

The context of our research lies in the field of explanatory visualizations of large-scale models of biological structures, such as viruses and bacteria, where relationships between various abstracted or transformed visual representations of a model should be conveyed without any need for user interaction. Such visualizations are employed by scientific illustrators and animators for conveying science to expert and non-expert audiences in an easily accessible and engaging way.

Each illustration which communicates a relationship starts with the two representations of the model. The first, source representation, is typically close to the mental model of the audience. The second, target representation, illustrates different aspects of the presented model, but its relationship to the source representation might not be obvious. In that case, the illustrator needs to manually create the visual transition between the two representations. We present a method for creating a continuum, or metamorphosis, between two arbitrary model representations that illustrates the relationship between these representations.

The continuum is defined as follows: the state of each data element is represented as a point in multidimensional "attribute" space. Each attribute of the data is present as one dimension of this space. The continuum is represented by curves in this multidimensional "attribute" space that connect, i.e., relate, the points of an element's source state

to its target state. Our method creates this continuum by describing the target representation on the basis of the original representation, thus alleviating the illustrator from creating the transition manually.

Figure 3a shows a source and a target representation. Both communicate certain aspects of a model, but they are disconnected, their relationship is not immediately clear. Our pipeline consists of two high level steps. In the first step, we *create* the continuum by explicitly defining relations between the data structures, visual, and spatial properties of the source and target representation (Fig. 4, left). However, this unstructured connection is not yet ready for illustrating the relationship between the representations (Figure 3b). The continuous space that we created can be sampled but we have to define *how* first. The second step of the pipeline prepares this continuum for *presentation* to an intended audience (Figure 3c) by specifying how the relations that we created in the first step should be presented (Fig. 4, right). With this step, the metamorphosis is finalized so that it illustrates the relationship between the source and the target representations.

The metamorphosis is carried out by applying a sequence of operators in our pipeline (Fig. 4), which we refer to as *metamorphers*. The operators can be arbitrarily combined by the illustrators to achieve results which they would otherwise have to create manually.

3.1 Continuum Creation

In the first step of the pipeline, the continuum between two model representations is created. The continuum forms the basis for the communication of the relationship between two desired data representations.

When illustrators manually create a transition across data representations in a 3D modeling tool, e.g., by key-framing it, the relation between the representations is not explicitly specified. Without such a relation, the transition that they modeled is only valid for the exact combination of the specified data, original representation, target representation, as well as the visual transition. The problem with this approach is that if one of these four aspects should be changed, e.g., because new findings about the data have been discovered, or a different information should be conveyed, the entire transition has to be manually remodeled from scratch.

To overcome this issue, we explicitly create this continuum in the first step of our pipeline by specifying relationships between all aspects of the underlying source and target representations. The continuum is created with the sequential execution of the metamorphers in the pipeline. The metamorphers define how an aspect A, e.g., the position, in the source state relates to aspect B in the target state. The relationship is explicitly modeled with these metamorphers. Therefore, if the underlying data is changed, the relationship remains. The transition does not have to be remodeled, simply the involved metamorphers have to be re-executed on the new data, thus saving significant effort for the illustrator.

3.1.1 Data restructuring

Biological data models often have a semantic hierarchy, such as the compartments that build up a cell. The hierarchy in a target representation does not necessarily have to be the same, e.g., due to abstraction of certain details. Therefore, the first step of connecting two representations, is to match their semantic hierarchy. The metamorphers in this stage, relate the original data structure with the data structure of the target representation by defining data subsets within the source model representation that match the semantics of the target representation,

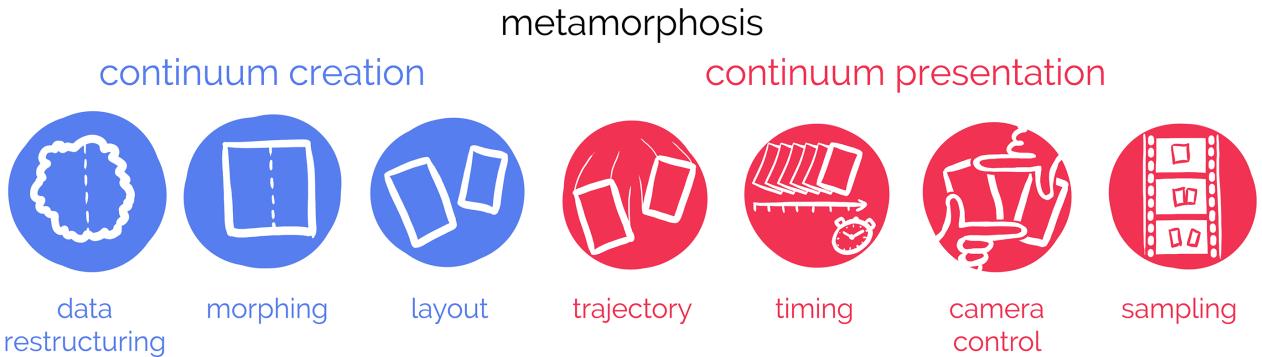


Fig. 4: The metamorphosis pipeline. Continuum creation: data restructuring, morphing, layouting. Continuum presentation: camera control, trajectory, timing, sampling.

