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Contours in Visualization

This thesis studies the visualization of set collections either via or defines as the relations among contours.

In the first part, dynamic Euler diagrams are used to communicate and improve semimanually the result of clustering methods which allow clusters to overlap arbitrarily. The contours of the Euler diagram are rendered as implicit surfaces called blobs in computer graphics. The interaction metaphor is the moving of items into or out of these blobs. The utility of the method is demonstrated on data arising from the analysis of gene expressions. The method works well for small datasets of up to one hundred items and few clusters.

In the second part, these limitations are mitigated employing a GPU-based rendering of Euler diagrams and mixing textures and colors to resolve overlapping regions better. The GPU-based approach subdivides the screen into triangles on which it performs a contour interpolation, i.e. a fragment shader determines for each pixel which zones of an Euler diagram it belongs to. The rendering speed is thus increased to allow multiple hundred items. The method is applied to an example comparing different document clustering results.

The contour tree compactly describes scalar field topology. From the viewpoint of graph drawing, it is a tree with attributes at vertices and optionally on edges. Standard tree drawing algorithms emphasize structural properties of the tree and neglect the attributes. Adapting popular graph drawing approaches to the problem of contour tree drawing it is found that they are unable to convey this information. Five aesthetic criteria for drawing contour trees are proposed and a novel algorithm for drawing contour trees in the plane that satisfies four of these criteria is presented. The implementation is fast and effective for contour tree sizes usually used in interactive systems and also produces readable pictures for larger trees.

Dynamical models that explain the formation of spatial structures of RNA molecules have reached a complexity that requires novel visualization methods to analyze these model's validity. The fourth part of the thesis focuses on the visualization of so-called folding landscapes of a growing RNA molecule. Folding landscapes describe the energy of a molecule as a function of its spatial configuration; they are huge and high dimensional. Their most salient features are described by their so-called barrier tree -- a contour tree for discrete observation spaces. The changing folding landscapes of a growing RNA chain are visualized as an animation of the corresponding barrier tree sequence. The animation is created as an adaption of the foresight layout with tolerance algorithm for dynamic graph layout. The adaptation requires changes to the concept of supergraph and it layout.

The thesis finishes with some thoughts on how these approaches can be combined and how the task the application should support can help inform the choice of visualization modality.