

# SECOND ANNOUNCEMENT AND REGISTRATION FORM

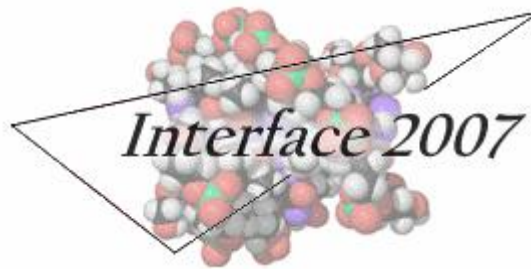
**39<sup>th</sup> Symposium on the Interface:  
Computing Science and Statistics  
Theme:  
Systems Biology**

23-26 May 2007  
DoubleTree Hotel, Philadelphia, PA

<http://www.interfacesymposia.org>  
<http://sbm.temple.edu/interface07>

**Keynote Speaker: David Botstein  
Princeton University**

*Title*  
**How the Genome and the Computer  
Have Changed Biological Science**



**SPONSORED BY**  
The Interface Foundation of North America

**HOSTED BY**  
Center for Statistical & Information Science  
Department of Statistics  
Center for Information Science & Technology  
Temple University

**Financial Sponsors**  
ASA Section on Statistical Computing  
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**COOPERATING ORGANIZATIONS**  
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This symposium is a long-standing forum focusing on the  
Interface between computing science and statistics.

# General Information

## **AN INVITATION**

The Interface Foundation of North America cordially invites you to participate in the 39<sup>th</sup> Interface Symposium, the premier annual conference on the interface of computing and statistics. The Foundation is a non-profit educational corporation founded in 1987 to sponsor the symposium and publish the proceedings. IFNA also co-publishes the *Journal of Computational and Graphical Statistics*. For further information about IFNA visit our web site at <http://www.interfacesymposia.org>.

The theme of Interface 2007 is Systems Biology. Systems Biology, through its focus on providing researchers quantitative information to explain the relationships between cellular environments and higher biological functions, uses database technology, computational systems, and statistical methodology to change the way we study biology. The lessons learned by those who work in Systems Biology have provided new approaches to those working at diagnosing and treating diseases.

The 2007 Symposium will include a strong scientific expository flavor emphasizing applied problems and synergy among solutions across biological areas. The program has invited sessions that will maximize opportunities for professional interactions not only among statisticians and computational scientists, but also biological scientists and others representing agencies and institutions facing challenging problems related to the theme of systems biology.

The Keynote Speaker is David Botstein of Princeton University. He is one of the most influential researchers in systems biology and bioinformatics. Many distinguished statisticians, computing scientists, and biologists who work in systems biology are also participating in Interface 2007.

## **CONTACT INFORMATION**

Conference Chairs:

Dr. Alan J. Izenman, Temple University, [alan@temple.edu](mailto:alan@temple.edu)

Dr. Zoran Obradovic, Temple University, [zoran@core.ist.temple.edu](mailto:zoran@core.ist.temple.edu)

Mail: Interface Foundation of North America, Inc.  
P.O. Box 7460  
Fairfax Station, VA 22039-7460

Phone: (215) 204-8166 Fax: (215) 204-1501

## **CALL FOR PARTICIPATION**

In 2007, we are focusing on statistical, computational, and biological problems connected with systems biology. Systems Biology, through its focus on providing researchers quantitative information to explain the relationships between cellular environments and higher biological functions, uses database technology, computational systems, and statistical methodology to change the way we study biology. The lessons learned by those who work in Systems Biology have provided new approaches to those working at diagnosing and treating diseases. The 2007 Symposium will include a strong scientific expository flavor emphasizing applied problems and synergy among solutions across biological areas. The program has invited sessions that will maximize opportunities for professional interactions not only among statisticians and computer scientists, but also biological scientists and others representing agencies and institutions facing challenging problems related to the theme of systems biology. Papers and presentations from all areas that connect statistics, computer science, and systems biology have been invited. Biological scientists are often at the frontier of work with new data types and we have encouraged them share their problems and solutions with us whether or not those solutions appeal to traditional statistical methods. Sessions will include invited and contributed paper sessions.

