Eve Zeyl Fiskebeck

Gjøstigen 18.
1914 Ytre Enebakk.
27/07/76
☎ +47 454 15 690
✉ evezeyl@gmail.com
Github
LinkedIn
Researchgate
ORCID

In a nutshell:

- I have used molecular genetics analysis methods to study micro and macro evolution mechanisms in order to understand adaptation and adaptability potential of different organisms. I use population genetics and phylogenetics theory and methods to help improve detection, characterisation and classification of pathogens to help improve disease control and management.
- I am interested in finding the best solutions to analyze data, understanding methods, combining methods, transposing methods between different scientific fields.
- My abilities are equally "practical" and "theoretical". I like to focus on working with methodologies that have practical applications in the context of a current research subject.
- I particularly enjoy working in an environment where each person provides its own expertise and contributes as a piece of a jigsaw puzzle to create a complete picture of a scientific question.
- I am enthusiastic and like to help others. I believe in the exchange of competencies. I thrive with constant learning.
- I enjoy coding and improving my data science abilities (an activity that I find relaxing and self-fulfilling).

Working experience:

10/02/2020 - Currently. Researcher in Bioinformatics (speciality: Evolutionary Biology).
01/12/2018 to 30/11/2019 Reconversion to Bioinformatics. Trainee and 40% employment (researcher) during 6 months on 2 projects. Norwegian Veterinary Institute.

- Ongoing: Reviewing the currently available methods for sources attributions (for planned contribution to analyses of attribution of food-borne pathogens to host-sources.
- Contributions to the methodological analysis of the SAV virus-typing pipeline development, and to the (ongoing) ILA variant-calling pipeline development.
- Contribution to the pilot analyses regarding the feasibility to detect virus (IPNV) from metagenomics samples.
- Phylogenetic analyses of *Escherichia coli* to investigate a putative persistent broiler outbreak and development of an analysis pre-Rpackage.
- Analyses for a pilot project aimed at tracing *Listeria monocytogenes* along a production chain in a fish processing facility to assist biosecurity measures.
- Perform proficiency tests for WGS of *Listeria monocytogenes* (included development scripts).
- Contribution to choice of methods of the *Listeria monocytogenes* typing pipeline.
- Contribution to the writing of the One Health Sequencing surveillance Handbook for bacterial pathogens.
- Tip-dated Bayesian phylogenetic inference on *Escherichia coli* ST38 of Broilers, and developing script for visualizing and annotating phylogenetic trees.
- Phylogenetics and phylogeography of *Yersinia ruckeri*.
- Data wrangling of absorbance data, Genome Wide Association Study (GWAS) and phylogenetics of *Listeria monocytogenes*.

Tasks:

- Exploring and understanding methods: de novo genome assembly, mapping, genome annotation, xxMLST and SNP typing, variants calling from deep sequencing, multiple sequence and whole genome alignment, distance based clustering and phylogenetic inference (core and pangenome) and associated methods for phylodynamics analyses and transmission trees reconstruction); for GWAS, source attribution/assignment... and for advising and sensibilize other bioinformatic users to the underlying assumptions, advantages and limitations of using those methods for their research questions.
- Contributing to the core bioinformatic team tasks: Developing tutorials for users: Conda, Poppunk, HPC usage, mapping and SNP calling, tree building and tree visualizing... and eg. contributing to knowledge transfer to other bioinformaticians and within the Bioinformatics

Core Team
- Some support to bioinformatic users: from helping to debug a Rscript, help launching pipelines.
- Contributions to research project development at VI. Soon: WPL in AMR Tanzania project.

References:

- Project/Work package leader:eg. Food security, Animal heath. Camilla Sekse ✆ **+47 92 456 888**
- Co-researcher in the bioinformatics Core-Team: Thomas Haverkamp ✆ **+47 48 094 932**

2009 to 2014 Laboratory Engineer. University of Oslo, Natural History Museum (NHM) and 2004 to 2010 Ph.D project.

