Bio: Our research uses data-driven systems biology, multi-omics and machine learning to study cardiometabolic diseases and progressive disorders for better early detection and precision medicine.

I would like to host a: **DDLS academic postdoc**

Contact: muhammad.arif@gu.se

Muhammad Arif

Affiliation: **University of Gothenburg**

Dept. of Molecular and Clinical Medicine

Bio: Specialist physician and associate professor at Umeå University, leading research on tumor stroma, fibroblast heterogeneity, and translational cancer models in pancreatic cancer.

Project idea: Pancreatic cancer is characterized by a dense stroma dominated by cancer-associated fibroblasts (CAFs), which play critical roles in tumor progression and therapy resistance. Recent research has revealed that CAFs are functionally heterogeneous, with some subtypes promoting tumor growth while others restrain it. However, the origins and defining features of tumor-restraining CAFs remain unclear. For the first time, this project will systematically compare fibroblast subtypes in normal wound healing with CAF subtypes, using advanced single-cell and spatial transcriptomics, organoid co-cultures, and integrative multiomics analyses. The recruited postdoc will lead this comparative analysis, mapping both similarities and differences in molecular and functional profiles of fibroblasts across the different phases of wound healing and contrasting these with CAF populations in tumors. A key aim is to identify which regenerative fibroblast states are missing or altered in the tumor context—insights that may explain why the tumor wound fails to heal. The ultimate goal is to determine whether such regenerative states can be induced or stabilized in the tumor microenvironment to suppress cancer progression.

I would like to host a: **DDLS academic postdoc**

Contact: daniel.ohlund@umu.se

Daniel Öhlund

Affiliation: **Umeå University**

Dept. of Diagnostics and Intervention

Andrea Fossati

Affiliation: **Karolinska Institutet**

Bio: We study how phages reprogram bacteria biology using proteomics, genetics and computation to map phage receptors, host responses and design smarter antimicrobials.

Project idea: The first step of any viral infection is binding to specific surface receptors on the host cell. In bacteriophages, these receptors and co-factors determine which bacteria can be infected, yet for most candidate therapeutic phages their receptors and entry pathways remain unknown. In the lab we work on how bacteriophages find, bind and rewire their bacterial hosts, with a particular focus on identifying phage receptors and co-factors on the bacterial surface using quantitative proteomics to link receptor usage to host range and resistance. This area would suit someone with solid experience in mass spectrometry based proteomics who wants to work at the interface of infection biology and data driven method development. Backgrounds that could fit include interaction proteomics, surface or membrane proteomics, DIA/PRM workflows or computational analysis of large proteomics datasets. Phage biology/microbiology knowledge is a plus but not necessary.

I would like to host a: **DDLS academic postdoc**

Contact: andrea.fossati@scilifelab.se

Rui Benfeitas

Affiliation: **Chiesi**

Global Clinical Development
Intervention

Bio: Translational & Precision Medicine Lead driving biomarker strategies, omic approaches and AI frameworks to advance patient endotyping and precision medicine in clinical trials.

Project idea: Large-scale patient profiling is helping identify new endotypes in asthma, chronic obstructive disease (COPD), and bronchiectasis (BE) by integrating multi-omic, and clinical data. This approach has revealed shared immune patterns across these diseases, creating opportunities for drug repurposing. Yet, recent clinical trials have shown minimal improvement over standard of care and the need to shift from disease- to pathobiology-focused therapies, highlighting a gap in systematic and multimodal patient characterizations that simultaneously address both lung and systemic circulation. We aim to develop precision medicine workflows for single- and cross-disease multi-modal patient endotyping and pathobiological characterizations in asthma, COPD, and BE, examining lung-blood crosstalk and disease similarities. By leveraging patient registries and data generated during clinical trials, we aim to develop both graph and deep-learning approaches for handling multi-omic data to identify patient subgroups, molecular signatures, pathobiological-drivers and facilitate computational inference of severity. This computational platform will enable hypothesis generation and identification of patient endotypes and biomarkers across diseases, tissues, and omic layers, at both bulk and single-cell levels. The hypotheses generated will be validated in independent cohorts. Project developed in collaboration with Prof. Muhammad Arif (University of Gothenburg).

I would like to host a: **DDLS industrial postdoc**

Contact: r.benfeitas@chiesi.com

Taner Arslan

Affiliation: **Chiesi Pharma AB**

Global Clinical Development

Bio: I am a lead bioinformatician specializing in machine learning and big data omics, dedicated to advancing translational science and precision medicine within clinical development.

Project idea: Dynamic Endotyping in Bronchiectasis: Integrating Imaging and Transcriptomics for Precision Medicine Bronchiectasis is a heterogeneous respiratory disease where current clinical phenotypes fail to capture biological diversity, limiting precision medicine. Leveraging the patient dataset with paired High-Resolution Computed Tomography (HRCT) scans (both at the baseline and follow-up) and blood RNA-seq (at the baseline), we aim to define dynamic endotypes that integrate structural progression and molecular signatures. Unlike static assessments, dynamic endotypes reflect disease trajectory and may predict exacerbation risk, progression, and therapeutic response. We propose a multimodal approach combining imaging and transcriptomics to uncover mechanistic subgroups. HRCT progression will be modelled using advanced computational techniques, such as deep learning, while RNA-seq may be encoded using graph-based methods to capture pathway-level biology. Fused representations, potentially learned through architectures such as autoencoders or attention-based models, will enable unsupervised clustering for endotype discovery and development of a baseline machine-learning classifier for prospective validation. This work will advance precision medicine in bronchiectasis, support patient stratification for clinical trials, and establish a blueprint for multimodal integration in chronic airway diseases.

I would like to host a: **DDLS industrial postdoc**

Contact: t.arslan@chiesi.com

Torsten Günter

Affiliation: **Uppsala University**

Dept. of Organismal Biology

Bio: I am a computational biologist with an interest in evolutionary biology and population genomics, analyzing ancient and modern DNA from humans and domestic animals. Group Website: www.gunther-lab.org

Project idea: Various different projects could be designed depending on the profile and interest of the candidate. Potential projects could involve method development for the analysis of genomic aDNA data, e.g. to better understand their population history, adaptation or social structure. We also have generated sequence data from different domestic animals that could be analyzed as part of the project. Together with collaborators, we also have access to large unpublished ancient DNA datasets from northern European Stone Age human populations, that could be analyzed with a focus on their evolutionary population history, social structure or pathogens. Other possibilities include the re-analysis of publicly available datasets, both ancient (e.g. AADR) and modern (e.g. UK Biobank). Other ideas are also very welcome. Please get in touch if you are interested!

I would like to host a: **DDLS academic postdoc**

Contact: torsten.gunther@ebc.uu.se

Erdinc Sezgin

Affiliation: **Karolinska Institutet**

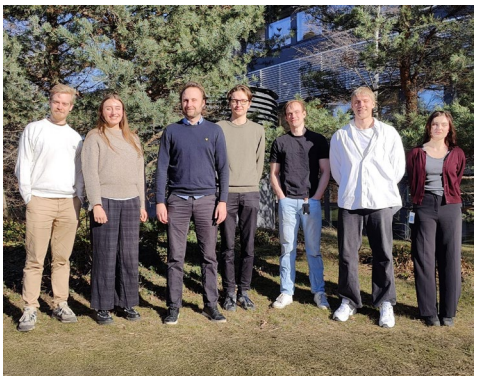
Women's and Children's Health

Bio: We study biophysical regulation of cellular events using advanced chemistry, optical, syntehtic biology and computational tools.

Project idea: Biophysics, immunology, advanced imaging, diseases, syntehtic biology, nanoscale bioparticles, smart probes

I would like to host a: **DDLS academic or industrial postdoc**

Contact: erdinc.sezgin@ki.se



Emil Marklund

Affiliation: **Stockholm University**

Dept. of Biochemistry and Biophysics

Bio: In our lab we investigate how biological macromolecules can manage to interact with each other with high specificity, and how sequence information determines quantitative macromolecular functions.

Project idea: We combine state of the art high-throughput measurements of molecular binding with simulations and mathematical modeling. Our goal is to gain a deep and quantitative understanding of life at the molecular level.

I would like to host a: **DDLS academic postdoc**

Contact: emil.marklund@scilifelab.se

Heidi Burdett

Affiliation: **Umeå University**

Dept. of Ecology, Environment & Geoscience

Bio: Our research seeks to understand the fundamental processes underlying photosynthesis in the coastal marine environment, applying this knowledge to coastal conservation and sustainability challenges.

Project idea: We seek to understand how coastal macrophytes (fleshy seaweeds, calcifying seaweeds, seagrasses, aquatic plants) photosynthesise, especially in marginal light environments where light intensity is low and/or spectral quality is constrained. This can be due to natural processes (e.g. polar latitudes, mesophotic depths), or because of climate change / human related causes (e.g. ocean darkening). Our recent research indicates that survival in marginal light environments is governed by a hierarchically-structured interaction between the environment, organismal physical structure and intracellular photo-physiology – which all have promising potential within DDLS: 1. Quantify environmental light conditions in marginal light environments, and predicting how this may shift under global change scenarios. This would involve optical modelling and remote sensing of the coastal water column to quantify the intensity and spectral composition of light available to seabed-fixed organisms; 2. Determine the role of organismal physical structure on the quantity and quality of light that is ultimately available for photosynthesis. Drivers of this include habitat-scale regulation of light niche diversity because of self-shading (e.g. habitat-scale photogrammetry analysis); 3. Establish the photo-physiological mechanisms operating within these environmental-physical constraints on light availability. We have a particular interest in investigating transcriptomic responses to light exposure extremes.

I would like to host a: **DDLS academic postdoc**

Contact: heidi.burdett@umu.se

Anne Tuiskunen Bäck

Affiliation: **Umeå University**

Clinical Microbiology/Public Health and Clinical Medicine

Bio: Cardiologist and translational researcher in virology and cardiogenetics, aiming to integrate molecular insights into precision medicine for individualized treatment.

Project idea: Our research focuses on how viral infections and human genetic variation influence cardiovascular disease, with a particular emphasis on myocarditis and virus-associated complications. We integrate metagenomic sequencing, genetic profiling, and molecular analyses with clinical data and advanced imaging to uncover mechanisms driving disease onset, progression, and long-term complications. Using longitudinal patient cohorts and multi-omics approaches, we aim to improve diagnostics, risk stratification, and individualized treatment strategies. Current projects include developing non-invasive biomarkers to complement cardiac MRI for myocarditis diagnosis and prognosis, and characterizing Puumala virus genetics to understand host-pathogen interactions and severe disease outcomes. By bridging molecular insights with clinical care, our multidisciplinary team contributes to precision medicine approaches that enhance patient management and long-term outcomes in cardiovascular and infectious diseases.

I would like to host a: **DDLS academic postdoc**

Contact: anne.tuiskunen@umu.se

Björn Schröder

Affiliation: **Umeå University**

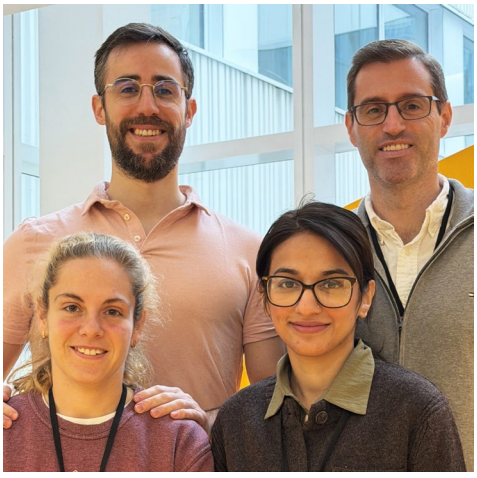
Dept. of Molecular Biology / MIMS

Bio: Research in the group of Björn Schröder focuses on the interaction between diet, gut microbiota and intestinal mucosal barrier function in health and disease. More details at www.mucubacter.org.

