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POWERING EVIDENCE-BASED GENOMICS

Genomenon Awarded Phase 2 NIH Grant to Apply Artificial Intelligence to Genomic Interpretation

Small Business Innovation Research Grant Accelerates Automated Genomic Literature Curation

ANN ARBOR, Mich., July 31, 2018 - Genomenon, the leading genomic data search company, today announced that it was awarded a Phase 2 Small Business Innovation Research (SBIR) grant by the National Institutes of Health (NIH). The grant was awarded to develop and apply machine learning (ML) and artificial intelligence (AI) algorithms to variant interpretation, the single biggest hurdle in scaling the adoption of genomic sequencing in both clinical and precision medicine applications.

Through this grant, Genomenon will be applying advanced ML and AI algorithms to its Mastermind genomic search database to provide suggested interpretations of genomic variants.

Genomenon has taken an innovative new approach when it comes to applying AI to genomic data sets. Many companies have applied natural language processing (NLP) and ML to genomic literature with little success. Genomenon has avoided the pitfalls of NLP, as there is nothing “natural” about the dozens of different ways that authors may describe genetic variations in the scientific literature.

Instead, the company has developed and patented its proprietary Genomic Language Processing (GLP) technique to find every disease, gene and variant in over 6 million full text genomic articles. Rather than applying ML and AI in a wholesale fashion to its search engine database, Genomenon uses specific GLP algorithms to refine the quality and priority of each individual search result. This leads to results that are both highly sensitive and highly specific in finding clinically relevant citations tied to a patient’s DNA.

The grant from NIH will help Genomenon further automate the literature curation process by applying GLP across American College of Medical Genetics and Genomics / Association of Molecular Pathologists (ACMG/AMP) guidelines to determine variant pathogenicity. Unlike some black-box solutions applying AI, Genomenon produces transparent results, displaying both the GLP evidence underpinning its conclusions and the citations and cited sentences that go into variant scoring.

“The NIH has been a key partner in helping us tackle the single biggest barrier at the center of genomic medicine – automating variant interpretation based on the scientific

evidence from the medical literature” said Mike Klein, CEO of Genomenon. “We are excited about the results that we are able to produce based on the work funded by this grant.”

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About Genomenon:

Genomenon is helping doctors, clinicians and researchers make sense of patient DNA data. With the world’s only comprehensive genomic-specific search engine, Genomenon helps doctors connect diseases and DNA profiles to the most impactful scientific genomic research to diagnose and treat patients. Our Mastermind Genomic Search Engine has the world’s largest collection of medical articles cataloguing the genetic relationships between DNA and human diseases, including cancer. Genomenon’s solutions lower the cost of genetic tests, deliver faster diagnoses, and help ensure that no data is missed that can save a patient’s life.

For more information, visit www.genomenon.com or email hello@genomenon.com

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