

**FALL 2017
BIOS 560R**

**Applied Biostatistics &
Bioinformatics in Cancer Research**

**2-Credit
FRIDAYS
2:00 - 3:50 PM**

Why Take this Course?

Learn how and when to apply bioinformatics analysis workflows to turn cancer genomics data into clinically applicable knowledge from a biostatistics perspective.

Some 'How To's' Covered:

- How to define a signature gene set for a tumor?
- How to define samples with a signature?
- How to obtain significance of clustering using a signature ?
- How to define clusters using genome-wide variants?
- How to perform biomarker-associated survival analysis?
- How to define prognostic and predictive biomarkers?
- How to obtain significance of prognostic biomarkers?
- How to test for 'early on' survival differences?



Topics Covered:

Single vs. Multiple data types genomic analysis, Microarray vs. NGS data, Clustering vs. Super PC, Permutation vs. Bootstrap, Bucket vs. Umbrella Clinical trials, Gene vs. Clinical associations

Instructor: Dr. Jeanne Kowalski

Associate Professor, Department of Biostatistics and Bioinformatics,
Director, Biostatistics and Bioinformatics Shared Resource, Winship Cancer Institute

**No Pre-Requisites: All RSPH & SOM
Students Welcome!**