The Taiwan International Graduate Program (TIGP) in Bioinformatics

Academia Sinica has established the Taiwan International Graduate Program (TIGP) in collaboration with a consortium of key national research universities in Taiwan. The purpose of the program is to develop the research manpower pool in those modern multidisciplinary fields that are important for Taiwan’s future economic and social development, and to enhance the innovative potential and academic standards of research in these and related fields. The TIGP has been established to attract highly qualified young researchers both domestically and abroad in order to help jumpstart the development of several frontier areas that are crucial to the future development of science and technology. The graduate program on bioinformatics is designed to offer specific training and research opportunities to PhD students who are interested in working in this particular area.

The TIGP Program on Bioinformatics (BP) is a joint-degree program sponsored by Academia Sinica (Institute of Information Science, Institute of Statistical Science, and Institute of Biomedical Sciences), National Tsing Hua University, National Chiao Tung University, and National Yang Ming University. Additional teaching support will soon be available from other major research universities in Taiwan. Unlike most bioinformatics programs offered in other universities that adopt existing courses in various departments, the programs are specifically designed for BP students and are taught by active and experienced bioinformatics researchers. The program provides interdisciplinary training and research opportunities that seamlessly integrate the related areas so that students will be well prepared for independent research in this new, fascinating area. The program focus on genetics and proteomics studies and emphasize data transfer, data analysis, biological information and biological feature extraction, knowledge management using advanced computation methodologies, and computer science technology. The program started in 2003; currently, 20 students are enrolled.

The TIGP provides full fellowship support for all graduate students for three years. In subsequent years, the financial support for outstanding students is general in the form of graduate research assistantships provided by the National Science Council or Academia Sinica. The stipend levels are about NT$32 000 (US$950) per month. All students can expect accommodation in the new student dormitory.
There are four basic research topics, as described below:

1. **Computational biology**—This area focuses on the design of various algorithms for sequence analysis, gene prediction, disease gene mapping, motif finding, and gene networks.

2. **Biological knowledge management**—This area focuses on the integration of various heterogeneous databases, biological knowledge representation, the automation of pipeline experiments, and the construction of various annotation databases. Biological literature search is also a crucial component.

3. **Bioinformatics applications**—This area focuses on using existing tools to analyze biological sequences, microarray data, proteomic data, etc. Statistical analyses and data mining techniques are used to reach the goal of information-driven biomedical research.

4. **Computational structural biology**—This area focuses on protein structure prediction and classification, automated biomolecule docking, and molecular dynamics.

The program's goal is to collaborate with biologists to speed up biological discovery using advanced informatics tools. In order to graduate, students are expected to publish two papers in leading bioinformatics journals or conferences as approved by the academic committee.

At present, publications from TIGP students include the following journals and conferences: *Nucleic Acids Research, Bioinformatics, Journal of Computational Biology, Journal of Bioinformatics and Computational Biology*, IEEE Computational Systems Bioinformatics Conference (CSB), International Conference on Research in Computational Molecular Biology (RECOMB), Asia-Pacific Bioinformatics Conference (APBC), and RECOMB Satellite Symposium on Regulatory Genomics. The subjects range from NMR backbone assignment, protein secondary structure prediction, transmembrane helix and topology prediction, to protein subcellular localization prediction and local structure prediction.