11th International Conference on Intelligent Systems for Molecular Biology
Brisbane, Queensland, Australia
June 29 – July 3, 2003
What are you going to see

- Institute for Molecular Biology, University of Queensland.
- Some statistics of the Conference.
- Singapore research.
- Selected papers.
Institute for Molecular Biology, University of Queensland.

• Research division:
  – Genomics and Computational Biology (Computational Genomics)
  – Cellular and Developmental Biology
  – Structural Biology and Chemistry (Structural and Functional Genomics)
  – Office of Public Policy and Ethics

New!
Institute for Molecular Biology, University of Queensland.

- 21 research groups.
- Offer undergraduate and graduate program.
- ~ 400 research staff.
- Have spin-off companies.
Overview of the Conference

• >800 Attendees
• 18 attendees from Singapore
  – 5 BII
  – 4 I2R
  – 3 NUS
  – 2 DSO
  – 2 GIS
  – 2 IMCB
Tracks in ISMB 2003

• Oral Sessions:
  – Phylogeny and Genome Rearrangements
  – Expression Arrays and Networks
  – Predicting Clinical Outcomes
  – Protein Clustering, Alignment and Patterns
  – Transcription Motifs and Modules
  – Structure and HMMs
  – Text Mining and High Throughput Methods
Tracks in ISMB 2003

• Poster Session
  – Data Mining
  – Data Visualisation
  – Databases
  – Functional Genomics
  – Genome Annotation
  – Microarrays
  – New Frontiers
  – Phylogeny and Evolution
  – Predictive Methods
  – Sequence Comparison
  – Structural Biology
  – Systems Biology
What are Singapore Researchers doing?

• DSO:
  – dbSTR: a database for short tandem repeats. (D16 - Databases)

• LIT:
  – Antimic: a database of antimicrobial peptides. (D34)

• BIC, NUS:
  – SDPS: small disulphide-bonded proteins structural database. (D38)
  – Modeling the main cysteine proteinase of the SARS virus. (J30 – structural biology)

• I2r
  – Prediction of protein function from primary structure. (H3 – Predictive methods)
What are Singapore Researchers doing?

- BII
  - Evolutionary significance of G1/S checkpoint among eukaryotes. (I6 – Sequence comparison)
  - Discovering novel regulatory controls of budding yeast cell cycle reverse engineering and Bayesian network modeling. (K7 – Systems biology)
  - Cellware: a modeling and simulation tool for large scale biological systems. (K9)
  - Parameter estimation for biochemical pathways using swarm algorithm. (K10)
Selected Oral Presentation

• Fast Identification and Statistical Evaluation of segmental homologies in comparative maps. (2)

• Glocal alignment: finding rearrangements during alignment. (3)
Fast Identification and Statistical Evaluation of segmental homologies in comparative maps. (2)

- Flexible dynamic programming algorithm for identification of segments.
- Model the probability of observing putative segmental homologies by chance and incorporate it into the method.
- Combining => rapid and automated.
- www.bio.unc.edu/faculty/vision/lab/
Glocal alignment: finding rearrangements during alignment.

• Combine global (LAGAN) and local (CHAOS) methods.

• http://Lagan.stanford.edu/glocal