

— Metamorphers —

A Formalization of Transitions in Illustrative Molecular Visualization

A, B, and C

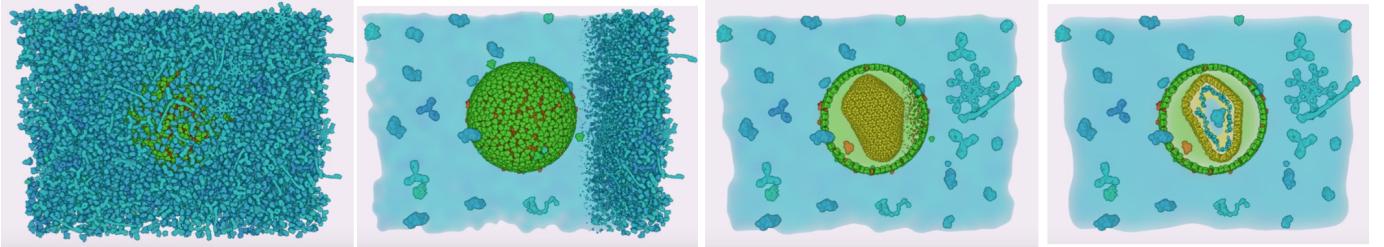


Fig. 1: Metamorphosis to a schematic representation of an HIV particle in blood serum.

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 more 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 XXX(could not read). 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 interactive 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, 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 se-

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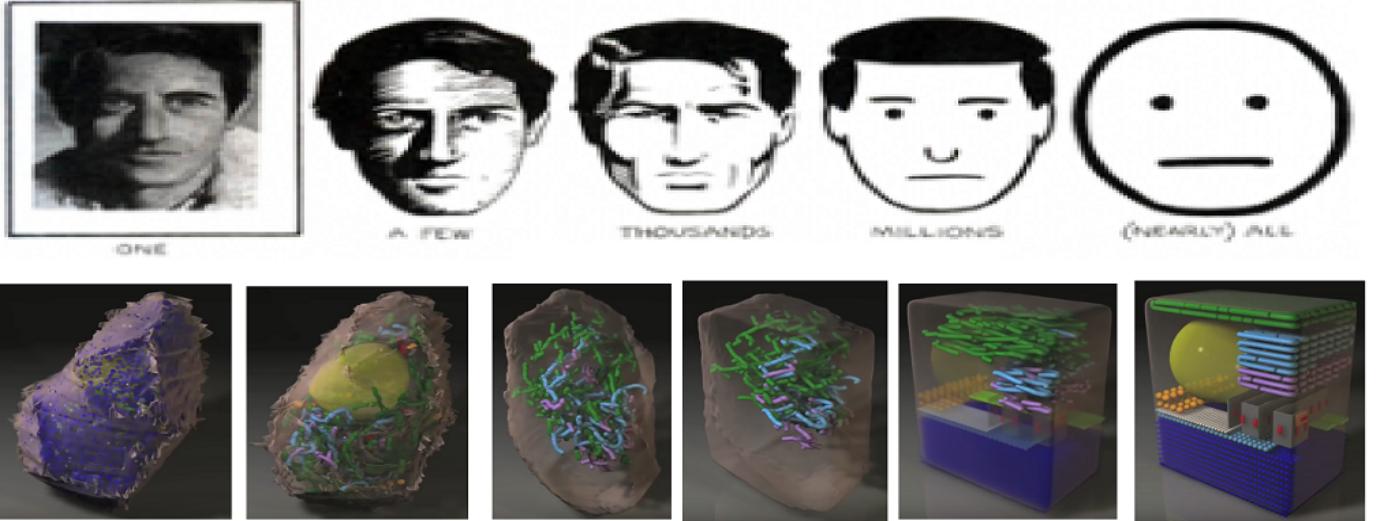


Fig. 2: Examples of transitions within the same visualization space (a), across different visualization spaces (b).

quence 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 [13]. Despite their immense popularity in the visual communication ... (cannot read), 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 [9] 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. [13] 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 [14] 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 [17] 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. [12] 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 Transitions between visual representations

Kosara et al. [10] use 3D scatter plot matrices to establish a link between physical layout and the abstract dimensions of the data. Their

