

## Curriculum Vitae

### Personal information

*Name:* Kuijjer, Marieke Lydia  
*Date of birth:* 05.02.1982  
*Sex:* Female  
*Nationality:* Dutch  
*Languages:* Dutch (native), English (full professional proficiency), Italian (full professional proficiency), Norwegian (upper intermediate)  
*Orcid ID:* 0000-0001-6280-3130  
*URL:* [www.kuijjerlab.org](http://www.kuijjerlab.org)



### Education

2008–2013 PhD in Bioinformatics and Cancer Genomics, Department of Pathology, Leiden University Medical Center (LUMC), the Netherlands  
2006–2008 Master of Science in Biomedicine, Leiden University, the Netherlands  
2003–2007 Bachelor of Science in Biomedicine, Leiden University, the Netherlands

### Current and previous positions

2020–2023 Assistant Professor in Computational Cancer Oncology (20%), Department of Pathology, LUMC, the Netherlands  
2018–2027 Group Leader in Computational Biology and Systems Medicine, Centre for Molecular Medicine Norway (NCMM), University of Oslo (UiO), Norway  
2013–2018 Research Fellow in Biostatistics and Computational Biology, Department of Biostatistics and Computational Biology, Dana Farber Cancer Institute (DFCI), USA; Department of Biostatistics, Harvard Chan School of Public Health (HSPH), USA

### Documented leave

5.5 months

### Mobility

2018– Group Leader, NCMM, UiO, Norway  
2013–2018 Postdoctoral Fellow, DFCI/HSPH, Boston, United States  
2008–2013 PhD student, LUMC, Leiden, the Netherlands

### Project management experience (selection)

2024–2028 Krafttak mot Kreft grant, Norwegian Cancer Society. **PI**  
2022–2023 Foundation for the Promotion of Cancer Research, University of Oslo, UNIFORM-FRIMED. **PI**  
2021–2026 Young Research Talents, Norwegian Research Council. **PI**  
2021–2025 Pink Ribbon grant, Norwegian Cancer Society. **PI**  
2020–2023 Four NCMM/Associate Investigator Collaborative grants. **Co-PI**  
2021–2022 Two NCMM/The Arctic University of Norway Tromsø (UiT) Collaborative grants. **Co-PI**  
2021 National Cancer Institute (NCI)/Department of Energy (DoE). **Co-PI**  
2020–2023 Leiden Center for Computational Oncology, Leiden University Medical Center. **Co-PI**  
2020–2023 Three Familien Blix Foundation grants. **(Co-)PI**  
2018–2027 NCMM, Computational Biology and Systems Medicine Group. **PI**

- 2018–2023 Dutch Research Council, VICI grant (to Judith Bovée). **Bioinformatics Lead**
- 2016–2018 Charles A. King Postdoctoral Fellowship, Charles A. King Trust, Sara Elisabeth O'Brien, Bank of America, co-Trustees. **PI**
- 2016–2017 National Cancer Institute (NCI) Brain Cancer Specialized Program of Excellence (SPORE) Career Enhancement Project (CEP) Award. **PI**
- 2015–2016 NVIDIA Compute the Cure. **Cancer Research Lead**

*For comprehensive list of funded projects, incl. amounts, please refer to the section below.*

### **Supervision of graduate students and research fellows**

- 2020–2024 Supervised at LCCO, LUMC, the Netherlands  
1 PhD student (co-supervised)
- 2018– Supervised at NCMM, UiO, Norway  
6 Postdoctoral Fellows (incl. 1 co-supervised, 3 Marie Curie Scientia Fellows)  
+4 Postdoctoral Fellows will start in 2024  
7 PhD students (incl. 1 co-supervised, 2 visiting)  
+1 PhD student will start in 2024  
1 Research Assistant (Master's student paid on project)  
9 Master's students (incl. 3 theses, 5 summer projects, 1 visiting)
- 2013–2018 Supervised at DFCI, HSPH, USA  
2 PhD students (incl. 1 rotation, 1 visiting)  
3 Master's students (incl. 1 thesis, 1 summer project)
- 2008–2012 Supervised at LUMC, the Netherlands  
2 Master's students (incl. 1 thesis)

*Total number of students: 4 high school, 10 Bachelor's (2 theses), 14 Master's (6 theses), 10 PhD students (2 co-supervised, 3 visiting, 1 rotation), 6 postdoctoral fellows (1 co-supervised).*

### **Teaching activities**

- 2024 Lecturer – MeInBio program, University of Freiburg, Germany (*upcoming*)
- 2022– Co-organizer – Nordic EMBL/UiO PhD course "Multi-omics data analysis and integration for precision medicine," UiO, Norway (5 ECTS)
- 2021 Lecturer – Frontiers in Genomics program, National Autonomous University of Mexico (UNAM), Mexico
- 2019– Lecturer & coordinator of grading – NCMM PhD course "Molecular Medicine," MF9120BTS, UiO, Norway (10 ECTS)
- 2015 Teaching Assistant – Harvard Catalyst course "Applications in Network Medicine," Harvard University, USA
- 2009–2010 Lecturer and workgroup leader – BSc Biomedical Sciences Pathology course, Leiden University, the Netherlands

### **Organization of conferences, workshops, seminars, and consortia**

- 2023 Co-organizer of the Institute for Computational and Experimental Research in Mathematics (ICERM) workshop on Mathematical and Computational Biology, Providence, RI, USA
- 2022– Co-organizer of the Nordic EMBL Partnership "Tools of the Trade—Data Science" Webinar Series
- 2022 Scientific Committee Member, Nordic EMBL Partnership Meeting, Aarhus, Denmark
- 2020 Scientific Committee Member, Nordic EMBL Partnership Meeting, Umeå, Sweden

- 2019 Organizer of the NCMM retreat, Sundvollen, Norway  
 2014–2015 Co-organizer of the Big Data Seminar, Department of Biostatistics, HSPH, USA

