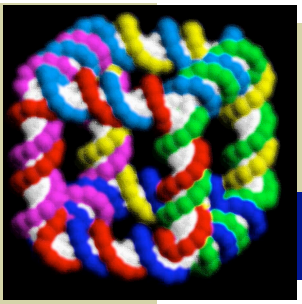

ISNSCE Newsletter

Newsletter September 2006

Volume 2, Issue 1

Letter from the President

n this issue:

The time flies very fast, especially on the scale of our watches that we use every day to confirm that we are again behind with so many activities and deadlines. Thus 2006 is almost over, but ... it was a good year for ISNSCE.

The main reason for this satisfaction is that our two conferences, "FNANO" in Snowbird in April and "DNA Computing" in Seoul in June, went really well. Big thanks to John Reif for all his work for "FNANO", and to Lila Kari and Byoung-Tak Zhang for their work for "DNA Computing".

When you will receive this Newsletter please consider your possible contribution to it. The Newsletter should reflect the activities of our community and it can be successful only if ISNSCE members will make it successful. We need reporters on various meetings/conferences that are of interest to our community, and we need volunteers to edit columns reporting on various research areas pursued within our community. Also reporters on interesting research activities going on in various institutes or within specific regions/countries are very welcome. I want to take this opportunity to thank Natasha Jonoska who puts a lot of work on purely voluntary basis into this Newsletter.

The prospects of getting the ISNSCE membership almost automatically when attending one or both of our meetings makes me quite optimistic about the growth of our organisation, something that I believe is important for the development of the broad research area that we represent.

According to our constitution, Andrew Turberfield, our current Vice President, will succeed me as President from January 1, 2007. You are all very much encouraged to contact either me (rozenber@liacs.nl) or Andrew (a.turberfield@physics.ox.ac.uk) with any comments that you think are relevant for the functioning of ISNSCE.

Grzegorz Rozenberg, President of ISNSCE
October 2006

Website:
www.isnsce.org

E-Mail:
contactisnsce@isnsce.org

Table of Contents

Report on the meeting DNA 12: The Twelfth International Meeting on DNA Computing, Seoul, Korea, June 5 – 9, 2006

by Satoshi Murata and Masayuki Yamamura

The 12th International Meeting on DNA Computer, chaired by Byong-Tak Zhang, was held from June 5 to 9, 2006 at Seoul National University, in Seoul, South Korea. The workshop which began in 1995 as a mini-workshop now attracts over a hundred participants from all over the world every year. To keep the friendly atmosphere for networking and to provide opportunity for deep discussion, single session style is maintained. Participants enjoyed good one-hour invited talks, other than oral presentations (25 min) and posters.

``..we had 120 participants from 17 countries of Asia, America and Europe''

Statistics

This year, we have 120 participants from 17 countries of Asia, America and Europe. The DNA 12 consists of 10 sessions with four invited talks. They are a wonderful collection of both theoretical and experimental results from leading edge research. 36 papers were accepted as full paper, 19 of them as oral presentation, other 24 papers with abstract only. Program committee of this year co-chaired by Chendge Mao and Takashi Yokomori worked hard to select these papers.

Prof. Stojanovic presenting his nano

Intensive Invited Talks

DNA automata and machines by Milan Stojanovic is the first invited talk, in which he fascinated audiences by his powerful picture of molecular mobile robot crawling on grassland of DNA. Ashis Goel's spoke about algorithmic self-assmbly of counters which he showed smart design of DNA tile counters with even less kind of tiles. The third invited talk is about beautiful mathematics in viral capsids is presented by Reidun Twarock. Roy Bar-Ziv's cell-free artificial biochemical networks showed one of the important future direction of application of DNA computation.

Topics

It is hard to select samples from many excellent talks in the oral session. William Shih presents large scale DNA-based molecular containers built on DNA-Origami technology recently developed by Paul Rothemund. David Zhang showed how catalytic systems can be driven only by entropy.
Satsuki Yaegashi's reported on experimental results on DNA memory made of four hairpins. Peng Yin showed a new design of DNA nanostructure called tile-less DNA ribbons and tubes. David Soloveichik's showed how to combine self-healing and proofreading properties in DNA tile self-assembly. Youdong Mao presented a proton driven DNA nanomachines which change morphology by pH and light. Bryan Wei spoke about their new software "Uniquimer" to design DNA sequences, which has user-friendly interface. The software is now open for public. Sadheer Sahu showed a simulation system which gives a framework for modeling DNA based molecular Systems.

