Bioinformatics

Algorithms and Software for Genomics and Proteomics

Lucian Ilie

www.csd.uwo.ca/~ilie

Genomics


Science
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THE HUMAN GENOME
American Association for the Advancement of Science


15 February 2001
nature
www.nature.com
the human genome
Nuclear fission
Five-dimensional energy landscapes
Seafloor spreading
The view from under the Arctic ice
Career prospects
Sequence creates new opportunities
naturejobs
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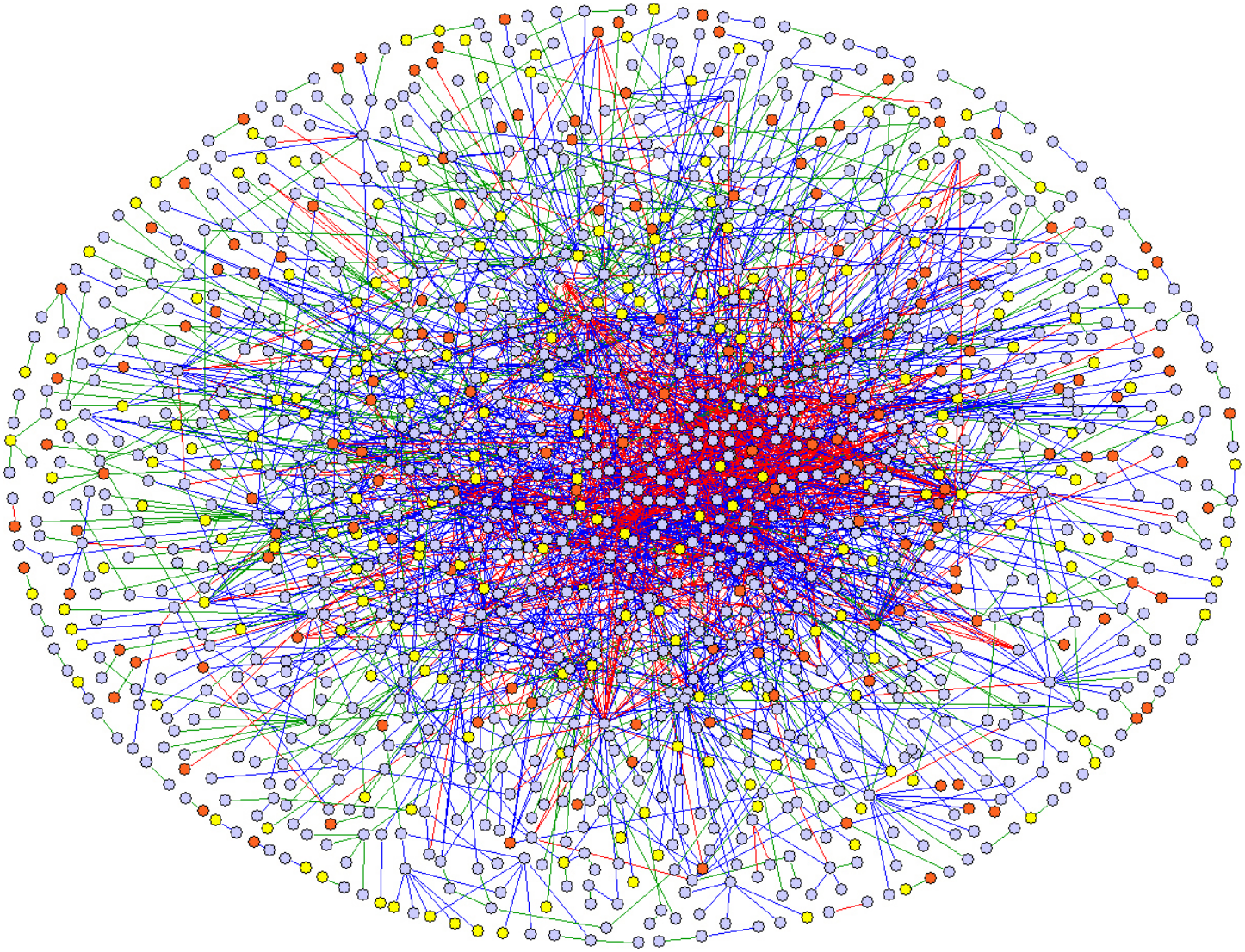
High Throughput DNA Sequencing

Genomics

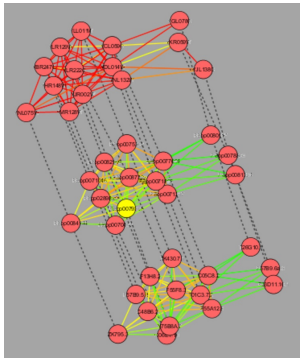
- DNA sequencing error correction (**HiTEC, RACER**)
- Genome assembly (**SAGE, SAGE2**)
- Genome assembly evaluation (**LASER**)
- Sequence similarity search (**SpEED, E-MEM**)
- Read mapping (**SHRiMP**)
- DNA probe design (**BOND**)
- PacBio read alignment (**HISEA**)

Proteomics

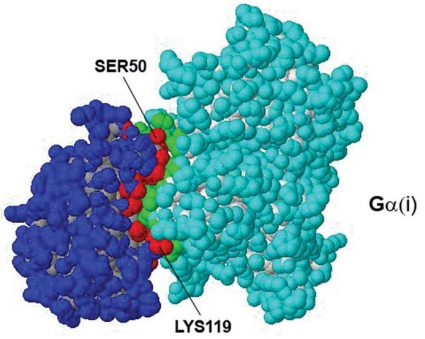


Proteomics

- Protein-protein interaction prediction (**SPRINT**)
- Protein-protein interaction network alignment improvement



- Protein-protein interaction site prediction



Applications

- Cancer research
- Cancer mutation discovery
- Genetic disorders
- Metagenomics
- DNA-protein interaction discovery
- Personalized medicine

Lab

PhD students:

- Mike Molnar
- Nilesh Khiste
- Yiwei Li
- Qin Dong
- Sabyasachi Patajoshi
- Jasleen Kaur

MSc students:

- Stephen Lu
- Nicholas DelBen
- Zaid Albirawi
- Valeria Portes de Cerqueira Cesar
- Debanjan Guha Roy

Computer clusters:

- 1TB RAM, 32 cores
- 4x 256GB RAM, 12 cores

Teaching

- **CS9877: Research Topics in Genomics and Proteomics**
  - Introduction to Bioinformatics
  - Hot research topics
  - No prerequisites
  - No assignments or exams