Kai Kammers

Curriculum Vitae

September 26, 2022

Current Position

Assistant Professor of Oncology
Quantitative Sciences Division
Department of Oncology
The Sidney Kimmel Comprehensive Cancer Center
The Johns Hopkins University School of Medicine

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Education and Training

Postdoctoral Training

2013 – 2016 Department of Biostatistics
Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, USA.
Advisors: Jeffrey T. Leek and Ingo Ruczinski

Degrees

2007 – 2012 **Dr. rer. nat. (Ph.D. equivalent), Statistics**
Dortmund University of Technology, Dortmund, Germany.
Dissertation title: *Survival models with gene groups as covariates.*
Dissertation referees: Jörg Rahnenführer and Katja Ickstadt.

2001 – 2007 **Diplom (M.Sc. equivalent) [with honors], Mathematics**
Heinrich-Heine-University, Düsseldorf, Germany.
Thesis title: *Central limit theorems for Kaplan-Meier integrals in censored models.*
Thesis referees: Arnold Janssen and Klaus Janßen.

Research Experience

2016 – present **Assistant Professor**
Quantitative Sciences Division, Department of Oncology, The Sidney Kimmel Comprehensive Cancer Center, The Johns Hopkins University School of Medicine, Baltimore, MD, USA.

2013 – 2016 **Postdoctoral Fellow**
Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, USA.

2007 – 2013 **Research Assistant**
Department of Statistics, Dortmund University of Technology, Dortmund, Germany.

2003 – 2007 **Student Research Assistant**
Mathematical Institute, Heinrich-Heine-University, Düsseldorf, Germany.

Publications

Peer-Reviewed Articles

45. Chen A, **Kammers K**, Larman HB, Scharpf RB, Ruczinski I. Detecting antibody reactivities in Phage ImmunoPrecipitation Sequencing data. *BMC Genomics.* 2022 Sep 15;23(1):654. doi: 10.1186/s12864-022-08869-y. [PMID: 36109689]

44. Chen A, **Kammers K**, Larman HB, Scharpf RB, Ruczinski I. Detecting and quantifying antibody reactivity in PhIP-Seq data with BEER. *Bioinformatics.* 2022 Aug 12;btac555. doi: 10.1093/bioinformatics/btac555. [PMID: 35959988]

43. Guo Y, Messner F, Beck SE, Iglesias Lozona M, Schwelberger H, Zhang Y, **Kammers K**, Oh BC, Greene ED, Brandacher G, Brockbank KGM. Gluconate-Lactobionate-Dextran Perfusion Solutions Attenuate Ischemic Injury and Improve Function in a Murine Cardiac Transplant Model. *Cells.* 2022 May 16;11(10):1653. doi: 10.3390/cells11101653. [PMID: 35626690]

42. Ngwa JS, Yanek LR, **Kammers K**, Kanchan K, Taub MA, Scharpf RB, Faraday N, Becker LC, Mathias RA, Ruczinski I. Inverting the model of genomics data sharing with the NHGRI Genomic Data Science Analysis, Visualization, and Informatics Lab-space. *Genet Epidemiol.* 2022 Mar 21;2(1):100085. doi: 10.1002/gepi.22448. Epub ahead of print. [PMID: 35312098]

41. Schatz MC, Philippakis AA, Afgan E, Banks E, Carey VJ, Carroll RJ, Culotti A, Ellrott K, Goecks J, Grossman RL, Hall IM, Hansen KD, Lawson J, Leek JT, O'Donnell Luria A, Mosher S, Morgan M, Nekrutenko A, O'Connor BD, Osborn K, Paten B, Patterson C, Tan FJ, Taylor CO, Vessio J, Waldron L, Wang T, Wuichet K, AnVIL Team (with **Kammers K** as a member of AnVIL Team). Inverting the model of genomics data sharing with the NHGRI Genomic Data Science Analysis, Visualization, and Informatics Lab-space. *Cell Genom.* 2022 Jan 12;2(1):100085. doi: 10.1016/j.xgen.2021.100085. Epub 2022 Jan 13. [PMID: 35199087]

40. Monaco DR, Kottapalli SV, Breitwieser FP, Anderson DE, Wijaya L, Tan K, Chia WN, **Kammers K**, Caturegli P, Waugh K, Roederer M, Petri M, Goldman DW, Rewers M, Wang LF, Larman HB. Deconvoluting virome-wide antibody epitope reactivity profiles. *EBioMedicine.* 2022 Jan 01;75:103747. doi: 10.1016/j.ebiom.2021.103747. Epub 2021 Dec 16. [PMID: 34922324]

39. Haussmann J, Matuschek C, Boelke E, Tamaskovics B, Corradini S, Wessalowski R, Maas K, Schmidt L, Orth K, Peiper M, Keitel V, Feldt T, Jensen BO, Luedde T, Fischer J, Knoefel WT, Ashmawy H, Pedotoa A, **Kammers K**, Budach W. Comparison of Different Systemic Therapeutic Regimes in Resectable Soft-Tissue Sarcoma-Results of a Network Meta-Analysis. *Cancers (Basel).* 2021 Nov 11;713(22):5631. doi: 10.3390/cancers13225631. [PMID: 34830786]

38. McGuire MR, Mukhopadhyay D, Myers SL, Mosher EP, Brookheart RT, **Kammers K**, Sehgal A, Selen ES, Wolfgang MJ, Bumpus NN, Espenshade PJ. Progesterone receptor membrane component 1 (PGRMC1) binds and stabilizes cytochromes P450 through a heme-independent mechanism. *J Biol Chem.* 2021 Nov;297(5):101316. doi: 10.1016/j.jbc.2021.101316. Epub 2021 Oct 20. [PMID: 34678314]