Nanoday

The final day was the customary Nanoday. There were four 90 minutes presentation. Two invited speakers were from Japan, Makoto Fujita and Mitsuhiko Shinoya. We simply amazed their magic of organic chemistry; it is fun to see how fascinating and complex structures such as cages, tubes, capsules that are self-assembled from simple small components. They are not only beautiful but actually work as nano-mechanical component such as molecular ball bearing. Varieties nano devices along with his own aptamer based DNA devices are introduced by Friedrich Simmel. The last talk was about DNA self-assembly and molecular machinery by Andrew Turberfield. This gives one of the feasible ways to build molecular machinery solely based on DNA hybridization.
(Power point slides of most of the above invited talks of DNA 12 and Nanoday can be downloadable at DNA12 website http://bi.snu.ac.kr/DNA12/)

The wet lab tutorial.

Student Award

From this year, excellent papers by student authors were presented to encourage younger generation in this field. "How crystals that sense and respond to their environments could evolve" by Rebecca Schulman in which she showed how inorganic materials such as DNA tile crystal can evolve got student paper award from DNA12 program committee, and "On the complexity of graph self-assembly in accretive systems" by Stanislav Angelov got student paper award from ISNSCE. In this paper he solved the open problem on complexity of the graph (AGAP) showing that AGAP is NP-complete on degree 3 planer graph.

Tutorials and Wet Lab Training

The first day of the workshop was a tutorial day, where students and beginners are warmly invited to learn basics of DNA computing, including wet lab training (by Susannah Gal), tutorial lectures on grammars of DNA computation (by Morgan Bishop), how to build logic in E.coli (by Yasubumi Sakakibara) and structural DNA nanotechnology (by Nadrian Seeman).

Excursion

On the third day, we enjoyed sightseeing by bus. Our first stop was at the many old palaces from Yi dynasty, and we walked around in the huge palaces. It was a soul-satisfying, refreshing change from the intense scientific discussions at the workshop. A villa called Secret Garden was especially memorable. Our next stop was at the town of Insadong, where delightful arrays of Korea's traditional crafts are sold in many shops. Then we satisfied our palate with Korean imperial cuisine, which consists of numerous varieties of dishes. To top it off, there were stage performances of traditional Korean songs, dances, and drums so entertaining, we experienced the Korean culture to our heart's content.

Nest year and beyond

The rewarding five days at DNA12 has passed very quickly. DNA13, the next year's workshop, will be held in Memphis, U.S.A. We look forward to an exciting experience at the town of Jazz and Blues.

Report from FNANO'06: 3rd Annuam Meeting on Foundations of Nano science, Snowbird, Utah USA, April 23-37, 2006.

By William Sherman & Peng Yin

Scientists gathered from around the globe this April at the Cliff Lodge in Snowbird, Utah for FNANO '06: the 3rd Annual Conference on Foundations of Nanoscience, Self-Assembled Architectures and Devices. The conference was chaired by John Reif and sponsored by the International Society For Nananoscale Science, Computation and Engineering and by the Defense Advanced Research Projects Agency. This year there was a particularly tight focus on bio-molecule based self-assembly, though, as usual, there were exciting talks from all main areas in self-assembly based nano-science. The tradition of having relatively few speakers, with lots of time between presentations to read posters and talk continued to work well. Keynote speakers were selected, which helped to focus each session quite nicely. The weather was fairly warm, so the skiing conditions were less than ideal, and again, the thin, mountain air caused numerous headaches and insomnia, but the general feeling was still upbeat. A party at the out-door pool and hot-tub was a big success, continuing the general feeling of camaraderie that keeps the discussions going over dinner and late into the night in the local bars.

Under the central theme of self-assembled architectures and devices, this year's conference was organized in 14 tracks: principles and theory of self-assembly, self-assembled system complexity, top-down meets bottom-up, self-assembly across scales, self-assembled DNA nanostructures, viral self-assembly, self-assembly of peptide-protein structures, fullerene nanostructures, self-assembled surface chemistry, nano-optics, DNA linked nanoparticle structures, molecular electronic devices and circuit assembly, self-assembled computer circuit and architectures, molecular motors, biomedical nanotechnolog.

