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## Newsletter Archives

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**ISCB Newsletter (February/March, 1999)**
**Volume 2, Number 2**

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### 1) ISCB RECRUITMENT

[Editors Note: We include here the recruitment letter for membership in the ISCB that is on the Society web page, and will be sent to targeted potential members. We include this letter in our ISCB mailing list in order to remind our members about the benefits that the Society has arranged for 1999, the prices for 1999, and the need for renewal on a new calender year schedule, in order to match the practices of the affiliated journals.

Dear Colleague;

I am writing to invite you to join the International Society for Computational Biology. Formed in 1997, the goal of the Society is to promote the scientific understanding of living systems through computation. Our emphasis is on the role of computing and informatics in advancing molecular biology. If you are involved in any aspect of computational biology yourself, or if you are planning to build a career in the field, or if you are just interested in the latest innovations, membership of the Society will be invaluable.

Why Join?

The Society, also called the ISCB, serves its membership in a variety of ways. Our primary goal is to help build computational biology into a robust and fertile scientific enterprise. We organize computational biology conferences and support high quality scientific publications. Our future plans include efforts to expand the awareness of our field in industry, academia and among funding agencies, and providing society-sponsored postdocs, fellowships and other awards.

Another way we serve our members is through dramatic savings on conference registrations and subscriptions to the key scientific publications in the field. In order to meet the diverse needs of the community ISCB offers three levels of individual membership: student-postdoc, basic and full. Each of these types of membership are rewarding both scientifically and financially. The benefits include:

*Access to the Leading Scholarly Journals*

Society members get access to the leading journals in the field. The savings on subscriptions alone is more than enough to cover your Society membership. Bioinformatics is the official journal of the society, and basic membership grants access to the on-line edition of the journal, including all published articles in full text, complete with graphics and tables. The online Bioinformatics is available in both PDF and HTML formats, and links to authors' servers allow you to download software, data and other supplementary information. Full members receive bound paper copies of both Bioinformatics and the Journal of Computational Biology (JCB). Student/postdoc and basic members may add a JCB subscriptions and/or bound volumes of Bioinformatics to their membership for a modest fee.

*Discounted Subscription to the Bioinform Newsletter*

The Bioinform newsletter covers industrial bioinformatics with weekly behind-the-scenes reports and analysis worldwide. It is available to all ISCB members for $495 per year, $90 off the regular price.

*Conference Registration Discounts*

We also sponsor a series of conferences, including Intelligent Systems for Molecular Biology (ISMB) and the Pacific Symposium on Biocomputing (PSB) and provide support for the International Conference on Research in Computational Molecular Biology (RECOMB). Our members get $50 registration discounts at all associated conferences, so if you go to all three, you'd save $150.

*And there's more*

Being a member of the Society can help show that you work in an established field, which can be important to employers or funding agencies. As an individual member, you are eligible for access to the ISCB Job Fair on our web site (www.iscb.org). Get the latest job listings, and maybe find that job of your dreams. We're hard at work on other services as well. Check our web site for information about possible ISCB sponsored pre- and post-doctoral fellowships, and other planned activities. Finally, you strengthen the Society just by joining. If you like to do more, or if you have an idea you'd like us to consider, please email us: iscb@iscb.org

The International Society for Computational Biology is a 501(c)3 non-profit corporation. Donations above the membership rate are tax-deductable in the United States, so please consider a gift of support if you can. And please contact us for information about possible institutional memberships as well.

We are building a vibrant, representative scientific society. We want your participation. The cost is low, and the benefits are substantial. Please take a few minutes to fill out the enclosed membership form, or visit the signup page on our web site: http://www.iscb.org/registration.html

Sincerely,

Lawrence Hunter
ISCB President

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**Membership Registration:**

Name (first, initial, last)
Highest degree
E-mail address
Personal webpage URL
Department
Institution
Telephone No
Fax No
Street address 1
Street address 2
City, State/Region, Postal code
Country
Status (Student, Postdoc, Basic, Full)
Areas of interest/keywords
Area of last degree
I want to receive email sent to the general society distribution list?