### **Institutional responsibilities**

- 2022– Member of the NCMM hiring board  
 2022– Advisory Board Member, Nordic Computational Biology (NCB) network (ISCB affiliate)  
 2021 Member of the pre-selection committee for the recruitment of two NCMM Group Leaders at NCMM  
 2020– Faculty Advisor of the ISCB Regional Student Group (RSG) Norway  
 2019– Member of the NCMM IT steering committee  
 2018– Hiring panel member for various positions at NCMM, UiO, UiB, Leiden University

### **Grant and position review**

- 2023–2024 Evaluation and Interview Committee Member for two Group Leader positions at the Laboratory for Molecular Infection Medicine Sweden (MIMS), University of Umeå, Sweden  
 2023 Evaluator for the renewal of Group Leader Balász Papp, the Hungarian Centre of Excellence for Molecular Medicine (HCEMM), Hungary  
 2022–2025 Data Science Committee Expert Member, Novo Nordisk Foundation, Denmark  
 2022– *Ad hoc* Grant Review, Medical Research Council, UK; Personal Research Grants Program, Israel Science Foundation (ISF); United States-Israel Binational Science Foundation (BSF), Israel Science Foundation (ISF)  
 2021–2022 Evaluator for the Doctoral Fellowship Programme of the Austrian Academy of Sciences  
 2021–2022 Expert and Rapporteur, HORIZON-MCSA-2021-PF-01 Life Sciences (LIF) proposal evaluations, EU  
 2020 Grant Review Committee Member, Omics Data Against Cancer (ODAC) competition, Québec Research Fund, Canada

### **Thesis opponent and review**

- 2023–2024 PhD Reviewer of 2 theses, University of Helsinki, Finland  
 2022– PhD Committee Member, University of Helsinki, Finland  
 2020–2022 PhD opponent of 4 national defenses, University of Oslo, Norway  
 2020–2021 PhD opponent of 2 international defenses (University of Helsinki, Finland; Leiden University Medical Center, the Netherlands)  
 2020– PhD midterm evaluation member for 7 PhD students at University of Oslo, Norway  
 2016–2021 MSc opponent/committee member of 2 defenses, incl. 1 international

### **Editorial and reviewer work**

- 2022 Reviewer for the Intelligent Systems for Molecular Biology (ISMB) 2022 Proceedings  
 2021– Associate Editor for the journal *Bioinformatics Advances*, Oxford University Press  
 2020–2021 Co-editor of the Research Topic in *Frontiers in Genetics*  
 2017 Conference proceedings review panel—Computational Methods in Systems Biology conference, Darmstadt, Germany  
 2016– Editorial Board Member for the journal *Cancer Research*

2013– Peer reviewer of a total of 63 manuscripts for 22 international journals, incl. *Nature Reviews Genetics*, *Nature Methods*, *Cancer Research*, *Journal of Pathology*, *Nucleic Acids Research*, *Bioinformatics*, *PLoS Computational Biology*, *Genome Medicine*

### **Participation in consortia**

2022– Executive Committee Member, biologist representative of the Fight Osteosarcoma Through European Research (FOSTER) consortium; Member of WP1 (basic research) and WP8 (research dissemination)

2008–2011 EuroBoNeT, a European network to promote research into uncommon cancers in adults and children, with focus on pathology, biology, and genetics of bone tumors

### **Memberships of academies / scientific societies**

2019– International Society for Computational Biology (ISBC)

2014– American Association for Cancer Research (AACR)

### **Major collaborations**

Norway Geir Kjetil Sandve (UiO), Vessela Kristensen (UiO), Xavier Tekpli (UiO), Erik Knutsen (The Arctic University of Norway UiT), Anthony Mathelier (NCMM/UiO)

International Judith Bovée (LUMC, the Netherlands), Priya Chudasama (German Cancer Research Center DKFZ, Germany), Kimberly Glass (Harvard Medical School, USA), John Quackenbush (HSPH, USA), Daniel Osorio (Boston's Children Hospital, USA)

### **Invited international presentations and seminars**

#### Invited keynotes

2024 CIBB 2024. September 4-6, Benevento, Italy (*upcoming*)

2024 TransSYS final conference. June 19-20, 2024, Belgrade, Serbia (*upcoming*)

#### Invited presentations at international conferences

2023 Genetics Society Spring Meeting, St. Catherine's College, University of Oxford. April 12-14, 2023, Oxford, UK

2022 EMBL Partnership conference. September 21-23, 2022, Heidelberg, Germany

2021 Panel discussion "Digital twins for cancer care." Fourth ISC Workshop on HPC Applications in Precision Medicine. July 2, 2021 (*virtual*)

2020 Nordic EMBL Partnership meeting. September 22-25, 2020 (Umeå, Sweden)

2020 Network Medicine satellite of NetSci. September 17, 2020 (Rome, Italy)

2016 LabRoots Genetics and Genomics virtual conference. May 11-12, 2016 (*virtual*)  
Presentation can be watched at: [tinyurl.com/bigdataintegration](https://tinyurl.com/bigdataintegration)

2015 Banff/BIRS conference Statistical and Computational Challenges in Bridging Functional Genomics, Epigenomics, Molecular QTLs, and Disease Genetics (BIRS/Banff 15w5142). August 3-7, 2015, Banff, Canada. Presentation can be watched at: [tinyurl.com/birsbanff-lioness](https://tinyurl.com/birsbanff-lioness)

*In addition to these invited talks, 9 presentations were selected for talks at international conferences (incl. USCAP, ISMB/ECCB).*

#### Invited seminars, international

2024 Medicine, Informatics and Biology (MeInBio) doctoral program. 2024 (*upcoming*).  
Freiburg, Germany

- 2023 Institute of Biotechnology, National Autonomous University of Mexico (UNAM). January 16, 2023. Cuernavaca, Mexico. Presentation can be watched at: [tinyurl.com/biotech-unam](https://tinyurl.com/biotech-unam)
- 2022 Institute for Molecular Medicine Finland (FIMM), University of Helsinki. June 28, 2022, Helsinki, Finland
- 2021 Program Frontiers in Genomics, National Autonomous University of Mexico (UNAM). November 23, 2021, Cuernavaca, Mexico. Presentation can be watched at: [tinyurl.com/netmed-unam](https://tinyurl.com/netmed-unam)
- 2021 Research Program in Systems Oncology, University of Helsinki. August 13, 2021, Helsinki, Finland
- 2021 Leiden Center for Computational Oncology, Leiden University Medical Center. February 1, 2021, Leiden, the Netherlands
- 2020 Molecular Tumor Genetics, Leiden University Medical Center. January 16, 2020, Leiden, the Netherlands

