

Workflows and Framework for Nutritional/Metabolic Phenotype/Genotype and Foods-for-Health Knowledge Integration

Matthew Lange^{1,2}, J. Bruce German¹, Jim Kaput²

¹Department of Food Science, University of California at Davis, CA, USA

²Division of Personalized Nutrition and Medicine, US Food and Drug Administration, Jefferson, AR, USA

Keywords: food, diet, health, gene, genetic, genome, genomics, metabolic, metabolism, metabolome, metabolomic, nutrition, nutritional, phenotype, ontology, public health, vocabulary

Metabolic syndrome affects more than one-third of the adults in the United States, and is known to be influenced by diet. When this basic statistic, and its public health implications, is taken into account with other diet-related illnesses, the importance of considering how different foods can improve or detract from human health could not be more clear. Yet, as food and nutrition research attempt to address their next set of challenges (post essential nutrient discovery) i.e. health improvement, performance enhancement, quality of life enrichment and prevention of diseases related to diet and food choices – it finds itself radically under-served from informatics and knowledge management perspectives.

Many life-science disciplines relating to health, nutrition, food, and agriculture have developed databases, thesauri, and/or ontologies to capture their domain knowledge. Unfortunately, the language used to describe substantially similar (even logically equivalent) concepts is often different between information systems. High throughput and omics technologies that are expanding both the amount and heterogeneity of available information – will only muddy the water unless a common unifying infrastructure is developed.

Increasing the future value of agriculture while decreasing the future cost of healthcare therefore, will depend on creating a process for generating ontological commonalities that stretch from the characterization of food production and processing; their impacts on organoleptic and nutrient characteristics of the food; food preferences and eating habits; health

characteristics driven by food choices and reflected by metabolic phenotype; the up/down-regulated pathways and single nucleotide polymorphisms that give rise to these phenotypes, and the frequencies and degree to which these nutritional phenotypes and genotypes are correlated with each other, as well as the extent to which they exist in populations.

Presented here is a suite of workflows for integrating nutritional phenotype/genotype experiment information, look-up libraries for inter-knowledge-domain queries, and an illustration of a unified framework for identifying and integrating the most important foods-for-health informata. A common system of language that describes the food – phenotype – health/performance continuum, and is shared by all relevant life-science disciplines, will provide immediate benefits in terms of:

- better understanding of the complex causes of diseases in humans,
- increased health-claims transparency and improved regulatory efficiency,
- predictive functions for individualized foods and diets,
- promoting health and well-being including people who are already healthy.

Next steps include the building of ontological maps across the identified knowledge domains that will enable cohesive semantic markup and robust food-for-health querying.