**Membership fees:**
Full membership $170

Basic membership $65
add Bioinformatics bound volumes +$30
add Journal of Computational Biology bound volumes +$75

Student/Postdoc $35
add Bioinformatics bound volumes +$30
add Journal of Computational Biology bound volumes +$35

Postage for non-US membership that includes JCB +$26

For student or postdoc rates, please include proof of status, such as photocopy of current ID or letter from your advisor, and your estimated graduation or fellowship end date.

Payment:

By credit card (Visa or Mastercharge):

Account number:
Expiration date:
Name exactly as it appears on the card:

By check: made out to The International Society for Computational Biology

Please send this form with your payment to:

International Society for Computational Biology
c/o David J. States
Institute for Biomedical Computing
Washington University
700 S. Euclid Ave.
St. Louis, MO 63110
USA

## 2) ISCB ANNUAL MEMBERSHIP FEES AND JOURNAL RATES

Since its inception in 1997, the ISCB has had a positive growth in membership and general interest. Because of the freshness of the Society we are experiencing, yet addressing, the growing pains that appear with the development of an endeavor of such great magnitude.

The rates for membership fees and choice of journal subscription have been adjusted somewhat, particularly affecting the student/trainee cost. The slight increase is due to an increase in publishing cost.

The three levels of membership offered by ISCB are: Student/Trainee, Basic (low cost) and Full. Each paid member receives on-line access to the official Society journal, Bioinformatics and substantial discounts to the three Society affiliated conferences: ISMB, PSB and RECOMB. Full members also receive bound volumes of Bioinformatics and the Journal of Computational Biology (which may also be added separately at other membership levels).

As of January 1999, the ISCB membership fees/journals are issued on a CALENDAR basis. Therefore, irrespective of when a member joins in 1999, payments will be applied to 1999 membership status and journal issues. If you are sending in a payment at the end of the year for the upcoming year, you MUST state which year to apply the membership fee/subscription. This can be noted on a mail-in payment, by email, or on-line notification. In order to keep the process running smoothly, we solicit your help, patience and support in this area.

As for access to Bioinformatics online for 1999, we are kindly giving this service to all members who sent in a payment in 1998. However, if you desire additional Journal subscriptions (on line or hard copies) you will need to send an additional payment for that particular subscription. Below is a breakdown of the options available.

The credit card payment process is still being worked out and we hope to have it in progress before the end of March.

Membership type Journals Dues Membership fees:

Full membership (represents Basic + 2 Journals) $170

Basic membership (Online Bioinformatics)
$65
add Bioinformatics bound volumes +$30
add Journal of Computational Biology bound volumes +$75

Student/Postdoc/Trainee (Online Bioinformatics)
$35
add Bioinformatics bound volumes +$30
add Journal of Computational Biology bound volumes +$35

A $26 postage fee will be charged for all non-US subscriptions to the Journal of Computational Biology.

Dues are listed in US dollars. We can accept foreign credit cards, and you will receive your bank's prevailing exchange rate (which is usually competitive). We can also accept checks made out in Euro dollars at an exchange rate of 1.15 US dollars to the Euro. This is not quite the prevailing exchange rate, but we have bank fees to cover on the exchange. Membership and journal subscriptions run for the calendar year. You will recieve back issues for the journals if you enter your membership later in the year.

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The Third Annual Conference on Research in Computational Molecular Biology (RECOMB 99) that will take place in Lyon (France) on April 11-14, 1999. Those who would like to attend the Conference are invited to register before

March 12, 1999

You will find a registration form as well as further information about the conference on the web site http://www.inria.fr/RECOMB99/

Warning: Future participants are suggested to make their hotel reservation as soon as possible. Please be aware that there are other congresses held in Lyon at that time and the hotel availability might be limited.

