

CURRICULUM VITAE

MARIEKE L. KUIJER, PhD



Date of birth February 5, 1982
Place of birth Zaanstad, the Netherlands
Nationality Dutch

PROFESSIONAL EXPERIENCE

PERIOD October 1, 2018–present
EMPLOYER Centre for Molecular Medicine Norway Oslo, Norway
UNIVERSITY University of Oslo
FACULTY Medicine
JOB TITLE Group leader

PERIOD November 1, 2020–October 31, 2023
EMPLOYER Leiden University Medical Center Leiden, the Netherlands
UNIVERSITY Leiden University
DEPARTMENT Pathology, Leiden Center for Computational Oncology
JOB TITLE Assistant Professor, 20% position

PERIOD May 6, 2013 – August 31, 2018
EMPLOYER Dana-Farber Cancer Institute Boston, MA, USA
UNIVERSITY Harvard T.H. Chan School of Public Health
DEPARTMENT Biostatistics and Computational Biology
JOB TITLE Research Fellow

PERIOD December 1, 2008 – November 30, 2012
EMPLOYER Leiden University Medical Center Leiden, The Netherlands
UNIVERSITY Leiden University
DEPARTMENT Pathology
JOB TITLE PhD student

EDUCATION

PERIOD December 1, 2008 – June 26, 2013
DEGREE Doctor of Philosophy in Cancer Genomics
UNIVERSITY Leiden University Leiden, The Netherlands

PERIOD September 2006 – December 2008
DEGREE Master of Science in Biomedical Sciences
UNIVERSITY Leiden University Leiden, the Netherlands

PERIOD January – June 2005, September – December 2006,
October 2007 – January 2008
STUDIES Biomedical Sciences
UNIVERSITY Karolinska Institutet Stockholm, Sweden
Full undergraduate semester and Master's degree specialization courses.

PERIOD	September 2003 – July 2007	
DEGREE	Bachelor of Science in Biomedical Sciences	
RANK	Propaedeutics with distinction	
UNIVERSITY	Leiden University	Leiden, the Netherlands

DOCUMENTED LEAVE

5.5 months

FUNDING (SELECTION)

The total amount of **external funding** allocated to my group is approximately **2,408 M EUR**. Internal funding: 3,165 M EUR.

- Norwegian Cancer Society, Krafttak mot Kreft (PI). 2024 – 2027 (7988k NOK)
- UNIFOR-FRIMED grant (PI). 2022 (125k NOK)
- Young Research Talents award (PI), Research Council of Norway. April 2021 – March 2026 (7984k NOK)
- Norwegian Cancer Society, Pink Ribbon (PI). April 2021 – March 2025 (3630k NOK)
- Department of Energy (DoE)/National Cancer Institute (NCI) Joint Design of Advanced Computing Solutions for Cancer (JDACS4C) program (Co-PI). January 2021 – December 2021 (\$100,000)
- NCMM start-up package (PI). October 2018 – September 2023 (18M NOK)
- Charles A. King Postdoctoral Fellowship, Sara Elizabeth O'Brien and Bank of America, co-Trustees. September 2016 – August 2018 (\$94,350)

PRIZES, HONORS, AND AWARDS

- Invited Participant, Department of Energy (DoE)/National Cancer Institute (NCI) Knowledge Labs. June 2020
- National Cancer Institute Brain Cancer Specialized Program of Research Excellence Career Enhancement Program Award. August 2016 – July 2017 (\$50,000)
- Harvard T.H. Chan School of Public Health Program in Quantitative Genomics travel award. January 2015
- Dutch Cancer Society (KWF) sponsorship. June 2013 (€1,500)
- Leiden University Fund travel grant. November 2012
- Best presentation award. Dutch Cancer Society (KWF) Tumor cell biology meeting, Lunteren, the Netherlands. November 2012
- Two Outbound Study Grants. September 2006 – December 2007
- Erasmus scholarship. January – June 2005

PROFESSIONAL SOCIETIES

- International Society for Computational Biology (ISCB), May 2019–present
- American Association for Cancer Research (AACR), December 2014–present

PARTICIPATION IN CONSORTIA

- Executive Committee Member, biologist representative of the Fight Osteosarcoma Through European Research (FOSTER) consortium. Member of WP1 (basic research) and WP8 (research dissemination). 2022–present
- Consortium Participant, EuroBoNeT, a European network to promote research into uncommon cancers in adults and children, with focus on pathology, biology, and genetics of bone tumors, 2008–2011

