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LEADS AI PRODUCT LIFECYCLE WITH AGILE METHODOLOGIES

EXPERTISE: MACHINE LEARNING ALGORITHMS | BIOINFORMATICS PROGRAMMING

Accelerating product innovation via deep learning and advanced analytics

Data-driven professional with immense success in building scalable machine learning algorithms, demos, POC's and AI-powered solutions that transform data into strategic outcomes.

Accomplished in optimizing large-language GenAI models, deep learning, and NLP frameworks focused on elevating algorithm performance through advanced statistical modeling and Docker cloud-based pipelines (**Azure, AWS, GPC**). Strengthened system resilience with robust monitoring, logging, and error handling for AI-driven applications using Lang-Chain and Lang Graph library. Skilled at delivering bioinformatics solutions by optimizing sequence analysis workflows and automating complex data pipelines. Chris is also a disabled veteran of the US military.
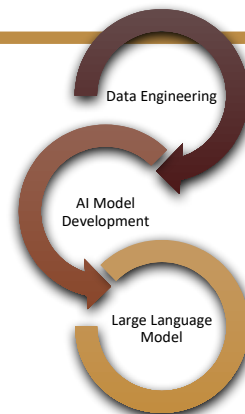
KEY QUALIFICATIONS

- AI / ML Model Development / Deployment
- API and Backend Systems Development
- Next-Generation Sequencing Pipelines
- Neural Networks, GenAI and CI/CD pipelines

- AI-driven Bioinformatics and Predictive Analytics
- Multimodal Workflow Data Integration
- Agentic AI (python, Langchain, Langgraph)
- Data Scientists Team Building

PROFESSIONAL HIGHLIGHTS

Mercola Health – Cape Coral, FL (Hybrid) | Oct 2024 to Present

SENIOR AI ENGINEER TEAM LEAD (CONTRACTOR)

Elevates algorithm accuracy and performance by leveraging computer vision, conversational voice AI, and predictive analytics derived from specialized blood laboratory data. Overhauls system responsiveness by reducing application latency and fine-tuning large language models (LLMs) through experimentation with Python programming, Sagemaker, GenAI, LlamaIndex, Lang chain, and Lang graph. Enhances developer proficiency by delivering high-impact "lunch-and-learn" sessions on engineering and RAG best practices, and Fargate, accelerating AI adoption across engineering team.

IMPACT SNAPSHOT: Achieve significant enhancement of FoodBuddy, PatentBuddy and Ask Dr. Mercola features by orchestrating agentic AI end-to-end development with Python, CI/CD automated pipelines, production deployment, and integration of advanced AI solutions within health apps using computer vision algorithms like CLIP, Deep gram, Eleven Labs, OpenAI and Hugging face repots.

Selected Contributions:

- Boost AI model efficiency and multimodal data handling by implementing Retrieval-Augmented Generation (RAG) workflows and embedding text, image, and voice data into vector databases, such as Qdrant / Zilliz Cloud.
- Enable hyper-personalized and actionable health recommendations by engineering sophisticated logic-based systems that harmonized Dr. Mercola's philosophy with USDA nutritional guidelines.
- Increase premium-feature conversions by 14% by reducing average system response time by 15% through rigorous POC model optimization and system performance enhancements.

- Enhance cross-platform application functionality and user engagement by optimizing AI model integration into applications built on Python, .NET, Blazor, and Maui frameworks.
- Reduce off-topic complaints by 33% by building real-time latency and accuracy dashboard, identifying and resolving vector-search edge cases.

Hawaii State Department of Health – Remote | Apr 2023 to Oct 2024

SENIOR SCIENTIST- BIOINFORMATICIAN (CONTRACTOR)

Streamlined large-scale genomic data analysis by architecting and managing high-throughput CI/CD bioinformatics pipelines for Whole Metagenomic Sequencing using the Nextflow workflow manager and Docker. Enhanced early detection and reporting accuracy by leveraging AI, advanced algorithms, and neural networks to predict and monitor SARS-CoV-2 and antimicrobial-resistant pathogens across Hawaiian wastewater facilities. Transformed pathogen detection and intervention strategies by pioneering AI-driven methodologies, accelerating response times. Enabled public health insights by deploying wastewater surveillance system for continuous monitoring.

