2013 Annual Conference
Where Software and Biology Connect

July 17 ('Developer Day') 18 – 19
Fred Hutchinson Cancer Research Center, Seattle, WA

Morning Scientific Presentations from Leading Researchers

Olivier Elemento *Cancer as a Darwinian process: insights from next-generation sequencing* • Levi Waldron *Meta-analysis for prognostic and predictive gene signatures of late-stage ovarian cancer* • Fabian Gruber *Extensive variation in chromatin states across human individuals and populations* • Josh Akey *Tales of human history from 6,500 exome sequences* • Kasper Hansen *A genome-wide look at DNA methylation* • New this year, short presentations from the *Bioconductor* community: Gregoire Pau; Laurent Gatto; Rory Stark; Matthew McCall; Tim Triche.

Afternoon *Bioconductor* Software Workshops

R / Bioconductor for everyone • Analysis of RNA-Seq differential gene expression and exon use with the *DESeq2* and *DEXSeq* • From reads to genes in less than 10 *R* commands• Efficient manipulation of high-throughput sequence data in *Bioconductor* • *ReportingTools*: an automated result processing toolkit for high throughput genomic analyses • Interactive visualization in Bioconductor using *Epivizr* • Reproducible research using *RStudio*, *knitr* and *git* • Developing apps with *BaseSpaceR* • Variant Calling with *Bioconductor* • Variant-transcription factor-phenotype networks • Discovering gene regulatory mutations • *minfi* and *shinyMethyl*: winning packages for methylation analysis • A *Bioconductor* pipeline for ChIP-Seq experiments • Differential analysis of ChIP-seq data • Cheminformatics of drug-like small molecule data • Accessing public data repositories with *Bioconductor* • Annotations in *Bioconductor* • *RGalaxy / AnnotationHub*

Posters and Social Hour

Details: http://bioconductor.org/bioc2013/