

Best Practices in Personalized Medicine
Vancouver, BC
March 8-9, 2011

“Workable” Ethics for Translational Research?

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McGill





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TCPS2

TRI-COUNCIL POLICY STATEMENT

Ethical Conduct for Research Involving Humans

2010

Canadian Institutes of Health Research
Natural Sciences and Engineering Research Council of Canada
Social Sciences and Humanities Research Council of Canada

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Note: For the most recent information on amendments, please consult the official online version of the TCPS at www.pseuethics.gc.ca.

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Clinical Trials

Guidance for Industry

Clinical Pharmacogenomics: Premarketing Evaluation in Early Phase Clinical Studies

DRAFT GUIDANCE

This guidance document is being distributed for comment purposes only.

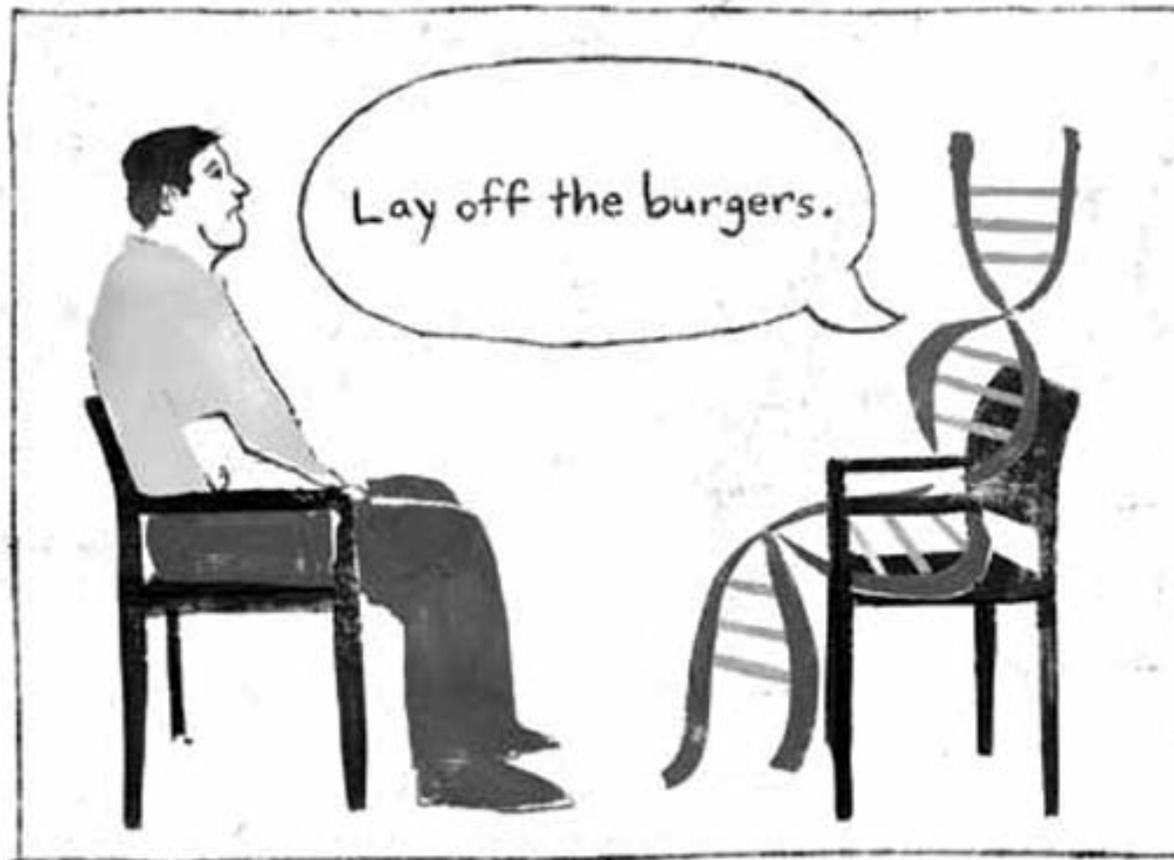
Comments and suggestions regarding this draft document should be submitted within 60 days of publication in the *Federal Register* of the notice announcing the availability of the draft guidance. Submit comments to the Division of Dockets Management (HFA-301), Food and Drug Administration, 5630 Fishers Lane, rm. 1061, Rockville, MD 20852. All comments should be identified with the docket number listed in the notice of availability that publishes in the *Federal Register*.