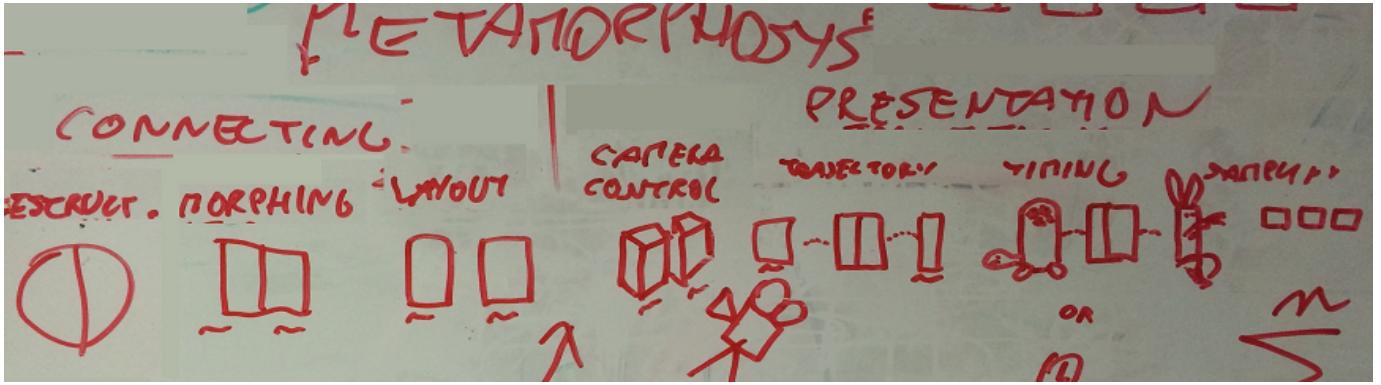


Fig. 3: The metamorphosis pipeline. Continuum creation: data restructuring, morphing, layouting. Continuum presentation: camera control, trajectory, timing, sampling.

work is an early attempt to connect information visualization and scientific visualization using points as data primitives. Elmquist 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. [7] 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.

Huron et al. [6] 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, 11, 8] 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 [15], 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 [13]. Tversky et al. [16] 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. Further, they acknowledge that the 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 is an explanatory visualization of large-scale structural models of viruses and bacteria that conveys relationships between various abstracted or transformed visual representations of the models without any need for user interaction. Such visualization techniques can then be easily employed by scientific illustrators and animators for easily accessible and engaging content authoring for popularising and conveying science to non-expert audiences.

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 continuum between two arbitrary model representations, or metamorphosis, and using it to illustrate the relationship between these representations. The metamorphosis is created automatically through describing the target representation, thus alleviating the illustrator from creating it manually.

Figure 4a shows the source and the target representations. They both communicate certain aspects of the model, but they are disconnected, their relationship is not immediately clear. Our pipeline consists of two steps. In the first step, we create a continuous space between these representations. However, this low-level connection is not yet ready for illustrating the relationship between the representations (Figure 4b). Therefore, the second step of the pipeline prepares this continuum for the presentation to the intended audience (Figure 4c). In 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, which we refer to as *metamorphers*.

3.1 Continuum Creation

In the first step of the pipeline, the continuum between two model representations is created. In this section, we describe the three stages of the continuum creation, with examples of metamorphers which can be used in these stages.

3.1.1 Data restructuring

Biological data models are organized in a hierarchy, which corresponds with the semantics of abstraction of the modelled phenomena. This hierarchy often differs in both representations. Therefore, the first step of connecting the representations is to match their semantic hierarchy. In this step of the pipeline, the illustrator defines data subsets within the source model representation, which match the semantics of the target representation, thus restructuring the data. Additionally, some of the data subsets can be duplicated, if the target representation requires it. All the data subsets are then organized in a hierarchy with

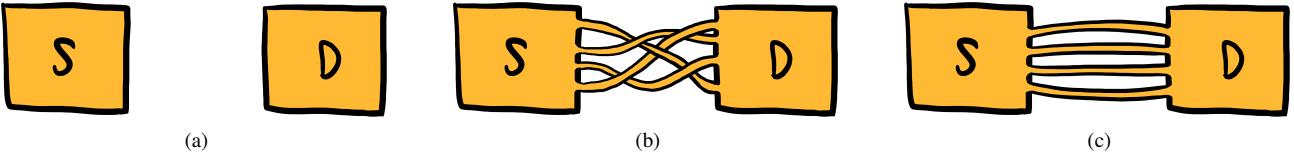


Fig. 4: The continuum between two representations describes the metamorphosis from one representation state to another: a) source and target representation. b) the continuum creation connects both representations. c) the continuum is restructured for presentation.

a tree structure, or a scene graph. All the subsequent pipeline stages can operate on any node of the scene graph, giving the illustrators the flexibility they are used to from the 3D modelling software.

Examples of metamorphers used in this stages are implicitly defined cutaway objects, such as those proposed by Le Muzic et al. ??, which specify spatial data subsets, or various data clustering algorithms.

