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Establishing the Genomic Knowledge Matrix for Nursing Science

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Abstract

Purpose: To establish the knowledge needed to integrate the multiple branches of omics into nursing research to accelerate achieving the research recommendations of the Genomic Nursing Science Blueprint.

Methods: The creation of the Genomic Knowledge Matrix occurred in three phases. In phase 1, the Omics Nursing Science and Education Network (ONSEN) Education Workgroup completed an evidence, bioinformatics, and technology review to inform the components of the Matrix. The ONSEN Advisory Panel then reviewed and integrated revisions. Phase 3 solicited targeted public comment focused on education and research experts, and applicable revisions were made.

Findings: The Genomic Knowledge Matrix establishes the following content areas: cellular and molecular biology, system physiology, microbiology, and translational bioinformatics as the minimum required preparation for nurse scientists to understand omics and to integrate this knowledge into research. The Matrix also establishes levels of understanding needed to function based on the role of the nurse scientist.

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Conclusions: The Genomic Knowledge Matrix addresses knowledge important for nurse scientists to integrate genomics into their research. Building on prior recommendations and existing genomic competencies, the Matrix was designed to present key knowledge elements critical to understand omics that underpin health and disease. Knowledge depth varies based on the research role.

Clinical Relevance: The Genomic Knowledge Matrix provides the vital guidance for training nurse scientists in the integration of genomics. The flexibility of the Matrix also provides guidance to inform fundamental genomic content needed in core science content in undergraduate and graduate level nursing curricula.

Keywords

Competency; education; genetics; genomics; knowledge; nursing; research

The National Human Genome Research Institute (NHGRI), National Cancer Institute (NCI), and National Institute of Nursing Research (NINR) collaboratively convened a group of multidisciplinary leaders with expertise in research, genetics, policy, nursing science, and evidence-based outcomes measurement to create a blueprint for genomic nursing science. The blueprint identified key genomic research priorities needed to inform the integration of genomics into nursing research, practice, and regulation. Preparation of the current and future nursing workforce, faculty, and scientists is a key priority, central to which is adequately preparing nurse scientists to conduct genomics research. Nurse scientists currently engage in this type of research; however, they are more often only a member of the team as opposed to lead investigators (Williams, Tripp-Reimer, Daack-Hirsch, & DeBerg, 2016). Developing resources to move these scientists toward assuming the role of principal investigator (PI) will contribute to more cost-effective health outcomes and accelerate the translation of evidence into practice (Genomic Nursing State of the Science Advisory Panel, 2013).

To operationalize the blueprint priorities, the NHGRI, NCI, and NINR assembled an advisory panel (AP) with expertise in key areas of genomics, education, clinical practice, and nursing research (Table S1). The AP was charged with defining ways to accelerate the uptake of genomics into nursing research, identifying researcher resources and gaps, exploring paradigms that support omics research, and envisioning a vehicle to promote genomics in collaborative nursing research. One of the significant gaps identified that currently limits nurse scientists' ability to conduct genomic research is their lack of educational preparation in following science content areas, such as cellular and molecular biology, system physiology, microbiology, and translational bioinformatics. They are not equipped with the necessary knowledge and skills to conduct omics research. A recommendation was made to develop fundamental core educational elements needed to prepare nurse scientists to integrate omics. The AP was expanded to form the Omics Nursing Science and Education Network (ONSEN) from a subset of the original members who were then divided into groups, including the Genomic Nursing Science Education Workgroup, which was charged with fulfilling this education mandate. The purpose of the Knowledge Matrix is not to prescribe an educational approach, as that would vary widely based on the institution, educational level, and knowledge or expertise of the faculty

teaching the content. Rather, the purpose of this article is to report the final recommendations for a set of core knowledge elements for omics nursing science.