37. **Kammers K**, Chen A, Monaco DR, Hudelson SE, Grant-McAuley W, Moore RD, Alter G, Deeks SG, Morrison CS, Eller LA, Blankson JN, Laeyendecker O, Ruczinski I, Eshleman SH, Larman HB. HIV Antibody Profiles in HIV Controllers and Persons With Treatment-Induced Viral Suppression. *Frontiers in Immunology.* 2021 Aug 26;12:740395. doi: 10.3389/fimmu.2021.740395. [PMID: 34512672]

36. Haussmann J, Budach W, Strnad V, Corradini S, Krug D, Schmidt L, Tamaskovics B, Boelke E, Simiantonakis I, **Kammers K**, Matuschek C. Comparing Local and Systemic Control between Partial- and Whole-Breast Radiotherapy in Low-Risk Breast Cancer - A Meta-Analysis of Randomized Trials. *Cancers.* 2021 Jun 13;13(12):2967. doi: 10.3390/cancers13122967. [PMID: 34199281]

35. Keramati AR, Chen M-H, Rodriguez BAT, Yanek LR, Gaynor BJ, Ryan K, Brody JA, Zhong X, Wei Q, NHLBI Trans-Omics for Precision (TOPMed) Consortium, NHLBI TOPMed Hematology and Hemostasis Working Group, **Kammers K**, Kanchan K, Iyer K, Kowalski MH, Pitsillides AN, Cupples LA, Li B, Schlaeger TM, Shuldiner AR, O'Connell JR, Ruczinski I, Mitchell BD, Faraday N, Taub MA, Becker LC, Lewis JP, Mathias RA, Johnson AD. Genome sequencing unveils a regulatory landscape of platelet reactivity. *Nature Communications.* 2021 Jun 15;12(1):3626. doi: 10.1038/s41467-021-23470-9. [PMID: 34131117]

34. **Kammers K**, Taub MA, Mathias RA, Yanek LR, Kanchan K, Venkatraman V, Sundararaman N, Martin J, Liu S, Hoyle D, Raedschelders K, Holewinski R, Parker S, Dardov V, Faraday N, Becker DM, Cheng L, Wang ZZ, Leek JT, Van Eyk JE, Becker LC. Gene and protein expression in human megakaryocytes derived from induced pluripotent stem cells. *Journal of Thrombosis and Haemostasis.* 2021 Jul.19(7):1783-1799. doi: 10.1111/jth.15334. Epub 2021 May 6. [PMID: 33829634]

    This article is highlighted in the journal by: Abbonante V, Di Buduo CA, Balduini A. iPSC diversity: A key for better use and improved targeting. *Journal of Thrombosis and Haemostasis.* 2021 Jul;19(7):1641-1643. doi: 10.1111/jth.15328. [PMID: 34176219]

33. Chen A, Laeyendecker O, Eshleman SH, Monaco D, **Kammers K**, Larman HB, Ruczinski I. A Top Scoring Pairs Classifier for Recent HIV Infections. *Statistics in Medicine.* 2021 May 20;40(11):2604-2612. doi: 10.1002/sim.8920. [PMID: 33660319]

32. **Kammers K***, Taub MA*, Rodriguez B, Yanek LR, Ruczinski I, Martin J, Kanchan K, Battle A, Cheng L, Wang ZZ, Johnson AD, Leek JT, Faraday N, Becker L, Mathias RA. Transcriptional profile of platelets and iPSC-derived megakaryocytes from whole genome and RNA sequencing. *Blood.* 2021;137(7):959-968. Published 2021 Feb 19. doi: 10.1182/blood.2020006115. [PMID: 33094331] (*contributed equally)

    This article is highlighted in the journal by: Middleton EA and Rowley JW. eQTLs in platelets and iPSC-megakaryocytes. *Blood.* 2021;137(7):869-870. Published 2021 Feb 19. doi: 10.1182/blood.2020009461. [PMID: 33599763]

31. Haussmann J, Budach W, Corradini S, Krug D, Tamaskovics B, Boelke E, Djiepmo-Njanang FJ, Simiantonakis I, **Kammers K**, Matuschek C. No Difference in Overall Survival and Non-Breast Cancer Deaths after Partial Breast Radiotherapy Compared to Whole Breast Radiotherapy-A Meta-Analysis of Randomized Trials. *Cancers* 2020;12(8):2309. Published 2020 Aug 17. doi: 10.3390/cancers12082309. [PMID: 32824414]

30. Haussmann J, Nestle-Kraemling C, Boelke E, Wollandt S, Speer V, Djiepmo-Njanang FJ, Tamaskovics B, Gerber PA, Ort K, Ruckhaeberle E, Fehm T, Corradini S, Lammering G, Mohrmann S, Audretsch W, Maas K, Roth S, **Kammers K**, Budach W, Matuschek C. Long-term Quality of Life After Preoperative Radiochemotherapy in Patients With Localized and Locally Advanced Breast Cancer. *Strahlenther Onkol.* 2020;196(4):386-397. Published 2020 Jan 9. doi: 10.1007/s00066-019-01557-z. [PMID: 31919547]

29. Haussmann J, Tamaskovics B, Boelke E, Djiepmo-Njanang FJ, **Kammers K**, Corradini S, Hautmann M, Ghadjar P, Maas K, Schuler PJ, Hoffmann TK, Lammering G, Budach W, Matuschek C. Addition of chemotherapy to hyperfractionated radiotherapy in advanced head and neck cancer-a meta-analysis. *Strahlenther Onkol.* 2019;195(12):1041-1049. Published 2019 Oct 4. doi:10.1007/s00066-019-01511-z. [PMID: 31586229]

