HARRISON PIELKE-LOMBARDO

PhD Researcher

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To Epistemic AI hiring team,

I am excited to discover the opportunity at Epistemic AI for implementing AI and NLP driven software tools for improving biomedical research. My thesis advisor, Lawrence Hunter, who serves as a scientific advisor for Epistemic AI suggested that I would be a good fit for building the type of software you use and solving the types of biomedical problems you solve.

There are two areas that have always interested me: software development and biology. Software development, for me, satisfies a creative itch when designing new systems while also being intellectually stimulating when solving domain specific challenges. Biology represents a uniquely complex system to untangle and understand while also being incredibly important to helping the people we know and love. To meet these interests, I have pursued a career in computational biology which lead me to study in the Computational Biosciences Program at the University of Colorado, Anschutz Medical Campus where my thesis research involved developing a method to reason about knowledge graphs of disease mechanisms in order to hypothesize drug treatments.

As a graduate of this program, I have developed skills in algorithm-development, domain-modeling, data science, machine learning, and artificial intelligence. Now, I am eager to apply what I have learned to solve challenges in the world. I have over 7 years of programming experience using programming languages from Python to Java and consider myself to have expert proficiency in them. I have contributed to the open-source ecosystem with a number of my own projects as well as by submitting pull-requests to several other libraries. As a member of our lab, I contributed to our team's diverse suite of tools which use Natural Language Processing and Artificial Intelligence to improve biomedical research. These tools incorporate several modern architectures for handling the large amount of data we use including cloud computing and containerization.

Below are listed a relevant selection of tools, packages, and concepts which I have experience using or have implemented in my own projects.

- Python, Tensorflow, Pandas, Numpy, Scikit-Learn
- Java, Swing
- Docker
- Data visualization, graph/network interaction
- Technical communication, API documentation, non-technical explanation,
- Inter-disciplinary communication
- Git, GitHub, CI/CD
- AWS, Google BigQuery
- Algorithm development
- FAIR data principles, Test-Driven-Development
- Artificial intelligence, machine learning, statistics model optimization/evaluation
- SQL, SPARQL, RDF, Neo4j, Datomic, Datascript

I hope that you will consider me in your decision-making process as I would like to contribute my expertise in biomedical data science and artificial intelligence to improving your products as well as learn from your team how to use software to improve the world.

Sincerely,

Harrison Pielke-Lombardo