

Marcin Kierczak: Curriculum Vitae

Training & Industry Outreach Coordinator and Data Scientist, NBIS / SciLifeLab, Uppsala, Sweden
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Profile

Bioinformatician and data scientist with a background in machine learning and statistical genomics. I coordinate training and industry outreach at the National Bioinformatics Infrastructure Sweden (NBIS), part of SciLifeLab, and am an associate professor of bioinformatics at Uppsala University. My research covers complex-trait and cancer genomics, conservation and ancient genomics, and metagenomics, mostly in collaboration with groups across Sweden. Since 2018 I co-organise RaukR, an advanced R summer school.

Experience

2024 – present	Training & Industry Outreach Coordinator, Data Scientist National Bioinformatics Infrastructure Sweden, SciLifeLab, Uppsala
2017 – 2024	Bioinformatics Data Scientist National Bioinformatics Infrastructure Sweden, SciLifeLab, Uppsala. Long-term support group (WABI)
2014 – 2017	Researcher Kerstin Lindblad-Toh's lab, Uppsala University & SciLifeLab
2010 – 2014	Postdoctoral researcher Örjan Carlborg's computational genetics group, Swedish University of Agricultural Sciences
2006 – 2010	Web consultant & database engineer Global Diversity Foundation

Education

2006 – 2009	PhD in Bioinformatics , awarded December 2009 Linnaeus Centre for Bioinformatics, Uppsala University. Thesis: <i>From Physicochemical Features to Interdependency Networks: A Monte Carlo Approach to Modeling HIV-1 Resistome and Post-translational Modifications</i> . Supervisor: Prof. Jan Komorowski; co-supervisor: Dr. Gunnar Andersson; opponent: Prof. Anna Tramontano
2003 – 2005	MSc, Molecular Biology Uppsala University. Thesis: <i>Rough Set-Based Classifiers for Predicting HIV-1 Resistance to NRTI Drugs</i>
2000 – 2003	BSc, Molecular Biology University of Warsaw. Thesis: <i>Role of CDK-5 Kinase in the Mammalian Central Nervous System</i>

Academic title

Associate professor (docent) in bioinformatics, Department of Cell and Molecular Biology, Uppsala University.

Certifications



FitSM® Foundation

Issued by APMG International, May 2026. [Verify credential](#)

Teaching and course organisation

- **RaukR**, *Advanced R Programming for Bioinformatics*, Visby. Co-organiser, annually since 2018.
- **R for non-programmers** and **Advanced R for data scientists**. Course leader.
- **R Programming for Life Scientists**, SciLifeLab, 2015–2020. Course responsible; teacher 2015–2017.
- **Statistical Methods in Genetic Mapping: An R-based Course**, 4 ECTS graduate course, 2013. Course responsible and teacher.
- **LUPA Workshop: GWAS Analyses in Stratified Populations**, Uppsala, 2011. Course responsible.
- **Next-Generation Sequencing: Bioinformatics and Data Analysis**, PhD-level course. Course responsible.
- **Boolean Reasoning** and **Knowledge-based Systems in Bioinformatics**, Uppsala University. Teacher and teaching assistant.

Invited and popular-science talks

- **From mythology to artificial intelligence: a short journey through statistical models** (in Swedish). Public lecture, [13x13](#), Uppsala University, 5 November 2025.

Supervision and examination

- **Examiner, PhD theses** (2): M. Dahlö (2021), A. García-Montaner (2020).
- **Opponent, licentiate thesis** (1): K. Ausmees (2019).
- **Co-advisor, PhD theses** (3): S. Sakthikumar (2020), S. Forsberg (2016), M. Ahsan (2014).
- **Subject reviewer, master's theses** (2): Y. Utkueri (2024), M. Qvarnlöf (2024).
- **Master's and research-project supervision**: further projects, listed on the [Training & Outreach](#) page.

Selected publications

36 peer-reviewed articles and preprints; 1,474 citations, h-index 22, i10-index 36 (Google Scholar, October 2026). The full list is on the [publications page](#).

- [Bayesian mixed model analysis uncovered 21 risk loci for chronic kidney disease in boxer dogs](#). *PLOS Genetics*, 2023.
- [Contribution of rare whole-genome sequencing variants to plasma protein levels and the missing heritability](#). *Nature Communications*, 2022.
- [GenErode: a bioinformatics pipeline to investigate genome erosion in endangered and extinct species](#). *BMC Bioinformatics*, 2022.
- [Genomic insights into the conservation status of the world's last remaining Sumatran rhinoceros populations](#). *Nature Communications*, 2021.
- [Genetic Barriers to Historical Gene Flow between Cryptic Species of Alpine Bumblebees Revealed by Comparative Population Genomics](#). *Molecular Biology and Evolution*, 2021.
- [Pre-extinction Demographic Stability and Genomic Signatures of Adaptation in the Woolly Rhinoceros](#). *Current Biology*, 2020.

- [SETD2 Is Recurrently Mutated in Whole-Exome Sequenced Canine Osteosarcoma](#). *Cancer Research*, 2018.
- [Genome-Wide Analysis in German Shepherd Dogs Reveals Association of a Locus on CFA 27 with Atopic Dermatitis](#). *PLoS Genetics*, 2013.

Skills

R, Python, Nextflow and Snakemake workflows, HPC environments, machine learning and feature selection, statistical genetics, proteomics, reproducible research and explanatory programming (tidyverse).

Languages

Polish (native) · English (fluent) · Swedish (fluent) · French, Latin and Spanish (basic)

Last updated October 2026.