Background

The urgent need to expand nursing education to include omics is based on the explosion of knowledge in this area of science that is being heralded as the new horizon for health care. Genomics provides a static view of an organism's genetic material (Topol, 2014); however, to understand the dynamic processes of the cell, other molecules such as RNA, proteins, and metabolites are also measured. Discoveries from the Human Genome Project led to a new collective field of study referred to as the omics, namely, genomics, transcriptomics, proteomics, epigenomics, metabolomics, and microbiomics. The term omics originated from systems-level studies involving all genes or gene products that rapidly broadened to include many other systems and interactions, such the microbiome (microbiomics) and host physiology (Tamez & Engler, 2017). Collectively, omics provides a comprehensive view of the biologic underpinnings of health and disease, which in the era of precision health captures the complexity of molecular biology and provides new tools for nurses to more accurately predict, prevent, diagnose, and treat disease and the related symptoms.

Currently nursing education does not adequately or universally contain the foundational information to allow nurses to integrate omics into their research program. Therefore, the Workgroup expanded its focus to develop fundamental core knowledge elements for omics. Recent publications support integrating omics across curricula in undergraduate and, especially, in doctoral level nursing programs (Conley et al., 2015; Henly et al., 2015).

Aims of This Initiative

The Workgroup mandate was to delineate the knowledge components necessary to integrate omics into nurse scientists' programs of research. The end product was development of a Genomics Knowledge Matrix that outlines the content underpinning comprehension of omics. The group purposively did not define the granular details of the content because they are inherently embedded in exploration of the topics, and the depth will vary widely based on learner needs and the role of the nurse scientist on a research project.

Methodological Development

Development of the Matrix was a multistep process whose inception was rooted in the branches of omics. Omics informs the types of knowledge and skills required to incorporate these sciences into a program of research. The central focus was to define factors that influenced human physiology including genomics and the microbiome, and subsequently epigenetics, proteomics, transcriptomics, and metabolomics.

Figure 1 provides a graphical representation of the central dogma of molecular biology (flowing from DNA to metabolites), the interacting omics, and examples of corresponding bioinformatics analytics. Genomics is the study of an organism's entire set of hereditary information (DNA). High-throughput sequencing captures variants that contribute to diseases and response to therapies. Environmental, behavioral, and social factors

significantly alter gene expression through physiologic pathways and epigenetics. Chromatin immunoprecipitation and bisulfite modification of DNA measure the epigenetic changes that regulate gene expression. Transcriptomics is the complete measure of genes that are transcribed into RNA at a given time in a specific cell or tissue. Driven by transcription, genes produce proteins that are the functional elements of the cell. Measuring protein levels (proteomics) and interactions can reveal molecular mechanisms of disease. Likewise, the ability to measure metabolic processes (metabolomics) reflects what has been encoded by the genome and modified by the environment. Finally, microbiomics is the study of commensal and pathogenic relationships among microorganisms living in and on humans and their contribution to health and disease. Bioinformatic analysis identifies the omic underpinnings of the risk factors, symptoms of diseases essential to evaluate treatment options unique to the individual (precision health).

Development of the Matrix began by surveying omics scientists to identify prerequisite knowledge needed to perform various functions used in their omics research. Cellular and molecular biology, system physiology, microbiology, and translational bioinformatics were identified as the minimum preparation required to understand omic science sufficiently for research integration. Knowledge in those domains provided the foundation to perform functions that ranged broadly from basic laboratory and research skills to complex higher order multifaceted tasks requiring extensive training. Similarly, how the necessary knowledge was attained ranged from basic training to formal education at the PhD level or above.

An iterative process was used to sort through the information and cluster similar concepts together. The clustered concepts were not amenable to individual leveling; therefore, a genomic knowledge continuum was developed to level across degrees of expertise using two frameworks, Bloom's Taxonomy and Webb's Depth of Knowledge (DoK; Anderson, Krathwohl, & Bloom, 2001; Webb, 1997; Table S2). Although both frameworks are cognitive classification systems, Blooms taxonomy was used to define the specificity and complexity of the research role, while Webb's DoK was used to distinguish the depth of understanding needed to function in the roles. The continuum can be applied to each of the knowledge elements defined in the Matrix as a means to categorize skills by level of expertise corresponding to the role of the nurse scientist on a study. For example, the PI of an animal model study examining the effect of a high-fat diet on coronary artery disease would perform at the applied level of the Matrix. Alternatively, a nurse running the clinical core of a human trial studying the same issue would perform at the proficient level. At that level, the individual is capable of hypothesizing cause-and-effect outcomes and revising the approach to correct problems and solve nonroutine issues as needed. However, the individual would not need to fully comprehend the scope or intricacies of the molecular processes involved in fat metabolism or perform experiments aimed at building a deep understanding of how omics influenced the physiologic mechanisms involved.

