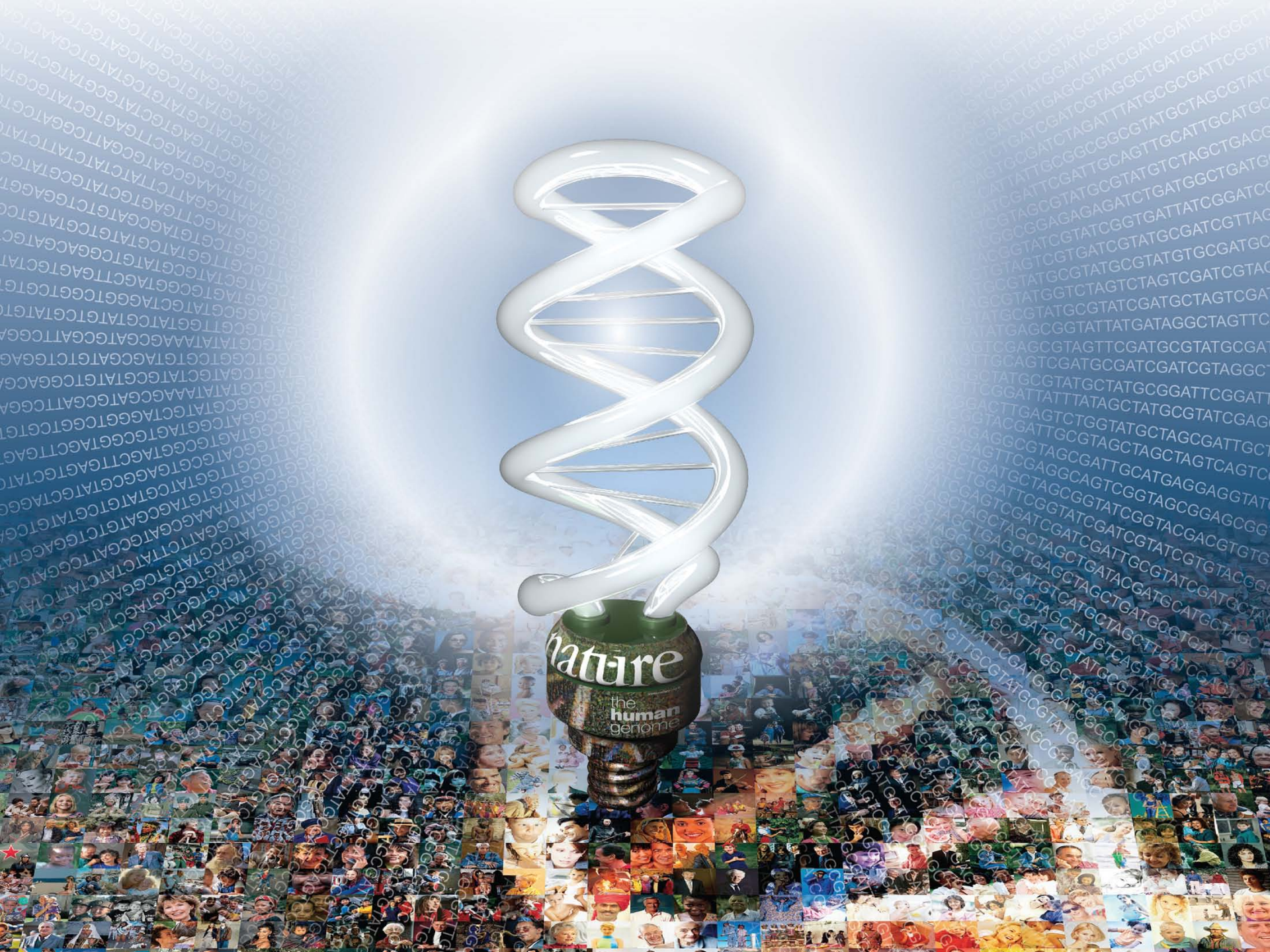
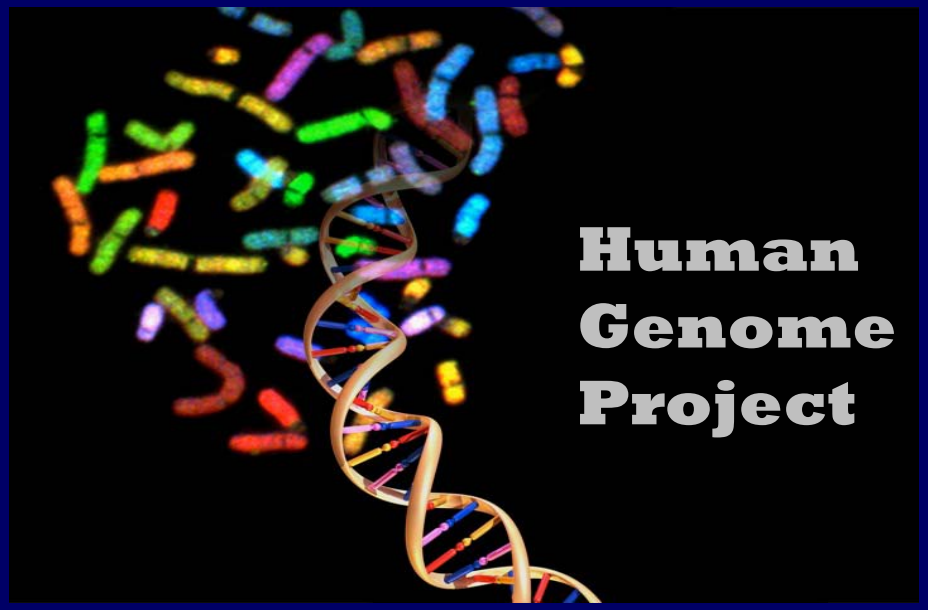
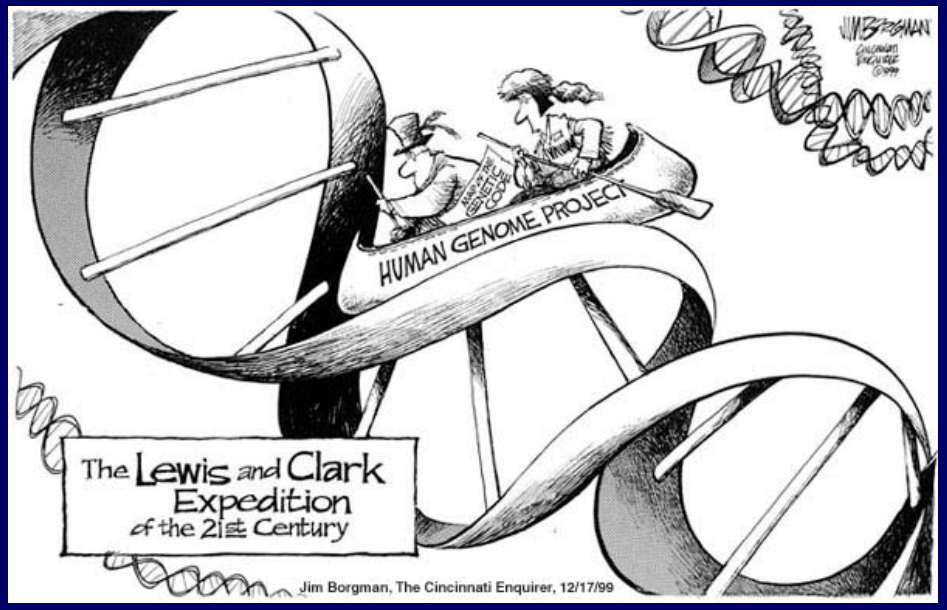