**Invited sessions** are organized by members of the Program Committee and designed to cover both the depth and breadth of current research related to the theme. See the section below on the Invited Program.

**Contributed sessions** have been organized by the Program Chairs from contributed abstracts.

## **REGISTRATION AND FINANCIAL SUPPORT**

The regular member of Interface registration is \$335. For individuals who are not members of Interface, registration is \$450. Members of cooperating societies receive discounted registration. For members of co-operating societies, registration is \$375. Regular participants in the Interface Symposium Series are strongly encouraged to join Interface. There also is a student registration fee of \$150, and a one-day registration fee \$170. **In order to enroll in the short courses, participants must be registered for the conference.** The one-day registration does not include the banquet. All other registered participants attend the banquet at no additional charge. Guest tickets for the banquet may be purchased for an additional \$65 per ticket. Limited funds may still be available to support travel and per diem expenses: preference will be given to young researchers and graduate students, with a priority to those presenting papers.

## **HOTEL ACCOMODATIONS**

The Interface 2007 conference hotel is the DoubleTree Hotel, located on Broad Street at Locust Street, Philadelphia, PA 19107, telephone (215) 893-1600 or (800) 222-TREE. The hotel is located on the Avenue of the Arts (Broad Street) in the heart of Center City. We have reserved a block of rooms for Interface attendees at the special rates of \$159 (single) and \$169 (double) per night (plus tax). Call the hotel directly and ask for Group Sales. We expect these rooms to go quickly, so book early!

## **SHORT COURSES**

### **Short Course I: Computational Systems Biology of Cancer: Measuring, Mining, and Modelling**

Bud Mishra (New York University)

**Time:** 8:00 am to 12:00 noon.

**Abstract:** Rapid and accurate solutions to many biomedical problems are beginning to rely on systems and computational approaches. A few notable examples are: genomic assays for cancer, genetic analysis of cancer genomes for marker detection, models of cancer progression, etc. While these examples focus on cancer and currently build upon microarray technology, the algorithmic approaches must aim to be scalable, agnostic to the technologies, and applicable to a wide variety of problems. This short course surveys many promises, challenges, and obstacles faced by the emerging field of systems biology as they tackle these biomedical problems. In particular, we will emphasize three highly-intertwined aspects of this problem: (1) Measuring: array and single-molecule measurements and their statistical analysis; (2) Mining: statistically combining gene expression and genomic patient data for discovery; (3) Modelling: systems biology algorithms for reasoning and redescription of time-course data. Various novel applications of mathematical ideas appear: 0-1 laws in experimental design, scan statistics applications to genetics, rate distortion theory and its applications to model building, hidden Kripke models and temporal logic redescrptions, nonlinear Kalman-Bucy filtering, efficient maximum a posteriori estimators, etc.

### **Short Course II: Copy-Number Variation in the Genome: Technologies, Statistics, and Applications**

John Marioni (University of Cambridge), Natalie Thorne (University of Cambridge), and Simon Tavare (University of Cambridge and University of Southern California)

**Time:** 1:00 pm to 5:00 pm.

**Abstract:** Array Comparative Hybridisation (aCGH) has become an established and important experimental tool for exploring how genomic variation impacts upon many areas of biology. The development of experimental and statistical techniques for analyzing aCGH data has been primarily motivated by its application to DNA taken from patients with a particular tumor. However, more recently, aCGH has been used to investigate a different problem, namely, the extent of Copy Number Variation (CNV) throughout (putatively normal) human genomes. This application has necessitated the development of novel tools for both pre-processing and downstream analysis of the data. One situation where the development of novel tools has been necessary is in the identification of regions of CNV. For tumors, a large number of genomic rearrangements (frequently covering many megabases) often occur and single outlying probes are generally assumed not to represent real biological changes. Moreover, tumors are very heterogeneous and this manifests itself in the presence of many different changes at a particular genomic locus across a cohort of samples. However, when finding regions of CNV using aCGH, the problems are quite different. In particular, regions of CNV tend to be small, with an average size of about 200kb. Furthermore, because there are no cellularity effects and sample heterogeneity is less of an issue, it is possible to use cross-sample information to not only remove technical probe effects but also to identify regions of CNV. In this session, we will describe the development of aCGH as an experimental platform, focusing on the statistical methods that have been devised for analyzing the data produced as the technology has evolved. In particular, we will describe the novel methods being used to find regions of CNV and on approaches for analyzing regions of CNV in conjunction with gene experiments, SNP, methylation, and other data generated from the same individuals whose CNV profiles have been determined.