The Matrix (Table 1) identifies the knowledge necessary for nurse scientists to integrate omics into their research based on the current state of the knowledge and makes no attempts to predict future developments in the field. Following development, the Matrix underwent two reviews prior to being finalized. First, the ONSEN workgroups reviewed the Knowledge

Matrix and provided input. This was followed by a public comment period targeting education and research nursing groups, including the American Association of Colleges of Nursing, National League for Nursing, and the Council for the Advancement of Nursing Science. All comments were reviewed, and revisions were instituted as applicable.

Discussion

The Matrix elements were rooted in the notion that nursing practice is centrally concerned with optimizing health. Nursing care is required across the spectrum of health, ranging from prophylactic interventions aimed at reducing future disease states, to measures focused on stabilization of acute exacerbations of a new or existing disease, to management of chronic illness aimed at maintaining homeostasis. Each phase along the spectrum of health requires nurses to critically assess the unique set of interactive factors that can promote physiologic disturbances associated with disease, including environmental, behavioral, social, and physical aspects. Building a comprehensive understanding of how factors combine to cause physiologic perturbations expressed as symptoms is essential to accurately diagnose a disorder and develop an appropriate plan of care (Committee for Assessing Progress on Implementing the Recommendations of the Institute of Medicine Report, The Future of Nursing, 2016).

Omics provides insights about the causal pathways of disease mechanisms at the molecular level (Conley et al., 2015). For example, nurses promote activities that improve health outcomes in the individual or their offspring, such as reduced dietary fat, exercise, breastfeeding, or other health-promoting actions. Similarly, during acute illness, nursing care is focused on interventions aimed at reestablishing homeostasis, such as intravenous fluids or pharmacologic therapies. In fact, all nursing interventions or care are purposively aimed at avoiding or resolving undesirable symptoms that characterize a disease process. Omics is vital knowledge for nursing practice because it contributes understanding about molecular function that underpins disease mechanisms that manifest as symptoms. Because nurses are proximal to the patient, they are uniquely positioned to observe how disturbances in physiologic function originate or respond to a specific intervention. However, without understanding the contribution of omics to the molecular basis of those health issues, the physiological basis of a patient’s condition is also not understood to help provide the optimal interventions and to limit adverse outcomes.

The Matrix recognizes the continuum of health from molecular function through to disease manifestation. It builds on the foundational work of Henly et al. (2015) and Conley et al. (2015) and existing competencies in genetics and genomics for nursing (Consensus Panel on Genetic/Genomic Nursing Competencies, 2009; Greco, Tinley, & Seibert, 2012). The Knowledge Matrix provides detail and structure about what knowledge is necessary to integrate omics into research. However, rather than prescribe specific competencies, the Matrix was designed to present key knowledge elements needed to understand the omics that underpin the health continuum. When the knowledge concepts in the Matrix are applied to the omics knowledge continuum, the depth of knowledge required to function in a particular research role is identified.

The Matrix was designed to be flexible enough to integrate the content across all core science and molecular human-based courses in undergraduate and graduate level nursing program curricula, up to and including the doctoral (PhD) program level. Early introduction of this content in the undergraduate program across the curriculum would be advantageous because it ensures nursing students recognize the critical importance of integrating this content into care and research.

Despite recognition of its importance, it has been almost 50 years since the first recommendations to integrate genetics into the nursing curriculum (Gratz, 1968), and more than 10 years since the first edition of the genomic nursing competencies were established (Consensus Panel on Genetic/Genomic Nursing Competencies, 2006); faculty capacity to teach this content remains mostly equivalent to the students they teach (Read & Ward, 2016). As the era of precision health unfolds, integrating omics information into practice across the entire healthcare continuum will become essential (Calzone et al., 2013).