28. Haussmann J, Budach W, Tamaskovics B, Boelke E, Corradini S, Djiepmo-Njanang FJ, **Kammers K**, Matuschek C. Which target volume should be considered when irradiating the regional nodes in breast cancer? Results of a network-meta-analysis. *Radiation Oncology.* 2019;14(1):102. Published 2019 Jun 11. doi: 10.1186/s13014-019-1280-6. [PMID: 31186015]

27. Matuschek C, Nestle-Kraemling C, Haussmann J, Boelke E, Wollandt S, Speer V, Djiepmo Njanang FJ, Tamaskovics B, Gerber PA, Orth K, Ruckhaeberle E, Fehm T, Corradini S, Lammering G, Mohrmann S, Audretsch W, Roth S, **Kammers K**, Budach W. Long-term cosmetic outcome after preoperative radio-/chemotherapy in locally advanced breast cancer patients. *Strahlenther Onkol.* 2019;195(7):615-628. Published 2019 May 17. doi: 10.1007/s00066-019-01473-2. [PMID: 31101954]

26. Eshleman SH, Laeyendecker O, **Kammers K**, Chen A, Sivay MV, Kottapalli S, Sie BM, Yuan Y, Monaco DR, Mohan D, Wansley D, Kula T, Morrison C, Elledge SJ, Brookmeyer R, Ruczinski I, and Larman HB. Comprehensive profiling of HIV antibody evolution. *Cell Rep.* 2019;27(5):1422-1433.e4. Published 2019 Apr 30. doi: 0.1016/j.celrep.2019.03.097. [PMID: 31042470]

25. Matuschek C, Haussmann J, Boelke E, Tamskovics B, Gripp S, Djiepmo FN, Orth K, Pieper M, Gerber PA, Anooshahr B, **Kammers K**, Budach W. Adjuvant Chemoradiotherapy vs Chemotherapy Alone in Gastric Cancer: A Meta-analysis and Review of Literature. *Strahlenther Onkol.*2019;195(8):695-706. Published 2019 Feb 22. doi: 10.1007/s00066-019-01431-y. [PMID: 30796495]

24. Matuschek C, Haussmann J, Boelke E, Gripp S, Schuler P, Tamskovics B, Gerber PA, Djiepmo F, **Kammers K**, Plettenberg C, Anooshahr B, Orth K, Budach W. Accelerated vs. conventionally fractionated adjuvant radiotherapy in high-risk head and neck cancer: a meta-analysis. *Radiat Oncol.* 2018;13(1):195. Published 2018 Oct 4. doi:10.1186/s13014-018-1133-8. [PMID: 30286777]

23. Buhren BA, Schrumpf H, Boelke E, **Kammers K**, Gerber PA. Standardized in vitro analysis of the degradability of hyaluronic acid fillers by hyaluronidase. *Eur J Med Res.* 2018;23(1):37. Published 2018 Aug 20. doi:10.1186/s40001-018-0334-9. [PMID: 30122153]

22. Oyinlade O, Wei S, **Kammers K**, Liu S, Wang S, Ma D, Huang ZY, Qian J, Zhu H, Wan J, Xia S. Analysis of KLF4 regulated genes in cancer cells reveals a role of DNA methylation in promoter- enhancer interactions. *Epigenetics.* 2018;13(7):751-768. Published 2018 Aug 25. doi: 10.1080/15592294.2018.1504592. [PMID: 30058478]

21. Heerma van Voss MR, **Kammers K**, Vesuna F, Brilliant J, Bergman Y, Tantravedi S, Wu X, Cole RN, Holland A, van Diest PJ, Raman V. Global Effects of DDX3 Inhibition on Cell Cycle Regulation Identified by a Combined Phosphoproteomics and Single Cell Tracking Approach.*Transl Oncol.* 2018;11(3):755-763. Published 2018 Apr 24. doi: 10.1016/j.tranon.2018.04.001. [PMID: 29684792]

20. Heerma van Voss MR, Vesuna F, Afzal J, Bergman Y, **Kammers K**, Lehar M, Malek R, Balew M, ter Hoeve N, Abou D, Thorek D, Berlinicke C, Yazdankheh M, Sinha D, Le A, Abrahams R, Tran P, van Diest PJ, Raman V. Targeting mitochondrial translation by inhibiting DDX3 for cancer treatment; a novel radiosensitization strategy. *Oncogene.* 2018;37(1):63?74. Published 2017 Sep 4. doi: 10.1038/onc.2015.336. [PMID: 28869602]

19. Urbschat S, Sippel C, Engelhardt J, **Kammers K**, Oertel J, Ketter R. Importance of Biomarkers in Glioblastomas patients receiving local BCNU wafer chemotherapy. *Mol Cytogenet.* 2017 May 4;10(1). doi: 10.1186/s13039-017-0317-5. [PMID: 28484518]

18. Collado-Torres L, Nellore A, **Kammers K**, Ellis SE, Taub MA, Hansen KD, Jaffe AE, Langmead B, Leek JT. Reproducible RNA-seq analysis using recount2. *Nat Biotechnol.* 2017 Apr 11;35(4):319-321. doi: 10.1038/nbt.3838. [PMID: 28398307]

17. Matuschek C, Bölke E, Hussmann J, Mohrmann S, Nestle-Kräming C, Gerber PA, Corradini S, Orth K, **Kammers K**, Budach W. The benefit of adjuvant radiotherapy after breast conserving surgery in older patients with low risk breast cancer- a meta-analysis of randomized trials. *Radiat Oncol.* 2017 Mar 23;12(1):60. doi: 10.1186/s13014-017-0796-x. [PMID: 28335784]

