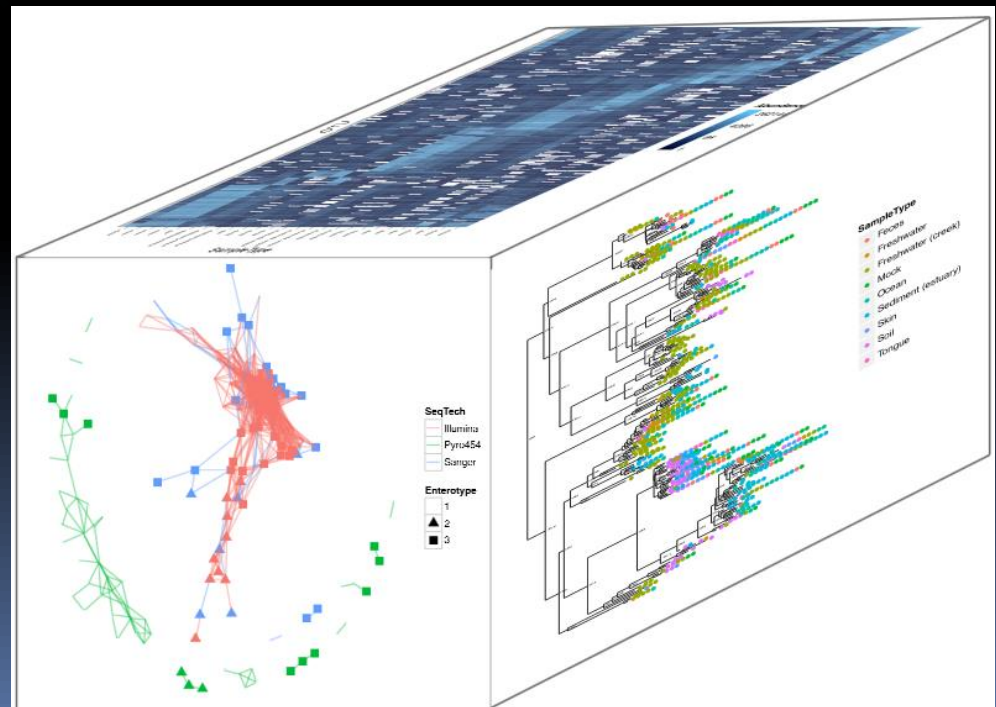# SAMSI 2014-15 PROGRAM ON BEYOND BIOINFORMATICS: STATISTICAL AND MATHEMATICAL CHALLENGES (BIOINFORMATICS)

Steve Qin
Dept of Biostatistics and Bioinformatics
Emory University

When

- September 1, 2014 - May 31, 2015
- Opening workshop:

  September 8-12, 2014

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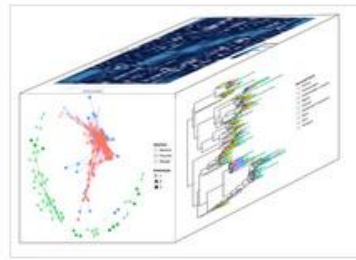
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2014-15 Program on Beyond Bioinformatics: Statistical and Mathematical Challenges (Bioinformatics)

The growing complexity and amount of genomic and related data are necessitating novel methods for data synthesis and analysis to answer previously inconceivable questions about biological processes. The Bioinformatics program will be devoted to statistical and mathematical challenges arising in the analysis of such data with the goal of addressing relevant biological questions.

In the planning stages, the structure of the program will revolve around at least the following general topics:

- Statistical pre-processing of emerging high throughput data
- Dependence in high-dimensional data, in particular, high dimensional discrete counts
- Integration of multi-omics data

Click to enlarge image.

Multi-dimensional aspects of metagenomic data illustrating evolutionary relationships, abundances, and a community network. (Bioconductor package

Workshops

- 2014-15: Bioinformatics: Opening Workshop: September 8-12, 2014

Courses

- Statistical and Mathematical Challenges in Molecular Evolution

Academic Year of Program

When: September 1, 2014 - May 31, 2015

Overview

The growing complexity and amount of genomic and related data are necessitating novel methods for data synthesis and analysis to answer previously inconceivable questions about biological processes. The Bioinformatics program will be devoted to statistical and mathematical challenges arising in the analysis of such data with the goal of addressing relevant biological questions.

Organizing committee program leaders:

- Alexander Alekseyenko
- Karin Dorman
- Nick Hengartner
- Susan Holmes
- Katerina Kechris
- Shili Lin
- Dan Nettleton
- Hongyu Zhao

Organizing committee (cont.)

- Directorate Liaison:
  - Snehalata Huzurbazar
- Local Scientific Coordinators:
  - David Dunson
  - Scott Schmidler
  - Fred Wright
  - Fei Zou
- National Advisory Committee Liaison:
  - Rebecca Doerge
- SAMSI-NISS Affiliates Liaison:
  - Zhaohui Qin

General topics

- Statistical pre-processing of emerging high throughput data

- Dependence in high-dimensional data, in particular, high dimensional discrete counts

- Integration of multi-omics data

- Modeling dynamics of mixtures; eg. populations of cells, variants, metagenomics

- Big data and machine learning for addressing 'omic' issues

Working groups and leaders

1. Simultaneous Inference, multiple hypothesis testing
   Fred Wright

2. Dependence in evolutionary models
   Scott Schmidler, Jeff Thorne, Seth Sullivan

3. Dynamics of 3-dim architecture in gene regulation
   Steve Qin, Shili Lin

4. Analysis of high dimensional discrete data
   Dan Nettleton, Fei Zou, David Dunson

5. Sparse Multiway data integration
   Susan Holmes, David Dunson

6. Graphical Modeling for data integration
   Katerina Kechris, Hongyu Zhao

7. Modeling dynamics of communities - metagenomics
   Alex Alekseyeko and Nick Hengartner

8. Imaging genetics
   Hongtu Zhu, Fei Zou

9. Modeling variation in metagenomic networks
   Anthea Monod and Sayan Mukherjee

Further information

- list is not exhaustive; if you are interested in suggesting and leading a new working group, please email huzurbazar@samsi.info

- For additional information about the program, send e-mail to bioinformatics@samsi.info

http://www.samsi.info/programs/research-programs