## **TRANSPORTATION FROM THE AIRPORT AND GETTING AROUND**

**Philadelphia International Airport (PHL)** serves arrivals and departures for international and domestic flights. It is located just 7 miles (11 km) from the center of Philadelphia. Ground transportation at Philadelphia International Airport is readily available and includes rail, bus, taxis, and shuttle bus and limousine services. Philadelphia is laid out in a basic grid pattern. SEPTA operates a large fleet of buses throughout the city and suburbs. Two subway lines serve the city: the Market-Frankford (E-W) and Broad Street (N-S). Because the streets are narrow in Center City, traffic is often congested, and travel on foot or by taxi is often recommended. There are historical tours, which include Victorian trolleys, double-decker buses, and horse-drawn carriages.

## **ABOUT PHILADELPHIA**

Philadelphia is famous as the birthplace of life, liberty, and the pursuit of happiness. There are cultural, culinary, artistic, and ethnic treasures within the city and its surrounding countryside. There are world-class museums in and around the city, such as the Philadelphia Art Museum, the Barnes Foundation, the Rodin Museum, the Franklin Institute, the Academy of Natural Sciences, the Norman Rockwell Museum, and the Institute of Contemporary Art. You can even visit the Philadelphia Zoo. You can take tours of Independence Hall (the birthplace of both the Declaration of Independence and the U.S. Constitution), the National Constitution Center, the Liberty Bell Center, and the Betsy Ross House. You can visit the Italian Market, the Reading-Terminal Market, and South Street, where you can savor an authentic Philly cheesesteak. Philadelphia is currently implementing a city-wide WiFi initiative so that high-speed Internet can be accessed free at numerous locations within the city. The normal daily temperature range in Philadelphia in May is 54-73 degrees F (12-23 degrees C). Average rainfall in May is 3.8" with about 11 days of rain during the month.

## **THE INVITED PROGRAM**

### **Genetic Association Studies**

**Charles Kooperberg, organizer**

Dan L. Nicolai, *Quantifying and Extracting Information in Whole-Genome Association Studies*  
James Y. Dai, *An Adaptive Clustering Algorithm to Model Haplotype-Disease Association in Case-Control Association Studies*  
Paul Scheet, *Patterns of Linkage Disequilibrium Reveal Errors and Deletions in Population Genetic Data*

### **Statistical Methods in Proteomics**

**Francoise Seillier-Moiseiwitch, organizer**

Kevin Coombes, *Statistical Preprocessing of Mass Spectrometry Data*  
Kimberley Sellers, *Modeling and Spot Detection of Two-Dimensional Gels*  
Valeriy Kosostyshevskiy & Francoise Seillier-Moiseiwitch, *Analysis of 2D-Gels; A Global Approach*

### **Problems and Prospects for Integrative Biology and the Grid**

**J. Robert Beck, organizer**

J. Robert Beck, *Good Cells, Bad Cells, and the Grid*  
Frank J. Manion, *Trustable Architectures for a Biomedical Research Grid*  
Eric A. Ross, *Local and Remote Data Mining and Implications for the Grid*

### **Statistical Methods for Genetic Association Studies**

**Gang Zheng, organizer**

Philip Rosenberg, *Aspects of the Statistical Multiple Comparisons Problem in Genetic Association Studies of Sporadic Disease*  
Jinbo Chen, *Conditional Likelihood Methods for Haplotype-Based Association Analysis Using Matched Case-Control Data*  
Gang Zheng, *Two-Stage Analyses of Case-Control Genetic Associations*