thus restructuring the data. Optionally, data subsets can be duplicated, if the target representation requires it. All data subsets are organized in a hierarchical tree structure, or a scene graph. The subsequent pipeline stages can operate on any node of the scene graph, giving illustrators the flexibility they are used to from 3D modeling software.

Examples of metamorphers used in this stage are explicitly defined cutaway objects, such as those proposed by Le Muzic et al. [ref our eurovis paper](#), which specify spatial data subsets, or data clustering algorithms, e.g., that group proteins by their type.

3.1.2 Morphing

An important aspect of relating two representations of the same biological data to each other, is understanding how the shapes of individual elements in those two representations relate to each other. For instance, molecules in mesoscale biological models can be displayed as space-filling models, stick models, or one of many other representations commonly used in molecular graphics. Alternatively, molecules can be represented in a different spatial frame of reference, as abstract shapes, such as cuboids, to illustrate quantitative information, such as their volume.

Metamorphers in this stage of the pipeline therefore specify the relationships between the shapes of the corresponding data elements. Depending on the target representation, two types of metamorphers can be applied to establish this relationship:

Object-space morphing metamorphers define how to transition between 3D shapes of the visual representations of the data elements. For instance, in molecular data, this can be achieved by continuously repositioning the individual atoms of a molecule to form the shape of the target representation, such as a different molecule, or an abstract shape (Fig. 5a).

Image-space morphing metamorphers define how to transform the visual representation of data elements in image space, for instance, through alpha blending or other image-processing operations (Fig. 5b). These metamorphers are used when the two representations cannot be adequately matched in the object space.

3.1.3 Layout

Depending on what illustrators intend to convey in a target representation, they often need to reposition data elements within the visualization. This might be done as means for occlusion handling, e.g., by exploding dense data to reveal the internal structures, or to simplify a noisy or complex spatial arrangement of the data elements to better fit the viewer's mental model. Elements could be positioned so that they represent an altogether different visualization space, such as a network that shows interactions between molecules.

Metamorphers in this stage of the pipeline therefore define how the spatial arrangements of data elements in both representations are related to each other, in order to allow illustrators to create spatial transitions between both layouts. Metamorphers define this relation with a sequence of transformations of the positions, rotations, and scales of the data elements. Layout metamorphers operate on the individual

nodes of the scene graph down to the individual data elements (e.g., molecules), so that whole data subsets can be transformed at once. Additionally, layout metamorphers can be arbitrarily stacked to achieve a wide range of spatial transformations. Such metamorphers can arrange data elements into various 3D volumes, such as cubes or spheres in order to illustrate their relative counts, or align them side by side for comparison.

3.2 Continuum Presentation

After the continuum between the two data representations is created, the "how?" of its presentation needs to be answered. The transition should be presented in a way that is engaging, readable, and valuable, i.e., so that it conveys the relevant information for the current scenario. There are three high level tasks that are essential in achieving this goal: occlusion handling, the steering of the viewer's attention, and the reduction of visual clutter. These tasks can be achieved during the second step of our pipeline, consisting of four different stages.

3.2.1 Trajectory

While the layout stage of the pipeline defines the "what" of the spatial relationship between data elements in different data representations, the actual "how", i.e., the trajectories between each source/target pair of spatial attributes is not yet specified. It is necessary to define the trajectory along which the data elements move in order to transit from the source representation to the target one. This is achieved in the first stage of the continuum presentation step.

Trajectory metamorphers define the "how" of the spatial relation based on arbitrary sets of control points between the source and target transformations of the data elements. These control points define the paths along which the data elements move, rotate, and scale during the metamorphosis.

The metamorphers of the trajectory stage can be used to structure the transition, such as through various edge-bundling methods. For instance, the molecules of the same type can move to their target positions along similar paths in order to minimize the visual clutter created by the transition (Fig. 5c).

3.2.2 Timing

In order to coordinate the transitions specified in the morphing and the layout stages, illustrators need to create an appropriate temporal arrangement for them. Such an arrangement can, on the one side, encode information about the chronology of the illustrated events. On the other side, illustrators use the speed and sequence at which individual transitions occur as means to suggest the transition's importance for the communicated message, as well as to draw a viewer's attention to different parts of the illustration.