16. **Kammers K**, Taub MA, Ruczinski I, Martin J, Yanek LR, Frazee A, Gao Y, Hoyle D, Faraday N, Becker DM, Cheng L, Wang ZZ, Leek JT, Becker LC, Mathias RA. Integrity of induced pluripotent stem cell (iPSC) derived megakaryocytes as assessed by genetic and transcriptomic analysis. *PLoS One.* 2017 Jan 20;12(1):e0167794. doi: 10.1371/journal.pone.0167794. [PMID: 28107356]

15. Ratovitski T, Chaerkady R, **Kammers K**, Stewart J, Zavala A, Pletnikova O, Troncoso J, Rudnicki D, Margolis R, Cole R, Ross C. Quantitative Proteomic Analysis reveals similarities between Huntington's Disease (HD) and Huntington's disease-like 2 (HDL2) human brains. *J Proteome Res.* 2016 Sep 2;15(9):3266-83. doi: 10.1021/acs.jproteome.6b00448. Epub 2016 Aug 3. [PMID: 27486686]

14. Foster DB, Liu T, **Kammers K**, O'Meally RN, Yang N, Papanicolaou K, Talbot CC Jr, Cole RN, O'Rourke B. Integrated omic analysis of a guinea pig model of heart failure and sudden Cardiac Death. *J Proteome Res.* 2016 Sep 2;15(9):3009-28. doi: 10.1021/acs.jproteome.6b00149. Epub 2016 Aug 3. [PMID: 27399916]

13. Matuschek C, Bölke E, Geigis C, **Kammers K**, Ganswindt U, Scheckenbach K, Gripp S, Simiantonakis J, Hoffmann TK, Greve J, Gerber PA, Orth K, Roeder H, Hautmann MG, Budach W. Influence of dosimetric and clinical criteria on the requirement of artificial nutrition during radiotherapy of head and neck cancer patients. *Radiother Oncol.* 2016 Jul;120(1):28-35. doi: 10.1016/j.radonc.2016.05.017. Epub 2016 Jun 10. [PMID: 27296411]

12. Budach W, Bölke E, **Kammers K**, Gerber PA, Nestle-Krämling C, Matuschek C. Adjuvant radiation therapy of regional lymph nodes in breast cancer - a meta-analysis of randomized trials- an update. *Radiother Oncol.* 2015 Dec 21;10:258. doi: 10.1186/s13014-015-0568-4. [PMID: 26691175]

11. Budach W, Bölke E, **Kammers K**, Gerber PA, Orth K, Gripp S, Matuschek C. Induction chemotherapy followed by concurrent radio-chemotherapy versus concurrent radio-chemotherapy alone as treatment of locally advanced squamous cell carcinoma of the head and neck (HNSCC): A meta-analysis of randomized trials. *Radiother Oncol.* 2016 Feb;118(2):238-43. doi: 10.1016/j.radonc.2015.10.014. Epub 2015 Nov 14. [PMID: 26589131]

10. Wilky BA, Kim C, McCarty G, Montgomery EA, **Kammers K**, Cole RN, Raman V, Loeb D. RNA Helicase DDX3 - A novel therapeutic target in Ewing sarcoma. *Oncogene.* 2016 May 19;35(20):2574-83. doi: 10.1038/onc.2015.336. Epub 2015 Sep 14. [PMID: 26364611]

9. te Riele AS, James CA, Groeneweg JA, Sawant AC, **Kammers K**, Murray B, Tichnell C, van der Heijden JF, Judge DP, Dooijes D, van Tintelen JP, Hauer RN, Calkins H, Tandri H. Approach to family screening in arrhythmogenic right ventricular dysplasia/cardiomyopathy. *Eur Heart J.* 2016 Mar 1;37(9):755-63. doi: 10.1093/eurheartj/ehv387. Epub 2015 Aug 27. [PMID: 26314686]

8. Matuschek C, Ochtrop T, Bölke E, Fenk R, Gripp S, Kröpil P, Gerber PA, **Kammers K**, Hamilton J, Orth K, Ganswindt U, Budach W. Effects of radiotherapy in the treatment of multiple myeloma: a retrospective analysis of a single institution. *Radiat Oncol.* 2015 Mar 28;10:71. doi: 10.1186/s13014-015-0374-z. [PMID: 25889851]

7. **Kammers K**, Cole RN, Tiengwe C, Ruczinski I. Detecting significant changes in protein abundance. *EuPA Open Proteom.* 2015 Jun;7:11-9. doi: 10.1016/j.euprot.2015.02.002. Epub 2015 Feb 25. [PMID: 25821719]

6. Linsler S, Kraemer D, Driess C, Oertel J, **Kammers K**, Rahnenführer J, Ketter R, Urbschat S. Molecular biological determinations of meningioma progression and recurrence. *PLoS One.* 2014 Apr 10;9(4):e94987. doi: 10.1371/journal.pone.0094987. [PMID: 24722350]

5. Hetzer S, Buhren BA, Schrumpf H, Bölke E, Meller S, **Kammers K**, Gerber PA, Homey B. Retrospective analysis of the frequency of centrofacial telangiectasia in systemic sclerosis patients treated with bosentan or ilomedin. *Eur J Med Res.* 2014 Jan 10;19:2. doi:10.1186/2047-783X-19-2. [PMID: 24410934]

4. Budach W, **Kammers K**, Bölke E, Matuschek C. Adjuvant radiotherapy of regional lymph nodes in breast cancer - a meta-analysis of randomized trials. *Radiation Oncol.* 2013 Nov 14;8:267. doi: 10.1186/1748-717X-8-267. [PMID: 24225206]

3. **Kammers K**, Lang M, Hengstler JG, Schmidt M, Rahnenführer J. Survival models with preclustered gene groups as covariates. *BMC Bioinformatics* 2011 Dec 16;12:478. doi: 10.1186/1471-2105-12-478. [PMID: 22177110]