nature
the human genome

~20 Years Ago

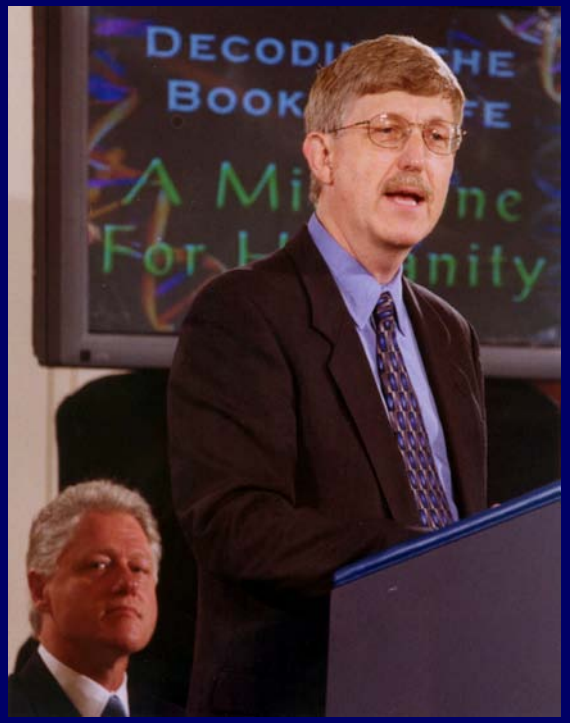


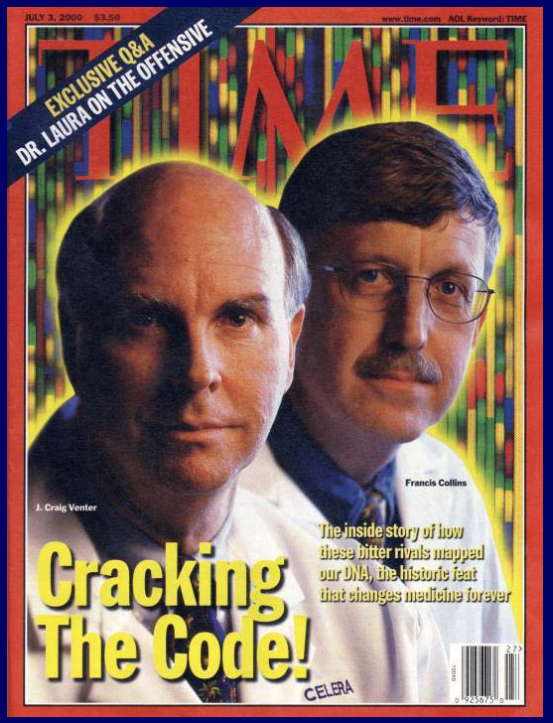


October 1990

Human Genome Project Begins

~10 Years Ago

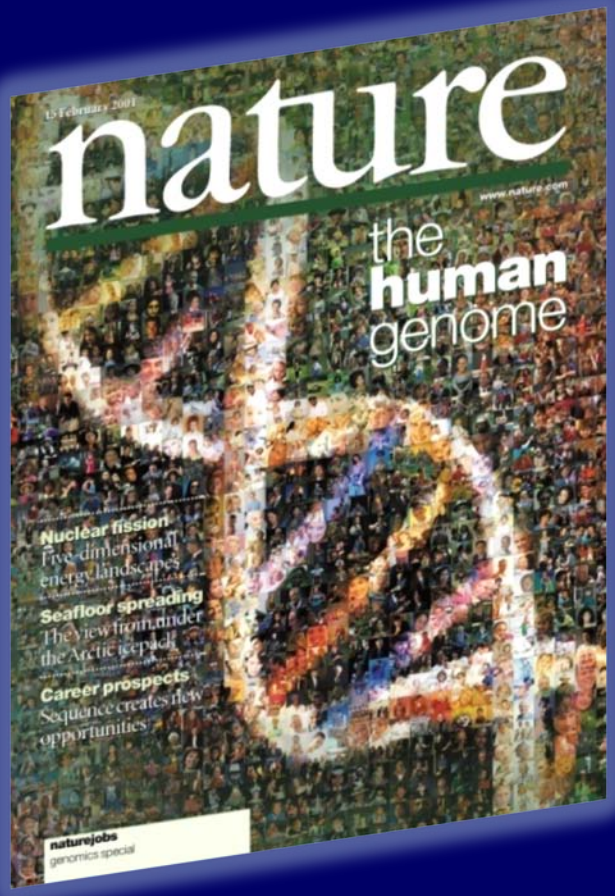




June 2000

Draft Human Genome Sequence Announced

~10 Years Ago



February 2001

Draft Human Genome Sequence Published

~1 Day Ago

PERSPECTIVE

doi:10.1038/nature09764

Charting a course for genomic medicine from base pairs to bedside

Eric D. Green[1], Mark S. Guyer[1] & National Human Genome Research Institute*

There has been much progress in genomics in the ten years since a draft sequence of the human genome was published. Opportunities for understanding health and disease are now unprecedented, as advances in genomics are harnessed to obtain robust foundational knowledge about the structure and function of the human genome and about the genetic contributions to human health and disease. Here we articulate a 2011 vision for the future of genomics research and describe the path towards an era of genomic medicine.

Since the end of the Human Genome Project (HGP) in 2003 and the publication of a reference human genome sequence[1,2], genomics has become a mainstay of biomedical research. The scientific community's foresight in launching this ambitious project[3] is evident in the broad range of scientific advances that the HGP has enabled, as shown in Fig. 1 (see rollfold). Optimism about the potential contributions of genomics for improving human health has been fuelled by new insights about cancer[4–7], the molecular basis of inherited diseases (http://www.ncbi.nlm.nih.gov/omim and http://www.genome.gov/GWAStudies) and the role of structural variation in disease[8], some of which have already led to new therapies[9–13]. Other advances have already changed medical practice (for example, microarrays are now used for clinical detection of genomic imbalances[14] and pharmacogenomic testing is routinely performed before administration of certain medications[15]). Together, these achievements (see accompanying paper[16]) document that genomics is contributing to a better understanding of human biology and to improving human health.

As it did eight years ago[17], 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 division 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 in agriculture, energy and other areas). Like the HGP, achieving this vision 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[18,19]), 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 quickly. Although genomics has already begun to improve diagnostics and treatments in a few circumstances, profound improvements in the effectiveness of healthcare cannot realistically be expected for many years (Fig. 2). Achieving such progress will depend not only on research, but also on new policies, practices and other developments. We have illustrated the kinds of achievements that can be anticipated with a few examples (Box 2) where a confluence of need and opportunities should lead to major accomplishments in genomic medicine in the coming 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 widely used. There is a compelling need to improve existing catalogues and to 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 disease-related traits require comprehensive catalogues of genetic variation, which provide both 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[20] and the International HapMap Project[21] (http://hapmap.ncbi.nlm.nih.gov), and is ongoing with the 1000 Genomes Project[22] (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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*Lists of participants and their affiliations appear at the end of the paper.

February 2011

NHGRI Published New Vision for Genomics

Understanding Our Genetic Inheritance

The U.S. Human Genome Project:

The First Five Years FY 1991-1995

U.S. DEPARTMENT OF HEALTH AND HUMAN SERVICES
Public Health Service
National Institutes of Health

U.S. DEPARTMENT OF ENERGY
Office of Energy Research
Office of Health and Environmental Research

1991-1995

POLICY FORUM

A New Five-Year Plan for the U.S. Human Genome Project

Francis Collins and David Galas*

The U.S. Human Genome Project is
of an international effort to develop
netic and physical maps and determin
DNA sequence of the human genome
the genomes of several model organ
Thanks to advances in technology a
tightly focused effort, the project i
track with respect to its initial 5-year
Because 3 years have elapsed since
goals were set, and because a much
sophisticated and detailed understandi
what needs to be done and how to do
now available, the goals have been re
and extended to cover the first 8
(through September 1998) of the 15
genome initiative.

In 1990, the Human Genome prog
of the National Institutes of Health (
and the Department of Energy (DOE
veloped a joint research plan with sp
goals for the first 5 years [fiscal year
1991–95] of the U.S. Human Gen
Project (1). It has served as a val
guide for both the research community
the agencies' administrative staff in d
oping and executing the genome p
and assessing its progress for the p
years. Great strides have been made to
the achievement of the initial set of
particularly with respect to constructin
tailed human genetic maps, impro
physical maps of the human genome
the genomes of certain model organ
developing improved technology for
sequencing and information handling
defining the most urgent set of ethica
gal, and social issues associated with th
quisition and use of large amounts
netic information.

Progress toward achieving the first
goals for the genome project appears
on schedule or, in some instances,
ahead of schedule. Furthermore, tec
logical improvements that could not
been anticipated in 1990 have in som
eas changed the scope of the project a
lowed more ambitious approaches. E
this year, it was therefore decided to u
and extend the initial goals to addres
scope of genome research beyond

physical maps; (iii) the definition of the sequence tagged site (STS) (5) as a common unit of physical mapping; and (iv) improved technology and automation for DNA sequencing. Further substantial improvements in technology are needed in all areas of genome research, especially in

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Environmental Research, Department of E
Washington, DC 20585.

* Present address: Darwin Molecular, 2405 C
Point, Kirkland, WA 98033.