Metamorphers in the timing stage define the "how" of this temporal arrangement. They operate on so called *time curves* that are associated with each node in the scene graph. These curves are used as transformations of the data elements' positions within their specified trajectories as functions of time.

Timing metamorphers are used to specify the starting time of each transformation, as well as its speed (Fig. 5d). As such, they can be used to create various temporal effects, such as staging [5] to reduce the visual clutter during the transition, and ease-in or ease-out curves for the movement of the data elements or entire data subsets. Time curves can also be modified to make some of the elements stop in the middle of the specified trajectory, or to reverse their movement.

3.2.3 Camera Control

To adequately follow the development of continuous transitions, e.g., when trajectories or target representations lie outside the original view frustum, and to guide the viewer’s attention towards important details of a representation, camera steering is a necessary component of a non-interactive explanatory visualization.

Camera control metamorphers define how camera settings change over time, to assure the visibility of all important data elements at each time step. These metamorphers access the temporally and spatially arranged data elements and use this information to automatically modify the position and the look-at vector of the camera. A camera control metamorpher could, for instance, set the look-at vector of the camera to point in the centroid of the data elements, while it moves the camera far enough to capture the entire data set for the given field-of-view.

3.2.4 Sampling

To present the created transition to the viewers, it is necessary to select a set of time steps that are going to tell the story intended by the illustrators. In the simplest case, the transition is sampled densely enough to form a seamless animation, given a certain number of frames per second and a desired length of the animation. In other situations, it might be more feasible to present only a few representative time steps which show the essential aspects of the transition, e.g., as a narrative sequence of single images.

Metamorphers of the *sampling* stage implement various strategies of how these time steps are chosen. While the previous stages of the pipeline can be called multiple times in order to create more complex transitions, the sampling stage is final, as it ties together the information from the previous stages to sample the visual result.

To sample the transition information created in the previous stages, the scene graph information is propagated down through the hierarchy to the individual data elements, to determine their absolute positions, orientations, and shapes at each point in time. There are no restrictions on how the sampling is performed. For instance, it is possible to create a hybrid visualization that displays a sparsely sampled narrative sequence of small multiples. Upon request, a continuous animated transition between two consecutive small multiples could be shown to provide additional information on how they relate to each other.

The sampling stage can also determine if the transition is pre-calculated or sampled on the fly in real-time. A continuous pre-calculated transition could be used not only for display in an animation but also for extracting information about the continuous change or motion of the transition. This extracted information could then be used for encoding the otherwise missing information about the transition in the form of glyphs within a static single result image.

4 USE CASES

After the description of the theoretical pipeline, we demonstrate its utility on several use cases. We show these examples on the structural model of the human immunodeficiency virus (HIV) which is built-up from thousands of macromolecules. The HIV particle is either contained within blood serum (Figures 1 and 6), or with the blood serum removed (Figure 7). The source visual representation is the direct rendering of the structural data set, which is then continuously transformed into a particular destination visualization space. Each example highlights a different aspect of the structure: 1) what does the three dimensional structure of the virus and its inner compartments actually look like and how do they relate to each other hierarchically? 2) what types of molecules are contained in which compartment of virus, what do they look like, and in which approximate quantity are they present?

3) how large is the collective volume of each molecule type within the HIV particle in respect to each other?

4.1 Explosion of Molecular Structures

Since molecular structures of the HIV data are very densely packed, it is difficult to inspect the outer and inner structures of the virus at the same time. The four structures that we want to show are assembled in an onion-like structure where one compartment is contained in another one. We therefore chose to convey the encapsulation of compartments in form of an exploded view (Figure 6), to answer our first question.

The specific pipeline for creating the continuum between the original visualization and the exploded view starts with the data restructuring. In order to create the relation of the original data to the four compartment structures of the target representation, we create subsets for all four compartments in the restructuring stage. To create the compartment subsets, we exploit the fact that each compartment contains molecules of different types, and implemented a *type range* metamorpher. The subsets created by the type range metamorpher contain all given molecules that match a specified type range. If each molecule type could exist within multiple compartments, we could achieve the creation of the compartment subsets, by spatially grouping the molecules with a *spatial splitting* metamorpher. A spatial splitting metamorpher checks the position of a given list of molecules in respect to a spatial object defined as an iso-surface of a distance field, like a plane, cube, or sphere, that the user can position freely in the scene. Molecules are then assigned to two new subsets, depending on which side of the object they are situated. To create the seam at which compartments are split for the explosion, we actually apply a spatial splitting metamorpher to spatially subdivide the three outer of the four subsets that we just created along a plane. At the end of the restructuring stage, the root node of the scene hierarchy has four child nodes for the compartment subsets. The nodes of the three compartments that are exploded in the final representation, have two additional child nodes containing the spatial subdivision.

