Immune Epitope DataBase (IEDB) Exercises

The Immune Epitope DataBase (IEDB) is a very useful resource for researchers of immunology and immunoinformatics. It is a highly organized database of epitopes (or more precisely: epitope assay results) that has a user-friendly search interface. It is maintained by the La Jolla Institute for Allergy and Immunology and has a dedicated team of curators and bioinformatitians that have mined the immunological literature. The IEDB is up to date with the immunological literature (within its scope) and is therefore a good place to get an idea of what has been studied and to what extent. Aside from this, they provide prediction tools that can be very useful when no experimental evidence exists. Best of all, it's all free (for academics)!

Today we will focus on building experience in querying the IEDB, so that you may search for data in your own research. Start by going to the IEDB home page.

Sequence Query

The goal here is to introduce you to the basic functionalities of the IEDB.

In the home page search (center field on homepage), in the 'Epitope' field, select 'Linear Epitope', 'Exact Match' and enter in the text box: 'ASNENMETM'. Leave remaining parameters as default and select 'Search' in the bottom of the page.

- **Q1: How many epitopes do you find?**
- **Q2: From which antigen molecule do the epitopes come from? What about the antigen organism?**

Under the 'Epitopes' search tab, inspect the column '# References' and note that the output table is sorted by this column. Click the column header names to change sorting order. Sort again by number of references and click the 'Details' number for the epitope with most references. This leads you to a summary page for said epitope. Note the tabulated T Cell Assay Results.

- **Q3: What is the number of positive results for the 'qualitative binding' assay? How about for 'pathogen burden after challenge'?**

Back on the top of the results page, click around the different tabs ('Epitopes', 'Antigen','Assays'...) for different vantage points of the results.

- **Q4: How many entries are under the Assay tab?**

The 'Assay' tab result can be further divided by tabs right above the results table ('T Cell Assays', 'B Cell Assays', 'MHC Ligand Assays').

- **Q5: How many 'MHC Ligand Assays' have been performed on the epitopes in question?**

Applied filters are shown under 'Current Filters' at the top of the results page. Try removing the 'Positive Assays Only' filter by clicking the red 'X' and pressing 'Search' (Top Left). You have now included negative results in your search.

- **Q6: How many negative 'MHC Ligand Assays' are added by doing this?**

You can add the ’Positive Assays Only’ filter back by refining your search. On the left side of the results page note the search fields (’Epitope’, ’Antigen’, ’Receptor’, ’Assay’...). Scroll down to the ’Assay’ field and select ’Positive Assays Only’. Scroll back to the top and select click ’Search’.

- **Q7: What is the ’MHC Ligand Assay’ count now? Does it match your initial count?**

Finally, inspect the results under the ’Reference’ tab. Click the PMID column entry for any row. This is a PubMed link to the reference. Back in the result table, sort the resulting references by the date by clicking the ’Date’ column header.

- **Q8: What is the time span of publications for the epitopes?**

Broaden your search. In the ’Epitope’ search field on the left of the results page, change the ’Exact Match’ search to a BLAST search with a 70% sequence homology.

- **Q9: How many Epitopes does your search yield?**

Pro tip: Start with a broad initial search (e.g. all T Cell epitopes) from the home page and then add filters in steps (in the search field on left of results page). This way you can get a feel for which filter is most restrictive (where do you lose most epitopes). This is also helpful for debugging a wrong search