GRANT REVIEW

- Member of the Committee for Data Science, Novo Nordisk Foundation, 2022–present
- *Ad hoc* grant review for United States-Israel Binational Science Foundation (BSF), Israel Science Foundation (ISF), Medical Research Council, UK, and Luxembourg National Research Fund, 2022–present
- Proposal evaluation expert and rapporteur, HORIZON-MSCA-2021-PF-01, 2021–2022
- Grant review panel member, Fonds de recherche du Québec, 2020

EDITORIAL AND REVIEW WORK

- Reviewer for the Intelligent Systems for Molecular Biology (ISMB) 2022 Proceedings, 2022
- Associate Editor, *Bioinformatics Advances*, 2021–present
- Guest Editor, *Frontiers in Genetics and Cancers*, 2020–2022
- Editorial Board member, *Cancer Research*, 2016–present
- Reviewed 62 manuscripts for 21 scientific journals, including *Nature Reviews Genetics*, *Nature Methods*, *Cancer Research*, *Nucleic Acids Research*, *Bioinformatics*, *PLoS Computational Biology*, and *Genome Medicine*. Publons account: <https://tinyurl.com/publons-mkuijjer>
- Tool evaluation board member for the conference “Computational Methods in Systems Biology.” CMSB 2017, Darmstadt, Germany.

TEACHING AND MENTORING ACTIVITIES

Mentoring

- Head of the Computational Biology and Systems Medicine group. Current core members include 1 Researcher, 2 Postdoctoral fellows (incl. 1 Marie Curie Scientia II fellow), 2 PhD students, 2 co-supervised PhD students, and 1 Master’s thesis student. 2018–present

- Mentored in total in current and previous positions: 6 postdoctoral fellows (of which 1 co-supervised), 8 PhD (2 co-supervised, 3 visiting), 13 Master's (6 theses), 10 Bachelor's (2 theses), and 4 high school students

Teaching

- Lecturer at the Medicine, Informatics, and Biology (MeInBio) program, University of Freiburg, Germany. November 2024 (*upcoming*)
- Co-organizer of and lecturer at the Nordic EMBL PhD course. Title: “Multi-omics data analyses and integration for precision medicine.” December 2022–present
- Lecturer at the Program Frontiers in Genomics, National Autonomous University of Mexico (UNAM), Mexico. November 2021
- Lecturer at NCMM PhD course “Molecular Medicine.” 2019–present. Grading of exams, 2020–2021. Coordinating grading of exams, 2021–present
- Teaching assistant at Harvard Catalyst course Applications in Network Medicine. November 2015
- Lecturer at Studium Generale, a science symposium for the general public, 2012
- Lecturer, working group, and journal club leader at the Pathology course of the undergraduate program of Biomedical Sciences, Leiden University, 2009–2010

INSTITUTIONAL RESPONSIBILITIES

Faculty hiring

- Hiring committee member for the position of two Group Leaders, the Laboratory for Molecular Infection Medicine Sweden (MIMS), Sweden (2023–2024)
- Evaluator for the renewal of a Group Leader position, the Hungarian Centre of Excellence for Molecular Medicine (HCEMM), Hungary (2023)

MSc/PhD defenses and committees

- Opponent in 2 international PhD defenses (University of Helsinki, Finland; Leiden University, the Netherlands)
- Opponent in 4 national PhD thesis defenses (1 second, 3 third opponent), Faculty of Medicine, University of Oslo
- PhD thesis Reviewer of 2 international PhD theses, University of Helsinki, Finland. 2023–2024
- Third semester evaluation committee member for 7 PhD students, Faculty of Mathematics and Natural Sciences and Faculty of Medicine, University of Oslo
- Committee member for 1 PhD student, University of Helsinki, Finland. 2022–present
- Proposal evaluation committee, Austrian Academy of Sciences, Austria. 2021–2022
- Opponent/committee member in 2 Master's thesis defenses, University of Bergen, Norway and Harvard Chan School of Public Health