1993-1998

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New Goal

Francis S. Collins,* Ari Patri and

REVIEW

The Human Genome Project has suc the major goals in its current 5-year p 1993–98. A new plan, for 1998–2003 human DNA sequencing will be the m bitious schedule has been set to com by the end of 2003, 2 years ahead of the course of completing the sequenc the human sequence will be produced plan also includes goals for sequencin ment; for studying human genome developing technology for functional ing the sequence of *Caenorhabditis melanogaster* and starting the mous the ethical, legal, and social implicatio for bioinformatics and computational of genome scientists.

The Human Genome Project (HGP) is f single most important project in biology es—one that will permanently change biol

F. S. Collins and E. Jordan are with the National H National Institutes of Health, Bethesda, MD 20892, of Biological and Environmental Research, Depart 20585, USA. A. Chakravarti is with the Department Genetics, Case Western Reserve University and U Cleveland, OH 44106, USA. R. Gesteland is at the H University of Utah, Salt Lake City, UT 84112, USA Institute of Ethics, Georgetown University, Washing

*To whom correspondence should be addressed:

682 23

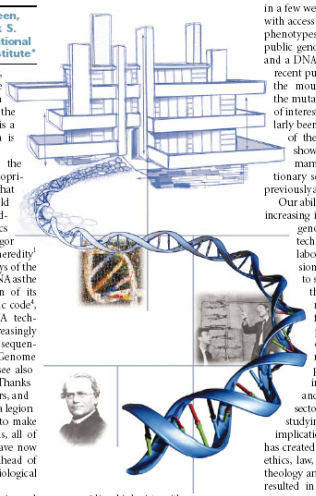
1998-2003

feature

A vision for the future of genomics research

A blueprint for the genomic era.

Francis S. Collins, Eric D. Green, Alan E. Guttmacher and Mark S. Guyer on behalf of the US National Human Genome Research Institute*



The completion of a high-quality, comprehensive sequence of the human genome, in this fiftieth anniversary year of the discovery of the double-helical structure of DNA, is a landmark event. The genomic era is now a reality.

In contemplating a vision for the future of genomics research, it is appropriate to consider the remarkable path that has brought us here. The rollfold (Figure 1) shows a timeline of landmark accomplishments in genetics and genomics, beginning with Gregor Mendel's discovery of the laws of heredity[1] and their rediscovery in the early days of the twentieth century. Recognition of DNA as the hereditary material[2], determination of its structure[3], elucidation of the genetic code[4], development of recombinant DNA technologies[5,6], and establishment of increasingly automatable methods for DNA sequencing[7–10] set the stage for the Human Genome Project (HGP) to begin in 1990 (see also www.nature.com/nature/DNA50). Thanks to the vision of the original planners, and the creativity and determination of a legion of talented scientists who decided to make this project their overarching focus, all of the initial objectives of the HGP have now been achieved at least two years ahead of expectation, and a revolution in biological research has begun.

The project's new research strategies and experimental technologies have generated a steady stream of ever-larger and more complex genomic data sets that have poured into public databases and have transformed the study of virtually all life processes. The genomic approach of technology development and large-scale generation of community resource data sets has introduced an important new dimension into biological and biomedical research. Interwoven advances in genetics, comparative genomics, high-throughput biochemistry and bioinformatics are providing biologists with a markedly improved repertoire of research tools that will allow the functioning of organisms in health and disease to be analysed and comprehended at an unprecedented level of molecular detail. Genome sequences, the bounded sets of information that guide biological development and function, lie at the heart of this revolution. In short, genomics has become a central and cohesive discipline of biomedical research.

The practical consequences of the emergence of this new field are widely apparent. Identification of the genes responsible for human mendelian diseases, once a herculean task requiring large research teams, many years of hard work, and an uncertain outcome, can now be routinely accomplished in a few weeks by a single graduate student with access to DNA samples and associated phenotypes, an Internet connection to the public genome databases, a thermal cycler and a DNA-sequencing machine. With the recent publication of a draft sequence of the mouse genome[11], identification of the mutations underlying a vast number of interesting mouse phenotypes has similarly been greatly simplified. Comparison of the human and mouse sequences shows that the proportion of the mammalian genome under evolutionary selection is more than twice that previously assumed.

Our ability to explore genome function is increasing in specificity as each subsequent genome is sequenced. Microarray technologies have catapulted many laboratories from studying the expression of one or two genes in a month to studying the expression of tens of thousands of genes in a single afternoon[12]. Clinical opportunities for gene-based pre-symptomatic prediction of illness and adverse drug response are emerging at a rapid pace, and the therapeutic promise of genomics has ushered in an exciting phase of expansion and exploration in the commercial sector[13]. The investment of the HGP in studying the ethical, legal and social implications of these scientific advances has created a talented cohort of scholars in ethics, law, social science, clinical research, theology and public policy, and has already resulted in substantial increases in public awareness and the introduction of significant (but still incomplete) protections against misuses such as genetic discrimination (see www.genome.gov/PolicyEthics).

These accomplishments fulfil the expansive vision articulated in the 1988 report of the National Research Council, *Mapping and Sequencing the Human Genome*[14]. The successful completion of the HGP this year thus represents an opportunity to look forward and offer a blueprint for the future of genomics research over the next several years.

The vision presented here addresses a different world from that reflected in earlier plans published in 1990, 1993 and 1998 (refs 15–17). Those documents addressed the goals of the 1988 report, defining detailed paths towards the development of genome-

*Endorsed by the National Advisory Council for Human Genome Research, whose members are Vickie Yates Brown, David R. Bergsma, Wylie Burke, Ronald W. Davis, William M. Gelbart, Eric T. Juengst, Bronya J. Keats, Raju Kucherlapati, Richard R. Lifton, Kim I. Nickerson, Maynard V. Olson, Janet D. Rowley, Robert Tepper, Robert H. Waterston and Tadataka Yamada.

2003-2010

PERSPECTIVE

doi:10.1038/nature09764

Charting a course for genomic medicine from base pa

Eric D. Green[1], Mark S. Guyer[1] & Natio

There has been much progress in g
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obtain robust foundational knowle
contributions to human health an
describe the path towards an era o

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understanding will accelerate the transition
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[1]National Human Genome Research Institute, National Inst
*Lists of participants and their affiliations appear at the end

REVIEW

doi:10.1038/nature09792

Initial impact of the sequencing of the human genom

Eric S. Lander[1]

The sequence of the human genome has dr
decade since its publication, on our unders
basis of inherited diseases and cancer, and
in fulfilling the promise of genomics for m

On 15 February 2001, a decade ago this week,
62-page paper entitled 'Initial sequencing a
human genome', reporting a first global look
the human genetic code. The paper[1] marked a mile
national Human Genome Project (HGP), a discovery
ceived in the mid-1980s and launched in 1990. The s
published a paper[2] from the company Celera Genc
draft human sequence based on their own prodigio
data from the public HGP.
The human genome has had a certain tendency to
excess: from early jeremiads that the HGP would st
consuming the NIH budget (it never rose to more thar
coverage of a late-breaking genome race between
protagonists; to a White House announcement of
sequence in June 2000, 8 months before scientific p
been written, peer-reviewed and published; to breathl
Wall Street and the press about the imminence of ge
and genome-based panaceas; to a front-page news
anniversary of the announcement that chided genom
yet having cured most diseases.
The goal of this review is to step back and assess th
from a scientific standpoint, addressing three questi
learned about the human genome itself over the past
the human sequence propelled our understanding
medicine, evolution and history? What is the road al
The past decade has shown the power of genomic m
for biomedical research. By providing a comprehe
human sequence has made it possible for scientists
fragmentary information into landscapes of biolog
function: maps of evolutionary conservation, gene t
matin structure, methylation patterns, genetic variatio
distance, linkage disequilibrium, association to inherit
alterations in cancer, selective sweeps during human
dimensional organization in the nucleus. By providi
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genes and proteins to be recognized based on unique 't
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spectrometer. In turn, these measurements have been
'cellular signatures' characteristic of specific cell types, st
and catalogues of the contents of organelles such as

[1]Broad Institute of MIT and Harvard, 7 Cambridge Center, Cambridge, M

PERSPECTIVE

doi:10.1038/nature09796

A decade's perspective on DNA sequencing technology

Elaine R. Mardis[1]

The decade since the Human Genome Project ended has witnessed a remarkable sequencing technology explosion that has permitted a multitude of questions about the genome to be asked and answered, at unprecedented speed and resolution. Here I present examples of how the resulting information has both enhanced our knowledge and expanded the impact of the genome on biomedical research. New sequencing technologies also have introduced exciting new areas of biological endeavour. The continuing upward trajectory of sequencing technology development is enabling clinical applications that are aimed at improving medical diagnosis and treatment.