*In addition, 4 presentations were selected for talks at international seminars/symposia.*

### **Prizes and awards**

- 2016 National Cancer Institute (NCI) Brain Cancer Specialized Program of Research Excellence (SPORE) Career Enhancement Program (CEP) Award
- 2015 Harvard Chan School of Public Health Program in Quantitative Genomics (PQG) travel award for the AACR conference "Computational and Systems Biology of Cancer"
- 2013 Leiden University PhD award for successfully completing the doctorate without extension of the contract
- 2013 Dutch Cancer Society (KWF) sponsorship to cover printing costs of the PhD thesis
- 2012 Leiden University Fund travel grant for the EMBO conference "From systems biology to functional genomics." November 17–20, 2012, Heidelberg, Germany
- 2012 Best presentation award. Dutch Cancer Society (KWF) Tumor cell biology meeting. November 6, 2012, Lunteren, the Netherlands
- 2006–2008 Two Outbound Study Grant scholarships for following Master's courses at the Karolinska Institute, Stockholm Sweden
- 2005 Erasmus scholarship, semester at the Karolinska Institute, Stockholm Sweden

### **Track record**

Dr. Kuijjer has a total of **65 scientific publications** (since 2011), incl. 56 peer-reviewed articles (50 original studies in journals, 3 computer science conference proceedings, 3 reviews). In addition, she published 4 editorial commentaries and a book chapter. She has 4 BioRxiv manuscripts currently in review/in revision. Her publication record includes 14 senior, 13 first, and 18 corresponding authorships. **h-index: 30**, i-10 index: 43, **citations: 4,660** (Google Scholar, accessed April 5, 2023).

Dr. Kuijjer has been invited for **2 keynotes** (*upcoming*) and has given **7 invited talks at international conferences** as well as 8 selected international talks, and 1 invited talk and 3 selected talks at national conferences. She presented 19 seminars (8 international), of which 14 invited and 5 selected for presentation. She participated in **2 panel discussions** (1 international).

Her group has published **9 computational softwares**, contributed to 3 additional softwares, and various large-scale open access data resources. For more details, see [www.kuijjerlab.org/tools](http://www.kuijjerlab.org/tools).

*Please refer to the last section of this document for a complete list of publications.*

## List of received funding sources

The total amount of external and internal funding my group received amounts to approximately **5,457,300 EUR**.

Please note that the amounts here are listed in EUR and are approximate, based on exchange rates of when the grants were funded.

### External funding sources

The total of amount of external funding to my group is approximately **2,413,000 EUR**. (Please note that this sum only includes funding specifically allocated to my group. Total funding of collaborative grants is not included, and presented in unbolded font below.)

- 2024–2027 UiO/NCMM – Precision network medicine for treatment stratification of metastatic breast cancer – Norwegian Cancer Society (NCS), Krafttak mot Kreft  
Role: **PI** – Amount: **675,000 EUR**
- 2023–2024 UiO/NCMM – Precision network medicine for treatment stratification of metastatic breast cancer – Astri og Birger Torsteds Legat til bekjempelse av kreft  
Role: **PI** – Amount: **5,000 EUR**
- 2023–2026 UiO/IBV – Decoding the unfolded protein response pathway for cancer therapy – Norwegian Cancer Society (NCS)  
Role: **Partner** – Amount: **750,000 EUR** (no funding to Kuijjer group, co-supervision of postdoctoral fellow)
- 2022–2024 UiO/NCMM – Mapping individual spatial regulatory genomic landscapes to identify drivers and targeted therapies in breast cancer – UNIFOR-FRIMED  
Role: **PI** – Amount: **11,000 EUR**
- 2022–2024 UiO/NCMM – Mapping individual spatial regulatory genomic landscapes to identify cancer drivers and targeted therapies in breast cancer – EU/FP7, Marie Curie Scientia Fellows (MCSF) II program  
Role: **PI** – Amount: **97,000 EUR**
- 2022–2023 UiO/NCMM – Drug combination prediction for the treatment of triple-negative breast cancer – Familien Blix Fond, Familien Blix Fond til fremme av medisinsk forskning  
Role: **PI** – Amount: **5,000 EUR**
- 2021–2026 UiO/NCMM – Large-scale personalized omics networks to model the disruption of gene regulation in cancer – Norwegian Research Council (NFR), Young Research Talents  
Role: **PI** – Amount: **750,000 EUR**
- 2021–2025 GRAMINOR AS – Genomic-based breeding technology for the improvement of pre harvest sprouting resistance in spring wheat under Norwegian climate – NFR, Innovation Project for the Industrial Sector  
Role: **Partner** – Amount: **1,700,000 EUR** (**19,000 EUR** to Kuijjer group)
- 2021–2024 UiO/NCMM – Towards identifying regulatory mechanisms driving breast cancer phenotypes by integrating multi-omic and multimodal single-cell data in a network-based approach – EU/FP7, Marie Curie Scientia Fellows (MCSF) II program  
Role: **PI** – Amount: **145,000 EUR**
- 2021–2025 UiO/NCMM – Large-scale personalized omics networks to identify novel regulatory subtypes and targeted therapies in breast cancer – Norwegian Cancer Society (NCS), Pink Ribbon/Rosa Sløyfe personalized breast cancer treatments  
Role: **PI** – Amount: **187,000 EUR** (original amount: **342,500 EUR**, partly overlap with

