China Scholarship Council – University Maastricht

PhD Programme Application form

Basic information

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1. Information on prospective UM supervisors and Promotor

- Title(s), initial(S), first name, surname: Prof. dr. J.C. (Judith) Sluimer
- Research group: Pathology/CARIM
- Address for correspondence: Postbus 616

  6200 MD Maastricht

- Telephone: +31644327274
- E-mail: Judith.sluimer@maastrichtuniversity.nl

1b. Second Supervisor:

- Title(s), initial(s), first name, surname: Prof. dr. (M) Ming, Chen
- Research group: Bioinformatics
- Address for correspondence: College of Life Sciences, Zhejiang University, China

- Telephone: +8657188206612
- E-mail: mchen@zju.edu.cn

Copromotor
- Title(s), initial(s), first name, surname:
- Research group:
- Address for correspondence:

- Telephone:
- E-mail:

2. Information on UM Faculty/ Department/ Institute/ School contact person:
- Initial(S), first name, surname: Carim-office@maastrichtuniversity.nl
- Research group: CARIM

4. Research field(s)

bioinformatics, single cell sequencing, cell metabolism, Vascular biology, ageing

- 人类健康与疾病的生物学基础 / Biological Foundations of Human Health and Diseases
- 重大新药创制 / Major New Drugs Discovery
- 前沿技术 / Frontier Technologies
- 信息技术 / Information Technology
- 基础研究 / Basic Research
- 人类健康与疾病的生物学基础 / Biological Foundations of Human Health and Diseases
- 支撑信息技术发展的科学基础 / Scientific Basis for Development of Information Technology

5. Title of research plan for CSC-UM PhD Programme

TITLE: Single-cell analysis of atherosclerosis and cell differentiation

6. Short summary of research plan

Background: Cardiovascular diseases (i.e., atherosclerosis) are leading causes of morbidity and death worldwide. Phenotypic and transcriptional heterogeneity within a celltype and transdifferentiation between cell types in atherosclerosis is tremendous, dictates cell function and could be a point of intervention for vascular diseases. Preliminary evidence suggests a new origin for smooth muscle cell. Hence, a single-cell (SC) approach is required to identify lineages and genetic regulators.

Study objective: Prof. Sluimer will provide SC and ATACseq datasets of murine lineage reporter mice, and human atherosclerosis to develop bioinformatics under supervision of Prof. Chen. Together, we develop and validate methodology to create a cross-species meta-analysis with our own and published data, and identify key differentiation tracks and their genetic drivers (coding and and long non-coding RNA) using single-cell sequencing data. We will identify differential cell subsets and genes, perform trajectory analysis, and predict transcription factors driving changes with atherosclerosis. Data will be used as input for drug repurposing predictions to stimulate beneficial phenotypes, or reverse detrimental phenotypes.

Expected Results: We will reveal and validate major drivers of cell heterogeneity and transdifferentiation in atherosclerosis, and to suggest first interventional targets for future exploitation. The developed workflows and tools are also applicable to other diseases. The meta-analysis will be made publically available.
The applicant for this joint-doctorate will therefore mature in a very interdisciplinary project and working environment. Together with career guidance by the host, training opportunities, and a clear plan for dissemination, the applicant will develop into an independent researcher.

Requirements: MSc degree in Computation biology or similar, and prior experience with bioinformatic languages (R and/or python) is crucial. We value team spirit, perseverance, a curious nature, a diligent way of working, and adequate English communication skills.

Group’s performance:

	Publications:	H-Index:	Number of citations
Prof. Sluimer	107	29 (WoS)	3729
Prof. Chen	236	47 (google scholar)	8907

Major publications related to this application: (>2017)