2. Matuschek C, Rudoy M, Peiper M, Gerber PA, Hoff NP, Buhren BA, Flehmig B, Budach W, Knoefel WT, Bojar H, Prisack HB, Steinbach G, Shukla V, Schwarz A, **Kammers K**, Erhardt A, Scherer A, Bölke E, Schauer M. Do insulin-like growth factor associated proteins qualify as a tumor marker? Results of a prospective study in 163 cancer patients. *Eur J Med Res.* 2011 Oct 10;16(10):451-6. doi: 10.1186/2047-783X-16-10-451. [PMID: 22024424]

1. Wemmert S, Bettscheider M, Alt S, Ketter R, **Kammers K**, Feiden W, Steudel WI, Rahnenführer J, Urbschat S. p15 promoter methylation - a novel prognostic marker in glioblastoma patients. *Int J Oncol.* 2009 Jun 1;34(6):1743-8. doi: 10.3892/ijo_00000305. [PMID: 19424593]

Book Chapters

1. **Kammers K**, Foster DB, Ruczinski I. Analysis of proteomic data. In Agnetti G, Lindsey ML, Foster DB (eds). *Manual of Cardiovascular Proteomics.* Springer International Publishing, Cham, Switzerland, 2016 Oct 17. doi: 10.1007/978-3-319-31828-8.

Reports

1. **Kammers K**, Rahnenführer J. Improved interpretability of survival models with gene groups as covariates. Technical Report, Department of Statistics, Dortmund University of Technology, 2010.

Preprints

6. Ngwa JS, Yanek LR, **Kammers K**, Kanchan K, Taub MA, Scharpf RB, Faraday N, Becker LC, Mathias, RA, Ruczinski I. Secondary Analyses for Genome-wide Association Studies using Expression Quantitative Trait Loci. *medRxiv.* 2021. doi: https://doi.org/10.1101/2021.07.20.21260862

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5. Schatz MC, Philippakis AA, Afgan E, Banks E, Carey VJ, Carroll RJ, Culotti A, Ellrott K, Goecks J, Grossman RL, Hall IM, Hansen KD, Lawson J, Leek JT, O'Donnell Luria A, Mosher S, Morgan M, Nekrutenko A, O'Connor BD, Osborn K, Paten B, Patterson C, Tan FJ, Taylor CO, Vessio J, Waldron L, Wang T, Wuichet K, AnVIL Team (with **Kammers K** as a member of AnVIL Team). Inverting the model of genomics data sharing with the NHGRI Genomic Data Science Analysis, Visualization, and Informatics Lab-space (AnVIL). *bioRxiv.* 2021. doi: https://doi.org/10.1101/2021.04.22.436044

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4. Keramati AR, Chen M-H, Rodriguez BAT, Yanek LR, Gaynor BJ, Ryan K, Brody JA, NHLBI Trans-Omics for Precision (TOPMed) Consortium, NHLBI TOPMed Hematology and Hemostasis Working Group, **Kammers K**, Kanchan K, Iyer K, Kowalski MH, Pitsillides AN, Cupples LA, Shuldiner AR, O'Connell JR, Mitchell BD, Faraday N, Taub MA, Becker LC, Lewis JP, Mathias RA, Johnson AD. Genome Sequencing Unveils a New Regulatory Landscape of Platelet Reactivity. *bioRxiv.* 2019. doi: https://doi.org/10.1101/621565

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3. Fu J, **Kammers K**, Nellore A, Collado-Torres L, Leek JT, Taub MA. RNA-seq transcript quantification from reduced-representation data in recount2. *bioRxiv.* 2018. doi: https://doi.org/10.1101/247346

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2. Monaco D, Kottapalli S, Yuan T, Breitwieser F, Anderson D, Wijaya L, Tan K, Chia WN, **Kammers K**, Caturegli M, Waugh K, Rewers M, Wang LF, Larman HB. Deconvoluting Virome-Wide Antiviral Antibody Profiling Data. *bioRxiv.* 2018. doi: https://doi.org/10.1101/333625

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1. Collado-Torres L, Nellore A, **Kammers K**, Ellis SE, Taub MA, Hansen KD, Jaffe AE, Langmead B, Leek JT. recount: A large-scale resource of analysis-ready RNA-seq expression data. *bioRxiv.* 2016. doi: https://doi.org/10.1101/068478

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Software

`recount` Collado-Torres L, Nellore A, **Kammers K**, Ellis SE, Taub MA, Hansen KD, Jaffe AE, Langmead B, Leek JT. Explore and download data from the recount project. *http://www.bioconductor.org/packages/recount.* 2022. doi: 0.18129/B9.bioc.recount, https://github.com/leekgroup/recount - R package version 1.20.0.

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Professional Activities

Memberships

2015 – 2019	Eastern North American Region, International Biometric Society.
2015 – 2019	American Society of Human Genetics.
2013	American Society for Mass Spectrometry.

Peer Review

2022 – present	Human Genetics and Genomics Advances.
2021 – present	Brain Sciences.
2021 – present	BMC Cancer.
2019 – present	Computational Statistics.
2018 – present	Nature Methods.
2017 – present	Biostatistics.
2016 – present	Journal of Proteome Research.
2016 – present	BMJ Open.
2016 – present	OncoTargets and Therapy.
2016 – present	Bioinformatics, subsection: European Conference on Computational Biology (ECCB).
2016 – present	Annals of Applied Statistics.
2014 – present	BioMed Central European Journal of Medical Research.
2013 – present	EEE/ACM Transactions on Computational Biology and Bioinformatics.
2012 – present	BioMed Central Bioinformatics.

