

## ~9 Months Ago

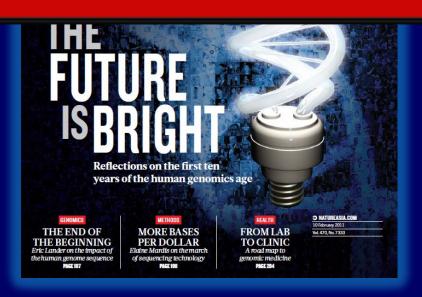
nature

### **PERSPECTIVE**

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Charting a course for genomic medicine from base pairs to bedside

# genome.gov/sp2011



omim and http://www.genome.gov/GWAStudies) and the role of structural variation in disease?, some of which have already led to new therapies "1.0 beher advances have already heaping and ended a practice (for example, microarrays are now used for dinical detection of genomic imbalances" and pharmacognomic testing is routinely performed before administration of certain medications"). Together, these achievements (see accompanying paper") document that genomics is contributing to a better understanding of human biology and to improving human health.

As it did eight years ago<sup>17</sup>, the National Human Genome Research Institute (NHGRI) has engaged the scientific community (http://www.genome.gov/Planning) to reflect on the key attributes of genomics (Box 1) and explore future directions and challenges for the field. These discussions have led to an update advision that focuses on understanding human biology and the diagnosis, prevention and treatment of human disease, including consideration of the implications of those advances for society (but these discussions, intentionally did not address the role of genomics, an agriculture, energy and other areas). Like the FiG. 2-chisving this wision is broader than what any single organization or country can achieve—realizing the full benefits of genomics will be a global effort.

This 2011 vision for genomics is organized around five domains extending from basic research to health applications (Fig. 2). It reflects the view that, over time, the most effective way to improve human health is to understand normal biology (in this case, genome biology) as a basis for understanding disease biology, which then becomes the basis for improving health. At the same time, there are other connections among these domains. Genomics offers opportunities for improving health without a thorough understanding of disease (for example, cancer therapies can be selected based on genomic profiles that identify tumour subtypes <sup>1407</sup>), and clinical discoveries can lead back to understanding disease or even basic biology.

The past decade has seen genomics contribute fundamental knowledge about biology and its perturbation in disease. Further deepening this understanding will accelerate the transition to genomic medicine (clinical care based on genomic information). But significant change rarely comes

decade. Similarly, we note three cross-cutting areas that are broadly relevant and fundamental across the entire spectrum of genomics and genomic medicine bioinformatics and computational biology (Box 3), education and training (Box 4), and genomics and society (Box 5).

### Understanding the biology of genomes

Substantial progress in understanding the structure of genomes has revealed much about the complexity of genome biology. Continued acquisition of basic knowledge about genome structure and function will be needed to illuminate further those complexities (Fig. 2). The contribution of genomics will include more comprehensive sets (catalogues) of data and new research tools, which will enhance the capabilities of all researchers to reveal fundamental principles of biology.

#### Comprehensive catalogues of genomic data

Comprehensive genomic catalogues have been uniquely valuable and widdy used. There is a compelling need to improve existing catalogues andto generate new ones, such as complete collections of genetic variation, functional genomic elements, RNAs, proteins, and other biological molecules, for both human and model organisms.

Genomic studies of the genes and pathways associated with diseaserelated traits require comprehensive catalogues of genetic variation, which provideboth genetic markers for association studies and variants for identifying candidate genes. Developing a detailed catalogue of variation in the human genome has been an international effort that began with The SNP Consortium<sup>20</sup> and the International HapMap Project<sup>21</sup> (http://hapmap. nchi.nlm.nih.gov), and is ongoing with the 1000 Genomes Project<sup>20</sup> (http://www.1000genomes.org)