Local services

- Member of the NCMM hiring board, 2022–present
- Advisory Board Member, Nordic Computational Biology (NCB) network, International Society for Computational Biology (ISCB) affiliate, 2022–present
- Faculty Advisor of the ISCB Regional Student Group (RSG) Norway, 2020–present
- Member of the NCMM IT steering committee, 2019–present
- Hiring panel member for various PhD, postdoctoral, researcher, scientific computing, and IT positions at NCMM, University of Oslo, University of Bergen, Leiden University, 2018–present

ORGANIZATION OF SCIENTIFIC MEETINGS AND SEMINARS

- Co-organizer of the Institute for Computational and Experimental Research in Mathematics (ICERM) workshop on Mathematical and Computational Biology. June 2023, Providence, RI, USA
- Executive Committee Member, biologist representative of the Fight Osteosarcoma Through European Research (FOSTER) consortium. 2022–present
- Co-organizer of the Tools of the Trade Data Science Webinar series, Nordic EMBL Partnership, 2022–present
- Scientific Committee Member, Nordic EMBL Partnership Meeting. February, 2022, Aarhus, Denmark
- Scientific Committee Member, Nordic EMBL Partnership Meeting. September 22–25, 2020, Umeå, Sweden
- Organizer of the NCMM retreat. June 12–13, 2019, Oslo, Norway
- Co-organizer of the 2014–2015 Big Data Seminar series of the Department of Biostatistics, Harvard T.H. Chan School of Public Health

CERTIFICATIONS

- Radiation Hygiene level 5B, Dutch Society for Radiation Hygiene, September 2003

LANGUAGES

Dutch	Native proficiency	English	Full professional proficiency
Norwegian	Upper intermediate proficiency	Italian	Full professional proficiency

PUBLICATIONS

Peer reviewed journal articles—original research

- 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 ML**, 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. Biological sample collection to advance bone sarcoma research and treatment: a position paper by two European consortia. 2024 *Accepted in Clin Cancer Res*
- **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***. Population-level comparisons of gene regulatory networks modeled on high-throughput single-cell transcriptomics data. *Nat Comput Sci*. 2024 Mar 4; online ahead of print
 - Struck E, **Belova T**, **Hsieh PH**, Odeberg J, **Kuijjer ML**, Dusart P, Butler L. Temporal transcriptome analysis of the endothelial response to tumour necrosis factor. *J Immunol*. 2024 Jan 1;212(1):117-129
 - **Hsieh PH**, Lopes-Ramos CM, Zucknick M, Sandve GK, Glass K, **Kuijjer ML***. Adjustment of false positive associations in co-expression measurements from RNA-Sequencing data. *Bioinformatics*. 2023 Oct;btad610
 - **Belova T**, Biondi N, **Hsieh PH**, Lutsik P, Chudasama P, **Kuijjer ML***. The gene regulatory landscape of leiomyosarcoma. *NAR Cancer*. 2023 Jul;5(3):zca037
 - 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. The Network Zoo: a multilingual programming language for the inference and analysis of biological networks. *Genome Biol*. 2023 Mar;24(1):45
 - Birkeälv S, Harland M, Matsuyama LSAS, Rashid M, Mehta I, Laye JP, Haase K, Mell T, Iyer V, Robles-Espinoza CD, McDermott U, Van Loo P, **Kuijjer ML**, Possik PA, Maria Engler SS, Bishop DT, Newton-Bishop J, Adams DJ. Mutually exclusive genetic interactions and gene essentiality shape the genomic landscape of primary melanoma. *J Pathol*. 2023 Jan 259(1):56-68
 - 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. Exploring Approaches for Predictive Cancer Patient Digital Twins: Opportunities for Collaboration and Innovation. *Front Digit Health*. 2022 Oct 6;4:1007784
 - Weber CR, Rubio T, Wang L, Zhang W, Robert PA, Akbar R, Snapkov I, Wu J, **Kuijjer ML**, Tarazona S, Conesa A, Sandve GK, Liu X, Reddy ST, Greiff V. Reference-based comparison of adaptive immune receptor repertoires. *Cell Reports Meth*. 2022 Aug 22;2(8)100269
 - Ben Guebila M, Weighill D, Lopes-Ramos CM, Burkholz R, **Pop R**, Palepu K, Shapoval M, Fagny M, Schlauch D, Glass K, Altenbuchinger M, **Kuijjer ML**, Platig J, Quackenbush J. An online notebook resource for reproducible inference, analysis, and publication of gene regulatory networks. *Nat Meth*. 2022 May;19(5):511-513
 - Ben Guebila M, Morgan DC, Glass K, **Kuijjer ML**, DeMeo DL, Quackenbush J. gpuZoo: Cost-effective estimation of gene regulatory networks using the Graphics Processing Unit. *NAR Genom Bioinf*. 2022 Feb 8;4(1):lqac002
 - 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, Hochreiter S, 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. immuneML: an ecosystem for machine learning analysis of adaptive immune receptor repertoires. *Nat Mach Intell*. 2021 Nov 16;3:936-944
 - Ben Guebila M, Lopes-Ramos CM, Weighill D, Sonawane AR, Burkholz R, Shamsaei B, Platig J, Glass K, **Kuijjer ML**, Quackenbush J. GRAND: A database of gene regulatory network models across human conditions. *Nucleic Acids Res*. 2021 Sep 11;gkab778
 - Lopes-Ramos CM, **Belova T**, **Brunner T**, Ben Guebila M, **Osorio D**, Quackenbush J, **Kuijjer ML***. Regulatory network of PD1 signaling is associated with prognosis in glioblastoma multiforme. *Cancer Res*. 2021 Nov 1;81(21):5401-5412
 - **Osorio D***, **Kuijjer ML**, Cai JJ. rPanglaoDB: an R package to download and merge labeled single-cell RNA-seq data from the PanglaoDB database. *Bioinformatics*. 2021 Jul 28;btab549
 - Grad I, Hanes R, Ayuda-Durán P, **Kuijjer ML**, Enserink JM, Meza-Zepeda LA, Myklebost O. Discovery of novel candidates for anti-liposarcoma therapies by medium-scale high-throughput drug screening. *PLoS ONE*. 2021 Mar 10;16(3):e0248140