Program Development

2015	Session Chair, 61th Biometric Colloquia of the International Biometrical Society - German Region, Dortmund, Germany.
2010	Local Conference Organization, 2nd Joint Statistical Meeting of the Germany Statistical Society, DAGStat2010, Dortmund, Germany.
2007	Local Organization, NGfN: Courses in Practical DNA Microarray Analysis, Dortmund, Germany.

Academic Service

Dortmund University of Technology

2011 – 2013	Member, Public Relations Committee.
2011 – 2013	Primary Curriculum and Career Advisor.
2010	Member, Summer Festival Planning Committee.
2009 – 2013	Member, Faculty Council.

Presentations

Scientific Meetings: Talks

2021	*Transcriptional landscape of platelets and iPSC-derived megakaryocytes. [invited speaker]* 28th Annual Meeting of the Royal Statistical Society of Belgium, Liège, Belgium.
2021	*eQTLs in platelets and IPSC-derived megakaryocytes.* CAAPA Virtual Annual Meeting, Denver, CO, USA.

2018 *Novel and concordant eQTLs from analysis of iPSC-derived megakaryocytes and platelets in the Genetic Studies of Atherosclerosis Risk (GeneSTAR) project.* The Casa Matematica Oaxaca (CMO) workshop 18w5202: Statistical and Computational Challenges in High-Throughput Genomics with Application to Precision Medicine, Oaxaca, Mexico.

2017 *Detecting eQTLs in high-dimensional sequencing data.* CEN ISBS Vienna 2017 Congress, Vienna, Austria.

2017 *Detecting eQTLs from high-dimensional sequencing data using recount2.* useR!2017, Brussels, Belgium.

2016 *Detecting eQTLs: a fast analysis protocol using high-dimensional sequencing data.* 2016 Joint Statistical Meetings (JSM), Chicago, IL, USA.

2016 *Detecting eQTLs in megakaryocytes (MKs) derived from induced pluripotent stem cells (iPSCs).* 2016 Eastern North American Region Meetings (ENAR), Austin, TX, USA.

2015 *Genetic and transcriptomic analysis of megakaryocytes.* Banff International Research Station for Mathematical Innovation and Discovery (BIRS) workshop 15w5142: Statistical and Computational Challenges in Bridging Functional Genomics, Epigenomics, Molecular QTLs, and Disease Genetics, Banff, Alberta, Canada.

2015 *Detecting significant changes in protein abundance.* 61st Biometric Colloquia of the International Biometrical Society - German Region, Dortmund, Germany.

2012 *Survival models with gene groups as covariates.* 9th Autumn Symposium of the Research Training Group "Statistical Modelling", Dortmund, Germany.

2012 *Survival models with preclustered gene groups as covariates.* 59th Biometric Colloquia of the International Biometrical Society - German Region, Berlin, Germany.

2008 *Survival models built from built from gene expression data with gene groups as additional covariates.* useR!2008 - the R User Conference, Dortmund, Germany.

2008 *Survival models with gene groups as covariates.* 1st Conference of the Central European Network 'LIFESTAT 2008', Statistics and Life Sciences: Perspectives and Challenges, 54th Biometric Colloquia & 25th ROeS Seminar, Munich, Germany.

Scientific Meetings: Posters

2018 *Novel and concordant eQTLs from analysis of iPSC-derived megakaryocytes and platelets in the Genetic Studies of Atherosclerosis Risk (GeneSTAR) project.* American Society of Human Genetics Annual Meeting, San Diego, CA, USA.

2018 *Replication of eQTLs in iPSC-derived megakaryocytes between ethnic groups.* Johns Hopkins Heart and Vascular Institute's 9th Annual Cardiovascular Research Retreat, Baltimore, MD, USA.

2017 *eQTL analysis of megakaryocytes (MKs) derived from induced pluripotent stem cells (iPSCs).* Symposium on Advances in Genomics, Epidemiology, and Statistics (SAGES), Philadelphia, PA, USA.

2016 *Integrity of induced pluripotent stem cell (iPSC) derived megakaryocytes as assessed by genetic and transcriptomic analysis.* Symposium on Advances in Genomics, Epidemiology, and Statistics (SAGES), Philadelphia, PA, USA.

2016 *Integrity of induced pluripotent stem cell (iPSC) derived megakaryocytes as assessed by genetic and transcriptomic analysis.* Genetics Research Day 2016 (MD-GEM), Baltimore, MD, USA.

2015 *Integrity of induced pluripotent stem cell (iPSC) derived megakaryocytes as assessed by genetic and transcriptomic analysis.* American Society of Human Genetics Annual Meeting, Baltimore, MD, USA.

2015 *Detecting differentially expressed proteins.* Symposium on Advances in Genomics, Epidemiology, and Statistics (SAGES), Philadelphia, PA, USA.

2013 *Challenges in including biological prior knowledge into survival models.* 3rd Joint Statistical Meeting of the Germany Statistical Society, DAGStat2013, including the 59th Biometric Colloquia of the International Biometrical Society - German Region, Freiburg, Germany.

2009 *Improving interpretability of survival models built from gene expression data with gene groups as additional covariates.* 17th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB) & 8th European Conference on Computational Biology (ECCB), Stockholm, Sweden.

2008 *Survival models with gene groups as covariates.* Workshop on Computational Systems Biology, Leipzig, Germany.

Invited Seminars

01/17/20 *Detecting Significant Changes in Protein Abundance.* Center for Statistics and Data Science Institute, Hasselt University, Belgium.

03/12/19 *Answering Biological Questions with Multiomics.* Department of Statistics, Dortmund University of Technology, Germany.

