Sophic Releases Cancer Biomarker Database

By Kevin Davies

July 2 | Following the completion of a three-year small business innovation research (SBIR) grant awarded by the National Cancer Institute, Sophic has released SCan-MarK Explorer -- a manually curated biomarker database.

SCan-MarK Explorer (Sophic Cancer Biomarker Knowledge Environment) is configured to support basic research, diagnostic development, drug discovery and personalized medicine.

"We'll continue to develop this," says Sophic's Pat Blake. "It's content-based. We have a manual curation team working on full-text papers to identify high potential candidate biomarkers."

The resource was developed with two SBIR awards worth $900,000 over the past three years. It is focused on five cancer disease types: breast, ovarian, colon, non-Hodgkin's lymphoma, and melanoma.
"Rather than boil the ocean, we decided to focus on these five deadly disease types," says Blake. "What differentiates us is that we've integrated the information into patient data from The Cancer Genome Atlas, so we're bridging into patient information from sequence and into pathways (through Reactome). We've also wrapped about 30 databases around this core such as mutations (COSMIC), sequence (dbSNP), and drugs (Drugbank)."

The database has been integrated into the BioXM Knowledge Management Software developed by Sophic's business partner, Biomax. "If you take their platform and add our content, that's where the benefit comes from," says Blake.

For the project, Sophic scientists extracted details for up to 33 often elusive Critical Data Elements (CDEs) from each paper. (A CDE represents evidence intended to improve a researcher's confidence that potential biomarkers will deliver value to the broad cancer community.) The CDEs were integrated into computational Sophic Cancer Biomarker Objects (SCBOs) that allow scientists to find correlations between valid semantic and scientific relationships between CDEs, SCBOs, enrichment databases and clinical information.

BioXM uses data models and ontologies to enable scientists to map complex biomarker knowledge networks. An intuitive Wiki interface allows researchers to visualize networks of valid semantic and scientific relationships connecting SCBOs, pathways, near‑neighbors, sequence data, mutations and drug compound information.

Sophic advisory board member K. Stephen Suh, director of the genomics program and tissue bank at Hackensack University Medical Center, has taken tissue from cancer patients to identify biomarkers for drug response. "We provided him with a shortlist for the 20 best candidates for colon cancer biomarkers," says Blake. "They've since found a very interesting colon cancer marker, which has been sent down to MD Anderson for further analysis."

Scan-MarK Explorer is available as an online hosted software-as-a-service for $4,800/seat. Similar to resources from Ingenuity or Thomson Reuters, Blake says users can't just take the data but they can use it for reference and can upload their candidate biomarkers to explore correlations with TCGA, Reactome, COSMIC and other databases. Potentially interested users can obtain a 2-week free trial at
www.sophicalliance.com

"This is to get us market share and visibility, but we're also selling to commercial enterprises," he notes. Last year, Sophic scientists (Blake *et al*.) published a paper in *The Cancer Journal*, which describes the current state of oncology informatics and lays out Sophic's vision and development strategy for SCan-MarK. Blake credits his organization's scientific advisory board, including principal scientists from NCI, big pharma, and cancer centers for helping to steer the project.