- Project 3: "Kinorhyncha - a poorly and neglected animal phylum" - artsprosjektet - managed by Artsdatabanken.
- Project 2: "Diversity mapping of Norwegian Gyrodactylid flatworms - mining natural history collections."
- Prosjekt 1 and PhD. project: Analyze of new material & analyses polar bears for Ph.D. Total > 900 samples).

Tasks:

- Sampling, microscope slides Preparations, microscopy, digitalisation.
- Testing and improving methods for DNA isolation and analysis (skin, plasma, blood).

- Routine DNA isolation, quantification, PCR, multiplex PCR, Sanger Sequencing, Genotyping, Sanger sequencing, sequence alignment, barcoding ...
- Competence transfer:
  - Instructor: introduction to laboratory courses for Ph.D. and master students (2 weeks, 2 different years): RNA and DNA isolation, quantification, PCR, reverse transcription, sanger sequencing, sequence visualizing (Staden package).
  - Advise and help for master students (Population genetics analyses, Kinorhycha).
- Statistical and data analysis.
- Contributions to publishing (all projects).
- Quality control of a part of the museum collection.

2003-2004 Laboratory Engineer. France Laboratoire d'Ecologie Alpine, CNRS, Grenoble.

Tasks:

- Testing and developing new markers for wildlife forensics.
- DNA isolation, sequencing, SNPs genotyping, species identification (barcoding).
- Contribution to daily laboratory management.
- Competence transfer: training of a bachelor student to laboratory work (1 month).

Education:

End 2004 to 2010. Ph.D. Population genetics of polar bears (Ursus maritimus) in the Svalbard area. Collaboration: University of Oslo (Natural History Museum) and Norwegian Polar Institute, Tromsø.

- Ph.D trial lecture: Microevolutionary responses to climate change and harvesting in wildlife: evidence and implications for management.

2002-2003 Second year Master-degree. Collaboration University Claude Bernard (UCB), Lyon I and University Joseph Fourier (UJF), Grenoble, France.

Courses (UCB): Analysis and modeling of biological systems (Statistics and modeling applied to biological research).

Research (UJF): Development and testing molecular methods to fight wildlife criminality (see publications).

2001-2002 First year Master-degree. Population genetics, population biology and ecosystems. UJF, France.

Including research project training (see publications).

2000-2001 Third year bachelor-degree: UJF, France.

Additional during summer vacations: 2 months research project (see publications).

1999-2000 Second Year bachelor-degree: University of Burgundy, Dijon, France. Cellular biology, microbiology, immunologi.

Additional special courses: bioinformatics, marketing.

Diverse

Languages

- French: Mother tongue.
- English: Fluent.
- Norwegian: Orally fluent, written: good. (Bergenstest: B2).
- German: (some understanding).

Computer literacy

OS: Ubuntu - Windows

Programming languages: R (90%), bash, python, SQLite, nextflow, HTML and CSS.

Some experience with making/using containers (Docker, singularity).

Note: Most of my Github repositories (work at the Veterinary Institute) are private.

Freetime

If I am in front of my PC, trying to develop a new function for analyses, you will find me in the swimming pool or at the local gym following crosstraining or hit-fighting classes.

Voluntary:

Previously coinstructor and helper at Carpentries Oslo and part of the Oslo Carpentry study group.

Results and publications

Eve Zeyl Fiskebeck, Snorre Gulla, Andreas Riborg, Duncan Colquhon. The ancestral history of Yersinia ruckeri in Norwegian aquaculture – four decades of repeated anthropogenic dissemination and clonal expansion. (currently writing).

Coipan Claudia, Fiskebeck Eve. Cluster delineation for genomic based infectious disease surveillance. (currently writing).

Eve Zeyl Fiskebeck, Monika Hjortaas, Hilde Sindre, Karin Lagesen and Arvind Sundaram. A high throughput amplicon-based virus classification method: library preparation and analysis pipeline. (currently writing).

Solveig Sølverød Mo, Eve Zeyl Fiskebeck, Jannice Schau Slettemeås, Karin Lagesen, Oskar Nilsson, Umaer Naseer, Silje Bakken Jørgensen, Thorunn R. Thorsteinsdottir, Marianne Sunde. Escherichia coli multilocus sequence type 38 from humans and broiler production represent two distinct monophyletic groups. To be submitted 08/2022.

