IgEvolution: A Novel Tool for Clonal Analysis of Antibody Repertoires

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BACKGROUND

Constructing antibody repertoires is an important error-correcting step in analyzing immunosequencing datasets that is important for reconstructing evolutionary (clonal) development of antibodies. However, the state-of-the-art repertoire construction tools typically miss low-abundance antibodies that often represent internal nodes in clonal trees and are crucially important for clonal tree reconstruction. Thus, although repertoire construction is a prerequisite for follow up clonal tree reconstruction, the existing repertoire reconstruction algorithms are not well suited for this task because they typically miss low-abundance antibodies that often represent internal nodes in clonal trees and are crucially important for clonal tree reconstruction.

TECHNOLOGY DESCRIPTION

Researchers at UC San Diego have developed a novel software tool, designated IgEvolution, to study and analyze antibody repertoires. It was tested on ~100 real datasets (the largest dataset contains 2M reads) and, from this point of view, presents an improvement upon the state-of-the-art. In particularly, IgEvolution detects important mutations in antigen-specific antibodies, identifies antibody sites with high mutability, and reveals antibody sites under high selective pressure. This part of the tool is novel and was not done before.

APPLICATIONS

The tool can be used for computational design of antibody drugs, analysis of vaccine efficacy, and humanization of nonhuman antibodies.

ADVANTAGES

Clonal analysis has the potential to reveal errors in the constructed repertoires and contribute to constructing more accurate repertoires, we advocate a *tree-guided construction of antibody repertoires* that combines error correction and clonal reconstruction as interconnected (rather than independent) tasks. We developed the IgEvolution algorithm for simultaneous repertoire and clonal tree reconstruction and applied it for analyzing multiple immunosequencing datasets representing antigen-specific immune responses.

STATE OF DEVELOPMENT

The inventors demonstrate that analysis of clonal trees reveals highly mutable positions that correlate with antigen-binding sites and light-chain contacts in crystallized antibody-antigen complexes. They also demonstrate that this analysis leads to a new approach for refining positions of complementarity determining regions (CDRs) in antibodies.

INTELLECTUAL PROPERTY INFO

Copyright software available for licensure.

RELATED MATERIALS

- Yana Safonova and Pavel A. Pevzner. IgEvolution: clonal analysis of antibody repertoires. Posted August 27, 2019. bioRxiv 725424; doi: https://doi.org/10.1101/725424 - 08/27/2019

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OTHER INFORMATION

KEYWORDS

Software, antibody repertoires, immunosequencing, repertoire sequencing, antibody clonal lineages, antigen-specific immune responses, somatic hypermutations.

CATEGORIZED AS

- **Computer**
  - Software
- **Medical**
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