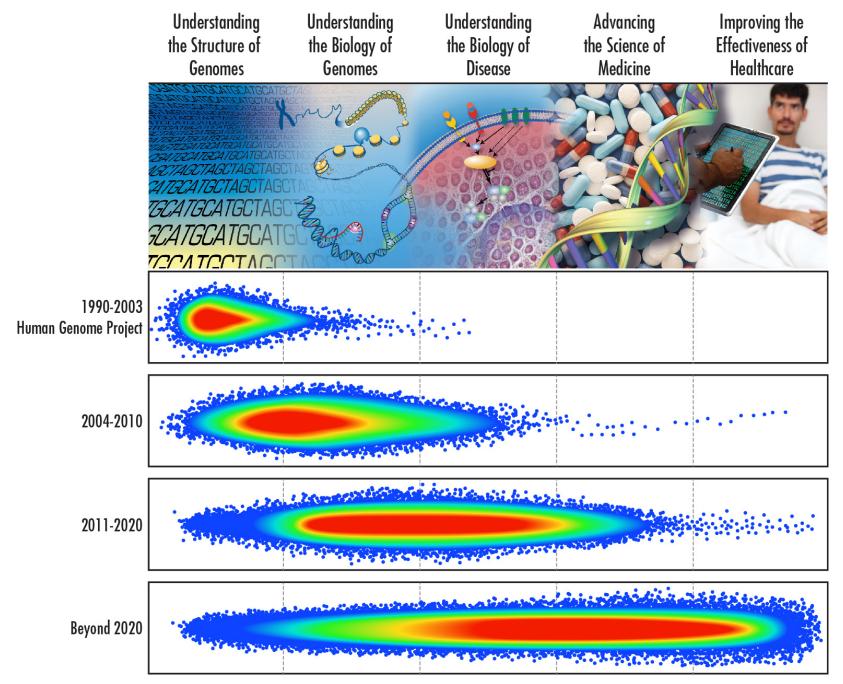
Over the past decade, these catalogues have been critical in the discovery of the specific genes for roughly 3,000 Mendelian (monogenic) diseases

Figure 1 | Genomic achievements since the Human Genome Project (see accompanying rollfold). ▶

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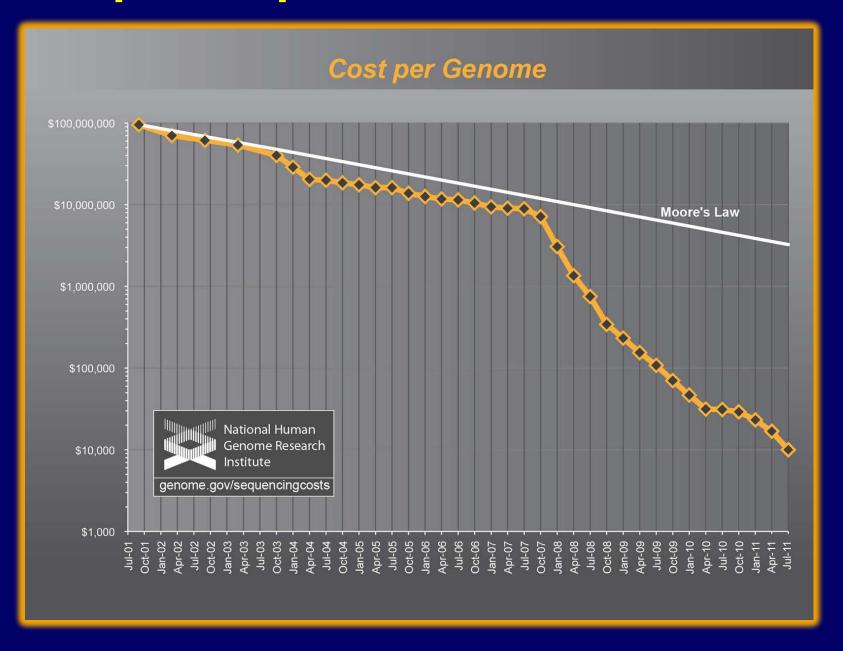
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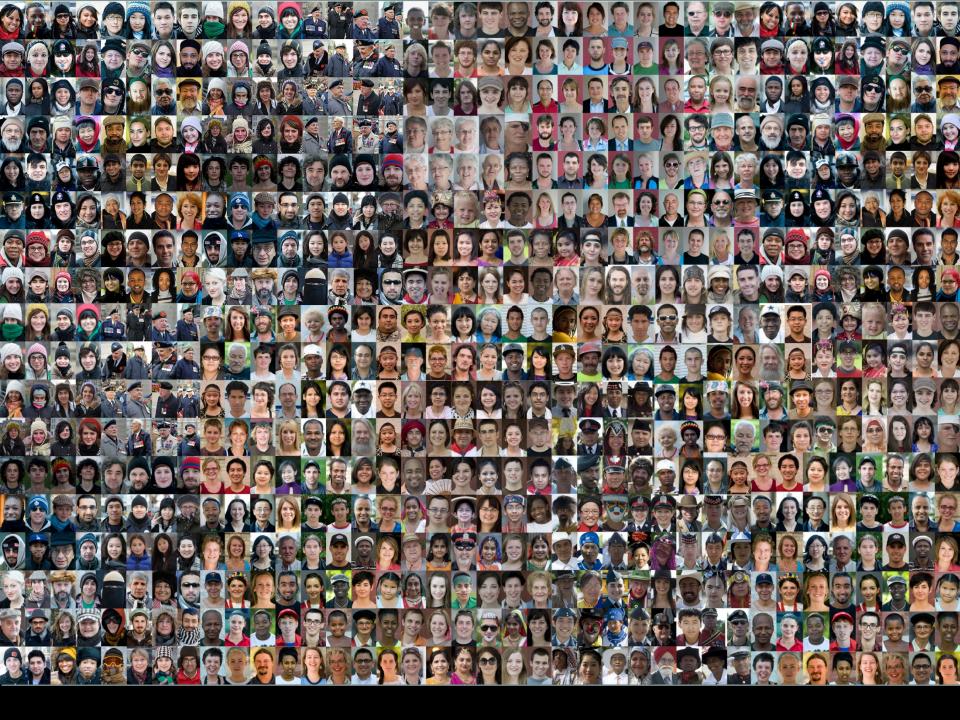
NHGRI Published New Vision for Genomics

