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Data Integration in the Life Sciences

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Preface

Understanding the mechanisms involved in life (e.g., discovering the biological function of a set of proteins, inferring the evolution of a set of species) is becoming increasingly dependent on progress made in mathematics, computer science, and molecular engineering. For the past 30 years, new high-throughput technologies have been developed generating large amounts of data, distributed across many data sources on the Web, with a high degree of semantic heterogeneity and different levels of quality. However, one such dataset is not, by itself, sufficient for scientific discovery. Instead, it must be combined with other data and processed by bioinformatics tools for patterns, similarities, and unusual occurrences to be observed. Both data integration and data mining are thus of paramount importance in life science.

DILS 2007 was the fourth in a workshop series that aims at fostering discussion, exchange, and innovation in research and development in the areas of data integration and data management for the life sciences. Each previous DILS workshop attracted around 100 researchers from all over the world. This year, the number of submitted papers again increased. The Program Committee selected 19 papers out of 52 full submissions. The DILS 2007 papers cover a wide spectrum of theoretical and practical issues including scientific workflows, annotation in data integration, mapping and matching techniques, and modeling of life science data. Among the papers, we distinguished 13 papers presenting research on new models, methods, or algorithms and 6 papers presenting implementation of systems or experience with systems in practice. In addition to the presented papers, DILS 2007 featured two keynote talks by Kenneth H. Buetow, National Cancer Institute, and Junhyong Kim, University of Pennsylvania.

The workshop was held at the University of Pennsylvania, in Philadelphia, USA. It was kindly sponsored by the School of Engineering and Applied Science of the University of Pennsylvania, the Penn Genomics Institute, and Microsoft Research, who also made available their conference management system. As editors of this volume, we thank all the authors who submitted papers, the Program Committee members, and the external reviewers for their excellent work. Special thanks go to Susan Davidson, General Chair, Chris Stoeckert, PC Co-chair, as well as Olivier Biton, Tara Betterbid, and Howard Bilowsky. Finally, we are grateful for the cooperation and help of Springer in putting this volume together.

June 2007

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