

Bioinformatics Center – Bio-knowledge Engineering –

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Tanta University, Egypt, 17 February–15 August
Iliia State University, Georgia, 8 April–5 July
Boston University, U.S.A., 30 May–19 August
National Cheng Kung University, Taiwan, 17 September–17 March

Scope of Research

We are interested in graphs and networks in biology, chemistry and medical sciences, which include metabolic networks, protein-protein interactions and chemical compounds. We have developed original techniques in machine learning and data mining for analyzing these graphs and networks, occasionally combining with table-format datasets, such as gene expression and chemical properties. We have applied the developed techniques to real data to demonstrate the performance of the methods and further to find new scientific insights.

KEYWORDS

Bioinformatics Machine Learning
Computational Genomics Systems Biology
Data Mining

MLAB Support 2013
2013 International Workshop on Machine Learning and Applications to Biology
August 5 - 6, 2013
Creative Research Institute, Hokkaido University

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— 16 inspiring talks —

Samuel Kaski (Khalifa University, Finland) Learning from Multi-Modal Data: Images, Posing, and Data Transition	Ziv Bar-Joseph (Carnegie Mellon University, USA) Algorithms in Biology
Masashi Sugiyama (Osaka Institute of Technology, Japan) Change Detection in Multi-Dimensional Time Series from Distributional Change to Structural Change	Jean-Philippe Vert (Mines ParisTech, France) Fast Linear-Score Feature Prediction from (Pseudo-)Data as a Flow Problem
Motoki Shiga (Osaka University of Technology, Japan) Non-negative Matrix Factorization with Auxiliary Information	Marin Fritsch (IST, Austria) Adaptive Clustering Algorithms: Techniques to Modern High-Throughput Data
Canh Hao Nguyen (Kyushu University, Japan) Explanatory Graph Embedding for Label Propagation	Yayoi Natsume (IST PRESTO, Japan) Detection of Time-Dependent In-Homogeneous Substructures
Koji Tsuda (IST, Austria) Mining Combinatorial Regulators	Shin-ichi Minato (Hokkaido University/IST PRESTO, Japan) Recent Research Activities of EDC/ODD-Based Economic Structure Identification
Ian Johnston (Boston University, USA) Spatially Weighting Clones in Variable Selection for GWAS	Satoshi Morinaga (IST, Austria) Fast and Accurate Bayesian Inference for Submodular Hierarchical Latent Variable Models
David duWard (IST, Austria) A Population Path-Following Approach for Discovering Interactions in High-Dimensional Survival Data	Toby Dylan Hocking (Osaka Institute of Technology, Japan) Learning to Compare Graph Layouts
Ichigaku Takigawa (Hokkaido University, Japan) Identifying Protein-Biomolecules Significantly Shared among Interacting Structure Pairs	Masayuki Karasuyama (Kyushu University, Japan) Local Factor-based Substructure Feature Selection

CRIS
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Hokkaido University

Organizers: Ichigaku Takigawa (Hokkaido University) / Hiroshi Mamitsuka (Kyoto University)

Selected Publications

Zheng, X.; Ding, H.; Mamitsuka, H.; Zhu, S., Collaborative Matrix Factorization with Multiple Similarities for Predicting Drug-Target Interactions, *Proceedings of the Nineteenth ACM SIGKDD International Conference on Knowledge Discovery and Data Mining (KDD 2013)*, 1025-1033 (2013).

Nakamura, A.; Saito, T.; Takigawa, I.; Kudo, M.; Mamitsuka, H., Fast Algorithms for Finding a Minimum Repetition Representation of Strings and Trees, *Discrete Applied Mathematics*, **161 (10-11)**, 1556-1575 (2013).

Takigawa, I.; Mamitsuka, H., Graph Mining: Procedure, Application to Drug Discovery and Recent Advance, *Drug Discovery Today*, **18 (1-2)**, 50-57 (2013).

Mamitsuka, H.; DeLisi, C.; Kanehisa, M., Data Mining for Systems Biology: Methods and Protocols *Methods in Molecular Biology*, **939**, (2013).

