Alma in Silico TRAINING - Transcriptomics data analysis

GOALS: This training aims at:

The goal of this training is to provide participants with the knowledge and practical skills to design, analyse and interprete results of a microarray transcriptomic experiments.

CONTENT:

Theoretical sessions will include the following:
- Quick overview of the technology behind some important platforms for microarray gene expression profiling (Affymetrix, Agilent, Illumina).
- Databases and other tools for microarrays (GEO, ArrayExpress, BioMart,...).
- Experimental design (+ how many replicates, Power Analysis).
- Data preprocessing, quality control and normalization (e.g. diagnostic plots, normalization for Affy: MAS5, RMA, GC-RMA,... How normalization differs for Agilent).
- Simple analysis of differential gene expression (FC, t-test and its variations,...)
- The issue of multiple testing, and corrections (Bonferroni, BH, SAM, Westfall and Young,...)
- Sophisticated models of differential expression (ANOVA, limma,...).
- Other multivariate analyses (clustering, classification, GSEA, Network analysis).
- Extraction of annotations for gene lists (biomaRt,...).
- Interpretation of gene lists (GO, DAVID, Networks, KeyDriver Analyses,...).
- Visualization (heatmaps, genomic coordinate plots,...).

Practical sessions will include the following:
- Very quick intro to the R/Bioconductor environment.
- Affymetrix data preprocessing and normalization, with diagnostics.
- Differential gene expression: gene filtering on fold-change and p-values, correction for multiple testing.
- Hierarchical clustering and heatmap visualization.
- Extraction of annotations for gene lists.
- Interpretation of gene lists (e.g. DAVID).

PLANNING: 3 day-training (theoretical and practical training): May 18,19 & 20 2010

NUMBERS OF PARTICIPANTS: 30 persons

PUBLIC AND PREREQUESITES:
This training session is primarily aimed at biologists wishing to use microarrays in their research. However, doctors in medicine, engineers, computer scientists and other researchers with a knowledge of basic concepts of molecular genetics will be welcome. Knowledge of English is necessary.

LANGUAGE: English

TRAINERS: Dr. David Henderson, Director of Scientific Computing at Sage Bionetworks, USA

LOCATION: This 3-day training will be held at the University of Liège, Building B32 (Psychology Faculty), Informatics room FAPSE, Boulevard du Rectorat 5, 4000 Sart-Tilman Liège, Belgium

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