



## 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

**Resolving metabolic regulators in vascular disease at the single cell level**

#### 6. Short summary of research plan

**Background:** Cell metabolism is an important driver of cell function and could be a point of intervention for vascular diseases. Preliminary evidence suggests metabolism differs between cell types, hence a single cell approach is required to identify metabolomic regulators. *In vivo* single cell metabolic profiling is not routine, and methods to infer metabolic pathways from single cell sequencing data (SCseq) are not well-established.

**Study objective:** Prof. Sluimer will provide SCseq datasets of human vascular diseases to develop bioinformatics under supervision of Prof. Chen. Together we develop and validate methodology to identify key metabolic drivers and pathways using single cell sequencing data. Integrate human, mouse and non-human primate data, identify differential cell subsets and genes, perform trajectory analysis, predict cell:cell communication and transcription factors driving changes with ageing. Data will be used as input for drug repurposing predictions.

**Expected Results:** We will reveal and validate major drivers of cell metabolism in vascular disease, and to suggest first interventional targets for future exploitation. The developed workflows and tools are also applicable to other diseases.

The applicant 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	235	45 (google scholar)	8427

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)