Since the visual representation of individual molecules does not change across the source and the target representation, we do not need to apply any metamorphers in the morphing stage of our pipeline.

In order to relate the original unexploded data to the final exploded representation, we apply metamorphers of the layouting stage performing the necessary spatial transformations. In this step, we finalized the creation of the continuum between the original unexploded and the exploded target representation. In order to present the transition in a pleasant way, we follow the remaining steps of our pipeline.

Since both, the source and the target representation, remain within the same view frustum, and we do not explicitly focus on any specific details, we do not apply any metamorphers in the camera control stage. The camera parameters are manually set beforehand, and the camera remains static throughout the animation.

Our original data differs from the exploded target representation only in position and topology (the split compartments). To present the transition, we move all compartment subsets as a unit so that they keep their shape during the transition. In the trajectory stage, we therefore apply the *linear interpolation* metamorpher to achieve a linear transition along the continuum between source and target representation.

In the layouting stage, we apply a total of five layout metamorphers to create the relation to the exploded representation (three compartments are split open, while two of them are also translated). If all these operations would be executed at the same time, the transition could be hard to follow [5]. In the timing stage, we make the presentation of the transition more pleasant, by applying a *delay* metamorpher. The delay metamorpher adjusts the time curve of each compartment subset so that each subsequent explosion starts only after the previous is finished.

In order to also support understanding for the structures of individual molecules/proteins and to convey the opening motion of each exploding compartment in the final representation, we show representatives of the proteins separated from the compartments in which they are contained. These representatives are molecules that simply do not complete their transition. To end the transition for these molecules

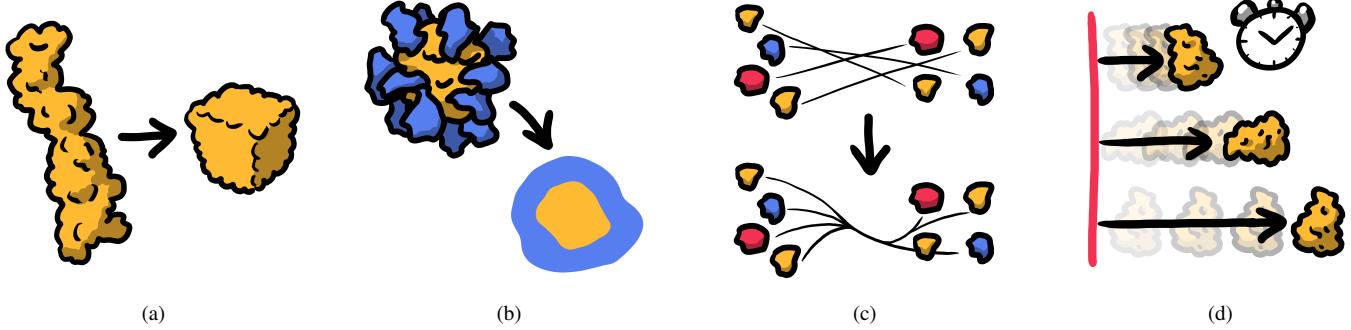


Fig. 5: Examples of different metamorphers: a) object space morphing, b) image space morphing, c) trajectory bundling, d) distance based time offset

before they reach their final position, we manipulate their timecurves with a *dust* metamorpher. During the transition, the opening compartments thus leaves a motion trail of molecules behind. In a static image, they suggest the opening motion leading to the final representation. In case the camera would zoom-in to show details of individual compartments, the motion trails would make the individual molecules surrounding the compartment discernible.

As the last step, the continuum created between the two representations is sampled. To create an animation, *continuous sampling* metamorpher is utilized, which generates a 10 seconds animation of 24 frames per second. This animation is shown in the supplementary video. For Figure 6, we apply *sparse sampling* metamorpher, which simply takes desired number of samples of the continuum at even intervals.

With the created transition, we can explain to the viewer how are the compartments enclosed within each other, as the final representation alone does not necessarily convey this information. This is especially the case for the viewers who are not familiar with the dataset. Furthermore, the transition explains where the isolated molecules, used as a context for the individual compartments, originate from.

4.2 Schematization of Molecular Structures

Besides the spatial organization of a cell, biologists are often also interested in the cell's molecular composition, i.e., what types of molecules are present in the data, in which compartment are they contained, what do the molecules look like? The HIV model, for instance, contains 42 different molecule types but due to their high count (thousands of molecule instances across these 42 types), their mostly random distribution and the dense packing of the data, the detailed information about the number of types and their individual shape is impossible to deduce from direct visualization of the original data. Illustrators therefore create atlas based views (such as in Figure 1d) that show a simplified schematic representation of a cell in order to highlight the shapes of different molecules, as well, as the shape and size of the structures that they collectively compose and are contained in. Low level details of the noisy molecule distribution, i.e., the exact count, position and shape of individual molecules are suppressed for this schematic representation.

