

Brief Bio and (PR)²: Problems & Pitches – Rants & Raves by *Mark Gerstein*

Self Introduction



Mark Gerstein is the Albert L Williams professor of Biomedical Informatics at Yale University. He is co-director the Yale Computational Biology and Bioinformatics Program, and has appointments in the Department of Molecular Biophysics and Biochemistry and the Department of Computer Science. He received his AB in physics summa cum laude from Harvard College in 1989 and his PhD in chemistry from Cambridge in 1993. He did post-doctoral work at Stanford and took up his post at Yale in early 1997. Since then he has received a number of young investigator awards (e.g. from the Navy and the Keck foundation) and has published appreciably in scientific journals. He has >250 publications in total, with a number of them in prominent journals, such as Science, Nature, and Scientific American. (His current publication list is at <http://papers.gersteinlab.org>.) His research is focused on bioinformatics, and he is particularly interested in large-scale integrative surveys, biological database design, macromolecular geometry, molecular simulation, human genome annotation, gene expression analysis, and data mining.

Publications:

<http://papers.gersteinlab.org/papers/structint/>
<http://papers.gersteinlab.org/papers/nethierarchy/>
<http://papers.gersteinlab.org/papers/sciam2/>
<http://papers.gersteinlab.org/papers/encodepgenes/>
<http://papers.gersteinlab.org/papers/intint/>
<http://gerstein.info>
<http://papers.gersteinlab.org/papers/subject/tools/>
<http://www.gersteinlab.org/>

General Questions

1) What is (are) your main interest(s) in attending the workshop?

I am interested in attending the workshop to expand my horizons on scientific visualization. Currently, I mostly know what has been done in the biomedical domain, particularly related to genomes and molecular structure. I'm, of course, also aware of impressive things happening on the web for the general public. I'm very curious on how other scientific domains have harnessed visualization and am interested in seeing if some of these approaches can be transferred to genome informatics.

2) What information/knowledge management needs do you have?

Explain your 'dream tool' for scientific discovery and innovation.

My dream tool for scientific discovery would be a genome visualization system that lets one browse the genome as effortlessly as one using Google maps to browse the earth. It would allow one to see the sequence as a simple linear line and also to some degree as 3D chromatin structure and as networks of molecular connections (e.g. those related to regulator and regulated). It would place annotation on the genome and inter-relate this annotation in detail with the full free text of the biomedical literature.

3) What is the most insightful visualization of static or dynamic phenomena you know?

The most insightful visualization that I know about was, of course, Watson & Crick's synthesis of Franklin and Wilkins' diffraction data into an easy to comprehend 3D model and then going on to show how this could explain many of the fundamental processes of genetics. The power of this visualization, of course, stems from the fact that the 3D structure represented a real chemical entity. It also connected two disciplines -- chemistry and genetics -- with a central visual metaphor that proves useful to this day.

4) What would you like to learn / achieve at the workshop?

I would like to see various applications people have developed for large-scale visualization, particularly how they enable one to bridge between different disciplines with a central visual metaphor. My inspiration for the later is the way that the visual network metaphor allows one to bridge between such diverse concepts as protein interactions, social relationships, and electrical circuits.