The sequencing of the Human Reference Genome, announced ten years ago, provided a roadmap that is the foundation for modern biomedical research. This monumental accomplishment was enabled by developments in DNA sequencing technology that allowed data production to far exceed the original description of Sanger sequencing[1]. Moving forward in the genomic era in which we now find ourselves, new (or 'next generation') DNA sequencing technology is enabling revolutionary advances in our understanding of health and disease. In essence, sequencing technology is the engine that powers the car that allows us to navigate the human genome roadmap. As that engine becomes ever more powerful, so will the questions we can ask and answer about the geography of our genetic landscape.

Of course, a car with only an engine is unworkable; as such, DNA sequencing technology provides an integral part of a larger system, one with multiple components that must be properly matched in order to achieve high throughput and efficiency. It has essentially never been as 'easy' as simply buying sequencing instruments, plugging them in, and generating data. We need the raw materials, such as fuel (DNA), sparks to ignite the fuel (reagents), mechanical parts to translate fuel and ignition into movement (robotics) and direction (bioinformatics), all working in a carefully engineered balance, and a driver (genome centre) to steer the automobile quickly and efficiently to the desired destination (biological understanding). By inference, as this 'engine' has achieved ever increasing horsepower, the supporting components have evolved to match its output with corresponding levels of performance, and new or completely revised components have been added as required.

In 2001, the technology that sequenced the human genome was based on capillary electrophoresis of individual fluorescent-labelled Sanger sequencing reaction products. Each instrument could detect 500–600 bases from each of 96 reactions in around ten hours, with 24-hour unattended operation producing 115 kbp (thousand base pairs) per day. Because of the increased scale required for the Human Genome Project, genome centres had developed a robust, highly automated and inexpensive preparatory process to feed their capillary sequencers. Once the data were produced, mature analysis software was applied to analyse the sequencing reads (each a ~500-bp sequence of A, C, G, T), then to assemble reads that shared sequence identity, reproducing that region of the genome. After assembly, each genomic region was further analysed to identify genes, repeat elements and other features. As the 'drivers' of these sequencing pipelines, genome centres could dial up capacity by increasing the amount of hardware used in the preparatory and sequencing processes, because sequence production, not sequence analysis, was rate limiting.

As I will describe, the ensuing 10 years has been marked by dramatic improvements in sequencing technology that have catapulted sequencing to the forefront of biological experimentation and have revolutionized the way that we approach genome-wide questions. One consequence of this revolution has been the coincident revitalization of bioinformatics, predominantly in development efforts aimed at data analysis and interpretation. Taken together, these unprecedented sequencing and analysis capabilities have inspired new areas of enquiry, have solved major questions about the regulation, variability and diaspora of the human genome, and have introduced a genomic era in medical enquiry and (ultimately) practice that will bring about the originally envisioned impact of the Human Genome Project.

Massively parallel sequencing

The first five years following the Human Genome Project provided further definition and annotation of the human genome sequence by comparative genomics; the sequencing of several model organism genomes—such as mouse[2], rat[3], chicken[4], dog[5], chimpanzee[6], rhesus macaque[7], duckbill platypus[8] and cow[9]—provided information about highly conserved genomic elements that are likely to be functional owing to their conservation. These genomes were largely produced by conventional methods, including Sanger-based capillary sequencing. Starting in 2005, a variety of new 'engines' for DNA sequencing that were radically different from the capillary sequencers used to sequence the human and model organism genomes became available from several different manufacturers (Fig. 1). These new engines were 'turbo-charged' by several orders of magnitude compared to their predecessors, because the basic mechanisms for data generation had changed radically, producing far more sequence reads per instrument run and at a significantly lower expense. The availability of multiple commercially available instruments alone represented a paradigm shift from the previous decade, where a single capillary instrument produced by Applied Biosystems dominated the market. Many of these innovative approaches were initially developed with National Institutes of Health (NIH) funding through the 'Technology development for the $1,000 genome' program (http://www.genome.gov/11008124#al-4) introduced during Francis Collins' directorship at the National Human Genome Research Institute (NHGRI).

Since the introduction of these platforms, the past five years have been marked by fierce competition between their manufacturers to greatly

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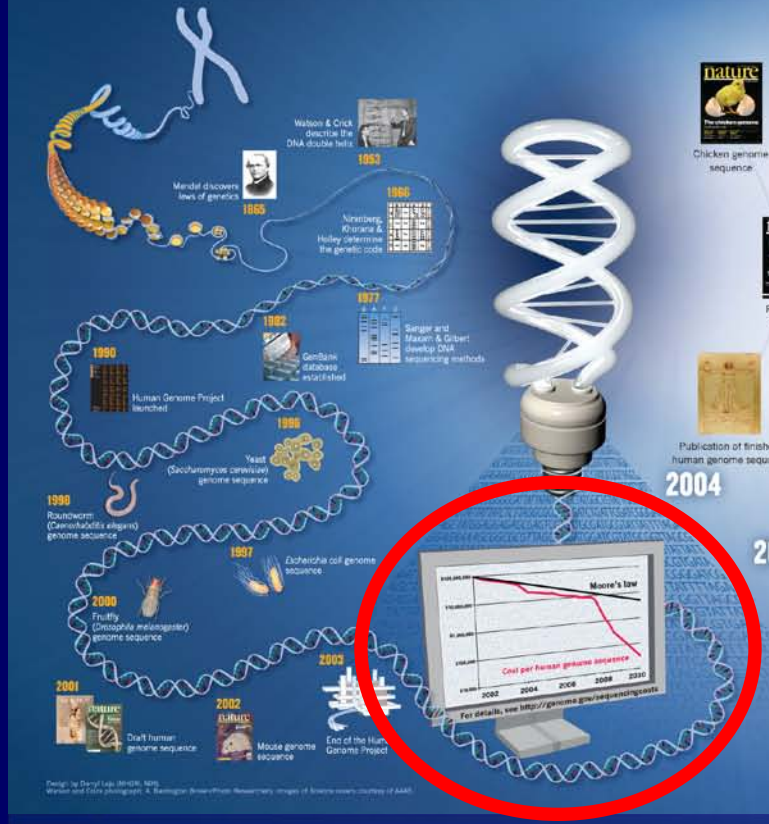
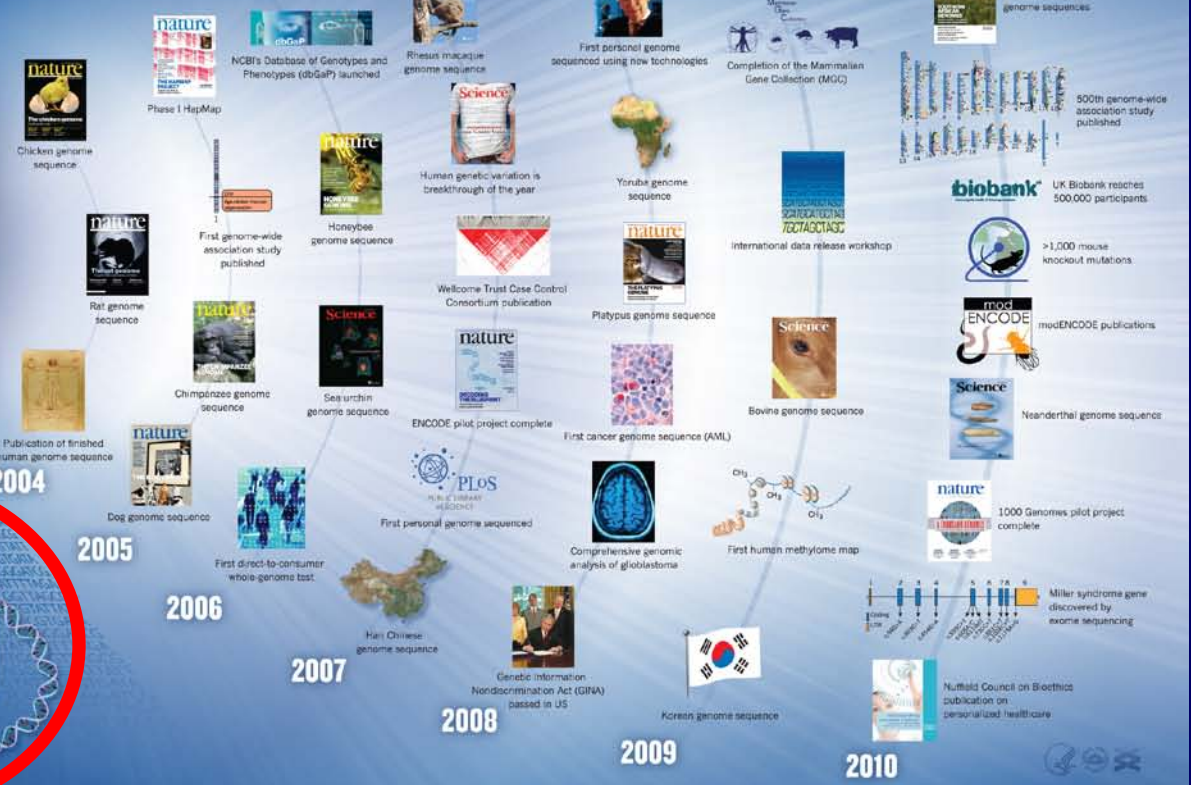
Genomic achievements since the Human Genome Project