1. van Kuijk K, Demandt JAF, Perales-Patón J, Theelen TL, Kuppe C, Marsch E, de Bruijn J, Jin H, Gijbels MJ, Matic L, Mees BME, Reutelingsperger CPM, Hedin U, Biessen EAL, Carmeliet P, Baker AH, Kramann RK, Schurgers LJ, **Saez-Rodriguez J, Sluimer JC**. Deficiency of myeloid phd proteins aggravates atherogenesis via macrophage apoptosis and paracrine fibrotic signaling. Cardiovasc Res 2021 (accepted 10.1093/cvr/cvab152) IF 13.1
2. Jin H, Goossens P, Juhasz P, Eijgelaar W, Manca M, Karel J, Smirnov E, Sikkink CJ, Mees BM, Waring O, van Kuijk K Fazzi GE, Gijbels MJ, Kutmon M, Evelo CT, Hedin U, Daemen MJ, **Sluimer JC**, Matic L, Biessen EA. Integrative multi-omics analysis of human atherosclerosis reveals a serum response factor driven network associated with intraplaque haemorrhage. Clinical and Translational Medicine 2021 (doi.org/10.1002/ctm2.458) IF 11.5
3. Vacante F, Rodor J, Mahmoud A, Miller E, Bruijn de J, Van Kuijk K, Gijbels MJ.; Scanlon JP, Doran AC, Newby D, Giacca M, Hadoke P, Denby L, **Sluimer JC,** Baker AH. CARMN Loss Regulates Smooth Muscle Cells and Accelerates Atherosclerosis in Mice. (Circ Res, 2021 128:9, 1258-1275) IF 17.3
4. Van Kuijk K, Kuppe C, Betsholtz C, Vanlandewijck M, Kramann R, **Sluimer JC**. Heterogeneity and plasticity in healthy and atherosclerotic vasculature explored by single cell sequencing. Cardiovasc Res. 2019, 115:1705-1715. IF 10.8
5. Marsch E, Demandt JA, Theelen TL, Tullemans BM, Wouters K, Boon MR, van Dijk TH, Gijbels MJ, Dubois LJ, Meex SJ, Mazzone M, Hung G, Fisher EA, Biessen EA, Daemen MJ, Rensen PC, Carmeliet P, Groen AK, **Sluimer JC**. Deficiency of the oxygen sensor prolyl hydroxylase 1 attenuates hypercholesterolaemia, atherosclerosis, and hyperglycaemia. Eur heart J 2016 37(39): 2993-2997 IF 19.6
6. Xiaotian Hu, Cong Feng, Yincong Zhou, Andrew Harrison, **Ming Chen*** (2022) DeepTrio: a ternary prediction system for protein-protein interaction using mask multiple parallel convolutional neural networks. *Bioinformatics*, 38(3): 694-702. (IF=6.931; 8.778)
7. Yuhao Chen, Yanshi Hu, Xiaotian Hu, Cong Feng, **Ming Chen*** (2022) CoGO: a contrastive learning framework to predict disease similarity based on gene network and ontology structure. *Bioinformatics*, btac520. (IF=6.931; 8.778)
8. Jiao Qu, Fa Yang, Tao Zhu, Yingshuo Wang, Wen Fang, Yan Ding, Xue Zhao, Xianjia Qi, Qiangmin Xie, Qiang Xu, **Ming Chen**, Yicheng Xie*, Yang Sun*, Dijun Chen* (2022) A reference single-cell regulomic and transcriptomic map of cynomolgus monkeys. *Nature Communications*, 13: 4069. (IF=17.694; 17.763)
9. Yuan Liao+, Lifeng Ma+, Qile Guo+, Weigao E+, Xing Fang+, Lei Yang+, Fanwei Ruan, Jingjing Wang, Peijing Zhang, Zhongyi Sun, Haide Chen, Zhongliang Lin, Xueyi Wang, Xinru Wang, Huiyu Sun, Xiunan Fang, Yincong Zhou, **Ming Chen**, Wanhua Shen*, Guoji Guo*, Xiaoping Han* (2022) Cell landscape of larval and adult Xenopus laevis at single-cell resolution. *Nature Communications*, 13: 4306. (IF=17.694; 17.763)