Project idea: The intestinal mucus layer is a critical barrier protecting the gut epithelium, yet its integrity is increasingly compromised in Western societies. When dietary fibre is scarce, gut microbes switch from fermenting fibres to degrading mucus, a process linked to inflammation and chronic diseases such as ulcerative colitis and type 2 diabetes. Our research revealed that low-fibre diets impair mucus secretion and increase mucus penetrability, effects reversible through microbiota transplants from fibre-rich donors. Building on a unique dataset of more than 400 samples integrating microbiome sequencing with functional mucus parameters from both human and mouse microbiota, a possible project could aim to develop machine-learning models predicting mucus function from gut microbiome profiles. Such an approach could eliminate invasive biopsies and enable early risk screening for Western lifestyle-associated diseases. The project will combine cutting-edge microbiome analysis, computational biology, and translational relevance, offering a postdoctoral researcher the opportunity to pioneer predictive tools at the intersection of diet, microbiota, and mucosal health. Other project ideas are also very welcome!

I would like to host a: **DDLS academic postdoc**

Contact: bjorn.schroder@umu.se



Nick Tobin

Affiliation: **Karolinska Institutet**

Oncology-Pathology

Bio: Cancer genomics scientist leveraging bioinformatics and AI-based methods to analyze genomic data and advance precision oncology.

Project idea: This project aims to quantify spatial heterogeneity of cancer hallmark processes in breast cancer by applying AI-based analysis to whole-slide histopathology images. Using SEQUOIA, a transformer-based model designed to infer transcriptomic programs from routine histology, the project will predict activity of MSigDB Hallmark gene signatures across spatial regions of individual whole-slide images. This enables mapping of hallmark processes such as proliferation, immune response, angiogenesis, and metabolic reprogramming directly from tissue morphology at high spatial resolution. By aggregating region-level predictions, the project will derive quantitative measures of intra-tumour hallmark heterogeneity across the entire slide. These heterogeneity metrics will then be related to clinical outcomes, with a specific focus on progression-free survival (PFS) in breast cancer patients. Survival analyses using Cox proportional hazards models and Kaplan-Meier estimates will assess whether spatial hallmark heterogeneity provides prognostic information beyond standard clinicopathological variables. By linking spatially resolved, image-derived hallmark activity to patient outcome, this project seeks to advance interpretable AI for digital pathology and to improve understanding of how functional tumour heterogeneity influences breast cancer progression.

I would like to host a: **DDLS academic postdoc**

Contact: nick.tobin@scilifelab.se

Avlant Nilsson

Affiliation: **Karolinska Institutet**

Cell and Molecular Biology

Bio: We are a systems biology group at SciLifeLab Solna and develop computer models of cellular processes in cancer, including resistance mechanisms, the effects of drugs, and cell-cell interactions.

Project idea: Our research focuses on biologically informed deep learning models of cellular systems. We constrain recurrent neural network models with prior knowledge of molecular interactions (including signaling, metabolism, and gene regulation) to learn interpretable relationships between genetic, molecular, and environmental inputs and resulting cell states and phenotypes. The project scope will be developed jointly with the candidate, and you are encouraged to bring complementary ideas within the scope of data-driven life science, deep learning, and systems biology. The work is fully computational and conducted using Python, PyTorch, and collaborative development via GitHub. While current efforts primarily focus on bulk data, extending the models to single-cell data offers opportunities to uncover correlation structures between cellular subsystems and to align bulk and single-cell representations, leveraging large public resources such as the Human Protein Atlas. One possible project direction is to link clinical data, molecular profiles, and health outcomes through learned cell-state representations using an autoencoder-like framework. Since many diseases, including cancer, are driven by dysfunctional cellular states, explicitly connecting clinical phenotypes and patient outcomes to these latent representations may improve both biological interpretability and predictive performance.

I would like to host a: **DDLS academic postdoc**

Contact: avlant.nilsson@ki.se

Johan Henriksson

Affiliation: **umeå university / scilifelab**

Dept. of molecular biology

Bio: Computer scientist & mechanical engineer, turned biologist. Methods developer in: single-cell assays, bioinformatics, CRISPR/transposon screens. Applied to CAR T cells, metagenomics and telomeres.

Project idea: We have a new method for whole-genome sequencing of up to a million cells at a time (http://zorn.henlab.org), applicable to microbes and cancer. It forms the basis for the largest ever genetic screen for new CAR T cells, as well as new telomere-based cancer diagnostics

I would like to host a: **DDLS academic postdoc**

Contact: johan.henriksson@umu.se

Erik Benson

Affiliation: **Karolinska Institutet**

MTC / Scilifelab

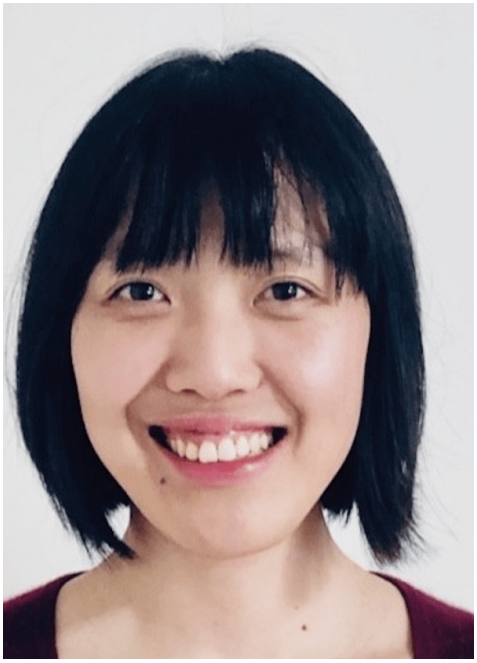
Bio: A young group based at Scilifelab affiliated to Karolinska Institutet funded by the ERC. I have background in physics, biomedicine and DNA nanotechnology.

Project idea: Decoding in vitro selection of DNA nanostructures Over the last years we have been working on a method to combine DNA nanotechnology with selection to find better structures to use as antibody alternatives or in cell specific targeting. Along the way we have been generating a lot of 'unusual' sequencing data documenting different types of selection experiments. From this data, we hope to both identify individual structures that perform their tasks exceptionally well and build models of the selection process allowing us to evaluate structures that were not included in the experiments from the start. We would be happy to host postdocs working on data driven modeling of in vitro evolution that could include topics such as:

• Stats/ML: Develop machine learning models trained on our selection data to deliver uncertainty aware, diversity promoting rankings of DNA nanostructures included or not in the selection process.
• High throughput structure prediction: Develop scalable tools to predict the 2D and 3D structures of millions of DNA nanostructures from sequencing data and use this information to drive the evaluation process.
• Data engineering/bioinformatics: Build a high throughput pipeline for UMI processing, cross/negative selection integration, QC, and dashboards for experiment in the loop candidate triage.

I would like to host a: **DDLS academic postdoc**

Contact: erik.benson@ki.se



Xiaonan Zhang

Affiliation: **Uppsala University**

Dept. of Immunology, Genetics and Pathology

Bio: Associate Professor, SciLifeLab Group Leader, IGP Goup Leader at Department of Immunology, Genetics and Pathology, UU

Project idea: My research aims to identify and characterize mutations that drive cancer development and to develop novel therapeutic strategies targeting cancer-specific vulnerabilities, particularly in cell-cycle–inactive cancer cell populations. For more information, please visit: https://www.scilifelab.se/researchers/xiaonan-zhang/

I would like to host a: **DDLS academic postdoc**

Contact: xiaonan.zhang@igp.uu.se

Christoph Ziegenhain

Affiliation: **Karolinska Institutet**

Dept. of Medical Biochemistry and Biophysics

Bio: In our group we are interested in shedding light on central molecular processes in human cells, in particular with regards to the control of alternative splicing of transcribed mRNAs. For this, we dev

I would like to host a: **DDLS academic or industrial postdoc**

Contact: christoph.ziegenhain@ki.se

Daniel Bojar

Affiliation: **University of Gothenburg**

Dept. of Chemistry and Molecular Biology

Bio: Our group focuses on data-driven glycobiology. We develop and apply AI and data science methods to elucidate glycan structure, interaction, and function at the system scale.

I would like to host a: **DDLS academic postdoc**

Contact: daniel.bojar@gu.se

Patrick Bryant

Affiliation: **Stockholm University**

Dept. of Molecular Biosciences,
The Wenner-Gren Institute
(MBW)

Bio: Development of advanced AI for peptide design wStockholm Universityith real-world therapeutic impact.

Project idea: Most current AI models in biology suffer from a critical flaw: they over-rely on memorizing evolution. While successful for standard proteins, this approach fails when designing for the “dark matter” of drug discovery—non-canonical modalities like cyclic peptides, macrocycles, and modified residues where evolutionary data is scarce. Our lab (The Bryant Lab) is pioneering a physics-aware, single-chain learning paradigm to solve this. Instead of overfitting to known protein-protein interfaces, we train deep learning models to master the fundamental grammar of folding and atomic interactions. This project aims to extend our proprietary framework (EvoBind/RareFold) to generate de novo binders with non-standard backbones.

I would like to host a: **DDLS academic or industrial postdoc**

Contact: patrick.bryant@scilifelab.se

Johan Zelano

Affiliation: **University of Gothenburg**

Clinical neuroscience

Bio: Professor of Neurology, Director of WCMTM, epilepsy physician with translational background now leading a VR-funded project on longterm outcomes of epilepsy treatments.

Project idea: We have a very big dataset of epilepsy treatment and concomitant other medication for over 100.000 individuals. I want a post doc that can use /develop advanced computational methods to find non-epilepsy medications potentiating the effect of anti seizure medications and influence the disease trajectory.The group consists of PhD-students and post docs doing standard epiidemiology and has extensive experience of studying epilepsy using big data.

I would like to host a: **DDLS academic postdoc**

Contact: johan.zelano@neuro.gu.se

Anna Gerdtsson

Affiliation: **Lund University**

Immunotechnology

Bio: Associate Professor at Lund University, Faculty of Engineering. Research focuses on spatial tumor-immune biology, integrating molecular and computational analyses.

Project idea: Machine Learning for Tissue Image Analysis - Feature Extraction and Prediction of Clinical Outcomes from Multiplex Immunofluorescence Images. Design of computational models that learn from mIF images to predict clinical outcomes, such as prognosis and treatment response. Identification of spatio-molecular features associated with survival and tumor microenvironment subtypes from routine pathology samples, to advance precision immuno-oncology.

I would like to host a: **DDLS academic postdoc**

Contact: anna.sandstrom_gerdtsson@immun.lth.se

Christos Samakovlis

Affiliation: **Scilifelab/Stockholm University**

Scilifelab and Molecular Biosciences, The Wenner-Gren Institite

Bio: Ph.D, 1991, Stockholm University, Postdoctoral researcher 1991-1994, Stanford University, Independent PI since 1995, SciLifeLab scientific director SU since 2021, Elected member KVA.

Project idea: We develop and use high-resolution, single cell analysis technologies to understand the cellular and molecular programs of lung development and to discover how these programs become misdirected in disease. We are working with several projects Integrating of spatial and multiomics data.

I would like to host a: **DDLS academic postdoc**

Contact: christos.samakovlis@scilifelab.se

Ian Hoffecker

Affiliation: **KTH Royal Institute of Technology**

Dept. of Gene Technology

Bio: The Molecular Programming Group, led by Ian Hoffecker, develops new technologies that use DNA as an information processing medium to do creative new and useful things with life science applications.

