NEWS

Video: Mining genes from whole genomes

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18 NOVEMBER 2010

Rapid advances in DNA sequencing technology are enabling researchers to comb quickly — and ever more cheaply — through whole genomes to learn about genetic variation involved in different traits and diseases.

In October 2010, **Evan Eichler** used data from the **1,000 Genomes Project** and found roughly 1,000 genes — including some associated with brain development — that **are prone to deletion or duplication**.

At the **Society for Neuroscience annual meeting** in San Diego, Eichler, professor of genome sciences at the University of Washington, talked to SFARI about what the rapid accumulation of genetic sequence information means for autism research.

For more reports from the 2010 Society for Neuroscience annual meeting, please **click here**.