We achieve a transition to such an atlas based view with our pipeline in the following way: Similar to the first step in the exploded view use case, we restructure the data with the type range metamorpher to create the relation to the three subsets that represent the compartments of our schematic target representation. Technically, we need each subset twice. Since the three subsets will be morphed in image space to create suggestions of the compartment shapes, we need a copy of each subset for the layouting stage. The *copy* metamorpher creates copies of the supplied subsets, resulting in copies A and B for each subset.

Since the shapes of compartments in the HIV particle are occluded in the original representation, we create a simplified representation of the shape of each compartment, marking its area, in the morphing

stage. We create the relation of our original noisy data to the simplified shape representation by applying a *blur* metamorpher. The blur metamorpher creates an additional render pass for each subset of copy A. The image of the molecules in the respective subset is blurred with a Gaussian kernel, removing high frequency noise from the image and leaving only a suggestion of the colors and the area of each respective compartment. By increasing the contrast of the alpha channel of the blurred image, sharp edges of each compartment area are created, thus making the shape representation more pronounced. The molecules in their original form are rendered on top of these shape representations.

To reveal the compartment areas created in the previous step, and to enable the display of enlarged representatives for each molecule type that are essential for conveying the molecule shapes, we have to reduce the noisy clutter of the molecules. We achieve this reduction in the layouting stage, where we create the relation of our dense and noisy original data to the sparse enlarged rendering of representative molecules and compartment shells in the final representation. For a given subset of copy B, the *schema* layout metamorpher differentiates between membrane molecule types, i.e., molecules that compose the shell of a compartment, and non-membrane types, i.e., the ones that are floating within a compartment, in order to create the final schematic representation. Since illustrators know, which molecule types the membranes of compartments are composed of, they can specify the membrane type so that they are treated differently than the molecules within compartments. For membrane molecules, the schema layout metamorpher picks the ones that are closest to the border of the compartment, from the viewing position. The picked membrane molecules remain their original size and rotation. The non-picked membrane molecules are scaled to zero to be invisible in the final representation, in order to reveal the compartments and molecules within. Alternatively, instead of scaling, transparency could be applied to membrane molecules in the morphing stage. For membranes, the schema layout operator thus preserves the membranes shells of compartments while revealing the inner structures of a compartment.

For non-membrane molecules, the illustrator has control over the total count of representatives that should be displayed in a compartment. Based on the specified number, the schema layout metamorpher calculates how many representatives of each molecule type of the given subset should be kept. The number of kept representatives depends on the ratio between the total number of molecules of each type within the subset, and the maximum number of allowed representatives. Each molecule type has one guaranteed representative.

Once the number of representatives for each molecule type is calculated, the schema layout metamorpher picks the representatives from the original data. In order to avoid visual clutter and to achieve a more pleasant result image, a greedy algorithm is used to approximate an uniform distribution of the representatives. Each representative molecule is picked so that its distance from the already picked molecules is larger than a pre-calculated threshold. The threshold is calculated from the total visible area of the compartment and the de-

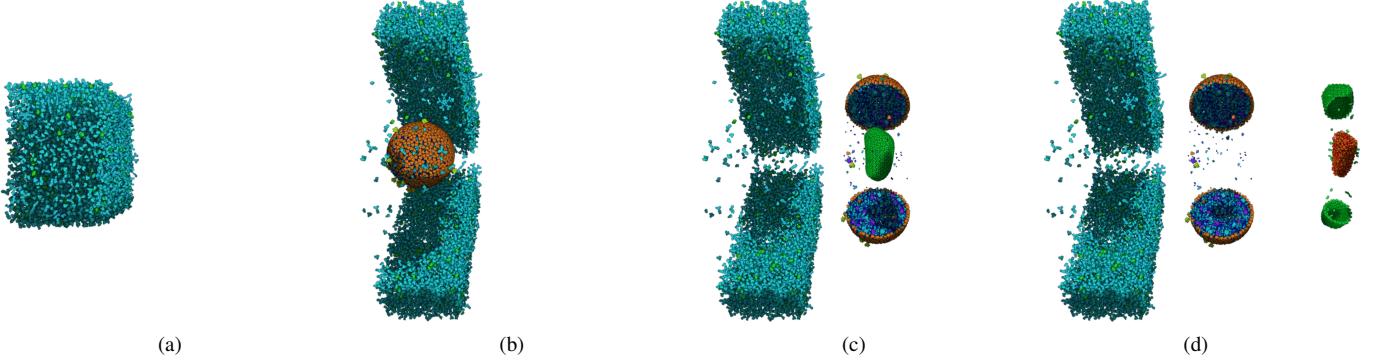


Fig. 6: Metamorphosis to an exploded representation of blood serum and HIV compartments. A trail of molecules is left behind during the transition to indicate their individual size and shape.

