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Using Big Data to Understand Immune Receptor Biology

# Introduction

What is immunoprofiling

What are we trying to do

# Background

1. Setting things up
2. Obtain / Access Data
3. Data Cleaning and Prep
4. Analyzing Datasets
5. Presenting Data

**Setting things up**

* Assigned Roles- Writer
* Jetstream
* Jupyter Notebooks
* Databases (benefits)

iReceptor, NCBI, SabDab, IEDB (ab-epitope)

* Python/Unix command line processing of data source content
* Epitopes on lung cancer cells - IEDB Immune Epitope Database
* Locate dataset(s) (Tumor Infiltrating T Cells) for further analysis

In today's meeting, we focused on utilizing big data to gain insights into immune receptor biology. We began by setting up the necessary infrastructure, assigning roles, and discussing the tools we will be using, including Jetstream, Jupyter Notebooks, and various databases such as iReceptor, NCBI, SabDab, and IEDB (antibody-epitope).

Data acquisition and preparation were essential aspects of our discussion. We obtained and accessed relevant datasets. Additionally, we explored datasets related to Tumor Infiltrating T Cells for further analysis.

Data cleaning and preparation were also addressed during the meeting to ensure that we work with high-quality and reliable information. Once the data was ready, we proceeded with analyzing the datasets using Python and Unix command line processing.

Finally, we discussed the upcoming presentation of our findings. We are excited to present the analyzed data to the team and discuss the insights gained from our research on immune receptor biology.