3.1.2 Morphing

An important aspect that might obfuscate the relationship between different representations of the biological data are the shapes, or visual representations, of the individual data elements. For instance, molecules in the mesoscale biological models can be displayed as space-filling models, stick models, or one of many different representations commonly used in molecular graphics. Alternatively, molecules can be represented by abstract shapes, such as balls or cubes illustrating their volume.

In this stage of the pipeline, the relationship between the shapes of the individual data elements is specified. We propose several metamorphers for this purpose.

3.2 Continuum Presentation

The Pipeline

3.3 Overview

[the paper story transition/flow is too hard here - restate what our paper is about and why we therefore explain now the pipeline stages - what is the pipeline about? it is for molecular models and allows for transitions to other visualization spaces. state the rationale, why a pipeline and why stages are necessary - currently too much "how i spent my summer" style - it is also important to state, why we did something (not only what we did)]

In this section, we present the eight stages that our pipeline consists of. The pipeline operates on the following data format.

[this should be part of the data structuring stage explanation:]

- Instances: instances have a spatial position, orientation, and geometrical representation, and can have an attribute vector. in our case, instances are molecules of different types that are composed of atoms. these atoms are represented by points and are the primitives in our data.
- Subsets: subsets are grouped instances, in our case groups of molecules. groups can be formed according to any internal or external attributes of instances, such as type or shape similarity.
- Entities: both instances and subsets are the entities that our pipeline operates on. this means, a metamorpher accepts either individual instances and/or groups of instances, e.g., in the layout stage, when repositioning a single molecule or a group of molecules.

Our pipeline takes a molecular data set in the described format and produces a user specified number of frames that show a transition from the provided original representation to a specified target representation.

The eight stages of our pipeline can be grouped into two high level tasks: the first four stages are responsible for creating a target representation. The final four stages are used to define the transition from

the original representation to the target representation. Each stage supports certain types of operators. These operators determine how a stage proceeds with the supplied data. Operators have to be implemented for each stage in consideration of desired target output. Here is where design considerations come into play. To convey their message, illustrators apply a combination of the three high level tasks of occlusion handling, and transformations within or across different visualization spaces. Subsequently, most pipeline stages supply measures for fulfilling these tasks with their individual means. These can, in combination, then enable other lower level tasks, such as, comparison,.. [check brehmer task taxonomy]

[this whole paragraph seems irrelevant to the reader:] In order to achieve a desired result, the respective operators have to be selected and parametrized for each stage. Depending on what kind of transition should be achieved, not all stages are mandatory. Further, the pipeline can be repeated for more complex stories or multi stage transitions. In the following we will discuss each stage in terms of its function within the pipeline and in terms of how it operates on the supplied data. How these stages can be applied in practice, will be demonstrated in the next Section, where we will discuss the creation of three exemplary transitions based on our proof of concept implementation.

3.4 Target State

The visual appearance of the final representation is defined in these stages.

3.4.1 Data Transformation

Before they start to visually transform their data, illustrators have to decide, which parts of the data and in which granularity it is handled, e.g., to determine, which parts to explode, or which parts to merge and render in a simplified manner. As such, the components on (most of) the following pipeline stages are operating on individual subsets of the data. Data Transformation, as the first stage in our pipeline, is therefore concerned with creating these subsets - or more precisely, a hierarchical scene-graph of subsets where the leave nodes are the individual molecules. These subsets are the building blocks that the final representation is constructed from.

Operators in this stage therefore define, according to which criteria to create these subsets. For instance, one operator could create a subset that contains all molecules of the same type, another according to the molecules' spatial positioning.

On a technical level, this means that operators of this stage will receive a list of entities (molecules or subsets) as input - will then group these entities according to specified criteria - and create a number of subsets, e.g, as many as there are molecule types. Each entity that fits the respective subset criteria is assigned to it as its child. Each child entity stores the id of its designated parent. The output of an operator will therefore be a list of the newly created subsets with the respective child / parent assignments.

To create a scenegraph, the operators of this stage have to be called hierarchically on the data. A user could, for instance, at first partition the scene spatially and then partition the resulting subsets by molecule type.

Multiple time steps, different data sets, or simply multiple copies of the same data can also be represented as high level nodes within such a scenegraph - provided the necessary operators to create or load them are implemented.