For questions regarding this draft document, contact (CDER) Lawrence Lesko at 301-796-1565 or Shiew-Mei Huang at 301-796-1541, or (CBER) Office of Communication, Outreach and Development at 800-835-4709 or 301-827-1800, or Changting Haudenschild at 301-827-3947, or (CDRH) Frances Kalush at 301-796-5408.

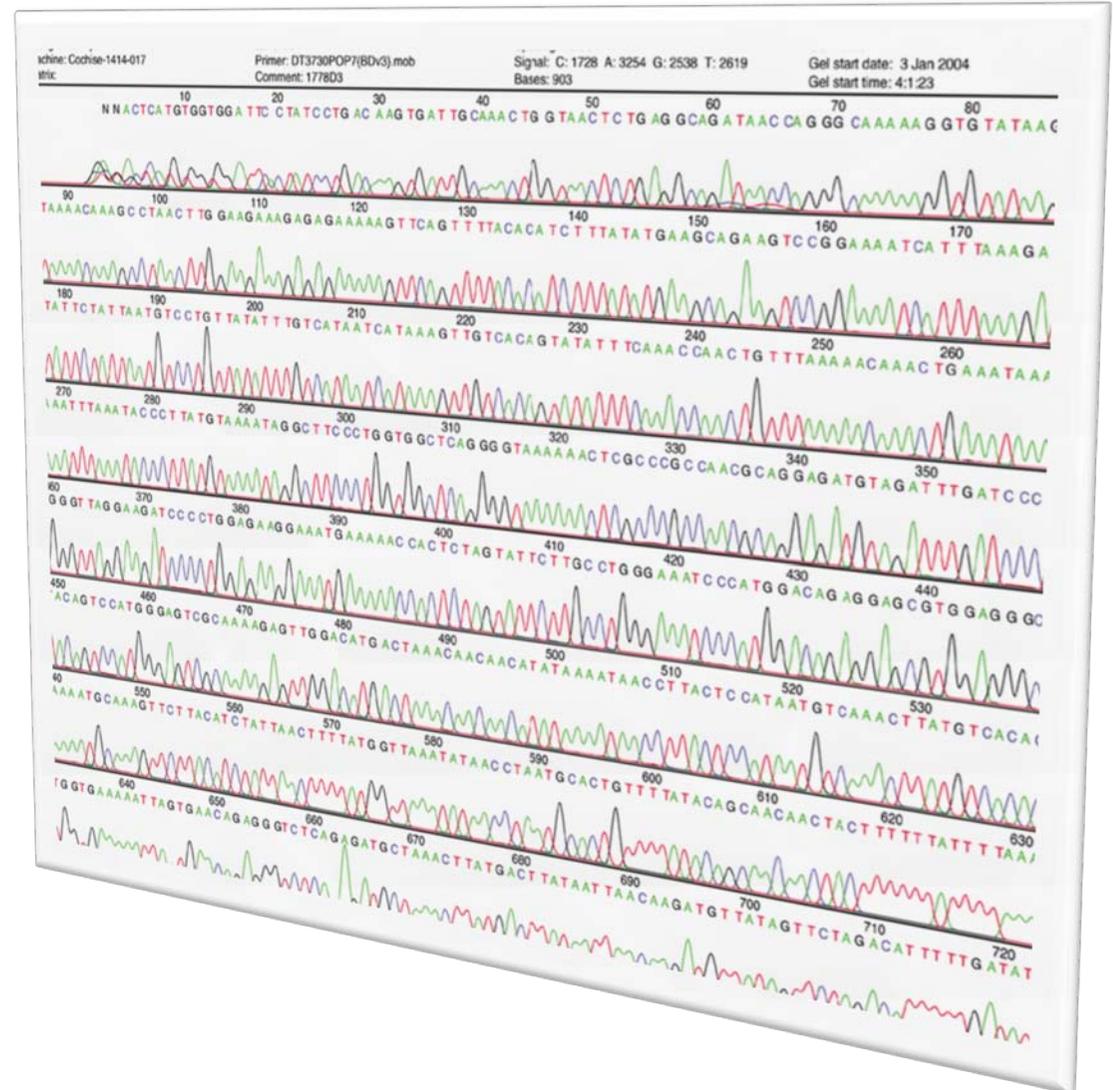
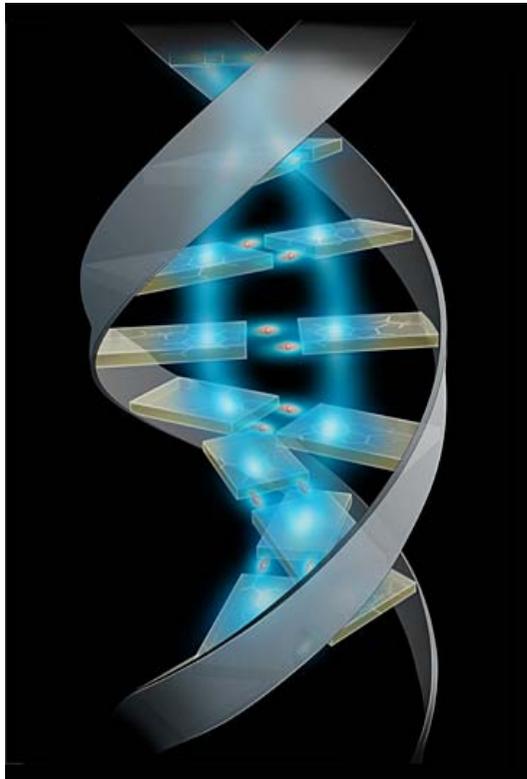
U.S. Department of Health and Human Services
Food and Drug Administration
Center for Drug Evaluation and Research (CDER)
Center for Biologics Evaluation and Research (CBER)
Center for Devices and Radiological Health (CDRH)

