

Graph Drawing Contest Report

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Abstract. This report describes the Tenth Annual Graph Drawing Contest, held in conjunction with the 2003 Graph Drawing Symposium in Perugia, Italy. The purpose of the contest is to monitor and challenge the current state of the graph-drawing technology.

1 The Contest Description

In the past the graph drawing contest had “challenge graphs” and the primary goal were “nice” drawings of these graphs. In addition there was an artistic category. Details can be found in the contest reports of the previous Graph Drawing Symposia.

The concept for this year’s contest has been revised with a focus on research directions and the hope for more entries. The contest theme was “drawing graphs within graphs”. This emphasizes the largely open question of how to visualize distinguished graph structures that are contained in larger graphs in a distinct way, such as: Describe algorithms that make explicitly or implicitly given subgraphs visible and display them, e.g., a (or all) $K_{3,3}$ and K_5 in a non-planar graph. Embed a distinguished subgraph in a given partial drawing of a graph in a suitable way. Make all occurrences of a small graph visible and show how they distribute over the graph, or how they relate to each other. Draw a graph using templates of certain subgraphs. Given a nested graph, place the contained graphs in a layout of their containers or vice versa. Make isomorphic subgraphs recognizable.

Two real world data sets were provided, that could be used for the illustration of the approaches. The first network shows the transcriptional regulation of *Escherichia Coli*. This network contains many occurrences of so-called motifs, which are described in [1]. Motifs are distinguished subgraphs which should be used in a graph drawing algorithm to clarify the structure of the network. The second network is a social network that represents organizations involved in drug policy making. There are confirmed and unconfirmed lines of communication between the organizations, and the inherent structure of the organization should be displayed. Text descriptions for the 2003 contest were made available via the World Wide Web and announced with the Graph Drawing Symposium. The data on the graphs was provided in several graph formats.

2 The Decisions

The seven entries address the contest theme in different ways, using hierarchical approaches and reduction techniques, 3D, and nice curves. The entries are of a high scientific level and describe research work at an early stage. They contained interesting new ideas with promising concepts for graph drawing. The authors spent much time and effort for the preparation of their entries, and students were strongly involved in the preparation of most entries.

The contest jury, formed by the authors of this report, evaluated the entries and made a pre-decision based on the originality and closeness towards the contest theme. Due to conflicting interests, the final decision on the first prize winners was made by an independent jury with Patrick Healy, Joe Marks, and Sue Whitesides.

2.1 The Winners

There are two first prize winning entries: “Drawing graphs within graphs: A contribution to the graph drawing contest 2003” by Daniel Gmach, Paul Holleis, and Thomas Zimmermann, students at the University of Passau, Germany, and “Graph pattern analysis with PatternGraffiti” by Christian Kuklas, Dirk Koschützki, and Falk Schreiber from the Bioinformatics Center, Gatersleben, Germany. Both teams are experienced graph drawing contest participants, since the Passau students were among the winners in 2002, and F. Schreiber was a contest winner in 1995.

Gmach, Holleis, and Zimmermann directly approach the contest theme and describe how to draw graphs within graphs. Distinguished subgraphs are mapped into supernodes, such that a summary graph remains from the given input graph. The subgraphs and the summary graph may be layouts separately, using even different drawing algorithms. Overlapping subgraphs are treated separately, taking their union or their symmetric difference as new subgraphs, or making copies of the overlapping parts. The edges between the supernodes are computed from exclusive connections between the subgraphs behind the supernodes. This process is illustrated in Fig. 1. The approach has been applied to the largest connected component of the transcriptional network of *Escherichia Coli* with then reduces from 328 vertices to a graph with just 16 supernodes, each representing a special motif (SIM). The summary graph clearly displays the connections between the SIMs, see Fig. 2. There is also a prototype implementation in Graffiti, a graph drawing tool from the University of Passau. A more detailed description of the approach is supposed to appear in a forthcoming paper.

Motivated by the GD2003 contest, Kuklas, Koschützki and Schreiber have developed PatternGraffiti as is a tool for the analysis and display of pattern. A pattern is a distinguished labeled subgraph. It is extended by regular expressions for the edge and node labels. A matching is a subgraph isomorphism of the pattern and a match of the labels. Matchings are computed by an adaptation of Ullmann’s algorithm [4]. Different pattern are distinguished by a colouring, and all occurrences of a pattern are drawn in the same way using an adapted