- Young Research Talents grant)
- 2021–2022 UiO/NCMM – *Quinolate phosphoribosyltransferase (QPRT) as a target gene for the reduction of resistance development in ER-positive breast cancer* – Familien Blix Fond, Familien Blix Fond til fremme av medisinsk forskning  
Role: **Co-PI** (with postdoctoral fellow Daniel Osorio) – Amount: **5,000 EUR**
- 2021 University of South Carolina – *Dynamic multiscale digital twin for a lung cancer patient*– National Cancer Institute (NCI)/Department of Energy (DoE), Joint Design of Advanced Computing Solutions for Cancer (JDACS4C) program  
Role: **Co-PI** – Amount: **94,000 EUR (14,000 EUR to Kuijjer group)**
- 2020–2023 Leiden University Medical Center (LUMC) – *SarCOma* – LUMC, Leiden Center for Computational Oncology (LCCO)  
Role: **Co-PI** – Amount: **1,500,000 EUR (200,000 EUR to Kuijjer group)**
- 2020–2023 UiO/NCMM – *Patient-specific modeling of gene regulatory networks and association to clinical characteristics in Alzheimer's disease* – EU/FP7, MCSF II program  
Role: **PI** – Amount: **145,000 EUR**
- 2020–2021 UiO/NCMM – *Identification and characterization of regulatory subtypes in leiomyosarcoma* – Familien Blix Fond (FBF), FBF til fremme av medisinsk forskning  
Role: **PI** – Amount: **5,000 EUR**
- 2018–2023 LUMC – *Sarcoma modeling towards patient-specific treatment* – Dutch Research Council (NWO), VICI grant to Judith Bovée  
Role: **Partner** – Amount: **1,500,000 EUR (20,000 EUR to Kuijjer group)**
- 2016–2018 DFCI – *Modeling the effects of gene regulation on cancer survival* – Charles A. King, Sara Elizabeth O'Brien, Bank of America, co-Trustees, Postdoctoral Fellowship  
Role: **PI** – Amount: **85,000 EUR**
- 2016–2017 DFCI – *Modeling the effects of gene regulation on glioblastoma development and progression* – National Cancer Institute, Specialized Programs Of Research Excellence (SPORE) Career Enhancement Project award  
Role: **PI** – Amount: **45,000 EUR**

### Internal funding sources

The total of amount of internal funding is approximately **3,165,300 EUR**.

- 2024–2026 UiO/NCMM – NCMM Collaborative Postdoctoral Program  
Role: **Co-PI** – Amount: **110,000 EUR**
- 2023–2027 UiO/NCMM – *Computational Biology and Systems Medicine group, second term* – The Norwegian Research Council, Helse Sør-Øst, University of Oslo  
Role: **PI** – Amount: **1,270,000 EUR**
- 2022–2023 UiO/NCMM – *Development of an epithelial–mesenchymal transition score for prognostic evaluation of breast cancer* – NCMM/UiT Collaborative Grant  
Role: **Co-PI** – Amount: **30,000 EUR**
- 2022–2023 UiT – *Towards precision treatment for lung cancer patients from serum cfRNA – a pilot study* – NCMM/UiT Collaborative Grant  
Role: **Co-PI** – Amount: **24,000 EUR**
- 2021–2023 UiO/NCMM – *Spatial tumor biology* – NCMM/Assoc. Investigator Collaborative Grant  
Role: **Co-PI** – Amount: **70,000 EUR**
- 2021–2023 UiO/NCMM – *Cold-induced neuronal degeneration: dissecting the mechanism, inducing resistance* – NCMM/Associate Investigator Collaborative Grant



- 2019–2021      Role: **Co-PI** – Amount: **38,300 EUR**  
UiO/NCMM – *Dynamic temporal network analysis of the induction, evolution and resolution of endothelial cell transcriptional responses to inflammatory stimuli* – NCMM/Associate Investigator Collaborative Grant
- 2019–2021      Role: **Co-PI** – Amount: **47,000 EUR**  
UiO/NCMM – *High dimensional and spatial analysis of osteosarcoma* – NCMM/Associate Investigator Collaborative Grant
- 2018–2023      Role: **Co-PI** – Amount: **36,000 EUR**  
UiO/NCMM – *Computational Biology and Systems Medicine group, first term* – The Norwegian Research Council, Helse Sør-Øst, University of Oslo
- Role: **PI** – Amount: **1,900,000 EUR**

## List of all scientific publications

Lab members are listed in *italics*. †shared authorship; #corresponding author

**Pre-prints and manuscripts in submission**—These include 1 first and 2 senior author manuscripts.

1. *Meijer DM*, Ruano D, Briaire-de Bruijn IH, Wijers-Koster PM, van de Sande MAJ, Gelderblom H, Cleton-Jansen AM, de Miranda N, **Kuijjer ML**†, Bovée JVMG† (2024) The variable genomic landscape during osteosarcoma progression: insights from a longitudinal WGS analysis. *MedRxiv*  
DOI:10.1101/2024.04.18.24306025
2. Unal B, Kuzu O, Jin Y, *Osorio D*, **Kuijjer ML**, Daugaard M, Oo HZ, Patterson J, Saatcioglu F (2024). Targeting IRE1 $\alpha$  alleviates the immunosuppressive tumor microenvironment in prostate cancer. *In revision*
3. Villaseñor-Toledo T, Valle-Garcia D, *Pop RT*, Osio-Beccero V, Meza-Sosa KF, Serrano C, Díaz de Leon-Guerrero S, Hernández-Pando R, Nava P, **Kuijjer ML**, Pérez-Martínez L, Pedraza-Alva G (2023) Exposure to enriched environment attenuates mouse experimental colitis by regulating a Myc-driven gene regulatory network and by improving colon epithelial barrier integrity. *BioRxiv* DOI:10.1101/2023.02.16.528051
4. *Osorio D*, Tekpli X, Kristensen V, **Kuijjer ML**# (2022) Drug combination prediction for cancer treatment using disease-specific drug response profiles and single-cell transcriptional signatures. *BioRxiv*  
DOI:10.1101/2022.03.31.486602 *In revision*
5. **Kuijjer ML**#, Glass K (2021) Reconstructing sample-specific networks using LIONESS. *BioRxiv*  
DOI:10.1101/2021.09.27.461954

