BioGeometry NEWS
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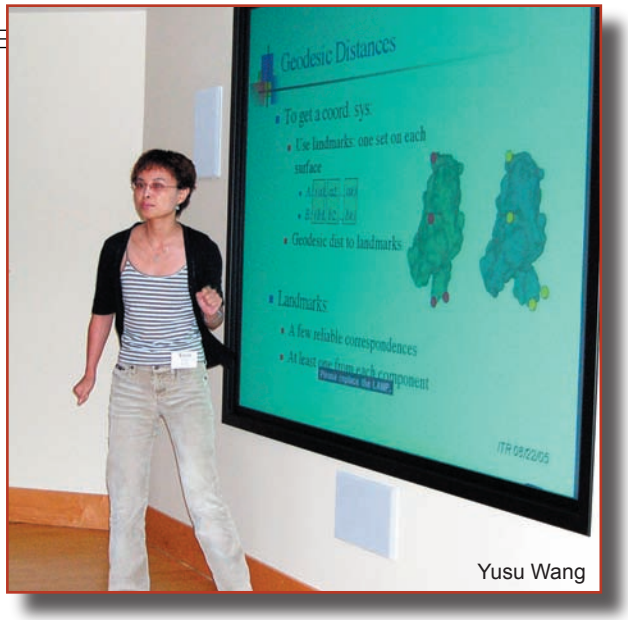
BioGeometry Meeting

Second Fifth Year Group Meeting

For the first time in the history of the project, the group met in Greensboro, at the North Carolina Agricultural and Technical State University. Solomon Bililign and Robert Gdanitz graciously organized the meeting on the top floor of the Fort Interdisciplinary Research Center on campus.

The technical program was divided into five sessions with a total of thirteen presentations. Opening the first session, Charlie Carter from UNC presented his work with Jeff Roach on linear encodings of the Delaunay tetrahedralization of a protein backbone for structural alignment of proteins. His crucial algorithmic insight is that the linearization of the tetrahedral structure enables the use of fast dynamic programming algorithms. Charlie was followed by Andrew Leaver-Fay from UNC, who reported on his work of speeding up the computation of the energy contribution of a rotamer using a trie (for re*trie*val) representation aimed at avoiding redundant atom-pair computations. The third and last talk of the first session was by Jeff Headd from Duke who told us about protein-protein interfaces and the insights he gained with a systematic statistical analysis of known complexes.

The second session featured two researchers from NCA&T. First, Iskra Magick presented the work from her master thesis project on the metal-binding to modified nucleocides. She described the structure determination of the mercury complex, which is of interest in cancer research, using experimental NMR and theoretical MD methods. Second, Divi Venkateswarlu talked about understanding protein-protein interactions in the blood coagulation cascade, a project he started in the group of Lee Pedersen at UNC in Chapel Hill.



Yusu Wang

The third session featured two researchers from Stanford. First, Daniel Russel told us about his work on comparing the structure of protein backbones using spanners, which are sparse graphs connecting the alpha carbon atoms in space so that the graph distance between any two is a good approximation of the Euclidean distance between them. In the last talk of the first day, Yusu Wang presented her work on segmenting low-resolution models of macro-molecules into relatively rigid domains connected to each other through hinge motions. This research exemplifies inter-institutional collaboration at its best, a key concept in this work being the elevation function, an idea she developed as a graduate student at Duke University before she joined Stanford as a postdoc working with Leonidas Guibas.

To round off the first day's program, the PIs of the project met to reflect on the past achievements, to ponder how to most productively convey what they have learned in this project, and to contemplate several possible paths into the future.

On the second day, Jean-Claude Latombe from Stanford opened the fourth session with a talk on the conformational flexibility of protein backbones. An intriguing aspect of his work is the exploration of a rank-2-deficient singularity identified by Jim Milgram using concepts from differential topology. He was followed by Andrew Ban from Duke who talked about his investigations of the quality of protein structures using local density measurements of protons in the full atom model. He found significant statistical differences between structures determined through x-ray and NMR experiments. In the last talk of the fourth session, Madhu Vaidya from Duke presented her work on alternative local measures that could alleviate some of the difficulties caused by Andrew's definition of local density as the fraction of a power cell occupied by the generating atom sphere. Her concept of local crowdedness weakens the artifacts encountered near the boundary of the protein, where local density tends to zero, and seamlessly expresses the whole range from under- to over-packing.

