

# HARRISON PIELKE-LOMBARDO

## PhD Researcher

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📍 Denver, CO

📅 12 May 1995



*"I am a Computational Bioscience graduate interested in developing software for artificial intelligence, health informatics, and game development. My work includes developing novel algorithms for symbolic AI and natural language processing. As a polyglot programmer, I enjoy turning difficult problems for people into easy solutions for computers."*

## EXPERIENCE

### PhD Researcher

#### University of Colorado, Anschutz Medical Campus

📅 2016 – 2022

📍 Aurora, CO

- Thesis title: Schematization of biological mechanisms using network alignment and computational analogy for hypothesizing about disease mechanisms and their interventions.
- Managed multiple, interconnected computational projects across different teams from planning to publication.
- Communicated with technical and non-technical audiences.
- Developed interpretable, symbolic artificial intelligence and machine learning methods for identifying drug-targets in text and performing inductive reasoning about drug-disease mechanisms.
- Maintained sustainable, open software development practices.

Knowledge graphs

Artificial intelligence

Biomedical data science

## PROJECTS

### Schematization of biological mechanisms using structural, semantic, and causal properties

- Developed algorithmic approaches in Clojure and Python for extending analogical reasoning of complex networks representing biological knowledge.
- Merged and harmonized large biomedical knowledge graphs.

### Knowtator: Concept/relation annotation for Protégé

- Deployed a WYSIWYG plugin for ontology development and text annotation that includes interactive graph visualization for textual features.
- Incorporated user feedback in several feature updates.

### Bootstrapped relation extraction using word embeddings and dependency paths

- Developed a novel bootstrapping relation extraction approach in Clojure that creates human-interpretable syntax patterns from dependency paths and word embeddings
- Performance optimized with GPU accelerated matrix operations.
- Evaluated the approach on a large corpus of biomedical text on its ability to identify drug-target relationships.

## SKILLS

### Clojure(script) (6 years)

Reagent

Re-frame

Datascript/Datomic

### Python (10 years)

NumPy

Pandas

scikit-learn

### Data visualization

Matplotlib

Vega

GraphViz

D3

### Communication

Jupyter(Lab)

LaTeX

RMarkdown

### Additional languages

Java

JavaScript

Bash

Common Lisp

C++

R

MATLAB

HTML/CSS

### Development tools

Git

GitHub

CI/CD

### Areas of expertise

Natural Language Processing

Statistics

Machine Learning

Semantic web

Artificial intelligence

Domain modelling

### Big data/Cloud

SQL

SPARQL

RDF

AWS

Kubernetes

BigQuery

HPC

Redis

## EDUCATION

### PhD Candidate in Computational Biosciences

#### University of Colorado, Anschutz Medical Campus

📅 2016 – Ongoing

📍 Aurora, Co

### MS in Biomedical Sciences

#### University of Colorado, Anschutz Medical Campus

📅 2016 – 2022

📍 Aurora, CO

### BS in Applied Mathematics

#### University of Colorado

📅 2013 – 2016

📍 Boulder, CO

## NOTE

References available upon request. Please see my GitHub page (@tuh8888) for my software projects as well as my contributions to various open-source projects.