



## BioC2009 Monday, July 27, 2009

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### Morning Talks • 8:30 am – 12:00 noon • Pelton Auditorium (Thomas Building)

- 8:30 – 9:15            Modeling and inference of transcriptional regulatory networks  
— *Ilya Shmulevich (ISB)*
- 9:15 – 10:00        Statistical inference for SNPchip data in the presence of genotype  
and copy number uncertainty — *Ingo Ruczinski (Johns Hopkins)*
- 10:00 – 10:30        COFFEE BREAK
- 10:30 – 11:00        Model-based quality assessment and base-calling for second-  
generation sequencing data — *Rafael Irizarry (Johns Hopkins)*
- 11:00 – 11:30        Non-specific filtering increases power for detecting differentially  
expressed genes — *Wolfgang Huber (European Bioinformatics  
Institute)*
- 11:30 – 12:00        Advances in ChIP-seq analysis — *Robert Gentleman (FHCRC)*
- 12:00 – 1:00        LUNCH

### Afternoon Practicals • 1:00 pm – 5:30 pm (Arnold Building)

- 1:00 – 3:00            LAB SESSIONS I
- Rm# M1-A303        Generating quality metrics reports for microarray data sets  
— *Audrey Kauffmann (EMBL-EBI)*
- M1-A307            String manipulations, efficient matching, and alignments using  
Biostrings — *Hervé Pagès and Patrick Aboyoun (FHCRC)*
- M1-A305            Data mining with biomaRt and data visualization using  
GenomeGraphs — *Steffen Durrinck (Illumina) and Jim Bullard*
- M4-A805/817        Integromics Biomarker Discovery for TIBCO Spotfire  
— *Alexandra Vamvakidou-Thomas (Integromics)*
- 3:00 – 3:30            COFFEE BREAK (Coffee provided on main level of Prentice Atrium)
- 3:30 – 5:30            LAB SESSIONS II
- Rm# M1-A303        Using limma for differential expression — *James MacDonald  
(University of Michigan)*
- M1-A307            Using annotations and metadata in Bioconductor — *Marc Carlson  
(FHCRC)*
- M4-A805/817        Using EBIimage and imageHTS for analysing High Content Screens  
— *Gregoire Pau (EMBL)*
- M1-A305            Using CellHTS2 for cell based assays — *Florian Hahne (FHCRC)*

6:00 – 7:30

Posters, Wine & Cheese – Prentice Atrium

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## BioC2009

Tuesday, July 28, 2009

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### Morning Talks · 8:30 am – 12:00 noon · Pelton Auditorium (Thomas Building)

- 8:30 – 9:15      Transcriptional variation and regulatory feedback in *Saccharomyces*  
— *Rachel Brem (UC Berkeley)*
- 9:15 – 10:00    Learning about the cell by breaking it: large-scale analysis of  
combinatorial perturbations — *Chad Myers (U of Minnesota)*
- 10:00 – 10:30    COFFEE BREAK
- 10:30 – 11:15    The importance of reproducibility in high-throughput biology: A case  
study — *Keith Baggerly (UT MD Anderson Cancer Ctr)*
- 11:15 – 11:45    Reconstructible analysis of genome-scale data: improving quality of  
scientific dissemination — *Vincent Carey (Harvard University)*
- 11:45 – 12:15    Bioconductor: past accomplishments, future challenges  
— *Martin Morgan (FHCRC)*
- 12:15 – 1:00     LUNCH

### Afternoon Practicals · 1:00 pm – 5:30 pm (Arnold Building)

- 1:00 – 3:00      LAB SESSIONS I
- Rm# M4-A805/817    *exploRase* - A GUI for exploratory analysis of 'omics data  
    — *Michael Lawrence (FHCRC)*
- M1-A303            Parallel Computing in R — *David Smith (REvolution Computing)*
- M1-A305            GGtools: genetics of gene expression with Bioconductor  
    — *Vincent Carey (Harvard University)*
- M1-A307            ShortRead: tools for input and quality assessment of high-  
    throughput sequence data — *Martin Morgan (FHCRC)*
- 3:00 – 3:30      COFFEE BREAK (Coffee provided on main level of Prentice Atrium)

3:30 – 5:30	LAB SESSIONS II
Rm# M1-A303	Automating the data import from the ArrayExpress database into Bioconductor — <i>Audrey Kauffmann (EMBL-EBI)</i>
M1-A307	Using the chipseq package to analyze high throughput sequence data — <i>Deepayan Sarkar (FHCRC)</i>
M4-A805/817	Analyzing flow cytometry data in Bioconductor — <i>Nishant Gopalakrishnan (FHCRC)</i>
M1-A305	<b>New</b> Using R in genome-wide analyses — <i>Ken Rice (U of Washington)</i>
6:00 – 7:30	Hors d'oeuvres and wine – Prentice Atrium

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