Hedwig Nordlinder

PhD student in Biostochastics, Karolinska Institutet

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About Me

My research combines stochastic processes, Bayesian inference and deep generative modelling. My PhD supervisors are Dr. Benjamin Murrell, Prof. Gunilla Karlsson Hedestam, Dr. Alexander Tong, and Prof. Jon Norberg (Stockholm University). Current projects include epistasis-aware ancestral reconstruction using protein language models, energy-based modelling of antibody–antigen binding, property-constrained generative sampling, and uncertainty-aware Bayesian models of phytoplankton dynamics.

Education

PhD in Biostochastics, Karolinska Institutet — Aug 2026 – Present

BSc Mathematical Statistics, Stockholm University (GPA: 4.9/5) — Sep 2023 – Dec 2025

BSc Mathematics, Stockholm University — Sep 2023 – Jun 2026

Danderyds Gymnasium, nationally recruiting mathematics specialisation programme (A in all mathematics courses; 21.05/22.5 overall) — Aug 2021 – Jun 2024

Publications and Preprints

Conference papers

1. Billera, L., **Nordlinder, H.**, Murrell, B. *Latent Process Generator Matching.* NeurIPS 2026. `https://arxiv.org/abs/2605.20547`
   Studies generator matching for generative modelling via tractable latent Markov processes.
2. Billera, L., **Nordlinder, H.**, Ryder, J. C., Oresten, A., Stålmarck, A., Björk, T. M., Murrell, B. *Branching Flows: Discrete, Continuous, and Manifold Flow Matching with Splits and Deletions.* NeurIPS 2026. `https://arxiv.org/abs/2511.09465`
   Extends flow matching to variable-length state spaces with split and deletion events

Preprints

1. Billera, L., **Nordlinder, H.**, Murrell, B. *Time-dependent loss reweighting for flow matching and diffusion models is theoretically justified.* `https://arxiv.org/abs/2511.16599`
2. Oresten, A., Sato, K., Stålmarck, A., Billera, L., **Nordlinder, H.**, Ryder, J. C., Kaduk, M., Murrell, B. *Spontaneous Emergence of Symmetry in a Generative Model of Protein Structure.* `https://doi.org/10.1101/2025.11.03.686219`
3. Sadiq, H., Truong, P., Danielsson, M., Kumar, V., **Nordlinder, H.**, Martin, D. P., Murrell, B. *difFUBAR: Scalable Bayesian comparison of adaptive evolution.* `https://doi.org/10.1101/2025.05.19.654647`

Research Experience

Research Assistant in Biostochastics, Karolinska Institutet — Oct 2024 – Aug 2026

Part of the Murrell Group, working on Bayesian phylogenetics and deep generative modelling of proteins and small molecules.

Awards

Outstanding Paper Award, ICLR 2026 DeLTa Workshop

Received the Outstanding Paper Award (given to the best oral presentations) at the DeLTa Workshop at ICLR for my co-first-authored paper *Latent Process Generator Matching* (oral presentation; top 6% of papers).

Mittag-Leffler Prize

Award given to exceptional bachelor's theses. Received the award for my thesis *Geometrically Aware Markov Chain Monte Carlo*.

Second place, Berlin Bio × AI Hackathon, Binder design track

Project included applying variable-length deep protein design models to a binder design task.

Third place, London Bio × AI Hackathon
Made an MCP for high-throughput screening of MHC class II allotype binding affinity to antigen-derived peptides, combined with structure prediction for promising candidates.

Theses

Geometrically Aware Markov Chain Monte Carlo (2025)
Bachelor's thesis in which I explored the Wasserstein mixing time of the Metropolis-adjusted Langevin algorithm on the Riemannian manifold of symmetric positive definite matrices.

A Note on a Central Limit Theorem of Ibragimov-Linnik (2026)
Bachelor's thesis in which I elucidated and repaired a proof of the Ibragimov-Linnik central limit theorem for mixing stochastic processes.

Skills

Julia programming. Experience using Julia for supervised deep learning (protein refoldability prediction), generative deep learning (flow matching / diffusion models), and MCMC for Gaussian process models in phylogenetics and regression.

MCMC and mathematical statistics. Experience with Hamiltonian Monte Carlo, Metropolis–Hastings and Gibbs sampling, including label-switching-aware samplers and Metropolis-within-HMC methods. Coursework in measure-theoretic probability, stochastic processes, functional analysis, linear regression and classical statistical inference.

Academic Service

Peer review. PLOS Computational Biology (February and July 2026); Molecular Biology and Evolution (June 2026).

Mattecentrum, volunteer (Aug 2022 – Oct 2024). Provided free one-on-one mathematics instruction to primary and secondary school students.