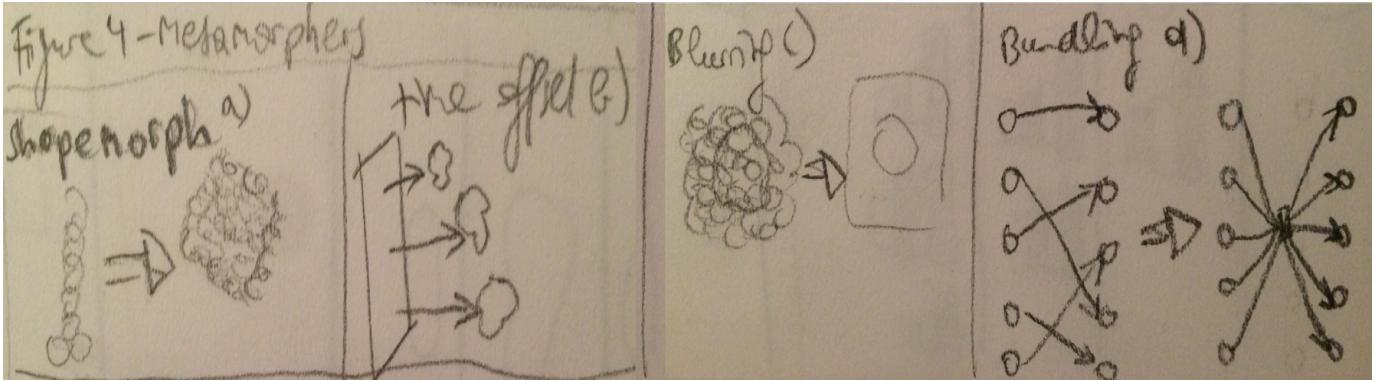


Fig. 5: Examples of different metamorphers: a) shape morphing, b) blurring, c) time offset, d) some layout

3.4.2 Annotations

This stage allows the illustrator to add various forms of annotations to the scene. Illustrators can use these annotations for multiple purposes: simple text labels could assist story telling by describing what is currently happening in the scene. Icons that point to specific events can be used to steer the viewer's attention. These elements can also be combined to 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.

Operators of this stage should therefore, in the simplest case, accept text input and should be able to create or load icons and other graphical representations. Annotations can be independently positioned and parametrized, but they can also be logically attached to specific entities, e.g., for creating a relative position or extracting and displaying an entity's attributes.

[we could also move this behind layouting]

3.4.3 Visual Transformation

Operators in this stage have access to the visual variables of transparency, color, and shape. Illustrators use these operators to change the visual mapping of parts or all of their data, in order to achieve a transformation within the same or across visualization spaces, e.g., to support tasks like simplification, abstraction, and occlusion handling. Operations can be applied on any level of the scenegraph, i.e., on individual molecules or subsets of molecules.

This allows the transparent rendering of occluding molecules, or the morphing of entities to different shapes, as can be seen in [Figure 2 - graham video].

From a technical perspective, the operators in this stage can implement specific shaders for creating a desired effect, e.g., by changing the molecule geometry, or doing post processing on the rendered image of a subset in a separate rendering pass.

3.4.4 Spatial Transformation (Layouting)

While the previous stage handled the visual variables of transparency, color, and shape, this stage is concerned with the transformation of the spatial variables of position, rotation, and scale. As the final stage of this part of the pipeline, it completes the transformation of the data, i.e., the creation of the final target representation.

With the spatial re-arrangement of the molecular data, various results can be achieved: occlusion handling, e.g., by exploding the dense data to reveal the inner workings of a cell. The noisy distribution of different molecules can be re-arranged, to simplify the complex and dense data so that it better fits 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.

The input for a layout operator is always a node in the scene hierarchy, i.e., an entity containing a list of molecules or subsets. For each child of the supplied node, the operator calculates a new position

rotation, and scale - depending on what kind of layout the respective operator is implementing. The output of a layout operator is therefore a new position, rotation, and scale for each child of the supplied node. Each entity has a vector of control points that stores positions and rotations and is initialized with the entity's original position and rotation (in the case of subsets, the bounding box). The new values calculated by the layout operators are added to this vector.

Layouts can be stacked upon each other - meaning they are called multiple times for the same node - this creates additional control points that can be used to transition the data into intermediate representations before arriving at the final state. The final representation is determined by the last layout that has been called. A user could, for instance, first call an explosion layout, to reveal the inner parts of the dense data set, before rearranging these parts into a simplified form.

3.5 Transition

These stages are responsible for defining the transition to the target representation, i.e., how each entity reaches its target position and when it reaches its target form.

3.5.1 Camera Operators

Control over camera parameters allows illustrators to steer a viewer's attention towards specific events or details in the scene, in a guided navigation fashion. An operator could also steer the camera to follow the development of a transition, if it leaves the current view frustum, to assure visibility of the entire data.

Operators in this stage modify the camera position & look-at vector. As such, they create a list of control points for these two values. For guided navigation, an operator could access the positional control points of user defined entities, for instance. A timing and trajectory is defined in the respective stages for the interpolation between these control points.