Project idea: Modern PCR-based diagnostics excel at single species detection (e.g. Covid tests), but cannot distinguish the complex multi-dimensional signatures of many human diseases like cancer. We are developing a new biochemical computing system that uses chemically synthesized DNA strands that behave like a neural network. The goal of this system is to perform complex diagnostic classification from nucleotide mixtures by allowing DNA and enzymatic reactions to perform molecular computations equivalent to the activation function and topology of a multilayer perceptron. We are looking for a postdoc candidate with physics. bioinformatics, or applied math (or similar) background interested in developing the computational framework needed to design DNA interaction energies and amplification products in parallel with our ongoing experimental implementation of this novel technology.

I would like to host a: **DDLS academic postdoc**

Contact: ian.hoffecker@scilifelab.se

Kemal Avican

Affiliation: **Umeå University**

Dept. of Molecular Biology and Icelab

Bio: Avican Lab bridges infection biology, AI, and single-cell technologies to uncover how pathogens survive and adapt in the host. Home of the µNordic Single Cell Hub (µNiSCH) and part of Icelab.

Project idea: Single-cell sequencing has revolutionized eukaryotic biology, providing high-resolution insights into tissue heterogeneity. However, a significant “computational gap” prevents the application of these powerful commercial technologies to microbiology. Current state-of-the-art bioinformatics pipelinesare rigidly optimized for eukaryotic genomes: they rely on polyadenylated mRNA capture, intron-exon splicing patterns, and nuclear compartmentalization to demultiplex data. These algorithms fail when applied to bacteria, which possess polycistronic operons, overlapping reading frames, low RNA content, and lack a nucleus. As wet-lab methods for bacterial single-cell multiomics (simultaneous DNA/RNA profiling) emerge at our facility (µNiSCH), there is an urgent need for software capable of processing this complex data. This project aims to establish a robust computational infrastructure for bacterial single-cell multiomics by benchmarking, hacking, and optimizing established commercial eukaryotic pipelines for prokaryotic use. We aim to unlock the potential of robust industrial algorithms by adapting them to the unique genomic architecture of bacteria or develop novel pipelines for bacterial single cell multiomics.

I would like to host a: **DDLS academic or industrial postdoc**

Contact: kemal.avican@umu.se

Petter Dyverfeldt

Affiliation: **Linköping University**

Dept. of health, medicine and caring sciences

Bio: Petter Dyverfeldt is Professor of Medical Imaging, developing AI- and physics-informed cardiovascular MRI to extract quantitative biomarkers from complex flow data in an interdisciplinary environment

Project idea: Cardiovascular disease remains the leading global cause of death1. A key but underused determinant of cardiovascular health is hemodynamics, i.e. the forces and dynamics of blood flow through the cardiovascular system2. Abnormal flow is mechanistically linked to major cardiovascular diseases such as atherosclerosis3, aneurysms4, and heart failure5. Therefore, advanced methodologies have been developed to comprehensively measure three-dimensional, time-varying (3D + time = 4D) blood velocity vector fields in the cardiovascular system. However, these methods are complex and limited to utility in specialized centers. Further, current analysis of the comprehensive cardiovascular velocity vector data is restricted to a small set of engineering-derived hemodynamic parameters, resulting in substantial information loss and limiting discovery of new mechanistic insights. The overall purpose of this project is to develop and evaluate a scalable, multimodal data-driven framework for automated generation, representation and interpretation of cardiovascular blood flow. By enabling automated generation of flow fields, physics-informed representation learning, and data-driven discovery of hemodynamic phenotypes, we hypothesize that our novel framework will enable large-scale, population-level hemodynamic studies and uncover new mechanistic links between blood flow and cardiovascular disease.

I would like to host a: **DDLS academic postdoc.**

Contact: petter.dyverfeldt@liu.se

Antonio Lentini

Affiliation: **Linköping University**

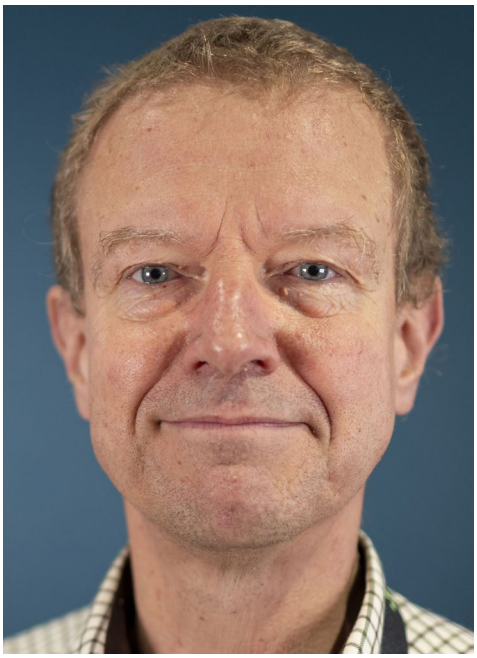
Dept. of Biomedical and Clinical Sciences

Bio: We study how cancers change and adapt over time, using experimental models, single-cell genomics, and computational modelling to uncover and target the mechanisms that drive tumour evolution.

Project idea: Single-cell genomics offers unprecedented resolution for dissecting cellular heterogeneity and the complex processes that drive cancer. By leveraging these data, we reconstruct evolutionary lineages to infer the trajectories underlying cancer initiation, development, and progression. As an interdisciplinary team, we integrate experimental model systems with computational expertise, enabling us to generate new datasets, rigorously test mechanistic hypotheses, and analyse large-scale, high-dimensional data to reveal fundamental principles of cancer evolution. We focus on two key windows of cancer evolution. First, we investigate early tumour initiation and development, asking how initial mutational events shape downstream molecular trajectories and whether distinct oncogenic drivers give rise to predictable evolutionary paths and vulnerabilities. Second, we study the emergence of treatment resistance, exploring how variation in therapeutic sensitivity arises and to what extent resistance, and ultimately treatment outcomes, can be anticipated from the state of the primary disease.

I would like to host a: **DDLS academic postdoc**

Contact: antonio.lentini@liu.se



Mats Nilsson

Affiliation: **Stockholm University**

Biochemistry and Biophysics

Bio: My research group has pioneered the in situ transcriptomic method in situ sequencing, based on padlock probes and rolling circle amplification.

Project idea: This is the method that runs in the Xenium in situ transcriptomic instrument from 10X Genomics. We are continuing developing spatial omics methods, and also developing novel Spatial Omics computational analysis tools. We apply new methods and tools to address diverse biological and medical questions. The postdoc would engage in developing and applying computational tools for Spatial Omics.

I would like to host a: **DDLS academic postdoc**

Contact: mats.nilsson@scilifelab.se

Stefanos Stagkourakis

Affiliation: **Karolinska Institutet**

Neuroscience

Bio: Assistant Professor at Karolinska Institutet and SciLifeLab studying distributed neural circuits underlying survival behaviors using large-scale recordings, optical control, and data-driven analysis.

Project idea: The project aims to uncover how distributed neural populations across the brain encode and control instinctive survival behaviors such as aggression and fear. Using large-scale neural recordings (Neuropixels), optical interrogation (two-photon imaging and holographic perturbation), and advanced behavioral quantification in freely moving animals, we will generate high-dimensional, multimodal datasets spanning neural activity, behavior, and internal state. The postdoctoral researcher will develop and apply data-driven computational approaches, including population decoding, latent variable models, and network-level analyses to identify neural ensemble dynamics that predict behavioral transitions and internal state changes. A key goal is to move beyond single-region or single-neuron descriptions toward principled models of distributed computations in the brain. The project is embedded within SciLifeLab's data-driven research environment and offers close integration between experimental systems neuroscience and modern computational analysis, providing strong training at the interface of biology, data science, and technology.

I would like to host a: **DDLS academic postdoc**

Contact: stefanos.stagkourakis@scilifelab.se

José Cerca

Affiliation: **Swedish Museum of Natural History**

Dept. for Bioinformatics and Genetics

Bio: I am an evolutionary biologist who uses genomic tools to investigate the evolutionary history of lineages, with a particular focus on insular species and adaptation, speciation and genome evolution.

Project idea: Reference genomes have revolutionized biology, serving as the foundation for comparative genomics, population genomics, transcriptomics, among others. However, reference genomes are typically constructed from a single individual, and therefore capture only a limited fraction of a species' genetic diversity. Even in well-studied species such as humans, reference genomes derived from a single individual, or from a single population, have been shown to introduce substantial biases in downstream analyses. In this project, we will explore the impact of reference genome bias and to evaluate the advantages of pangenome-based approaches. Specifically, we will assess associations between reference bias and dataset divergence, and estimate the extent to which additional structural variation is captured by a pangenome relative to a single reference genome. The main deliverable will be a set of practical guidelines to help researchers minimize reference bias and improve genomic data analyses.

I would like to host a: **DDLS academic postdoc**

Contact: jose.cerca@gmail.com

Rachel Foster

Affiliation: **Stockholm University**

Ecology, Environment and Plant Sciences

Bio: I am a microbial oceanography facinated by microbial interactions between nitrogen fixing microbes and photosynthetic eukaryotic plankton (e.g., symbioses, consortia).

Project idea: Are you interested in data driven discovery of planktonic symbioses? Work in the Foster lab aims to use open-source image archives and platforms to study symbiotic and multicellular plankton in the wild. Fully reversible image to omic workflows are available for discovering new partnerships, studying biogeography, and ecology for uncultivated populations. A primary aim is to relate changes in the community composition of symbiotic and multicellular phytoplankton to carbon export in the context of climate change.

I would like to host a: **DDLS academic postdoc**

Contact: rachel.foster@su.se

Ilaria Piazza

Affiliation: **Stockholm University / SciLifeLab Solna**

MBW / SciLifeLab Solna

Bio: Ilaria Piazza is a SciLifeLab group leader at campus Solna hosted by Stockholm University and a Wallenberg Academy Fellow. She also leads a group at the Max Delbrück Center in Berlin. Her research com

Project idea: We are recruiting a DDLS Research School postdoctoral fellow to join our research program at the interface of proteomics, metabolism, chromatin biology, and data science. Our group studies the dynamic proteome and how metabolism directly regulate protein structure, activity, and gene expression. We are particularly interested in how environmental and metabolic cues are sensed by proteins to control chromatin architecture, protein synthesis, and cell fate decisions The successful candidate will develop a data-driven research project focusing on one or more of the following themes:

- Proteome-wide discovery of protein–metaboliteinteractions and allosteric regulation
- Quantitative modeling of proteomics data and protein conformational dynamics
- Mechanistic links between metabolism, chromatin state, and gene expression programs
- Drug target deconvolution using low-input proteomics and imaging

I would like to host a: **DDLS academic postdoc**

Contact: ilaria.piazza@scilifelab.se

Nele Brusselaers

Affiliation: **Karolinska Institutet**

Women's and Children's Health (KBH)

Bio: As an epidemiologist working in the microbiome field, I focus on early life, women's health and cancer, with a particular interest in non-antibiotic drug effects on health and long-term health.

Project idea: SweMaMi is a large cohort of ~5000 women followed through pregnancy (stool/saliva/vaginal samples), and for this collaboration we want to focus on the infant microbiome, prescribed drug use and health of the child up to age 10 (neurodevelopment, GI issues, infections, weight gain, ...).

I would like to host a: **DDLS academic postdoc**

Contact: nele.brusselaers@ki.se

Mats Ohlin

Affiliation: **Lund University**

Department of
Immunotechnology

Bio: Research focus on antibodies and antibody technology.

Project idea: Our team operates in the domains of antibody engineering and development. We are part of the SciLifeLab Drug Discovery and Development Platform with a focus on therapeutic antibody development, and the Lund University ATMP environment. We also focus our research on antibody repertoire development in health and disease, such as during allergic disease. Projects with a strong focus on computational antibody design and repertoire analysis is a high priority within the team. We recently acquired a Beacon Optofluidic Platform designed to, in high throughput, study functional properties of immune cells and their products (e.g. antibodies) at the single-cell level. This resource opens up for a host of studies of adaptive immune responses. Overall, projects within the domains of immune repertoire development is thus in line with our research focus.