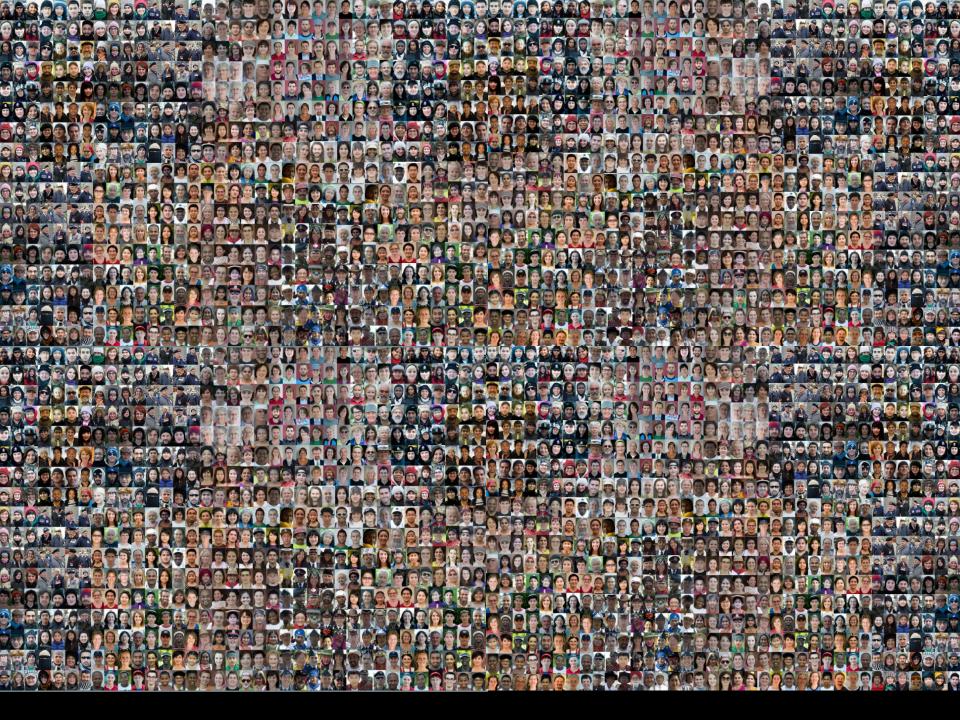


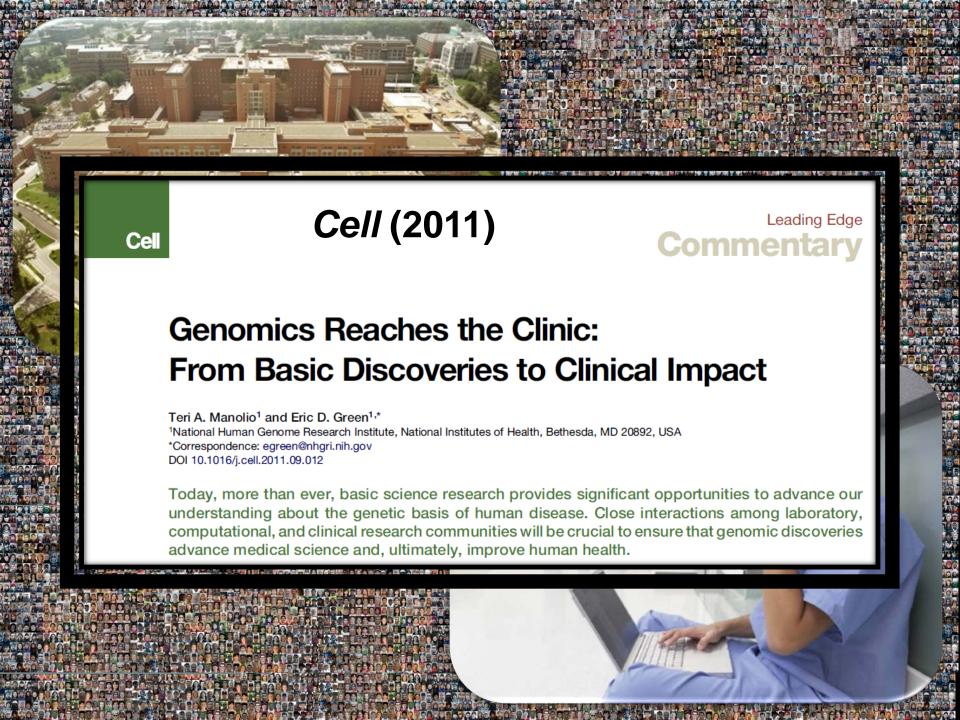
Green et al. 2011

## Cost per Sequenced Human Genome









## NHGRI Strategic Plan: 'No Brainers'

### Imperatives for genomic medicine



Opportunities for genomic medicine will come from simultaneously acquiring foundational knowledge of genome function, insights into disease biology and powerful genomic tools. The following imperatives will capitalize on these opportunities in the coming decade.

Making genomics-based diagnostics routine. Genomic technology

development so far has been driven by the research market. In the next decade, technology advances could enable a clinician to acquire a complete genomic diagnostic panel (including genomic, epigenomic, transcriptomic and microbiomic analyses) as routinely as a blood chemistry panel.

**Defining the genetic components of disease.** All diseases involve a genetic component. Genome sequencing could be used to determine the genetic variation underlying the full spectrum of diseases, from rare Mendelian to common complex disorders, through the study of upwards of a million patients; efforts should begin now to organize the necessary sample collections.

Comprehensive characterization of cancer genomes. A comprehensive genomic view of all cancers<sup>4–7</sup> will reveal molecular taxonomies and altered pathways for each cancer subtype. Such information should lead to more robust diagnostic and therapeutic

Practical systems for clinical genomic informatics. Thousands of genomic variants associated with disease risk and treatment response are known, and many more will be discovered. New models for capturing and displaying these variants and their phenotypic consequences should be developed and incorporated into practical systems that make information available to patients and their healthcare providers, so that they can interpret and reinterpret the data as knowledge evolves.