IMPACT SNAPSHOT: Strengthened global data collaboration and laboratory accuracy by designing, developing and programming Meta AMR Tracker Pipeline for tracking and surveying antimicrobial resistant genes in bacteria in wastewater using multi-platform computational pipelines and contributing to NCBI data submissions, establishing gene prioritization guidelines, and advising on strategic laboratory procedures.

Selected Contributions:

- Advanced genomic classification precision by engineering Python deep learning models and classification algorithms (Deeplasmid, DeepArg, PlasmidFinder) for plasmid-versus-chromosome differentiation and Antibiotic-Resistant Gene (AMR) detection.
- Fostered cross-functional innovation by orchestrating "data jam" workshops, streamlining insights exchange between bioinformatics, lab operations, and policy teams to drive data-driven decision-making.
- Saved $20K/month by optimizing AWS batch genome assembly workflows, maintaining throughput with right-sized instances and efficient job scheduling.
- Accelerated antimicrobial resistance identification by 25% through design and deployment of natural language processing algorithms using Docker, improving response capability for emerging threats.
- Accelerated pathogen alerts by 25% by developing an AI-driven anomaly detection pipeline for wastewater surveillance.
- Improved AMR detection precision by 40% by engineering Deeplasmid and DeepArg classification models for antibiotic-resistance gene identification.

Johnson & Johnson – New Jersey | Jan 2022 to Feb 2023

AI ARCHITECT NLP (CONTRACTOR)

Maximized adoption of AI-driven Q&A systems by developing Python NLP framework that eliminated limitations of static algorithms and manual workflows. Enhanced relational accuracy within databases by engineering score calculation framework using distance metrics. Designed and implemented DrBot.Health's doctor-patient matching system, applying Siamese Neural Networks and Triplet Networks to identify optimal cancer specialists. Advanced precision in radiation therapy planning by leading proof-of-concept (PoC) for the proton radiation dosimetry program.

IMPACT SNAPSHOT: Spearheaded AI transformation of HAQ Q&A tracker database by architecting advanced Natural Language Processing (NLP) solutions and Large Language Models (LLMs) to modernize legacy systems.

Selected Contributions:

- Modernized the HAQ Q&A tracker database architecture by migrating to Python machine learning-based platform, integrating ChatGPT with Azure OpenAI for enhanced query handling and data management.

- Optimized system efficiency and model performance by deploying state-of-the-art LLMs—including ChatGPT 3.5, GPT-4o, Falcon, and LLaMA2, resulting in accurate information retrieval.
- Elevated internal research visibility by authoring whitepaper on combining Siamese networks with triplet loss for physician matching, leading to increasing correct specialist recommendations by 45%.
- Elevated answer accuracy by 22% and cut average call time by 1 minute by migrating HAQ knowledge base to Siamese-network model via Azure OpenAI, reclaiming 800 labor hours quarterly.
- Doubled throughput and cut query time by 60% by migrating HAQ Q&A Tracker to an LLM-driven platform powered by ChatGPT Azure OpenAI.

M2GEN Biotechnology Company/Contractor– Tampa, FL | Jan 2021 to Feb 2022

PRINCIPAL ENGINEER IN ML & BIOINFORMATIC SCIENCE

Advanced cancer research by leading development and launch of precision-medicine data platform. Delivered AI-driven solutions by forging strategic partnerships with three key tech and business leaders. Cut cloud infrastructure costs by 44% by optimizing resource allocation across Synapse, Blob Storage, EC2, and Databricks environments. Reduced data cleaning time by 60% and improved ML pipeline readiness by standardizing and preprocessing data with SpaCy and NLTK.

IMPACT SNAPSHOT: Engineered and automated end-to-end Whole Exome and RNA-Seq pipelines for ORIEN Avatar cancer genomics—integrating Sentieon/BWA-MEM alignment, Sentieon GATK-equivalent variant calling (germline & somatic), STAR-based fusion detection & expression quantification, and Funcotator annotation under GRCh38.p13 to deliver standardized CRAM/VCF/TMB/MSI/CNV/HRD outputs and slash total analysis turnaround by 50%.

