Technique for refining multi-source genomic data

A scientific team from the National Institute of Standards and Technology, Harvard, and the Virginia Bioinformatics Institute says they have developed new methods to integrate data from different sequencing platforms, thus producing a reliable set of genotypes to benchmark human genome sequencing.

The techniques put forth by the researchers are designed to make it increasingly possible to use an individual's genetic profile to guide medical decisions to prevent, diagnose, and treat diseases. Their report ("Integrating human sequence data sets provides a resource of benchmark SNP and indel genotype calls") appears in Nature Biotechnology.

Read the full, original story: Technique Developed for Refining Multi-Source Genomic Data