

Scientists develop DNA sequence analysis software for immunity research

July 28 2016

A team of scientists from the IBCh RAS Laboratory of Genomics of Adaptive Immunity has developed VDJviz – a multifunctional browser designed to work with large volumes of data produced using modern DNA sequence analysis. This breakthrough development could be instrumental in accelerating the data analysis process for a the new field of immunogenetics, which will yield treatments and therapies for serious diseases associated with disruptions in the formation and normal functioning of the adaptive immunity system.

The program is available [here](#). The results of this research work were published in *BMC Genomics*.

"VDJviz got its name from certain groups of genome fragments from which mature B [receptor genes](#) and T-cells are formed for the [immune system](#), as well as antibodies—immunoglobulins, which are soluble forms of the antigen-recognizing B cell receptors—V – variable, D – diversity and J – joining," says Ivan Zvyagin, researcher IBCh RAS. "This complex process of maturation of these genes, called V (D) J recombination, underlies the formation of the adaptive immune system – the body's defense system, which is theoretically capable of resisting any foreign pathogenic organism, as well as preventing the development of tumors."

During VDJ recombination, the V, D and J groups are joined together using one fragment from each to form a unique sequence for encoding the antigen-recognizing part of the receptor. This process occurs in the

body multiple times during the maturation of each of the B or T cells, resulting in the formation of a huge set of B- and T-cells, each of which has a unique antigen-recognizing receptor. The entire set of possibilities for the structure of these receptors is called a B- or T- cell repertoire.

Recent advances in molecular biology make it possible to determine the encoding sequence of these hypervariable receptors and immunoglobulins. Rep-Sec is a prime example of this sophisticated technology. After processing the data using various tools, researchers make use of bioinformatics to restore the cell repertoires of the adaptive immune system. Obviously, the possible sequences and combinations are so diverse that analyzing the data without using specific applications is difficult and time consuming. Therefore, VDJviz also helps scientists perform their tasks much more quickly and efficiently.

Depending on the preferences of the researcher, the program can be installed on any suitable desktop computer. There is also an online version. The program's main advantages include information support for the six most popular tools for processing Rep-Seq data (MiTCR, MIGEC, MiXCR, IgBlast, IMGT HighVQuest, ImmunoSEQ), a user-friendly GUI, the ability to provide a visual representation of the characteristics of hypervariable receptor sequences, the ability to use the samples to make a variety of comparisons based on a host of parameters and an easy data export process. Free for academic projects, the program does not require any special programming skills, and any biologist can access it.

"Our program optimizes the work performed by researchers and helps develop and test new hypotheses on the formation and operation of the adaptive immune system," Ivan says. "Most importantly, Rep-Seq data analysis in immunology and immunogenetics is important not only for theoretical research, but also for practical problems. The developers of the program believe that new knowledge in this area is vital for the

development of new therapies for many serious autoimmune and oncological diseases, as well as allergies."

More information: Dmitriy V. Bagaev et al. VDJviz: a versatile browser for immunogenomics data, *BMC Genomics* (2016). [DOI: 10.1186/s12864-016-2799-7](https://doi.org/10.1186/s12864-016-2799-7)

Provided by Institute of Bioorganic Chemistry of the Russian Academy of Sciences

Citation: Scientists develop DNA sequence analysis software for immunity research (2016, July 28) retrieved 24 April 2024 from <https://medicalxpress.com/news/2016-07-scientists-dna-sequence-analysis-software.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.