Eric Alcaide Machine Learning

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Achievements

- **Invented Protein-Ligand CoFolding (1st hire @CharmTx):** From raw data in the PDB (parsed w/ 1000+ CPU cores) to 3D structure prediction (training on 100+ GPUS) to Screening to a Menin inhibitor in clinical trials.
- **LLM Inference Platform (Founding Engineer@poolside):** Support automatic evals with zero adaptation inference for (model factory) for Attention, Sliding Window, RNN / SSM, Hybrid (horizontal, vertical), MoEs, RL inference, etc.
- **Code Completion Product Ownership (Founding Engineer@poolside):** Owned the entire stack from ablations to model pre-training to finetuning to [tab] completions in the editor.

Skills

Multi-Language Coding
Python (and scientific stack pytorch, triton, cython, jax, etc), CUDA, Bash, JS, PHP, Ruby

Cloud & HPC
Algorithms optimization, CPU (1000+ cores) and GPUs (1000+ A/H1/200s), Async data pipelines

Machine Learning
NLP, LLMs (pretraining, long context, RL, inference), GNNs, 3D, computer vision, etc

Strategic Thinking, Operational Excellence, Change Management, Long Term Planning, Complex Problems, People Leadership

Education

2024
Lugano, Switzerland
PhD Student, *IDSIA, Università della Svizzera Italiana*
Avised by Prof. Jürgen Schmidhuber. Reasoning over Multimodal Molecular Representations. Intelligent Processing of Multi-format Information with Applications to Chemistry

Barcelona, Spain
Medicine Degree, *University of Barcelona*
Medical Degree. Multiple distinctions.

Barcelona, Spain
Physics Degree, *University of Barcelona*
Theoretical Physics Mention

Professional / Research Experience

2024 – present
Switzerland
Founding Engineer, *poolside*
Scaling LLMs. Foundations team, working on (Pre)Training, Inference, Evals, Research. Distributed workloads on thousands of CPU/GPUs. From core research to product. FP8 training, scaling RL, distributed novel optimizers, alternative silicon.

2021 – 2024
London, United Kingdom
Machine Learning & Translational Scientist, *CHARM Therapeutics*
From Bits to Molecules, and Everything in between: data ingestion pipeline (1000s of CPUs), geometric deep learning research, model training (100s of GPUs), evaluation, drug target research, virtual screening, etc. First employee, architect of DragonFold

2021 – present
Open Source Researcher, *EleutherAI, OpenBioML*
Research at the intersection of Natural Language Processing, Structural Biology and High Performance Computational Methods. Author of RWKV, an RNN Model for the Transformer Era (up to 14B models). RWKV versions 4, 5, 6, and 7. Diverse international research collaboration for the promotion of Open Source AI. Lead efforts of teams of 25+ researchers

2020 – 2021
Machine Learning Researcher, *VIR Biotechnology*
Machine Learning for Structural Biology. Geometric Deep Learning and Natural Language Processing techniques for organic molecules, proteins and monoclonal Antibodies (mAbs).

Peer Reviewed Papers

2025
RWKV-7 "Goose" with Expressive Dynamic State Evolution,
CoLM 2025, Conference on Language Modelling
First non-TC0 RNN trained at scale to recognize any DFA

2025
RADLADS: Rapid Attention Distillation to Linear Attention Decoders at Scale,
CoLM 2025, Conference on Language Modeling
Converted Qwen2.5 72B to RWKV. Created the best RNN on just a few hours and tokens

2024 **Eagle and Finch: RWKV with Matrix-Valued States and Dynamic Recurrence,**
CoLM, Conference on Language Modelling
Next generation RWKV 5 & 6. Best scalable RNNs for their time. 0.1B - 14B models

2023 **RWKV: Reinventing RNNs for the Transformer Era,** *EMNLP*
Rearrangement of typical RNNs compute graph to allow for GPT training. Trained multilingual Large Language Models from 0.1B to 14B parameters, with chat interface and Open Source release. Future developments sponsored by the Linux Foundation.

2023 **UMD-fit: Generating Realistic Ligand Conformations for Distance-Based Deep Docking Models,** *NeurIPS 2023 Generative AI In Biology Workshop*
Addressed chemical inaccuracies in Deep Learning Molecular Docking models.

2023 **Advancing structural biology through breakthroughs in AI,**
Current Opinion in Structural Biology
Major recent advances driven by technology and applications to novel therapeutics.

2022 **InterDocker: End-to-End Cross-Attentive and Geometric Transformers for Efficient Iterative Protein Docking,** *LMRL-Learning Meaningful Representations of Life, NeurIPS2022*

2021 **MP-NeRF: Massively Parallel Natural Extension of Reference Frame,**
Journal of Computational Chemistry
Parallelized the Natural Extension of Reference Frame for folding polymers (proteins, RNA, etc) from internal angles, 1000x faster. Usage in MD simulations and ML training.

Courses

2020 – 2020 **HPC-based Computational Biomedicine,** *Barcelona Supercomputing Centre*
Barcelona, Spain
Impact and Hands-on experience of applied supercomputing to biomedical problems (molecular simulations, genomic analysis, tissue modelling, etc.)

2018 – 2019 **Deep Learning, Natural Language Processing and AI for Medicine,** *Coursera*
Contents include: foundations of Deep Learning, project management, Computer Vision, sequential data, Natual Language Processing, AI in healthcare, etc

2017 – 2017 **Artificial Intelligence Micromasters Program,** *Columbia University*
CSMM.101x: Artificial Intelligence (AI) - (through edx.org). Average qualification: 8.1 / 10
Search methods, games, ML introduction, CSPs, NLP, robotics introduction, etc.

Side Projects

2020 – present **Open Source Contributions**
Cutting-edge Open Source Software packages (Pytorch Geometric, Fastformers, etc)

2018 – present **Open Source projects**
Projects and modules for scientific computing which recieved a high degree of community acceptance:

- **2023: Uni-Mol** : Accuracy improvements for ML-based molecular docking.
- **2021: AlphaFold2 open replication** **:** Main contributor to the Open Source effort for the replication (and improvement) of the AlphaFold2 architecture (state of the art, deep learning engine for protein structure prediction).
- **2021: E(n) Equivariant GNN, Geometric Vector Perceptron:** Graph Neural Network architectures on invariant representations in 3D or arbitrary dimensions.
- **2019: AlphaFold1 imitation: MiniFold**: Predict protein foldings from raw sequences
- **2018: Keras-WRN:** Wide Residual Networks for image recognition in Keras.

2017 **Deep Learning - Can Computers Learn?**
Research project focused on the AI and Deep Learning field, subfields and the state of the art techniques. Evolutionary Strategies for architecture optimization in Neural Networks.

Languages

Spanish	**English**	**German**	**Mandarin**
Native	C2 level	B1 level	HSK 2