working on, explaining that they are able to look at individual cells using optics and/or electrical signals, thus enabling scientists to view cell content. Dr. Nobel discussed his long history with systems biology, beginning over 40 years ago when the molecules responsible for heart beating was determined. He was able to perform systems-level simulation of the heart and described how 90% of research is experimental while 10% is computational, but it is important in that it brings the experimental portion of research together to a unified whole. Dr. Green presented his work using multiple-species sequence comparison to determine not the coding sequences of genes, which are relatively easy to find, but the non-coding functional sequences. His work is part of the ENCODE project (ENCyclopedia Of DNA Elements), which utilizes multispecies comparison to identify highly conserved DNA sequences throughout evolution. These sequences are assumed to be strong indicators of functionally important regions of the human genome. Dr. Alon presented his work on "network motifs" which are recurring patterns in the graph representation of biological networks, and the final talk was by Dr. David Lipman, who described his historical work on protein sequence comparison. He also made clear his congenial relationship with Drs. Temple Smith and Michael Waterman by describing his first encounters with them. Interestingly, he concluded by questioning whether systems biology is truly possible, considering semantic shifts and polysemous in natural language. He explained that it may be difficult because of the nature of evolving systems, noise, etc., providing the attendants with some food for thought before returning home.

Finally, the best paper award was awarded to two papers: Robert Edgar for MUSCLE and Chuong Do et. al. for PROBCONS, both very new methods for multiple sequence alignment. Seeing as both works expressed their intention to combine together to perform even better multiple sequence alignments in the near future, both were equally considered to be of high quality.

All in all, the enormous number of participants told of the increasing popularity and importance of computational biology, and the advancement of techniques that will most definitely affect all our lives in the future.

■ Fourth International Workshop on Bioinformatics and Systems Biology

馬見塚 拓（京都大学化学研究所）

6月に京都で開かれた題名の会議に、Program Committee Co-chairとして参加したので報告する。本会議は、日本バイオインフォマティクス教育プログラムにより組織され、学生の教育を目的とするユニークな会議である。米国からはボストン大学バイオインフォマティクスプログラム、インドからはフロリダ大学を中心としたシステムバイオロジープログラム、日本からは京大・東大の共同研究プログラム（ゲノム情報科学研究教育機構）が参加した。日本は昨年の参加である。会議プログラムは通常の国際会議とほぼ同様の形式（oral presentation, poster presentation, reception, banquet等）で3日半であり、論文はfull paperとshort paperの2つのカテゴリーに分けられ、oral presentationと poster presentationに対応している。前者は査読のした25件（19,15,9,5）を採択し、Genome Informatics誌の最新号を予稿集として、後者は3件（21,13,13,2）の投稿を見送りし、ポスターブラウザが公開されている。全ての論文はJSBIのホームページからダウンロード可能なので、興味のある方は参照されたい。参加者は海外から約40名、全体で約120名ほどであった。

Excursion（奈良散策）が用意され、また学生を中心に参加者、かつ既に3プログラム間の交換留学が開始されているためもあり、参加者は同士の交流の密度は非常に高かった。特に、教育プログラムに属する学生にとって、異文化で育まれた学生が分野の研究者と拠点で交流できる貴重な機会となったと思われる。また、3プログラムを重用しての研究の交流や教員の交流プログラムが多多少っており、特に、ボストンは生物学者発信、ドイツは（理論）物理学者発信の割合が高い、このような交流により新しい研究成果の発表が行なわれた。本会議の詳細に興味のある方は、以下の会議のホームページを参照されたい：http://www.bic.kyoto-u.ac.jp/proteome/workshop/index.html

最後に、予編集作成等に尽力していただいた宮野悟先生はじめ関係各位のご協力に心より感謝いたします。

Michael Gribskov (President, International Society for Computational Biology)

When asked to provide a short letter for this issue of the JSBI newsletter, I naturally looked over the one I provided for the last newsletter. In that letter I concentrated on my hope for closer ties between JSBI and ISCB, I still strongly believe that this is an important goal, and continue to work to achieve it. Progress, however, has been slower than I would like, a fact to which I attribute the very difficult year that ISCB has had financially after the poor attendance at the 2003 ISMB meeting in Brisbane, and to personal concerns on my part (I am soon moving to a new University).

However, progress is being made on a number of fronts that, I believe, will allow us to take major steps forward in the near future. Restructuring of the membership fee and a record turnout for the joint ISMB/ECCB 2004 meeting places ISCB on a much more secure financial footing. The SIGs and Affiliates committee has established new definitions for what it means to be an ISCB affiliated society. While this may seem minor, it opens the door to closer ties and to our ability to offer benefits to ISCB affiliated societies such as JSBI.

A major effort of ISCB this year has been to improve Bioinformatics, the society journal. Many members have commented on the growing pains experienced