

Breaking the genome bottleneck

The genomic data generated from next-generation sequencing machines doesn't amount to much more than alphabet soup if it's not subjected to significant computational processing and statistical analysis. For the data to be useful, the trick is to turn those As, Ts, Gs, and Cs into a manageable description of disease risks and other genetic predispositions. That requires a lot of computational power and time—already a significant bottleneck for some genomic analysis companies.

View the original article here: [Breaking the Genome Bottleneck – MIT Technology Review](#)