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Machine Learning Researcher in Protein Design (f/m/*)

Location
Zürich

Employment Type
Full time

Department
Software

OverviewApplication

This is Cradle

Proteins are the molecular machines of life, used for many therapeutic, diagnostic, chemical, agricultural and food applications. Designing and optimizing proteins takes a lot of expert knowledge and manual effort, through the use of custom computational and biological tools.

Machine learning is revolutionising this space, by enabling high-fidelity protein models. At Cradle, we offer a software platform for AI-guided discovery and optimization of proteins, so that biologists can design proteins faster and at scale. We are already used by clients across pharma, biotech, agritech, foodtech, and academia.

We're an experienced team of roughly 60 people. We've built many successful products before and have enough funding for multiple years of runway. We are distributed across two main locations, Zurich and Amsterdam, and are focused on building the best possible team culture.

We offer our employees a very competitive salary, a generous equity stake (for full time employees) in the company and a wide range of benefits and career progression opportunities.

Position summary

Cradle is hiring machine learning researchers, ideally but not exclusively those with backgrounds in protein modelling, to contribute to our mission of developing ML systems for lab-in-the-loop discovery and optimization of proteins. We build a SaaS

platform for clients across multiple industries (biopharma, agtech, food, chemical, ...), multiple modalities (antibodies, enzymes, ...), and we're already used in production by 4 of the top 20 big pharma companies, top 2 industrial biotech firms, and top 3 in agg. These partners use the Cradle platform to engineer proteins from initial discovery of single sequences and libraries to guiding the development of fully functional programs.

The role's primary focus is on developing, validating, and deploying models that address key challenges in protein engineering. The work concentrates on several key research areas:

- Designing, Training and fine-tuning foundation models: Training novel large-scale protein models from scratch, as well as fine-tuning existing ones, using a combination of public and proprietary datasets from our in-house lab and customer projects.

- Predictive and generative modeling: Creating robust methods for multi-property prediction and conditional sequence generation that can efficiently sample the protein design space to guide laboratory experiments.

- Active learning strategies: Designing and implementing active learning loops to close the design-build-test-learn cycle, ensuring new experimental data provides maximum information gain for model improvement.

- Multi-modal learning: Researching and implementing models that integrate diverse data modalities, including protein structure, sequence, function, laboratory machine metadata, and other relevant contextual metadata.

In this role, you're expected to actively push the status quo by researching and developing novel methods in machine learning for protein engineering. You will closely work with other researchers and engineers to implement these new concepts from initial research into robust, production-ready code in a way that is scalable and adheres to high software engineering standards.

A key advantage at Cradle is our dedicated, in-house wet lab, used exclusively to validate our protein designs and research ideas. With industry-leading turnaround times of 2-3 weeks and high-throughput capabilities, this facility enables us to rapidly test ML research hypotheses and generate proprietary foundational datasets. This tight feedback loop, combined with access to numerous industry-relevant datasets for evaluation, provides a unique environment for building and validating state-of-the-art models that work not just in-silico but also on real-world problems.

Need to have (technical)

- PhD in Computer Science, Mathematics, Physics, Computational Biology or a related discipline.

- Excellent skills in software development.

- Strong experience in applying deep learning to problems related to protein sequence-function relationships (e.g., protein property prediction, de novo design, structure prediction, directed evolution, etc.).

- Modern generative modelling: diffusions; masked language modelling etc.

- Familiarity with PyTorch or JAX.

Need to have (non-technical)

- You are self-directed. You will be asked to solve abstract tasks independently, produce results and organize your work without constant supervision.

- You want to grow. Cradle is a high-growth company providing a lot of new opportunities. You enjoy taking on challenging projects and are able to process honest feedback.

- You are able to communicate well. We are working at the intersection of biology and software where good communication is key.

- You are kind and work well in teams. We look for team players who contribute to a positive and friendly working environment.

Nice to haves

- We operate a highly automated ML model provisioning system. Experience with popular machine learning, pipelining and deployment libraries will be of high value (Kubernetes, Docker, ...).

- Languages beyond Python: Rust, Haskell, Julia, Elixir etc, in particular those which lean towards functional programming. Much of our code is architected in this fashion. (Likewise knowledge of compiler theory, type theory etc is beneficial.)

- Inference time optimization; Triton, Pallas, etc.

- Demonstrated ability to deliver deep learning models to production use.

- An understanding of genomics, immunology or molecular biology.

- Familiarity with typical protein design and synthetic biology tasks: bispecifics, CAR-T, metabolic engineering, etc.

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