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Sommario/riassunto	The publication date is one day earlier then the EST date to provide the proceedings to attendees in Australian on the first day of the conference It is our great pleasure to welcome you to the ACM Ninth International Workshop on Data and Text Mining in Biomedical Informatics (DTMBIO'15), in conjunction with ACM Conference of Information and Knowledge Management (CIKM'15). As biomedical "big-data" are rapidly growing in quantity and quality, computational techniques to handle, store and analyze such information to acquire more valuable knowledge is now essential for relevant researchers. Along with the traditional medical records including electronic medical records (EMR), clinical test results and environmental records, high-throughput observations upon biological entities such as genes, transcripts, proteins and metabolites are coupled with individual phenotype information to infer elements that are associated with a specific phenomenon of our interest. This also requires an exploration of previously reported knowledge that exists in a form of canonical database and literature, to build a hypothesis and confirm the consistency. Accordingly, it is doubtless that application of cutting-edge techniques in data and text mining is a key for efficient biomedical knowledge generation in this "big-data" era. Since its inaugural meeting in 2006, started as the Text-mining in bioinformatics (TMBIO), DTMBIO has been continuously bringing

together multidisciplinary pioneers from computer and biomedical communities. Over 100 high-quality studies have been presented in the past DTMBIO workshops, many of which are finally published as full paper in scientific journals. Although highly diverse in terms of methods, information sources and target phenotypes (diseases), we have been maintaining two major themes: (1) method development and improvement for data and text mining in bioinformatics that forms a basis for more efficient and accurate analyses, and (2) novel biomedical discoveries from high-throughput data based upon data and text mining techniques. We regard the balanced combination between pure computer science and biology as the primary factor for being successful in holding a creative and innovative workshop for both groups. And we anticipate this tradition will be kept for upcoming DTMBIO workshops too. The papers accepted for presentation and publication in this volume cover a variety of topics, including bio-text mining, bio-data mining, pathway and bio-network analysis, bio-ontology management, sequence analysis for massively parallel sequencing, protein-protein interactions, biomedical data classification, and biomedical information retrieval. We hope that these proceedings will serve as a valuable and up-to-date reference about the application of data- and text-mining techniques within biomedical informatics.