**Original scientific publications arising from my independent laboratory**—1 first and 5 senior authorships.

6. McCabe M, Green D, van Ewijk R, Tirtei E, Andreou D, Baecklund F, Baumhoer D, Bielack S, Rajesh B, Boye K, Brennan B, Capra M, Cottone L, Dirksen U, Fagioli F, Fernandez N, Flanagan AM, Gambarotti M, Gaspar N, Gelderblom H, Gerrand C, Gomez-Mascard A, Harges J, Hecker-Nolting S, Kabickova E, Kager L, Kanerva J, Kester L, **Kuijjer M**, Laurence V, Lervat C, Marchais A, Marec-Berard P, Mendes C, Merks J, Ory B, Palmerini E, Pantziarka P, Papakonstantinou E, Piperno-Neumann S, Raciborska A, Roundhill E, Rutkauskaite V, Safwat A, Scotlandi K, Staals E, Strauss S, Surdez D, Sys G, Tabone MD, Toulmonde M, Valverde C, van de Sande M, Wörtler K, Campbell-Hewson Q, Nathrath M (2024) Biological sample collection to advance bone sarcoma research and treatment: a position paper by two European consortia. *Accepted in Clin Cancer Res*
7. *Osorio D*#, Capasso A, Eckhardt SG, Giri U, Somma A, Pitts TM, Lieu CH, Messersmith WA, Bagby SM, Singh H, Das J, Sahni N, Yi SS#, **Kuijjer ML**# (2024) Population-level comparisons of gene regulatory networks modeled on high-throughput single-cell transcriptomics data. *Nat Comput Sci Mar 4;online ahead of print* DOI:10.1038/s43588-024-00597-5
8. Struck E, Belova T, Hsieh PH, Odeberg J, **Kuijjer ML**, Dusart P, Butler L (2024) Temporal transcriptome analysis of the endothelial response to tumour necrosis factor. *J Immunol* Jan 1;212(1):117-129  
DOI:10.4049/jimmunol.2300419
9. *Hsieh PH*, Lopes-Ramos CM, Zucknick M, Sandve GK, Glass K, **Kuijjer ML**# (2023) Adjustment of false positive associations in co-expression measurements from RNA-Sequencing data. *Bioinformatics* Oct;btad610 DOI:10.1093/bioinformatics/btad610
10. *Belova T*, Biondi N, *Hsieh PH*, Lutsik P, Chudasama P, **Kuijjer ML**# (2023) The gene regulatory landscape of leiomyosarcoma. *NAR Cancer*. Jul;5(3):zca037 10.1093/narcan/zcad037
11. Ben Guebila M, Wang T, Lopes-Ramos CM, Fanfani V, Weighill D, Burkholz R, Schlauch D, Paulson J, Altenbuchinger M, Sonawane AR, Lim J, *Calderer G*, *van IJzendoorn D*, Morgan D, *Marin A*, Chen CY, Song A, Shutta K, DeMeo D, Padi M, Platig J, **Kuijjer ML**, Glass K, Quackenbush J (2022) The Network Zoo: a

multilingual programming language for the inference and analysis of biological networks. *Genome Biol* 24(1):45. DOI:10.1186/s13059-023-02877-1

12. Birkeälv S, Harland M, Satiko L, Matsuyama AS, Rashid M, Laye JP, Haase K, Mell T, Iyer V, Robles-Espinoza CD, McDermott U, van Loo P, **Kuijjer ML**, Possik PA, Engler SSM, Bishop DT, Newton-Bishop J, Adams DJ (2021) Mutually exclusive genetic interactions and gene essentiality shape the genomic landscape of primary melanoma. *J Pathol* 259(1):56-68. DOI:10.1002/path.6019
13. Stahlberg EA, Abdel-Rahman MH, Aguilar B, Asadpoure A, Beckman RA, Borkon L, Bryan JN, Cebulla CC, Chang YH, Chatterjee A, Deng J, Dolatshahi S, O Gevaert, EJ Greenspan, Hao W, Hernandez-Boussard T, Jackson P, **Kuijjer ML**, Lee AV, Macklin P, Madhavan S, McCoy MD, Mirzaei NM, Razzaghi T, Rocha H, Shahriyari L, Shmulevich I, Stover DG, Sun Y, Syeda-Mahmood T, Wang J, Wang Q, Zervantonakis I (2022) Exploring Approaches for Predictive Cancer Patient Digital Twins: Opportunities for Collaboration and Innovation. *Front Digit Health* 4:1007784. DOI:10.3389/fdgth.2022.1007784
14. Weber C, Rubio T, Wang L, Zhang W, Robert P, Akbar R, Snapkov I, Wu J, **Kuijjer ML**, Tarazona S, Conesa A, Sandve GK, Liu X, Reddy ST, Greiff V (2022) Reference based comparison of immune repertoires. *Cell Rep Meth* 100269. DOI:10.1016/j.crmeth.2022.100269
15. Ben Guebila M, Weighill D, Lopes-Ramos C, Burkholz R, *Pop R*, Palepu K, Shapoval M, Fagny M, Schlauch D, Glass K, Altenbuchinger M, **Kuijjer ML**, Platig J, Quackenbush J. (2022) An online notebook resource for case studies in network medicine. *Nat Meth* 19(5),511-513. DOI:10.1038/s41592-022-01479-2
16. Ben Guebila M, Morgan DC, Glass K, **Kuijjer ML**, DeMeo DL, Quackenbush J (2022). gpuZoo: Cost-effective estimation of gene regulatory networks using the Graphics Processing Unit. *NAR Genom Bioinf* 4(1):lqac002. DOI:10.1093/nargab/lqac002
17. Pavlovic M, Scheffer L, Motwani L, Kanduri C, Kompova R, Vazov N, Waagan K, Bernal FLM, Costa AA, Corrie B, Akbar R, Al Hajj GS, Balaban G, Brusko TM, Chernigovskaya M, Christley S, Cowell LG, Frank R, Grytten I, Gundersen S, Hobaek Haff I, Hovig E, *Hsieh PH*, Klambauer G, **Kuijjer ML**, Lund-Andersen C, Martini A, Minotto T, Pensar J, Rand K, Riccardi E, Robert PA, Rocha A, Slabodkin A, Snapkov I, Sollid LM, Titov D, Weber CR, Widrich M, Yaari G, Greiff V, Sandve GK (2021) immuneML: an ecosystem for machine learning analysis of adaptive immune receptor repertoires. *Nat Mach Intell* 3:936-944. DOI:10.1038/s42256-021-00413-z
18. Ben Guebila M, Lopes-Ramos CM, Weighill D, Sonawane AR, Burkholz R, Shamsaei B, Platig J, Glass K, **Kuijjer ML**, Quackenbush J (2021) GRAND: a database of gene regulatory network models across human conditions. *Nucleic Acids Res* gkab778. DOI:10.1093/nar/gkab778
19. Lopes-Ramos CM, *Belova T*, *Brunner T*, Ben Guebila M, *Osorio D*, Quackenbush J, **Kuijjer ML**# (2021) Regulatory network of PD1 signaling is associated with prognosis in glioblastoma multiforme. *Cancer Res* 81(21):5401-5412. DOI:10.1158/0008-5472.CAN-21-0730
20. *Osorio D*, **Kuijjer ML**, Cai JJ (2021) rPanglaoDB: an R package to download and merge labeled single-cell RNA-seq data from the PanglaoDB database. *Bioinformatics* 38(2):580-582. DOI:10.1093/bioinformatics/btab549
21. Grad I, Hanes R, Ayuda-Duran P, **Kuijjer ML**, Enserink J, Meza-Zepeda L, Myklebost O (2021) Discovery of novel candidates for anti-liposarcoma therapies by medium-scale high-throughput drug screening. *PLoS ONE* 16(3):e0248140. DOI:10.1371/journal.pone.0248140
22. Fagny M, **Kuijjer ML**, Stam M, Joets J, Turc O, Roziere J, Pateyron S, Venon A, Vitte C (2021) Identification of key tissue-specific, biological processes by integrating enhancer information in maize gene regulatory networks. *Front Genet* 11:606285. DOI:10.3389/fgene.2020.606285
23. Quang J, Ding W, **Kuijjer ML**, Quackenbush J, Chen P (2020) Clustering sparse data with feature correlation with application to discover subtypes in cancer. *IEEE Access* 8:67775-67789. DOI:10.1109/access.2020.2982569

