HARRISON PIELKE-LOMBARDO

Computational Biologist

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EXPERIENCE

Computational Biologist
2016 – 2022
University of Colorado, Anschutz Medical Campus
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 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 $O(4^n)$ ($4^{3\text{ billion}}$) 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
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 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. 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

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
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
- Problem-solving
- 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
- Adaptability
- Communication
- Teamwork
- Time management

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.