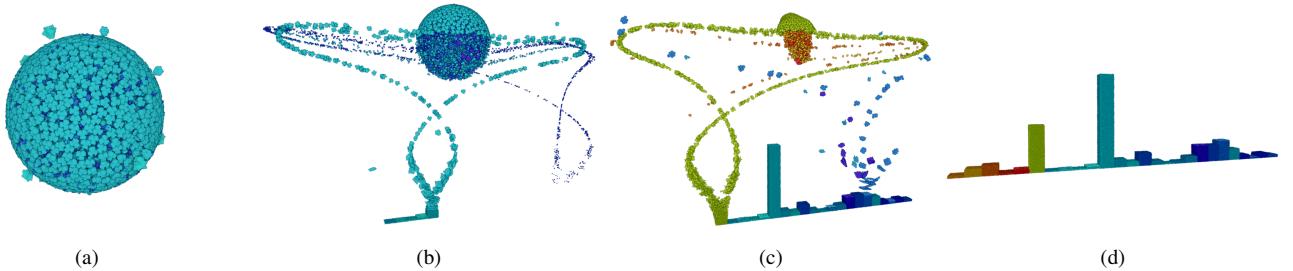


Fig. 7: Metamorphosis of molecules into histogram bars that display the volume that each molecule takes up in the HIV particle. A distance based time offset reveals the layered compartments one by one during the metamorphosis.

sired number of the representatives.

To make the atomic structures of molecule representatives better visible, the schema layout metamorpher enlarges them. Since the rotations of the molecules are randomly distributed, the schema layout metamorpher rotates them to face the camera view direction. In order to achieve more organic look of the final representation, the random rotation along the view direction axis is maintained.

To achieve smooth rotations during the transition, the trajectory stage uses a *SLERP* metamorpher that implements spherical linear interpolation [17] between the original and the target orientation, which are internally represented as quaternions.

Since inner structures are occluded by the outer structures of the blood serum and HIV particle, we use the timing stage to reveal the structures step-by-step. A *staged timing* metamorpher manipulates the time curve of the molecules of a compartment in such a way, that the transition of each compartment starts with a specified delay. Additionally, in order to create a peel-away effect that reveals the inner structures and molecule representatives of each compartment from left to right, we use a *distance offset* metamorpher. The distance offset metamorpher calculates the distance of each molecule to a plane, or other 3D object, that the illustrator can place in the scene. The distance to the plane is then used as a measure for creating an additional per-molecule delay offset.

Since the original and the target representation occupy the same space, we do not need to apply any guidance in the camera control stage. The animation is again created through the continuous sampling metamorpher in the sampling stage.

The presentation of the continuum between the original data representation and the schematization emphasizes aspects of the data that may not be self explanatory. The transition of the scaling more directly shows how small the original molecule representatives were. The transition of rotations emphasizes the fact that molecules can have different orientations in the original data. The staging per compartment enables occlusion handling as it reveals inner structures in intermedi-

ate states of the transition which would not happen in a side by side comparison and non-staged animation. The distance offset delay reduces the transformation at any given time to a small vertical stripe of the data, thereby reducing the amount of simultaneous visual stimuli, making the animation more readable, and directing the users attention to the one specific location that is transforming at each point in time.

4.3 Representation of Quantitative Relations

To understand the molecular data, it is often necessary to show quantitative aspects of the data elements. In our example, we convey how many different molecule types does the HIV particle contains, and how much of the volume within the particle does each of the types occupy. Such quantification is necessary, for instance, when analyzing different life cycle stages of a cell.

The comparison of such information on the direct rendering of the original 3D models can deceive due to the complexity of the molecular structures. Illustrators therefore often supply quantitative information in the form of infographics, which are based in a different visualization space than the original biological data. In this space, spatial dimensions are not used to convey spatial information but rather abstract dimensions, such as aggregations, e.g., of atom counts [18]. The relation between the original spatial and the transformed abstract representations is even harder to grasp. Continuous transitions are especially suitable for depicting such complex relations, as was successfully demonstrated in the award-winning animation of the decomposition of a cell (Figure 2b). In this video, scientific illustrator Graham Johnson used an animated transition to convey the relation between the 3D model of a pancreas cell and an abstract depiction of volumetric relations between the elements of the cell.

In this final use case, we demonstrate how we can achieve such a transition to an abstract visualization space with our pipeline. As a demonstration, we chose to convey the quantitative information about the number of molecule types in the HIV particle and the volumetric relation between types by a histogram (Figure 7d). The number of his-

togram bars corresponds to the number of molecule types. The height of each bar corresponds to the volume that the respective molecule type occupies in the HIV particle. Since we are concentrating on displaying relations within the HIV particle, we remove the blood serum from our original representation before we restructure our data hierarchy to match the intended target representation.