Håkon Kaspersen and Eve Zeyl Fiskebeck. (Submitted). ALPPACA - A tooL for Prokaryotic Phylogeny And Clustering Analysis. JOSS, submitted.

Maduna, Simo, Jon Aars, Ida Fløystad, Cornelya Klutsch, Eve Marie Louise Zeyl Fiskebeck, Øystein Wiig, Dorothee Ehrich, et al. 2021. Sea Ice Reduction Drives Genetic Differentiation among Barents Sea Polar Bears. Proceedings of the Royal Society of London. Biological Sciences 288,1958:1–10.

Håkon Kaspersen, Eve Zeyl Fiskebeck, Camilla Sekse, Jannice Schau Slettemeås, Anne Margrete Urdahl, Madelaine Norström, Karin Lagesen, Roger Simm. 2020. Comparative genome analyses of wild type- and quinolone resistant *Escherichia coli* indicate dissemination of QREC in the Norwegian broiler breeding pyramid. Frontiers in Microbiology.

Håkon Kaspersen, Camilla Sekse, Eve Zeyl Fiskebeck, Jannice Schau Slettemeås, Roger Simm, Madelaine Norström, Anne Margrete Urdahl, Karin Lagesen. 2020. Dissemination of quinolone resistant *Escherichia coli* in the Norwegian broiler and pig production chain, and possible persistence in the broiler production environment. Applied and Environmental Microbiology, 18;86(7).

Zeyl, E.; Marcotegui, P.; Harris, P.D.; Bakke, T.A.; Bachmann, L. (2012). New parasites from old fishes. Naturen, 6, 27-280.(In Norwegian).

Peacock, Elisabeth et al. (2015). Implications of the circumpolar genetic structure of polar bears for their conservation in a rapidly warming Arctic. PLoS ONE,Volum 10:0112021.(1) s.

Zeyl E. Population genetics of polar bears in the Svalbard area. (2010). University of Oslo, Natural History Museum (Ph.D. thesis. With additional data).

Zeyl E., Ehrich D., Aars J., Bachmann L., Wiig Ø. (2010). Denning area fidelity and mitochondrial DNA diversity of female polar bears (*Ursus maritimus*) in the Barents Sea area. Canadian Journal of Zoology, 88, 1139-1148.

Lindqvist C., et al. (2010). Complete mitochondrial genome of a Pleistocene jawbone unveils the origin of polar bear. Proceedings of the National Academy of Sciences, 106, 5053-5057.

Zeyl E., Aars J., Ehrich D., Bachmann L., Wiig Ø. (2009). The mating system of polar bears: a genetic approach. Canadian Journal of Zoology, 87, 1195-1209.

Zeyl E., Aars J., Ehrich D., Wiig Ø. (2009). Families in space: relatedness in the Barents Sea population of polar bears (*Ursus maritimus*). Molecular Ecology,18, 735-749.

Beja-Pereira A., Zeyl E., Ouragh L., Nagash H., Ferrand N., Taberlet P., Luikart G. (2004). Twenty polymorphic microsatellites in two of North African most threatened ungulates: *Gazella dorcas* and *Ammotragus lervia* (Bovidae, Artiodactyla). Molecular Ecology Notes, 4, 452-455.

Maudet C., Beja-Pereira, A., Zeyl E., Nagash, H., Kence A., Özüt D., Biju-Duval, M.-P., Boolormaa S., Coltman D.W., Taberlet P., Luikart G. (2004). A standard set of polymorphic microsatellites for threatened mountain ungulates (Caprini, Artiodactyla). Molecular Ecology Notes, 4, 49–55.

Zeyl E. (2003). Wildlife forensics: developing and evaluating molecular tools to assign Middle East wild sheep (*Ovis spp.*) to their population of origin. Usefulness to fight poaching (Master degree research thesis, in French).

Zeyl E. (2003). Uses of molecular genetics tools in wildlife forensics (Master degree bibliographic thesis, in French).