I would like to host a: **DDLS academic postdoc**

Contact: mats.ohlin@immun.lth.se

Virginia Dignum

Affiliation: **Umeå University**

AI Policy Lab / Computing
Science Dept.

Bio: Virginia Dignum is Professor of Responsible AI at Umeå University and leads the AI Policy Lab, which develops practical tools, audits, and policy guidance for governing AI systems.

Project idea: Develop data-driven methods for the responsible governance of foundation models in medical imaging, which can introduce significant governance challenges related to data provenance, demographic bias, data leakage, and accountability in clinical contexts. The postdoc will examine real-world foundation models used in radiology and digital pathology, integrating empirical analysis, computational risk assessment, and policy analysis. Using case studies drawn from publicly available imaging repositories, the project will examine how these practices shape medical, ethical, and regulatory risks:

1. map data provenance, reuse, and dataset composition, identifying how demographic and institutional biases propagate into clinical models;
2. develop quantitative indicators for governance-relevant risks, including performance disparities, memorization of image features, and misuse risks;
3. translate these indicators into actionable policy instruments, such as model documentation standards, audit protocols, and regulatory

I would like to host a: **DDLS academic or industrial postdoc**

Contact: virginia@cs.umu.se

Brinton Seashore-Ludlow

Affiliation: **Karolinska Institutet**

Dept. of Oncology-Pathology

Bio: The Seashore-Ludlow research group at Karolinska Institutet and SciLifeLab focuses on functional precision medicine, with an emphasis on ovarian cancer and other hard-to-treat malignancies.

Project idea: We develop and apply near-patient 3D culture systems (including short-term patient cultures, spheroids, and microenvironment-informed models) combined with multiparametric imaging and systematic perturbation profiling. A central aim is to understand how tumor cell states—such as epithelial–mesenchymal transition, dormancy, and metabolic adaptation—emerge and can be therapeutically targeted. A key component of the lab is the development and application of advanced image analysis and data-driven methods, including machine learning and deep learning approaches, to extract biologically meaningful phenotypes from complex imaging and multi-omics data. Experience or interest in AI-enabled image analysis, representation learning, and integrative modeling is therefore highly welcome. The lab operates at the interface of biology, technology development, and data science, closely linked to national and international infrastructures including SciLifeLab and the Chemical Biology Consortium Sweden.

I would like to host a: **DDLS academic postdoc**

Contact: brinton.seashore-ludlow@ki.se

Kristiina Tammimies

Affiliation: **Karolinska Institutet**

Women’s and Children’s Health

Bio: Associate Professor / Senior Lecturer in Neurogenetics with focus on improving the understanding of neurodevelopmental disorders.

Project idea: Our lab combines large scale genomic and clinical data with advanced molecular and cellular models to better understand neurodevelopmental disorders. On the clinical side, we work with population-level genomics, multi-omics, and rich clinical phenotyping to identify genetic mechanisms, developmental pathways, and predictors of intervention outcomes. In parallel, our cellular work uses 2D and 3D human derived neural systems to dissect molecular pathways and gene–environment interactions at early developmental stages. A potential project idea is to develop a multi-omics framework within either the clinical or cellular projects. For example, integrating genomic, transcriptomic, and methylation data in clinical cohorts to identify convergent risk pathways, or building a multi-layer molecular map of gene perturbations in neural models.

I would like to host a: **DDLS academic postdoc**

Contact: kristiina.tammimies@ki.se

Sara Hallin

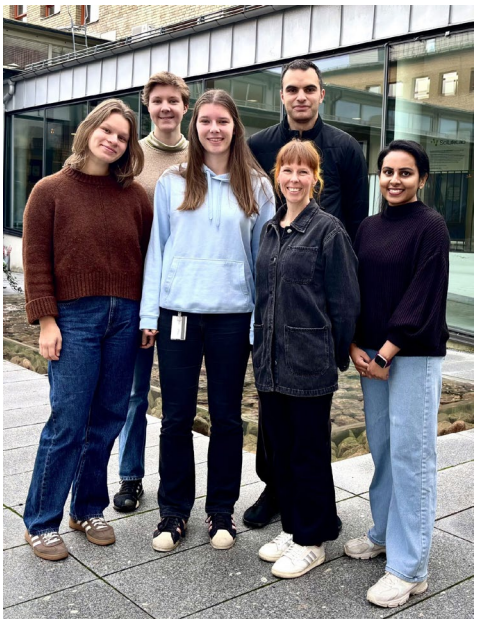
Affiliation: **Swedish University of Agricultural Sciences, Uppsala**

Mycology and Plant Pathology

Bio: I am professor of soil microbiology and lead a group dedicated to advancing the understanding of the ecology and physiology of soil microorganisms, and their roles in nitrogen and carbon cycling.

I would like to host a: **DDLS academic postdoc**

Contact: sara.hallin@slu.se



Astrid von Mentzer

Affiliation: **University of Gothenburg**

Microbiology and Immunology

Bio: The von Mentzer Lab explores bacterial evolution, host adaptation, and AMR spread across humans, animals, and environments using genomics, phylogenetics, and machine learning in a One Health context.

Project idea: Plasmid-mediated spread of antimicrobial resistance (AMR) is a growing threat, especially in Gram-positive pathogens that cause serious infections such as sepsis and hospital-acquired UTIs. Many conjugative plasmids in these bacteria carry both Type IV Secretion Systems (T4SS) and LPxTG-anchored adhesins—structures that help bacteria stick to surfaces and host tissues, promote biofilm formation, and increase DNA transfer efficiency. These modules likely work together to drive persistence and spread of AMR, but how they co-evolve and function as a unit is still unclear. In this project, we aim to explore the diversity, distribution, and evolutionary relationships between adhesins and T4SS across plasmids from Gram-positive bacteria. The project will involve large-scale genome mining, structure prediction (e.g. AlphaFold2), clustering, and comparative genomics. We are particularly interested in identifying plasmid architectures that may act as “mobile risk units” for resistance spread. Experimental work will be limited to validation of key findings. The project combines microbial genomics, protein structure prediction, and evolution. It would suit a candidate with interests in bacterial evolution, AMR, and data-driven biology. There is room to shape the direction depending on the postdoc’s background.

I would like to host a: **DDLS academic postdoc**

Contact: astrid.von.mentzer@gu.se

Pol Solé-Navais

Affiliation: **University of Gothenburg**

Wallenberg Laboratory/ Dept of Molecular and Clinical Medicine

Bio: Our group tackles questions in human quantitative genetics by using computational and statistical methods to understand the mechanisms behind pregnancy loss and reproductive health.

I would like to host a: **DDLS academic postdoc**

Contact: pol.sole.navais@gu.se

Andreas Höglund

Affiliation: **NeoTargets AB**

Tumour biology

Bio: At NeoTargets, a Stockholm based drug discovery company, we utilize our proprietary oncotarget discovery platform to identify novel and safe drug targets in cancer.

Project idea: We are looking for a PostDoctoral candidate in Bioinformatics to help us develop our proprietary oncotarget discovery platform.

What you will work on:

- Implementing AI-driven target evaluation and biomarker identification
- Building/operationalizing tools to assess druggability, target biology, and patient stratification/identification
- Mining and integrating large-scale oncology datasets (e.g., functional genomics, multi-omics, and clinical/genomic resources)

What we're looking for:

Strong bioinformatics and data-science skills with experience working with large datasets . It's a plus if you have hands-on experience with cancer biology repositories such as DepMap, cBioPortal, TCGA, and single-cell resources

I would like to host a: **DDLS industrial postdoc**

Contact: andreas.hoglund@neotargets.se

David Díez del Molino

Affiliation: **Stockholm University**

Centre for Palaeogenetics,
Department of Zoology

Bio: We use bioinformatic and computational methods to generate and integrate ancient, historical, and modern genomic data into evolutionary, population, and conservation genomics studies.

Project idea: In several current projects, we are investigating changes in genomic diversity during the last 200 years in response to population decline in key insect pollinators, specifically bumblebees and butterflies. A suggested project for a DDLS Postdoc fellow would be to investigate the adaptive responses of these pollinators to rapid anthropogenic environmental shifts over the last century in Sweden. Using a combination of historical and modern genomic data already generated, the fellow will reconstruct genetic baselines to identify signatures of selection associated with agricultural intensification, land-use changes, and pesticide exposure. Ultimately, this project will elucidate the capacity for pollinators to adapt to human-driven pressures, providing critical data to inform conservation strategies for these essential ecosystem service providers.

I would like to host a: **DDLS academic postdoc**

Contact: david.diez@zoologi.su.se

Gabriela Montejo-Kovacevich

Affiliation: **Uppsala University**

Ecology and Genetics

Bio: Assistant Professor & SciLifeLab Fellow at Uppsala University, studying climate adaptation using field ecology, behaviour and population genomics, with a focus on insects and rapid evolution.

I would like to host a: **DDLS academic postdoc**

Contact: gabriela.montejo-kovacevich@scilifelab.uu.se

Ludvig Lizana

Affiliation: **Umeå University**

Physics, Integrated Science Lab (IceLab)

Bio: Lizana works at the intersection of physics and cell biology, using theory and simulations to explore gene regulation, epigenetics, aging, and networks, and values curiosity and collaboration.

Project idea: Synthetic biology aims to reprogram cellular behavior by assembling molecular components into functional circuits. Cells process information through molecular networks, much like electronic circuits process signals through logic gates, but with a crucial difference: cellular networks have evolved through natural selection, whereas electronic circuits are engineered. Although recent advances now make cellular reprogramming feasible, building synthetic circuits remains labor-intensive, and their behavior is often difficult to predict. This project will develop computational models to support the understanding and optimization of synthetic molecular circuits. The postdoctoral researcher will model individual molecular gates and use simulations to study their behavior in larger circuits. These models will identify critical system parameters that determine circuit behavior and enable predictable molecular gate design. Because systematic parameter sweeps are difficult experimentally, simulations provide an efficient way to explore parameter space and establish design principles. The project will be conducted in close collaboration with Prof. Yaowen Wu at Umeå University, integrating computational modeling with his wet-lab experiments. The candidate should have experience in stochastic simulation, programming, and ordinary differential equations.

I would like to host a: **DDLS academic postdoc**

Contact: ludvig.lizana@umu.se

Anders Eklund

Affiliation: **Linköping university**

Department of biomedical engineering

Bio: AE is a professor working on a range of topics, including radiotherapy, cancer, and orthopedics. The common theme is to use deep learning for image data.

Project idea: Anything related to deep learning for medical images, cancer and orthopedics, such as federated learning, generative AI, foundation models, fusion of multimodal data. We currently have one project in federated learning, one in radiotherapy, two in orthopedics, and one in cardiovascular disease. We use deep learning in all projects.

I would like to host a: **DDLS academic postdoc**

Contact: anders.eklund@liu.se

Juliette Griffie

Affiliation: **Stockholm University**

Dept. of Biochemistry and Biophysics

Bio: Griffie's laboratory (host lab, https://www.scilifelab.se/researchers/juliette-griffie/). Research interests: Bioimage analysis, deep learning, data driven life science.

