This landmark issue of *JAMIA* is the first to introduce articles reflecting our extended scope in translational bioinformatics (TBI), as described in the editorial by Butte and Shah (*see page 352*). Just as medicine has evolved to rely on both molecular and clinical phenotyping, biomedical informatics has evolved to encompass the integration and analysis of information from different biological levels. Sarkar (*see page 354*) reviews the role of TBI and explains how it bridges biology and medicine through methods for information handling that significantly overlap those used in clinical informatics. Altman (*see page 358*) reviews the most notable TBI articles in 2010, some of which were published in *JAMIA*. Wei (*see page 370*), who was the recipient of the 2011 Marco Ramoni Award, presents a Bayesian approach to using data from genome-wide association studies for predictive modeling.

The TBI articles cover a range of clinical and molecular approaches. Pathak (*see page 376*) reports on the challenges of and solutions for phenotype mapping across institutions participating in the Electronic Medical Records and Genomics (eMERGE) Network, while Xu (*see page 387*) reports how natural language processing significantly helped researchers conduct pharmacogenetic studies at an institution participating in the same network. Chen (*see page 392*) describes how using a new approach to integrate data from different biological levels can help in the investigation of genes responsible for prostate cancer progression. Foran (*see page 403*) describes software used to process information from tissue microarrays using grid technology, and Helmer (*see page 416*) describes a network framework designed to accommodate collaborative biomedical research. Related to this topic, advanced networking and high performance computing are reviewed by Locati (*see page 523*).

However, a network cannot be fully functional unless the information that it carries is semantically mapped across its nodes. Rector (*see page 432*) discusses the problems in using SNOMED in practical applications, and Nelson (*see page 441*) describes the challenges and solutions for standardizing medication names and formulations. This is critical for studies such as those conducted by Hasan (*see page 449*), in which the goal is to detect omissions in medication lists, and for studying the tradeoffs between manual versus automated record review for detection of adverse events, as described by Tinoco (*see page 491*). Related to recognition of concepts in electronic health records (EHRs), Savova (*see page 459*) describes a method to construct a resource for public sharing of gold standard annotations from clinical narratives, and Wilcox (*see page 511*) provides a method to estimate mismatches (ie, inclusion of information from the wrong patient) in EHRs. Related to information access in EHRs, Boxwala (*see page 498*) describes a method to monitor potentially inappropriate accesses, and Welte (*see page 506*) reports on difficulties in conducting content-based image retrieval. Archer (*see page 515*) reviews specific issues encountered in personal health records.

All this fascinating work for structuring, analyzing, and disseminating data through a network is prerequisite to the end goal of improving care and preventing disease. Clinical decision support (CDS) is one way to move toward this goal. Carroll (*see page 485*) describes a specific CDS for screening used in pediatric clinics associated with a major academic center, and Seidling (*see page 479*) reports on factors associated with CDS. Related to CDS for quality improvement and public health, Carnevale (*see page 466*) describes a CDS to detect nosocomial infections, and Kirchhoff (*see page 473*) reports on the feasibility of utilizing machine learning methods to translate public health information into different languages. Finally, because research in our field is still primarily funded by federal agencies, it is important to understand some factors that are associated with funding. Boyack (*see page 423*) studies the positive association of funding and the impact of articles. This author also reports an increasing trend in co-funding by NIH institutes, reflecting the current collaborative nature of biomedical research.

The articles from this special issue are prime examples of the diversity and richness of research and innovative uses of applications. However, we must recognize that the field of biomedical informatics could not have attained the achievements exemplified in these articles without the pioneering work of colleagues who dedicated their professional lives to it. This issue of *JAMIA* celebrates exceptional individuals who helped establish the foundations of biomedical informatics and who have touched our lives in many different ways. We remember them fondly, knowing that, by following their footsteps, we will keep their legacy alive for current and future generations of biomedical informatics professionals.