The last session was opened by Andrea Mantler from UNC telling us about her exploration of protein allostery using tools


Above: Dmitriy Morozov, Herbert Edelsbrunner, Yuriy Mileyko


Left: Solomon Bililign, Joseph Graves, Robert Gdanitz


Above: Alex Tropsha, Fred Brooks, Johannes Rudolph

from mathematical rigidity. In this approach, she represents bonds by rods thus obtaining a geometric graph in space which may or may not be rigid and if it is not will consist of rigid domains allowing for non-rigid interactions between them. Second, Jeff Phillips from Duke presented his work on the alignment of two or more protein structures and the related concept of mean shape. Finally, in the last talk in this meeting, Michael Levitt from Stanford continued the theme presenting his work on the automatic classification of protein structures. He raised intriguing questions about the interpretation of data he obtained by standard dimension reduction techniques.

From listening to the talks it was evident that we have come a long way assimilating each other's different academic heritage. We have arrived at biogeometry, a field in which the languages of structural biology, computing, and mathematics are inseparably interwoven.

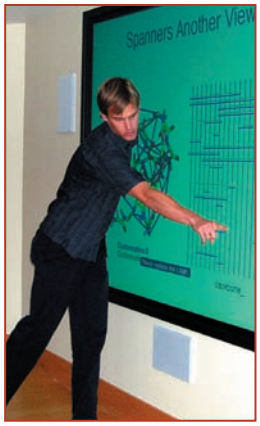
Leo Guibas, Pankaj Agarwal

Jeff Phillips, Charlie Carter

Jack Snoeyink, Jeff Headd

Yuriy Mileyko, Jeff Phillips, Bei Wang, Andrew Leaver-Fay, Amit Patel, Jack Snoeyink, Dmitriy Morozov

Michael Levitt



Daniel Russel

Jean-Claude Latombe

Schedule

Monday, August 22

9:00	Welcome by Solomin Bililign and Robert Gdanitz
9:10- 10:50 Chair: Jack Snoeyink	
9:10	Structural alignment via Delaunay tetrahedralization by Charlie Carter (UNC)
9:50	Pruning rotamer "trie"s by Andrew Leaver-Fay (UNC)
10:20	Protein interfaces, flat and in detail by Jeff Headd (Duke)
10:50	Break
11:10-12:10 Chair: Alex Tropsha	
11:10	Metal-binding to modified nucleosides (4-thio uridine) by Iskra Magick (NCAT)
11:40	Understanding protein-protein interactions in blood coagulation cascade: application of protein docking and MD simulation methods by Divi Venkateswarlu (NCAT)
12:10	Lunch
2:00-3:00 Chair: Johannes Rudolph	
2:00	Comparing proteins using spanners by Daniel Russel (Stanford)
2:30	Segmentation for low-resolution macro-molecules under large motion by Yusu Wang (Stanford)
3:00	Break
3:30	PI Meeting
6:00	Restaurant Dinner

Tuesday, August 23

9:00-10:40 Chair: Yusu Wang	
9:00	Study of the conformational space of flexible protein loops by Jean-Claude Latombe (Stanford)
9:40	Evaluating the quality of NMR structures by local density of protons by Andrew Ban (Duke)
10:10	A new local density measure for protein structure by Madhu Vaidya (Duke)
10:40	Break
11:00-12:40 Chair: Charlie Carter	
11:00	Exploring protein allostery by mathematical rigidity by Andrew Mantler (UNC)
11:30	Mean shape and protein backbone alignment by Jeff Phillips
12:00	Automatic classification of protein structures by Michael Levitt
12:40	Lunch

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