

HARRISON PIELKE-LOMBARDO

Computational Biologist

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🎂 12 May 1995

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EXPERIENCE

Computational Biologist

📅 2016 – 2022

University of Colorado, Anschutz Medical Campus

📍 Aurora, CO

- Managed multiple, interconnected computational projects written in `Clojure`, `Java`, and `Python` across different teams resulting in 6 publications, 4 dataset releases, and 5 package releases.
- Developed interpretable, symbolic `Artificial Intelligence`, `Machine Learning`, and `Natural Language Processing` methods for identifying drug-targets in text and performing inductive reasoning about drug-disease mechanisms using a `Knowledge Graph` constructed from 10 biomedical ontologies and 10 databases containing 1 trillion triples.

IEEE Undergraduate Grant

📅 2015 – 2016

University of Colorado, Boulder

📍 Boulder, CO

- Used an Aho-Corrasick automata representation of CRISPR-Cas9 binding sites to reduce the complexity of the estimation of binding coverage from $O(4^n)$ (4^3 billion) combinations to a $O(1)$ (constant time statistical approximation when n is large). Implemented mathematical models in `Python` and `MATLAB` and evaluated using genetic data from the Human Genome Project.

Cancer Center Summer Fellow

📅 Jun 2015 – Aug 2015

University of Colorado, Anschutz Medical Campus

📍 Aurora, CO

- Optimized and evaluated a drug-efficacy scoring algorithm which incorporates multi-omic data including cancer genomes and drug-target profiles. Communicated results with domain experts using heat-map visualizations of kinase scores for selected cancer subtypes.

PROJECTS

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

- Conceptualized and tested algorithmic approaches in `Clojure` and `Python` for extending analogical reasoning of complex networks representing biological knowledge. Merged and harmonized large biomedical knowledge graphs represented in `RDF`, `Datomic`, and `SQL` formats.

Knowtator: Concept/relation annotation for Protégé

- Deployed a WYSIWYG `Java` plugin for ontology development and text annotation that includes interactive graph visualization for textual features. It was used to annotate over 100k concept and relation annotations. Later became a `Clojurescript` web application. `CI/CD`: Incorporated user feedback in several feature updates.

Bootstrapped relation extraction using word embeddings and dependency paths

- Automated relation extraction by implementing a novel bootstrapping approach in `Clojure` that creates human-interpretable syntax patterns from dependency paths and word embeddings. Performance optimized with GPU accelerated matrix operations. Improved precision for relation extraction for drug-targets from biomedical texts by 10%.

EDUCATION

Master of Science in Biomedical Sciences and Biotechnology

📅 2016 – 2022

University of Colorado, Anschutz Medical Campus

📍 Aurora, CO

Bachelor of Science in Applied Mathematics

📅 2013 – 2016

University of Colorado

📍 Boulder, CO

SKILLS

- Python
- Java
- JavaScript
- Clojure
- Clojurescript
- C++
- Creativity
- Organization
- NumPy
- Pandas
- Reagent
- Re-frame
- Datascript
- Datomic
- NLTK
- R
- MATLAB
- HTML
- CSS
- Git
- GitHub
- CI/CD
- AWS
- Kubernetes
- Natural language processing
- Statistics
- Machine learning
- Semantic web
- Artificial intelligence
- SQL
- SPARQL
- BigQuery
- Redis
- Communication
- Teamwork

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.