### **Proteomics Data Analysis**

**Slobodan Vucetic, organizer**

Olga Troyankaya, *From Diverse Genomics Data to Protein-Protein Interaction Networks*  
Milos Hauskrecht, *Enhancing the Analysis of MS Proteomic Profiles Using Prior Knowledge and Past Data Repositories*  
Predrag Radivojac, *Methods for Protein Identification and Quantification from Tandem Mass Spectrometry Data*

### **Genomic Analysis Across Platforms**

**Giovanni Parmigiani, organizer**

Rafael Irizarry, *Multiple Laboratory Comparisons of Microarray Platforms*  
Robert Scharf, *A Hierarchical Model and R Software for Finding Differential Gene Expression in Multiple High-Throughput Platforms*  
Zoltan Szallazi, *Probe Sequence and Biological Knowledge-Based Approaches to Increase the Consistency of DNA Microarray Analysis*

### **Computational Analysis of Gene Regulation**

**Vincent Carey, organizer**

Christina Leslie, *Learning Regulatory Programs that Accurately Predict Gene Expression*  
Anirvan Sengupta, *SVMs and Probabilistic Approaches for Classifying Promoters*  
Harmen Bussemaker, *Data-Driven Biophysical Modeling of Gene Expression Regulation*

### **Information Extraction from Biomedical and Clinical Text**

**David Shera, organizer**

Keven Cohen, *The Global Linguistic Challenge and Approaches*  
Peter S. White, *AMining the Bibliome: Supervised Extraction of Biomedical Entities from Text for Biological Application*  
Andrey Rzhetsky, *Striving to Make Text-Mining Useful for Disease-Gene Identification*

### **Computational and Statistical Methods for Genome-Wide Studies of Biological Systems**

**Sandrine Dudoit, organizer**

Imola K. Fodor, *Systems Biology Insights from Host-Pathogen Interaction Studies*  
Steve Horvath, *Simple Models for Integrating Gene Expression and Genetic Marker Data to Characterize Disease-Related Genes*  
Sunduz Keles, *Enhancing Motif-Finding Models Using Multiple Sources of Genome-Wide Data*

### **Data and Decision Fusion**

**Frank Hsu, Amy Braverman, organizers**

Tin K. Ho, *Uniform Random Guesses and Random Decision Forests*  
Guy Lebanon, *A Censored-Data Approach to Modelling Partial Rankings on the Ranking Lattice*  
Li-San Wang, *Regulatory Module Discovery with Heterogeneous Data by Multipartite Coclustering*

### **Computational Techniques for Structural Genomics**

**Daisuke Kihara, organizer**

Carlos J. Camacho, *In Silico Prediction of Protein Interactions: Nothing that Nature Does Not Already Know*  
Yaoqi Zhou, *From Sequences and Structures to Interactions of Proteins: Some Recent Developments*  
Daisuke Kihara, *Surface-Shape-Based Protein Structure Classification and Search*

### **JCGS Highlights**

**Luke Tierney, David van Dyk, organizers**

Hana Sevcikova, *Simulating 2D Gaussian Random Fields: Fast and Exact Algorithms*  
Ben B. Hansen, Stephanie Olsen Klopfer, *Flexible, Optimal Matching for Comparative Studies: A Network Flows Algorithm and an R Package*  
Richard M. Heiberger, *Mean-Mean Multiple Comparison Displays for Families of Linear Contrasts*

**Indexing and Search in Biological Data**  
**Mohammed J. Zaki, organizer**

Jeremy Buhler, *Indexed Biosequence Similarity Search in the Age of Comparative Genomics*  
Jignesh Patel, *Indexing for Success: Effective Index-Based Methods for Querying Biological Sequences*  
Ambuj Singh, *Querying and Mining in Graph Databases*

**Integrative Systems Biology in Cancer Research**

**Ramana V. Davuluri, organizer**

Andrea Califano, Herbert Irving, *Genome-Wide Identification of Modulators of Transcriptional Regulation in Human B Lymphocytes: The Kinome Meets the Transcriptome*  
Michael Q. Zhang, *CAdaptively Inferring Human Transcriptional Subnetworks*  
Michael Ochs, *Integration of Annotations for Guiding Analysis of Signaling in Cancer Cells*  
Mike West, *Stochastic Modelling and Estimation in Dynamic Cellular Networks*