Project idea: Biomedical research heavily relies on images as they provide valuable insight about local context and spatial relationship. Thus, microscopy is crucial to unravel and characterise complex cellular processes. As rapid development in optics and sample preparation provide ever larger and more informative image-based data sets (e.g., improved resolution, increased content), the analysis of such data is rapidly becoming a critical bottleneck. Deep learning (DL) has proven a very powerful tool for image processing (from denoising to segmentation), but it typically relies on broad and big annotated data sets for training and benchmarking. In contrast, the vast majority of molecular and cell biology laboratories produce small image-based data sets (often only few hundreds of cells) with limited annotations, tailored to answer a very specific biological question. For DL to attack these pressing biological issues, these shortcomings (small data sets, limited annotations) need to be addressed computationally. The Griffie's laboratory (SciLifeLab) and Volpe's laboratory (University of Gothenburg) propose a joint project to investigate how interpretable machine learning can be tailored to improve annotation strategies in biomedical imaging, with a focus on microscopy data sets. The data sets are already available and this is a purely computational project. We are looking for candidates with strong expertise in machine learning.

I would like to host a: **DDLS academic postdoc**

Contact: juliette.griffie@scilifelab.se

Peter Heintzman

Affiliation: **Stockholm University**

Geological Sciences / Centre for Palaeogenetics

Bio: Research Group Leader in ancient DNA/palaeogenomics. Specifically: Molecular/computational methods, sedimentary ancient DNA ecological community reconstruction, extinct megafaunal population genomics

I would like to host a: **DDLS academic postdoc**

Contact: peter.d.heintzman@geo.su.se

Zheng Zhao

Affiliation: **Linköping University**

Division of Statistics and
Machine Learning

Bio: Assistant professor (tenure-track), Division of Statistics and Machine Learning, working on computational statistics and machine learning, especially, generative diffusion models.

Project idea: Our group (with frequent collaborators locally and at Uppsala University) has a strong background in the foundation of statistical machine learning methods, especially differential equations and generative diffusion models, demonstrated by publications in many prestigious ML venues (e.g., ICML, ICLR, and AISTATS). We are very happy to host postdocs working on the intersection between within DDLS strategic research areas and data-driven statistical machine learning. For instance, applying and developing machine learning methods and models for estimation and sampling problems (e.g., parameter estimation in epidemiology modelling and generating molecule design in biology, and Bayesian inverse problems in general). For more details of the group, see, https://zz.zabemon.com.

I would like to host a: **DDLS academic postdoc**

Contact: zheng.zhao@liu.se

David Gisselsson Nord

Affiliation: **Lund University**

Division of Clinical Genetics

Bio: David Gisselsson Nord is a Lund University professor studying genomics in childhood cancer and genetic-security risks, leading national projects. He represents Sweden with NATO and WHO.

Project idea: Bioconvergence is the fusion of biotechnology, advanced computation, and AI. It already drives development in life sciences by accelerating drug discovery, improving disease surveillance, and enabling precision medicine. These capabilities rely on automated data analysis, machine learning pipelines, and tools that integrate biological, digital, and behavioral datasets. Alongside these benefits, recent assessments show that bioconvergence also creates new societal risks. Our previous research indicates that the most immediate threats lies in software enabled misuse of biodata in intelligence, influence operations, and cognitive warfare. Civil defense and biosecurity frameworks have not yet adapted, leaving policy development behind technology. This multidisciplinary project uses AI assisted open-source intelligence (OISINT) analysis to evaluate how bioconvergence will likely impact intelligence and disinformation over the next 5–10 years. It focuses on innovating AI OSINT agents and LLM based structured analytic techniques to identify threat actors and to trace technical trends and deployment of bioconvergence technology in conflict zones. We will thereby identify early warning signs and different counterstrategies for policy makers to prevent and manage risks of bioconvergence being used to violate ethical norms. This work of vigilance will be necessary to avoid excessive regulation of bioconvergence, which would risk slowing down data driven life science development severely.

I would like to host a: **DDLS academic postdoc**

Contact: david.gisselsson_nord@med.lu.se

Kasper Karlsson

Affiliation: **Karolinska Institutet**

Oncology-Pathology

Bio: We are an ERC-funded group at SciLifeLab Solna developing data-driven single-cell and spatial approaches to model tumor heterogeneity, evolution, and therapy resistance.

Project idea: Our goal is to develop more effective cancer therapies that improve patient outcomes. To achieve this, we leverage the most relevant experimental and cell culture models and combine them with data-driven hypotheses to address clinically relevant challenges in cancer biology and therapy response. Within the lab, one ongoing DDLS-funded effort aims to establish better single-cell perturbation prediction models in order to enable in-silico screening for interventions that can shift resistant tumor cell states toward more therapeutically favorable states, such as differentiated or drug-sensitive phenotypes. We have access to large, well-annotated pediatric cancer genome and transcriptome datasets through Barntumörbanken, enabling tight coupling between patient-derived data and experimental model systems. Potential research directions include mapping differentiation landscapes in pediatric cancers (e.g. neuroblastoma), developing endogenous lineage-tracing strategies based on naturally occurring genomic variation, and modeling cellular responses to drugs and genetic perturbations. These examples highlight possible research directions, but the project will be developed together with the candidate, who is encouraged to bring complementary ideas within data-driven life science and translational cancer research.

I would like to host a: **DDLS academic postdoc**

Contact: kasper.karlsson@ki.se

Erik Sonnhammer

Affiliation: **Stockholm University**

Department of Biochemistry and Biophysics

Bio: Professor of Bioinformatics at Stockholm University, previously at Karolinska Institutet, Stockholm. Ph.D. in bioinformatics at the Sanger Institute. Present H-index 72 and ~90000 citations.

Project idea: The goal of the project is to develop and apply gene regulatory network (GRN) inference methods from spatial and single-cell multi-omics data with AI and gene perturbations. By building a deep learning framework with a specialized architecture to efficiently connect data with perturbed genes, inference reliability will be boosted. To enable accurate GRN inference from spatial multi-omics data, a system will be developed for inferring the perturbation design based on gene expression and chromatin accessibility data. This way inferred region-specific GRNs can be connected to particular tissue phenotypes such as different cancer stages. The developed system will be applied to spatial liver cancer data generated by the group. Understanding cancer dysregulation can lead to new therapies to curb one of the major causes of death. The project involves programming, data analysis, benchmarking, and modelling, as well as application of the developed methods to experimental data. The successful candidate should be highly motivated and have a Ph.D. in bioinformatics or related field. Alternatively, a Ph.D. in molecular biology or related field and 2 years of postdoctoral experience in bioinformatics research and programming, documented by scientific publications. Proficiency with gene expression data analysis techniques is essential. Excellent skills in computer programming (primarily Python, Matlab, and R), AI methods, and UNIX are necessary merits.

I would like to host a: **DDLS academic postdoc**

Contact: erik.sonnhammer@scilifelab.se

Laura Carroll

Affiliation: **Umeå University**

Department of Clinical Microbiology

Bio: As a computational microbiology group, we develop bioinformatic methods, which can leverage massive microbial (meta)genomic data sets to improve pathogen surveillance and source tracking efforts.

Project idea: High-throughput single-cell metagenomic sequencing (scMetaG) methods have the potential to transform microbiology...but dealing with the massive amounts of complex data that they generate is a massive challenge! Our group is developing novel computational methods, which can make sense of all this data! Specifically, we've developed Bascet, a command-line suite designed to scale to massive scMetaG datasets (>1 million cells), and Zorn, an R package/workflow manager that enables reproducible scMetaG data analysis, exploration, and visualization. Here, the project is flexible; postdocs can work on improving methods within Bascet/Zorn (e.g., trimming, de-barcoding, de novo assembly, genome annotation, scMetaG data visualization), developing novel analysis methods (e.g., novel methods for longitudinal scMetaG analysis, machine learning-based methods for genome annotation)...or improving the many methods/tools we're currently developing!

I would like to host a: **DDLS academic postdoc**

Contact: laura.carroll@umu.se

Anna Plym

Affiliation: **Karolinska Institutet**

Dept. of Medical Epidemiology and Biostatistics

Bio: Our group, lead by Associate Professor Fredrik Wiklund and Assistant Professor Anna Plym, conducts studies in genetic epidemiology, aiming to identify inherited genetic factors for prostate cancer.

Project idea: The proposed project idea aims to identify not only high-risk groups but also men at low risk for prostate cancer who can safely omit frequent prostate cancer testing. Based on genetic susceptibility and other biomarkers/ risk factors, we estimate that at least 40% of men, and likely higher, can be reliably classified as having a low risk of developing potentially fatal prostate cancer (Plym et al, Clinical Cancer Research 2022 & Plym et al, JAMA Network Open 2024).

I would like to host a: **DDLS academic postdoc**

Contact: anna.plym@ki.se

Ran Friedman

Affiliation: **Linnaeus University (LNU)**

Chemistry and Biomedical Sciences

Bio: Ran Friedman leads the Computational Chemistry and Biochemistry Research Group at LNU. We have strong interest in cancer therapies drug resistance, protein-ion interactions and protein-ligand binding.

Project idea: We wish to provide a mechanistic understanding how a single point mutation leads to a new function in isocitrate dehydrogenase (IDH) enzymes and furthermore how the enzymes can be inhibited efficiently. IDH are enzymes whose activity is important to cellular metabolism. Mutations in IDH1 and IDH2 lead to the development of new functionality, whereby the product of the catalytic reaction (normally α-ketoglutarate, αKG) is reduced to D-2- hydroxyglutarate (D2HG). Production of D2HG leads to tumourigenesis. Importantly, how IDH mutations lead to their new, oncogenic functionality is not clear. Although IDH inhibitors are used in cancer therapy, their efficacy is reduced due to resistance. Understanding resistance to IDH inhibitors is therefore another aim of this study.

I would like to host a: **DDLS academic postdoc**

Contact: ran.friedman@lnu.se

Carsten Daub

Affiliation: **Karolinska Institutet**

Medicine Huddinge

Bio: We study how gene regulation shapes health and disease, combining clinical samples, high-throughput sequencing, and advanced bioinformatics at Karolinska Institutet.

Project idea: The 10x Genomics Visium Spatial Transcriptomics (ST) platform relies on the Space Ranger pipeline, which maps sequencing reads to gene models to produce spot-level gene expression matrices. However, alterations in pre-mRNA processing, especially changes in 3′ untranslated region (3′UTR) lengths, are increasingly recognized in cancer and have been linked to disease severity and subtype. This project aims to systematically assess transcript-structure variation in ST datasets to determine whether 3′UTR dynamics can serve as spatial biomarkers of cancer severity and subtype identity. The results have the potential to expand the biological insights extractable from ST data and may be broadly relevant across diverse disease-related ST datasets.

I would like to host a: **DDLS academic or industrial postdoc**

Contact: carsten.daub@scilifelab.se

Alexander Lyubartsev

Affiliation: **Stockholm University**

Dept. of Chemistry

Bio: PhD in Physics 1988. Assoc. professor (2001) and full professor (2007) in Physical Chemistry at Stockholm University. Research in modeling and simulations of biomolecular systems.

Project idea: Biological membranes, consisting of a variety of lipids, steroids, polysacharides, membrane proteins, constitute outer shells of all biological cells, as well as of various intracellular organells. Biomembranes are involved in critically important cellular processes and take active role in the life of cell. Understanding of molecular processes and molecular mechanisms of membrane functioning is crucially important question in molecular and cell biology. In experiments it is difficult to reveal molecular details of biomembrane functioning since they are inherently disordered systems and subject to temporal and spacial fluctuations. Computer simulations and modeling provide atomic-level insight into molecular behavior, mechanisms, and interactions, complementing experiments with detailed, predictive data, revealing how molecular interactions give rise to biological functioning. I am inviting to host a DDLS post-doc project dealing with biomembranes modeling using physics-based computational methods (molecular dynamics, multiscale simulations) and data-driven - machine learning/AI approahes to adress actual problems in biomembranes research.

