

Learning the language of DNA

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An international consortium of scientists, including a team from The University of Queensland's Institute for Molecular Bioscience (IMB), is a step closer to the next generation of treatments to combat disease, after publishing a comprehensive analysis of the human and mouse transcriptomes.

A senior member of the consortium and IMB researcher Professor David Hume said transcriptome describes all of the information read from the genome by a cell at any given time.

"Essentially, we need to understand the language that cells use to read DNA in order to know how processes in the body are controlled," Professor Hume said.

"This knowledge will be a major resource to the biomedical research community."

Part of understanding the language of cells lies in identifying promoters - the DNA regions at the start of genes that regulate their activity.

"We have identified the core promoters of the large majority of genes in the mouse and human genomes, expanding the number of known promoters by five- to ten-fold," Professor Hume said.

The findings of the consortium have also upended the traditional view that each gene has a single promoter and a single starting position.

The team found that, while genes that are only turned on in a specific tissue or at a specific point in time use the traditional model of a single start site, genes used in many tissues have a broad distribution of start sites.

This new model may help explain why some organisms, such as humans, are much more complex than simple organisms such as worms, despite having a similar number of genes.

If some genes have a broad range of start sites, individual species can differ subtly in the way they control these genes, meaning the genes can evolve faster, and organisms with these genes can become more complex.

The consortium also found that many pseudogenes – traditionally thought to be "fossils" of ancient genes – are actually active, and are therefore likely to have some as yet unknown function.

The results obtained by the FANTOM consortium, led by the Japanese scientific institute RIKEN and Genome Network Project, have been published in the current edition of the prestigious journal Nature Genetics in a paper of which Professor Hume is corresponding author and first co-author.

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