10. Renying Wang+, Peijing Zhang+,*, Jingjing Wang+, Lifeng Ma+, Weigao E+, Shengbao Suo+, Mengmeng Jiang+, Jiaqi Li+, Haide Chen, Huiyu Sun, Lijiang Fei, Ziming Zhou, Yincong Zhou, Yao Chen, Weiqi Zhang, Xinru Wang, Yuqing Mei, Zhongyi Sun, Chengxuan Yu, Jikai Shao, Yuting Fu, Yanyu Xiao, Fang Ye, Xing Fang, Hanyu Wu, Qile Guo, Xiunan Fang, Xia Li, Xianzhi Gao, Dan Wang, Peng-Fei Xu, Rui Zeng, Gang Xu, Lijun Zhu, Lie Wang, Jing Qu, Dan Zhang, Hongwei Ouyang, He Huang, **Ming Chen**, Shyh-Chang NG*, Guang-Hui Liu*, Guo-Cheng Yuan*, Guoji Guo*, Xiaoping Han* (2022) Construction of a cross-species cell landscape at single-cell level. *Nucleic Acids Research*, gkac633. (IF=19.16; 17.21)
11. Jingjing Wang#, Huiyu Sun#, Mengmeng Jiang, Jiaqi Li, Peijing Zhang, Haide Chen, Yuqing Mei, Lijiang Fei, Shujing Lai, Xiaoping Han, Xinhui Song, Suhong Xu, **Ming Chen**, Hongwei Ouyang, Dan Zhang*, Guo-Cheng Yuan*, Guoji Guo* (2021) Tracing cell-type evolution by cross-species comparison of cell atlases. *Cell Reports*, 34: 108803. (IF=9.995; 10.99)
12. Xiaoping Han*, Ziming Zhou, Lijiang Fei, Huiyu Sun, Renying Wang, Yao Chen, Haide Chen, Jingjing Wang, Huanna Tang, Wenhao Ge, Yincong Zhou, Fang Ye, Mengmeng Jiang, Junqing Wu, Yanyu Xiao, Xiaoning Jia, Tingyue Zhang, Xiaojie Ma, Qi Zhang, Xueli Bai, Shujing Lai, Chengxuan Yu, Lijun Zhu, Rui Lin, Yuchi Gao, Min Wang, Yiqing Wu, Jianming Zhang, Renya Zhan, Saiyong Zhu, Hailan Hu, Changchun Wang, **Ming Chen**, He Huang, Tingbo Liang, Jianghua Chen, Weilin Wang, Dan Zhang, Guoji Guo* (2020) Construction of A Human Cell Landscape at Single Cell Level. *Nature*, 581(7808): 303-309. (IF=69.504; 63.58)
13. Xinjian Yu, Siqi Lai, Hongjun Chen, **Ming Chen*** (2020) Protein-protein interaction network with machine learning models and multiomics data reveals potential neurodegenerative disease-related proteins. *Human Molecular Genetics*, 29(8): 1378-1387. (IF=5.121; 5.999)
14. Dijun Chen*, Liangyu Fu, Dahui Hu, Christian Klukas, **Ming Chen***, Kerstin Kaufmann* (2018) The HTPmod Shiny application enables modeling and visualization of large-scale biological data. *Communications Biology*, 1: 89. (IF=6.548; 6.816)
15. Xiaoping Han*, Renying Wang, Yincong Zhou, Lijiang Fei, Huiyu Sun, Shujing Lai, Assieh Saadatpour, Zimin Zhou, Haide Chen, Fang Ye, Daosheng Huang, Yang Xu, Wentao Huang, Mengmeng Jiang, Xinyi Jiang, Jie Mao, Yao Chen, Chenyu Lu, Jin Xie, Qun Fang, Yibin Wang, Rui Yue, Tiefeng Li, He Huang, Stuart H. Orkin, Guo-Cheng Yuan, **Ming Chen**, Guoji Guo* (2018) Mapping the Mouse Cell Atlas by Microwell-seq. *Cell*, 172: 1091-1107. (IF=66.85; 59.901)
16.

