Verge Genomics Announces Publication of New Approach for Uncovering Novel Drug Targets from Human Genetics

- Verge's "Bayesian Annotation Guided eQTL Analysis (BAGEA)" technology predicts how genetic variants may lead to disease, a key bottleneck in genetics-driven drug development
- Allows the company to translate large human genetic datasets into biological insights that will accelerate drug development

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SAN FRANCISCO--(BUSINESS WIRE)--Verge Genomics, a drug discovery company developing therapies for neurological diseases by integrating a unique all-in-human genomic platform with machine learning, announced today the publication of an original scientific research paper in the journal PLOS Computational Biology, a journal of the Public Library of Science in association with the International Society for Computational Biology.

Over the last decade analysis of human genetic data has revealed hundreds of genetic variants associated with disease. Yet, a major bottleneck to using this data for drug development is understanding how changes in DNA sequence ultimately result in disease, often requiring long and expensive experimentation. This paper describes a novel computational method developed at the company named BAGEA that uncovers the functional impact of genetic mutations using only the genome sequence. The paper illustrates BAGEA's ability to predict the effects of genetic variants and validates its predictive power in a number of tissues and cell types.

"Designing medicines that functionally counteract known genetic causes of disease is core to our strategy to unlock clinical success in neurodegeneration. Key to this strategy is understanding the functional impact of disease causing genetic mutations, which may lead to therapies that are effective in more patients than those focused solely on correcting the mutation," said Alice Zhang, CEO and Co-Founder of Verge Genomics, "We are excited by this novel statistical approach that allows us to more effectively mine large human genetic datasets to identify previously undiscovered drivers of disease. The peer-review and publication of this paper is an important independent examination of our platform and approach."

Verge develops medicines that functionally counteract known genetic mutations in defined patient populations, but with broad translational potential. Its platform is designed to identify convergent pathways shared by multiple genetic drivers of disease by integrating multiple types of human data. The paper published in PLOS Computational Biology by Lamparter *et al*. describes the development of a method to map the consequences of genetic variation, including gene expression, enabling a better understanding of the pathways through which genetic mutations may act to cause disease. Furthermore, the method predicts the directional impact of each genetic variant, which enables scientists to develop more precise therapeutic hypotheses about whether inhibition or activation is appropriate for treating disease.

“Our new approach allows us to combine gene expression data with epigenomic data giving us a new understanding of gene regulators, their importance in given cell types, and whether they act as gene activators or gene inhibitors” said Victor Hanson-Smith, Head of Computational Biology at Verge,. “This information will allow us to uncover new biological targets that can be used to develop drugs that either enhance or inhibit genes involved in disease processes. This is the first of several methods we have been developing to further our mission of bringing new treatments to patients with neurological diseases like ALS and Parkinson’s Disease.”

The paper published in PLOS Computational Biology is titled, “A framework for integrating directed and undirected annotations to build explanatory models of cis-eQTL data”, and can be accessed here.

About Verge Genomics

Verge is focused on developing therapeutics for neurological diseases using human genomics to accelerate drug discovery. Verge has created a proprietary all-in-human platform, generating one of the field’s largest and most comprehensive databases of ALS and Parkinson’s Disease patient genomic data. The Company is led by experienced computational biologists and drug developers who are successfully advancing therapeutic programs in ALS and Parkinson’s disease toward the clinic. For additional information, please visit www.vergegenomics.com.

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