

Research: Computing Gene Regulation

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From: Robert Karl Stonjek (*rstonjek_at_bigpond.net.au*)

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Computing Gene Regulation

Researchers take a statistical glimpse at how gene expression is controlled

By David Secko

Eukaryotic gene regulation as a field has matured much during decades of study, but understanding it on a genome-wide basis has started in earnest only with the assembly of genomic data. Identifying genome-wide regulatory motifs is problematic due to their typically low consensus sequences; grasping which transcription factors bind to such motifs is even more difficult, as numerous factors can bind to any one motif. Nonetheless, with many diseases linked to malfunctions in transcription factors, and many cellular processes relying on multitiered transcriptional regulation, this information is invaluable.

Today, researchers combine powerful statistical techniques with their belief that the information to regulate every gene is somewhere in the sequence database; they seek to flush out common regulatory motifs and examine their roles in regulating genomes. And better assays provide more information for such approaches. Beyond understanding genomic regulation, common motifs may lead to better modeling. It comes down to "predictive power" says Frank Pugh, assistant professor at Pennsylvania State University; soon, sequence alone could accurately predict how a newly discovered gene is regulated

Read the rest at The Scientist

http://www.the-scientist.com/yr2004/jun/research2_040621.html

Posted by

Robert Karl Stonjek.