3.5.2 Trajectory

This stage describes for each molecule, how it reaches the target position and the control points in-between that have been defined in the spatial transformation/layouting stage. This is in the simplest case a linear interpolation between a molecule's control points. However, if applied wisely, illustrators can use this stage for multiple purposes: Simplification: they can make the transition more readable and visually engaging, by bringing structure into its elements' motion paths, e.g., by creating a well positioned point in space for each molecule type through which it has to "travel" to reach its target position. This can also serve occlusion handling, e.g., by placing these transit points in a way that the molecules flying through them reveal essential parts of the scene. Trajectories can also encode topological information that was not present in the original data, e.g., in the form of meaningful data highways that transport molecules from one cellular compartment to another, or to simulate the flow of blood between two organs.

To achieve this spatially structured transition, operators in this stage can implement techniques such as edge bundling. This means that an

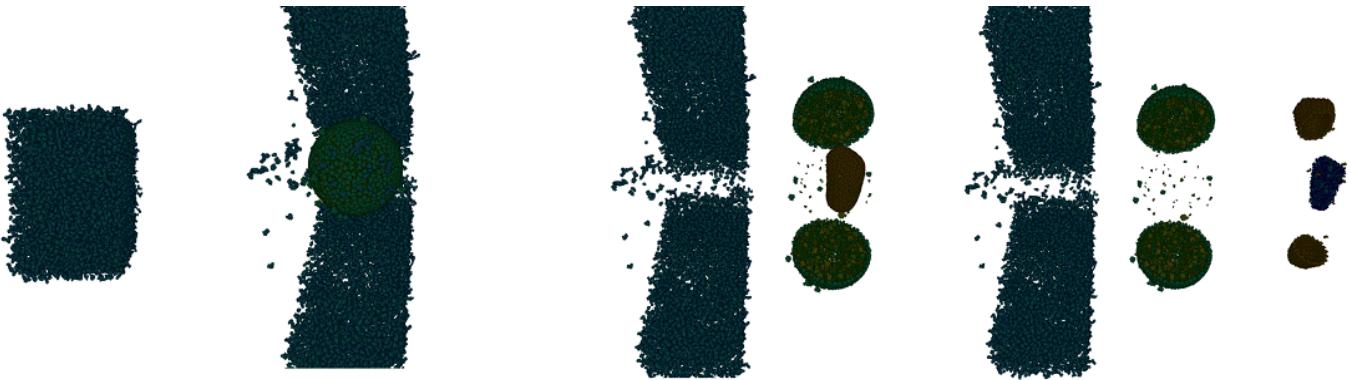


Fig. 6: Explosion

operator can introduce new control points into the motion path of a molecule, e.g., to re-direct it so that it does not occlude the existing scene. Operators in this stage also determine, whether to interpolate linearly between control points, or whether to use other strategies, such as cubic splines.

As such, this stage, takes a subset from the scene hierarchy as input. The child elements of this subset are analyzed in terms of their control points (at the very least original and target position) and their relation to the control points of the remaining elements of this subset (or the entire scene). Depending on the operator type, new control points that fulfill a desired function, such as clutter reduction in the form of more orderly transition paths, are created as the output of the stage.

3.5.3 Timing

The timing stage is responsible for the temporal coordination of the transition by determining the order and speed at which entities or subsets reach their target position and visual form. As such, this stage is the illustrators' canvas in the temporal dimension.

While the inherent purpose of this stage is to encode chronological information, i.e., the sequence of events, illustrators can also use it for additional purposes: they can make the transition more readable & visually engaging by reducing the number of simultaneous visual stimuli, i.e., by starting the transition of individual molecules / subsets with a time offset to each other, thus creating staged transitions/animations [cite heer?]. Timing can also be used for occlusion handling, i.e., by first starting the transition of elements that occlude important structures or that are closer to the viewing position, while other elements remain in their positions until they are revealed. Further, timing can also be used for controlling visual stimuli. The transition can be timed in a way that the attention is steered to a currently important structure or event by animating what should be in focus while keeping the remaining scene still.

As such, operators of this stage, depending on the intent that they implement, create a time curve for each entity. This time curve determines the start time and speed of the spatial and visual transition. Optionally, also an end time can be created, i.e., to determine, when an element should cease to exist but also, when the transition should stop, i.e., whether an element should reach its final destination as well as how close it should get. This can be used to create a target representation that looks like it stopped in mid-motion.

3.5.4 Sampling

This final stage determines the sampling strategy, i.e., at which rate the transition is sampled. The operator, that the illustrator chooses, therefore determines, whether the transition will be continuous or if sparser sampling will be applied, e.g., to extract a narrative sequence like in a comic strip. The lowest rate would therefore just output the final image of the target representation.

While the previous stages of the pipeline can be called multiple times in order to create more complex animations/transitions/stories,

the sampling stage is final, as it ties together the information from the previous stages to sample the visual result.

