

Using genetic identification as the key principle, we perform innovative research and technological developments in a wide range of societally relevant areas such as in forensics, evolution, epidemiology, and other medically relevant fields.

## ***Vacancy: MSc Bioinformatics student***

The Department of Genetic Identification at Erasmus MC is looking for a motivated bioinformatics Master's student to conduct a 4/5-month summer internship in the field of epigenomics. The central scientific question of the proposed research project is: "Can genome-wide DNA methylation analysis in blood reveal hypervariable sites with low heritability that can be used to discriminate identical twins?". Our Department has recently acquired a research grant to answer this question, and you will be part of a multidisciplinary team, including biologists, epigenetics and bioinformaticians. This sub-project forms part of a bigger project and includes the development of a data analysis pipeline based on data from Illumina Methylation Beadchip 450K microarray generated from a total of 660 monozygotic (MZ) twins, to comprehensively investigate their genome-wide methylomes. Prior to analysis, various standard and novel quality control steps will be performed using available R packages and available phenotypic data. The developed pipeline will be designed to allow for the discovery of hypervariable CpG sites of low heritability but relatively high over-time stability, which can further be verified in other existing 450K datasets we have in our laboratory. A pilot study in a small number of twin pairs revealed some sites that showed methylation differences between more than one pair, and our aim is to investigate this hypothesis in a larger scale. The identification of such twin-differentiating epigenetic markers is expected to increase not only our understanding of potential environmental influences on our DNA (why are the twins different?), but also allow for the future development of a forensic 'CpGforID' tool to be used in criminal cases where MZ twins are involved (can

we tell 'who did it?'), which cannot be currently separated via standard DNA profiling methods. Therefore, the outcomes of this project will be useful for the purpose of, among others, forensics, epigenetics, and twins research. The work of this project will be published in a high-impact scientific journal (where you would get an authorship position), presented in various conferences and the identifier markers will be shared with the scientific community. If you are a creative, independent, highly motivated bioinformatics student with good skills in working with Linux, Python -and preferably R- and are interested in epigenetics and/or forensics, this internship could provide you with an opportunity to get a close view into a field of human epigenetics and forensics, where you can contribute with your research. Good results might also lead to PhD/job opportunities within our department.

Additional information can be obtained from  
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