Cardiovascular biology

My research interests are on identifying and understanding the (epi)genetic causes of atherosclerosis underlying ischemic stroke and coronary artery disease. With my work I ultimately aim to identify novel therapeutic targets and (surrogate) biomarkers for cardiovascular diseases through statistical (epi)genetics and in vitro modelling. We use different methods, including statistical fine-mapping, co-localisation, and causal inference (Mendelian Randomisation), (single-cell) molecular quantitative trait loci analyses (expression and methylation), genetic epidemiology, and high-throughput whole-slide imaging using machine learning. This has resulted in the identification of 28 genetic regions with a substrate in atherosclerotic plaques that harbour genes potentially causal to atherosclerosis and amenable to therapy. We are currently pursuing several targets in vitro to better understand the molecular mechanisms in collaboration with the labs of dr. Mokry and prof. dr. Asselbergs.
Did I raise your interest? Looking for an internship at the interface of statistical (ep)genetics and cardiovascular disease? Consider yourself competent in bioinformatics? Or are you up for the challenge to combine bioinformatics with in vitro experimentation? I will try to be the best mentor I can be for you, while you learn to work with some unique datasets and exciting in vitro methods.

For more information please contact:
Dr. Sander W. van der laan
s.w.vanderlaan-2@umcutrecht.nl
visit https://swvanderlaan.github.io for my on my work.

Atherosclerosis is a progressive disease that is the leading global cause of death. The current understanding of the atherosclerotic plaque that leads to myocardial infarction and stroke is predominantly driven by pathological characteristics. These studies found that plaque rupture is the primary substrate of vulnerable plaque. As compared to plaque rupture, our knowledge of other mechanisms – like plaque erosion, is minimal. To better understand these processes, we use plaques isolated from patients and generate multiple omics datasets like transcriptomes (including single-cell RNA sequencing), DNA methylation, genotyping, ATAC-seq or ChIP-seq. We offer dry lab projects (computational analysis) where we aim for discovering new processes involved in symptomatic plaques and wet lab projects where we use primary cells from plaques grown in cell cultures for further validations and in-depth molecular mechanistic studies

For additional information please contact:
Dr. Michal Mokry
m.mokry@umcutrecht.nl

Or:
Prof. Dr. G. Pasterkamp
g.pasterkamp@umcutrecht.nl