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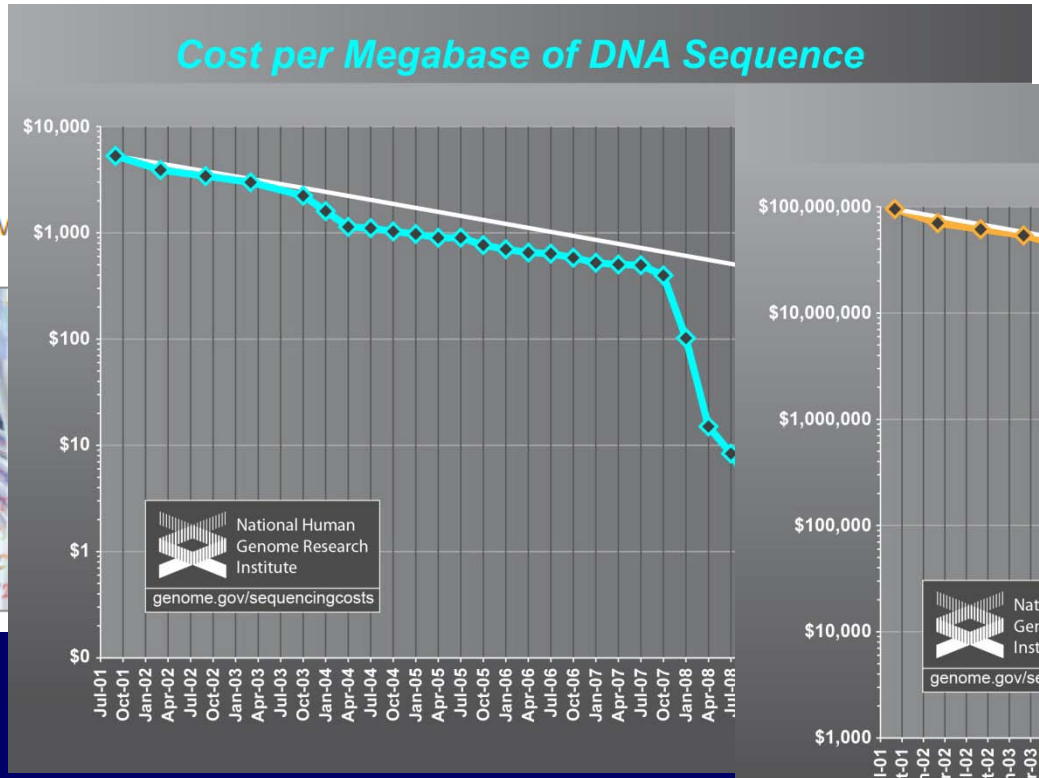
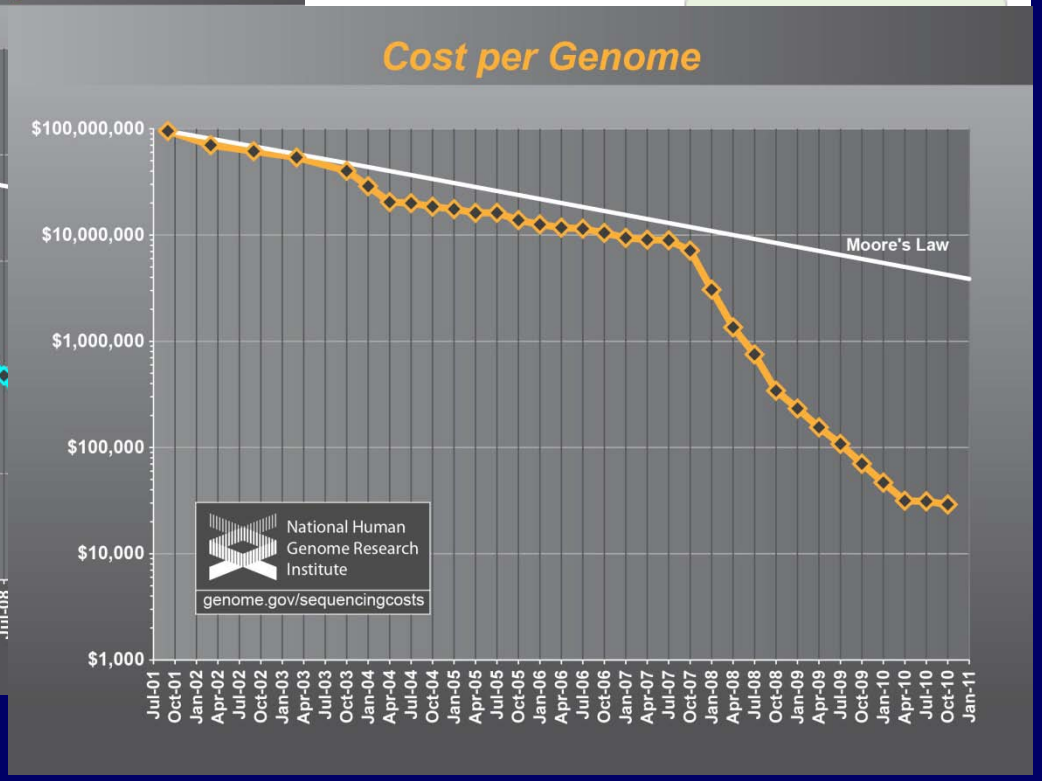
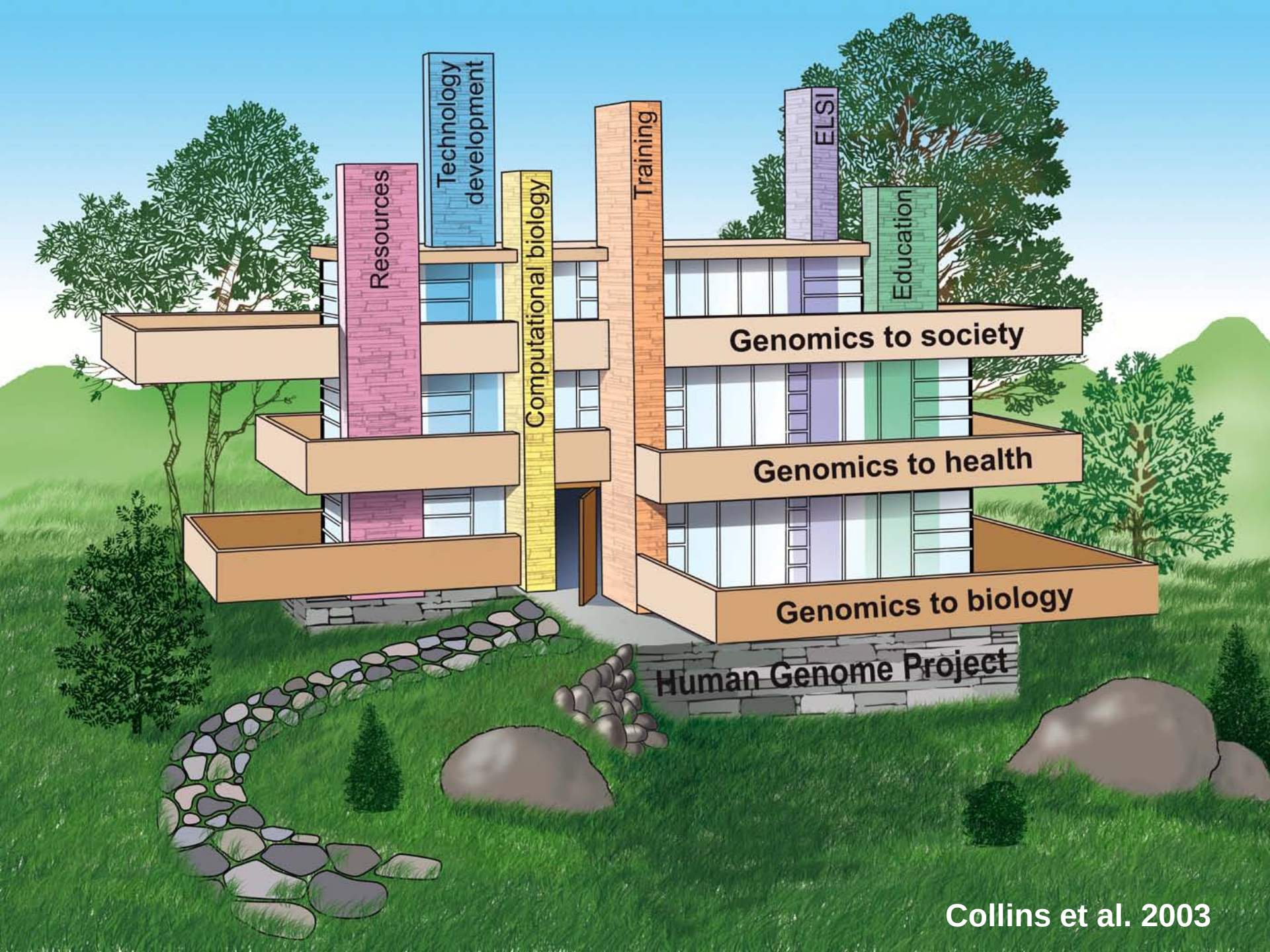
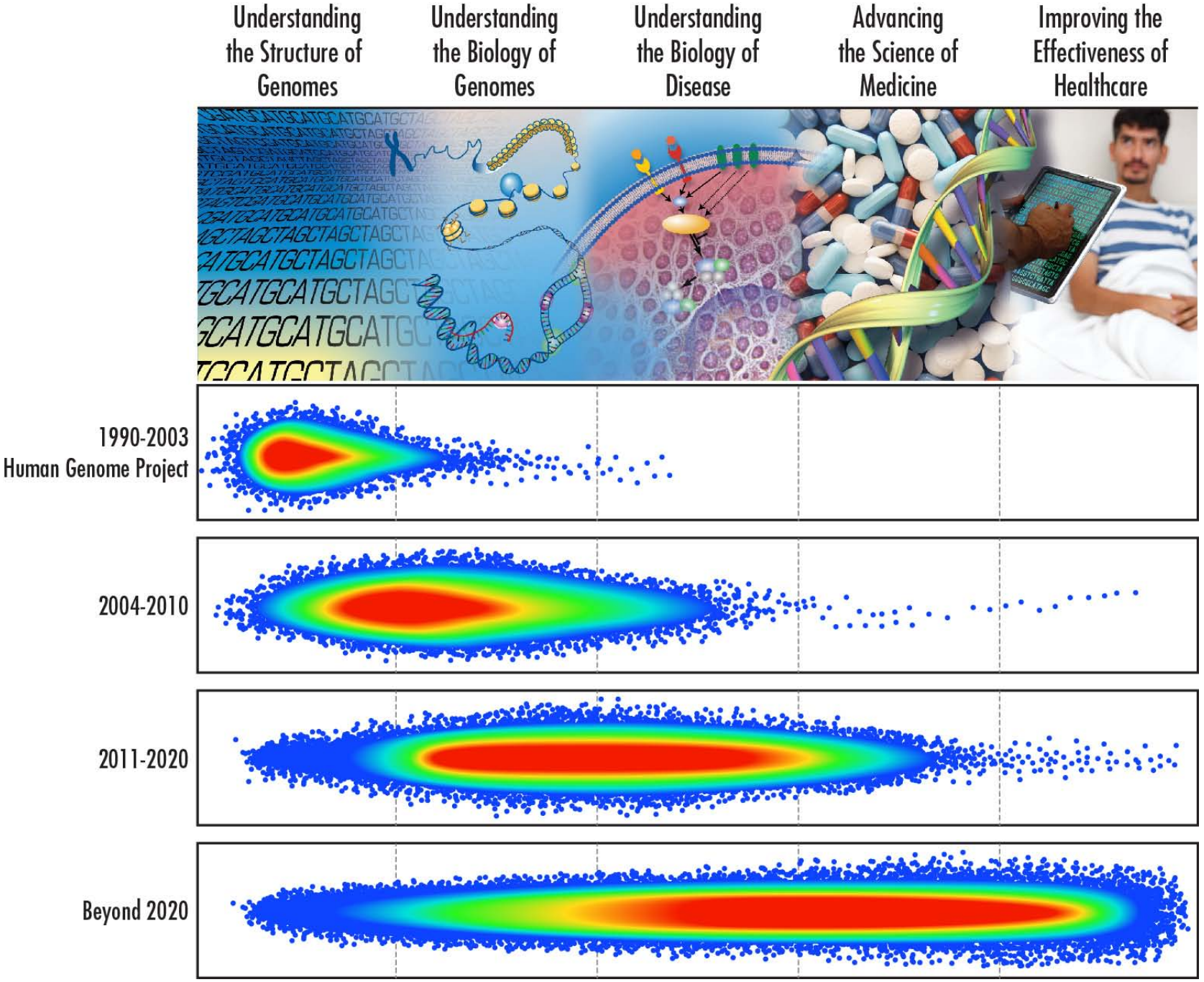




