

Software Tools *and* Algorithms for Genome Sequence Analysis

Bioinformatics has become essential in biology due to our increasing ability to rapidly acquire massive amounts of data. The human genome project and in its wake other genome projects have driven technology development. Without accelerated technology development it would have been impossible to successfully complete the human genome project. Furthermore, the analysis of genome sequences has contributed to new biological insights and thereby enormously increased available biological data, opening new challenges for bioinformatics. Computational biology and bioinformatics augment traditional laboratory-based biology e.g. by curation of large databases of diverse biological information and providing software tools for analysis of data, establishing the bases for functional genomics. The unfolding genomics scene provides enormous gains for the research of infectious and genetic diseases. Bioinformatics software tools can be used to e.g. analyze data to reveal target candidate genes for further study. Often a large scale analysis of massive amounts of data is demanded to prioritize laboratory-based research. This requires the availability of efficient and rapid algorithms to complete all necessary tasks in a reasonable time. I will present a novel approximate sequence pattern matching algorithm, a multiple alignment construction method and their essential applications, such as software specifically designed for analysis and finishing of complex repeated genome projects.

Dr. Martti T. Tammi

Centre for Genomics and Bioinformatics
Karolinska Institutet
Stockholm, Sweden

Date: 10 Sept 2003, Wed

Time: 4 pm

Venue: DBS Conference Room,
Blk S3 Level 5

Host: A/P Shoba Ranganathan

All are welcome

**Department of Biological Sciences
Seminar Announcement**

