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containing large numbers of sequences polymorphisms structures and gene expression profiles of normal and diseased tissues are being rapidly generated for human and model organisms Bioinformatics is thus rapidly growing in importance in the annotation of genomic sequences the understanding of the interplay among and between genes and proteins the analysis of genetic variability of species the identification of pharmacological targets and the inference of evolutionary origins mechanisms and relationships This proceedings volume contains an up to date exchange of knowledge ideas and solutions to conceptual and practical issues of bioinformatics by researchers professionals and industrial practitioners at the 5th Asia Pacific Bioinformatics Conference held in Hong Kong in January 2007 Proceedings of the 6th Asia-Pacific Bioinformatics Conference Alvis Brazma,Tatsuya Akutsu,Satoru Miyano,2008 High throughput sequencing and functional genomics technologies have given us the human genome sequence as well as those of other experimentally medically and agriculturally important species thus enabling large scale genotyping and gene expression profiling of human populations Databases containing large numbers of sequences polymorphisms structures metabolic pathways and gene expression profiles of normal and diseased tissues are rapidly being generated for human and model organisms Bioinformatics is therefore gaining importance in the annotation of genomic sequences the understanding of the interplay among and between genes and proteins the analysis of the genetic variability of species the identification of pharmacological targets and the inference of evolutionary origins mechanisms and relationships This proceedings volume contains an up to date exchange of knowledge ideas and solutions to conceptual and practical issues of bioinformatics by researchers professionals and industry practitioners at the 6th Asia Pacific Bioinformatics Conference held in Kyoto Japan in January 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