

Education

- 2017–2021 **PhD. Statistical genetics**, *University Medical Center Groningen*
PhD focused on building statistical methods to identify causal gene expression from observational data. Supervised by Lude Franke, Cisca Wijmenga and Serena Sanna (ongoing)
- 2015–2017 **MSc. Molecular Biology**, *University of Groningen*, 98th grade percentile
Master of Science, Molecular biology and biotechnology, following a bioinformatics track. The curriculum consisted of statistical methodology, machine learning and computer science
- 2010–2014 **BSc. Molecular Biology**, *University of Groningen*
Bachelor of Science degree, Molecular biology, Bachelor thesis on epigenetic mutation rates in *Arabidopsis thaliana*

Master thesis #1

- title *Polygenic risk modeling of celiac disease*
- supervisors Peter Visscher, University of Queensland, Australia
- description Celiac disease is a heritable autoimmune disease affecting $\approx 1\%$ of European populations. In this master project I developed and built sophisticated polygenic risk models for Celiac disease that take into account the peculiar genetics of celiac disease. This resulted in a polygenic risk model that matched the gold standard

Master thesis #2

- title *Covariate specific allele specific expression*
- supervisors Lude Franke, University Medical Center Groningen, The Netherlands
- description Expression quantitative trait loci (eQTL) are often dependent on covariates such as cell type proportions. In this master project, I developed a statistical method to identify covariate specific allele specific eQTL. Identifying known and novel covariate specific eQTL

Experience

Vocational

- 2014–2015 **Research Assistant**, *University of Groningen*
I analyzed bisulfite sequencing data in *Arabidopsis thaliana* to identify heritable epigenetic mutation rates. I was invited to work as a research assistant to turn my bachelor thesis into a publication.
- Published the project in Proceedings of the National Academy of Sciences (PNAS)
 - Keynote speaker at the AllBio conference 2014, Bari, Italy
 - Taught a graduate course on bisulfite sequencing that detects DNA methylation status of cytosines

2017–2021 **PhD candidate**, *University medical center Groningen*

PhD candidate in statistical genetics, working on statistical methodology to identify causal relationships between gene expression and complex traits. Particularly focused on celiac and heart disease.

- Built and published a new Mendelian randomization method identifying causality between gene expression and complex traits
 - Identified eQTL in a large RNA-seq dataset
 - Simulated causal relationships informed by RNA-seq observations
 - Applied MR to gene expression, identifying *PVRL2* expression as causal to LDL cholesterol levels
- Systematically identified likely causal genes for celiac disease using methods such as coloc, closest gene and Mendelian randomization.
 - Successfully identified causal genes using a *trans*-mediation analysis approach.
 - Experimentally validated a gene, *TRAFD1* in siRNA experiments
- Performed and published a PheWAS analysis on COVID-19 relevant genes

2020–2021 **Visiting Researcher**, *MRC Integrated epidemiology unit, Bristol University*

Visiting researcher working together with Professor George Davey Smith working on extended integration of -omics datasets to identify causal networks in human biology.

2021–Now **Postdoctoral Fellow**, *Statistical Genetics Group, University of Lausanne*

Postdoctoral researcher with an interest in causal relationships

- Developing new ways of benchmarking causal inference methods
- Developing and testing new causal inference methods

Awards and honors

2014	Keynote speaker, Allbio Conference	<i>Bari, Italy</i>
2019	Best Presentation, European Mathematical Genetics Meeting	<i>Dublin, Ireland</i>
2019	Best poster nominee, European Society of Human Genetics	<i>Gothenburg, Sweden</i>
2020	Editorial highlight for van der Graaf et al. 2020	<i>Nature Communications</i>

Languages

Dutch	Fluent	<i>Mother tongue</i>
English	Fluent	<i>Professional language</i>
German	Limited proficiency	<i>Occasional usage</i>
French	Limited proficiency	<i>Occasional usage</i>

Programming language and computer skills

R	Full proficiency	C	Proficient
Python	Full proficiency	Java	Proficient
SQL	Proficient		

Interests

- Rowing I have rowed in Dutch national championships, Furthermore I won the bronze medal at the European youth championships in 2009
- Light design I enjoy designing and building custom lamps in my free time
- Volunteering I have volunteered at a local music venue for 8 years

Selected Publications

- 1 Alexander Kurilshikov, Carolina Medina-Gomez, Rodrigo Bacigalupe, Djawad Radjabzadeh, Jun Wang, Ayse Demirkan, Caroline I Le Roy, Juan Antonio Raygoza Garay, Casey T Finnicum, Xingrong Liu, et al. Genetics of human gut microbiome composition. *BioRxiv, accepted in Nature Genetics*, 2020.
- 2 Esteban A Lopera Maya, Alexander Kurilshikov, Adriaan van der Graaf, Shixian Hu, Sergio Andreu-Sanchez, Lianmin Chen, Arnau Vich Villa, Ranko Gacesa, Trishla Sinha, Valerie Collij, et al. Effect of host genetics on the gut microbiome in 7,738 participants of the dutch microbiome project. *BioRxiv, under review in Nature Genetics*, 2020.
- 3 Lopera Maya, A Esteban, Adriaan van der Graaf, Pauline Lanting, Marije van der Geest, Jingyuan Fu, Morris Swertz, Lude Franke, Cisca Wijmenga, Patrick Deelen, et al. Lack of association between genetic variants at *ace2* and *tmprss2* genes involved in sars-cov-2 infection and human quantitative phenotypes. *Frontiers in Genetics*, 11:613, 2020.
- 4 Sipko van Dam, Urmo Vosa, Adriaan van der Graaf, Lude Franke, and Joao Pedro de Magalhaes. Gene co-expression analysis for functional classification and gene-disease predictions. *Briefings in bioinformatics*, 19(4):575–592, 2018.
- 5 Adriaan van der Graaf, Annique Claringbould, Antoine Rimbart, Harm-Jan Westra, Yang Li, Cisca Wijmenga, and Serena Sanna. Mendelian randomization while jointly modeling cis genetics identifies causal relationships between gene expression and lipids. *Nature Communications*, 11:4930, 2020.
- 6 Adriaan Van Der Graaf, René Wardenaar, Drexel A Neumann, Aaron Taudt, Ruth G Shaw, Ritsert C Jansen, Robert J Schmitz, Maria Colomé-Tatché, and Frank Johannes. Rate, spectrum, and evolutionary dynamics of spontaneous epimutations. *Proceedings of the National Academy of Sciences*, 112(21):6676–6681, 2015.
- 7 Adriaan van der Graaf, Maria Zorro, Annique Claringbould, Urmo Vosa, Raul Aguirre-Gamboa, Chan Li, Joram Mooiweer, Isis Ricano-Ponce, Zuzzana Borek, Frits Koning, et al. Systematic prioritization of candidate genes in disease loci identifies *trafd1* as a master regulator of $\text{ifn}\gamma$ signalling in celiac disease. *Frontiers in Genetics, accepted*, 2020.