I would like to host a: **DDLS academic postdoc**

Contact: alexander.lyubartsev@su.se

Shafqat Ahmad

Affiliation: **Södertörn University**

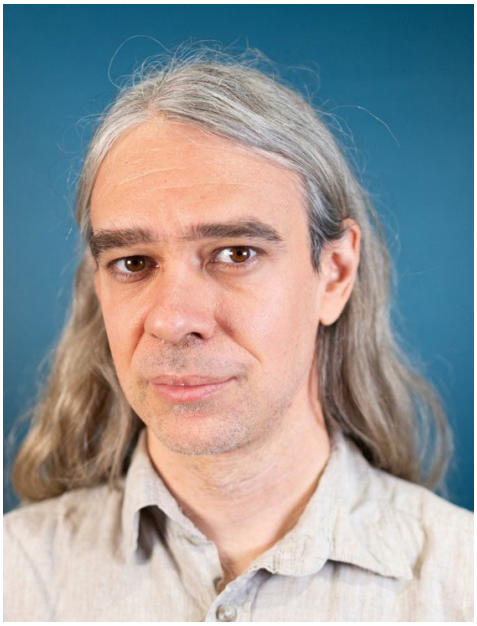
Dept. of Environment, Development and Sustainability Studies, School of Natural Sciences, Technology and Environmental Studies

Bio: I am an Associate Professor and Senior Lecturer. My research investigates how environmental, genetic, metabolomic, and gut microbiota factors influence cardiometabolic and cardiovascular disease.

Project idea: This project explores how alcohol consumption affects cardiometabolic disease risk. Using large-scale population cohorts, we will examine the relationships between alcohol intake patterns—type, frequency, and volume—and disease outcomes. By integrating molecular, genetic, and epidemiological data, including biomarkers from blood and urine, we aim to identify the pathways through which alcohol influences cardiometabolic health. The findings will enhance understanding of alcohol-related disease mechanisms and may guide strategies for prevention and early intervention.

I would like to host a: **DDLS academic postdoc**

Contact: shafqat.ahmad@sh.se



Carl Nettelblad

Affiliation: **Uppsala University**

Dept. of Information Technology

Bio: Professor in scientific computing, focusing on iterative optimization of data-driven models, HMMs and deep learning for eukaryotic genome SNP data analysis. Competed in IMO, IOI, IBO, ICPC.

Project idea: I am open to host a student with a novel distinctive idea. Our main current lines of work include contrastive learning methods for creating embeddings of read sequences, with efficient techniques to do mapping in a novel ways on GPU, possibly extending to assembly. We also want to push our contrastive genome embeddings to phenotype prediction through fine-tuning. Within the group, we have also explored using diffusion models for genotype imputation, with no member actively considering that aspect right now (so it's up for the taking!). An older line of work that would be relevant to explore is the method COACS (Alberto Pietrini, Carl Nettelblad, Optics Express 2019) for low-photon count X-ray single particle imaging. This method could be made usable in practice by exploring the proper application of preconditioners, possibly with Dykstra's projection algorithm. There is considerable experience in preconditioners for other problems at our division. We see understanding the numerical behavior of iterative optimization within life science, be it COACS, an HMM, or deep learning approaches, as our overaching theme.

I would like to host a: **DDLS academic postdoc**

Contact: carl.nettelblad@it.uu.se

Axel Abelein

Affiliation: **Karolinska Institutet**

Medicine Huddinge

Bio: Group Leader & Docent at Karolinska Institutet. Our group studies how naturally occurring molecular chaperones target amyloids in neurodegenerative diseases.

Project idea: "Harnessing molecular chaperones to combat amyloid toxicity": We are seeking a postdoctoral researcher with a background in structural biology and protein biochemistry who will contribute to elucidate the interplay of molecular chaperones with amyloid-forming proteins associated to neurodegenerative disorders, such as Alzheimer's and Parkinson's disease. The postdoctoral project may include::

- Structural characterization of amyloids and molecular chaperones using cryo electron microscopy (cryo EM)
- NMR spectroscopy to probe chaperone–amyloid interactions and molecular dynamics
- Integration of AI assisted protein structure prediction
- Characterization of liquid–liquid phase separation (LLPS) and its role in amyloid regulation Homepage: https://ki.se/en/bionut/axel-abelein-group

I would like to host a: **DDLS academic postdoc**

Contact: axel.abelein@ki.se

Julian Walfridsson

Affiliation: **NeoTargets AB**

NeoTargets

Bio: NeoTargets is a Stockholm-based drug discovery company using a proprietary AI-driven platform to identify novel, safe cancer drug targets and enable next-generation targeted therapies.

I would like to host a: **DDLS industrial postdoc**

Contact: julian.walfridsson@neotargets.se

Joan Camunas-Soler

Affiliation: **University of Gothenburg**

Institute of Biomedicine

Bio: Joan is a Wallenberg Molecular Medicine Fellow focused on data-driven genomics and precision medicine, integrating single-cell technologies and liquid biopsies.

Project idea: I am particularly interested in supporting applicants interested in working on data-driven methods related to:

* Mining RNA- or DNA-based liquid biopsy datasets to study infectious diseases.
* Analysis and interpretation of long-read sequencing data for liquid biopsy applications
* Development of deconvolution algorithms for single-cell electrophysiology data
* Joint analysis of single-cell transcriptomic and physiological measurements (e.g. Patch-seq, functional imaging)
* Novel computational and statistical approaches for spatial transcriptomics analysis

I would like to host a: **DDLS academic or industrial postdoc**

Contact: joan.camunas@gu.se

Golnaz Taheri

Affiliation: **KTH Royal Institute of Technology**

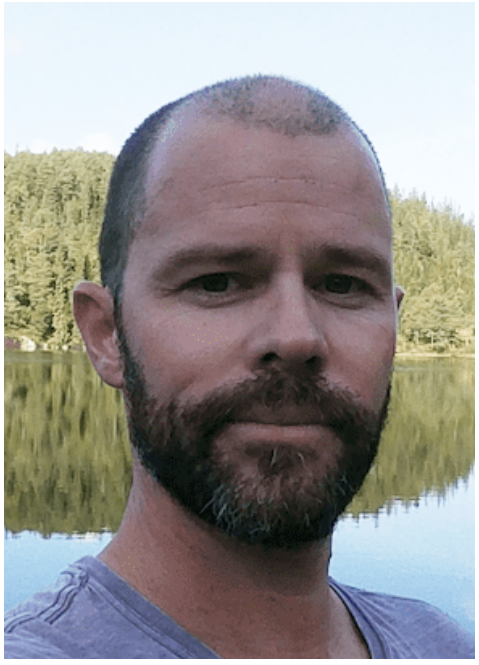
Dept. of Computational Science and Technology

Bio: My lab's research focuses on machine learning and graph-based methods for multi-omics data integration, cancer biomarker discovery, drug discovery, and precision medicine.

Project idea: I have two postdoctoral project topics, one academic and one industrial. The industrial project is in collaboration with Taner Arslan at Chiesi and focuses on building machine-learning–based pipelines that integrate imaging data with molecular profiles to enable patient endotyping in respiratory diseases. The other project is academic and focuses on drug safety and the molecular profiling of drugs for interaction prediction.

I would like to host a: **DDLS academic or industrial postdoc**

Contact: golnazt@kth.se



Nicolas Dussex

Affiliation: **Swedish Museum of Natural History**

Dept. of Population Analysis and Monitoring

Bio: Evolutionary biologist focusing on the genomics of small populations and responses of marine species to climat change

Project idea: My research focuses on two main topics:

1) marine species museomics, genome erosion, adaptation
2) marcogenomics of sea warming (methods dev. or empirical data)

I would like to host a: **DDLS academic postdoc**

Contact: nicolas.dussex@gmail.com

Janne Lehtiö

Affiliation: **Karolinska Institutet and SciLifeLab**

Dept. of Oncology and Pathology, Karolinska Institutet

Bio: Janne Lehtiö is professor of proteomics at KI with shared position at the Karolinska Hospital. Lehtiö's group has pioneered proteogenomics to decode molecular mechanisms to improve cancer treatments

Project idea: We are seeking postdoctoral researchers with a strong background in computational science to join an ambitious project developing agentic AI approaches for mining proteogenomic data to improve personalized cancer treatment selection. The project addresses real clinical needs and spans the full translational pipeline from advanced method development to clinical implementation. Our research group offers an innovative, open, and collaborative multidisciplinary environment bringing together computational scientists, biologists, clinicians, and proteomics and multi-omics experts. The position is ideally suited for candidates eager to apply cutting-edge AI methods to complex biomedical data and to make a tangible impact on precision oncology. We encourage applicants interested in the DDLS postdoctoral call to apply together with us.

I would like to host a: **DDLS academic postdoc**

Contact: janne.lehtio@scilifelab.se

Tara Stanne

Affiliation: **University of Gothenburg**

Dept. of Laboratory Medicine, Institution of Biomedicine

Bio: By integrating multi-omics data—specifically proteomics and genetics—with machine learning, we aim to decode the mechanisms underlying various stroke etiologies to improve clinical prevention

Project idea: Stroke is a major cause of death and long term disability. Most cases arise from a blood clot blocking a vessel in the brain, yet in roughly a quarter of ischemic strokes the clot's origin remains unknown (cryptogenic stroke). Our research aims to uncover the biological mechanisms underlying different ischemic stroke subtypes, with a particular focus on cryptogenic stroke. This project integrates human genetics with deep, bottom up proteomics to map proteins and protein isoforms in blood samples from stroke patients and controls. We will apply Seer's Proteograph® platform together with data independent acquisition mass spectrometry to generate unbiased, high resolution plasma proteomes. These proteomic data will be combined with genomic information to identify protein altering variants and isoforms. By comparing controls with major ischemic stroke subtypes—including cryptogenic stroke—we aim to discover novel isoform level signatures that can improve diagnosis, patient stratification, and precision therapy development. The postdoc will lead analyses to identify molecular signatures shared across, or unique to, specific etiologic subtypes. The position is well suited for candidates with experience in mass spectrometry–based proteomics, DIA workflows, or computational analysis of large proteomics datasets. Additional opportunities include: • Developing ML models • Building tools for 3D isoform prediction • Developing a Shiny App to disseminate results

I would like to host a: **DDLS academic postdoc**

Contact: tara.stanne@gu.se

Charlotte Ling

Affiliation: **Lund University**

Dept. of Clinical Sciences, Malmö

Bio: Charlotte Ling is Professor and PI at Lund University Diabetes Centre (LUDC), leading research on epigenetic mechanisms in type 2 diabetes using large-scale human and single-cell genomics.

Project idea: Type 2 diabetes (T2D) affects hundreds of millions worldwide. It is characterized by hyperglycemia due to impaired insulin secretion from pancreatic islets and insulin resistance. Pancreatic islets contain several hormone-secreting cell-types, making cell-type–specific profiling essential for fully understanding disease mechanisms. Our team has generated the world's largest single-nucleus multiomic resource from human islets—snRNA-seq and snATAC-seq—from 126 donors (100 non-diabetic, 26 T2D), complemented by bulk RNA-seq, DNA methylation, and genotypes from >400 donors. We also have snCUT&Tag data from some donors. Together, these datasets provide an unprecedented foundation for data-driven discovery of disease mechanisms in an important human tissue. The postdoc will leverage these multi-layered datasets by conducting data-driven integrative analyses that uncover a cell-type–specific regulatory architecture and its perturbation in T2D. The candidate is encouraged to design and implement scalable and interpretable computational strategies — such as integrative statistical modeling, multiomic factor analysis, and machine learning–based regulatory inference — to identify regulatory mechanisms disrupted in T2D. In addition to bioinformatics expertise, Professor Lings' lab has extensive wet-lab knowledge and facilities, where discovered regulatory elements and candidate genes will be experimentally tested using e.g., CRISPR–dCas9 epigenetic editing to establish causal relevance.

I would like to host a: **DDLS academic postdoc**

Contact: charlotte.ling@med.lu.se

Anna Tomberg

Affiliation: **AstraZeneca**

Discovery Science

Bio: I am an Associate Principal Scientist at AstraZeneca R&D in Gothenburg, working on AI in drug discovery.

