GENOOX

TRANSFORMING COMPLEX DATA
INTO CLINICAL ANSWERS

END OF THE DIAGNOSTIC ODYSSEY: Resolving Old Cases in Minutes with Genoox

THE EDITH WOLFSON MEDICAL CENTER

The Genoox platform was employed to reanalyze a rare disease case which had remained unsolved for years, and achieved astonishing results in a matter of only minutes.

We are in the explosive era of a rapidly evolving genomics space. New discoveries are found every day and new methods are being published at a pace that is increasingly difficult to manage. Even with the gigantic strides made in recent years, less than 30% of familial cases are genetically resolved with most other cases remaining open. Reanalyzing these cases periodically is critical, as new discoveries may shed new light on any given case delivering an actionable clinical diagnosis.

The Case

The index patient is an 8 year-old girl that presented severe epileptic encephalopathy from infancy. Due to multiple seizures and low compliance to medications, a psychomotor development halt was observed. Both parents were healthy.

In their search for an answer, the child was taken to numerous clinics. Whole exome sequencing (WES) conducted five years ago (2012) was followed by direct sequencing of SCN1A gene, which is formerly known to be associated with early infantile epileptic encephalopathy and therefore found to be a good candidate gene. Both WES and direct sequencing did not reveal any pathogenic mutation.

The Result

The breakthrough came when one of the physicians contacted Genoox with a request to assist in the detection of the driver mutation responsible for causing this rare syndrome. The sample data was uploaded to the Genoox platform which detected a heterozygous variant in the splicing region of SCN1A (c.2589+3A>T) within a matter of minutes. The mutation was found close to a homopolymer region which renders alignment and variant calling in this region complicated, and therefore been missed by previous analyses. Employing proprietary machine learning algorithms, the Genoox classification engine ranked the variant with high relevance to the phenotypes and its pathogenic impact. The mutation was later confirmed and validated by family segregation.

Key Takeaways

Today, many cases remain unresolved during initial analysis and are later resolved performing reanalysis. In most cases this requires the application of a more advanced bioinformatic process which can reveal new discoveries overlooked by older technologies. Additionally, newly published discoveries are not always available for bioinformaticians. New publications can shed light on recent discoveries and variants of previously unknown significance (VUS) can be re-classified as known pathogenic variants.

Genoox offers a unique resource in tackling these challenges, removing the genome interpretation barrier. The Genoox platform automatically keeps up to date with millions of in-house and public data points, enabling researchers and medical experts to obtain genomic insights rapidly and accurately. The platform's data mining tools process, store, and uncover insights that can reveal previously hidden gene mutations, and classify complex relationships.

The Genoox platform employs sensitive statistical modeling algorithms for superior bioinformatics, using a proprietary data structure that allows users to detect variants with better accuracy, while utilizing historical data. Our advanced algorithms allow for extremely high variant detection sensitivity, providing an exceptional level of confidence with variant calls as well as a significant reduction in sequencing costs.

Our method ensures fast turnaround time for rapid discovery and accurate clinical interpretation by enabling clinicians and researchers to perform complex genomic analyses, uncover hidden clinical insights and make new discoveries with only a few mouse clicks.