Nucleic acids, and in particular DNA, were the most popular construction material among this year's FNANO-ers. In the Track on Self-assembled DNA Nanostructures, the keynote talk by Rothemund was one of the major highlights of the conference. Rothemund's talk presented his landmark work on folding long bacterial DNA with the help of many short strands to produce arbitrary 2D shapes and patterns. Rothemund has used these DNA origami techniques to construct planar figures with complex shapes as exemplified famously by the smiley-faces that recently graced the cover of Nature. He has also adapted techniques for putting bumps onto planar figures to emboss illustrations onto molecules, such as a map of the Americas. The shapes are about 100 nm x 100 nm in size and with a pixel resolution of about 6 nm. Beyond the dazzling pictures, however, Rothemund's research has shifted one of the main paradigms in the field of structural DNA nanotechnology. Prior to Rothemund's origami, the base sequences used in the field had always been

synthesized with careful optimization to make sure there was the least possible symmetry within the sequences (in hope for the least possibility of mis-folding). Similarly, the strands were generally purified quite carefully to minimize the chance that even a single base could introduce an improper symmetry. Rothemund's successful construction with naturally occurring DNA shows that even with some limited level of sequence symmetry, many structures can still form with substantial yield. Further, by keeping the concentration of helper-strands much higher than the long, scaffold DNA, Rothemund could eliminate the onerous, rate-limiting step of purifying all the DNA strands in his system. Together, these breakthroughs allow him to build much larger systems, and to use modular construction methods that allow, for example the writing of virtually any three letters onto a DNA rectangular substrate. Another particularly impressive talk was delivered by Mao. Going against the conventional wisdom of minimizing sequence symmetry and structural flexibility in planar DNA tilings, Mao intentionally introduced both elements into his tiles and obtained amazingly large and uniform DNA lattices, with dimensions up to 1 mm. In addition to the above progress in 2D DNA structures, Goodman from Turberfield's group reported the construction and characterization of a new class of 3D structures, DNA tetrahydra. Shih's excellent poster presented three preliminary constructions of nano-containers designed to satisfy a broad set of engineering demands: high strength/weight ratio, compact size suitable for in-cell formation, or pore sizes varying from 1 to 100 nm. DNA can also be used to manufacture much larger structures. Luo's talk in the Track on Assembly Across Scales, reported using DNA as a construction material to produce structures ranging from nanometer scale to centimeter scale. One particularly interesting example is Luo's DNA hydrogel. Many of the properties of the DNA hydrogel can easily be tuned by varying the lengths of the arms or the sticky ends holding the units together. The resulting gels form easily at room temperature, are stronger than agarose gels, and can encapsulate living cells for biological studies and medical applications. Further, if a gene is incorporated into the DNA sequence, Luo reports that the coded protein will get synthesized with extremely high yield in the presence of the appropriate enzymes.

cont. on page 10

Column on Self-Assembly

Edited by Andrew Tturberfield

Self-assembly of biopolymers is the impatient scientist's approach to making molecular devices. It relies on design of non-covalent interactions – often between nucleic acids and peptides – to control structure with atomic precision. DNA, RNA and peptides are particularly suitable as their interactions can be controlled by specifying the sequences in which bases or amino acids are incorporated in the polymer – and automated synthesis allows these designs to be tested within days. Working with biomolecular self-assembly is also a wonderful opportunity for an imaginative physical scientist – it creates opportunities to talk to biologists and spark ideas for interdisciplinary research. This column will focus on new ways of making things by self-assembly and on new ideas for using self-assembled devices to do things that could not be done before. It will inevitably concentrate on nanofabrication using DNA, but I hope that it will stray widely.

A very striking recent development was Paul Rothemund's paper on DNA origami [*Nature* **440**, 297 (2006)], which introduced a new approach to design for self-assembly. Paul uses one long template strand of DNA which, for economic reasons, is a viral genome, and many short 'staple' strands.

