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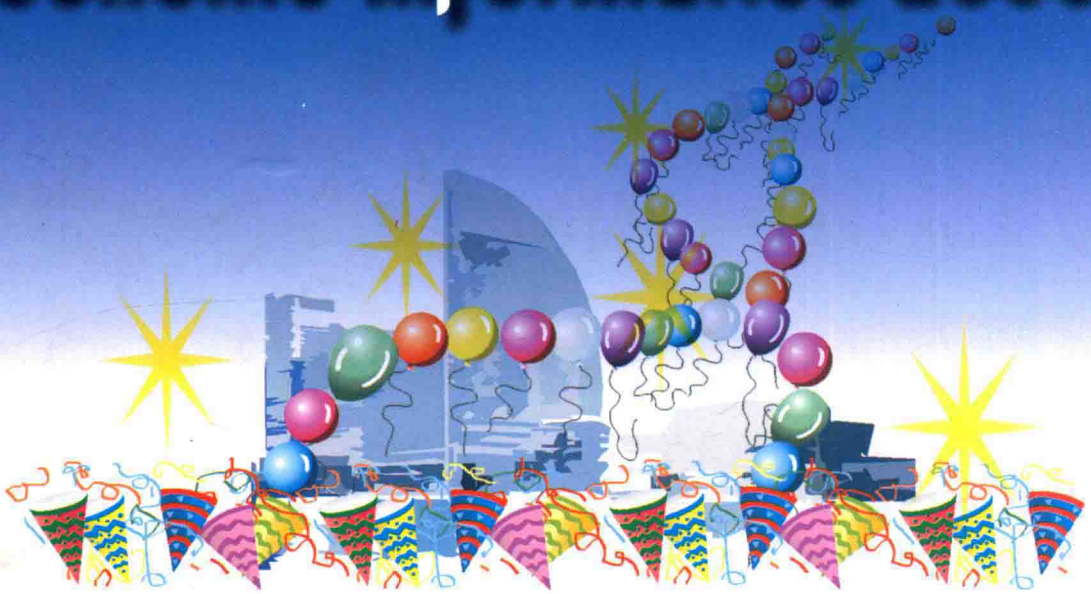

Shinichi Morishita • Sang Yup Lee • Yasubumi Sakakibara
Editors

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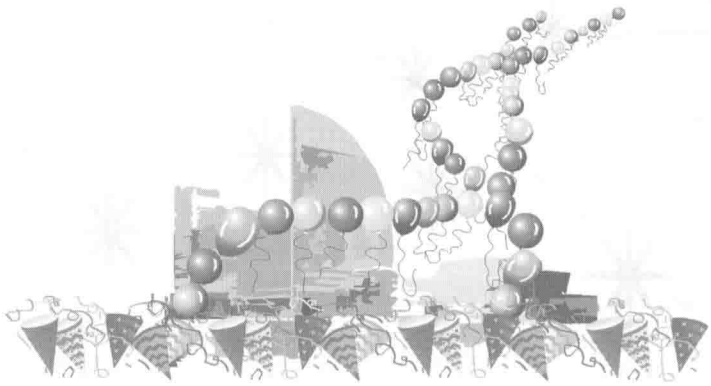

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4	Genome Informatics Workshop IV	1993	4-946443-20-7
5	Genome Informatics Workshop 1994	1994	4-946443-24-X
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PREFACE

This issue of Genome Informatics contains papers presented at the Twentieth International Conference on Genome Informatics (GIW 2009) held in Yokohama, Japan from December 14th to 16th, 2009.

The first Genome Informatics Workshop (GIW) was held in Tokyo in 1990, the dawn of human genome sequencing. Remarkably, the invited talks by Akiyoshi Wada, Ross Overbeek, and Yoshiyuki Sakaki that year were all on the subject of the computational support for genome sequencing. Since then, GIW has provided unique opportunities to encourage bioinformatics and create bridges between theory and experiments, academia and industry, and East and West. GIW is the longest running international bioinformatics conference.

The 20th International Conference on Genome Informatics (GIW 2009) was held at PACIFICO Yokohama Convention Center, Japan, on December 14-16, 2009. We accepted 18 papers from the 39 submissions. The two best papers were:

- C. Nelson Hayes, Diego Diez, Nicolas Joannin, Minoru Kanehisa, Mats Wahlgren, Craig E. Wheelock, and Susumu Goto. "Tools for investigating mechanisms of antigenic variation: new extensions to varDB."
- Kouichi Kimura and Asako Koike. "Localized suffix array and its application to genome mapping problems for paired-end short reads."

In addition, this book contains abstracts from the five invited speakers: Sean Eddy, HHMI's Janelia Farm (USA), Minoru Kanehisa, Kyoto University (Japan), Sang Yup Lee, KAIST (Korea), Hideyuki Okano, Keio University, (Japan), and Mark Ragan, University of Queensland (Australia).