February 2011
Clinical Pharmacology

Physician – Patient Relationship



Whole-Genome Sequencing



Population Biobanks

POLICYFORUM

RESEARCH FUNDING

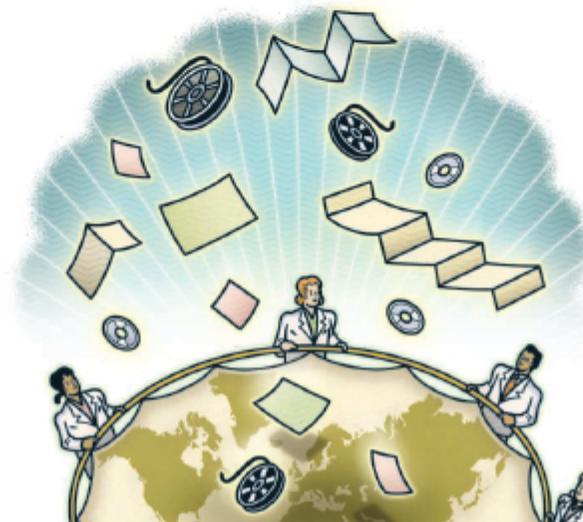
Sustaining the Data and Bioresource Commons

Paul N. Schofield,^{1,2*} Janan Eppig,² Eva Huala,³ Martin Hrabe de Angelis,⁴ Mark Harvey,⁵ Duncan Davidson,⁶ Tom Weaver,⁷ Steve Brown,⁸ Damian Smedley,⁹ Nadia Rosenthal,¹⁰ Klaus Schughart,¹¹ Vassilis Aidinis,¹² Glauco Tocchini-Valentini,¹³ John M. Hancock⁸

Development of powerful, high-throughput technologies, together with globalization of scientific research, presents the biomedical research community with unprecedented challenges for the management, archiving, and distribution of data and bioresources (1). We need a social contract between funding agencies and the scientific community to accommodate “bottom-up” integration and “top-down” financing of databases and biorepositories on an international scale.