**Methods for Integrating Disparate Molecular Datasets for Prediction**  
**Peter S. White, organizer**

Yves Lussier, *Ontology Similarity Networks and Database Interoperability*  
John Maris, *Interactive Genomics of Human Neuroblastoma: Promises and Pitfalls for Translation to the Clinic*  
Michael Krauthammer, *Data Integration for Disease Pathway Mapping*

**Roles of Protein Intrinsic Disorder in Interaction Networks**  
**Keith Dunker, organizer**

Pedro Romano, *The Interplay Between Alternative Splicing and Intrinsic Disorder and Its Implications on Multicellular Complexity*  
Richard Kriwacki, *Proteomics Studies of Intrinsically Unstructured Proteins (IUPs) in Mammalian Cells*  
Celeste Brown, *Structure and Function of Rapidly-Evolving Proteins Involved in Yeast Protein-Interaction Networks*  
Jake Chen, *Exploring Relationships Among Protein Disorders, Network Hubs, and Disease Targets in Protein Interactome Studies*

**IASC Session: Current Issues in Statistical Biocomputing**  
**Michael G. Schimek, organizer**

Alexander Ploner, *Pathway-Specific Predictors for Gene Expression Data*  
Eva Budinska, Eva Gelnarova, Michael Schimek, *A Median Absolute Deviation Method for Detecting Copy-Number Changes in Array-CGH Data*  
Florian Markowitz, Olga G. Troyanskaya, Rainer Spang, *Building Phenotypic Hierarchies from Nested Effects of Gene Perturbations*

**Best of SIAM Data Mining 2007**  
**Vipin Kumar, organizer**

**Inferring Genetic Networks from Genomics Data**  
**Grace S. Shieh, organizer**

Satoru Miyano, *Computational Challenges for Modelling and Simulating Biological Pathways*  
Hongyu Zhao, *Inferring Genetic Regulatory Networks Using Genomics Data*  
Henry Hornng-Shing Lu, *Is Less More?: On Statistical Investigation for Large Biological Networks*

**Best of CAMDA 2006**  
**Patrick McConnell, organizer**

Madhuchhanda Bhattacharjee, *Bayesian Joint Disease-Marker-Expression Analysis Applied to Clinical Characteristics of Chronic Fatigue Syndrome*  
Anja Presson, Steve Horvath, *Integration of Genetic and Genomic Approaches for the Analysis of Chronic Fatigue Syndrome Implicates Forehead Box N1*  
Roumyana Kirova, *A Systems Genetic Analysis of Chronic Fatigue Syndrome: Combinatorial Data Integration from SNPs to Differential Diagnosis of Disease*  
Simon M. Lin, *QA/QC of Clinical SELDI-TOF Data with Wavelets*

**Providing Biological "Confidence" from Computational Analysis**  
**Gregory E. Gonye, organizer**

Ronald Pearson, *Pharmacovigilance Maps: Quantifying Associations Between Prescription Drugs and Adverse Reactions*  
Rajanikanth Vadigpalli, *Identification of Perturbation-Relevant Gene Regulatory Networks from Statistical Enrichment Analysis of Gene Co-Expression Clusters*  
Isadore Rigoutos, *Of microRNA Targets and microRNA Precursors*

**Statistical Learning and Management of Biological Data**  
**Parthasarathy Srinivasan, organizer**

Dennis Pearl, Liang Liu, *Using Molecular Data to Estimate the Evolution of Species – Not Just the Phylogeny of Genes*  
Jieping Ye, Sudhir Kumar, *Machine-Learning Approaches for Drosophila Gene Expression Pattern Image Analysis*  
Chris Bystroff, *I-Sites 2007: Protein Local Structure Motifs Have Covariant Sequence Patterns*  
Golan Yona, *Integration and Analysis of Complex, Heterogeneous and Interrelated Biological Data – Towards a New Generation of Biological Databases*