Omics is a fundamental component of precision health but is not sufficient to study on a stand-alone basis. Omics must be considered in relation to the population of interest as well as the outcome initiated by interaction with environmental, behavioral, or social factors (see Figure 1). When viewed in this manner, this definition supports early integration of this content across the curriculum at all levels, starting at the undergraduate program level.

There are limitations to the Matrix. The development of the Matrix included university and federal government experts in genomics, PhD level nursing education, continuing education for nursing scientists, and genomic competencies. Consensus was limited to ONSEN members and therefore may not reflect the broadest input. This limitation was addressed by seeking public comment that targeted nursing researchers and educators. While all input was carefully reviewed and addressed, it is possible that input from some critical individuals who did not contribute could be lacking. The Matrix is designed to be nimble because of the rapidly evolving nature of omics. This necessitates an ongoing review that the Workgroup will perform on an annual basis to integrate updated material and to strengthen the Matrix over time.

Critical to the successful implementation of the Matrix is the availability of materials to both teach and learn this content. The granular detail of the knowledge element in the Matrix is embedded within the topics requiring resources to map to the content. Mapping educational resources to each content area in the Knowledge Matrix is the logical next step in the extension of this work. Full versions of the Matrix and the knowledge continuum are open access documents that are available in the education section of the ONSEN website (http://omicsnursingnetwork.net/). The Matrix will be reviewed and updated at regular intervals to ensure that the concepts stay aligned with knowledge discovery.

Conclusions

If nursing is to continue contributing meaningfully to safe and effective precision health care, integrating omics content into nursing education and research can no longer be delayed (Williams, Feero, Leonard, & Coleman, 2017). The Matrix is the first attempt to articulate

the foundational knowledge that needs universal integration across all PhD level nursing programs in order to accelerate the inclusion of the research recommendations in the genomic nursing science blueprint. The flexibility within the Matrix also provides guidance for genomic content needed as part of a core science in all undergraduate and graduate nursing program curricula.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Resources

- Genetics/Genomics Competency Center. http://genomicseducation.net/
- ONSEN. http://omicsnursingnetwork.net/