The biological commons is evolving away from a traditional differen-

Globalization of biomedical research requires sustained investment for databases and biorepositories.



data models to accommodate new data types. The associated bioontologies and other informatics tools need to continue to be developed, maintained, and applied to data to standardize and maximize access, retrieval, and exploitation for discovery. Repositories also need to innovate and respond to emerging disruptive technologies. Consequently, any distinction between time-delimited research projects and long-term, relatively static infrastructures is being eroded. The traditional distinction between “infrastructure” and “research” is even less appropriate, presenting a challenge to those funders who continue to think in these

II. IMPLICATIONS

A. Recruitment

HapMap and 1000Genomes

The screenshot shows the top portion of the International HapMap Project website. It features a dark blue header with the project logo on the left and navigation links (Home, About the Project, Data, Publications, Tutorial) on the right. Below the header is a language selection menu with options for English, Français, and Yoruba. The main content area includes a brief description of the project and a 'Project Information' sidebar with links to 'About the Project', 'HapMap Publications', 'HapMap Tutorial', and 'HapMap Mailing List'. A 'News' section contains a dated entry from 2011-02-02 regarding Haploview issues with release 28 data.

The screenshot displays the homepage of the 1000 Genomes project. The header features the title '1000 Genomes' and the subtitle 'A Deep Catalog of Human Genetic Variation'. A navigation bar includes links for Home, About, Data, Analysis, Participants, Contact, Browser, and Wiki, along with a search bar. The main content is divided into two columns. The left column, titled 'LATEST ANNOUNCEMENTS', contains two entries: 'February 2011 Data Update' (dated Wednesday, February 16, 2011) and 'Mapping copy number variation by population scale genome sequencing' (dated Thursday, February 03, 2011). The right column, titled 'LINKS', contains icons and text for 'All Project Announcements', 'Sample and Project Information', 'Media Archive', 'Download the 1000 Genomes Pilot Paper', 'Project Contacts', and 'RSS Feed'.

ization different from HapMap. Please contact Haploview help desk (haploview@broadinstitute.org) for
on GRCh37
genome build b35 to GRCh37 is available. Data is available for bulk download.
now available for data in merged HapMap phases I+II+III release #28 (NCBI build 36, dbSNP b126)
able for browsing. Click here to read the latest release notes.
now available for data in HapMap phase 3 release #3 (NCBI build 36, dbSNP b126). Data is
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the new genome. Click here to read the latest release notes
available for chromosome X

II. IMPLICATIONS

A. Recruitment

“Citizens” and Population Biobanks

TAKING IT TO THE **BioBANK**
By CATHERINE HARRIS



Genotyping and Clinical Trials

Commentary

Ethical challenges in genotype-driven research recruitment

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³Department of Medicine, Division of Neurology, Duke University Medical Center, Durham, North Carolina 27710, USA

Many genetic and genomic studies are conducted using a phenotype-driven approach: Cases and controls are identified based on the presence or absence of a particular condition and analyses are undertaken to identify gene variants associated with that condition. The inverse—a genotype-driven approach—is receiving increasing attention as another powerful research tool. In this

from among patients attending adult and pediatric epilepsy clinic at Duke; subjects in another study on the genetics of memory served as controls. The consent form for the epilepsy study stated that participants would not receive individual research results (B1). Participants were also asked to sign a separate "biobanking consent form to permit the long-term storage of biological samples" (B2). The consent form for the epilepsy study did not mention the biobanking consent form, and the biobanking consent form did not mention the epilepsy study. This situation raises ethical questions about the transparency of research recruitment and the potential for unintended consequences. For example, the biobanking consent form may have been used to recruit subjects for other studies, or the epilepsy study may have been used to identify subjects for other studies. These questions are particularly relevant in the context of genotype-driven research, where the identification of subjects is based on their genetic profile rather than their clinical presentation.

II. IMPLICATIONS

A. Recruitment

Personal Genome Project

Personal Genome Project

Home [Project Overview](#) Participation Overview PGP Community [DONATE](#)

Volunteers from the general public working together with researchers to advance personal genomics.

We believe individuals from the general public have a vital role to play in making personal genomes useful. We are recruiting volunteers who are willing to share their genome sequence and many types of personal information with the research community and the general public, so that together we will be better able to advance our understanding of genetic and environmental contributions to human traits and to improve our ability to diagnose, treat, and prevent illness. Learn more about how to [participate](#) in the Personal Genome Project.



Project Overview. The PGP hopes to make personal genome sequencing more affordable, accessible, and useful for humankind. Learn more about our [mission](#).