24. Fagny M, Patig J, **Kuijjer ML**, Lin X, Quackenbush J (2020) Nongenetic cancer-risk SNPs affect oncogenes, tumor suppressor genes, and immune function. *Br J Cancer* 122(4):569-577. DOI:10.1038/s41416-019-0614-3
25. **Kuijjer ML**#, Hsieh PH, Quackenbush J, Glass K (2019) lionessR: single sample network inference in R. *BMC Cancer* 19(1):100. DOI:10.1186/s12885-019-6235-7
26. Barnett I, Malik N, **Kuijjer ML**, Mucha P, Onnela JP (2019) Endnote: Feature-based classification of networks. *Network Science* 7(3):438-444. DOI:10.1017/nws.2019.21
27. van IJzendoorn DGP, Szuhai K, Briaire-de Bruijn IH, Koster M, **Kuijjer ML**†#, Bovée JVGM†# (2019) Machine learning analysis of gene expression data reveals novel differential diagnostic and prognostic markers for soft tissue sarcomas. *PLoS Comput Biol* 15(2):e1006826. DOI:10.1371/journal.pcbi.1006826
28. Wong K, van der Weyden L, Schott CR, Foote A, Constantino-Casas F, Smith S, Dobson JM, Murchison EP, Wu H, Yeh I, Fullen DR, Joseph N, Bastian BC, Patel RM, Martincorena I, Robles-Espinoza CD, Iyer V, **Kuijjer ML**, Arends MJ, Brenn T, Harms PW, Wood GA, Adams DJ (2019) Cross-species genomic landscape comparison of human mucosal melanoma with canine oral and equine melanoma. *Nat Commun* 10(1):353. DOI: 10.1038/s41467-018-08081-1

**Original scientific publications arising from post doctoral work**—3 first and 2 senior author publications.

29. **Kuijjer ML**#, Fagny M, Marin A, Quackenbush J, Glass K (2020) PUMA: Panda Using MicroRNA Associations. *Bioinformatics* 36(18):4765-4773. DOI:10.1093/bioinformatics/btaa571
30. Lopes-Ramos CM, Chen CY, **Kuijjer ML**, Paulson JN, Sonawane AR, Fagny M, Platig J, Glass K, Quackenbush J, DeMeo DL (2020) Sex differences in gene expression and regulatory networks across 29 human tissues. *Cell Rep Jun* 23;31(12):107795. DOI:10.1016/j.celrep.2020.107795
31. **Kuijjer ML**†, Tung MG†, Yuan G, Quackenbush J, Glass K (2019) Estimating Sample-Specific Regulatory Networks. *iScience* 14:226-240. DOI:10.1016/j.isci.2019.03.021
32. Lopes-Ramos CM, **Kuijjer ML**, Ogino S, Fuchs C, DeMeo DL, Glass K, Quackenbush J (2018) Gene regulatory network analysis identifies sex-linked differences in colon cancer drug metabolism processes. *Cancer Res* 78(19):5538-5547. DOI:10.1158/0008-5472.CAN-18-0454
33. **Kuijjer ML**#, Paulson JN, Salzman P, Ding W, Quackenbush J (2018) Cancer subtype identification using somatic mutation data. *Br J Cancer* 118(11):1492-1501. DOI:10.1038/s41416-018-0109-7
34. Sonawane AR, Paulson JN, Fagny M, Chen CY, Lopes-Ramos CM, Platig J, Quackenbush J, Glass K†#, **Kuijjer ML**†# (2017) Understanding Tissue-Specific Gene Regulation. *Cell Reports* 21(4):1077-1088. DOI:10.1016/j.celrep.2017.10.001
35. Paulson JN, Chen CY, Lopes-Ramos CM, **Kuijjer ML**, Platig J, Sonawane AR, Fagny M, Glass K, Quackenbush J (2017) Tissue-aware RNA-Seq processing and normalization for heterogeneous and sparse data. *BMC Bioinformatics* 18(1):437. DOI:10.1186/s12859-017-1847-x
36. Lopes-Ramos CM†, Paulson JN†, Chen CY, **Kuijjer ML**, Fagny M, Platig J, Sonawane AR, DeMeo DL, Quackenbush J, Glass K (2017) Regulatory network changes between cell lines and their tissues of origin. *BMC Genomics* 18(1):723. DOI:10.1186/s12864-017-4111-x
37. Fagny M, Paulson JN, **Kuijjer ML**, Sonawane AR, Chen CY, Lopes-Ramos CM, Glass K, Quackenbush J, Platig J (2017) Exploring regulation in tissues with eQTL networks. *Proc Natl Acad Sci U S A* 114(37):E7841-E7850. DOI:10.1073/pnas.1707375114
38. Hill KE, Kelly AD, **Kuijjer ML**, Barry W, Rattani A, Garbutt CC, Kissick H, Janeway K, Perez-Atayde A, Goldsmith J, Gebhardt MC, Arredouani MS, Cote G, Hornicek F, Choy E, Duan Z, Quackenbush J, Haibe-Kains B, Spentzos D (2017) An imprinted non-coding genomic cluster at 14q32 defines clinically relevant

