IMAG/MSM PI Consortium Meeting April 11-12, 2006
Questions for MSM PI's

PI Name: Peter J. Ortoleva
PI Project Title: Intercellular Genomics of Subsurface Microbial Colonies

1. Please highlight your scientific progress from year 1, where did you hope to be after year 1?

Year 1 Progress: A comprehensive transcriptional regulatory network discovery system has been developed and made available online (http://sysbio.indiana.edu) for other researchers. A reaction transport model for microbes in complex media has been implemented. A rigorous all-atom, multiscale approach to the simulation of nanosystems has been developed; we have developed novel order parameters for capturing nanoscale features and an innovative ensemble has been designed for nanosystems. The objective of these multiscale studies is to predict the behavior of viruses and other nanosystems from a calibrated interatomic force field.

Year 2 Goals: Extend the regulatory network discovery system to include proteomics and genomics, and apply this extended system with the multiscale simulator to understand microbial colonies. Use the nanosystem simulator to predict structural transitions and other viral-life cycle processes.

2. What challenges did you experience?

Only a limited amount of validated regulatory information was available, which was needed for our bioinformatics modules. This was overcome using a variety of network discovery system, which was integrated through an objective Bayesian approach.

3. What unexpected outcomes did you encounter?

Not applicable.

4. What are the major advances that have occurred in your field this year?

Other than our own advances (see Question 1), databases on protein-protein interactions and improved promoter analyses for discovering gene regulatory sites have been developed. Computer molecular dynamics has been accelerated and will facilitate our multiscale approach to nanosystem simulation.

5. How successful were your proposed tools, and did you adopt new tools?

Using our TRND system, we demonstrated the feasibility of developing genome-wide transctipional regulatory networks, meeting a major objective of our study. The approach was tested on E.coli and human B cells.

6. Please share your individual experiences of collaborating with the broader community.

A great deal of interest from other research groups in our TRND system has been expressed, and we have made plans for integrating our software and that of others to create a more powerful network discovery system.

7. Please highlight your plans for year 2.

Please see Year 2 Goals outlined in Question 1.

8. What is your primary MSM Working Group? WG1

9. Please comment on your MSM Working Group(s), and what needs to be improved?

WG1: This group has been one of the factors that encouraged me to further develop our multiscale nanosystem approach.

WG4: This groups places, in my opinion, too much emphasis on model integration instead of the development of innovative models.

10. How do you foresee logical linking of models with others in the MSM?

I believe the regulatory network reconstruction and analysis tools, as well as the bionanosystem-simulation approach, will ultimately be a key part of a larger modeling effort for complex, intracellular phenomena.

11. Are you writing grants?

Yes. New proposals are being written on the application of the regulatory network discovery system to diabetes, stem cells in the context of cancer, and for the application of multiscale approaches for the design of drug-delivery nanocapsules. Another proposal is being developed for multicellular simulation with applications in the modeling of tissues and tumors.

12. Are you finding new collaborations?

Yes. We have assembled a group of researchers that is focusing on the application of multiscale approaches to whole-virus simulation, with the objective of arriving at the computer-aided design of antiviral drugs and vaccines.