Bioinformatics

Algorithms and Software for Genomics and Proteomics

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Genomics

Human genome sequence
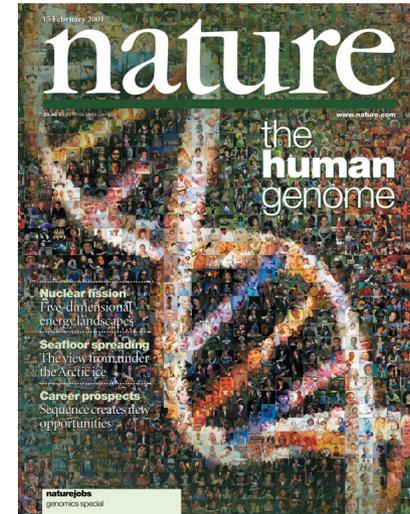
High-throughput DNA sequencing

Proteomics

Human protein interactions
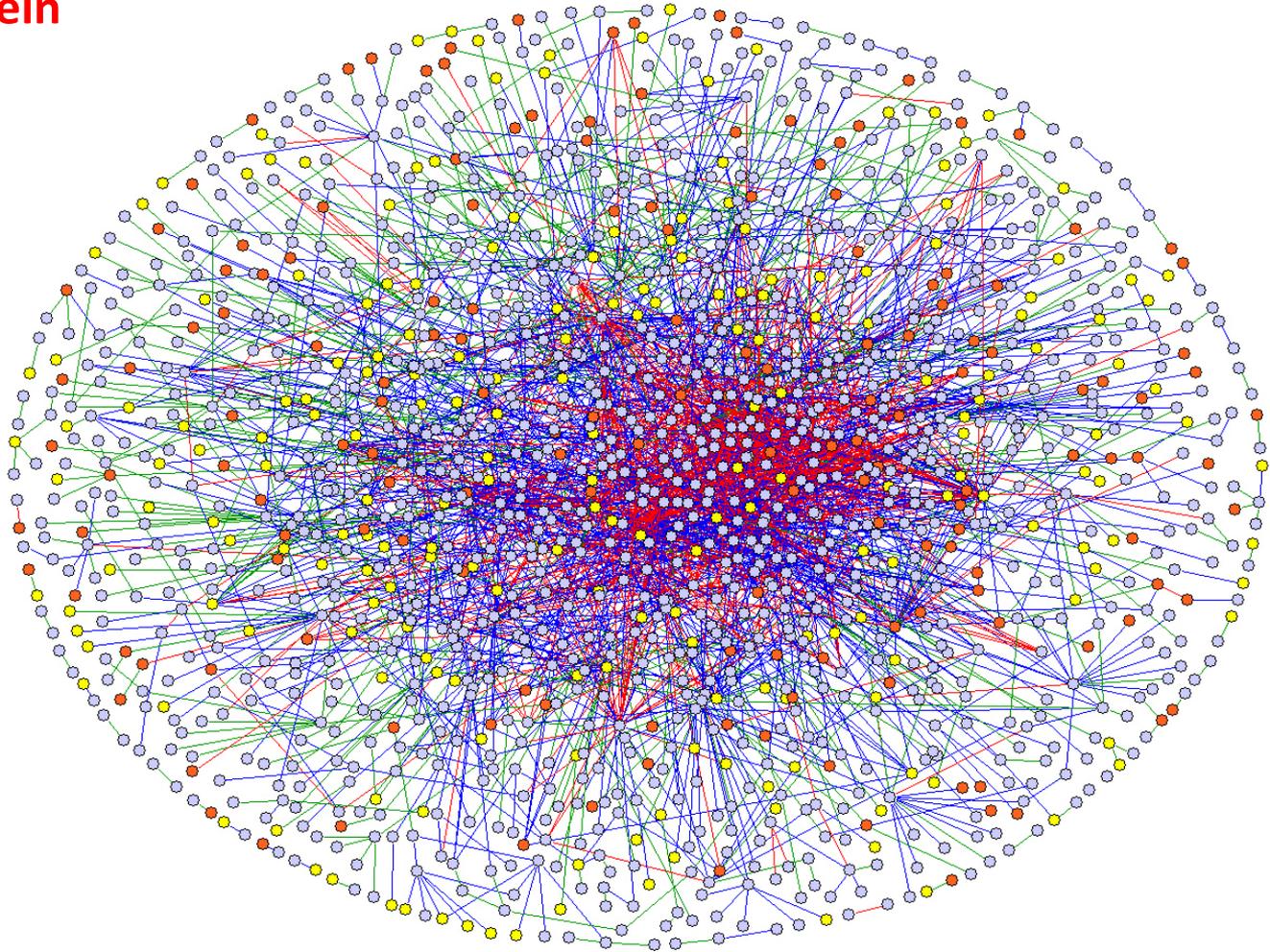
Software

- DNA sequencing error correction
  - **HiTEC** – Bioinformatics 2010
  - **RACER** – Bioinformatics 2013
- Genome assembly
  - **SAGE** – BMC Bioinformatics 2014
  - **SAGE2** – Bioinformatics 2017
- Genome assembly evaluation
  - **LASER** – BMC Research Notes 2015
- Sequence similarity search
  - **SpEED** – Bioinformatics 2007, Bioinformatics 2011
  - **E-MEM** – Bioinformatics 2014
- Read mapping
  - **SHRiMP2** – Bioinformatics 2011
- DNA probe design
  - **BOND** – BMC Genomics 2011, BMC Bioinformatics 2013
- PacBio read alignment
  - **HISEA** – BMC Bioinformatics 2017
- Protein-protein interaction prediction
  - **SPRINT** – BMC Bioinformatics 2017

Applications

- Cancer research

- Cancer mutation discovery

- Genetic disorders

- Metagenomics

- DNA-protein interaction discovery

- Personalized medicine

Lab

PhD students:

- Yiwei Li
- Qin Dong
- Sabyasachi Patajoshi
- Jasleen Kaur

MSc students:

- Nicholas DelBen
- Zaid Albirawi
- Valeria Portes de Cerqueira Cesar
- Debanjan Guha Roy
- Caocao Liu
- Arnab Mallik

Computer clusters:

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

Teaching

- On sabbatical 2018 - 2019