

The Medical College of Wisconsin

Division of Biostatistics

Proudly Presents:
A Statistical Research Seminar
Talk By:



Andrea Rau, PhD

Research Scientist, French National Institute for Agricultural Research

Title: Exploring drivers of gene expression in The Cancer Genome Atlas

ABSTRACT: The Cancer Genome Atlas (TCGA) has greatly advanced cancer research by generating, curating, and publicly releasing deeply measured molecular data from thousands of tumor samples. In particular, gene expression measures, both within and across cancer types, have been used to determine the genes and proteins that are active in tumor cells. To investigate the behavior of gene expression in TCGA tumor samples, we introduce a statistical framework for partitioning the variation in gene expression due to a variety of molecular variables including somatic mutations, transcription factors (TFs), microRNAs, copy number alternations, methylation, and germ-line genetic variation. We provide a freely available, user-friendly, browseable interactive web-based application, called [EDGE in TCGA](#), for exploring the results of our transcriptome-wide analyses across 17 different cancers in TCGA. As proof-of-principle, I will illustrate how we used our web tool to identify and validate specific TFs that influence the expression of PTPN14 in breast cancer cells.

**Tuesday, December 4, 2018
3:30 PM – 4:30 PM**

**Medical College of Wisconsin
M2050**

Light refreshment provided 3:10 PM