Project idea: The Mission: Use AI to automate analytical data processing for high-throughput experimentation and metabolomics. Why This Matters: Right now, scientists spend countless hours processing analytical data. Your work could change that—freeing up time for discovery, accelerating drug development, and pushing the boundaries of what's possible in chemical research. The Team: You'll collaborate with Prof. Belén Martín-Matute (Stockholm University: https://www.organ.su.se/bm/) and work alongside AstraZeneca experts who are as passionate about innovation as you are. Who We're Looking For: Someone with a strong background in AI/ML or computational chemistry who's tired of theoretical problems and wants to tackle messy, real-world data. You should be comfortable working across disciplines—bridging code and chemistry—and excited about the challenge of making AI tools that scientists will actually use.

I would like to host a: **DDLS industrial postdoc**

Contact: anna.tomberg@astrazeneca.com

Aelys Humphreys

Affiliation: **Stockholm University**

Dept. of Ecology, Environment and Plant Science

Bio: Comparative biologist studying the evolution and extinction of biodiversity using phylogenetic and modelling approaches. Often global in scope, studies involve synthesising large-scale datasets.

Project idea: Probabilistic modelling of species extinction Loss of biodiversity is one of the most serious environmental challenges of our time. However, evidence for the biodiversity crisis rests on a small fraction of all species and approaches for scaling up and improving accuracy of our understanding of ongoing species losses are sorely needed. In this context, I propose a project aimed at implementing and developing methods for estimating species extinction using probabilistic and machine learning approaches and the masses amounts of information stored globally in natural history collections and other biodiversity observation platforms. Most of my work centres on plants but approaches are suitable for any group with poorly known extinction levels (e.g. fungi, insects). Further reading: Humphreys et al. 2025. New Phytologist. https://doi.org/10.1111/nph.70552. Suitable for DDLS research area Evolution & Biodiversity.

I would like to host a: **DDLS academic postdoc**

Contact: aelys.humphreys@su.se

Ingemar André

Affiliation: **Lund University**

Biochemistry and Structural Biology

Bio: We develop machine learning methods for protein structure prediction and de novo design, and study how protein expression and folding is controlled in the cell with evolutionary and machine learning

Project idea: Large protein complexes are central to many biological processes in the cell. Formation of large assemblies requires tight control of the rate of synthesis to control the relative concentrations of protein subunits, but also to control the assembly mechanism. The goals of this project is to build a deep learning model that can describe assembly formation based, trained on genome and protein sequences but also so transcriptomics and proteomics data. The goal is to make predictions from this model that can be experimentally validated.

I would like to host a: **DDLS academic postdoc**

Contact: ingemar.andre@chem.lu.se

Jens Sjölund

Affiliation: **Uppsala University**

Information Technology

Bio: Primary research interests: machine learning, optimization, experiment design, precision medicine (especially cancer, my background is in radiotherapy and MRI). WASP Fellow and ELLIS member.

I would like to host a: **DDLS academic or industrial postdoc**

Contact: jens.sjolund@it.uu.se

Dominik Dietler

Affiliation: **Lund University**

Faculty of Medicine

Bio: We are an interdisciplinary research environment spanning epidemiology, precision medicine, data science, virology, and law focusing on the development of novel AI methods in public health research.

Project idea: The goal is to develop a generic foundation AI model that enables new scientific discoveries from large-scale, deeply characterized population cohorts including biological material and linked longitudinally with Sweden's rich population and health-care registers. Similar to how GPT-3 is pretrained on natural language, our model will be pretrained on an extensive "cohort language" constructed from multimodal data describing lifelong health trajectories. This model will be used for a broad range of cutting-edge research tasks, including identifying risk factors and biomarkers, developing more effective therapies and preventive measures, and assessing health impacts. As one specific example, a downstream application may uncover differences in omics profiles associated with cardiovascular risk factors such as blood pressure. Interventions that shift these profiles could point to new therapeutic opportunities and preventive strategies, while subtle data patterns may help identify hidden high-risk individuals who would benefit most from treatments like blood-pressure-lowering therapy. By integrating cohort data with biological material and register data, the project opens the door to diverse novel and unforeseen research opportunities and maximizes the value of Sweden's exceptional data landscape, positioning AI as a transformative tool for population-level health research.

I would like to host a: **DDLS academic postdoc**

Contact: dominik.dietler@med.lu.se

Bo Jacobsson

Affiliation: **University of Gothenburg**

Dept. of Obstetrics and Gynecology

Bio: We advance the field of human quantitative genetics by leveraging cutting-edge computational and statistical approaches to uncover the biological mechanisms causing preterm birth

I would like to host a: **DDLS academic postdoc**

Contact: bo.jacobsson@obgyn.gu.se

Amir Aminifar

Affiliation: **Lund University**

Dept. of Electrical and Information Technology

Bio: Amir Aminifar is an Associate Professor and Docent, the Director of the Intelligent Systems Laboratory, and a Wallenberg AI, Autonomous Systems and Software Program (WASP) Fellow.

Project idea: Large Language Models (LLMs) have attracted a lot of attention in the past few years. LLMs can be adopted in various contexts, including healthcare and the medical domain. Trust in LLMs, however, represents a major challenge, particularly when it comes to precision medicine and diagnostics. An interesting research direction is to investigate the potential risks associated with the adoption of LLMs in such domains and build trust in the decisions made by the LLMs and machine learning techniques. In our group, we have a successful history of working on fostering trust in machine learning techniques and LLMs, including in the context of medical applications, in collaboration with university hospitals, e.g., Lausanne University Hospital in Switzerland, and in collaboration with major industries, e.g., Google DeepMind in the US.

I would like to host a: **DDLS academic or industrial postdoc**

Contact: amir.aminifar@eit.lth.se

Sebastian Lewandowski

Affiliation: **Karolinska Institutet**

Clinical Neuroscience

Bio: Can brains heal their scars? We aim to understand the brain fibrotic response to neurodegeneration and the mammalian evolution of scar free recovery.

Project idea: Damage to the central nervous system (CNS) in mammals is currently considered irreversible. In most mammals, regardless of the source of injury, the resulting brain fibrotic lesions permanently prevent from efficient regeneration after brain trauma, ischemia or age-related neurodegeneration. Our project will identify the mechanisms behind the scarless regeneration of the central nervous system in African spiny mice (Acomys sp.). Traditional approaches to studying CNS tissue scarring are bound to an inherent paradox. Repair is typically studied in mice and rats which develop fibrotic scarring and do not regenerate well, or in worms and salamanders which do regenerate well but are evolutionarily too distant from mammals to practically translate these observations. Recent studies revealed that African spiny mice (Acomys genus) can regenerate multiple tissues without fibrotic scarring and to restore coordinated walking after complete spinal cord transection (Fig. 1). This unique mammalian regenerative ability was somehow acquired through biological evolution to escape predators and is controlled by yet unknown genetic factors. Our project will identify uniquely evolved genes in the Acomys cahirinus genome which can contribute to the regenerative capacity. We will also distinguish the mechanisms that reduce lesions in the CNS during neurodegenerative autoimmune injury using single-cell multiomics.

I would like to host a: **DDLS academic or industrial postdoc**

Contact: sebastian.lewandowski@ki.se

Helga Westerlind

Affiliation: **Karolinska Institutet**

Dept. of Medicine Solna

Bio: I'm a computational epidemiologist working within the field of rheumatic diseases. I use data driven methods and integration of various types of data, aiming to answer clinically important questions.

Project idea: Patients with rheumatoid arthritis (RA), a chronic inflammatory disease, are currently all started on the same treatment despite only one third achieving a good response. No reliable predictors for treatment response are known and prediction models are needed. As a post-doc, you will use data-driven methods to integrate biological, register, various clinical EHR and lab data to build a prediction model for treatment response in RA. The foundation is our study Epidemiological Investigation of RA (EIRA). EIRA has been linked to the Swedish Rheumatology Quality register (SRQ), which contains data on the RA disease. Through EIRA, you will also have access to genome-wide genetic data, proteomics, and an array of various auto-antibodies related to rheumatic diseases. Moreover, EIRA has been linked to the Stockholm region health care data, containing health care visits from specialist and primary care, medical chart data, referral letters, medications and results from laboratory tests. The project will take place at the Division of Clinical Epidemiology (KEP), at the Department of Medicine Solna, Karolinska Institutet, in professor Johan Askling's research group, which focuses on the clinical epidemiology of chronic inflammatory diseases. The project will use a collaborative, interdisciplinary approach, involving experts from the relevant fields such as rheumatology, epidemiology, immunology, machine learning, biostatistics, and data science.

I would like to host a: **DDLS academic postdoc**

Contact: helga.westerlind@ki.se

Pierre Nyquist

Affiliation: **Chalmers and University of Gothenburg**

Mathematical Sciences

Bio: Applied mathematician working on topics in probability, statistics, computational mathematics and machine learning.

Project idea: Generally interested in all problems related to computational questions, primarily using stochastic methods (special focus on Markov chain Monte Carlo) or tools from machine learning. See some of my past work, e.g. with researchers at SciLifeLab in Stockholm related to brain modelling: https://pierrenyq.github.io. Interested in both theoretical problems motivated by questions in life science, and more applied, computational problems that require more than vanilla-type methods.

I would like to host a: **DDLS academic postdoc**

Contact: pnyquist@chalmers.se

Paulo Czarnewski

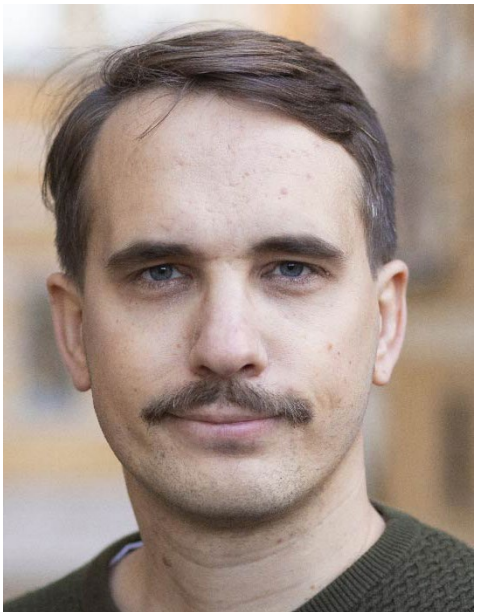
Affiliation: **Precisium AI**

Precisium AI

Bio: I'm Paulo Czarnewski, CEO of Precisium AI, leading the development of atlas-level AI models for precision medicine, transforming database-scale omics data into actionable insights for drug discovery.

I would like to host a: **DDLS industrial postdoc**

Contact: paulo.czarnewski@precisium.ai



Erik Smedler

Affiliation: **University of Gothenburg**

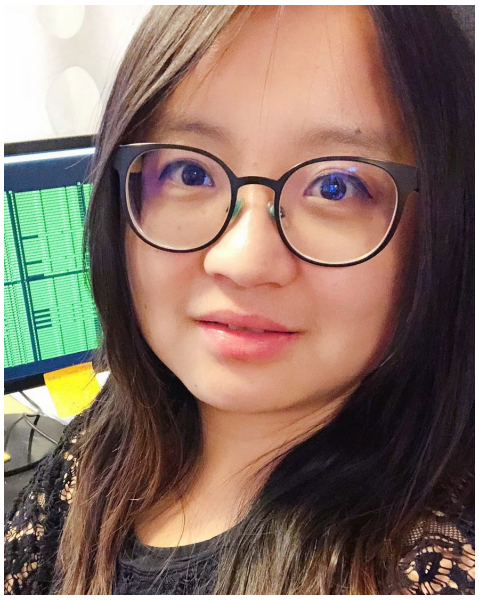
Neuroscience and physiology

Bio: Clinician-scientist leading a molecular neurobiology lab focusing on both the biology of mental disorders and glioma. General interest in how stem cells become neurons and connect in networks.