- Fagny M, Kuijjer ML, Stam M, Joets J, Turc O, Roziere J, Pateyron S, Venon A, Vitte C. Identification of key tissue-specific, biological processes by integrating enhancer information in maize gene regulatory networks. *Front Genet.* 2021 Jan 11;11:606285
- Quang J, Ding W, Kuijjer ML, Quackenbush J, Chen, P. Clustering sparse data with feature correlation with application to discover subtypes in cancer. *IEEE Access (in press)*. 2020 Dec;8(1)67775-67789
- **Kuijjer ML***, Fagny M, Marin A, Glass K, Quackenbush J. PUMA: Panda Using MicroRNA Associations. *Bioinformatics.* 2020 Sep 15;36(18):4765-4773
- Lopes-Ramos CM, Chen CY, Kuijjer ML, Paulson JN, Sonawane AR, Fagny M, Platig J, Quackenbush J, Glass K, DeMeo DL. Sexual dimorphism in gene expression landscapes across 29 human tissues. *Cell Reports.* 2020 Jun;31(12):107795
- Fagny M, Platig J, Kuijjer ML, Lin X, Quackenbush J. Nongenic cancer-risk SNPs affect oncogenes, tumor suppressor genes, and immune function. *Br J Cancer.* 2020 Feb;122(4):569-577
- **Kuijjer ML***, Hsieh PH, Quackenbush J, Glass K. lionessR: single-sample network reconstruction in R. *BMC Cancer.* 2019 Oct 25;19(1):1003
- Barnett I, Malik N, Kuijjer ML, Mucha P, Onnela JP. Endnote: feature-based classification of networks. *Network Science.* 2019 Sep 23;7(3):438-444
- **Kuijjer ML†**, Tung M†, Quackenbush J, Yuan GC, Glass K. Estimating sample-specific regulatory networks. *iScience.* 2019 Apr 15;79(8):2084
- van IJzendoorn DGP, Szuhai K, Briaire-de Bruijn IH, Kostine M, **Kuijjer ML†***, Bovée JVMG†*. Machine learning analysis of gene expression data reveals novel diagnostic and prognostic biomarkers and identifies therapeutic targets for soft tissue sarcomas. *PLoS Comput Biol.* 2019 Feb 20;15(2):e1006826
- 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. Cross-species genomic landscape comparison of human mucosal melanoma with canine oral and equine melanoma. *Nature Communications.* 2019 Jan 21;10(1):353
- Lopes-Ramos CM, Kuijjer ML, Ogino S, Fuchs C, DeMeo DL, Glass K, Quackenbush J. Gene regulatory network analysis identifies sex-linked differences in colon cancer drug metabolism processes. *Cancer Research.* 2018 Oct 1;78(19):5538-5547
- **Kuijjer ML***, Paulson JN, Salzman P, Ding W, Quackenbush J. Cancer subtype identification using somatic mutation data. *Br J Cancer.* 2018 May;118(11):1492-1501
- Sonawane AR, Platig J, Fagny M, Chen CY, Paulson JN, Lopes-Ramos CM, Quackenbush J, Glass K†*, **Kuijjer ML†***. Understanding Tissue-Specific Gene Regulation. *Cell Reports.* 2017 Oct 24;21(4):1077-1088
- Paulson JN, Chen CY, Lopes-Ramos CM, Kuijjer ML, Platig J, Sonawane AR, Fagny M, Glass K, Quackenbush J. Tissue-aware RNA-Seq processing and normalization for heterogeneous and sparse data. *BMC Bioinformatics.* 2017 Oct 3;18(1):437
- Lopes-Ramos CM†, Paulson JN†, Chen CY, Kuijjer ML, Fagny M, Platig J, Sonawane AR, DeMeo DL, Quackenbush J, Glass K. Regulatory network changes between cell lines and their tissues of origin. *BMC Genomics.* 2017 Sep 12;18(1):723
- Fagny M, Paulson JN, Kuijjer ML, Sonawane AR, Chen CY, Lopes-Ramos CM, Glass K, Quackenbush J, Platig J. Exploring regulation in tissues with eQTL networks. *Proc Natl Acad Sci U S A.* 2017 Sep 12;114(37):E7841-E7850
- Hill K, Kelly A, Kuijjer ML, Barry W, Rattani A, Kissick H, Janeway K, Perez-Atayde A, Goldsmith J, Gebhardt MC, Arredouani M, Cote G, Hornicek F, Choy E, Duan Z, Quackenbush J, Haibe-Kains B, Spentzos D. An imprinted non-coding genomic region at 14q32 defines clinically relevant molecular subtypes in osteosarcoma across multiple independent datasets. *J Hematol Oncol.* 2017 May 15;10(1):107
- van IJzendoorn DGP, Quackenbush J, Glass K, **Kuijjer ML***. PyPanda: A Python package for gene regulatory network reconstruction. *Bioinformatics.* 2016 Nov 1;32(21):3363-3365
- Baranski Z, Booij TH, Kuijjer ML, de Jong Y, Cleton-Jansen AM, Price LS, van de Water B, Bovée JVMG, Hogendoorn PCW, Danen EH. MEK inhibition induces apoptosis in osteosarcoma cells with constitutive ERK1/2 phosphorylation. *Genes Cancer.* 2015;6(11-12):503-512