molecular subtypes in osteosarcoma across multiple independent datasets. *J Hematol Oncol* 10(1):107. DOI:10.1186/s13045-017-0465-4

39. van IJzendoorn DGP, Quackenbush J, Glass K, **Kuijjer ML** (2016) PyPanda: A Python package for gene regulatory network reconstruction. *Bioinformatics* 32(21):3363-3365. DOI:10.1093/bioinformatics/btw422

**Original scientific publications arising from PhD work**—These include 5 first author publications.

40. Baranski Z, Booij TH, **Kuijjer ML**, de Jong Y, Cleton-Jansen AM, Price LS, van de Water B, Bovée JVGM, Hogendoorn PCW, Danen EH (2015) MEK inhibition induces apoptosis in osteosarcoma cells with constitutive ERK1/2 phosphorylation. *Genes Cancer* 6(11-12):503-512. DOI:10.18632/genesandcancer.91
41. Buddingh EP, Ruslan SEN, Reijnders CMA, Szuhai K, **Kuijjer ML**, Roelofs H, Hogendoorn PCW, Egeler RM, Cleton-Jansen AM, Lankester AC (2015) Mesenchymal stromal cells of osteosarcoma patients do not show evidence of neoplastic changes during long-term culture. *Clin Sarc Res* 5:16. DOI:10.1186/s13569-015-0031-1
42. Pahl JHW, Santos SJ, **Kuijjer ML**, Boerman H, Sand L, Szuhai K, Cleton-Jansen AM, Egeler RM, Bovée JV, Schilham MW, Lancaster AC (2015) Expression of the immune regulation antigen CD70 in osteosarcoma. *Cancer Cell Int* 15:31. DOI:10.1186/s12935-015-0181-5
43. Wouters MC†, Dijkgraaf EM†, **Kuijjer ML**, Jordanova ES, Welters MJP, Nortier JWR, van der Hoeven JJM, Kroep JR, Deamen T, Nijman HW, van der Burg SH (2015) IL-6, IL-6 receptor, pSTAT3 and myeloid cell populations in ovarian cancer. *Oncol Immunology* 3(12):e962397. DOI:10.4161/21624011.2014.962397
44. Pahl JHW, Kwappenberg KMC, Varypataki EM, Santos SJ, **Kuijjer ML**, Mohamed S, Wijnen JT, van Tol MJD, Cleton-Jansen AM, Egeler RM, Jiskoot W, Lankester AC, Schilham MW (2014) Macrophages inhibit human osteosarcoma cell growth after activation with the bacterial cell wall derivative liposomal muramyl tripeptide in combination with interferon-gamma. *JECCR* 33(1):27. DOI:10.1186/1756-9966-33-27
45. **Kuijjer ML**, van den Akker BEWM, Hilhorst R, Mommersteeg M, Buddingh EP, Serra M, Bürger H, Hogendoorn PCW, Cleton-Jansen AM (2014) Kinome and mRNA expression profiling of high-grade osteosarcoma identifies genomic instability, and reveals Akt as potential target for treatment. *BMC Med Genomics* 7:4. DOI:10.1186/1755-8794-7-4
46. Kansara E, Leong HS, Lin DM, Popkiss S, Pang P, Garsed DW, Walkley CR, Cullinane C, Ellul J, Haynes NM, Hicks R, **Kuijjer ML**, Cleton-Jansen AM, Hinds PW, Smyth MJ, Thomas DM (2013) Senescence-related immunologic functions of the RB1 tumor suppressor in radiation-induced osteosarcoma. *J Clin Invest*. 2013 123(12):5351-60. DOI:10.1172/JCI70559
47. de Vos van Steenwijk PJ, Ramwadhoebe TH, Goedemans R, Doorduijn E, van den Ham JJ, Gorter A, van Hall T, **Kuijjer ML**, van Poelgeest MIE, van der Burg SH, Jordanova ES (2013) Tumor infiltrating CD14 positive myeloid cells work side by side with T cells to prolong the survival in patients with cervical carcinoma. *Int J Cancer* 133(12):2884-94. DOI:10.1002/ijc.28309
48. **Kuijjer ML**, Peterse EFP, van den Akker BEWM, Briaire-de Bruijn IH, Serra M, Meza-Zepeda LA, Myklebost O, Hassan AB, Hogendoorn PCW, Cleton-Jansen AM (2013) IR/IGF1R signaling as potential target for treatment of high-grade osteosarcoma. *BMC Cancer* 20(13):245. DOI:10.1186/1471-2407-13-245
49. Mohseny AB, Cai Y, **Kuijjer ML**, Xiao W, van den Akker B, de Andrea CE, Jacobs R, Ten Dijke P, Hogendoorn PC, Cleton-Jansen AM (2012) The activities of Smad and Gli mediated signalling pathways in high-grade conventional osteosarcoma. *Eur J Cancer* 48(18):3429-38. DOI:10.1016/j.ejca.2012.06.018
50. Lenos K, Grawenda AM, Lodder K, **Kuijjer ML**, Teunisse AF, Repapi E, Grochola LF, Bartel F, Hogendoorn PC, Wuerl P, Taubert H, Cleton-Jansen AM, Bond GL, Jochemsen AG (2012) Alternate splicing of the p53 inhibitor HDMX offers a superior prognostic biomarker than p53 mutation in human cancer. *Cancer Res* 72(16):4074-84. DOI:10.1158/0008-5472.CAN-12-0215

