# A gentle introduction to ML via antibody-engineering

NCBI: Building Transparent ML/AI Solutions to Advance Biological Research Virtual Codeathon Feb. 26 – Mar 1, 2024

# **Project Goals**



#### **Motivation**

- ML/Al is hot
- Antibodies are important in therapeutics, diagnostics, and as reagents (spatial omics, flow cytometry, histology)
- Antibodies are used to teach protein purification, ELISAs, etc. in community college workforce education
- We get requests for ML modules

## **ML Education Challenges**

- Vocabulary
- Methods, appropriateness
- Need infrastructure: data, tools, models
- Reproducing papers is hard/impossible
- Examples lack context (maps, apples, cars)
- Step by step examples are lacking
- Teaching: sysadmin >> coding

## Can we?

- Identify a small number of key concepts (regression vs neural nets vs language models)
- Identify illustrative data sets, test cases
- Create infrastructure, libraries, install commands/scripts
- Documents steps and concepts taught
- Target different levels of experience

# Many Computational Tools, Resources, Methods

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AbLang: An antibody language model for completing antibody sequences

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#### **Antibody H3 Structure Prediction** C. Marks\*, C.M. Deane Department of Statistics, University of Oxford, 24-29 St Giles', Oxford OX1 3LB, United Kingdom ARTICLE INFO ABSTRACT Article history: Received 16 Decem Received in revised f Accepted 27 January Available online 1 Fe **Generating Human Antibodies Using Language** Keywords: Antibodies Models Loop modelling Protein structure pr

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# **Emerged in the past 5-6 yrs**

Antibody Watch: Text Mining Antibody Specificity from the Literature

Chun-Nan Hsu¹, Chia-Hui Chang¹,², Thamolwan Poopradubsil², Amanda Lo¹, Karen A. William¹, Ko-Wei Lin¹, Anita Bandrowski¹,³, Ibrahim Burak Ozyurt¹, Jeffrey S. Grethe¹, and Maryann E. Martone¹,³\*

## **Patterns**

Deciphering the language of antibodies using selfsupervised learning

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EpiBERTope: a sequence-based pre-trained BERT model improves linear and structural

Review

Linear B-Cell Epitope Prediction for In Silico Vaccine Design: A Performance Review of Methods Available via Command-Line Interface

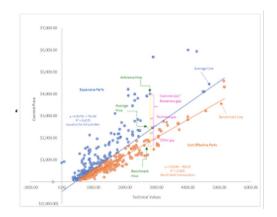
Kosmas A. Galanis , Katerina C. Nastou †, Nikos C. Papandreou, Georgios N. Petichakis, Diomidis G. Pigis and Vassiliki A. Iconomidou \*

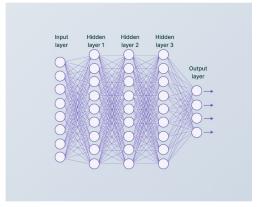
# Machine Learning (ML) Concepts



- Methods
  - Regression
  - Neural nets
  - Language models
- Training data & models
  - Features (attributes)
  - Data structures
- Data resources & code

Jason's machine learning - https://docs.google.com/presentation/d/1kSuQyW5DTnkVaZEjGYCkfOxvzCqGEFzWBy4e9Uedd9k/edit#slide=id.g2397597de6 0 71





## Previous work



## DWB antibody engineering - https://antibody-engineers.org

2022 Hackathon

https://antibody-engineers.org/event/antibody-engineering-hackathon-august-2022 https://github.com/AntibodyEngineers/covid-not-covid

- ML Ablang, covid not covid, a developer was successful
- Others learned some programing, jupyter notebooks

#### 2023 Hackathon

https://antibody-engineers.org/event/antibody-engineering-hackathon-august-2023 https://github.com/AntibodyEngineers/immune-profiling

- Immune profiling data, pandas, graphing, some success with data set -> tools -> science
- Still a lot of jupyter/basic python how tos
- 2024 Hackathon (Aug 5-8: Zoom)
  - Build on this hackathon



Project aims 1) develop modules to support course-based undergraduate research experiences. (CUREs) 2) investigate hackathons as a novel strategy for engaging participants in collaborative curriculum development.



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## **ML** and Antibodies



- A big goal:
  - Given an epitope sequence can we design an antibody de novo
- Other applications
  - Humanize mouse antibodies
  - Improve solubility, stability
  - Tune binding affinities
  - Convert Fab/scFab/svFv fragments into VHH (single domain, "nanobody") fragments
  - Multivalent antibodies
  - CAR-T / Immunotherapy
  - Antibodies to proteins in non-model organisms (one of ours)

# **Tools and Data**



## **Tools**

- AbLang 2022 hackathon
   https://github.com/oxpig/AbLang,
   https://github.com/TobiasHeOI/AbLang2
- AntiBERT (AntiBERTy)
   https://github.com/dohlee/antiberty-pytorch
- SAM (Simple Antibody Model)
   <a href="https://github.com/Wang-lab-UCSD/AntPack">https://github.com/Wang-lab-UCSD/AntPack</a>
   <a href="https://github.com/jlparkl/humanness\_evaluation">https://github.com/jlparkl/humanness\_evaluation</a>
- IgFold Ab structure prediction (IgFold -> iCn3d?) https://github.com/Graylab/IgFold
- More at: <a href="https://github.com/topics/antibody-design">https://github.com/topics/antibody-design</a>

### Data

- OAS Observed Antibody Space https://opig.stats.ox.ac.uk/webapps/oas
  - >1 billion sequences from 80 studies
- iReceptor <a href="http://ireceptor.irmacs.sfu.ca">http://ireceptor.irmacs.sfu.ca</a>
  - Federated database
  - 5.2 Billion annotated sequences from 10,019 repositories
  - 67,000 clones from 64 repertoires
  - 133,000 sorted B/T cells from 142 repositories
- NCBI SRA
  - Raw data from various experiments
  - Gotta dig

# Schrödinger's Cat



- Trying to simplify ML requires learning it.
- Once you learn, your view of what's hard changes. You are no longer a novice.