Selected Contributions:

- Reduced data processing time by 60% by deploying and optimizing NGS pipelines for RNA-Seq and Whole Exome Sequencing using Cromwell on AWS and Azure platforms.
- Boosted variant calling accuracy by 65% by engineering clustering and classification algorithms to refine VCF file outputs.
- Enhanced data quality by 33% by developing Python custom entity extraction programs and transformer-based algorithms.
- Accelerated deployment cycles by 35% by automating Azure DevOps CI/CD workflows with Docker, WDL, and Cromwell on Azure.

ADDITIONAL EXPERIENCE

- **Senior Artificial Intelligence Engineer and Solutions Architect contractor** (NCI Information Systems, VA) Enhanced NLP model performance and persona-based AI using LLM's, NMF and Top2Vec language embedding tech. Employed Python and R to deploy topic clustering NLP models with Kubernettes deployment for government GSA contract   **Jan 2020 to Feb 2021**

- **Computational Biologist contractor** (Boehringer-Ingelhaim Research Laboratory, CT)

- Managed complex biomedical data using advanced computational approaches including unsupervised learning and dimensionality reduction. Led exploratory research on single-cell and bulk RNA analysis, investigating diverse gene expression levels in liver/renal diseases and in healthy states, leveraging practical expertise in artificial intelligence. Applied Next-Generation Sequencing (NGS) to introduce single-cell analysis pipelines, identifying biomarkers for drug therapeutics; applied clustering algorithms and dimensionality reduction methods (UMAP, T-SNE, PCA) **Feb 2019 to Jan 2020**

EDUCATION

PhD. Computer Science (ABET Accredited), University of Florida, **2029**

Masters Computer Science (ABET Accredited), University of New Haven, Tagliatella College of Engineering, CT. **2019**

Bachelors Health Sciences, Thomas Edison State College, NJ. **2012**

CERTIFICATIONS / PROFESSIONAL DEVELOPMENT

A-Z"- Machine Learning / Data Science Training Course

"COUSERA"- Basic Machine Learning Course | Stanford University "AWS"- Solutions Architect Training

"Zero to Mastery Academy"- Tensorflow Developer Certification

"Agentic AI" Workflow Deployment training ourse

 Agentic AI Engineering Coursework

TECHNICAL SKILLS PROGRAMS:

Python (Advanced), CUDA parallel programming, C / C++ (Basic), Linux / Unix Shelling Scripting, Bash Scripting, .NET / Blazor / Maui, MySQL, Github repot, FastAPI, FlaskAPI, Jenkins, Docker, Singularity containerization, Kubernettes, Fargate, SageMaker, Cloudwatch, ML pipelines with GitLab, Prometheus, Grafana, Kubeflow, high performance computing, R programming, AI Agents, Streamlit, REST APIs, NGINX, copilotAI, n8n, CrewAI, Autogen, MCP, "HiPerGator" HPC super-computer, CLIP computer vision algorithm

Tableau, Structured Query Language (SQL), MYSQL, HTML, CSS, JSP (Basic), Machine Learning / Deep Learning, Sklearn

Keras, TensorFlow, PyTorch ML Platforms, Linux / Unix Programming, AWS / Azure Cloud Platform Services, CUDA

ETL Pipelining (SSIS), Pyspark API, NoSQL Databases, Econometrics, Time-Series, Cromwell on Azure, WDL Files, Nextflow NGS programming.

BIOINFORMATICS TOOLS:

GATK Toolkit, Picard Tools, STAR Aligner, BWA Aligner, Tophat2 / Bowtie2 / Cufflinks, Sentieon

Cellranger, Samtools, HT-Seq, Trimmomatic, FastQ Screen, Funcotator, Cromwell, Nextflow, DNA Nexus, Single RNA-Seq

Analysis, WGS/WES DNA NGS analysis, Spatial Transcriptomics, Bulk RNA Seq, DNA Metagenomics MSI scoring, Sentieon, GATK suite, Nanopore sequencing, Illuminia sequencing, single-cell RNA Seq.