**MetaCore™** is an integrated curated knowledge database and software suite for pathway analysis of experimental data and gene lists. The scope of data types includes microarray and sequence-based gene expression, SNPs and CGH arrays, RNAi screens, gene variants, proteomics, metabolomics, Co-IP pull-out and other custom interactions which can all by analyzed in tandem. In this session, we’ll be analyzing data published recently in PNAS about NOTCH1 signaling in chronic lymphocytic leukemia <http://www.pnas.org/content/114/14/E2911.abstract>.

Agenda:

* MetaCore Basics Training [9:30am – 12:30pm]
	+ MetaCore Overview
	+ EZ searching for interactions and pathways involved with NOTCH1
	+ Uploading data into MetaCore.
	+ Pathway analysis of ICN1 RNA-seq data bound to NOTCH1 in ChIP-seq experiments.
	+ Compare pathways enriched by leading edge genes from peripheral blood of chronic lymphocytic leukemia patients.
* MetaCore Advanced Training [1:30pm – 4:00pm]
	+ Use overconnectivity analysis to associate transcription factors regulating the ICN1 RNA-seq dataset.
	+ Find other publicly available GEO microarray datasets to find similar signatures in other diseases.
	+ Identifying causal networks and synergistic pathways from ICN1 RNA-seq data bound to NOTCH1 in ChIP-seq experiments using Key Pathway Advisor.