Before the sampling starts, the scene hierarchy is flattened again - which means that all information from higher level nodes is projected into the leaves, i.e., the individual molecules. The transformation matrices of higher level nodes are multiplied recursively with all their lower level children for each control point - so that each molecule knows about its global position for each control point.

The sampling stage then uses the output of the timing stage to determine at which rate/speed to interpolate between control points for each molecule. And it uses the output of the trajectory stage to determine how to interpolate between the supplied control points, e.g., linear, cubic,..

The sampling stage can also determine if the transition is pre-baked or sampled on the fly in real-time. This makes it possible to use a continuous pre-baked transition to create, for instance, a single result image that encodes the missing transition information within glyphs. These glyphs can be calculated from the continuous pre-baked information.

The continuously sampled information could also be exploited to create a hybrid visualization that displays a discretely sampled narrative sequence of small multiples. Upon clicking one of these small multiples, it could show the continuous transition to the next discrete element in the narrative sequence.

4 USE CASES

Real world illustrators now can use this pipeline of metamorphers to create continuous representations that depict a desired metamorphosis of a given source representation to an intended target representation by combining the metamorphers on each pipeline stage that create the intended relations between the source and the target representation. To actually enable an illustrator to apply our method, we created a proof of concept implementation of our pipeline. In order to apply our method to solve relevant problems, we approached an illustrator and, in collaboration, created three different use cases for a data set of HIV. This data set represents an HIV particle contained within blood serum (**see Figure XXX**). The three questions that we helped to answer with our demonstration are: 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, how do they look like, and in which approximate quantity are they present? 3) how large is the volume of each compartment and the molecules contained within in respect to each other?

4.1 Explosion of Molecular Structures

Since molecular structures of the HIV data are very densely packed, it is impossible to inspect the outer and inner structures of the virus at the same time. Since the four structures that we want to show, hierarchically contain each other, much like a Russian matryoshka doll,

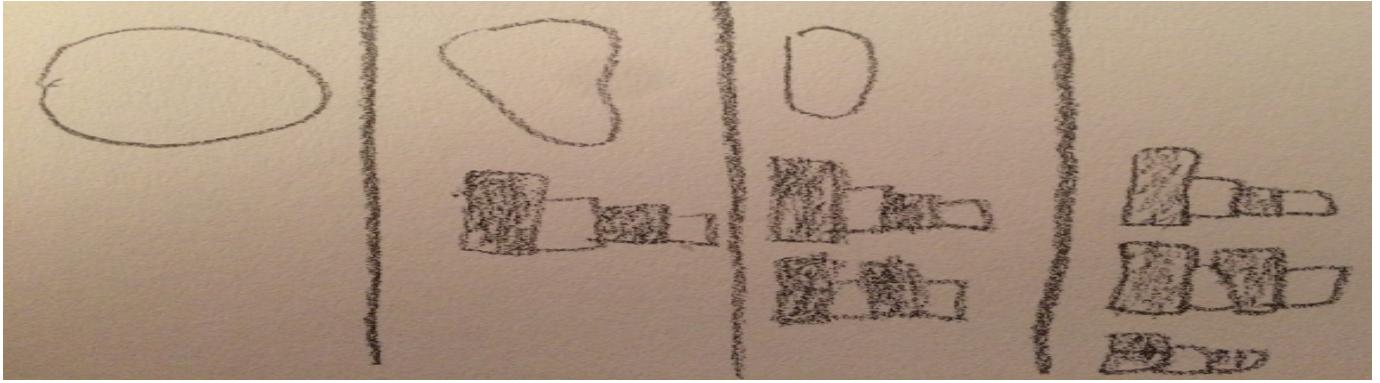


Fig. 7: Infovis

we chose to transform the virus representation to an exploded view (Figure ??), to answer our first question.

We can achieve the transition of the HIV data to an exploded view in the following way: First, we want to create the relation of the original data to the four compartment structures of the target representation. In the data re-structuring stage, we therefore need to create four subsets from our original data that correspond to these compartments. Since each compartment contains molecules of differing types, we implemented the *type range* metamorpher that creates subsets that contain all given molecules that match a specified type range. These four subsets are added to the root node of our data that contains all molecules. Since three of the four compartments that we just created are exploded in our desired target representation, we further have to spatially subdivide these compartments along a plane. We therefore implemented the *plane splitting* metamorpher that checks the position of a given list of molecules in respect to a plane that the user can freely position in the scene. Molecules are then assigned to two new subsets, depending on which side of the plane they are situated. The scene hierarchy is therefore extended by two additional child nodes containing the spatial subdivision for each subset that we just spatially subdivided.