Want to participate? We aim to enroll 100,000 informed participants from the general public. Learn more about [participation](#) in the PGP and how you can get involved.



Meet our volunteers. Participants may volunteer to publicly share their DNA sequence and other personal information for research and education. Meet the "[PGP-1K](#)".



Documentary Film about PGP. Two-time Emmy Award-winning documentary producer [Marilyn Ness](#) is making a film about the PGP.



CC0. We are committed to making [research data](#) from the PGP freely available to the public. Read about PersonalGenomes.org's use of the



Help Us Build. Are you a Rails developer interested in supporting the PGP through volunteer web application development? See our

Project News

Keep up-to-date with PersonalGenomes.org news and events. [Subscribe to our newsletter](#).

November 9, 2010: George Church wins Franklin Institute Bower Prize. [Read news](#).

October 12, 2010: Announcing new collaborations, new tools, and the PGP-1K. [Read newsletter #4](#).

October 11, 2010: Welcome to the team, [PGP-1K](#)! This week we are enrolling the next 1000 participants in the PGP.

July 2, 2010: New eligibility screening and enrollment software launched. We removed the need for invitation codes. [Sign up now](#).

April 27, 2010: A majority of individuals with a personal genome sequence on one stage at the [GET Conference 2010](#).

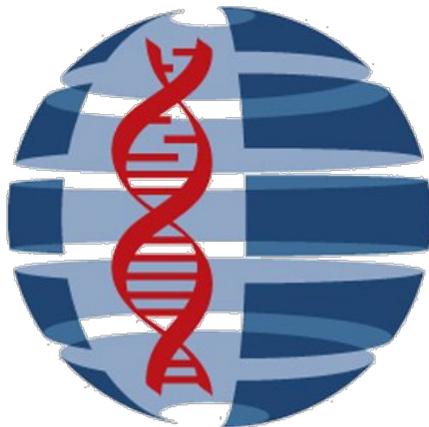
II. IMPLICATIONS

B. Privacy

Controlled Access Databases (ICGC)



The screenshot shows the ICGC Data Access Compliance Office website. At the top, there is a navigation bar with the ICGC logo, the text "DATA ACCESS COMPLIANCE OFFICE", and a search bar. Below the navigation bar, there are several tabs: "Overview", "Access Forms", "Research Practices", "International Data Access Committee", "DACO Approved Projects", and "Contacts". The main content area is titled "Data Access Compliance Office" and features three steps: 1. Create your account (with a "Learn How" button), 2. Fill your application (with a "Learn How" button), and 3. Submit to DACO (with a "Learn How" button). Below this, there is a description of the DACO: "The Data Access Compliance Office (DACO): Handles requests from scientists for access to controlled data from the International Cancer Genome Consortium (ICGC)." and a "Please note" section with additional information.



International Cancer Genome Consortium

DataSHIELD

Int. J. Epidemiol. Advance Access published July 14, 2010

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© The Author 2010; all rights reserved. doi:10.1093/ije/dyq111

DataSHIELD: resolving a conflict in contemporary bioscience—performing a pooled analysis of individual-level data without sharing the data

Michael Wolfson,¹ Susan E Wallace,^{2,3} Nicholas Masca,⁴ Geoff Rowe,¹ Nuala A Sheehan,⁴ Vincent Ferretti,^{3,5} Philippe LaFlamme,^{5,6} Martin D Tobin,⁴ John Macleod,⁷ Julian Little,^{3,8} Isabel Fortier,^{3,8,9} Bartha M Knoppers^{2,3} and Paul R Burton^{3,4,8,10*}

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Accepted 27 May 2010

Background Contemporary bioscience sometimes demands vast sample sizes and there is often then no choice but to synthesize data across several studies and to undertake an appropriate pooled analysis. This same need is also faced in health-services and socio-economic research. When a pooled analysis is required, analytic efficiency and flexibility are often best served by combining the individual-level data

Identification?

