Lusheng Wang
Daming Zhu (Eds.)

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Preface

This volume contains the papers presented at the 24th International Computing and Combinatorics Conference (COCOON 2018), held during July 2–4, 2018, in Qing Dao, China. COCOON 2018 provided a forum for researchers working in the areas of algorithms, theory of computation, computational complexity, and combinatorics related to computing.

The technical program of the conference included 62 contributed papers selected by the Program Committee from 120 full submissions received in response to the call for papers. All the papers were peer reviewed by at least two (2.83 in average) Program Committee members or external reviewers. The papers cover various topics, including algorithms and data structures, complexity theory and computability, algorithmic game theory, computational learning theory, cryptography, computational biology, computational geometry and number theory, graph theory, and parallel and distributed computing. Some of the papers were selected for publication in special issues of *Algorithmica, Theoretical Computer Science* (TCS), and *Journal of Combinatorial Optimization* (JOCO), with the journal version of the papers being in a more complete form.

The conference also included three invited presentations, delivered by Michael Segal (Ben-Gurion University of the Negev), Ming Li (University of Waterloo), and Russell Schwartz (Carnegie Mellon University). Abstracts of their talks are included in this volume. We would like to thank all the authors for contributing high-quality research papers to the conference. We express our sincere thanks to the Program Committee members and the external reviewers for reviewing the papers. We thank Springer for publishing the proceedings in the *Lecture Notes in Computer Science* series. We thank the Shandong University for hosting COCOON 2018. We are also grateful to all members of the Organizing Committee and to their supporting staff. electronic Program Committee meetings, and to assist with the assembly of the proceedings.

May 2018 Daming Zhu

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Abstracts of Invited Talks

Privacy Aspects in Data Querying

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Abstract. Vast amounts of information of all types is collected daily about people by governments, corporations and individuals. The information is collected, for example, when users register to or use online applications, receive health related services, use their mobile phones, utilize search engines, or perform common daily activities. As a result, there is an enormous quantity of privately-owned records that describe individuals finances, interests, activities, and demographics. These records often include sensitive data and may violate the privacy of the users if published. The common approach to safeguarding user information, or data in general, is to limit access to the storage (usually a database) by using and authentication and authorization protocol. This way, only users with legitimate permissions can access the user data. However, even in these cases some of the data is required to stay hidden or accessible only to a specific subset of authorized users. Our talk focuses on possible malicious behavior by users with both partial and full access to queries over data. We look at privacy attacks that meant to gather hidden information and show methods that rely mainly on the underlying data structure, query types and behavior, and data format of the database. The underlying data structure may vary between graphs, trees, lists, queues, and so on. Each of these behaves differently with regard to data storage and querying, allow for different types of attacks, and require different methods of defense. The data stored in databases can be just about anything, and may be a combination of many different data types such as text, discrete numeric values, coordinates, continuous numeric values, timestamps, and others. We will show how to identify the potential weaknesses and attack vectors for each of these combinations of data structures and data types, and offer defenses against them. This is a joint work with Eyal Nussbaum.

Challenges from Cancer Immunotherapy

Ming Li

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There are currently two revolutions happening in the scientific world: deep learning and cancer immunotherapy. The former we have all heard, but I believe it is the latter [1–4] that is more closely related to the CPM/COCOON community and personally to each of us.

In principle, cancer immunotherapy is to activate our own defense system to kill cancer cells. When a cell in our bodies (for all vertebrates) becomes sick beyond repair, the MHC complex brings fragments of 8-15 amino acids, or (neo)antigens, from the foreign invader or cancerous proteins, to the surface of the cell inviting the white blood cells to kill that cell.

Short peptide immunotherapy uses these short sequences (of 8-15 amino acids) as the vaccine. One key obstacle for this treatment to become a clinical reality is how to identify and validate these somatic mutation loaded neoantigens (peptides of 8-15 amino acids) that are capable of eliciting effective anti-tumor T-cell responses for each individual. Currently, to treat a patient, we take a biopsy, do exome sequencing, perform somatic mutation analysis and MHC binding prediction. This process is a long, unreliable, and very expensive detour to predicting the neoantigens that are brought to the cancer cell surface [3, 4]. This process potentially can be validated by mass spectrometry (MS) [3–5] or even replaced by MS altogether if MS has sufficient sensitivity to capture the low abundant neoantigens on the cancer cell surface.

There is a promising MS technology called Data-Independent Acquisition (DIA) [6, 7] that has unbiased fragmentation of all precursor ions within a certain range of m/z. In this talk we will present our preliminary work [8] on how to find these mutated peptide sequences (de novo sequencing) from the cancer cell surface using deep learning and DIA data. We will discuss major open problems.

This is joint work with NH. Tran, R. Qiao, L. Xin, X. Chen, C. Liu, X. Zhang, and B. Shan. This work is partially supported by China's National Key R&D Program under grants 2018YFB1003202 and 2016YFB1000902, Canada's NSERC OGP0046506, Canada Research Chair Program, MITACS, and BSI.

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Reconstructing Tumor Evolution and Progression in Structurally Variant Cancer Cells

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Abstract. Cancer is disease governed by the process of evolution, in which a process of accelerated genomic diversification and selection leads to the formation of tumors and a process of generally increasing aggressiveness over time. As a result, computational algorithms for reconstructing evolution have become a crucial tool for making sense of the immense complexity of tumor genomic data and the molecular mechanisms that produce them. While cancers are evolutionary systems, though, they follow very different rules than standard species evolution. A large body of research known as cancer phylogenetics has arisen to develop evolutionary tree reconstructions adapted to the peculiar mechanisms of tumor evolution and the limitations of the data sources available for studying it. Here, we will explore computational challenges in developing phylogenetic methods for reconstructing evolution of tumors by copy number variations (CNVs) and structural variations (SVs). CNVs and SVs are the primary mechanisms by which tumors functionally adapt during their evolution, but require very different models and algorithms than are used in traditional species phylogenetics. We will examine variants of this problem for handling several forms of tumor genomic data, including particular challenges of working with various bulk genomic and single-cell technologies for profiling tumor genetic variation. We will further see how the resulting models can help us develop new insight into how tumors develop and progress and how we can predict their future behavior.

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