- Buddingh EP, Ruslan SEN, Reijnders CMA, Szuhai K, Kuijjer ML, Roelofs H, Hogendoorn PCW, Egeler RM, Cleton-Jansen AM, Lankester AC. Mesenchymal stromal cells of osteosarcoma patients do not show evidence of neoplastic changes during long-term culture. *Clin Sarcoma Res.* 2015 Jun 23;5:16
- 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. IL-6, IL-6 receptor, pSTAT3 and myeloid cell populations in ovarian cancer. *OncoImmunology.* 2015 Jan 7;3(12):e962397
- Pahl JHW, Santos SJ, Kuijjer ML, Boerman H, Sand L, Szuhai K, Cleton-Jansen AM, Egeler RM, Bovée JV, Schilham MW, Lankester AC. Expression of the immune regulation antigen CD70 in osteosarcoma. *Cancer Cell Int.* 2015 Mar 18;15:31
- 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. Macrophages inhibit human osteosarcoma cell growth after activation with the bacterial cell wall derivative liposomal muramyl tripeptide in combination with interferon-gamma. *JECCR.* 2014 Mar 10;33(1):27
- Kuijjer ML, van den Akker BEWM, Hilhorst R, Mommersteeg M, Buddingh EP, Serra M, Bürger H, Hogendoorn PCW, Cleton-Jansen AM. Kinome and mRNA expression profiling of high-grade osteosarcoma identifies genomic instability, and reveals Akt as potential target for treatment. *BMC Med Genomics.* 2014 Jan 21;7:4 *Highly accessed*
- Kansara E, Leong HS, Lin DM, Popkiss S, Pang P, Garsed DW, Walkley CR, Cullinane C, Elul J, Haynes NM, Hicks R, Kuijjer ML, Cleton-Jansen AM, Hinds PW, Smyth MJ, Thomas DM. Senescence-related immunologic functions of the RB1 tumor suppressor in radiation-induced osteosarcoma. *J Clin Invest.* 2013 Dec 2;123(12):5351-60
- 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. 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.* 2013;133(12):2884-94
- 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. IR/IGF1R signaling as potential target for treatment of high-grade osteosarcoma. *BMC Cancer.* 2013;20(13):245
- Namløs HM, Meza-Zepeda LA, Barøy T, Østensen IHG, Kresse SH, Kuijjer ML, Serra M, Bürger H, Cleton-Jansen AM, Myklebost O. Modulation of the Osteosarcoma Expression Phenotype by MicroRNAs. *PlosONE.* 2012;7(10):e48086
- 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. The activities of Smad and Gli mediated signalling pathways in high-grade conventional osteosarcoma. *Eur J Cancer.* 2012 Dec;48(18):3429-38
- 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. Alternate splicing of the p53 inhibitor HDMX offers a superior prognostic biomarker than p53 mutation in human cancer. *Cancer Res.* 2012 Aug 15;72(16):4074-84
- Kuijjer ML, Rydbeck H, Kresse SH, Buddingh EP, Lid AB, Roelofs H, Bürger H, Myklebost O, Hogendoorn PC, Meza-Zepeda LA, Cleton-Jansen AM. Identification of osteosarcoma driver genes by integrative analysis of copy number and gene expression data. *Genes Chromosomes Cancer.* 2012 Jul;51(7):696-706
- 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, Tokar 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, Bovée JV. Somatic mosaic IDH1 and IDH2 mutations are associated with enchondroma and spindle cell hemangioma in Ollier disease and Maffucci syndrome. *Nat Genet.* 2011 Nov 6;43(12):1256-61
- 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. mRNA expression profiles of primary high-grade central osteosarcoma are preserved in cell lines and xenografts. *BMC Med Genomics.* 2011 Sep 20;4:66
- Kuijjer ML†, Buddingh EP†, Duim RA, Bürger H, Agelopoulos K, Myklebost O, Serra M, Mertens F, Hogendoorn PC, Lankester AC, Cleton-Jansen AM. Tumor-infiltrating macrophages are associated with metastasis suppression in high-grade osteosarcoma: a rationale for treatment with macrophage activating agents. *Clin Cancer Res.* 2011 Apr 15;17(8):2110-9

