

TOOLS AND RESOURCES WORKSHOP

Genespring workgroup at NASC

N.Graham, D.Belfield, Z.Emmerson, G.Gill, N.James, L.Kacinova, N.Leftley,
L.Lucas, S.May, T.Milsted, A.Mortimore, B.Parkinson, R.Roberts, B.Schildnecht,
M.Topham, H. Townsend, E.Wigmore
*NASC, Plant Sciences Division, University of Nottingham, Sutton Bonington Campus,
Loughborough, LE12 5RD*
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NASC has recently obtained a grant from the BBSRC to implement a Genespring workgroup database (Agilent technologies). This will allow users to easily access all the data held within the NASCArrays database and perform detailed statistical analysis of the data.

Genespring GX is powerful visualisation and analysis tool for use with a variety of expression data including Affymetrix, spotted-array and real-time PCR data. The data can be viewed in a number of ways (scatter plots, chromosome maps, box plots etc.) and analysed using a wide range of techniques. Differentially expressed genes can be identified using volcano plots or ANOVA tests. More detailed analysis can be performed including principal component analysis, clustering (hierarchical, K-means, self-organising maps etc.) pathway analysis and promoter motif identification. The workgroup database will allow users to directly access all the .CEL files held in the NASCArrays database (currently over 3500 slides). Whole experiments, individual or groups of .CEL files can be downloaded and analysed locally or large analysis jobs can be sent to the server. Personal data (experiments, gene lists, analysis results etc.) can be shared with the whole community or selected users.

Genespring workgroup training sessions will be held at NASC and at selected meetings. Further information can be found at <http://affymetrix.arabidopsis.info>