

Riley Densley  
CS 6900

Dr Kaundal

1. What are the major research areas of the presenter?
  - a. Artificial Intelligence, Advanced Bioinformatics Laboratory
2. List the names of the projects that the presenter's research group did in the pastor has been doing recently. Among these projects, which project is the most appealing to you and which project is the least appealing to you? Why?
  - a. DNA Sequencing, Host Pathogen Interaction, Supervised (machine) learning
  - b. I found the DNA sequencing interesting. Looking for different patterns and seeing how patterns relate to different human conditions sounds like a mystery waiting to be solved.
  - c. Host Pathogen Interaction did not seem quite as interesting. As far as I could tell it was similar to DNA Sequencing but instead you were just looking at specific proteins and seeing what different combinations were possible.
3. List two researchers in the other universities who has the same research interests as the presenter.
  - a. Professor Tom Tullius from Boston University
  - b. Professor John Weinstein from the University of Texas
4. Summarize two most interesting research projects from each of the two researchers.
  - a. Professor Tullius is doing research on DNA, DNA-protein complexes, and RNA. He is investigating the connection between structural properties of DNA and genomics. He is utilizing the National Human Genome Research. He is also researching Genome damage and aging. He is looking into oxidation damage that are in the DNA. He uses an advanced sequencing platform to comprehensively identify sites of DNA breaks.
  - b. A lot of Professor John Tullius's research is focused on cancer. One research project is focused on tumor type cancer-testis antigens and their use as possible biomarkers and immunotherapeutic targets for cancers. He performed a comprehensive genome-wide analysis, incorporating exome sequence, DNA copy number, DNA methylation, messenger RNA and microRNA expression and targeted protein expression. Molecular data was integrated with clinical outcomes to identify biologically robust subtypes.