

Variations on the genetic theme

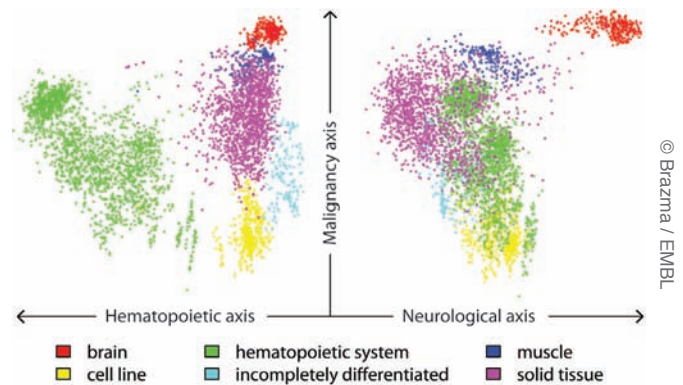
EMBL-EBI researchers present global map of human gene expression

Hinxton, 8 April 2010 - Just like members of an orchestra are active at different times although playing the same piece of music, every cell in our body contains the same genetic sequence but expresses this differently to give rise to cells and tissues with specialised properties.

By integrating gene expression data from an unprecedented variety of human tissue samples, Alvis Brazma and his team at the European Bioinformatics Institute, an outstation of the European Molecular Biology Laboratory (EMBL), and their collaborators have for the first time produced a global map of gene expression. The full analysis behind this unique view of the genetic activities determining our appearance, function and behaviour is published today in *Nature Biotechnology*.

The analysis used data collected from 163 laboratories worldwide involving 5,372 human samples from various tissues, cell types and diseases. Most transcriptomics experiments compare gene expression in only a few cell types or conditions and although technically challenging, integrating this data on a large-scale has created a new way for scientists to explore gene expression. The analysis is visualised as a map subdividing the human gene expression space into six distinct major groups or 'continents'.

The continents emerged by grouping samples with similar gene expression signatures. This established the identity of the six groups: brain; muscle; hematopoietic (blood related); healthy and tumour solid tissues; cell lines derived from solid tissues;



This image shows the 5,372 samples as dots colour-coded for the six major clusters identified by comparing gene expression profiles. The left and right panels of the figure are projections of the same three-dimensional shape viewed from two different perspectives.

and partially differentiated cells. By visualising these subsets in 3D, comparisons can be made on the degree of similarity in the gene expression profiles on each grouping. For example, analysis of the continents showed that cell lines are usually more similar to each other than to their tissue of origin.

A new bioinformatics service allowing anyone to explore this expression map has been developed by the European Bioinformatics Institute as part of the ArrayExpress Gene Expression Atlas resource (www.ebi.ac.uk/gxa/). ●

Source Article

Lukk, M., Kapushesky, M., Nikkilä, J., Parkinson, P., Goncalves, A., Huber, W., Ukkonen, E. & Brazma, A. A global map of human gene expression. *Nature Biotechnology*, 8 April 2010.

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About EMBL

The European Molecular Biology Laboratory is a basic research institute funded by public research monies from 20 member states (Austria, Belgium, Croatia, Denmark, Finland, France, Germany, Greece, Iceland, Ireland, Israel, Italy, Luxembourg, the Netherlands, Norway, Portugal, Spain, Sweden, Switzerland and the United Kingdom) and associate member state Australia. Research at EMBL is conducted by approximately 85 independent groups covering the spectrum of molecular biology. The Laboratory has five units: the main Laboratory in Heidelberg, and Outstations in Hinxton (the European Bioinformatics Institute), Grenoble, Hamburg, and Monterotondo near Rome. The cornerstones of EMBL's mission are: to perform basic research in molecular biology; to train scientists, students and visitors at all levels; to offer vital services to scientists in the member states; to develop new instruments and methods in the life sciences and to actively engage in technology transfer activities. Around 190 students are enrolled in EMBL's International PhD programme. Additionally, the Laboratory offers a platform for dialogue with the general public through various science communication activities such as lecture series, visitor programmes and the dissemination of scientific achievements.

About EMBL-EBI:

The European Bioinformatics Institute (EBI) is part of the European Molecular Biology Laboratory (EMBL) and is located on the Wellcome Trust Genome Campus in Hinxton near Cambridge (UK). The EBI grew out of EMBL's pioneering work in providing public biological databases to the research community. It hosts some of the world's most important collections of biological data, including DNA sequences (EMBL-Bank), protein sequences (UniProt), animal genomes (Ensembl), three-dimensional structures (the Protein Databank in Europe), data from gene expression experiments (ArrayExpress), protein-protein interactions (IntAct) and pathway information (Reactome). The EBI hosts several research groups and its scientists continually develop new tools for the biocomputing community.

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