06/14/17 *Adventures in Genomics and Proteomics.* Assistant Professor Summer Series at The Johns Hopkins University School of Medicine, Baltimore, MD, USA.

09/30/16 *Reproducible, Hypothesis Driven Research in Genomics.* The MITRE Corporation, Windsor Mill, MD, USA.

03/04/16 *Statistics for genomics and proteomics.* Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, USA.

02/18/16 *Improving Statistical Practice and Procedures in Collaborative Projects with Omics Data.* Johns Hopkins University School of Medicine, Baltimore, MD, USA.

07/13/15 *eQTL analysis of megakaryocytic cell lines.* Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, USA.

12/01/14 *Analysis of proteomic data.* Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, USA.

06/11/14 *Analysis of proteomic data.* Department of Statistics, Dortmund University of Technology, Germany.

11/04/13 *Integrating prior biological knowledge into high-dimensional survival models.* Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, USA.

03/13/12 *Survival analysis.* Department of Radiation Oncology, Düsseldorf University Hospital, Germany.

02/28/12 *Statistics in medicine.* Department of Radiation Oncology, Düsseldorf University Hospital, Germany.

01/11/12 *Survival models with preclustered gene groups as covariates.* Mathematical Institute, Heinrich-Heine-University, Düsseldorf, Germany.

12/01/11 *Survival models with preclustered gene groups as covariates.* Institute for Medical Informatics, Münster University, Germany.

11/01/11 *High-dimensional survival models.* Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, USA.

Funding

Ongoing Research Support

09/20 – 08/25 UE5CA254170 (NCI), Leek et al. (PIs), Responsibility: Co-Investigator.
Scalable multi-mode Education to increase use of ITCR Tools by diverse Analysts.
We propose to create a complete training resource including content and both online and offline courses to improve cancer informatics knowledge throughout the research enterprise. The project will create an informatics training network hosted at www.itcrtraining.org that can be used by everyone from community members, to basic scientists, to ITCR tool developers, to medical doctors, to principal investigators to improve their knowledge of informatics.

04/20 – 03/24 R01GM136724 (NIGMS), Larman/Ruczinski (PIs), Responsibility: Co-Investigator.
Design and Analysis of Displayed Peptidomes.
This project seeks to address current limitations in peptide library design. Innovative principles will be established and ultimately utilized for the construction of an efficient gut microbiome library.

01/20 – 12/24 U01CA247576 (NCI), Staedtke/Bai (PIs), Responsibility: Co-Investigator.
Adrenergic modulation of cellular immune functions in CAR T cell-induced cytokine release syndrome.
The project's goal is to assess the translational potential of catecholamines in preventing, predicting and treating immunotoxicity and cytokine release syndrome in human patients receiving therapies with chimeric antigen receptor (CAR) T cells.

07/19 – 06/22 U01CA241953 (NIH), Schnaar (PI), Responsibility: Co-Investigator.
Ganglioside Interactome Toolkit.
It is the goal of this project to provide new adaptable and accessible chemical biology tools to investigate ganglioside functions in health and disease.

05/19 – 04/23 R01HL143818 (NHLBI), Becker/Resar (PIs), Responsibility: Co-Investigator.
Clonal Hematopoiesis in Healthy Individuals from Families with Early Onsetcoronary Artery Disease.
Using whole genome sequencing, we will examine these oncogenic mutations and determine whether they are more prevalent in people with a family history of early coronary disease and if they are related to markers of early aging. We will also perform functional studies in cultured cells and mice to further understand the process.

09/18 – 06/23 U24HG010263 (NHGRI), Schatz et al. (PIs), Responsibility: Co-Investigator.
Implementing the Genomic Data Science Analysis, Visualization, and Informatics.
The goal of this project is to create cloud-based computational analysis and visualization workspace for genomic research. The research enabled by this workspace will accelerate our understanding of the genetic components of human health and disease and progress towards precision genomic medicine.

01/18 – 11/22 R01HL104608 (NHLBI), Mathias/Barnes/Kenny (PIs), Responsibility: Co-Investigator.
New Approaches for Empowering Studies of Asthma in Populations of African Descent.
There are three primary objectives of this study is to (1) expand and integrate multi-omic resources for asthma research in African Diaspora populations and identify novel genetic determinants for risk of asthma in CAAPA cohorts; (2) broadly disseminate CAAPA results through web-based resources that empower the asthma research community for new discoveries; and (3) develop and apply novel approaches for prioritizing CAAPA results in 3 independent biobanks enriched for US minority populations (Nashville, New York City, and the Rocky Mountain region).

11/16 – 10/22 R01AI095068 (NIAID), Eshleman (PI), Responsibility: Co-Investigator.
HIV incidence testing in an evolving epidemic: identification of accurate multi-assay algorithms that include serosignatures from a novel antibody profiling system.
The major goal of this project is to expand a repository of well-characterized samples with information on the duration of HIV infection; use these samples to evaluate performance of HIV incidence assays.

Completed Research Support

06/18 – 05/20 R01HL141944 (NHLBI), Mathias/Ruczinski (PIs), Responsibility: Co-Investigator.
Integrative Computational Biology Approaches to Identify Functional Determinants of Platelet Aggregation in African Americans and European Americans.
We propose the integration of whole genome DNA and RNA sequencing to understand the true biological mechanism of action of the previously identified genetic associations, and to uncover the determinants of high residual heritability with this multi-omics approach.

05/17 – 04/22 P30CA006973 (NCI), Nelson/Cope/Wheelan/Yegnasubramanian (PIs), Responsibility: Co-Investigator.
Regional Oncology Research Center: Experimental and Computational Genomics.
The primary mission of the Core is to allow SKCCC investigators to harness the ongoing revolution in cancer genomics to accelerate their basic discovery and translational research.

