

Computational R&D in Action: Integrating Correlation and Knowledge Networks For Treatment Response Modeling and Decision Support

Erich Gombocz¹, Robert Stanley¹, Jason Eshleman¹

¹ IO Informatics, 2550 Ninth Street, Suite 114, Berkeley, CA 94710, U.S.A.
[Correspondence: rstanley@io-informatics.com]

Abstract

With computational R&D spanning multiple information domains - dynamic, flexible and extensible solutions are required to cope with the demand for knowledge management and data sharing. In addition to privacy and security concerns, analytical and demographic data from instruments, files, images, databases and the web need to be put together in the context of biological mechanisms and clinical relevance in order to generate applicable knowledge. The integration challenges become even more apparent when addressing complex medical data from hospitals, research laboratories, external facilities and public resources. Such considerations require a new approach in order to harvest data relationships and interactions in a meaningful way to generate valuable knowledge. This approach creates applicable models for effective decision making in discovery, development and personalized medicine applications.

This poster demonstrates how semantic data integration, where data are placed in their functional context with other data, changes the playing field. Semantics harmonize synonyms and nomenclature to account for common terminology and data relationships across life sciences research and clinical domains. Additionally, semantics allow for relationship mining, inference and reasoning in a systems approach. Dynamic, flexible resource description framework (RDF) databases, ubiquitous SPARQL endpoints and "linked open data" initiatives are becoming important tools and are keys for research demanding global collaboration. Graph representations of merged data, including correlation networks and formally mechanistic reference networks, allow for identifying target classifiers in discovery and focusing on relevant dimension-reduced subnets. Furthermore, knowledge from powerful systems-biology based models foster an understanding of complex biological processes (e.g., diseases & disease states, pre-disposition to certain biological responses, patient stratification for trials and treatment, predictive risk assessment for tumor growth, organ rejection, toxicity assessment and severity of drug side effects).

The poster presents several customer cases – utilizing reasoning for excipient influence on drug formulation stability despite imprecise connections; comparative assessment of effectiveness of combination prostate cancer treatment; and combinatorial biomarker-based toxicity classification. These examples demonstrate capabilities gained from semantic integration of analytical correlation networks with public knowledge networks towards a better understanding of complex biologic interactions relevant to personalized medicine. This technology is actively applied in production environments for 1.) combining and reasoning across experimental and published data to create target profiles identifying effective compounds and warning of toxic indication; and 2.) creating actionable inferences and intelligent screening patterns about disease states and treatments. These methods combine clinical, genomic and molecular phenotypic data within Applied Semantic Knowledgebases (ASK™) to assert optimum pharmaceutical development towards patient-centric personalized medicine.

The implications of using Applied Semantic Knowledgebases (ASK™) in drug development, personalized therapy, improvement of quality of life for patients and its impact on pharmaceutical development and healthcare in general are demonstrated.