

Reading and writing genomes

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The human genome draft published in 2004 was a milestone, but achieved at a cost of \$3 billion it is inapplicable to diagnostics for global health. We have reduced the cost of sequencing by over a million times in the past six years. The next step is integrating Genome + Environment = Trait (GET) data on large diverse cohorts enabled by a new consent mechanism (<http://www.personalgenomes.org>) in a globally shareable, unrestricted form (<http://evidence.personalgenomes.org>). This includes time-series studies of microbiomes and immune responses to such microbes, allergens, vaccines and allele-specific expression in pluripotent stem cells. To move from correlations to causations and cures requires a similar million-fold improvement in DNA writing technology - via use of DNA synthesized on chips and Multiplex Automated Genome Engineering (MAGE). Applications include metabolic engineering and multivirus resistant cells.

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