

SCHEDULE

12:50—1:10 pm	Sign-in, meet and greet
1:10—1:15 pm	Welcome remarks , Juli Petereit, VPRI-Bioinformatics
1:15—1:25 pm	Grant Schissler, Mathematics & Statistics <i>Gene Set Analysis of Correlated, Paired-sample Transcriptome Data to Enable Precision Medicine</i>
1:25—1:35 pm	So Young Ryu, Community Health Science <i>Missing Imputation in Mass Spectrometry Data</i>
1:35—1:45 pm	Pedro Miura, Biology <i>RNA-seq Analysis of circRNA Expression</i>
1:45—1:55 pm	Ana de Bettencourt-Dias, Associate Vice President for Research <i>Status of the Cores</i>
1:55—2:05 pm	Break
2:05—2:15 pm	Tin Nguyen, Computer Science and Engineering <i>Date Integration and Disease Subtyping</i>
2:15—2:30 pm	Graduate Student Presentation: Junchao Shi, Physiology and Cell Biology <i>SPORTS1.0: a tool for annotating and profiling non-coding RNAs optimized for rRNA- and tRNA- derived small RNAs</i>
2:30—2:40 pm	David Alvarez-Ponce, Biology <i>The Evolution of Genes and Genomes</i>
2:40—2:50 pm	Timothy L Bailey, Pharmacology <i>Biological Sequence Motifs</i>
2:50—3:00 pm	Tina Slowan-Pomeroy, Biology, TMCC <i>Bioinformatics - It's A Blast</i>
3:00—3:10 pm	Break
	- Core Presentations -
3:10—3:20 pm	Dave Quilici, Nevada Proteomics Center <i>Differential Expression of Proteomes</i>
3:20—3:30 pm	Craig Ulrich, Pharmacology and NV INBRE Bioinformatics <i>Ingenuity Pathway Analysis</i>
3:30—3:37 pm	Craig Osborne, Nevada Genomics Center <i>Next-Generation Sequencing at the NGC</i>
3:37—3:45 pm	Richard Tillett, NV INBRE Bioinformatics <i>Lahontan: an RNA-seq pipeline for any scale</i>
3:45—3:53 pm	Juli Petereit, VPRI-Bioinformatics <i>Beautiful World of Networks</i>
3:53 —4:00 pm	Closing remarks