Project idea: Global meta-analysis of RNAseq data etc from stem cell-based neural models of mental disorders. We want to develop methodologies for merging highly complex data from wide range of sources to identify replicable biological markers of mental disorders.

I would like to host a: **DDLS academic postdoc**

Contact: erik.smedler@gu.se



Ping Chen

Affiliation: **Karolinska Institutet**

Dept. of Laboratory Medicine

Bio: Computational biologist and group leader interested in multi-omics and AI approaches for non-invasive diagnostics and mechanistic insight in metabolic disease.

Project idea: I am interested in and would like to support projects that (1) develop novel AI-enabled digital tools for non-invasive diagnostics and risk stratification, and (2) use data-driven multi-omics approaches to dissect cellular and molecular mechanisms underlying human disease progression.

I would like to host a: **DDLS academic or industrial postdoc**

Contact: ping.chen@ki.se

Matthew Webster

Affiliation: **Uppsala University**

Medical Biochemistry and Microbiology

Bio: My group works on population and evolutionary genomics, mainly using bees. More information can be found here: www.websterlab.net

Project idea: The cause of ageing is a question of fundamental importance for both evolutionary biology and medicine. A prominent theory suggests that mutations in somatic cells are significant drivers of ageing. Long-lived mammals have much lower somatic mutation rates than those with short lifespans. However, there is so far no evidence that inter-individual variation in lifespan correlates with somatic mutation rate. Frontline research in this field is hampered by the fact that somatic mutations in normal tissue are extremely difficult to reliably assay. To address this, the Webster lab has been using NanoSeq, a duplex sequencing protocol with single-molecule accuracy. We propose to measure somatic mutation rates in experimental evolution lines of seed beetles (Acanthoscelides obtectus). Early- and late-reproducing lines have evolved a more than two-fold difference in longevity over the course of >400 generations of evolution. Differences in expression of mismatch repair genes have been observed between lines, suggesting that they may differ in response to DNA damage. We wish to test the hypothesis that differences in lifespan are caused by differences in somatic mutation rate. We will estimate somatic mutation rates in multiple individuals and ages across replicate lines using NanoSeq. This will allow us to test how somatic mutations accumulate over time and whether rates differ between lines with different lifespans. This has broad implications for our understanding of ageing.

I would like to host a: **DDLS academic postdoc**

Contact: matthew.webster@imbim.uu.se

Alek Erickson

Affiliation: **Stockholm University**

Molecular Biosciences

Bio: Our group studies epigenetic regulatory mechanisms in craniofacial development using clonal lineage tracing, multi-omic analysis, and in vivo functional genomics.

Project idea: In my research group, we study how shape emerges during embryonic development by deconstructing how cells compute, transmit, and retain spatiotemporal information. We ask how positional identity from body patterning influences clonal diversification to shape the early face. To do this, we combine in vivo models with gene editing, lineage tracing, single-cell genomics, microscopy, cell sorting, and CT-based phenotyping. In this DDLS project, we will profile gene regulatory networks (GRNs) governing progenitor fate decisions across space and time and link these programs to distinct facial shapes. The postdoctoral fellow will integrate high-throughput clonal lineage tracing with a multi-omic atlas of human craniofacial development, identify regulatory motifs associated with multipotency, and model how spatial fields of GRN activity drive morphogenesis over developmental time.

I would like to host a: **DDLS academic postdoc**

Contact: alek.erickson@su.se

Mauricio Esguerra Neira

Affiliation: **AstraZeneca AB**

Safety Sciences

Bio: Associate Director in Computational Chemistry in the Safety Innovation Department Chemical Toxicology Group. In-silico models to design safe drugs early.

Project idea: The central research question driving this project is: Can we develop a comprehensive in-silico platform that leverages state-of-the-art AI technologies to predict off-target interactions for biologics across the complete human proteome with accuracy comparable to current experimental methods? Can these initial methods also provide a platform for expansion to other drug modalities?

I would like to host a: **DDLS industrial postdoc**

Contact: mauricio.esguerra@astrazeneca.com

Nicholas Pearce

Affiliation: **Linköping University**

Physics, Chemistry and Biology

Bio: In the d3ms group, we develop ML/AI-based methods for determining and analysing macromolecular structures solved using biophysical techniques (X-ray/Cryo-EM/NMR).

Project idea: We have lots of opportunities for the analysis of data from X-ray crystallography and Cryo-EM for ligand identification, flexibility analysis, heterogeneity characterisation, structural dynamics etc.

I would like to host a: **DDLS academic or industrial postdoc**

Contact: nicholas.pearce@liu.se

Alexa McIntyre

Affiliation: **Linköping University**

Dept. of Biomedical and Clinical Sciences

Bio: Our lab studies autoimmune diseases and adaptive immunity using experimental molecular biology and computational methods. Group website: amcintyrelab.github.io

Project idea: We are developing new approaches to detect and characterize autoreactive cells and their targets in the context of autoimmune diseases. Potential projects include combining spatial transcriptomics and high-throughput imaging data to detect and characterize autoreactive B cells or focusing on analysis of proximity labelling proteomics and immunopeptidomics data.

I would like to host a: **DDLS academic postdoc**

Contact: alexa.mcintyre@liu.se

Erik Sonnhammer

Affiliation: **Stockholm University**

Dept. of Biochemistry and Biophysics

Bio: Professor of Bioinformatics at Stockholm University, previously at Karolinska Institutet, Stockholm. Ph.D. in bioinformatics at the Sanger Institute. Present H-index 72 and ~90000 citations.

Project idea: This is a collaboration between Stockholm University and Merck AB. The project will have a base in the Sonnhammer group at Science for Life Laboratory in Stockholm, which is a strong research environment for large-scale life science research, and a joint physical center for a number of computational and life science groups at Stockholm's three Universities. The project will be jointly supervised by Professor Erik Sonnhammer, SU, and Dr. Dimitri Guala, Merck AB. A new exciting opportunity is combining spatial biology with AI-driven modeling of gene expression responses to drug treatment in the field of drug repurposing. Drug repurposing involves identifying new therapeutic uses for existing medications. The project will use AI models such as CycleGANs, that by learning from complex spatial gene expression profiles and cellular heterogeneity within tissues can predict how existing drugs might act on previously uncharacterized disease mechanisms or cellular subtypes. The project involves programming, modelling, and data analysis. The PostDoc should be have a Ph.D. in bioinformatics or related field. Alternatively, a Ph.D. in molecular biology or related field and 2 years of postdoctoral experience in bioinformatics research and programming, documented by scientific publications. Extensive experience with Python, deep learning techniques, and good UNIX knowledge are essential skills. Matlab, R, scripting, and familiarity with omics data analysis techniques are desirable merit

I would like to host a: **DDLS industrial postdoc**

Contact: erik.sonnhammer@scilifelab.se

Fredrik Levander

Affiliation: **Lund University**

Immunotechnology

Bio: Using computational (prote)omics to enable cancer precision medicine

Project idea: Large amounts of omics data have been collected for different tumor types but remain to some degree unexploited. By leveraging new data analysis approaches to dissect complex tumors, we could potentially classify tumors in new ways to select the best treatment options for each patient based on predictive modeling. The project can encompass proteomics data or other expression omics data, as well as multi-omics data approaches. Would be happy to discuss possibilities!

I would like to host a: **DDLS academic postdoc**

Contact: fredrik.levander@immun.lth.se

Andi Alijagic

Affiliation: **Örebro University**

School of Science and Technology

Bio: Andi Alijagic is a docent in biology employing phenomic and multi-omics approaches to decode how complex environmental exposures reshape cellular states and drive variability in biological responses.

Project idea: This project aims to establish Phenomics for Precision Environmental Health by developing AI-driven models that map, interpret, and predict how environmental perturbations reshape cellular state space through high-content imaging integrated with multi-omics data. Large-scale phenomic profiles will be combined with complementary proteomics, metabolomics, and glycomics layers to generate a systems-level view of exposure-induced cellular reprogramming. Using advanced machine learning and representation learning approaches, the project will identify mechanistic phenotypic signatures linked to molecular pathway alterations, including inflammatory activation, metabolic rewiring, and stress adaptation, and determine how these response patterns vary across biological contexts. A central component is the close collaboration with Örebro University's interdisciplinary ARC – AI, Robotics and Cybersecurity Center, providing cutting-edge expertise in artificial intelligence, data engineering, and computational infrastructure. The project will be embedded in a cross-disciplinary data science ecosystem together with image analysis expert Assoc. Prof. Stephanie Lowry, bioinformatician Prof. Dirk Repsilber, and AI/ML expert Dr. Oleksandr Kotlyar. This cross-disciplinary approach will enable the creation of interpretable, generalizable phenomic-multi-omic models that lay the foundation for predictive, data-driven assessment of cellular susceptibility to environmental exposures.

I would like to host a: **DDLS academic postdoc**

Contact: andi.alijagic@oru.se

Gustav Nilsonne

Affiliation: **Karolinska Institutet**

Dept. of Clinical Neuroscience

Bio: MD, PhD, Associate professor of neuroscience, leader of the KI Metascience team. We try to make science more trustworthy and useful.

Project idea: In our team, we collect, process, and analyse data about scientific processes on a large scale. Examples include clinical trial registry data, regulatory approvals data, and data about scientific publications. We assess transparency and reproducibility and try to build better ways to determine what is good science. We also do meta-analyses and large-scale secondary analyses of existing data to answer substantive questions in neuroscience. Depending on the interests and background of the candidate, projects may involve any of these topics or others in the broad field of metascience. Candidates without a fully defined project are very welcome.

I would like to host a: **DDLS academic postdoc**

Contact: gustav.nilsonne@ki.se

Johan Trygg

Affiliation: **Sartorius Stedim Data Analytics AB**

Advanced Data Analytics,
Corporate Research

Bio: Professor of Chemometrics, Umeå University; Head of Advanced Data Analytics, Sartorius Corporate Research. Research at the techbio–AI–digital biology nexus to accelerate biopharma drug R&D.

Project idea: In drug discovery, multimodal profiling captures a fuller picture of cell state, clarifies mechanism, and improves predictive power for drug responses. We develop AI and advanced chemometrics to simplify analysis and biological readouts from time series of complex multimodal data, especially metabolomics combined with live-cell imaging. We collaborate with the Swedish Metabolomics Center for metabolomics data, while live-cell imaging is performed within Sartorius. Our long-term goal is to deliver next-generation data-analytical tools for more efficient drug development across modalities. As a postdoc, you will search out promising tools and instigate new methods when existing ones fall short, driving real impact.

I would like to host a: **DDLS industrial postdoc**

Contact: Johan.Trygg@Sartorius.com

Qiaoli Wang

Affiliation: **Lund University**

Dept. of Translational Medicine

Bio: Assistant Professor, DDLS Fellow, iPanCare Group Leader at Lund University. A young group at SciLifeLab working on population science and multi-omics research.

Project idea: Our research employs integrative approaches of genetic, molecular epidemiology, and machine learning algorithms to dissect this lethal disease by leveraging large population-based cohorts, national registries, biobanks, and clinical images. Through innovatively applying diverse data sources with advanced analytical methodologies, our lab is interested in developing strategies for personalized prevention and prediction, early detection, and tailored prognostic tools for pancreatic cancer. The ultimate goal of our research is to identify key factors contributing to the development and metastasis of pancreatic cancer, to improve early diagnosis and survival of pancreatic cancer through facilitating personalized screening programs, treatments, and surveillance strategies.

I would like to host a: **DDLS academic postdoc**

Contact: qiaoli.wang@med.lu.se