The electronic versions of all these papers in this issue are also freely available from the website of the Japanese Society for Bioinformatics (JSBi) (`http://www.jsbi.org/journal.html`).

Shinichi Morishita
Sang Yup Lee
GIW 2009 Program Committee Co-Chairs

Yasubumi Sakakibara
GIW 2009 Conference Chair

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First of all, we would like to thank the authors for their efforts in preparing their manuscripts. We also appreciate the great efforts made by the program committee members and the external reviewers in the reviewing process. We further acknowledge the assistance from the local organizing committee members for arranging the conference venue. Special thanks are due to the conference editorial staff for their excellent work, especially, Emi Ikeda, Ayumu Saito, and Asako Suzuki. Finally, GIW 2009 was sponsored by the Human Genome Center of the Institute of Medical Science at the University of Tokyo, and the Japanese Society for Bioinformatics.

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CONTENTS

PART A

Full Papers

PREDICTING PROTEIN-PROTEIN RELATIONSHIPS FROM LITERATURE USING LATENT TOPICS

TATSUYA ASO[1] KOJI EGUCHI[1]
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This paper investigates applying statistical topic models to extract and predict relationships between biological entities, especially protein mentions. A statistical topic model, Latent Dirichlet Allocation (LDA) is promising; however, it has not been investigated for such a task. In this paper, we apply the state-of-the-art Collapsed Variational Bayesian Inference and Gibbs Sampling inference to estimating the LDA model. We also apply probabilistic Latent Semantic Analysis (pLSA) as a baseline for comparison, and compare them from the viewpoints of log-likelihood, classification accuracy and retrieval effectiveness. We demonstrate through experiments that the Collapsed Variational LDA gives better results than the others, especially in terms of classification accuracy and retrieval effectiveness in the task of the protein-protein relationship prediction.

Keywords: Biomedical text mining; probabilistic topic models.

1. Introduction

There have been increasing demands for organizing knowledge accumulated in documents and then generating potential hypotheses in biomedical fields. This paper focuses on the task to predict relationships between biological entities. Research trends on the biomedical relationship extraction can be categorized into: (1) methods using manually or automatically generated templates, (2) methods based on natural language processing, and (3) statistical co-occurrence-based methods [1, 2]. This paper focuses on the third approaches targeting a specific type of biomedical entities, proteins. While the natural language processing-based approaches usually extract entity relationships within a document, statistical methods are based on co-occurrence of biomedical entities or their related statements in a set of documents to extract relationships between the entities. Statistical topic models are promising for this objective.

Statistical topic models (e.g., [3, 4]) are based on the idea that documents are mixtures of topics, where a topic is a probability distribution over words, in order to capture semantics or to achieve dimensionality reduction. "Probabilistic Latent Semantic Analysis" (pLSA) [5], proposed by Hoffman, can model underlying topics for given documents; however, it cannot model the topics for *unseen* documents that were not used for parameter estimation. Blei et al. [3] proposed one of the

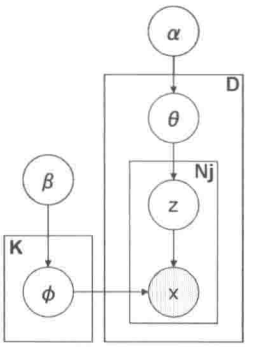

Fig. 1. The graphical model of LDA.

topic models called "Latent Dirichlet Allocation" (LDA) in an extension of pLSA, introducing a Dirichlet prior on a multinomial distribution over topics for each document. This makes the model applicable to unseen documents. The LDA model has been accepted in various fields; however, it has not been investigated for predicting biological entity relationships, to our knowledge. In this paper, we investigate applying the LDA model to extract and predict protein-protein relationships from biomedical literature. In the statistical topic modeling, a set of topics are usually assumed to be unobserved in a document collection, and so we need to infer such unknown distributions from the documents. To estimate the LDA model, "Collapsed Gibbs Sampling inference"[a] method can be used [4]. "Collapsed Variational Bayesian inference" (CVB) [6] is alternative approach to estimate the LDA model.

The focus of this paper is to investigate how to apply the LDA model to the task of protein-protein relationship prediction from biomedical literature, and to evaluate, in an extrinsic manner, the effectiveness over different model estimation methods.

2. LDA and Estimation Algorithms

2.1. *Generative Process of LDA*

Figure 1 shows the graphical model of LDA. We formally describe generative process of LDA [3], as follows,

(1) For all j documents sample $\theta_j \sim Dir(\alpha)$
(2) For all k topic sample $\phi_k \sim Dir(\beta)$
(3) For each of the N_j words x_i in document d_j
  (a) Sample a topic $z_i \sim Mult(\theta_j)$
  (b) Sample a word $x_i \sim Mult(\phi_{z_i})$

[a]It is sometimes simply called "Gibbs Sampling inference" [4].