diseases are influenced by the microbial communities that inhabit our bodies (the microbiome)<sup>101</sup>. Recent initiatives<sup>102,103</sup> (http://www.human-microbiome.org) are using new sequencing technologies to catalogue the resident microflora at distinct body sites, and studying correlations between specific diseases and the composition of the microbiome<sup>104</sup>. More extensive studies are needed to build on these first revelations and to investigate approaches for manipulating the microbiome as a new therapeutic approach.

Practical systems for clinical genomic informatics:

"...New models for capturing and displaying these variants and their phenotypic consequences should be developed and incorporated into practical systems that make information available to patients and their healthcare providers..."

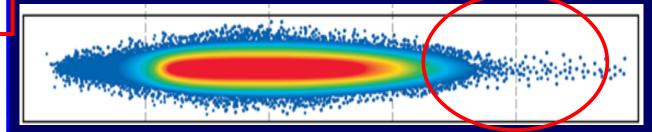
Structure of Genomes

Biology of Genomes

Biology of Disease

Advancing Science of Medicine

Improving
Effectiveness of
Healthcare



# Clinical Genomic Information Systems







# Characterizing and Displaying Genetic Variants for Clinical Action



- Collaboration between NHGRI & Wellcome Trust
- Goal: Consider processes, databases, and other resources needed to:
  - Identify clinically relevant variants
  - Decide whether they are actionable and what the action should be
  - Provide information for clinical use





## **Planning Committee**

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