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| **School/Department:** | **Department of Immunology Erasmus MC** |
| **Supervisor information:** | * Prof dr. Anton W Langerak (supervisor) * Dr. Harmen JG van de Werken & Dr. Marco WJ Schreurs (co-supervisors) * **Email:** [a.langerak@erasmusmc.nl](mailto:a.langerak@erasmusmc.n) and/or [h.vandewerken@erasmusmc.nl](mailto:h.vandewerken@erasmusmc.nl) and/or [m.schreurs@erasmusmc.nl](mailto:m.schreurs@erasmusmc.nl) * **Website:** [Anton Langerak](https://www.immunology.nl/research/anton-langerak/)and [Harmen van de Werken](https://www.immunology.nl/research/harmen-van-de-werken/)& [II](https://www.erasmusmc.nl/en/research/researchers/werken-harmen-van-de) and [Marco Schreurs](https://www.immunology.nl/research/marco-schreurs/) **Personal Grants:**  1. DDHF CCBC (2018) 2. EU-TRANSCAN NOVEL (2019)  * **Most important recent relevant publications:|**  1. **van de Werken, H. J. G.**\*, van Riet, J.\*, …, Mostert, B. The genomic landscape of 85 advanced neuroendocrine neoplasms reveals subtype-heterogeneity and potential therapeutic targets. **Nat. Commun.** **12,** 1–14 (2021). 2. **Assmann JLJC\*, Kolijn PM\*, Schrijver B\*, … Langerak AW.** TRB sequences targeting ORF1a/b are associated with disease severity in hospitalized COVID-19 patients. J Leukoc Biol. 2021. Epub ahead of print. 3. van Riet, J., …, **van de Werken, H. J. G.** SNPitty: An Intuitive Web Application for Interactive B-Allele Frequency and Copy Number Visualization of Next-Generation Sequencing Data. **J. Mol. Diagnostics** **20,** 166–176 (2018). 4. **van de Werken, H. J. G.**, …, Joffe, B. Small chromosomal regions position themselves autonomously according to their chromatin class. **Genome Res**. **27,** 922–933 (2017). 5. **van de Werken, H. J. G**.\*, Landan, G\*., …, de Laat, W. Robust 4C-seq data analysis to screen for regulatory DNA interactions. **Nat. Methods** 9, 969–972 (2012) |
| **Project Title:** | **Precision medicine in an immune disease and cancer context using Machine learning and Artificial intelligence** |
| **Abstract:** | Machine Learning (ML) and Artificial Intelligence (AI) are key to better predict clinical outcome with highly complex clinical and molecular data sets. Moreover, these sophisticated methods can be applied to develop new algorithms and visualization tools to better understand basic cellular and molecular principles.In this project we aim to improve our biological understanding, diagnostic tools and response to therapy through ML and AI using different context-dependent -omics data sets in three subprojects:  **1.** We will deeply interrogate whole transcriptome data to understand transcription and aberrant splicing in cancer. We will develop new algorithms5 and visualization tools3 and integrate whole genome data and chromosome conformation data when necessary 1,4.This can lead to many novel insights in cancer development and potential new therapies in this devastating disease.  **2.** We will use immune receptor repertoire ("immunome") data from lymphoproliferative disease to identify context-dependent profiles of immune cells2. These profiles can support precision medicine through 1) definition of benign and malignant immune cell clones (diagnostics/prognostics) 2) traceability of clones upon therapy (monitoring), and 3) identification of disease-specific patterns to guide therapeutic decision making (theranostics). Examples of the impact of immunome analysis in a broader context include: Stereotyped BCR subsets in chronic leukemia with different prognostics, minimal disease monitoring, eligibility for immune therapy, TCR profiles with disease impact in cancer but also infectious disease, e.g. COVID-19.  **3**. We aim to improve allergy diagnostics based on the IgE profile of allergic individuals. The newly developed Allergy Explorer (ALEX) allows the acquisition of an IgE profile comprising 282 allergen extracts and components. The major challenge is the correct and clinically useful interpretation of such extensive IgE profiles, including reactivity of variable clinical implication. AI may support the clinician in the interpretation of the IgE profiles in combination with clinical signs and symptoms, and other clinical and demographic patient characteristics.  Based on these projects we hope to show that ML and AI supported clinical decision making as such may significantly benefit future treatment of cancer and immunological disease at a personal level (Precision Medicine). |
| **Requirements of candidate:** | * We are looking for a candidate with strong analytical and problem-solving skills, being highly motivated and having excellent communication and writing skills and being able to work independently. A background in immunology and/or cancer biology is of significant added value. * Master’s degree in bioinformatics, computational biology, statistics, or a related field. * The candidate should have demonstrated excellent scientific writing and software engineering skills in R and Python or Perl. * Scholarship that will, at least, cover subsistence allowance and international airplane ticket (we could help with the scientific part of your scholarship proposal) * English language requirement:   + English speaking countries & Netherlands: no requirement   + Other countries: IELTS 7.0 (min 6.0 for all subs), TOEFL 100 (min 20 for all subs) |

**English requirements：**

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*Erasmus University China Center -> CSC Scholarship -> “I am a prospective CSC PhD Candidate” -> Table 1*

Please note:

Each institute requires difference level of English, make sure to find the right institute. 2022 CSC-PhD programme information will be shared and updated soon!