The base sequence of the template is known, so a staple can be designed to hybridize at one or more predetermined locations: staples that bind to two or three different locations simultaneously force the template to fold back on itself in a zig-zag pattern to create sheets of many different shapes which can be patterned by attaching labels to the staples. This technique is a big step forward – it allows larger, more information-rich arrays to be created than was previously possible. It is also remarkable robust: the genomic template can be relied on to be more-or-less perfect, and assembly is very tolerant of synthesis and stoichiometry errors in the zoo of staples required to complete the origami. At FNANO06 William Shih also showed origami sheets that were designed to curl to create cylinders.

An interesting use of origami sheets is to provide well-defined edges from which to grow arrays by more traditional DNA tiling techniques. One fascinating development in DNA tiling, presented at FNANO06 and DNA12, is work by Rebecca Schulman and Erik Winfree on evolution [*Lecture Notes In Artificial Intelligence* **3630**, 734 (2005)]. They are studying ribbon-like arrays of tiles with an internal structure (genetic information) that repeats as they extend. Ribbons reproduce by breaking across their width, creating new growth fronts. Evolutionary pressure can be applied, for example, by restricting the supply of tiles needed for growth.

Not all developments are in two-dimensional assembly. Russell Goodman's DNA tetrahedra [*Science* **310**, 1661 (2005)] are a new addition to the select group of three-dimensional DNA nanostructures. They are remarkable because, like the origami structures, they can be made with very high yield, making it reasonable to explore applications such as 3D fabrication using tetrahedral bricks and as cages for drug delivery. As a first step in this direction Christoph Erben showed at FNANO06 that a protein could be caged within a DNA tetrahedron.

Paul Paukstelis has also explored DNA structures as hosts for proteins [*J. Am. Chem. Soc.* **128**, 6794 (2006)]. He showed that a 3D DNA crystal containing 9nm cylindrical pores adsorbed proteins with an affinity that depended on the protein size – it acted as a molecular sieve. This is a step towards the use of DNA lattices to position guest proteins for X-ray structure determination.

The range of chemical functionalities of peptides is vastly greater than that of DNA, but peptide self-assembly is much harder to design. Using staggered heterodimers of peptide alpha helices it is possible to make coiled-coil fibrils with sticky ends; now Max Ryadnov and Dek Woolfson [*J. Am. Chem. Soc.* **127**, 12407 (2005)] have shown that branched linkers can be used to create networks and that other peptides create kinks or stall growth. Rationally designed peptide-based materials are on the way.

A promising new journal, Nature Nanotechnology, will appear in October. The following is taken from their website. '*Nature Nanotechnology* is a multidisciplinary journal that publishes papers of the highest quality and significance in all areas of nanoscience and nanotechnology. The journal covers research into the design, characterization and production of structures, devices and systems that involve the manipulation and control of materials and phenomena at atomic, molecular and macromolecular scales. Both bottom-up and top-down approaches - and combinations of the two – are covered.' This could be good!

From the Nominating Committee

There are two important items on our ballots this year:

1. Next year (2007) the ISNSCE President will be our current Vice President, Dr. Andrew Turberfield. So, the next year's Vice President's position is up for election. The person elected for Vice President will serve as President the year after (2008). The Nominating Committee has identified two candidates that are presented to the ISNSCE members, **Prof. Masami Hagiya** and **Dr. Philip Kuekes.** With this Newsletter we introduce the candidates to the members.
2. In order to strengthen the ties between ISNSCE and the two conference series that it supports, and to boost ISNSCE membership, we will automatically include one year's subscription to ISNSCE as part of the registration package for FNANO and DNAx starting in 2007. This requires that certain rules in the Constitution of ISNSCE are changed accordingly. Below we include the proposed changes that will be included in the ballot.

All members are eligible to vote and ballots will be distributed later this Fall.

Masami Hagiya

Birth year: 1957.