**Modelling of Ethanol Abuse and HIV/AIDS**  
**Yasmin H. Said, organizer**

Kendall J. Bryant, Ron Braithwaite, *Developing Integrative Models of the Interaction of Alcohol Use and HIV/AIDS Progression Using Behavioral and Biological "Bedside and Bench"*  
Yasmin H. Said, Edward J. Wegman, *Assessing Interventions Related to Negative Effects of Ethanol on HIV/AIDS Spread*  
W.F. Wieczorek, K.S. Marczyński, T.H. Nochajski, S. Tetewsky, *Using Research Data to Parameterize Risky Sexual Behavioral and Alcohol Use*

**Metrology and Inference of Complex Biological and Engineered Systems**

**Z.Q. John Lu, organizer**

Marc Salit, *Standards in Microarray Gen Expression Experiments*  
 Inyoung Kim, *Bayesian Semiparametric Methods for Pathway Analysis*  
 Jim Filliben, *Sensitivity Analysis Methodology for a Complex System Computational Model*

**Metagenome Informatics**

**Hongwei Wu, Ying Xu, organizers**

Mihai Pop, *Assembling the Human Gut Biome*  
 Kostas Mavrommatis, *Benchmarking the Fidelity of Metagenomic Sequences Using Simulated Datasets*  
 Hongwei Wu, *On Incorporating Genomic Neighborhood Information for the Prediction of Orthologous Genes*

**Systems Approaches for Alcohol Use Modelling**

**Yasmin H. Said, organizer**

Gregory Bloss, *Systems Perspectives on Prevention of Alcohol-Related Problems: Research Opportunities and Resources*  
 Paul J. Gruenewald, *Systems Ecology and Community Systems: Understanding Social Problems in Social Terms*  
 K.S. Marczynski, W.F. Wieczorek, A.M. Delmerico, T.H. Nochajski, and S.J. Tetewsky, *Geocomputational Methods in the Assessment of Alcohol Use in a Population of DWI Offenders*

**Immunological Proteomics**

**Keith Baggerly, organizer**

Keith Baggerly, *Statistical Analysis of Reverse-Phase Protein Arrays*  
 Debashis Ghosh, *Phage Arrays*  
 Francis Tong, *Antibody Arrays*

**Biological Networks**

**Natasa Przulj, organizer**

Teresa Przytycka, *TBA*  
 Chris Wiggins, *TBA*  
 Natasa Przulj, *TBA*

**Accessible Interfaces to Advanced Statistics Software**

**Richard Heiberger, organizer**

Erich Neuwirth, Thomas Baier, *An Office-Software and Menu-Driven Interface for Advanced Statistics in the Biological Sciences*  
 Narasimhan Balasubramanian, *Disseminating Statistical Methodology and Results via R and Excel: Two Examples*  
 Robert Gagnon, *Analysis and Visualization of Microarray Gene Expression Data Using Excel, SAS, and S-Plus*

**Analysis of DNA Barcode Data**

**Woolcott K. Smith, Javier Cabrera, organizers**

David Schindel, *TBA*  
 Javier Cabrera, John Lau, Albert Y. Lo, *Weighted Chinese Restaurant Process for Clustering Barcodes*  
 Bogdan Paraniuc, *TBA*

**A Starter Kit for Systems Biology: First Useful and Usable System Model of Protein Cycle, Pursuit of Uncertainty, and Interdisciplinary Collaboration**  
**Arnold Goodman, organizer**

Date	Events
Wednesday, May 23	<p>Registration Begins for Interface 2007</p> <p>Short Course I:  <i>Computational Systems Biology of Cancer: Measuring, Mining, Modeling</i>                      (8:00 a.m. – noon)                      Bud Mishra                      Courant Institute, New York University</p> <p>Short Course II:  <i>Copy-Number Variation in the Genome: Technologies, Statistics, and Applications</i>                      (1:30 p.m. – 5:30 p.m.)                      John Marioni, University of Cambridge, Natalie Thorne, University of Cambridge, and Simon Tavaré, University of Cambridge and University of Southern California</p> <p>Evening Mixer                      (8:00 p.m. – 10:00 p.m.)</p>
Thursday, May 24	<p>Keynote Address:  <i>How the Genome and the Computer Have Changed Biological Science</i>                      (8:00 a.m. – 9:45 a.m.)                      David Botstein                      Princeton University</p> <p>Technical Sessions begin                      (10:30 a.m. – 5:45 p.m.)</p> <p>Conference Banquet                      (7:00 p.m. – 10:30 P.m.)                      Speaker  <i>A View of Systems Biology from 30,000 Feet</i>                      Richard Klavans                      University of California, San Diego</p>
Friday, May 25	<p>Technical Sessions Continue                      (8:00 a.m. – 5:45 p.m.)</p>
Saturday, May 26	<p>Technical Sessions Continue                      (8:00 a.m. – noon)</p>