**3) PRELIMINARY PROGRAM OF RECOMB'99**
April 11-14,
Hotel de Lyon Metropole, Lyon, France

**Saturday, April 10, 1999**
16:00 - 19:00 - Welcome and registration at Lyon Metropole Hotel
18:00 Cocktail offered by the City Hall of Lyon

**Sunday, April 11, 1999**
8:45 Opening Remarks:
Sorin Istrail, General RECOMB Vice-Chair
1999 Program Committee Chair
Mireille Regnier, 1999 Conference Chair
Ron Shamir, 2000 Program Committee Chair

Distinguished New Technologies Lecture - Chair: S. Istrail

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9:00 Large DNA Microarrays - the How and the Why
Ed Southern

10:00 Break

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10:15 Algorithms for Choosing Differential Gene Expression Experiments
R. M. Karp, R. Stoughton, K. Y. Yeung

10:40 An Algorithm for Clustinering cDNAs for Gene Expression Analysis
E. Hartuv, A. Schmitt, J. Lange, S. Meirer-Ewert, H. Lehrach, R. Shamir

11:05 A Dictionary Based Approach for Gene Annotation
L. Pachter, S. Batzoglou, V. I. Spitkovsky, W. S. Beebee Jr.,
E. S. Lander, B. Berger, D. J. Kleitman

11:30 Break

Session on Sequencing - Chair: R. Karp

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11:45 De Novo Peptide Sequencing via Tandem Mass Spectrometry: A Graph-Theoretical Approach
V. Dancik, T. Addona, K. Clauser, J. Vath, P. A. Pevzner

12:10 On the Power of Universal Bases in Sequencing by Hybridization
F. P. Preparata, A. M. Frieze, E. Upfal

Lunch: 12:35 - 14:00

Distinguished Biology Lecture - Chair: P. Pevzner

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14:00 Whole Genome Association Studies in Humans
Daniel Cohen

15:00 Break

Session on Protein Structure - Chair: M. Levitt

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15:15 Recognition of Remote Protein Homologies Using Three-Dimensional Information to Generate a Position Specific Scoring Matrix in the Program 3D-PSSM
L. Kelley, R. MacCullum, M. J. E. Sternberg

15:40 A Solvation Potential with Improved Contact Definitions and Optimized by Extensive Threading
A. Dombkowski, G. M. Crippen

16:05 Fast Detection of Common Geometric Substructure in Proteins L. P. Chew, D. Huttenlocher, K. Kedem, J. Kleinberg

16:30 Break

Plenary Lecture Session - Chair: M. Levitt

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16:45 The Past, Present and Future of Protein Structure Prediction
John Moult

18:00 - 20:00 Business Meeting

**Monday, April 12, 1999**
Plenary Lecture Session - Chair: R. Karp

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8:30 Computational Analysis of Molecular Diversity for Drug Discovery
Peter Willett

9:30 Break

Session on Genomic Rearrangements - Chair: R. Shamir

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9:45 Reconstructing the Pre-Doubling Genome
N. El-Mabrouk, D. Bryant, D. Sankoff

10:10 Formulations and Hardness of Multiple Sorting by Reversals
A. Caprara

10:35 Probability Models for Genome Rearrangement and Linear Invariants for Phylogenetic Inference
D. Sankoff, M. Blanchette

11:00 Break

Session on Trees - Chair: A. Guenoche

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11:15 Modeling Protein Families Using Probabilistic Suffix Trees
G. Bejerano, G. Yona

11:40 Faster Reliable Phylogenetic Analysis
V. Berry, D. Bryant

12:05 Obtaining Highly Accurate Topology Estimates of Evolutionary Trees from Very Short Sequences
D. H. Huson, S. Nettles, T. J. Warnow

Lunch: 12:30 - 14:00

Plenary Lecture Session - Chair: D. Slonim

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14:00 Progress Toward the Whole-Genome Shotgun Sequencing of Drosophilia
Gene Myers

15:00 Break

Session on Statistics - Chair: J. Kececioglu

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15:15 Searching Gene Transfers on Bacillus Subtilis Using Hidden Markov Models
L. Bize, F. Muri, F. Samson, F. Rodolphe, S. D. Ehrlich,
B. Prum, P. Bessieres

15:40 Significance Testing for Genomic Mismatch Scanning
G. R. Grant, R. S. Spielman, E. Manduchi, V. G. Cheung, W. J. Ewens

