Mathematical Methods and Models in Biosciences
June 15–20, 2025, Sofia, Bulgaria
https://biomath.math.bas.bg/biomath/index.php/bmcs
Biomath Forum

Application of Graphs for System Level Analysis of the Repertoire of Antibody Reactivities

Anastas Pashov[1], Peter Petrov[2]

[1]Institute of Microbiology
Bulgarian Academy of Sciences, Bulgaria
a_pashov@microbio.bas.bg

[2]Institute of Mathematics and Informatics
Bulgarian Academy of Sciences, Bulgaria
pk5rov@gmail.com

The current understanding of antibodies in immunology presents a limited paradigm that overlooks crucial aspects of their diversity. Our studies introduce an innovative analytical framework that integrates phage display, mimotope, igome, and high-throughput binding assays into a unified pipeline for system level analysis of the antibody repertoire.

We employ graph-based formalisms to analyze the data, aligning with the intuitive concept of antigen and antibody reactivity landscapes. This approach reveals novel insights into the relationship between public specificities and idiotypic interactions across various pathologies.

The resulting innovative analytical paradigm yields new information about the relationship between public specificities and idiotypic interactions in the context of different pathologies. Different clustering algorithms and spectral analysis helped in finding large scale structures in the repertoire. This information informed filtering and recursive feature elimination algorithms for dimensionality reduction in the design of proof of principle machine learning models.

Thus, we could show the potential of this approach as a novel diagnostic platform in cancer (brain tumors), autoimmune disease (antiphospholipid syndrome), neurodegenerative disease (Alzheimer's disease and frontotemporal dementia), and probably in all pathologies involving inflammation and immune disturbance.

Keywords: antibody repertoire, graphs, bioinformatics, machine learning