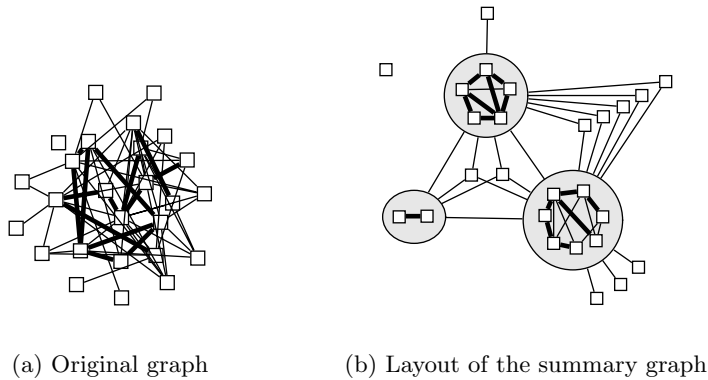


Fig. 1. Social network and connection sets

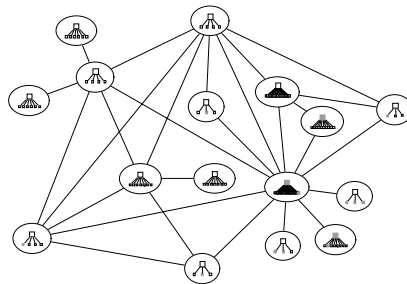


Fig. 2. SIMs in transcriptional network

spring embedder algorithm. PatternGraffiti is a plug-in to Graffiti. It enables to the user to specify a set of patterns, which are then searched in the input graph and visualized by the algorithm. A screenshot with a part of the transcriptional network and a motif (the original is coloured) is shown in Fig. 3. The approach has also been applied to the data from the social network. A more detailed description of the approach is supposed to appear in a forthcoming paper.

2.2 The Runners-Up

The following entries are the second prize winners:
Breanne Byck, Jill Joevenazzo, Elspeth Nickle, Jon Wilsdon, and Steve Wismath from the University of Lethbridge, Canada, address the social network and use a 3D approach to highlighten the inherent structure within the given network. Green and red edge colourings are used to emphasize the confirmed and unconfirmed relationships. Their central image in a stereogram, a 2D drawing which appears to be 3D. See also their poster in this volume.

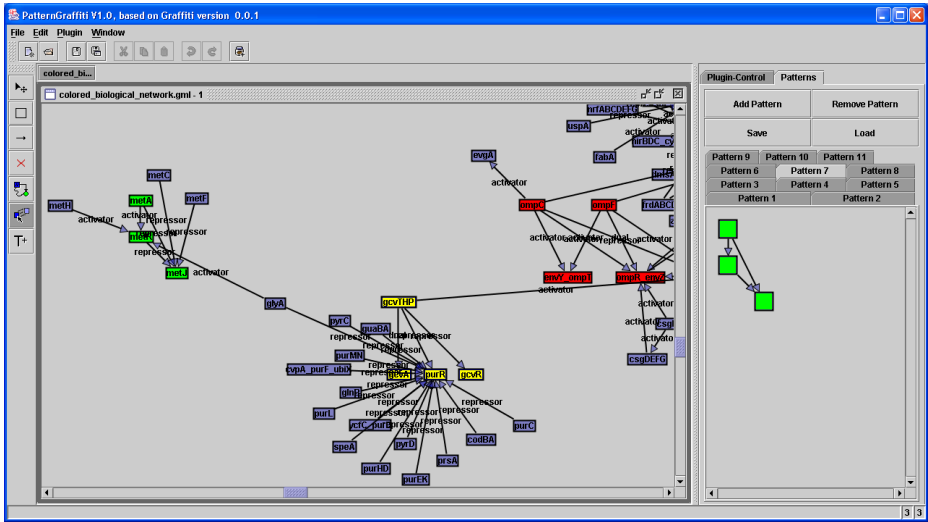


Fig. 3. Screenshot from PatternGraffiti

David Eppstein, Michael T. Goodrich, and Jeremy Y. Meng, University of California, Irvine, CA, applied their recent approach on confluent drawings [3] to reduce the visual complexity of drawings. The outcome are “dancing bicliques”, showing the famous Tower of Pisa in a new way, see Fig. 4. Given a layered graph, the edges between two adjacent layers are covered by bicliques i.e., complete bipartite graphs, which are then displayed by confluent drawings. Bicliques are drawn in colours, since the planarity constraint from [3] cannot be preserved.

Ken Frank, Michigan State University, East Lansing, MI, uses his KliquesFinder clustering algorithm to produce crystalized sociograms, and has applied it to express and represent friendships among the French financial elite.

Marco Gärtler from the University of Karlsruhe, Germany, has introduced an advanced reduction technique to decompose a network into smaller pieces. Besides the motifs from [1] he has found other remarkable patterns in the regulatory network which are collapsed for the contraction of the network. The remainder is drawn in a DAG layout style. This technique is suitable for the interactive exploration of other structural data.

Nestor Sosa, Andreas Kremling, Esther Ratsch, and Isabel Rojas from the European Media Laboratory, Heidelberg, Germany, and the Max Planck Institute for Dynamic Complex Technical Systems in Magdeburg describe the development of an application for the visualization of the transcriptional networks. The main concept towards a visualization is a simplification of the network using the given motifs and other substructures. The reduction is enormous, so that a three layer network remains from the transcriptional network of *Escherichia Coli*, which can be drawn right away.

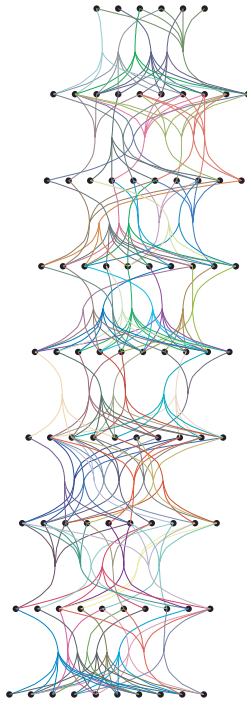


Fig. 4. Tower of Pisa

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