genome.gov/sequencingcosts



Collins et al. 2003


Understanding the Structure of Genomes
Understanding the Biology of Genomes
Understanding the Biology of Disease
Advancing the Science of Medicine
Improving the Effectiveness of Healthcare
1990-2003 Human Genome Project
2004-2010
2011-2020
Beyond 2020

NHGRI Publishes 2011 Strategic Plan

PERSPECTIVE

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Charting a course for genomic medicine from base pairs to bedside

Eric D. Green[1], Mark S. Guyer[1] & National Human Genome Research Institute*

There has been much progress in genomics in the ten years since a draft sequence of the human genome was published. Opportunities for understanding health and disease are now unprecedented, as advances in genomics are harnessed to obtain robust foundational knowledge about the structure and function of the human genome and about the genetic contributions to human health and disease. Here we articulate a 2011 vision for the future of genomics research and describe the path towards an era of genomic medicine.

Since the end of the Human Genome Project (HGP) in 2003 and the publication of a reference human genome sequence[1,2], genomics has become a mainstay of biomedical research. The scientific community's foresight in launching this ambitious project[3] is evident in the broad range of scientific advances that the HGP has enabled, as shown in Fig. 1 (see rollfold). Optimism about the potential contributions of genomics for improving human health has been fuelled by new insights about cancer[4–7], the molecular basis of inherited diseases (http://www.ncbi.nlm.nih.gov/omim and http://www.genome.gov/GWAStudies) and the role of structural variation in disease[8], some of which have already led to new therapies[9–13]. Other advances have already changed medical practice (for example, microarrays are now used for clinical detection of genomic imbalances[14] and pharmacogenomic testing is routinely performed before administration of certain medications[15]). Together, these achievements (see accompanying paper[16]) document that genomics is contributing to a better understanding of human biology and to improving human health.

As it did eight years ago[17], 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 updated vision 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 in agriculture, energy and other areas). Like the HGP, achieving this vision 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[18,19]), 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 quickly. Although genomics has already begun to improve diagnostics and treatments in a few circumstances, profound improvements in the effectiveness of healthcare cannot realistically be expected for many years (Fig. 2). Achieving such progress will depend not only on research, but also on new policies, practices and other developments. We have illustrated the kinds of achievements that can be anticipated with a few examples (Box 2) where a confluence of need and opportunities should lead to major accomplishments in genomic medicine in the coming 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 widely used. There is a compelling need to improve existing catalogues and to 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 disease-related traits require comprehensive catalogues of genetic variation, which provide both 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[20] and the International HapMap Project[21] (http://hapmap.ncbi.nlm.nih.gov), and is ongoing with the 1000 Genomes Project[22] (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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A Decade with the Human Genome Sequence

Charting a Course for Genomic Medicine

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National Human Genome Research Institute

Anticipating the Next Decade of the Genome
Francis Collins, M.D., Ph.D.
National Institutes of Health

The Human Genome at 10: An Overview
Eric Lander, Ph.D.
Broad Institute

Reading Genomes Bit by Bit
Sean Eddy, Ph.D.
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Genes, Genomes, and the Future of Medicine
Richard Lifton, M.D., Ph.D.
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Fevers, Genes, and Targeted Therapies: Adventures in the Genomics of Inflammation
Dan Kastner, M.D., Ph.D.
National Human Genome Research Institute

Exploring Your Genetic Blueprint: A Panel Discussion
Moderated by Sharon Terry, M.A.
Genetic Alliance
Featuring James Watson, Ph.D.
Cold Spring Harbor Laboratory