## MEETING REGISTRATION FOR INTERFACE 2007

39<sup>th</sup> Meeting of the Interface, INTERFACE 2007, May 23-26, 2007

Name \_\_\_\_\_ (As will appear on your nametag)

Job Affiliation \_\_\_\_\_ (As will appear on your nametag)

(Indicate whether this is a  work address or  home address.)

Address \_\_\_\_\_

City \_\_\_\_\_ State or Province \_\_\_\_\_

ZIP or Postal Code \_\_\_\_\_ Country \_\_\_\_\_

Telephone \_\_\_\_\_ E-mail \_\_\_\_\_

Join Interface now (and attend at the Member rates of \$335). Pay \$35 membership plus \$335 registration.

### Conference fees (with 1 Banquet ticket included, except single-day registrants)

- Interface member, \$335
- Member of Cooperating Societies, \$375
- Not a member of either Interface or Cooperating Societies, \$450 (I do not wish to join Interface.)
- Student Registration (no proceedings), \$150
- Single Day Registration (no banquet, no proceedings), \$170

### Interface Short Course Registrations (At least one-day Conference Registration Required)

- Attendees who are members of Interface or Cooperating Societies, one course, \$165
- Attendees who are members of Interface or Cooperating Societies, both courses, \$225
- Attendees who are not members of Interface or Cooperating Societies, one course, \$225
- Attendees who are not members of Interface or Cooperating Societies, both courses, \$350
- Students, one course, \$75
- Students, both courses, \$100

If only one course is taken, circle appropriate one: **I: Biology of Cancer II: Copy-Number Variation**

Guest Banquet Tickets @ \$65 each Total Amount Enclosed \_\_\_\_\_

Make checks payable to Interface. Mail to: Interface 2007, P.O. Box 7460, Fairfax Station, VA 22039-7460, USA, or fax to: (703) 993-9299 (attention: Ms. Elizabeth Quigley). Visa, MasterCard, or Discover Credit Cards are accepted. Please supply also the following information.

Type of Card \_\_\_\_\_ Expiration Date \_\_\_\_\_

Credit Card Number \_\_\_\_\_ / \_\_\_\_\_

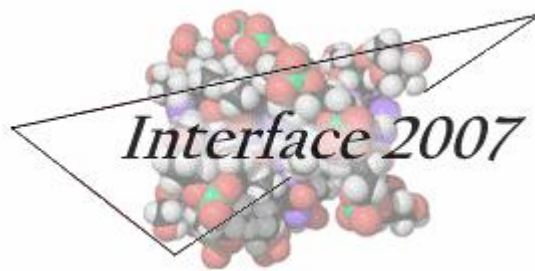
All card users, please note: Please include the 3-digit number that follows credit card number. This is found on the back of credit card in the signature line.

Cardholder's Name \_\_\_\_\_ Signature \_\_\_\_\_

Credit Card Billing Address & Email address: (If different from mailing address or attendee information. If Cardholder is not the attendee, please furnish email address for confirming receipt.)

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(Please Print.)

Notes: For enquiries contact Ms. Liz Quigley (703) 993-1212 or via email, equigley@gmu.edu. Registration for Interface includes all Interface sessions, breaks, the banquet, and conference CD. For student registration, attach a letter from department chair or major professor. Participants in the short course(s) must be registered for at least a single day. On-site registration will be available. If you select and pay for Interface membership, then you can register at member rates for the meeting and the short courses (i.e. membership becomes effective immediately.) Cooperating societies are ASA, CSNA, ENAR, IASC, IMS, INFORMS, SIAM, and WNAR.



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