ENPICOM

www.enpicom.com

ENPICOM
DECODING THE IMMUNE SYSTEM

Decoding the immune system through immunomics data analysis

ENPICOM's ImmunoGenomiX (IGX) Platform offers state-of-the-art immunomics data analysis, management and visualization for academic researchers, drug developers, and related service providers.

The immune system has always been central to understanding and treating infectious diseases and autoimmune conditions, and in recent decades has been recruited to fight cancers in immunotherapies from vaccines and bispecific antibodies, to a growing range of cell-based therapies. ENPICOM, an innovative bioinformatics software engineering company, is dedicated to supporting immunological research in academic research centers, and improving and accelerating the discovery and development of novel vaccines and immunotherapies by biopharma companies, through ground-breaking products and customized solutions for immunomics data analysis.

ENPICOM, based in the Netherlands, was founded in 2017, and today employs more than 25 scientists and software engineers. Last year, ENPICOM was listed as one of the top 15 most promising biotech start-ups in Europe by StartupCity, and this year was recognized as one of the 50 fastest-growing companies working in the field of data science in the Netherlands.

Understanding the adaptive immune system

One of the major challenges of decoding the immune system is characterizing an individual's immune repertoire: the genetic code of the trillions of T and B cell receptors of the adaptive immune system. The DNA/RNA data generated by immune repertoire sequencing is the most informative way to probe the immune system, but the millions of short sequencing reads it generates per sample—derived from highly variable receptor-encoding regions of the genome—are impossible to analyze with standard sequencing algorithms.

With the growing demand for personalized immunotherapies and accessible vaccines, especially against threats such as COVID-19, life scientists increasingly need new and efficient data management, analysis and integration tools to gain more insights into the adaptive immune system.

ENPICOM's solution: the IGX Platform

To address this need, ENPICOM has brought together immunological expertise and innovative bioinformatics methods with robust and scalable software engineering to develop the IGX Platform, the first end-to-end solution on the market for the management, analysis and visualization of immune sequencing data. IGX combines proprietary sequence-analysis algorithms, an intuitive user interface and several analysis apps to enable scientists in academic research centers and biopharmaceutical companies to accurately interpret large-scale repertoire data,
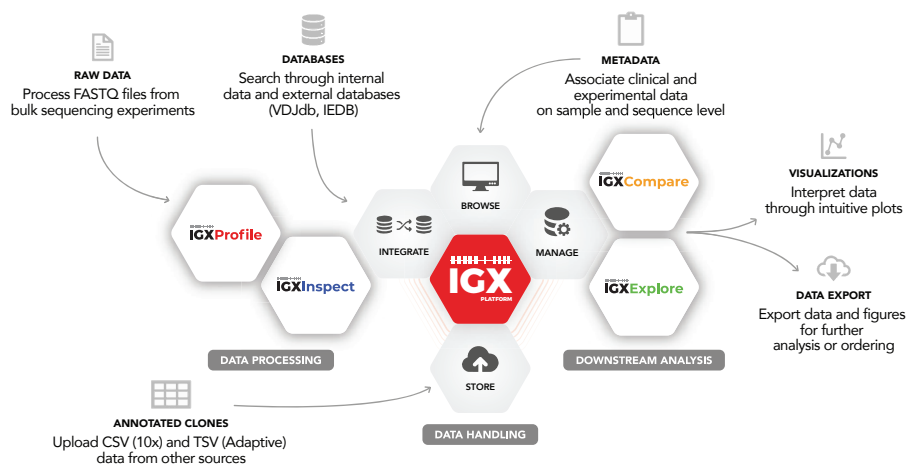

Fig. 1 | ENPICOM's IGX Platform overview.

speed up the extraction of biologically and clinically relevant information, and, most importantly, unlock insights that otherwise would remain obscured.

The IGX Platform is scalable by design, so users can browse hundreds of millions of sequences in internal and public databases with confidence and ease. In addition, IGX allows researchers to integrate data with (meta)data from other domains, clinical as well as experimental. IGX requires no programming, so scientists can focus on research rather than coding (Fig. 1).

The IGX Platform can be used with any sequencing technology, and can handle T and B cell receptor sequencing data derived from DNA or RNA, and prepared with any protocol. Additionally, IGX can store, annotate and analyze paired receptor chains, and includes new search options tailored to the structure of paired receptor data, making it easier than ever to find and analyze single-cell data.

Instead of using folders or groups to organize immune repertoire data, the IGX Platform offers an extensive, customizable tagging system that means data can be annotated at any level, providing limitless possibilities for organizing repertoire sequencing data in a meaningful way. Tags are native to the IGX user experience and offer an intuitive way to add metadata to repertoire sequences and organize them without endless layers of folders.

In immunomics, finding and selecting relevant clones is similar to finding the proverbial needle in a haystack, so it is essential that scientists have robust systems to explore, prioritize and select clones based on structured metadata and sequence information. The IGX Clone Browser, a powerful tool

for exploring immune sequencing data, helps users to find what they are looking for, and was designed from scratch to provide a structured overview of all data, while allowing powerful and highly customizable searches. Users can look for specific patients, genes or sequences of interest, while taking into account paired chain information, and filters can be applied for various purposes—for example, finding the right samples for downstream analysis, or for browsing specific clones of interest.

IGX's Clone Browser integrates a number of apps independently developed by ENPICOM that enable a range of analyses and visualization methods, allowing users to create reproducible, end-to-end workflows tailored to specific research questions.

The IGX Platform is not only valuable for researchers working on basic immunological questions in academic settings and R&D scientists developing new drugs in the biopharmaceutical sector, but also provides an ideal way for sequencing service providers to share information with their customers. ENPICOM welcomes discussions with all potential end-users about how the IGX Platform can help them achieve their goals in immunomics data analysis and management.

CONTACT

Svitlana Lozova
Marketing Communications Manager
ENPICOM
's-Hertogenbosch, the Netherlands
Tel: +31 85 250 0 575
Email: communications@enpicom.com