

R/Bioconductor Course – Cuernavaca, January 21-25

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1/21 Monday

morning Introduction

1. Background/Introduction
2. Using R (Emacs/ESS, GUI)
3. Getting help
4. Reading in Data

afternoon Programming R

1. Syntax
2. Types (factors, numbers, characters) / Data Structures (matrices, data.frames, lists, environments)
3. Control Structures
4. Functions
5. Classes S4/S3

1/22 Tuesday

morning Exploratory Data Analysis in R

1. Numerical Summaries
2. Statistical Graphics
3. Smoothing / Advanced Plotting

afternoon EDA in practice: Examining Yeast Cell Cycle Data

1. Working with Bioconductor Data Sets
2. Microarray Graphics

1/23 Wednesday

morning Statistical Data Analysis

1. Statistical Tests and Tools
2. Simulation
3. Linear Models

afternoon Statistical Data Analysis in Practices: HapMap Data

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1. Introduction to HapMap
 2. Data Visualization
 3. Classification/Clustering

1/24 Thursday

morning Hidden Markov Models in Practice

1. HMM review
2. Tiling array data
3. Simulating Data, Fitting Models

afternoon Hidden Markov Models in Practice

1. Building S4 Classes
2. Building R packages

1/25 Friday

morning Bioconductor

1. Overview of Bioconductor Packages
2. Package overview *Biobase*
3. Package overview *affy*
4. Package overview *limma*
5. Package overview *BiomaRt*
6. Package overview *graph*, *Rgraphviz*

afternoon Bioconductor In Practice

1. Working with graphs/networks
2. Working with microarray data and the RMA pipeline