Systematic Surveys of Human Epigenomes
Bradley Bernstein, M.D., Ph.D.
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Functionalizing the Cancer Genome
Lynda Chin, M.D.
Harvard Medical School

Ethical, Legal, and Social Issues in Genomics: Reflecting Back, Planning Ahead
Amy McGuire, J.D., Ph.D.
Baylor College of Medicine

The Public Place in Personal Genomics
Amy Harmon
New York Times

The Path Ahead
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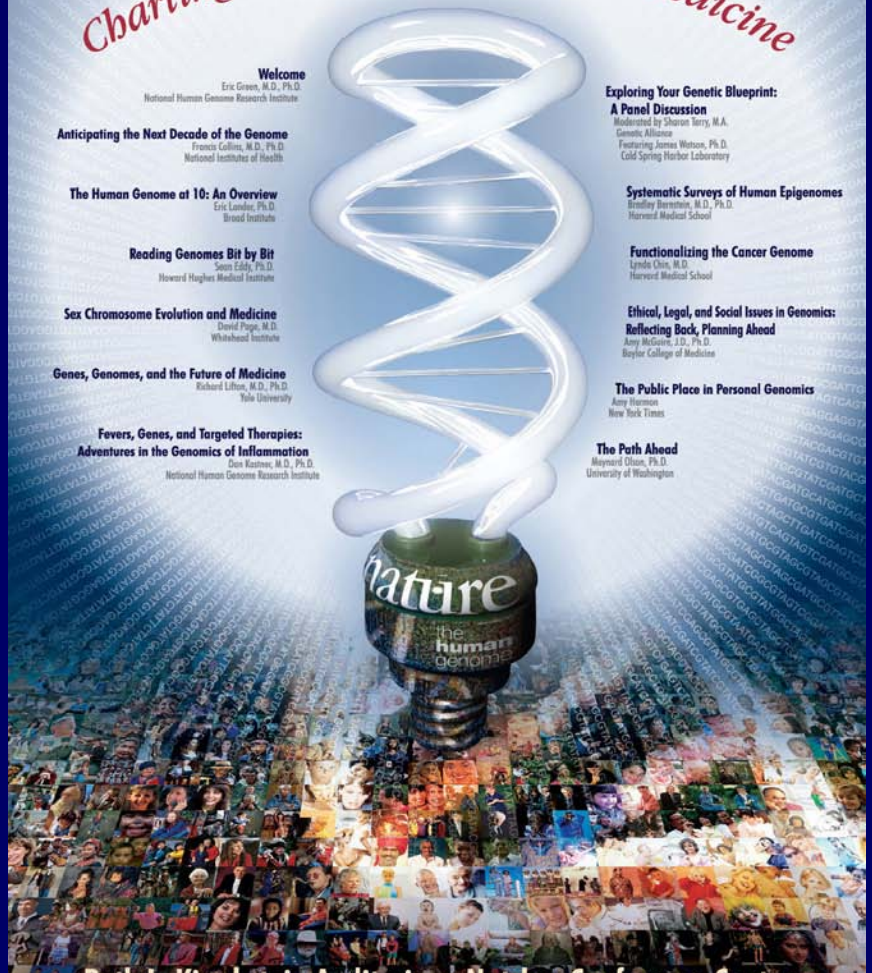

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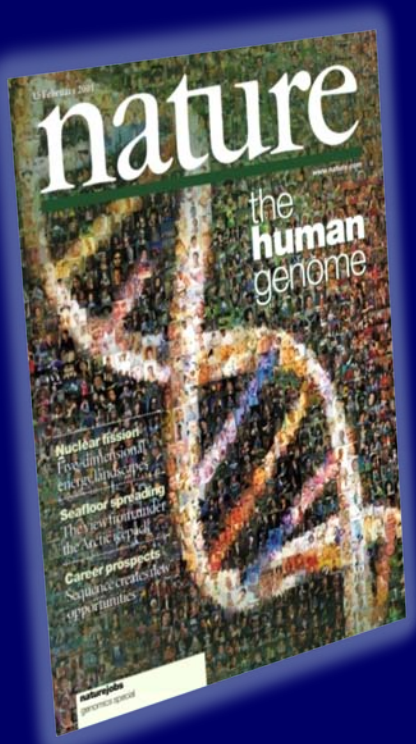

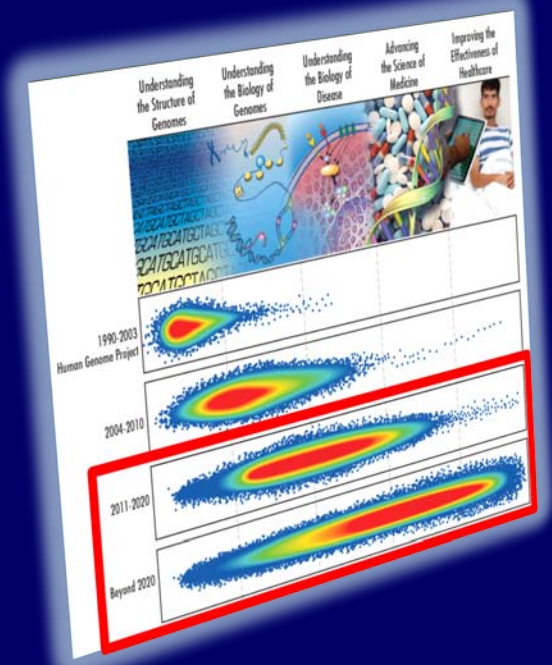

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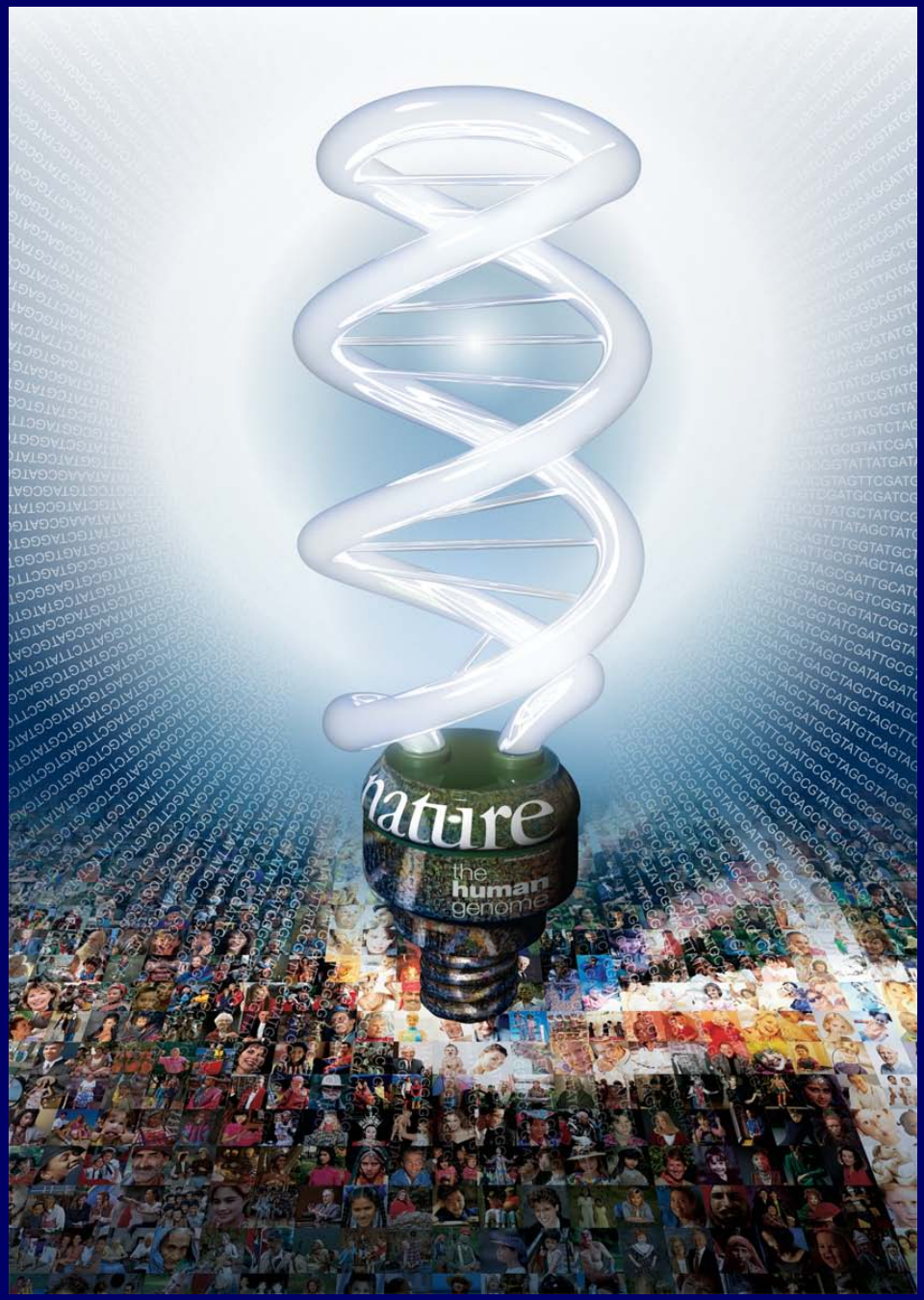

