In the morning of December 18, I left Singapore to attend GIW2005 conference with great excitement as this is the second time that I am attending the GIW conference, but what a wonderful journey it has been! Last year, I was still a freshman in the bioinformatics domain, being a computer scientist who had not yet crossed over into the fascinatingly complex world of biology. I had just joined Dr. See-Kiong Ng’s acclaimed bioinformatics team at the Institute for Infocomm Research (I2R) in Singapore because I was excited by the research advances in biology that I have been hearing about since the Human Genome Project, and I was very eager to apply my computer science techniques to help biologists understand the secrets of life. For my baptism in bioinformatics, the wise Dr. Ng suggested that I should attend the GIW2004 conference. He was right, of course, because I learned so much from GIW2004, and a year later, we won the Best Paper Award for GIW2005. Having attended the GIW conference previously, I was well aware of the high standard of the papers presented. As such, you can imagine our surprise when we received an email on December 6 from program co-chair Prof Mamitsuka and Prof Reinhard Heinrich who informed us of the good news.

After my return from GIW2004, Dr. Ng began to assign me a number of projects on how to computationally mine the protein interaction networks to discover useful knowledge – this is a main research focus for Dr. Ng’s bioinformatics group at I2R. We became interested in the possibility of discovering protein complexes from protein-protein interaction networks. Protein complexes are molecular aggregations of proteins assembled from multiple stable protein-protein interactions. They are biologically very important as many proteins are functional only after they are assembled into a complex. However, while the current high throughput experimental techniques have detected many pair-wise protein-protein interactions, the experimental determination of protein complexes is still a highly laborious task. As a result, relatively few protein complexes have been identified to-date. Given that there are much data on protein-protein interactions but comparatively little data on protein complexes, we wondered whether we could help bridge this information gap by mining for putative protein complexes in the vast available protein interaction networks. We eventually came out with a graph-based technique, using a novel concept of local cliques to explore the protein-protein interaction network and merging the local cliques found in the networks to find the bigger protein complexes. After some initial disappointments, we began to obtain some promising results on this work around August 2005, and Dr. Ng suggested that we should write up our work and submit to GIW2005. It was a mad dash to meet the submission deadlines (which was thankfully postponed for another week), but of course we are now truly glad that we had made it.

I was very fortunate to work with a very talented and interdisciplinary team: Soon-Heng Tan, a biologist, Chuan-Sheng Foo, who is good in programming and mathematics, and Dr See-Kiong Ng, who is a leading bioinformatics expert with great vision and insights. This turned out to be a good recipe for success as we were able to work out novel solutions for difficult but real problems. Nevertheless, we still feel very fortunate to have been selected because there were many qualified papers in the conference that deserved the Best Paper award.

It is easy to understimate the invaluable contributions by GIW to the successfully growing field of bioinformatics. Over the years, being the longest running international bioinformatics conference, GIW has continued to inspire and nurture countless aspiring bioinformaticians like me. I salute the tireless efforts of the organizers (especially, Prof Satoru Miyano) of this marvelous conference. For me, GIW was the door through which I first entered into the exciting world of bioinformatics. Now, the award has provided me with an even greater gift of confidence that will help me greatly in my continued journey in bioinformatics. For this, I am truly grateful for the kind considerations of the program committee of GIW2005. GIW, and the beautiful city of Yokohama in December, will always have a treasured place in my heart.

On behalf of my co-authors, let me wish everyone a happy and productive new year. I shall be looking forward to the next GIW meeting, where many more exciting work and achievement will be reported, and which is also where many more young and aspiring scientists will begin their fruitful journey into the exciting world of bioinformatics that will help us understand the secrets of life eventually.

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**Oxford University Press Bioinformatics Prize**

受賞ポスター：‘A Maximum Likelihood Method for Inference of Spliceosomal Intron Evolution’,
Hung Dinh Nguyen, Maki Yoshihama, Naoya Kenmochi
Hung Dinh Nguyen (Frontier Science Research Center, University of Miyazaki)

On the afternoon of December 21st, 2005 I had just finished lunch with my supervisor, Prof. Kenmochi, and returned to the poster section of the GIW2005 conference. It was still lunch time and nobody was around. I sat down in a chair away from my poster for a rest. Suddenly, a young man with a camera in his hand came to my poster and was about to take a picture of it. Since I thought that he might be interested in my research, I came over him and offered to explain it. "No, thanks," he said, "I just want to take a picture of your poster because it was chosen by the GIW committee to be awarded the poster prize." This was the first time I knew my poster had received the prize. I was surprised and exited to know this good news.

I just started my research in April 2005 after I received a JSPS fellowship. I work in collaboration with Dr. Yoshihama and under the guidance of Prof. Kenmochi to study the evolution of spliceosomal introns. As we already knew, many spliceosomal introns exist in eukaryotic genes. These introns are extra bits of DNA sequences that have to be spliced out after the genes are transcribed into RNA (and hence the name spliceosomal introns). Two natural questions that should be raised are when did these introns originate and what is their role? These questions are the central subject of the introns-early versus introns-late debate. The intron-early theory proposes that introns already existed in the progenitor (i.e., the last common ancestor of prokaryotes and eukaryotes) to facilitate the construction of the first genes. The introns-late theory, on the other hand, holds that introns were gained later after the emergence of eukaryotes. There is still no decisive answer, and inference of intron evolution from the observed data is vital for resolving this debate.

Since intron sequences degrade quickly but their positions in the genes are well conserved, the pattern of intron position conservation is the most reliable information for such inference. So far, different methods of two approaches, maximum parsimony (MP) and maximum