

## Evolutionary Computation In Gene Regulatory Network Research Wiley Series In Bioinformatics

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Evolutionary Computation in Gene Regulatory Network Research is a reference for researchers and professionals in computer science, systems biology, and bioinformatics, as well as upper undergraduate, graduate, and postgraduate students.

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Provides a reference for current and future research in gene regulatory networks (GRN) using evolutionary computation (EC) Covers sub-domains of GRN research using EC, such as expression profile analysis, reverse engineering, GRN evolution, applications Contains useful contents for courses in gene regulatory networks, systems biology, computational biology, and synthetic biology Delivers state-of-the-art research in genetic algorithms, genetic programming, and swarm intelligence Evolutionary ...

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Introducing a handbook for gene regulatory network research using evolutionary computation, with applications for computer scientists, computational and system biologists. This book is a step-by-step guideline for research in gene regulatory networks (GRN) using evolutionary computation (EC).

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Using evolutionary algorithms to study the evolution of gene regulatory networks controlling biological development Alexander Spirov Computer Science and CEWIT, SUNY Stony Brook, Stony Brook, NY, USA; and the Sechenov Institute of Evolutionary Physiology and Biochemistry, St. Petersburg, Russia

Using evolutionary algorithms to study the evolution of ...

The evolution of high throughput technologies that measure gene expression levels has created a data base for inferring GRNs (a process also known as reverse engineering of GRNs). However, the nature of these data has made this process very difficult.

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