16h05 Break

Session on Statistics - Chair: G. Kucherov

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16:20 Classifying Proteins by Family Using the Product of Correlated p-values
T. L. Bailey, W. N. Grundy

16:45 Sequence Homology Detection Through Large Scale Pattern Discovery
A. Floratos, I. Rigoutsos, L. Parida, G. Stolovitzky, Y. Gao

17:30 - 19:30 Poster Session

**Tuesday, April 13, 1999**
Plenary Lecture Session - Chair: M. Regnier

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8:30 Genome Sequences and Protein Structures
Cyrus Chothia

9:30 Break

Session on Mapping - Chair: R. Karp

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9:45 Algorithms for Whole Genome Shotgun Sequencing
E. Anson, G. Myers

10:10 Construction of Physical Maps from Oligonucleotide Fingerprints Data
G. Mayraz, R. Shamir

10:35 Computing Physical Maps of Chromosomes with Nonoverlapping Probes
by Branch-and-Cut
T. Christof, J. Kececioglu

11:00 Break

Session on Threading - Chair: M. Vingron

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11:15 A Method for Optimal Design of a Threading Scoring Function
J. R. Bienkowska, R. G. Rogers Jr., T. F. Smith

11:40 An Anytime Algorithm for Gapped Block Protein Threading with Pair Interactions
R. H. Lathrop

12:05 Efficient Algorithms for Protein Sequence Design and the Analysis of Certain Evolutionary Fitness Landscapes
J. M. Kleinberg

12:30 - 14:00 Lunch

Lecture Session - Chair: S. Istrail

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14:00 Trends in Computational Biology
John Wooley

15:00 Break

Session on Sequence Alignment - Chair: A. Apostolico

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15:15 An Analytic Study of the Phase Transition Line in Local Sequence
Alignment with Gaps
R. Bundschuh, T. Hwa

15:40 Winnowing Sequences from a Database Search
P. Berman, Z. Zhang, Y. I. Wolf, E. V. Koonin, W. Miller

16:05 q-gram Based Database Searching Using a Suffix Array (QUASAR)
S. Burkhardt, A. Crauser, P. Ferragina, H-P. Lenhof, E. Rivals,
M. Vingron

17:00 - 23:00 Evening program at Saint-Romain-en-Gal

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17:00 Departure to Saint-Romain-en-Gal

18:00 Stanislaw Ulam - Computational Biology Address - Chair: M. Waterman
Comparison of Complete Genomes: Organisation and Evolution
Piotr Slonimski

19:00 Visit of the Museum

21:00 Cocktail

**Wednesday, April 14, 1999**
Plenary Lecture Session: Chair R. Shamir

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9:00 Comparing Genes and Genomes: From Polymorphism to Phylogeny
Peer Bork

10:00 Break

Session on Drug Design - Chair: R. Lathrop

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10:15 Efficient Database Screening for Rational Drug Design Using Pharmacophore-Constrained Conformational Search
S. M. LaValle, L. E. Kavraki, P. W. Finn, J-C. Latombe

10:40 Coupled Optimization in Protein Docking
J. C. Mitchell, A. T. Phillips, J. B. Rosen, L. F. Ten Eyck

11:05 Derivation of Sensitive Discrimination Potential for Virtual Ligand Screening
M. Totrov, R. Abagyan

11:30 Break

Session on Molecular Structure - Chair: J.M. Claverie

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11:45 Optimizing Combinatorial Library Construction via Split Synthesis
B. Cohen, S. Skiena

12:10 Internal Loops in RNA Secondary Structure Prediction
R. B. Lyngso, M. Zuker, C. N. S. Pedersen

12:35 - 14:00 Lunch

Session on Gene Networks - Chair: T. Lengauer

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14:00 Identifying Gene Regulatory Networks from Experimental Data
T. Chen, V. Filkov, S. S. Skiena

14:25 Evolution of Metabolisms: A New Method for the Comparison of Metabolic Pathways
C. V. Forst, K. Schulten

14:50 Clustering Gene Expression Patterns
A. Ben-Dor, Z. Yakhini

15:15 Closing session

15:30 End of the conference

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