Hancock, T.; Takigawa, I.; Mamitsuka, H., Identifying Pathways of Co-ordinated Gene Expression Data Mining for Systems Biology: Methods and Protocols, *Methods in Molecular Biology*, **939**, 7, 69-85 (2013).

Global Graph Comparison for Biological Networks

We investigate the new problem of global graph comparison from statistical viewpoint, with the application in studying evolutions and preservations of biological networks of different species. Previous works on comparing graphs mainly focused on comparing graphs locally, considering graphs as a collection of subgraphs (as in the case of large chemical structures consisting of many independently functioning substructures). This does not satisfy the requirement of our application in comparing species through their corresponding metabolic, signaling or protein-protein interactions networks. Instead, in our application, the global structures of networks, such as connectivity and robustness of the networks determine the species' biological functionalities. This can contribute to building phylogenetic trees.

We formulate this problem as a graph comparison problem for labeled graphs. Considering orthologous genes from different species as the same node in different graphs, the problem boils down to comparing different graph structures on the same node set. Taking into account biological interpretation of network connectivity and robustness, we require that graph pairs are similar if they differ in the well-connected parts, and similar in sparse parts. For example, in Figure 1, graph G1 should be close to G2, and

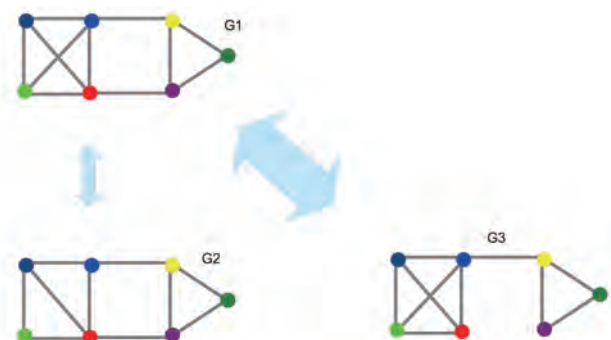


Figure 1. G1 is closer to G2 than to G3 as G3 is not robust, can be disconnected by removing one edge.

far from G3, even though both pairs have one edge difference. Therefore, we use eigenvectors and eigenvalues of graph Laplacians to derive similarities and distances (*ged*) for graphs globally [1,2].

Our formulation for this problem is shown to have many properties. It is shown to have the ability to weight edges in graphs according to their roles in network structures, potentially showing the important steps in biological processes. It is a generalization of comparing embeddings of graphs with graph Laplacians, paving way for more extensions with desirable statistical properties [2]. It has unexpected applications beyond our initial intention. We can also use it to select graph-cut clustering solutions, making it a general tool for graph data analysis. As shown in Figure 2, *ged* can differentiate bad clustering solutions with disconnected clusters from good ones [2]. This cannot be seen from usual clustering algorithms. The next step would be applying the method to comparing biological networks of different species to studies their evolutions and preservations in terms of these biological networks.

References

- [1] Wicker, N.; Nguyen, C. H.; Mamitsuka, H., A New Dissimilarity Measure for Comparing Labeled Graphs, *Linear Algebra and its Applications*, **438-5**, 2331–2338 (2013).
- [2] Nguyen, C. H.; Wicker, N.; Mamitsuka, H., Selecting Graph Cut Solutions via Global Graph Similarity, *IEEE Transactions on Neural Networks and Learning Systems* (in press).

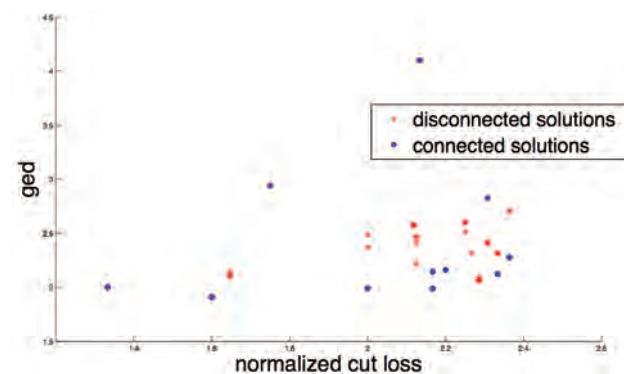


Figure 2. Small *ged* distances usually mean good clustering solutions (connected clusters).