

Genomics and Health Information Technology Systems: Exploring the Issues
April 27 - 28, 2011, Bethesda, MD
Brief Meeting Summary, prepared by Greg Feero, M.D., Ph.D. (planning committee chair)

Overview

The two day meeting brought together a broad representation of stakeholders to discuss the increasing intersection of clinical health information technology systems and genomic data. The meeting was convened to provide a high level overview of the challenges and opportunities for research and policy development in this space. NHGRI's interest in this area stems from its recent Strategic Plan focusing on the path towards genomic medicine; the Institute is interested in identifying areas where it could make a unique contribution and how it might stimulate untapped areas of research. Approximately 90 individuals participated in the event, which consisted of presentations, panel sessions and small breakout groups charged with exploring challenges and opportunities in basic discovery research, clinical implementation research, interoperability standards development and clinical computing capacity requirements.

Overarching observations

There was universal consensus that now is the time to be examining the intersection of health information technology systems and genomic data. This was felt to be true for both research and clinical applications of genomics. The consensus also was that basic discovery research would greatly benefit from the ability to more effectively harness the vast amounts of information generated in clinical care, assuming that issues of consent, oversight, data access and data quality could be addressed adequately. There was some debate regarding how much demonstrated utility genomic information has in routine health care; however there was also a general consensus that opportunities to garner evidence of clinical benefit are lost unless genomic and clinical information are captured in ways that can be queried to follow outcomes. Most attendees felt that computing capacity and data storage would not be a limiting factor in the integration of genomic information into clinical health information technology systems.

Recurring themes

1) Development of a "learning health system"

Discussions repeatedly reflected the need for health information technology systems to evolve to a level of function where genomic and clinical data capture and manipulation supports real time clinical decision making, evaluation of outcomes of decisions, as well as discovery research. Without such systems the expense of clinical outcomes research as well as discovery research required moving forward becomes problematic. In such an environment the distinction between discovery and implementation research becomes less apparent, as do the traditional boundaries separating clinical and research informatics infrastructures. Developing such a system is a dramatic departure from the traditional role of medical records in health care and will necessitate a considerable amount of dialogue with the public and health professionals.

Related issues include:

- Discomfort with the blurring of research and clinical care, and a potential mismatch between researcher and public acceptance of such blurring
- Adequacy of patient consent and oversight of data access
- Lack of clarity of when information generated (such as a newly identified disease risk conferring variant) is clinically actionable
- Determination of the how representative studies derived from HIT systems are of phenotypic and subject diversity
- Accurate phenotyping (prospective "neat" vs. retrospective "scruffy")
- Determining the most appropriate time to introduce new data elements or capabilities into systems
- Determining when it is appropriate to reinterpret an individual's genotype/sequence information, given changes in the underlying knowledge base

Example suggested projects/research activities:

- Study representation of poor, minorities, uninsured, underrepresented in current EHRs to determine if there is a problem
- Create an EHR-light software solution with minimal data fields linked to larger EHR or web/cloud based system
- Create bi-directionality between EHR and PHR, so patients can enter data directly into PHR that transfers to EHR either only for research or for research and clinical use
- Methods to integrate relevant EHR data longitudinally across multiple health care systems as well as across feeder systems such as pharmacies and laboratories.
- Family history – need to link through one EHR FH to another EHR, consent & mechanisms to allow connectivity
- ELSI study to assess public attitudes toward the scale and scope of EHR research and what level of consent is needed
- Computer in doctor's office where could ask research participation questions of patients based on EHR information; adds specificity to research request rather than generic access to EHR

2) Development of a clinical variation database for clinical purposes

Concerns were raised repeatedly regarding the currently fragmented patchwork of human genetic variation databases. The current balkanization affects the ability to assess data accuracy and quality, greatly hinders routine clinical interpretation of genomic test results, and effectively limits the construction of high quality clinical decision support tools. In addition, the level of curation according to common standards for clinical relevance or utility varies widely. The advent of low cost NGS in a diversity of research and clinical environments will exponentially compound the current situation.

