Jonathan Gray

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Technical Skills

- **Experienced:** Python, TypeScript/Javascript, R, Node, React, Redux, Express, PostgreSQL, Docker, Bash, HTML5, CSS/SCSS, Snakemake, Python Libraries (Pandas, Numpy, Matplotlib, Seaborn, Scikit-learn, Tensorflow)
- **Strong:** C/C++, Matlab, MongoDB, AWS, Prometheus, Grafana, Jest

Experience

Docketeer Extension (Open Source Product for Docker Desktop)   **Sept 2023 - Present**

- Implemented Kubernetes monitoring within Docketeer, leveraging Prometheus for efficient data collection capabilities and Grafana for intuitive visualization tools to deliver a comprehensive cluster health overview and granular performance metric insights to users.
- Built REST API using Express for its rapid development capabilities, extensive middleware support, and integration with frontend technologies.
- Created comprehensive documentation for the REST API for easier developer onboarding.
- Achieved a 70x improvement in processing speed and significantly reduced user wait times by optimizing backend log message parsing through streamlined logic, eliminating redundant string manipulations, and implementing regular expressions.
- Introduced search feature for logs allowing filtering by date time and message text for an easier user experience.
- Implemented a browser-based development environment that bypassed Docker Desktop extension limitations through a Docker API wrapper and integrated build tools, enabling real-time hot reloading and significantly enhancing development and productivity.

Paratus Sciences (Startup), New York, NY   **Nov 2021 - May 2023**

Research Associate II

- Led design and implementation of Benchling (Electronic Laboratory Notebook based on PostgreSQL) system for metadata tracking and QC which served as main platform for tracking samples for the Genomics team.
- Developed dashboards to display sequencing coverage, status, and sample information for genomic samples using Benchling and PostgreSQL allowing for live tracking of sample progress and aggregation of sequencing stats to inform decisions about final genome assembly.
- Used Python, Benchling API and Pacbio's SMRTlink API to automate metadata transfer from sequencing systems to Benchling, feeding into the sample progress and sequencing stats dashboards.
- Responsible for genome assembly using NextFlow Tower Pipelines and publishing of final assemblies to NCBI.
- Trained team members on pushing and pulling data to/from AWS S3 buckets using the AWS CLI, running RNAseq Pipelines with NextFlow Tower, and using Benching to track samples.

Icahn School of Medicine, New York, NY   **Sept 2020 - Nov 2021**

Research Assistant III

- Used Snakemake to automate sequencing pipeline for Differential Expression processing of RNAseq sample, reducing number of manual steps by 80%.
- Created visualization using Python and R for various types of sequencing data including ATACseq, RNAseq, and ChIPseq

Education

BS, Biomedical Engineering (2016-2020) Minor in Chemistry

University of South Carolina, Columbia, SC

- Outstanding Senior Award - Biomedical Engineering

Certificates

Mathematics for Machine Learning Certificate, Coursera (View Certificate)   **April 2023**

Hobbies

Muay Thai, Brazilian Jiu Jitsu, Tennis, Powerlifting, Guitar