BS and PhD degrees:
1988 Ph.D., Kyoto University
1980 B.S., University of Tokyo

Positions: 1995-now, Professor, Department of Information Science (Department of Computer Science from 2001), University of Tokyo.1992-1995, Associate Professor, 1988-1992, Associate Professor, Research Institute for Mathematical Sciences, Kyoto University. 1982-1988, Research Associate,

Awards and recognitions: IBM Japan Science Award in 1989. I led three research projects on DNA and molecular computing:Theory and Construction of Molecular Computers in 1996-2001;Molecular Memory in 2001-2007;Molecular Programming in 2002-2007
Representative publications: My research contributions in this field of DNA and molecular computing to date can be summarized as exploring the computational power ofhairpins and secondary structures of DNA: (1) computing with hairpin formation, (2) computing with hairpin dissociation, and (3) computing with repeated hairpin formation and dissociation (known as Whiplash PCR).

(1) K. Sakamoto, H. Gouzu, K. Komiya, D. Kiga, S. Yokoyama, T. Yokomori and M.Hagiya: ``Molecular Computation by DNA Hairpin Formation'', *Science,* **288**, 2000,pp.1223-1226. (2) A. Kameda, M. Yamamoto, H. Uejima, M. Hagiya, K. Sakamoto and . Ohuchi: ``Hairpin-based state machine and conformational addressing: Design and experiment'', *Natural Computing*, **4,** No.2, 2005, pp.103-126.

(3) K. Komiya, K. Sakamoto, A. Kameda, M. Yamamoto, A. Ohuchi, D. Kiga, S. Yokoyama and M. Hagiya: ``DNA polymerase programmed with a hairpin DNA incorporates a multiple-instruction architecture into molecular computing'', *BioSystems*, **83**, No.1, 2006, pp.18-25.
Professional affiliations: ISNSCE, ACM, IFIP WG2.2, IPSJ (Information Processing Society of Japan)
Research interest: autonomous DNA computing, DNA nanorobotics
Personal statement: Working in this field for ten years, I feel that the research goal of the field is becoming clearer and clearer. We are developing a new kind of science and technology for constructing nanoscale systems that can be programmed to behave autonomously in an environment. As a computer scientist, I would like to say that computer science and related engineering disciplines are now invading into material and even biological worlds. Although the current focus of the society is mainly on DNA-based nanosystems, I think its research target should be enlarged along the above mentioned research direction. For example, synthetic biology aims to achieve a similar goal by engineering genetic circuits of cells. I think that this society should be at the center of this big research movement and try to make it stronger, broader, and more visible to academia and even to industry.

Philip J. Kuekes

Birth year: 1947.

BS and PhD degrees:
1988 Ph.D., Kyoto University
1969 B.S., in Physics, Yale University

Positions: 1991 - present HP Laboratories, Project Manager for Teramac, a trillion operations per second defect-tolerant reconfigurable computer. (91-95) Chief Architect Quantum Science Research group working on self-assembly of molecular electronics. (96-present) 1990 Director of Architecture at Plus Logic, Inc. a startup Field Programmable Gate Array company.1980-90 Computer Architect, TRW. created a number of highly parallel special purpose giga-op computers for DARPA and the Navy. 1975-1979 Consulting Computer Architect, Kuekes Engineering, designing hardware and microcode for highly pipelined systems. 1972-74 Project Engineer, Ling Electronics - designed the Ling Array Processor used in the first Doppler weather radar. 1970-71 Engineer, Raytheon Computer - designer of the first commercial array processor.

Awards and recognitions: Received the 2000 Feynman Prize in Nanotechnology. Member of the National Academies Committee for the Review of the National Nanotechnology Initiative. Named to the 'Scientific American 50' list of technology leaders for 2002. Named Small Times 2005 Researcher of the Year.
Representative Publications: (1) DeHon, A., Goldstein, S.C., Kuekes, P.J., Lincoln, P. ``Nonphotolithographic nanoscale memory density prospects'' (2005) *IEEE Transactions on Nanotechnology*, **4** (2), pp. 215-228.(2) Snider, G., Kuekes, P., Hogg, T., Williams, R.S. Nanoelectronic architectures (2005) *Applied Physics A: Materials Science and Processing*, **80** (6), pp. 1183-1195.

(3) Heath, J.R., Kuekes, P.J., Snider, G.S., Williams, R.S. ``A defect-tolerant computer architecture: Opportunities for nanotechnology'' (1998) *Science,* **280** (5370), pp. 1716-1721.

He has twenty-two patents in molecular electronics and parallel computer architectures.

