

Bioinformatics

The bioinformatics group analyzes genetic, epigenetic, transcriptomic and proteomic data from basic research and clinical trials and develops necessary software and databases.

Group Leader: Dr Wei

Bioinformatics Facility

The bioinformatics group analyzes genomic (i.e., SNP, promoter and CpG-island microarrays and next generation sequencing), transcriptomic (i.e., Affymetrix expression and exon microarrays, RNA-seq) and proteomic (i.e., ELISA and MALDI-TOF MS) data from basic research and clinical trials and develops necessary software and databases. It advises researchers on experimental design and does both low level and high level analyses.

Low level analyses involve data quality assessment, background subtraction and normalization. High level analyses involve the identification of abnormal genomic regions and differentially expressed genes and proteins and the classification of patient samples using supervised and unsupervised analyses, such as ANOVA, multiple regression, hierarchical clustering, principle component analysis, logistic regression, partial least square analysis and neural network. The results are presented according to the requirements of individual research projects.

The facility also provides advice on gene ontology analysis, promoter analysis and building gene interaction networks. Commercial software, such as Expression Console, Genotyping Console, Affymetrix Power tools, IGB, MatLab and PLS_Toolbox, and academic software, such as Bioconductor, SAM, dChip, PAINT, CisGenome, CytoScape and SNVMix is used. In addition, new computer programs are developed using several programming languages such as R, VBA, MatLab and C#.

The bioinformatics facility uses a combination of locally installed and public databases. It is involved in several aspects of cancer research, for example, (i) the identification of human genes whose expression are significantly changed following some treatment such as EBV virus infection, irradiation, demethylation or addition of CD40 ligand, or (ii) genes that are up or down regulated at different stages of tumour development, and (iii) the diagnosis and prognosis of cancers according to ELISA and mass spectrum data of blood and urine samples.

Selected papers...

[Automated Pub Med Search for Dr. Wenbin Wei \(http://www.ncbi.nlm.nih.gov/pubmed?term=Wei%20W%20AND%20Birmingham%20AND%20UK\)](http://www.ncbi.nlm.nih.gov/pubmed?term=Wei%20W%20AND%20Birmingham%20AND%20UK)

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