

Visibility Equalizer

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Abstract

In molecular biology and similar fields, knowledge transfer is commonly carried out through schematic illustrations. Traditionally, illustrations of biological processes on the molecular level have been created by manual hand drawing. Nowadays, complex models of various biochemical structures and micro-organisms exist. These models can be utilized in creating computer-generated biological illustrations through various molecular-visualization algorithms. When using such algorithms, it is beneficial for illustrators to be able to apply techniques common in traditional illustration, such as cutaway views. In this paper, we propose a method for enhancing real-time molecular-visualization algorithms with the capability to apply cutaway views. In contrast with existing cutaway algorithms, we take advantage of the specific nature of the biochemical models, which consists of multiple instances of a limited number of different molecular types. Our approach to cutaway views allows the illustrators to reintroduce some of the removed instances into the scene to communicate the presence of the given molecular type, yet maintaining the visibility of the internal structures of the model. This process is enabled through a novel interaction method for controlling the visibility in the instance-based scene. We refer to this method as visibility equaliser.

Categories and Subject Descriptors (according to ACM CCS): I.3.3 [Computer Graphics]: Picture/Image Generation—Viewing algorithms

1. Introduction

In the field of molecular biology, micro-biology, and medicine, illustrations are essential for the inter- and intra-disciplinary knowledge transfer. Over the years, illustrators have developed various techniques for capturing specific aspects of the displayed objects and processes. One of the most common methods utilized in the technical illustration are so-called *cutaway views*. When a cutaway view is applied, parts of the illustrated object are left out, such as if they were physically cut away. In this way, internal structures, which are to be communicated by the illustration, can be shown.

Creating hand-drawn illustrations of complex polymolecular structures, or even entire microorganisms, is an extremely tedious task. Such structures can contain hundreds

of thousands of molecules. Therefore, to communicate the intended message, it is often necessary to adequately simplify the structure in question. The illustration then consists of appropriate abstractions, while certain amount of information is lost.

A different approach is to utilize computational models of the structures which are to be illustrated, and utilizing software packages for visualization of these models. Such models, typically generated through simulation and statistical modelling, consists of large numbers of instances of several molecular types. The different molecular types contained within the model represent the chemical composition of the modelled object, while the distributions of the instances of the individual types represent the concentrations of the respective chemical compounds. High number of molecular instances, as well as their large densities, often make task of visualizing such models non-trivial. The advantage of this approach is the possibility to generate illustrations exhibiting high degree of accuracy, which would require extremely high effort.

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When utilizing the molecular models for the illustrative purposes, algorithmic equivalents of the traditional illustrative techniques are often employed. For instance, software packages for computer-aided illustration often offer an option to manipulate and apply culling objects for creating cut-away views of the illustrated models or scenes. The culling objects work in such a way that the part of the rendered scene enclosed by the surface of the cutting object is removed, thus making previously occluded structures visible.

In general, illustrators choose such placements of the culling objects that only unimportant parts of the scene are removed and no essential information is lost. Specifically in molecular visualization, it is often desired that the culling objects are positioned so that all molecular types are represented in the generated scene. However, the placement of the culling objects also needs to correspond with the geometrical structure of the model, so that it is obvious what are the artificial cuts introduced in the illustration, and what is their purpose. Given the high complexity inherent to most of the molecular models, meeting both of these requirements at the same time is a difficult task. With each additional culling object that the illustrator introduces into the scene, it gets progressively more difficult to keep overview of which molecular types are still represented in the scene in sufficient amounts.

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An example is shown in Figure 1. Figure 1a shows an illustration of a HIV virus. In Figure 1b, a cutaway view is used to reveal internal structures of the virus - the capsid containing the RNA. Some of the glycoproteins (yellow molecules) are left in the illustration to communicate their presence on the surface of the virus particle. In particular, those glycoproteins which are not occluding the object of interest, were chosen to be kept in the illustration providing the contextual information.