Peer-reviewed conference papers

- **Hsieh PH**, Hsiao RX, **Belova T**, Ferenc K, Mathelier A, Burkholz R, Chen CY, Sandve GK, **Kuijjer ML***. 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)
- Kang T, Zarringhalam K, **Kuijjer ML**, Quackenbush J, Ding W. Clustering on sparse data in non-overlapping feature space with applications to cancer subtyping. *IEEE International Conference on Data Mining (ICDM'18)*. 2018 Dec 1;18367133
- Andreeva O, Li W, Ding W, **Kuijjer ML**, Quackenbush J, Chen P. Catalysis Clustering With GAN By Incorporating Domain Knowledge. *KDD '20: Proceedings of the 26th ACM SIGKDD International Conference on Knowledge Discovery & Data Mining*. 2020 Aug;1344-1352

Pre-prints

- **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†. The variable genomic landscape during osteosarcoma progression: insights from a longitudinal WGS analysis. *MedRxiv* 2024 Apr 819; DOI: 10.1101/2024.04.18.24306025
- **Osorio D†**, Shahrrouzi P†, Tekpli X, Kristensen V, **Kuijjer ML***. Drug combination prediction for cancer treatment using disease-specific drug response profiles and single-cell transcriptional signatures. *BioRxiv* 2024 Feb 8; DOI: 10.1101/2022.03.31.486602
- 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. Exposure to enriched environment attenuates mouse experimental colitis by regulating a Myc-driven gene regulatory network and by improving colon epithelial barrier integrity. *BioRxiv*. 2023 Feb 16; DOI: 10.1101/2023.02.16.528051
- **Kuijjer ML***, Glass K. Reconstructing sample-specific networks using LIONESS. *BioRxiv*. 2021 Sep 27; DOI: 10.1101/2021.09.27.461954

