A Visual Comparison of Hand-Drawn and Machine-Generated Human Metabolic Pathways

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Abstract

This poster abstract presents a visual comparison between three hand-drawn and one machine-generated human metabolic pathway diagrams. The human metabolic pathways, which describe significant biochemical reactions in the human body, have been increasingly investigated due to the development of analysis processes and are compiled into pathway diagrams to provide an overview of reaction in human body. This complex network includes about $5,000$ *metabolites and* $7,500$ *reactions, which are hierarchically nested and difficult to visualize. We collect and analyze well-known human metabolic pathway diagrams, and summarize the design choices of these diagrams, respectively. Together with a machine-generated diagram, we can understand the visual complexity of three hand-drawn and one machine-generated diagrams.*

CCS Concepts

•***Human-centered computing*** → ***Graph drawings;*** *Information visualization;*

1. Introduction

Human metabolic pathways, structures depicting our knowledge on molecular interactions in human physiological systems, have been studied in the past 20 years. This relationship network is built by carefully controlled experiments, and new findings and errors are continuously added and revised to improve this hierarchical dynamic network. To understand this complex network, biologists manually arrange the position of nodes and edges to maintain the high visual quality of the node-link diagrams, pathway diagrams. Although the hand-drawn diagrams provide high understandability, this is a very time-consuming and it becomes an impractical task when the network grows.

Since relationship has been considered as the most important information for biologists, several studies were conducted to generate high-quality pathway diagrams. The popular graph drawing algorithm such as forced-directed and hierarchical layouts are naturally incorporated to visualize pathway datasets [BBS14]. Other techniques including rebuilding sub-diagrams from well-known KEGG database [GKK14], overlaying omics information on pathway diagrams [JP14], and aligning network nodes on grids [LK05] are also conducted. Nonetheless, those techniques are developed for small biological networks.

Human metabolic pathways collected by biologists nowadays include about $5,000$ metabolites and $7,500$ reactions and are often used to accomplish disease treatment. Several metabolic pathway diagrams are manually drawn by community-driven research groups, including *KEGG pathway maps* [KG00], *Recon-Map* [NDG*17], and *Roche Biochemical Pathways* [Mic17] are all manually drawn to achieve their high visual quality.

In this paper, we summarize the primary drawing principles of each selected hand-drawn human metabolic pathway diagram and the diagram automatically generated using our system [WNV18]. This will provide a quick visual comparison between human-generated and machine-generated pathway diagrams.

2. Comparison between Manually-Drawn Map and Automatically-Drawn Map

Figure 1 shows our selected human metabolic pathway diagrams, including the overview map of Kyoto Encyclopedia of Genes and Genomes (KEGG) - GenomeNet (Figure 1(a)) [KG00], the overview map of the Virtual Metabolic Human database (Figure 1(b)) [NDG*17], the metabolic pathway map of Roche (Figure 1(c)) [Mic17], and the diagram automatically generated using our system (Figure 1(d)). These diagrams are strongly depending on the preferences of diagram designers, and thus selected information shown on the diagrams is also various. We summarize these designs as follows:

Overview diagram of KEGG

A1. Undirected graph: The arrow in a pathway diagram represents significant chemical reactions, while the reversed reaction could exist even though it is not experimentally signifi-