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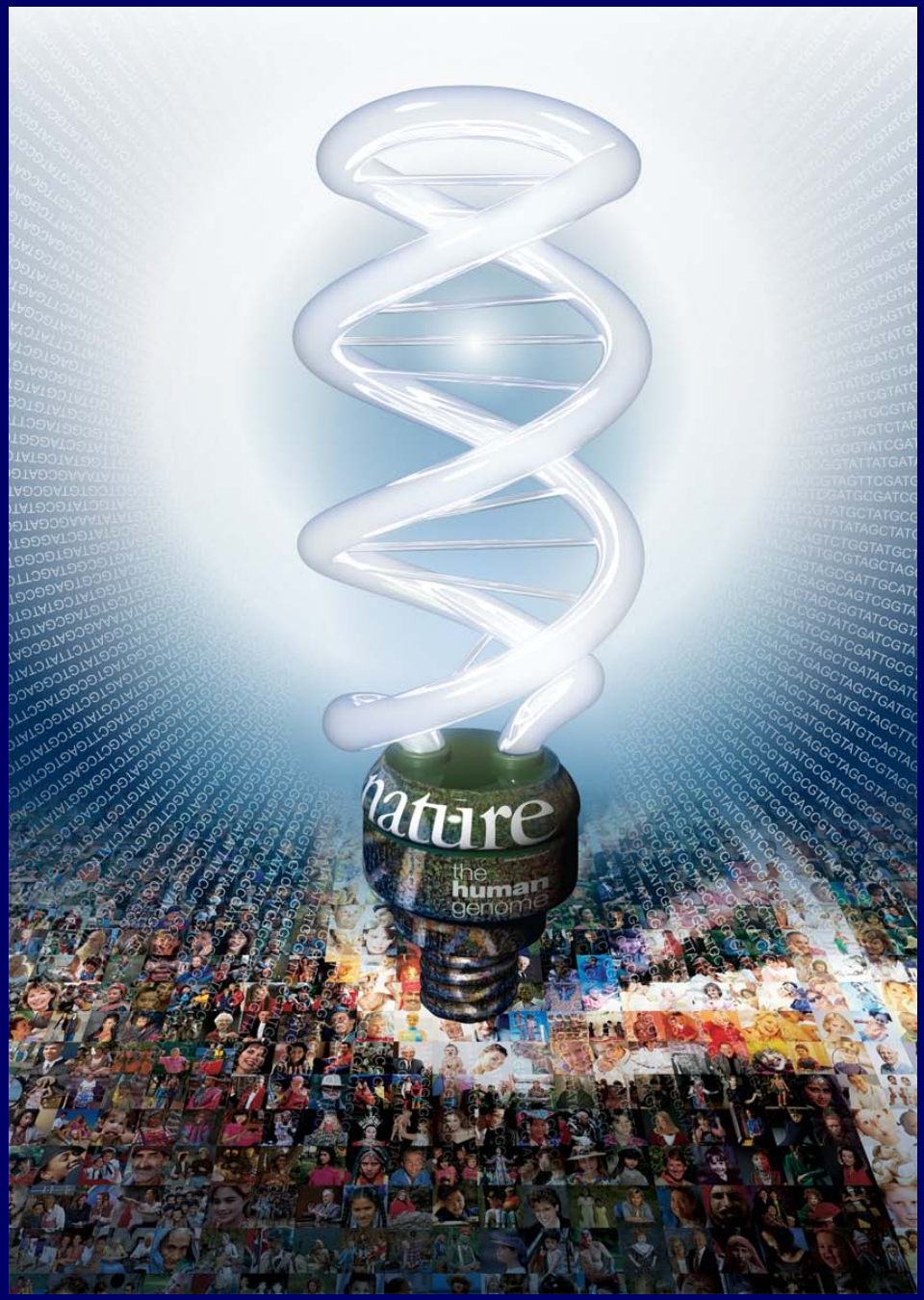

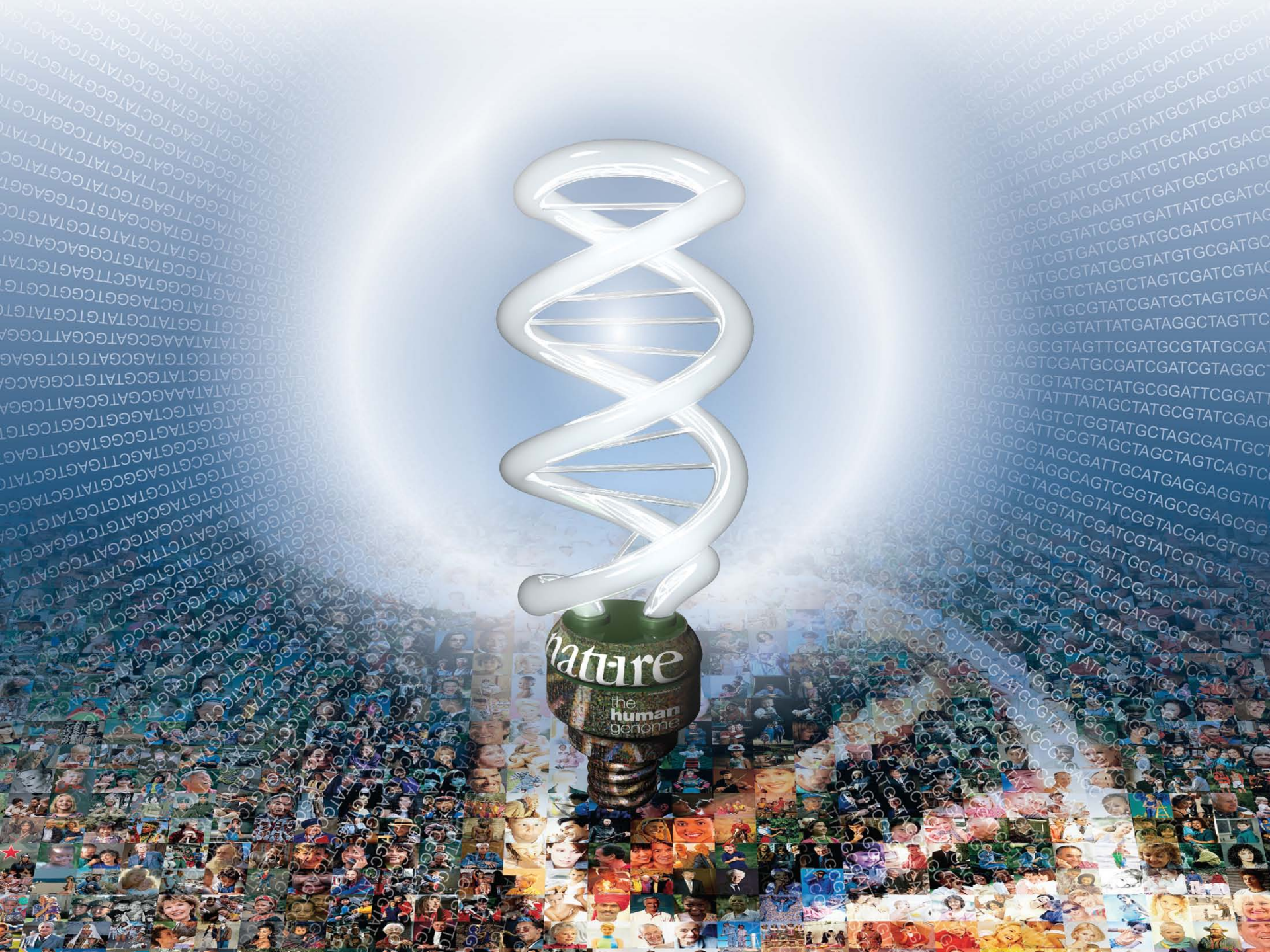
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