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   Nota di contenuto   Association Study between Gene Expression and Multiple Relevant
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                         Using Kernel Machines -- Simulating Evolution of Drosophila
                         Melanogaster Ebony Mutants Using a Genetic Algorithm -- Microarray
                         Biclustering: A Novel Memetic Approach Based on the PISA Platform --

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| Sommario/riassunto | This book constitutes the refereed proceedings of the 7th European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics, EvoBIO 2009, held in Tübingen, Germany, in April 2009 colocated with the Evo* 2009 events. The 17 revised full papers were carefully reviewed and selected from 44 submissions. EvoBio is the premiere European event for experts in computer science meeting with experts in bioinformatics and the biological sciences, all interested in the interface between evolutionary computation, machine learning, data mining, bioinformatics, and computational biology. Topics addressed by the papers include biomarker discovery, cell simulation and modeling, ecological modeling, uxomics, gene networks, biotechnology, metabolomics, microarray analysis, phylogenetics, protein interactions, proteomics, sequence analysis and alignment, as well as systems biology. |