7. Motivation for CSC-UM PhD application (max. 250 words)

To whom it may concern

I am He Xu, graduated from Guangzhou University. I am writing this letter to express my deep interest in the PhD position” Bioinformatics” .First, I learned the relevant skills of bioinformatics during my postgraduate study. I think it is very meaningful to solve practical problems by combining information technology with biological knowledge. So I firmly chose the bioinformatics occupation When I graduated. In more than one year of work, I have studied WES analysis, RNA-seq analysis and scRNA-seq analysis. However, I found that my education have limited the development of my career prospects, and I think a higher education can help me improve my personal value. Secondly, I am a person who likes to explore new things. In the field of bioinformatics, scRNA-seq analysis is currently a hot trend, because of its very large data dimension, its data processing becomes extremely difficult and diverse. I think It's very challenging. My ideal mentors, Professor Sluimer and Chen, have complimentary expertise in the physiological mechanism of cardiovascular diseases, and bioinformatics I am very interested in this research direction, because my hometown is in the northeast of China, and a large number of people in our region have related family medical history, so I have attached great importance to this since childhood.

Finally I know that the doctoral program you offer has attracted many promising candidates, but I believe that my professional knowledge, enthusiasm and persistence can help me to complete this challenge.

Best
He Xu

Applicant's Curriculum Vitae (if available)

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8. Personal details

Applicant
- Title(s), initial(s), first name, surname: He Xu

CSC-UM PhD programme start 1-9-2021

- Surname: Xu
- Nationality: Chinese
- Date of Birth: 1997-01-04
- Country and place of birth: Tongliao City, Inner Mongolia Autonomous Region, the People's Republic of China

9. Master's degree (if applicable)

Note! Add a copy of your Master's degree to your application

University (211 or 985 if available): Guangzhou University
Faculty/discipline: College of Life Science
City and country: China Guangzhou
Date:2019-09 to 2022-06
Grade average: Better than average
Title Master's thesis (if applicable): Optimization of extraction and purification process of total flavonoids from Flowering Chinese cabbage and analysis of the difference of total flavonoids content in different Flowering Chinese cabbage.
Thesis grade: Excellent

Personal Resume

Basic information

Name:Xing He xu
Nationality: Mongolian
Phone: 19120509511

Year of birth: 1997.01
Native place: Guangzhou China
Height and weight: 188CM/86kg
Mailbox: 1457576928@qq.com

Apply information

Apply academy: Maastricht University
Apply major: bioinformatics

Educational

2019.09-2022.06 **Guangzhou university** **Master Degree**
Major courses: bioinformatics, molecular biology, biochemistry, epigenetics, genetics, R language, Linux.

Experience

2018.09-2019.08 **Luoyang Oriental Hospital** **Department of Medical Engineering**

- Responsible for the medical equipment maintenance and debugging

2021.08-2022.11 **Beijing Bofurui Gene Diagnosis Co. LTD** **Head of bioinformatics Department**

- I work in Beijing Bofurui Medical Diagnosis Co., LTD., director of bioinformaticsResponsible for the management of the Department of Bioinformatics, bioinformatics process construction of the whole exon sequence project, genetic counseling work, and cooperation with several hospitals to analyze Bulk RNA-seq data and single cell sequencing data.

Award

Excellent athlete of Henan Province in CUBA Basketball League

Self-evaluation

I am a bioinformatics practitioner and a master's student. I am good at WES, RNA-seq, Single cell sequencing and other data analysis. I am mainly familiar with R language and Linux. I have processed thousands of exon data and several RNA-seq data, and I believe that I can meet the complex data processing needs. At the same time, I like to communicate and help others

硕士学位证书

徐赫，男，1997年 1 月 4 日生。在广州大学完成了 化学工程领域工程 硕士专业学位培养计划，成绩合格。根据《中华人民共和国学位条例》的规定，授予 工程 硕士学位。

校　长　魏明海

学位评定委员会主席

证书编号：1107832022101357

二〇二二年　六月　二十日

（专业学位证书）

硕士研究生

毕业证书

研究生 **徐赫** 性别 **男**，**一九九七** 年 **一** 月 **四** 日生，于 **二〇一九** 年 **九** 月至 **二〇二二** 年 **六** 月在 **化学工程** 专业 **全日制** 学习，学制 **三** 年，修完硕士研究生培养计划规定的全部课程，成绩合格，毕业论文答辩通过，准予毕业。

培养单位：广州大学

校　长：魏明海

证书编号：110781202202000925

二〇二二 年 六 月 三十 日