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Dr. Ken Kennedy
c/o Prof. Fran Berman
Director, San Diego Supercomputer Center
University of California San Diego
9500 Gilman Drive
La Jolla CA 92093-0505

March 17, 2001

Dear Dr. Kennedy:

The program development and execution system to be developed within the GrADS Science and Technology Center promises to be a major contribution to biologists. I would be very interested in being involved as an application developer for the GrADS system. We are presently inundated with biological data at the molecular level. While the human genome has captured the attention of the public the lesser know fact is that a new genome of a lesser species is being released every 1-2 weeks. At the same time data on gene expression, protein structure, protein-protein interactions, complex biological pathways etc. are being made public at exponential rates. Our approach to processing such data is to establish pipelines of existing software components developed by us and others, rigorously benchmark and test those pipelines, and then process large amounts of data in this way. Genome annotation and protein models are two results we are currently seeking through pipelining. The latter will provide targets in drug design experiments.

These pipeline codes are amenable to Grid computing and would be greatly improved by developing them in an environment which promotes their performance. Given the expertise of the GrADS Science and Technology Center proposal PIs, I would be eager to collaborate with this group to target biological codes we plan to develop to perform well in Grid environments. This effort should complement funded efforts and provide us an expanded platform on which to run our codes. I wish you luck with the proposal.

Sincerely,

Philip E. Bourne PhD
Professor of Pharmacology
Project Leader, The Protein Data Bank
Senior Principal Scientist, San Diego Supercomputer Center