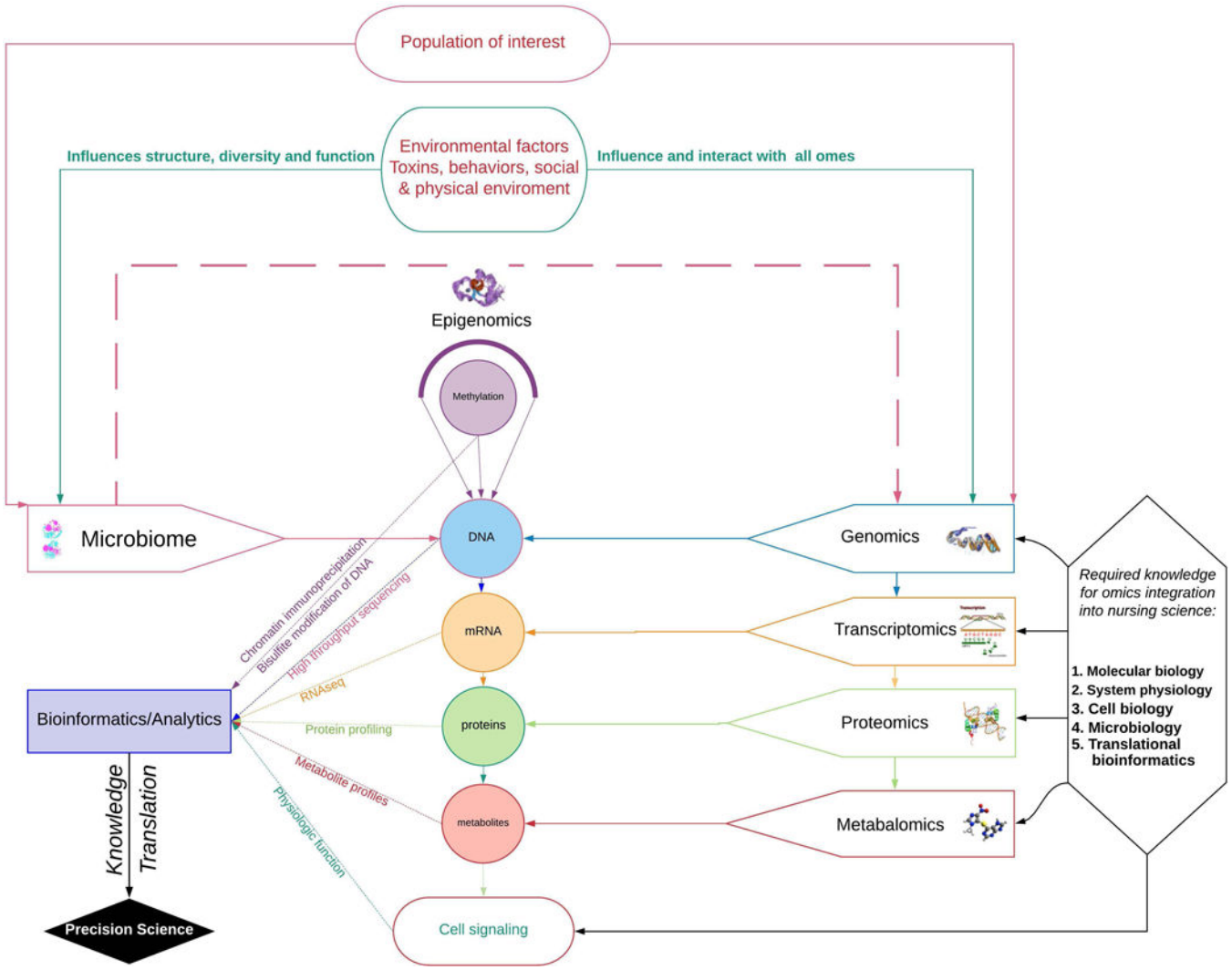

Figure 1.

Identifies the core knowledge required for integration of OMICS into nursing science, taking into account the mediating effects of the variables (i.e., environment, microbiome) that influence OMICS within the population of interest.

Table 1.

Knowledge Matrix (Abridged for Publication)

Knowledge category	Knowledge elements				
Molecular biology: Knowledge and applied understanding of the formation and function of macromolecules.					
Genomics	Genome structure/gene structure				
	Genome variation (e.g., molecular evolution, mutations, polymorphism)				
	Gene expression and epigenetics (e.g., methylation)				
Mitochondrial DNA	Structure/function				
	Variants				
Epigenetics	Methylation				
	Histone modification				
Transcriptomics	Transcription and transcription regulation (e.g., polyA sites and microRNA)				
	RNA variants, mutations, base modification				
	Transactivation response and open reading frame				
Proteomics	Translation				
	Structure and function of peptides and implication of genetic variation				
	Post-translational modifications				
	Protein–protein interaction				
	Polysome-associated messenger RNAs				
Metabolomics	Metabolic byproducts-lipidomics				
	Signaling molecules and hormones (e.g., chemokines)				
Systems physiology: Systems physiology is integrated with systems biology to provide a functionally in-depth insight into the system as a whole by combining experimental, computational, and theoretical studies to advance understanding of humans and other living creatures.					
Cardiovascular	Renal	Lymphatic	Endocrine	Musculoskeletal	Reproductive
Pulmonary	Immune	Neurology	Nervous	Digestive	Integumentary
Cell biology: Knowledge of cell formation, structure, components, and function.					
Tissue organization					
Cell type and structure	Somatic and germline				
Organelles					
Metabolism and transport	Protein, lipid, and carbohydrate metabolism (e.g., Kreb cycle, mitochondria)				
Cell communication	Cell excitability (ion channels, action potentials)				
	Endocrine, paracrine, autocrine signaling				
Growth, maintenance, repair (conception, development, aging)	Mitosis and meiosis (chromosome structure and function)				
	Stem cells and differentiation				
Immune cell function					
Microbiology: Knowledge and understanding of structure, function, and interaction between microbes living in and on the human body (microbiome). Microbiology is the study of					

