HARRISON PIELKE-LOMBARDO

Computational Biologist

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EXPERIENCE

Computational Biologist

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 written in Clojure, Java, and Python across different teams from planning to publication.
- 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 Knowledge Graphs.

IEEE Undergraduate Grant

University of Colorado, Boulder

2015 – 2016 | Boulder, CO

Used an Aho-Corrasick automata representation of CRISPR-Cas9 binding sites to reduce the complexity of the estimation of binding coverage from $O(4^n)$ ($4^{3\text{ billion}}$) 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

University of Colorado, Anschutz Medical Campus

Jun 2015 – Aug 2015 | 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 heatmap visualizations of kinase scores for selected cancer subtypes.

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 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. Later became a Clojurescript web application.
- CI/CD: 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.
- Improved precision for relation extraction for drug-targets from biomedical texts by 10%.

EDUCATION

Master of Science in Biomedical Sciences and Biotechnology

University of Colorado, Anschutz Medical Campus

2016 — 2022 Aurora, CO

Bachelor of Science in Applied Mathematics

University of Colorado

2013 – 2016 Boulder, CO

SKILLS

- Python
- Java
- JavaScript
- Clojure
- Clojurescript
- C++
- 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

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.