Today it takes a significant amount of time and a team of specialists to examine a piece of cancerous tumor and determine whether it was caused by harmful genetic mutations. But having that information can help better determine the type of cancer, how advanced it is, and what the most effective treatment might be.

The Solution

University of Michigan Medical School faculty, Mark Kiel, M.D., Ph.D., Kojo Elenitoba-Johnson, M.D., and Megan Lim, M.D., Ph.D., are the award-winning team of pathologists who recognized a need to more quickly interpret genetic information — to find informative mutations among the three billion bits of DNA that make up a patient’s genome. As a result, they developed GENOMENON, an innovative suite of software tools that automates the process, focuses on what the researchers call “clinically important mutations,” and makes information available to doctors in just minutes.

The team has identified the limitations to automation of genome sequence interpretation and addressed these shortcomings using a combination of innovative approaches in their products that democratize genome-sequencing interpretation.
GENOMENON is an innovative suite of software tools (SAVANT, PRODIGY, and MASTERMIND) that speeds discovery work and diagnosis by allowing rapid, automated, and accurate analysis of next-generation sequencing data.

**Significant Need**
Doctors spend a lot of time tediously reviewing next-generation sequencing data for genetic mutations. This enormous amount of work is frustratingly inefficient, extremely expensive, and prone to human error.

**Compelling Science**
- **SAVANT** – Analysis software for molecular diagnosticians, pathologists, and geneticists that automatically identifies clinically-actionable genetic variants from gene panels, exomes, or entire genomes from individual patients.
- **PRODIGY** – Analysis software for research applications that automatically identifies disease-causing genetic variants from complex, multi-sample datasets in academic- and pharmaceutical-scale research projects.
- **MASTERMIND** – Comprehensive, clinically-curated knowledge base of variant data from millions of primary scientific articles.

**Competitive Advantage**
GENOMENON automates the genome interpretation process, helping doctors find clinically important mutations and providing results in just minutes, as opposed to manual review which can take several hours per data point.

**MTRAC Project Key Milestones**
- Assembly and testing of data processing algorithm (SAVANT/PRODIGY)
- Collection and analysis of external datasets
- Sequencing of test samples
- Development of MASTERMIND backend architecture
- Optimization of back end data processing (SAVANT/PRODIGY)
- Graphical user interface design (SAVANT/PRODIGY)
- Implementation of software front end (SAVANT/PRODIGY)
- Company Launch

**Overall Commercialization**
- **Commercialization Strategy**
  Business model is software as a service. Researchers to pay per sample and clinical health systems to purchase annual licenses.
- **Intellectual Property**
  Two patents pending covering database assembly and data processing algorithm. Licensing arrangement with University of Michigan.
- **Regulatory Pathway**
  FDA approval unlikely to be required for clinical genomic sequencing decision support software.
- **Completed Business Formation**
  Internal team assembled, website launched.
- **Engage Investors**
  A number of angel and venture investors have expressed interest in GENOMENON.

**MTRAC Funding and Guidance**
MTRAC funding and guidance provided the resources we needed to finalize our first software product and produce demonstration data to present to our first customers.

**Mark Kiel, M.D., Ph.D.**
**Megan Lim, M.D., Ph.D.**
**Kojo Elenitoba-Johnson, M.D.**