Professional affiliations: American Physical Society, IEEE, ISNSCE
Research interest: The integrated circuit, manufactured by optical lithography, has driven the computer revolution for four decades. If we are to continue to build complex systems of ever-smaller components, we must find a new technology that will allow massively parallel self-assembled construction of electronic circuits at the atomic scale. Biology offers an existence proof that extremely complex structures can be assembled bottom-up. But living organisms have evolved to propagate genes not to implement a design from a specification. To design from a specification and also self-assemble the resulting design my research involves developing both the molecular electronics building blocks and computer aided design algorithms for a defect-tolerant reconfigurable technology. The technical problem we face is to make extremely small electronic components (at the atomic scale), use very large numbers of these components to make very complex circuits, but manufacture these circuits at much less cost than today's integrated circuits. This requires many disciplines to work together. To make them function at the smallest scales we use quantum physics. To achieve massive complexity we use computer architecture. To keep them inexpensive we use low mechanical precision and do self-assembly. And to deal with the inevitable defects of self-assembled devices we use a reconfigurable architecture. The device is either partially or completely self-assembled, and the key to the scaling is that the location of the active devices on the substrate are defined after the devices have been assembled, not prior to assembly. This architectural approach allows us to address the functions of interconnect, memory, logic and I/O. The key task of the architectural community in the immediate future is to develop a sense of the trade-offs between the computational costs of computer aided design algorithms to repair defects and the manufacturing costs of avoiding defects in the first place. Biology through evolution has struck one balance. We need to find the balance for self-assembled nanotechnology.
Personal Statement: We are off to a good start by sponsoring the two most important conferences on self-assembly, FNANO and DNA. I have been working to interest funding agencies and computer designers in the opportunity that design for self-assembly holds for a practical manufacturing of nanotechnology. The problem is that such an effort is incredibly interdisciplinary. Our society has the promise of becoming a focal point to bring together researchers from many backgrounds to attack the problem of design for self-assembly. The funding agencies are committed to nanotechnology. I would like ISNSCE to take the lead in providing the interdisciplinary forum that will be needed to succeed.

Change in the Constitution of ISNSCE

In order to strengthen the ties between ISNSCE and the two conference series that it supports, and to boost ISNSCE membership, we will automatically include one year's subscription to ISNSCE as part of the registration package for FNANO and DNAx starting in 2007. The membership year runs from January 1st: non-members will be given the option of immediate membership (until December 31st) instead of membership for the next year; existing members who have already obtained membership for the next year will be offered a discount on the conference registration fee as a bonus for society membership OR membership for an additional year (with no limit on how many years' membership can be accumulated). Members of ISNSCE will be balloted (at the same time as the election of the next Vice President) on a proposal to alter the society's Rule I Sections 2,3,4, which are concerned with membership renewal, in order to ensure that they are consistent with this scheme.

Proposed changes (current constitution available at www.isnsce.org)

Rule 1 Membership.

Section 2. Bills for annual membership dues not yet paid shall be mailed before October 30 preceding the year to which they apply, requesting payment to arrive not later than December 1. Second bills shall be mailed before the following March 1. Members whose dues are not paid will be kept on the membership list for one year. During the new annual billing cycle such members will receive bills for the unpaid dues of the current year plus dues for the following year. Members still in arrears on January 1 of this second annual billing cycle will be dropped from the membership list.

Section 3. Members desiring to terminate their membership may submit resignations to reach the Treasurer at any time not later than December 31 of the last year of membership.

Section 4. Any person paying a membership subscription may elect to have membership start on January 1st of the following year or, if already a member for that year, on January 1st of the first year for which he or she is not yet entitled to membership.

Section 6. Annual dues may be waived by vote of Council for a full member or a former full member who notifies the Treasurer in writing of current unemployment. A separate notification and a new vote of Council must be made for each subsequent year for which dues are to be waived. A member whose dues are so waived shall retain all the rights of membership.