51. **Kuijjer ML**, Rydbeck H, Kresse SH, Buddingh EP, Lid AB, Roelofs H, Bürger H, Myklebost O, Hogendoorn PC, Meza-Zepeda LA, Cleton-Jansen AM (2012) Identification of osteosarcoma driver genes by integrative analysis of copy number and gene expression data. *Genes Chr Cancer* 51(7):696-706. DOI:10.1002/gcc.21956
52. Namløs HM, Meza-Zepeda LA, Barøy T, Østensen IHG, Kresse SH, **Kuijjer ML**, Serra M, Bürger H, Cleton-Jansen AM, Myklebost O (2012) Modulation of the Osteosarcoma Expression Phenotype by MicroRNAs. *PlosONE* 7(10):e48086. DOI:10.1371/journal.pone.0048086
53. Pansuriya TC, van Eijk R, d'Adamo P, van Ruler MA, **Kuijjer ML**, Oosting J, Cleton-Jansen AM, van Oosterwijk JG, Verbeke SL, Meijer D, van Wezel T, Nord KH, Sangiorgi L, Toker B, Liegl-Atzwanger B, San-Julian M, Sciot R, Limaye N, Kindblom LG, Daugaard S, Godfraind C, Boon LM, Vikkula M, Kurek KC, Szuhai K, French PJ, Boveé JVGM (2011) Somatic mosaic IDH1 and IDH2 mutations are associated with enchondroma and spindle cell hemangioma in Ollier disease and Maffucci syndrome. *Nat Genet* 43(12):1256-61. DOI:10.1038/ng.1004
54. **Kuijjer ML**, Namløs HM, Hauben EI, Machado I, Kresse SH, Serra M, Llombart-Bosch A, Hogendoorn PC, Meza-Zepeda LA, Myklebost O, Cleton-Jansen AM (2011) mRNA expression profiles of primary high-grade central osteosarcoma are preserved in cell lines and xenografts. *BMC Med Genom* 4:66. DOI:10.1186/1755-8794-4-66
55. Buddingh EP†, **Kuijjer ML**†, Duim RA, Bürger H, Agelopoulos K, Myklebost O, Serra M, Mertens F, Hogendoorn PC, Lankester AC, Cleton-Jansen AM (2011) Tumor-infiltrating macrophages are associated with metastasis suppression in high-grade osteosarcoma: a rationale for treatment with macrophage activating agents. *Clin Cancer Res* 17(8):2110-9. DOI:10.1158/1078-0432.CCR-10-2047

### Original articles in scientific peer-reviewed congress publications

Conference proceedings arising from my independent laboratory—Includes 1 senior author publication.

56. *Hsieh PH*, Hsiao RX, *Belova T*, Ferenc K, Mathelier A, Burkholz R, Chen CY, Sandve GK, **Kuijjer ML**# (2023) Using hierarchical variational autoencoders to incorporate conditional independent priors for paired single-cell multi-omics data integration. *NeurIPS LMRL Workshop*. 2022 Oct 9 (modified: 05 May 2023)
57. Kang T, Zarringhalam K, **Kuijjer ML**, Quackenbush J, Ding W (2018) Clustering on Sparse Data in Non-Overlapping Feature Space with Applications to Cancer Subtyping. *IEEE International Conference on Data Mining (ICDM)*, 1079-1084. DOI:10.1109/ICDM.2018.00138
58. Andreeva O, Li W, Ding W, **Kuijjer ML**, Quackenbush J, Chen P (2020) Catalysis clustering with GAN by incorporating domain knowledge. *KDD2020 Knowledge Discovery and Databases*. KDD '20: Proceedings of the 26th ACM SIGKDD International Conference on Knowledge Discovery & Data Mining Aug 23;1344-1352. DOI:10.1145/3394486.3403187

### Reviews and editorials in international scientific publication series and textbooks

Arising from my independent laboratory—Includes 2 first and 4 senior author publications.

59. *Osorio D*#, **Kuijjer ML**# (2024) Enabling comparative gene regulatory network analysis on single-cell data with SCORPION. *Research Briefing. Nat Comput Sci*. Mar 12;online ahead of print
60. DeMarzio M, Glass K#, **Kuijjer ML**# (2023) Single-sample network modeling on omics data. *BMC Biol* Dec 29;21(1):296. DOI:10.1186/s12915-023-01783-z
61. Fagny M, Glass K, **Kuijjer ML**# (2022) Applications and methods in genomic networks. *Front Genet* Jun 8;13:936015 *Editorial*. DOI:10.3389/fgene.2022.936015

62. van Oost St, Meijer Dt, **Kuijjer ML**, Bovée JVGM, de Miranda N (2021) Linking immunity with genomics in sarcomas: is genomic complexity an immunogenic trigger? *Biomedicines* Aug 19;9(8):1048 *Review*. DOI:10.3390/biomedicines9081048
63. Calderer G, **Kuijjer ML**# (2021) Community detection in large-scale bipartite biological networks. *Front Genet* Apr 21;12:649440 *Mini review*. DOI:10.3389/fgene.2021.649440
64. **Kuijjer ML**# (2020) Predicting cancer evolution using cell state dynamics. *Cancer Res* Aug 1;80(15):3072-3073 *Commentary*. DOI:10.1158/0008-5472.CAN-20-1878
65. **Kuijjer ML**, Paulson JN, Quackenbush J (2020) Expression analysis. In: *Bioinformatics: A practical guide to the analysis of genes and proteins*, 4th edition. Editors: Baxevanis AD, Bader G, Wishart DS. 2020 Feb 12. *Book chapter*. Publisher: Wiley. ISBN: 978-1-119-33595-5

**Arising from PhD work—1 first author publication**

66. **Kuijjer ML**, Hogendoorn PC, Cleton-Jansen AM (2013) Genome-wide analyses on high-grade osteosarcoma: making sense of a genomically most unstable tumor. *Int J Cancer* 133(11):2512-21 *Review*. DOI:10.1002/ijc.28124