

# Autonomous Exploration of Dynamic Biological Systems by Scouting

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Given a large model of a complex biological system, we usually face the problem that there are many parameters to adjust. Extensive factor interaction among the parameters makes the analysis difficult. Systematic tests (e.g., n-factorial designs) are not scalable in terms of the parameter dimension because of the exponential growth of designate sampling points. An evolutionary exploration method (called *scouting*) has been introduced in the light of evolutionary experimentation with the help of communication theory [1]. The main objective of the scouting algorithm is to maximize information gain from limited experimental resources. As a result of the application of the scouting algorithm, experiments are more concentrated on the region where unexpected observation yields. The scouting algorithm can be used both to control real automatic experimentation systems [2] and to analyze theoretic computer models [3]. We extended the work by modifying the algorithm and applied it to several models of biological systems.

The modifications aimed at a problem independent method and at reducing the number of parameters the user has to set. We introduced an adaptive mutation rate and adaptive population size, such that only one parameter (the minimal experimental resolution) remains to be chosen by the user. We present results from applying scouting to a mathematical model of the relationship between HIV and the immune system [4]. Ongoing work applies scouting to an Erythropoietin-Receptor signal transduction pathway model, which is especially interesting because of its high dimensionality (more than 1000 dimensions).

## References

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