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| **School/Department:** | **Department of Medical Oncology Erasmus MC** |
| **Supervisor information:** | * Prof dr. John Martens (supervisor) * Dr. Harmen van de Werken (co-supervisor) * **Email:** [j.martens@erasmusmc.nl](mailto:j.martens@erasmusmc.nl) and/or [h.vandewerken@erasmusmc.nl](mailto:h.vandewerken@erasmusmc.nl) * **Website:** [John Martens](https://www.erasmusmc.nl/en/cancer-institute/research/groups/medical-oncology-translational-cancer-genomics)and [Harmen van de Werken](https://www.erasmusmc.nl/en/research/researchers/werken-harmen-van-de) & [II](https://www.immunology.nl/research/harmen-van-de-werken/) * **Personal Grants:**   DDHF CCBC (2014 & 2018)  Astellas (ML; 2014)  NKB EMCR (2014)   * **Most important recent publications:**   **1.** Lindsay Angus, …, **Harmen J.G. van de Werken** , …, **John W.M. Martens** 2019. “Genomic landscape of metastatic breast cancer and its clinical implications”. **[Nature Genetics](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6858873/)** [51(10):1450-1458](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6858873/).. **2. Harmen J.G. van de Werken\*, van Riet, J.\*,**  ... and Mostert, B. 2021 The genomic landscape of 85 advanced neuroendocrine neoplasms reveals subtype-heterogeneity and potential therapeutic targets. [**Nature Communications**. 12, 1–14.](https://www.researchsquare.com/article/rs-50333/v1) **3.** Nik-Zainal, Serena, ... **John W. M. Martens**, ..., and Michael R. Stratton. 2016. “Landscape of Somatic Mutations in 560 Breast Cancer Whole-Genome Sequences.” [**Nature** 534(7605):47–54](https://pubmed.ncbi.nlm.nih.gov/27135926/). **4.** Smid, Marcel, .., **John W. M. Martens**. 2016. “Breast Cancer Genome and Transcriptome Integration Implicates Specific Mutational Signatures with Immune Cell Infiltration.” [**Nature Communications** 7:12910](https://www.nature.com/articles/ncomms12910). **5. Harmen J.G. van de Werken** et al.. 2017 Small chromosomal regions position themselves autonomously according to their chromatin class. [Genome Res. 27, 922–933](https://pubmed.ncbi.nlm.nih.gov/28341771/)  **6.** **van de Werken, Harmen J. G.**, 2012 et al. ”Robust 4C-Seq Data Analysis to Screen for Regulatory DNA Interactions.” [**Nature Methods** 9(10):969–72](https://pubmed.ncbi.nlm.nih.gov/22961246/). |
| **Project Title:** | **Cancer Computational Biology to Gain Insights in Biology and Create Clinical Value Using Multi-Omics Data Sets of Advanced and Metastatic Patients** |
| **Abstract:** | A Dutch initiative involved the biobanking of tumor biopsies and matched blood samples from cancer patients with locally advanced and metastatic diseases and subjecting them to Whole Genome Sequencing (WGS). The heroic effort generated a database of currently more than 4000 WGS datasets revealing pan-cancer and subtype specific driver events and mutational programs relevant for disease progression and therapy failure. In these first studies matched transcriptomics, in addition to WGS data, were not included as these data were generated at a later time point. Therefore, the next intruding step is to interrogate available transcriptome data and integrate them with matched WGS data. This provides us with the opportunity, in metastatic cancer, 1) to identify the phenotypic heterogeneity, 2) the clinical significance of RNA-seq beyond WGS data 3) and identify novel disease progression and cancer drug-resistances modules. Currently, we have access to 2072 matched RNA-seq datasets from 36 cancer types and eight different treatment categories, including chemotherapy and immunotherapy. We will interrogate this very comprehensive data set by applying state-of-the art- bioinformatic and computational biology methods including regularized multivariate analyses and machine learning methods, such as Random Forest and Neural Networks. The insights we will gain from this interrogation will be incorporated in patient stratification statistical models to ultimately support physicians in their clinical decision making, which may improve the health of cancer patients in the future. |
| **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 able to work independently. A background in 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：**

**Please refer to Erasmus University China Center official website for your information** [www.eur.nl/eucc](http://www.eur.nl/eucc)

*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!