Description: BBISR is pleased announced our first ever series of ‘do it yourself’ workshops to introduce biostatistics and bioinformatics application tools we developed for cancer research. We certainly do not literally expect nor intend for investigators to ‘do it yourself.’ Instead, the intent is to equip investigators with tools to enable efficient data mining that will help in formulating a specific research question to discuss with us on how best to address it. The workshop topics include, but are not limited to the following: integrated genomic data analysis, survival analysis of early vs. later and landmark times, heatmap analysis (yes, analysis, not just, but including construction), ensemble gene outlier analysis, boxplot jitters and beeswarms, defining tumors with a molecular signature, and more! These and other menu-driven tools developed by BBISR are available for use on our website (https://BBISR.winship.emory.edu). The workshops will provide detailed instruction on the use of each tool in addition to informing on the guiding principles behind them. Participants must bring their own laptops to the workshop and are encouraged to bring their own data, in addition to the supplied data. The workshops will be hosted in our location at 718 Gatewood Road NE (the house on the hill next to the Blomeyer gym). The number of participants in each workshop is limited to 10. We hope to see you there!

For Information and Registration: https://BBISR.winship.emory.edu/#workshops
BBISR “Do it Yourself” Workshop Series
Bioinformatics & Biostatistics Tools for Cancer Research

Register at https://BBISR.winship.emory.edu/#workshops

- **Integrated Genomic Analysis of:**
  Genes using **GISPA:** Gene Integrated Set Profile Analysis (06/02/17)
  Samples using **SISPA:** Sample Integrated Set Profile Analysis (06/09/17)
  Gene Outliers using **GOPEA:** Gene Outlier Profile Ensemble Analysis (06/16/17)
- **Clustering Analysis with** **NOJAH** Not Just Another Heatmap! (06/23/17)
- **Survival Analysis with** **CASAS:** Cancer Survival Analysis Suite (06/30/17)

**Fridays, 1:00 - 3:30 pm**
718 Gatewood Rd. NE

**RSVP by 05/15/2017**
Limited to 10 seats per workshop!

Pre-Requisites: Winship members and their affiliates (lab personnel, postdoc, fellows) are welcome!
A laptop with an internet connection.

**Presented by:**
Biostatistics & Bioinformatics Shared Resource
Winship Cancer Institute of Emory University

For further inquires, email jeanne.kowalski@emory.edu
With GISPA, you can use:

- Any combination of genome-wide molecular data
- As few as a single sample per phenotypic group

With GISPA, you can define:

- Gene signatures for as few as a single sample
- Subtype based on integrating gene microarray-based expression with RNA-Seq-based expression.
With SISPA, you can use:
- Any combination of molecular data types
- As few as a five samples

With SISPA, you can define:
- Samples with molecular changes based on a pathway/network
- Cell lines with genomic and IC50 changes

How to define samples with a gene signature that is based on combined changes in expression, copy number, methylation, and variant allele frequencies?
With G-OPEA, you can use:

- Any genomic data set with 2-sample groups
- Common methods to detect outliers or their combinations

With G-OPEA, you can define:

- Cancer gene outliers using expression, methylation, copy number or other genomic data
- Statistical significance of gene outlier
- Sample outliers for the detected gene outlier

How to define genes as outliers based on a combination of outlier statistics and a combination of changes in expression, copy number, methylation, and variant allele frequencies?
With NOJAH, you can use:
• Any quantitative data type

With NOJAH, you can define:
• Clustering using various distance measures
• Most variable genes
• Statistical significance of a gene set in clustering samples
• Number of clusters
• Cluster of clusters using multiple genomic datasets

How much do you really know about clustering? How do you address clustering problems? What genes to choose? How to select number of clusters? How to identify cluster significance? How to generate clusters based on different genomic platforms?

BBISR “Do it Yourself” Workshop Series:
Cluster Analysis
Using Not Just Another Heatmap (NOJAH)

June 23rd 2017
Friday, 1:00 - 3:30 pm
718 Gatewood Rd. NE
Survival analysis in cancer research is one of the most fundamental analysis methods, answering the frequent question of whether a marker is associated with overall survival. We dive deeper into this question by testing marker associations that occur ‘early’ vs. later vs. a landmark start time.

**With CASAS, you can use:**
- Any data set with survival information

**With CASAS, you can define:**
- Markers associated with survival starting with either a ‘landmark’ time or ‘early on’ post treatment
- Several gene associations for single cancer type or several cancer types associations for a single gene
- Statistical significance of a prognostic signature