

# CLINICAL DECISION SUPPORT SYSTEM FOR PERSONALIZED MEDICINE

## INTRODUCTION

Personalized medicine are strategies focused on the ability to predict which patients are more likely to respond to specific treatment modalities. And as such this approach is founded upon the fundamentals that disease biomarkers are associated with patient prognosis and response to treatments. Additionally, “omic” (DNA, RNA, protein and metabolomics profiles) and environmental factors can be associated with drug metabolism, drug response and drug toxicity, thereby demining the overall efficacy of treatment options. So as to deliver personalized treatment options to patient’s powerful informatics systems that aggregates, analyses and provides insights are necessary. iPhronesis™, by design is built to address the personalized medicine segment. This is accomplished by integrating disparate unstructured data sources such as literature, EMR records and applying powerful, meaningful analytics and providing otherwise hidden insights. This empowers healthcare providers to gain deeper understanding of the underlying pathophysiology, generate patient longitudinal views and provide new treatment options backed by evidences.

## IPHRONESIS™

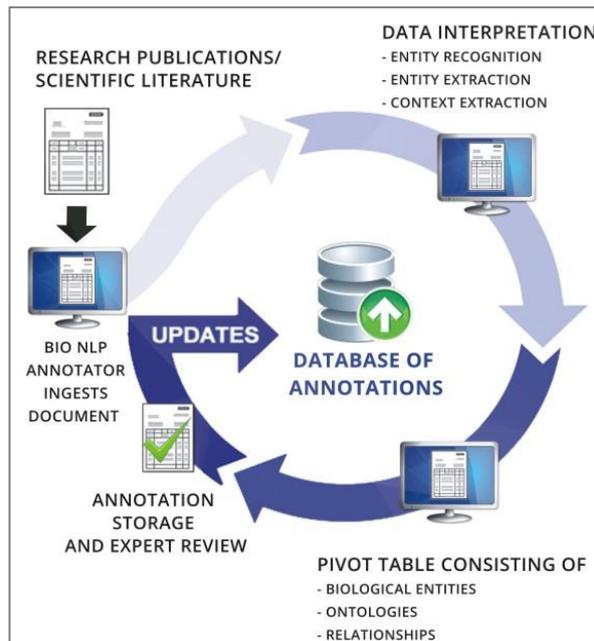
iPhronesis™ is out Knowledge Automation Platform that has all the essential modules for such end-to-end analysis and in the context of Personalized Medicine is delivered by employing the following modules.

## KNOWLEDGE AUTOMATION

Generating result is only part of the problem but combining data from different omic experiments is a complex problem. It requires that databases our different domains are integrated and the input data accurately referenced. iPhronesis™ database wrapper modules allow for easy integration with disparate datasources. Structured databases contain data that is mined by human/ computational methods, yet, these databases are not complete. To overcome this gap, iPhronesis™ offers powerful knowledge automation modules which are designed to work with unstructured data such as from experiments, scientific publications, EMR and clinical trials. By identifying relationships, entities, keywords and more from scientific literature, we generate a syntax tree using NLP technologies that

represents a structured form of unstructured document data. Further, this data is queried using NLP allowing for contextual queries and rich search results.

This approach extends the reach of conventional research by combining various datasets. For e.g. when profiling studies are conducted such as lipid profile or metabolomics, identified moieties are queried against many databases including corpora, this leads to detailed understanding of the entity such as its control mechanism, cellular pathways it participates in, its metabolism and



other entities it interacts with, databases such as ENCODE, KEGG, RNA Seq from 1000 Genomes, BIND, MINT and SIDER are useful. With this information, iPhronesis™ generates a molecular signature that comprises its genomics, proteomic, metabolomics and when available phenotypic information. Which is mathematically represented as networks where the connections specify the type of relationship and its relevance. Such logic is extended to include data of all types and this is accomplished by using other modules of iPhronesis™.

## LONGITUDINAL VIEW

So that we empower healthcare providers with all the tools to make mission critical decisions, a patient longitudinal view is required. This is not just a graphics view but is rooted into being able to aggregate data from complex backend systems and the knowledgebase that we generate as stated above. iPhronesis™ used EMR, imaging and other disparate unstructured data to generate longitudinal views. This view represents all the instances the patient is seen by a healthcare provider and all medical details associated with it. Machine learning algorithms are used to generate novel insights as described below.