Knowledge category	Knowledge elements			
microscopic organisms such as bacteria, virus, archaea, fungi, and protozoa (nature.com, 2016).				
The human microbiome	Microbiology in the postgenomic era			
Forms of microorganisms	Bacteria	Archaea	Eukaryota (animal, fungi, and plants	
	Viruses are not organisms in the same sense but are of considerable biological importance			
Bacterial taxonomy (rank-based classification of bacteria)	Kingdom	Phylum	Class	Order
	Family	Genus	Species	
Composition, diversity, complexity at different locations in and on the human	Skin			
	Respiratory track (e.g., nasal passages)			
	Oral cavity			
	Gastrointestinal tract			
	Urogenital tract			
	Body fluids (e.g., blood, breast milk, amniotic fluid)			
Function	Environmental factors that influence structure of microbial communities (e.g., antibiotics, food contaminants)			
	Immune system (adaptive, innate, antigen-antibody)			
	Novel diagnostics			
	Drug targets			
Microbes and disease (pathogen and commensal/indigenous microbes)	Routes of transmission			
	Biofilms			
	Structure, function, and dynamics			
	Virome			
Identification methods	Phenotypic analyses			
	Genetic analyses 1. DNA–DNA hybridization 2. DNA profiling 3. Sequencing			
Phylogenetic analyses (HMP developed)	16S-based phylogeny			
	Whole-genome sequence based analysis			
Interaction/interrelationships	Transcriptome and metabolome Whole and/or pan genome sequencing			
Analytic approaches and bioinformatics (translational bioinformatics): Translational bioinformatics is the growth and advancement of various data storage, analytical, and interpretive methods to enhance the conversion of progressively large amounts of genomic and biomedical data into preemptive, preventative, prognostic, and participatory health (American Medical Informatics Association, 2017).				
Big data analytics potential	Delivery of higher quality of care (e.g., evidence-based medicine)			
	Lower costs			
	Save lives			
Types of health-related data	Clinical	Behavioral	Environmental	Financial
	Diet	Administrative/operational		
Genomics and big data	Data sources and types			
	Improved analytic tools			

Knowledge category	Knowledge elements
	Increasingly rapid development of big data technology
	Need to personalize health care
	Increased amounts of genomic and other types of data
Sequencing methods	Sequencing platform, interpretation, and reporting standards
	Goal to identify genetic variants that have known impacts on health and disease
	Multiple variant results in a single gene, in multiple genes in a single disease, and in multiple diseases at the same time (e.g., gene panels)
	Multiple findings are possible, including incidental findings
	Sequencing results can have variable clinical relevance to patients' and provider's decision making and patients' outcomes.
Genomic data processing: pathway analysis and the reconstruction of networks	Functional effects of genes differentially expressed are analyzed
	Reconstruction of networks from signals measured using high-throughput techniques, analyzed to reconstruct underlying regulatory physiological networks Pathway analysis toolkits (e.g., Onto-Express Go Miner, ClueGo, GSEA, Pathway-Express)
	Reconstruction of metabolic networks toolkit (e.g., Recon 2)
	Reconstruction of gene regulatory networks methods (e.g., Boolean methods, ODE models)
Genomics study designs	Twin-based epidemiological studies (used to estimate disease heritability)
	Linkage studies (used to find disease-associated loci)
	Genome-wide association studies (GWAS) 1. Used for identification of a large number of disease-associated genomic loci 2. Group-based association tests a. GWAS analysis evaluates each single nucleotide polymorphism individually with univariate statistic b. GWAS meta-analysis methods also used c. Genomic functional annotation is required for prioritizing variants and interpreting results in association studies (statistical tools available)
	Next-generation sequencing/high-throughput sequencing: 1. Used to identify not only single nucleotide variants but also single variants 2. Targeted sequencing and whole-genome sequencing study design
	Examples of other DNA measurement techniques: 1. Copy number variants 2. Cell free DNA (e.g., tumor, mitochondrial, nuclear)
Limitations to genomics study design	Difficulty in interpreting GWAS results
	Missing heritability or large gap between proportion of variance
Limitations to data-oriented science	Sampling bias (individuals being analyzed are not representative of the broader population)
	Completeness (risk that the most important items have not been measured and/or analyzed)
	Repeatability (reproducibility is critical but difficult without controls)
	Constraints (much is not known about the data)

Note. GSEA = gene set enrichment analysis; HMP = Human Microbiome Project; ODE = ordinary differential equation.