Reviews, editorials, commentaries, and book chapters

- **Osorio D***, **Kuijjer ML***. Enabling comparative gene regulatory network analysis on single-cell data with SCORPION. *Research Briefing. Nat Comput Sci*. 2024 Mar 12; online ahead of print
- De Marzio M, Glass K*, **Kuijjer ML***. Single-sample network modeling on omics data. *Short Commentary. BMC Biol*. 2023 Dec 29;21(1):296
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- **Calderer G**, **Kuijjer ML***. Community detection in large-scale bipartite biological networks. *Mini review. Front Genet*. 2021 Apr 21;12:649440
- **Kuijjer ML***. Predicting cancer evolution using cell state dynamics. *Commentary. Cancer Research*. 2020 Aug 1;80(15):3072-3073
- **Kuijjer ML**, Paulson JN, Quackenbush J. Expression analysis. Book chapter in *Bioinformatics: A practical guide to the analysis of genes and proteins, 4th edition*. Editors: Braxevanis AD, Bader G, Wishart D. Feb 2020, ISBN: 978-1-119-33558-0
- **Kuijjer ML**, Hogendoorn PCW, Cleton-Jansen AM. Genome-wide analyses on high-grade osteosarcoma; making sense of a most genomically instable tumor *Review. Int J Cancer*. 2013;133(11):2512-21

CONFERENCE TALKS AND INTERNATIONAL SEMINARS

Keynotes – invited

- Computational Intelligence methods for Bioinformatics and Biostatistics (CIBB). September 4–6, 2024, Benevento, Italy (*upcoming*)
- TransSYS closing conference. June 19–20, 2024, Oxford, Belgrade, Serbia (*upcoming*)

Conference talks – invited

- Genetics Society Spring Meeting, St. Catherine’s College, University of Oxford. April 12–14, 2023, Oxford, United Kingdom
- EMBL Partnership conference. September 21–23, 2022, Heidelberg, Germany
- Panel discussion, Fourth ISC Workshop on HPC Applications in Precision Medicine. July 2, 2021 (*virtual*)
- Nordic EMBL Partnership Meeting. September 22–25, 2020 (*virtual*, originally Umeå, Sweden)
- Network Medicine satellite, NetSci. September 17, 2020 (*virtual*, originally Rome, Italy)
- National Consortium for Sequencing and Personalized Medicine (NorSeq) conference. October 3, 2019, Oslo, Norway
- LabRoots Genetics and Genomics virtual conference. May 11–12, 2016 (*virtual*). Presentation can be watched at: <https://tinyurl.com/bigdataintegration>
- 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: <https://tinyurl.com/birsbanff-lioness>

Conference talks – international (selection)

- Intelligent Systems for Molecular Biology (ISMB). July 13–16, 2020 (*virtual*, originally Montreal, Canada)
- Medical and Health Informatics (MedInfo) 2019. August 26–30, 2019, Lyon, France
- Intelligent Systems for Molecular Biology (ISMB)/European Conference on Computational Biology (ECCB). July 21–25, 2019, Basel, Switzerland. Presentation can be watched at: <https://tinyurl.com/ismb-eccb-glioblastoma>
- Statistical Modeling of Epigenomics and Gene Regulation conference. August 27–28, 2015, Cambridge (MA), USA
- United States and Canadian Academy of Pathology (USCAP) annual meeting. February 26 – March 4, 2011, San Antonio (TX), USA

Seminars – invited, international

- Medicine, Informatics and Biology (MeInBio) doctoral program, University of Freiburg, Germany. 2024 (*upcoming*)
- Institute of Biotechnology, National Autonomous University of Mexico (UNAM), Mexico. January 16, 2023
- Institute for Molecular Medicine Finland (FIMM), University of Helsinki, Finland. June 29, 2022
- Program Frontiers in Genomics, National Autonomous University of Mexico (UNAM), Mexico (*virtual*). November 23, 2021. Presentation can be watched at: <https://tinyurl.com/netmed-unam>
- Research Program in Systems Oncology, University of Helsinki, Finland. August 13, 2021
- Leiden Center for Computational Oncology seminar, Leiden University Medical Center. February 1, 2021, Leiden, the Netherlands (*virtual*)
- Molecular Tumor Genetics seminar, Leiden University Medical Center. January 16, 2020, Leiden, the Netherlands