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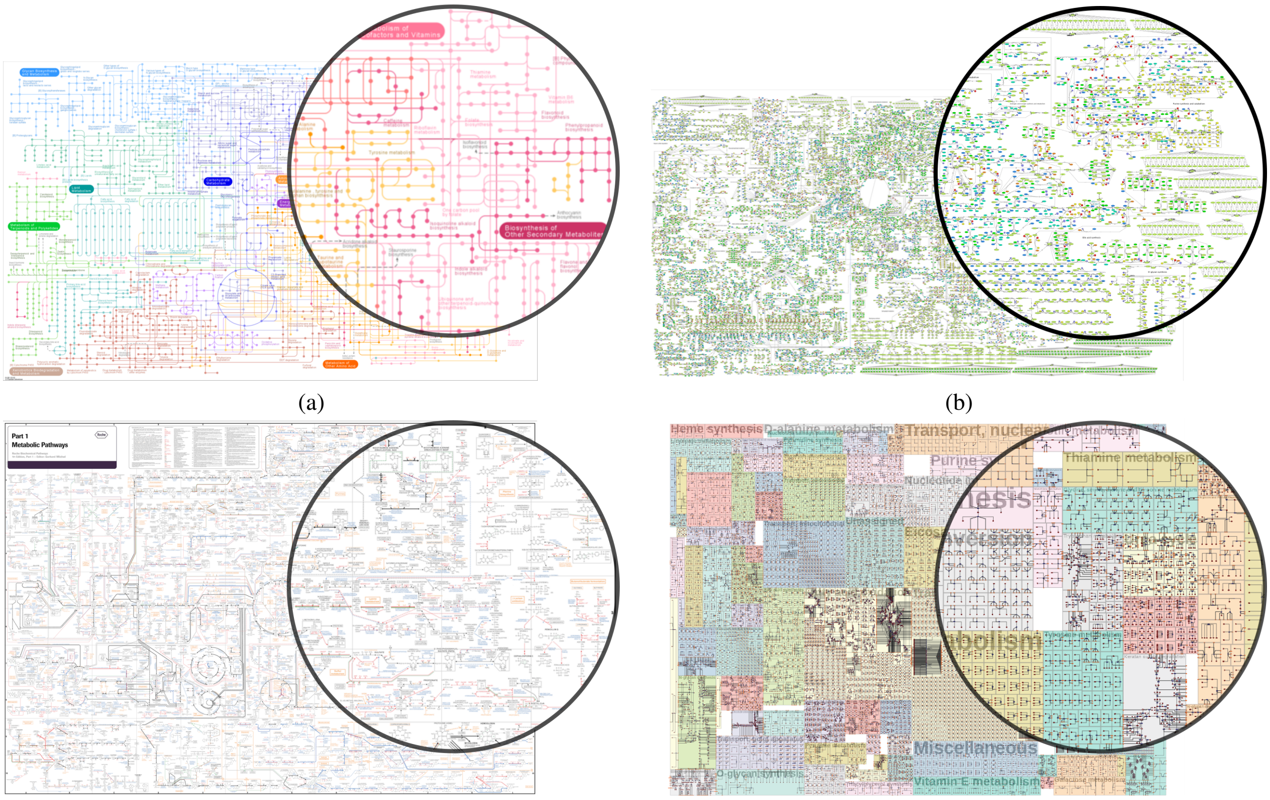

(a) (b)

(c) (d)

Figure 1: *Human metabolic pathways manually drawn by (a) Kyoto Encyclopedia of Genes and Genomes (KEGG) - GenomeNet [KG00], (b) Virtual Metabolic Human (VMH) database [NDG* 17], (c) Roche Pathway [Mic17], and (d) Human Metabolic Pathway automatically generated using our system.*

cant. Removing the arrows improves the visual representation and the aforementioned uncertainty.

A2. Category based color encoding: Color is used to visually guide the users to the correct theme of each sub diagram.

A3. Pattern: Local layout is preserved from the diagram of the same theme.

Overview diagram of VMH

B1. Directed graph: The arrows are used to represent significant chemical reactions.

B2. Color encoding of metabolites: The color of nodes shows the types of the metabolites, including ion, water, antioxidant and free radicals, and cofactors.

B3. Node name: Metabolite names are drawn on the diagram.

Overview diagram of Roche

C1. Directed graph: The arrows are used to represent significant chemical reactions.

C2. Edge based color encoding: Reactions are highlighted using different colors.

C3. Structural formula: graphic representation of the molecular structure is embedded in the diagram.

System generated pathway diagram

D1. Directed graph: The arrows are used to represent significant chemical reactions.

D2. Bundled edges: Long edges are bundled to improve the visual clutter.

D3. Global and local context: Category information is constrained within a rectangle and detailed relationship is represented in nearly orthogonal fashion.

D4. Customization: Users can customize the diagram by arranging the neighboring rectangles.

3. Conclusion

In this poster, we investigate several hand-drawn and automatic generated pathway diagrams and summarize their corresponding design principles. In the future, we plan to investigate the understandability and usability in comparison between hand-drawn diagrams and automatically generated diagrams.

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