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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

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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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