FNANO report cont. from page 5

Besides DNA, viruses and peptides are also popular bio-systems for nano-construction. The talks in the Track on Viral Self-Assembly reported progress in understanding and utilizing the assembly of virus subunits into virus capsids (Douglas and Prevelige) as well as in using either the viral subunits (Zlotnick) or the whole virus capsids (Wang) as building blocks to assemble non-viral structures. Of particular interest was Wang's talk on using the rod-like plant tobacco mosaic virus to assemble 1D fibers, 2D monolayer films, and 3D viral composites. The two talks in the Track on Self-Assembly on Peptide-Protein Structures share a similar spirit in utilizing evolutionary approaches to engineer synthetic proteins with novel functions. Chaput utilizes in vitro selection techniques to construct proteins with novel enzymatic functions and has successfully identified four novel ATP binding proteins, while Tamerler uses an iterative selection, modeling, mutation process to identify inorganic-binding proteins that can be used for self-immobiliztion of enzymes and other nanoscale objects.

Biomolecules are also popular materials among the speakers in the Track on DNA-Linked Nanoparticles and the Track on Surface Chemistry. Yet non-biological molecules also receive much attention as evidenced by the many excellent talks in the Track on Fullerene Nanostructures, the Track on Molecular Electronic Devices and Circuit Assembly, and the Track on Self-Assembled Computer Circuit and System Architectures, and the Track on Self-Assembly Across Scales.

In addition to the numerous tracks studying relatively static nano-structures, FNANO featured the Track on Molecular Motors. The motor track opened with a beautiful keynote talk by Block on single molecule studies of RNA polymerase. Block started by introducing the emerging field of single molecule biophysics and the powerful enabling technology of optical traps, and proceeded to describe their group's remarkable achievement in constructing optical traps with Angstrom level resolution for displacement measurement. With this capacity, they conducted an amazing real time study of a single RNA polymerase molecule, revealing the enzyme's single base steps along its DNA template. Following Block's talk on natural motors are four talks describing clever constructions of synthetic molecular motors: (1) the small organic molecule based rotary motors constructed by Pollard to

generate macroscopic work, (2) the fullerene based NanoCars driven by Kelly to engineer and study controlled motion on surfaces, (3) the DNAzyme based multivalent nano-spiders raised by Taylor that move in a substrate matrix and release cleaved products, and (4) the microorganism bugs harnessed by Weibel to transport microscale cargos.

Though the majority of talks are on experiments, theory is also an important and indispensable part of the conference. A particularly elegant talk in the Track on the Principles and Theory of Self-Assembly was delivered by Bois from Pierce group. The talk presented the first algorithm for calculating the partition function of an unpseudoknotted complex of multiple interacting nucleic acid strands. This is a major step forward in the field of computational study of nucleic acids and provides a powerful tool for the burgeoning community working on rational designed DNA/RNA nanostructures. Besides the talks in the Track on Principles and Theory of Self-Assembly, FNANO featured many other excellent theory talks as well as talks with substantial theoretical components, in particular, the talks in the Track on Self-Assembled Compute Circuit and System Architecture and the Track on Self-Assembled System Complexity. As the field of self-assembled nanostructures further matures, we expect an increasingly intimate interplay between theory and practice.

In addition to the above eleven conventional tracks, this year's conference features three new special tracks, the Track on Top-down Meets Bottom-up, the Track on Self-Assembled System Complexity, and the Track on Biomedical Nanotechnology. These thoughtful additions added great value to the conference and help further expand our community. One particularly impressive talk was delivered by Rasmussen on constructing minimal self-replicating nanomachines in the Track on Self-Assembled System Complexity. Rasmussen reported on the exciting experimental progress and prospect of constructing minimal self-replicating molecular systems, termed as protocells, using a pure synthetic approach. The work on protocells is a beautiful example where design simplicity enables crucial progress toward system complexity.

Mark your calendars for the ISNSCE upcoming meetings!

FNANO: Foundations of Nanoscience

Website:

www.cs.duke.edu/~reif/FNANO/

Dates to remember:

- Submission: *January 15st, 2007*
- Meeting: *April 18-21, 2007*
- Cut-off date for reservations at the meeting hotel: *February 15th*

Place: Snowbird, Utah. Take your skis!

DNA13: DNA based computing

Website:

http://dna13.memphis.edu

Dates to remember:

- Submission: *February 26th, 2007*
- Notification of acceptance: *April 15th, 2007*
- Revised manuscripts due: *May 5th, 2007*
- Meeting: *June 3-8, 2007*

Place: Memphis TN, USA