

Advancing Vaccine Research Through Sequence Analysis



Link: bit.ly/VAXPATH

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CONTEXT: WHY THIS MATTERS

Understanding how the immune system evolves is key to developing better vaccines.

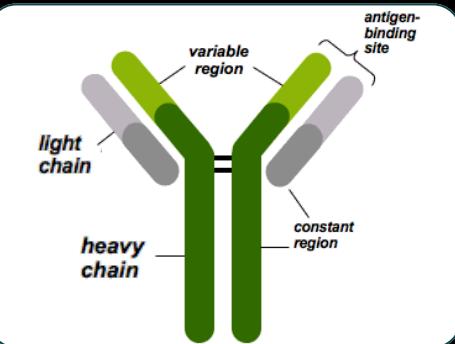
When we get sick or vaccinated, our B cells produce antibodies that improve over time. Researchers use antibody sequence data to study this – but most tools for analyzing these sequences are hard to use, not scalable, and require programming skills.



SCIENCE BEHIND OUR PROJECT

Antibodies are made of two chains: a heavy chain & a light chain. These chains change through somatic hypermutation, a natural process that helps the immune system improve its response.

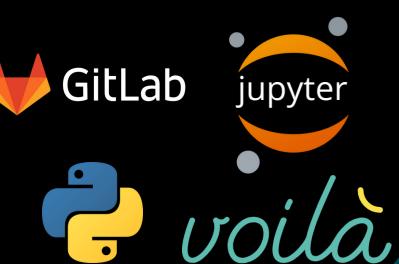
We focus on visualizing how these changes occur over time.



OUR SOLUTION

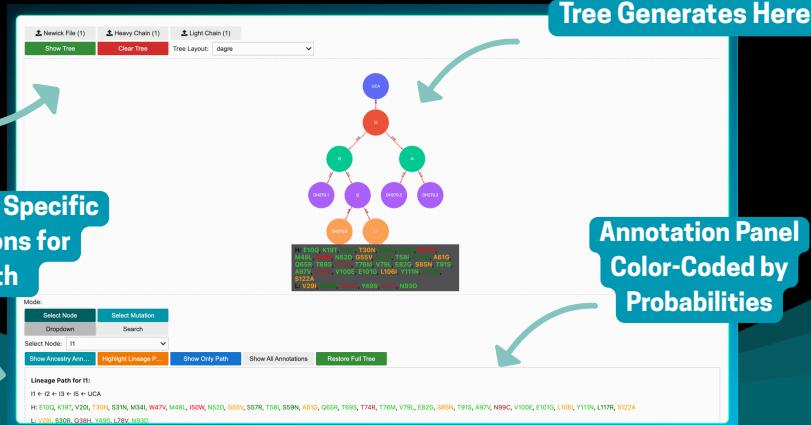
We built an interactive web tool that helps researchers:

- Upload antibody sequence data (FASTA + Newick)
- Generate interactive clonal lineage trees
- Visualize key mutations in heavy and light chains
- Track how antibodies change over time



User Uploads

Search & Click on Specific Nodes/Mutations for Lineage Path



Tree Generates Here

Annotation Panel Color-Coded by Probabilities

NEXT STEPS

- Integration with Armadillo tool
- Gather feedback from immunology researchers for iterative design
- Potential Data Storage feature
- Update visualization option