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Jisca Huisman

Experience

Data manager, *EBMT*, Leiden, Netherlands (32h/w). **2021–2022**
Automating several data QC steps; writing scripts to bridge the gap between SPSS-using data managers and R-using statisticians; translating SPSS scripts to R.

R package maintainer. **2019–current**
Maintenance, expansion, and user support for R package `sequoia`, which performs pedigree reconstruction from SNP data. In 2021 it was downloaded on average 670x/month from CRAN¹. I wrote extensive documentation for this package, including a [website](#)².

Freelance consultant. **2019–current**
Reconstruction of pedigrees and similar tasks for clients from academia and industry, including written reports with data visualisation.

Post-doctoral researcher, *University of Edinburgh*, UK. **2015–2018**
Investigation why the level of inbreeding in the Rum red deer study population is higher than expected under panmixia. Tasks included:

- Co-supervising MSc projects;
- Catching, ear-marking and measuring calves, after obtaining the appropriate license;
- Designing forms for a observational study.

Post-doctoral researcher, *University of Edinburgh*, UK. **2012–2015**
Estimating inbreeding depression in a range of life history traits in the Rum red deer study population using SNP data. Tasks included:

- Inventarising and DNA extraction of thousands of samples, and the record keeping thereof;
- Quality control of new data and its integration with existing data.

Temporary scientific staff, *NTNU*, Norway. **2008–2012**
Student assistant at statistical computer practicals using R, and several other undergraduate courses at the biology and mathematics departments (25% of hours during PhD).

Data entry, *Numico*, Netherlands. **2007**

Student assistant at statistics course, *Wageningen University*, Netherlands. **2005**
Helping undergraduates learn statistics with SPSS.

¹<https://CRAN.R-project.org/package=sequoia>

²<https://jiscah.github.io>

Education

PhD

Biology, NTNU, Norway.

2008–2012

Thesis title Gene flow and natural selection in Atlantic salmon

Description Population genetic modelling of a heritable fitness trait differing between escaped farmed salmon and wild salmon, as well as two empirical studies on natural selection in salmon.

Selected courses Modern statistical methods (Bayesian, cross-validation, clustering), Quantitative genetics with integration of molecular genetics for animal breeding (Nordic PhD course)

MSc + BSc

Animal Science, Wageningen University, Netherlands.

2001–2006

Specialisation in Animal Breeding & Genetics

Master Thesis: Genetic diversity of Dutch adder populations

Selected courses: Advanced Statistics, Modern Statistics for the Life Sciences, Gene Technology, Animal Ecology, Introduction to Programming (Java)

Languages

English: Fluent

Norwegian: Intermediate

Dutch: Native

German, French: Elementary

Computer skills

R: Expert knowledge regarding functions, simulations, package development, Rmarkdown reports, and creating an interface with Fortran. Moderate experience with Shiny.

Other languages: Extensive experience with Fortran and Latex; basic knowledge of SPSS, Shell, C, Java, Python, HTML

MS office: Extensive experience with Word, Excel, and Access

Writing/coding tools: Notepad++, Rstudio, TexnicCenter

Other: Moderate experience with linux, version control with git, and RegEx.

Other skills

Statistics: I performed the statistical analysis for several scientific publications. This included generalized and mixed models, likelihood optimisation, and Bayesian approaches.

Scientific writing: I was lead author on several scientific publications, and co-author on several more (for a complete list, please see [google scholar](https://scholar.google.com/citations?user=p_btglIAAAAJ&hl)³). I performed peer review for dozens of manuscripts.

Presentations: I have presented posters and given oral presentations at various international scientific conferences

Lab: DNA extraction from various tissues using various protocols, including for high molecular weight; PCR

Code examples

R package: <https://github.com/JiscaH/sequoia>

Functions: <https://github.com/JiscaH/R-functions>

How-to's: <https://github.com/JiscaH/HowTo>

³https://scholar.google.com/citations?user=p_btglIAAAAJ&hl