Related issues include:

- Lack of clarity regarding the most appropriate model for establishing a reference database
- Lack of clarity regarding how best to curate and disseminate information from a clinical reference database

- Need to come to agreement on:

Data representation (format, content, quality metrics)

Interpretation (genotype/phenotype correlations, sufficiency of evidence)

Actionability (Recommended next steps when a variation is present, sufficiency of evidence)

Example suggested projects/research activities:

- Some form of centralized annotated & curated variant data base for clinical use
- Guidelines & policy around clinical community generation of variant information
- Workshop to bring together experts to hash-out feasibility and myriad of issues that need to be considered in developing a database
- Research to inform policy on critical genome values that need to be unmasked regardless of circumstances

3) Development of interoperability

There was broad consensus that genomic data must be stored in a structured format that permits exchange of information between health information technology systems. Interoperability is crucial to research as well as clinical use of genomic information, especially for germline sequence data.

Related issues include:

- Standards development , harmonization, and curation
- Need for standards to be extensible as the range of variation types expands to minimize disruption to clinical informatics systems
- Lack of incentives for standards adoption until very late in the translation of genomic knowledge.
- A need to harmonize existing standards based on evidence of effectiveness and adoption.

Example suggested projects/research activities:

- Develop broad forum for genomics standards discussion
- Development of open tools to check clinical nomenclature vs standards
- dbGAP-like model for metadata around consent
- Research on drivers to standards adoption by spectrum of generators and consumers of genomic data
- Ensure funding requirements drive standards development/ harmonization/adoption
- Training of individuals in bioinformatics and clinical informatics → intersection of programs

4) Development of clear consent and oversight guidelines

Representatives of basic and clinical research communities as well as health professional groups all agreed on the desirability of developing nationally acceptable guidelines for consent and oversight for the integration and use of genomic information in the context of clinical health information technology systems. Requiring specific individual consent for every analysis of a HIT-derived dataset would effectively preclude any useful research, yet having no dialog with stakeholders and considering it not Human Subjects research is similarly untenable. It was recognized that the reasons and requirements of consent in clinical and research settings differ and that “one size does not fit all”. However benchmarks for acceptable handling of genomic information in various HIT contexts would help to alleviate uncertainty in both environments.

Related issues include:

- Uncertainty in how to handle return of results, whether anticipated or not?
- Establishing a balance between patient autonomy and “DNA paternalism”.
- Establishing the boundaries of longitudinal responsibility for data reinterpretation.
- Establishing acceptable national recommendations for genomic data confidentiality, privacy and security (CPS).

Example suggested projects/research activities:

- Study flow of genomic information in the context of clinical informatics systems
- Study patient controlled models of use of genomic information in clinical informatics systems
- Software for instruments and middleware for medical purposes should be required to adhere to federal regulations regarding CPS
- Research funding agencies should require that any new tools developed for clinical patient care adhere to federal CPS regulations
- Research needs to be done on whether we can enable online clinical genetic informed consent in a manner that all patients understand fully their risks (and that of biological family members) without feeling pressure to consent
- A standard of care for whole genome variation reporting needs to be developed, this will require workshops and consensus building

5) Development of an evidence base regarding the clinical implementation/representation of genomic information

Due to the rapid evolution of genomic discoveries, there has been little time to accrue understanding of the most effective approaches for clinical implementation of genomic scale data in patient care. It was generally agreed that at least some genomic information will eventually become part of nearly all patient’s health records. It was also generally agree that little data exists regarding how to represent

that information, or how to most effectively measure the consequences of making the information available in the context of health information technology systems.

Related issues include:

- Uncertainty about how much genomic information should be incorporated in the electronic environment (targeted variation information or complete variant data sets).
- Uncertainty regarding the most effective models for the development of clinical decision support/ interpretation (e.g. built into the EHR, or in third party systems interoperable with the EHR, stand alone third party systems generating interpretive reports).
- Lack of clarity regarding patient and provider preferences for the representation of genomic information.
- Lack of understanding of patient and health care provider's preferred outcomes from access to genomic information in the context of EHRs.
- Lack of infrastructure to measure outcomes associated with the integration of genomic information in EHRs.

Example suggested projects/research activities:

- Develop additional pilot projects to explore multiple models for genomic information integration into EHRs (eMERGE 2.0). Consideration should be given to whether these pilot projects would largely encompass leading institutions who have already invested heavily in EHR infrastructure and/or incentivize institutions who are not as far along.
- Survey to learn perceived value of whole genome sequence information (consumers, providers, payers, organizations, researchers)
- Design project to develop metrics for determining the effectiveness of point of care genomics tools for providers and health care consumers
- Use chromosomal microarray data as a proxy for investigating issues surrounding future use of genomic information in clinical informatics systems