OPEN ACCESS Freely available online

PLoS GENETICS

Viewpoints

Public Access to Genome-Wide Data: Five Views on Balancing Research with Privacy and Protection

P³G Consortium^{1*}, George Church^{1*}, Catherine Heeney^{2*}, Naomi Hawkins², Jantina de Vries², Paula Boddington², Jane Kaye², Martin Bobrow^{3*}, Bruce Weir^{4*}

1 Department of Genetics, Harvard Medical School, Cambridge, Massachusetts, United States of America, **2** The Ethox Centre, Department of Public Health and Primary Care, University of Oxford, Oxford, United Kingdom, **3** Department of Medical Genetics, University of Cambridge, Cambridge, United Kingdom, **4** Department of Biostatistics, University of Washington, Seattle, Washington, United States of America

Introduction by Greg Gibson and Elizabeth Fisher

Just over twelve months ago, *PLoS Genetics* published a paper [1] demonstrating that, given genome-wide genotype data from an individual, it is, in principle, possible to ascertain whether that individual is a member of a larger group defined solely by aggregate genotype frequencies, such as a forensic sample or a cohort of participants in a genome-wide association study (GWAS). As a consequence, the National Institutes of Health (NIH) and Wellcome Trust agreed to shut down public access not just to individual geno-

research. George Church posits that actions directed toward restricting data access are likely to exclude researchers who might provide the most novel insights into the data and instead makes the argument that full disclosure and consent to the release of genomic information should be sought from study participants, rather than making difficult-to-guarantee promises of anonymity. Martin Bobrow weighs the risks and benefits and proposes four steps that represent a middle ground: Retain restricted access for now, make malicious de-identification practices illegal, increase public awareness of the issues, and encourage recognition that scientists

DNA mixture including up to 1,000 participants. Although in hindsight it is clear that basic statistical theory would predict this to be the case, the reality is that it had previously gone completely unrecognised.

This situation illustrates the need to raise the level of discussion, thereby avoiding the ad hoc resolution of immediate privacy concerns and anticipating future scientific possibilities with a view to providing prospective guidance.

The implications of the Homer paper were discussed by the international Public Population Project in Genomics (P³G) (<http://www.p3g.org>). The consensus was

The subscription of the Homer paper to bioethical bioethics literature. The subscription of the Homer paper to bioethical bioethics literature. The subscription of the Homer paper to bioethical bioethics literature.

II. IMPLICATIONS

C. Communication

Biobanks Websites

CORIELL
INSTITUTE
for Medical Research

home | about | personalized medicine | biorepository

search us:
search...

- Home
- About Coriell
- Research and Faculty
- Personalized Medicine
- Biorepository Catalog
- Stem Cell Biobank
- Services
- Science Fair
- Education and Training
- Giving to Coriell
- Contact Us
- Partners

COURIER-POST
Coriell tackles personal medicine
It plans to enroll 10,000 in innovative gene-based program

Breaking News >>
Press Release: CPMC Data Going Into EMRs (2/8/11)
CPMC Risk Estimation (2/1/11)
Biobanking Revitalized (1/15/11)
Health Watch: Stem Cells (12/16/10)
Determining Continental Origins
More News >>

Videos >>
ABC Action News 6 (3:10)
NJN News (2:31)

Biorepository Catalog

Coriell Institute for Medical Research
The Coriell Institute for Medical Research is an independent, not-for-profit research organization dedicated to understanding human genetic diseases and providing the highest quality genetic resources.

II. IMPLICATIONS

C. Communication

Return of Results?



McGill



CENTRE OF GENOMICS AND POLICY
CENTRE DE GÉNOMIQUE ET POLITIQUES

THE JOURNAL OF
LAW, MEDICINE & ETHICS

A Journal of the American Society of Law, Medicine & Ethics

Lexicon

International Context and General Principles

Biobanks and Populations

Paediatric Research

Intrafamilial Communication

Deceased Individuals

International Consortia

“Incidental” Findings



UK
10K
RARE GENETIC VARIANTS IN HEALTH AND DISEASE

ETHICAL GOVERNANCE FRAMEWORK

Drafted by the Ethical Advisory Group of the UK10K project

Data-Sharing

International Code of Conduct for Data Sharing in
Genomic Research



Genomic Research: Quo Vadis?

PERSPECTIVE

doi:10.1038/nature09764

Charting a course for genomic medicine from base pairs to bedside

Eric D. Green¹, Mark S. Guyer¹ & 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.

CONCLUSION