Since each histogram bar has to represent a single molecule type, we use a *group-by-type* metamorpher to create a subset for each type.

The histograms in the final representation are constructed from the individual molecules in our original data. Each molecule is represented as a slice with given base area and a height that represents the molecule's volume. The volume depends on the number of atoms that the molecule is composed of. By stacking the molecule slices, we receive a height that is representative of the total volume of all molecules of the respective type. In the morphing stage, we therefore apply an *object space* metamorpher on each type subset, in order to morph the shape of each molecule to the aforementioned slice, by repositioning the atoms of the molecule.

In order to layout the morphed molecule slices into the shape of a bar, we use a *bar layout* metamorpher on each type subset. The bar layout simply stacks the molecule slices in a subset on top of each other. The bars are then positioned side-by-side along a line with a *line layout* metamorpher.

Since we position the histogram bars in the final representation below the HIV particle, the molecules on top of the particle would, with a linear trajectory between their origin and destination point, fly through the particle, and exit the particle on the bottom side, before reaching their final position in the histogram. To present the transition in a manner where molecules do not cross the HIV particle on their way to their destination, we introduce additional control points to the path of the molecules in the trajectory stage of our pipeline. [TODO: description of first (sideways) CP]

Further, we add a control point for each molecule type above its respective histogram bar to create a trajectory that looks like the molecules are filling the bar by pouring into it. We therefore bundle the trajectories of the molecules above each bar with a *trajectory bundling* metamorpher. We place the control point at the same height for all bars. To calculate the x/y position for a control point, we use the center of the bounding box of the respective molecule type subset. Each subset in the scene hierarchy has a bounding box. Bounding boxes are calculated when a subset is created and updated when a layout is applied.

Due to the onion like structure of the HIV particle, inner structures are occluded by outer structures. Inner structures should therefore not start their transition before the outer structures, as they would never be visible in their original representation. Further, if the inner structures would fly through the outer structures to their target representation, a viewer would not understand, from which part of the virus exactly they would be coming from. To present the transition in a manner, that reveals each original structure before it starts its transition, we apply the *staged timing* metamorpher to peel HIV particle like an onion, starting with its outer layers. In contrast to the previous two use cases, here, we stage the timing by molecule type to transition each molecular type individually into its histogram bar representation. The transition of each type starts after a certain delay / when the previous transition is finished. To create the order of the staging that results in the peeling effect, we use a *distance offset* metamorpher. The distance of each molecule of a specific type to the center of the particle is calculated and averaged. The average distance per type is then used for the ordering of the staging. As the center of the particle we assume the center of the bounding box of the root node of the scene hierarchy.

In contrast to the previous use case, the position of the final representation (the histograms) differs from the position of the original representation (the HIV particle). A camera position that shows both representations at the same time would use the screen space inefficiently, since only during the transition both representations are visible. The original and the target representation would be shown with unused screen space where the respective other representation would be positioned. We therefore implemented a simple *guided navigation*

metamorpher to use the available screen space efficiently by zooming in as closely as possible to the displayed data, while assuring that entire scene (all molecules) are visible at all times during the transition. The metamorpher checks if molecule instances are culled from the view. If yes, then the camera is zoomed out until no more instances are culled. If no, the camera zooms in until instances are culled. A constant zooming in and out at the optimal position is avoided by smoothing the camera transition. The camera look-at vector is updated to look at the center of our scene, where our HIV particle is positioned.

Finally, to produce the animated transition to the histogram bars, why apply the same continuous sampling as in the previous two use cases.

The transition conveys two aspects of the data that a simple side-by-side presentation of original and target state would not. One the one side, the relation between the histogram bars and the molecular structures that they represent is established. On the other side, the inner structures of the HIV particle that are not visible in the original representation and not present in the target representation are revealed in the course of the transition.

4.4 Expert Feedback

We demonstrated the three usecases to two experts in illustration and animation in order to gather their feedback. Each use case was presented in form of a video of the respective animated transition. We supplied the experts with questionnaires that contained specific questions for each use case. [mention the questions or list a few examples of the questions?]

4.4.1 Exploded Views

...waiting for feedback...

4.4.2 Schematization

...waiting for feedback...

4.4.3 Histograms

...waiting for feedback...

5 IMPLEMENTATION

We implemented the pipeline within the CellVIEW framework [12], which is a tool for real-time visualization of large mesoscale molecular models. We treat individual molecules as data elements that are rearranged in the scene within the transitions. In this way, we support large variety of illustrative effects.