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 need to call *translation* and *rotation* metamorphers in the layouting stage that create the translation (and slight rotation) of the explosion for each pair of spatially split subsets (Figure ??b). An additional translation moves each inner compartment to the left of its previously encapsulating compartment (Figure ??c).

We now created 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, source and target representation, remain within the same view frustum, and we do not want to explicitly point the camera on any specific details, we apply no metamorpher in the camera control stage.

Our original data differs from the exploded target representation only in position and topology (the split compartments). To present the transition, we therefore want to move all compartment subsets as a unit - they should 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 XXX layout metamorphers/operations to create the relation to the exploded representation. If all these operations would be executed at the same time, the transition could be hard to follow [cite Heer paper here]. In the timing stage, we can 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 start only after the previous is finished. To suggest the opening

motion of each exploding compartment in the final representation, we apply a *[need fitting name]* metamorpher that adjusts the time curve of a few random molecules in such a way, that they do not finish their transition. During the transition, the opening compartments thus leave a trail of molecule "breadcrumbs" behind.

The only thing that is left to do now is to sample the continuum representation that we created. We chose a *dense/continuous sampling* metamorpher to create a ten second animation with twenty four frames per second for the supplemental video. For the Figure ?? we applied a *sparse sampling* metamorpher [or we took stills from this video?][or we have one sampling metamorpher that we used for video and figures but with different parametrizations - how to spin/sell this?].

4.2 Schematization of Molecular Structures

The data consists of 42 types of molecules, that have a total of XXX number of instances, consisting of a total number of YYY atoms.

4.3 Representation of Quantitative Relations

[this is the old usecase section]

4.4 Schematization of Molecular Structures

In scientific illustrations, atlas based views schematic representations of cellular structures are used to give an insight of the molecular and atomic composition of these cells. The focus lies therefore on displaying individual molecules to convey their atomic composition, as well as on selected constellations of molecules to convey the structures that they collectively create. However, the original data model consists of millions of mostly noisy distributed atoms. To achieve this schematic representation therefore, one the one side, specific molecules have to be chosen as representatives of their type to be displayed at a sufficiently large scale (focus), while suppressing the noisy distribution of millions of atoms (context). On the other side, molecules that do not have a noisy distribution but form coherent structures, such as cell membranes, have to be preserved. This representation sacrifices the low level detail of the noisy atomic distribution, i.e., the exact count, position and shape of individual molecules. It aims to preserve the shape and size of compartments as well as molecule type overview, compartment relation (zugehörigkeit), and molecule shape. This metamorphosis corresponds with a transformation within the same visualization space.

@discussion of results: transition = more intuitive to follow.

because this type of automatic illustrative schematization has not been presented/solved yet in literature, we present it as our tertiary contribution...

4.5 Representation of Quantitative Relations

For the explanation of the molecular data, often also the relation of quantitative aspects is important for its understanding, e.g, how many different molecules of each type does the HIV particle contain, or how much of the volume within the particle does each type occupy? Graham Johnson answered this question in his award-winning video

demonstration of the decomposition of an XXX cell. In order to achieve this sort of representation, the molecular data has to be transformed into a different visualization space. A stronger abstraction than in the previous two examples takes place. To convey these quantitative information about aggregated volumetric and count information, shapes and positions of compartments and molecules are sacrificed. Since this transformation is across visualization spaces, the target representation is harder to relate to the original representation.

@discussion: here, large distance between representation forms in visualization space - a continuous transition is therefore especially suitable for conveying the transition..

4.5.1 Grouping by Type - use case C

We need to visually or spatially transform all molecules of the same type in a uniform fashion, e.g., to spatially transform them into a collective shape. [refer to all usecases here?] The output of this metamorpher is therefore a list of subsets that contain entities of the same type. The metamorpher parses a given list of entities and creates a new subset for each new type-ID that it finds. Entities of the matching type are then assigned as children to this subset.

4.6 Schematization of Molecular Structures

4.6.1 Applied Metamorphers

-data transform: 1) [type range grouper] create three high lvl subsets: the blood serum, the membrane, the capsid 2) [copy] the entire partitioned data set because we will render it in two different representations = \in results in copy A & B

-annotations: do the circular annotations?