2. Related Work

[VKG05] [BHW*07] [BF08] [LRA*07] [LHV12] [MAPV15]

3. Overview

3.1. Design principles

There are several issues with using cutaway views in illustrations. First one is that it has to be clear from the visual representation of the cut that the given part of the object has been removed artificially for the sake of illustration. Otherwise the viewers might believe that the hole created by the cut is in fact inherent part of the object. This is commonly solved by using specific shapes of the cuts which significantly differ from the shapes naturally occurring within the object (e.g., using circular cut on object which only have straight edges).

Another issue is that the information about the part of the

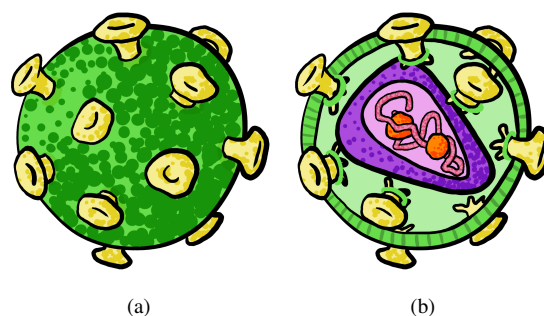


Figure 1: (a) Illustration of a HIV virus. Here, outside membrane of the virus particle is visible. (b) Cutaway view of the HIV virus. Despite the cutaway, some of the glycoproteins (yellow molecules) are kept in the view to provide adequate context.

object that is being cut away is lost. In technical illustration, this issue is often circumvented by displaying contours of the cutaway part of the object. Alternatively, small portions of the cutaway parts can be reintroduced into the scene. These graphical elements are not occluding the objects of interest, but at the same time they help to convey the overall shape of the cutaway part.

References

- [BF08] BURNS M., FINKELSTEIN A.: Adaptive cutaways for comprehensible rendering of polygonal scenes. In *ACM SIGGRAPH Asia 2008 Papers* (New York, NY, USA, 2008), SIGGRAPH Asia '08, ACM, pp. 154:1–154:7. URL: <http://doi.acm.org/10.1145/1457515.1409107>, doi:10.1145/1457515.1409107. 2
- [BHW*07] BURNS M., HAIDACHER M., WEIN W., VIOLA I., GRÖLLER M. E.: Feature emphasis and contextual cutaways for multimodal medical visualization. In *Proceedings of the 9th Joint Eurographics / IEEE VGTC Conference on Visualization* (Aire-la-Ville, Switzerland, Switzerland, 2007), EUROVIS'07, Eurographics Association, pp. 275–282. URL: <http://dx.doi.org/10.2312/VisSym/EuroVis07/275-282>, doi:10.2312/VisSym/EuroVis07/275-282. 2
- [LHV12] LIDAL E. M., HAUSER H., VIOLA I.: Design principles for cutaway visualization of geological models. In *Proceedings of Spring Conference on Computer Graphics (SCCG 2012)* (May 2012), pp. 53–60. 2
- [LRA*07] LI W., RITTER L., AGRAWALA M., CURLESS B., SALESIN D.: Interactive cutaway illustrations of complex 3d models. In *ACM SIGGRAPH 2007 Papers* (New York, NY, USA, 2007), SIGGRAPH '07, ACM. URL: <http://doi.acm.org/10.1145/1275808.1276416>, doi:10.1145/1275808.1276416. 2
- [MAPV15] MUZIC M. L., AUTIN L., PARULEK J., VIOLA I.: cellview: a tool for illustrative and multi-scale rendering of large biomolecular datasets. In *Eurographics Workshop on Visual Computing for Biology and Medicine* (Sept. 2015), B'uhler K., Linsen L., John N. W., (Eds.), EG Digital Library, The Eurographics Association, pp. 61–70. URL:

http://www.cg.tuwien.ac.at/research/publications/2015/cellVIEW_2015/.
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- [VKG05] VIOLA I., KANITSAR A., GROLLER M. E.: Importance-driven feature enhancement in volume visualization. *IEEE Transactions on Visualization and Computer Graphics* 11, 4 (July 2005), 408–418. URL: <http://dx.doi.org/10.1109/TVCG.2005.62>, doi:10.1109/TVCG.2005.62.2