04/14 – 03/19 R01HL118356 (NHLBI), Becker (PI), Responsibility: Co-Investigator.
Gene transcripts and proteomics in families with platelet hyperaggregation.
We propose to discover new pathways regulating platelet aggregation by determining which genes are expressed in subjects with platelet hyperaggregation. By sequencing the entire platelet transcriptome we will identify changes in the amount or quality (e.g., splice variants) of mRNA transcripts that are associated with specific platelet hyperaggregation phenotypes.

09/13 – 04/19 R01GM105705 (NIGMS), Leek (PI), Responsibility: PDC and Co-Investigator.
Statistical models for biological and technical variation in RNA sequencing.
Genome-wide gene expression measurements are widely used to understand the molecular basis for diseases and to develop predictive and prognostic biomarkers. RNA-sequencing is a new technology for making expression measurements that is more flexible but produces larger and more complex data. We propose to develop statistical methods and software for analyzing these data, accounting for biological and technological errors.

07/13 – 06/15 KA 3884/1-1 (DFG, German Research Foundation), Kammers (PI).
Integration of prior biological knowledge into survival models for different types of omics data.
The major goal of this projects is the integration of prior biological knowledge and the aggregation of genomic information from different data sources into statistical models.

09/12 – 05/18 R01HL112064 (NHLBI), Mathias (PI), Responsibility: Co-Investigator.
A family-based exome sequencing approach to Identify platelet aggregation genes.
Native and residual post aspirin platelet hyper aggregation, a strong risk factor for ischemic syndromes, is moderately to highly heritable. Our preliminary data using a genome-wide association study (GWAS) in African American and European American families suggest high 'missing heritability' (i.e. that not explained by the common GWAS signal detected). The primary hypothesis is that genes harboring rare genetic variants determining platelet aggregation account for a substantial fraction of missing trait heritability, and an integrative family-based approach of GWAS and exome-sequencing will be applied to test this hypothesis.

07/11 – 06/17 U01HL107446 (NHLBI), Becker (PI), Responsibility: PDC.
Functional genomics of platelet aggregation using iPS and derived megakaryocytes.
In 3 phases, we will (1) create pluripotent stem cells (iPS) from peripheral blood mononuclear cells, then differentiate these stem cells into megakaryocytes (2) efficiently produce iPS and megakaryocytes using a novel pooling method, and (3) produce iPS and megakaryocytes from 400 subjects in GeneSTAR (200 whites, 200 African Americans), selected based on specific hypotheses derived from GWAS signals in native and post aspirin platelet function.

Postdoctoral Awards and Research Support

2016 **Poster Award** [1st place, Postdoctoral Fellows], 2016 Genetics Research Day of the Maryland-Genetics, Epidemiology, Medicine Training Program (MD-GEM), Baltimore, MD, USA.

2015 **Travel Award**, Symposium on Advances in Genomics, Epidemiology, and Statistics (SAGES), Philadelphia, PA, USA.

2013 – 2015 **Postdoctoral research fellowship**, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, USA; funded by the German Research Foundation (DFG).

2012 – 2013 **Postdoctoral research fellowship** within the research training group (Graduiertenkolleg) 'Statistical Modelling' at Dortmund University of Technology, Germany; funded by the DFG.

Teaching

Department of Biostatistics, Johns Hopkins University

2015 – 2016 **Survival Analysis**, Teaching Assistant.

Department of Statistics, Dortmund University of Technology.

2011 – 2013 **Data Analysis with SAS**, Teaching Assistant.

2011 **High-dimensional Survival Analysis**, Primary Instructor.

2010 **Analysis of Mircoarray Data**, Primary Instructor.

2010 **Survival Analysis with R and SAS**, Primary Instructor.

2008 – 2011 **Statistical Methods in Bioinformatics**, Teaching Assistant.

2007 – 2011 **Clinical Trials**, Teaching Assistant.

2007 **Statistical Learning**, Teaching Assistant.

2007 **Survival Analysis**, Teaching Assistant.

Mathematical Institute, Heinrich-Heine University Düsseldorf

2006 **Analysis I**, Teaching Assistant.

Mentoring

Pre-doctoral Advisees /Mentees

2016 – 2018 Jack Fu, Bsc, Graduate Student within the Department of Biostatistics.
2017 – 2021 Siruo Wang, Bsc, Msc, Graduate Student within the Department of Biostatistics.
2018 – 2021 Daniel Monaco, Bsc, Graduate Student within the Department of Medicine.
2016 – 2021 Kayode Sosina, Bsc, Msc, Graduate Student within the Department of Biostatistics.
2018 – 2022 Athena Chen, Bsc, Graduate Student within the Department of Biostatistics.

Thesis committees

2018 Jack Fu, PhD, Biostatistics, doctoral thesis reader and final oral examination committee member.
2018 Kayode Sosina, PhD, Biostatistics, preliminary schoolwide oral exam committee member.
2018 Daniel Monaco, PhD, Pathology, thesis committee member.
2021 Yoris van Houtven, PhD, Statistics, doctoral thesis reviewer and final oral examination committee member.
2021 Siruo Wang, PhD Biostatistics, doctoral thesis reader and final oral examination committee member.

Additional Skills

Languages German: native speaker
English: fluent
French: basics

Computer Skills R, Bioconductor, SAS, Stata, SPSS, LaTeX, unix shell scripts, Microsoft Office.

Lecturer mibeg-Institute for Medicine, Cologne, Germany: Courses in Statistics for Clinical Research Associates (2009 – 2013, multiples times a year).

Professional Development Participation in 'Research Leadership for Postdocs' [Course fulfills NIH expectation for 'instruction and training in leadership skills'], Johns Hopkins Medical Institutions, Professional Development Office (2015).