PhD Project Description

School/Department:	Department of Radiology and Nuclear Medicine Erasmus MC
Supervisor information:	• *Prof dr Wiro Niessen,*: w.niessen@erasmusmc.nl www.bigr.nl • **Personal Grants:** *Wiro Niessen is (co-PI) of numerous Dutch and European research grants, including on Imaging Genetics (1 MEuro), Radiomics (600 kEuro). He received personal VICI grants (1.25 MEuro) and Simon Stevin award (500 kEuro). Total research funding over last 10 years is more than 15 MEuro. He has supervised 42 PhD students.* • **Most important publications:** - Hofer, E., Roshchupkin, G.V., Adams, H.H… Niessen WJ… Sudha Seshadri ., 2020. Genetic correlations and genome-wide associations of cortical structure in general population samples of 22,824 adults. Nature Communications, 11(1), pp.1-16.. - Van der Lee SJ, Roshchupkin GV, Adams HHH, Schmidt H, Hofer E, Saba Y, Schmidt R, Hofman A, Amin N, van Duijn CM, Vernooij MW, Ikram MA, Niessen WJ. Gray matter heritability in family-based and population-based studies using voxel-based morphometry. Human Brain Mapping. 2017;38(5):2408-23. - Wang, J., Knol, M.J., Tiulpin, A., Dubost, F., de Bruijne, M., Vernooij, M.W., Adams, H.H., Ikram, M.A., Niessen, W.J. and Roshchupkin, G.V., 2019. Gray matter age prediction as a biomarker for risk of dementia. Proceedings of the National Academy of Sciences, 116(42), pp.21213-21218.. - Hibar DP, Adams HHH, Jahanshad N, …. , Niessen WJ, … , Thompson PM, Ikram MA. Novel genetic loci associated with hippocampal volume. Nature Communications. 2017;8. - Roshchupkin GV, Gutman BA, Vernooij MW, Jahanshad N, Martin NG, Hofman A, McMahon KL, Van Der Lee SJ, Van Duijn CM, De Zubicaray GI, Uitterlinden AG, Wright MJ, Niessen WJ, Thompson PM, Ikram MA, Adams HHH. Heritability of the shape of subcortical brain structures in the general population. Nature Communications. 2016;7. - Santos EMM, Yoo AJ, Beenen LF, Berkhemer OA, den Blanken MD, Wismans C, Niessen WJ, Majoie CB, Marquering HA. Observer variability of absolute and relative thrombus density measurements in patients with acute ischemic stroke. Neuroradiology. 2016;58(2):133-9. - Roshchupkin GV, Adams HHH, Vernooij MW, Hofman A, Van Duijn CM, Ikram MA, Niessen WJ. HASE: Framework for efficient high-dimensional association analyses. Scientific Reports. 2016;6. - Roshchupkin GV, Adams HH, van der Lee SJ, Vernooij MW, van Duijn CM, Uitterlinden AG, van der Lugt A, Hofman A, Niessen WJ, Ikram MA. Fine-mapping the effects of Alzheimer's disease risk loci on brain morphology. Neurobiology of Aging. 2016;48:204-11. - Niessen WJ. MR brain image analysis in dementia: From quantitative imaging biomarkers to ageing brain models and imaging genetics. Medical Image Analysis. 2016;33:107-13. - Huizinga W, Poot DHJ, Guyader JM, Klaassen R, Coolen BF, Van Kranenburg M, Van Geuns RJM, Uitterdijk A, Polfliet M, Vandemeulebroucke J, Leemans A, Niessen WJ, Klein S. PCA-based groupwise image registration for quantitative MRI. Medical Image Analysis. 2016;29:65-78.
Project Title:	**Distributed Machine Learning in application for large-scale omics studies**
Abstract	**Artificial Intelligence** field has seen dramatic advances in the past few years with much excitement around the use of deep learning (DL), many-layered convolutional neural networks (CNN). The world has witnessed striking advances in the ability of machines to understand and manipulate data, including images, language, and speech. CNN showed ability to detect a complex pattern in high-dimensional data, but also are able to integrate data from various resources by having many input channels into neural network. Human genetics can benefit immensely from DL. However, the application of AI in genetics analysis is still quite limited. The main issue is the restriction for data sharing between cohorts and loss of power, compare to the pooled analysis. Distributed Learning is a distributed machine learning approach which enables model training on a large corpus of decentralized data. **The main goal of this project** is to develop new distributed learning framework for multi-center genetics analysis in collaboration with **NVIDIA company**, which will be able to utilize machine learning approaches and increase power of gene discovery. We aim to apply these methods on large datasets from population-based Rotterdam study, UK Biobank as well as within **world-wide genetics consortiums**.
Requirements of candidate:	We are looking for a highly motivated, hardworking student to join our very international team. Successful candidates are expected to have a strong quantitative or computer science background, excel at critical thinking, with a strong motivation to engage in the development and application of advanced analytical methods. • Master degree in mathematics, computer science, statistics, bioinformatics, physics, electrical engineering, or in an equivalent discipline. •Strong knowledge of: Python. •Experience with machine learning and deep learning methods. •Scholarship that will, at least, cover subsistence allowance and international air plane ticket (we could help with the scientific part of your scholarship proposal) •English language requirement: - English speaking countries & Netherlands: no requirement - Other countries: IELTS 6.0