-visual transform: A: blurrin & increasin contrast of alpha channel for nice sharp edges of each subset individually B: scalin

-layouting (spatial transform): A: renderin them on top of each other (occlusion management) B: rotatin

-navigation: not necessary, because we stay in the same visualization space / spatial extents

-trajectory: B: linear interpolation between rotations

-timing: staged per compartment distance field left to right for each

-sampling: continuous

4.7 Representation of Volumetric Relations

4.7.1 Applied Metamorphers

-data transform: 1) [type range grouper] create 3 hierarchical compartments by typerange 2) [single type grouper] split all three by type = \in subsets containing all molecules of same type for each hierarchical compartment

-annotations: 3) [txt-label] for each type subset 10) [representative] molecule for type subset

-blending: 4) [slice-flatterer] create target rep for each molecule with blending: slice with hight representing the molecule volume

-layouting: 5) [bar layout] for each type compartment - the layout puts all molecule slices on top of each other to create histogram bars
6) the [line layout] puts all the bars within a compartment side by side
7) the [translate layout] then moves the new center for the next line layout for the next compartment

8) layout: put label below each bar 9) layout: put rep below label

-trajectory: 10) [top-down-fall-in-component]: for each molecule in bar subset, we add a control point to the top of the bar, so that the molecule seems like falling into the bar instead of going straight from its original position to the designated position within the bar.

-timing: 11) [distance offset] a plane can be positioned in space. the distance of each molecule/compartmetn to this plane is measured and used for a the creation of a time offset that specified when each molecule is allowed to start its transition

12) timing: make label & rep appear when animation is finished

-guided navi: 13) [whole-data-in-view-keeper] update the camera pos & lookat to keep all molecules in the view frustum.

-sampling: 14) continuous sampling

4.8 Metamorphers

[just for reference] [describes PoC components that we implemented per pipeline stage]

[should we describe beforehand what (which representations) we try to achieve with these implementations?]

4.8.1 Partitioning

spatial subselection by clipping plane/object,

splitting into types,

splitting into type ranges

cloning

—not showcased but implemented: *spatial splitting operations into equal parts (pie splitter),

4.8.2 Annotations

text labels, icons (textures), maybe: data representatives (for each type), optional addon to each operator: connectors between annotation & assigned subset

4.8.3 Blending / Morphing

blur into collective shape, morph,

—not showcased but implemented: blending to texture

—other not implemented & not used examples: unfolding

4.8.4 Layouting

bar, line, translate, rotate, scale, schematization layout = combi of scale & rotate but selection of elements where what op is applied is very specific

—not showcased but implemented: slice, sphere, circle

4.8.5 Camera / Guided Navi

[whole-data-in-view-keeper] update the camera pos & lookat to keep all molecules in the view frustum.

other examples:

4.8.6 Trajectory

linear: from A straight to B, bundling/transit points

—other not implemented & not used examples: curved

4.8.7 Timing

offset function: delay timing by distance to plane & staging by type ... anything else?

—other not implemented & not used examples: offset according to: inherent spatial parameters (position, distance to other entities, density)

4.8.8 Sampling

continuous sampling,

—other not implemented & not used examples: sparse (comic strip / narrative sequence),

post-processing operators: motion blur,

5 IMPLEMENTATION

6 DISCUSSION

6.1 Discussion of Results

6.2 Expert Feedback

6.3 General Applicability of Our Approach

compatible data formats: point cloud, volume, polygonal?

compatible data types: dense hierarchical data with lots of repeating entities of a few dozen types

6.4 general discussion

6.4.1 additional outcomes

side products of our pipeline - free of charge / easily achievable with minimal additional effort: sequence: comic strips, static image with glyph

6.4.2 animation

tversky: congruence principle: the structure and content of an external representation should match the structure and content of the desired mental representation.

apprehension principle: the structure and content of the external representation should be readily and accurately perceived and comprehended.

6.4.3 things that should be preserved:

depending on the usecase / representation - not all properties are essential for each representation form.

- instance level: position of instances
- type level: shape of types, relative size of types, color of types (?), number relation between types
- compartment level: shape/pos/size/color of compartments / structures
- global level: volumetric dimensions of the data
- todo: what else?

6.5 occlusion

is of course a central factor that could hinder a user's understanding of a transition. can be dealt with at various stages of the pipeline. grouping: choose groups so that they dont interfere with each other (depending on how you plan to transform the data) TODO: come up with examples that describe which kind of grouping would be beneficial for which kind of target state e.g., group the data first into layers parallel to the viewing plane that basically peel the data layouts inner bar: within the bar occlusion does not matter, as long as the bar represents entities of the exact same type todo: other inner layouts & general outer general: the placement of entities/subsets should be chosen so that they dont occlude each other from the viewing angle. maybe we should not distinguish between inner and outer layout since this kind of restricts us to having two layouts instead of n.

then again, we could argue that there can be n-outer layouts, and one inner layout morphing: same as inner layout: within the shape occlusion is not an issue

trajectory: the trajectories offer two of techniques for avoiding occlusion.

edge bundling: setting control points so that paths don't occlude each other todo: anything else?

timing: coordination of timing and speed of elements, e.g., staging

7 CONCLUSION

7.1 future work

implementation of comic strip / animation hybrid

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