Science Visualization Workshop

- Virtual School for Computer Science and Engineering (VSCSE), UMichigan
- 2 day workshop: August 24-25, 2015. 2520C UCC, U Iowa.
- Course Details from previous years:
  - Introduction to Data Visualization
  - Conceptual Scientific Visualization
  - Introduction to Informational Visualization
  - Introduction to Scientific Visualization
  - Scientific Visualization with Paraview
  - Scientific Visualization with VisIt
  - Scripting with Paraview and VisIt
  - Parallel Visualization
- To register: [https://portal.xsede.org/course-calendar/-/training-user/class/382/session/742](https://portal.xsede.org/course-calendar/-/training-user/class/382/session/742)
- Contact: Sai Ramadugu (saikumar-ramadugu@uiowa.edu)

Only 3 slots left
4th annual IIHG Bioinformatics Summer Course
Welcome

- Thanks
  - Speakers/Instructors
  - Lisa Koizumi, Mycah Kimble
  - Richard Smith, Colleen Campbell
  - IIHG
Two problems with any “bioinformatics course”

Which side of the equation do you cater to the “bio” or the “informatics”

What part of the field do you target

   Biology is a pretty broad field
   Informatics is also very broad
   Bioinformatics…
Re-arrangements for this year

We dropped the concept of a “theme”
Past years centered around chip-seq and exome sequencing
More flexibility
Less (hopefully) expectation that you will master a topic
Added an additional hands-on session
  more advanced R
Still have UCSC and Galaxy sessions
Still looking for the “goldilocks” talk
Why have a bioinformatics class?
The Sloan Foundation, first supported postdoctoral fellows, and then in 1999 began providing funding for professional MS degree programmes in bioinformatics and computational biology.

Many individuals who first applied bioinformatics to biological problems were self-taught. However, the demand for bioinformaticists rapidly outstripped the supply. Recent articles have highlighted the dearth, both in industry and academia, of bioinformaticists.
Whole Exome Sequencing

For Whole Exome Sequencing with Professional RUO Interpretation, [click here](#)

Description

Average 70X Coverage.

The exome contains the functionally important coding regions of the human genome. Exome sequencing selectively targets these portions of the genome and has proven to be efficient and an extremely cost-effective method of identifying DNA variants. In contrast to traditional Sanger sequencing tests that analyze a single gene or small group of genes at once, exome sequencing has the ability to simultaneously analyze approximately 60 million base pairs, representing 22,000 genes using next-generation sequencing (NGS). Sequencing of the exome can help identify variants that may be the genetic cause of a wide range of traits and conditions. NGS relies on a method that enriches a sample by using DNA capture probes targeted only to the exome portion of the genome.

Gene By Gene is excited to announce the implementation of the Arpeggi engine pipeline. Arpeggi, Inc., now part of Gene By Gene, developed internal bioinformatics...
A little knowledge is a dangerous thing:

Per capita consumption of mozzarella cheese correlates with Civil engineering doctorates awarded

Correlation: 95.86% (r=0.958648)

http://tylervigen.com/spurious-correlations
Give us feedback

Let us know what was good
Let us know what topics you would like
Let us know what tutorials you would like
Course wiki

http://tinyurl.com/iihg-2015

Slides and schedule

Note on schedule