The pipeline is implemented as an application programming interface (API) that can be easily scripted in C# language. All metamorphers are supported as simple function calls taking as the input arbitrary nodes of the scene graph, down to the individual data elements.

6 DISCUSSION AND FUTURE WORK

Our method allows the generation of transitions for arbitrary molecular data sets, which has the advantage target representations and transitions do not have to be manually modeled and key-framed in a tool like Maya. Our pipeline implementation offers a simple API for access and parametrization of the implemented metamorphers. The API can be extended with additional metamorphers that support further transitions and target representations, that can then again be applied to arbitrary molecular data. Currently illustrators can access our API with a scripting interface, where metamorphers along the pipeline are called on subsets of the data with specific parametrizations. The scripting does not pose a challenge to illustrators as they are used to high level scripting interfaces of tools such as Maya. Nevertheless, we plan to implement a visual interface for our API so that also non-experts can plug metamorphers together with a few clicks.

The ease of use and speed in generating results with our method has the tradeoff of sacrificing the flexibility the time consuming manual modeling these modeling tools supply with manual creation.

Since we designed our pipeline to produce visualizations for presentation purposes, we did not build it explicitly with interaction in mind. It is built to produce static images or animation sequences.

The environment in which we implemented our method, however (cellVIEW), natively supports user interactions as it is based on the Unity3D engine. The formal pipeline, as well as the implementation could be extended to support user interactions, e.g., to make it also applicable in interactive analysis scenarios. Such an extension of our approach could allow user interactions, e.g., on the final representation, to create a partial transition of a selected subset back to the original representation.

At one point during the design of our formal pipeline, we were contemplating to add a stage for annotations to our pipeline, as they can assist story telling by describing what is currently happening in the scene. They can point to specific events in the transition to steer the viewer's attention. They can create frames of reference, such as coordinate axes, scales, and legends, that can improve the viewers' orientation within and their understanding of the presented information. However, we decided to rather discuss them in this part of our paper, as they are orthogonal to what our pipeline is designed to do and therefore do not match the conceptual scope of our pipeline. Further, the implementation of simple annotations, e.g., as billboards in the scene, is trivial, so we did not deem them as an essential contribution in the scope of our work.

Even though we described our pipeline only for the application with molecular data, it could be also applied on other data formats. The molecular data is comparable with point cloud data on a non uniform grid. Point cloud and volume data are therefore supported out of the box if the matching data importer is supplied. What these data formats have in common is that the geometric topologies of objects can be easily split up, e.g., as is the case when splitting a spherical structure along a plane. In polygon data, the splitting of the geometric topology is not as trivial. In order to make our pipeline compatible with polygonal data, the data restructuring stage would have to be extended with metamorphers that support topological changes of the mesh data.

While we only inspected our method from the perspective of molecular mesoscale data, our approach could also be applied to other application domains at different visualization scales, e.g., to explain physical phenomena. Further, our approach could also be used to transition between different scales of data, such as in the work of Hsien et al. [cite!]. Different scales of a data set could be managed in different hierarchy levels by the data re-structuring stage. Each node of the hierarchy could be rendered with a different level of detail mechanic in the morphing stage.

Since our pipeline produces a continuum between two representation states, it can be used out of the box to generate animations and narrative sequences (comic strips). However, another interesting direction for future work would be to explore the possibilities that different sampling metamorphers could provide. As we discussed in Section 3.2.4, our pipeline supports pre-calculated as well as real-time sampling for the presentation of the created continuum. Real-time sampling could be explored in regard to possible applications for user interaction. Concerning the pre-calculated continuum, we could investigate, how to actually extract information about the change during a transition to substitute the missing information about motion within static glyphs. Further, the possible applications of the mentioned narrative sequence-animation hybrid could be explored.

7 CONCLUSION

In this paper, we present a formal method for creating continuous transitions between two representations. These target representations and transitions have historically been modeled and key-framed manually by illustrators and animators in 3D modeling tools. Our method is described in the form of a pipeline, that creates and presents a continuum between two representations in seven stages based on a simple scripting interface. Representations and transitions can be created with a few lines of code and executed for arbitrary data sets, which is a huge improvement over the previous manual workflow for creating such representations. Each stage of our pipeline supports a certain type of so called metamorphers, that are responsible for relating the original to the target representation for certain aspects of the continuum. We implemented our method and showcased its flexibility based

on three use cases that highlight certain aspects of a HIV data set, and we discussed further possible applications of the metamorphers that we provide. Each pipeline stage can be extended with metamorphers to further increase the range of supported target states and transitions. The metamorphers can then be applied to arbitrary molecular data sets. In a discussion we describe how our approach can be applied to other data types and other visualization domains. We gathered feedback from domain experts in illustration and animation that confirmed the benefit of our approach in respect to their habitual workflow.

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