

Kai Kammers

Curriculum Vitae

November 2, 2018

Current Position

Assistant Professor of Oncology

Division of Biostatistics and Bioinformatics
Department of Oncology
The Sidney Kimmel Comprehensive Cancer Center
The Johns Hopkins University School of Medicine

✉ 550 North Broadway, Suite 1103, Baltimore, MD 21205, USA

☎ +1 410 502 0946

✉ kai.kammers@jhu.edu

🌐 www.biostat.jhsph.edu/~kkammers

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**
TU 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**
Division of Biostatistics and Bioinformatics, 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, TU Dortmund University of Technology, Dortmund, Germany.
- 2003 – 2007 **Student Research Assistant**
Mathematical Institute, Heinrich-Heine-University, Düsseldorf, Germany.

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 TU Dortmund University of Technology, Germany; funded by the DFG.

Publications

Submitted Manuscripts

1. Eshleman SH, Laeyendecker O, **Kai Kammers**, Chen A, Sivay MV, Kottapalli S, Sie BM, Yuan Y, Mohan D, Wansley D, Kula T, Morrison C, Elledge SJ, Brookmeyer R, Ruczinski I, and Larman HB. Comprehensive profiling of HIV antibody evolution. *Cell Host & Microbe*.
2. Matuschek C, Haussmann J, Boelke E, Tamskovics B, Gripp S, Djiepmo FN, Orth K, Gerber PA, Anooshahr B, **Kammers K**, Budach W. Adjuvant Chemoradiotherapy vs Chemotherapy Alone in Gastric Cancer: A Meta-analysis and Review of Literature. *Strahlentherapie und Onkologie*.

Peer-Reviewed Articles

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. *Radiation Oncology*. 2018 Oct 4;13(1):195. doi: 10.1186/s13014-018-1133-8. [PMID: 30286777]
23. Buhren BA, Schrupf H, Bölke E, **Kammers K**, Gerber PA. Standardized in vitro analysis of the degradability of hyaluronic acid fillers by hyaluronidase. *Eur J Med Res*. 2018 Aug 20;23(1):37. 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 Jul 30. doi: 10.1080/15592294.2018.1504592, [Epub ahead of print]. [PMID: 30058478]
21. 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 Apr 20;11(3):755-763. doi: 10.1016/j.tranon.2018.04.001. [PMID: 29684792]
20. 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 Jan 4;37(1). doi: 10.1038/onc.2015.336. Epub 2017 Sep 4. [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, 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. 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, TU Dortmund University of Technology, 2010.

Preprints

- 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>.
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>.
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>.

Professional Activities

Memberships

- 2015 – present Eastern North American Region, International Biometric Society.
- 2015 – present American Society of Human Genetics.
- 2014 American Society for Mass Spectrometry.

Peer Review

- 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

TU 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

- 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

- 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, TU 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

- 06/18 – 05/20 R01HL141944 (NHLBI), Mathias/Ruczinski(PI), 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.
- 12/17 – 11/22 R01HL104608 (NIH), Mathias/Barnes/Kenny (PI), 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).
- 07/17 – 04/22 P30CA006973 (NCI), William Nelson and Leslie Cope (PI), Responsibility: Co-Investigator.
Regional oncology research center: Bioinformatics Core.
The bioinformatics shared resource guarantees the availability of comprehensive Bioinformatics expertise to Cancer Center members.
- 11/16 – 10/20 R01AI095068 (NIAID), Susan 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.
- 04/14 – 03/19 R01HL118356 (NHGRI), 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.

Completed Research Support

- 01/13 – 08/18 R01GM105705 (NHGRI), 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.
- 07/11 – 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.
- 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.
- 05/06 – 04/18 P30CA006973 (NCI), Nelson/Cope (PI), Responsibility: Co-Investigator.
Regional Oncology Research Center: Bioinformatics Core.
 The bioinformatics shared resource guarantees the availability of comprehensive Bioinformatics expertise to Cancer Center members.

Teaching

Department of Biostatistics, Johns Hopkins University

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

Department of Statistics, TU Dortmund University of Technology.

- 2011 – 2013 **Data Analysis with SAS**, Teaching Assistant.
 2011 **High-dimensional Survival Analysis**, Primary Instructor.
 2010 **Analysis of Microarray 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.

Main Collaborators

Local at Johns Hopkins University

- 2017 – present Benjamin Larman, PhD, Department of Pathology.
 2017 – present Susan Eshleman, MD, PhD, Department of Pathology.

- 2015 – present Lewis Becker, MD, Department of Medicine.
- 2015 – present Margaret Taub, ScD, Department of Biostatistics.
- 2015 – present Rasika Mathias, ScD, Department of Medicine.
- 2015 – present Margaret Taub, ScD, Department of Biostatistics.
- 2015 – present Jeffrey Leek, PhD, Department of Biostatistics.
- 2013 – present Ingo Ruczinski, PhD, Department of Biostatistics.
- 2013 – present Robert Cole, PhD, Department of Biological Chemistry.

National

- 2017 – present Kathleen Barnes, PhD, Department of Medicine, University of Colorado, Denver, CO, USA.
- 2016 – present Jennifer Van Eyk, PhD, Cedars-Sinai Heart Institute and the Advanced Clinical Biosystems Research Institute, Los Angeles, CA, USA.

International

- 2016 – present Stefan Canzar, PhD, LMU Munich, Munich, Germany.
- 2014 – present Holger Schwender, PhD, Mathematical Institute, Heinrich-Heine University, Düsseldorf, Germany.
- 2010 – present Bettina Alexandra Buhren, PhD and Peter-Arne Gerber, MD. Department of Dermatology, Düsseldorf University Hospital, Düsseldorf, Germany.
- 2010 – present Wilfried Budach, MD, Edwin Bölke, MD, and Stephan Gripp, MD, Department of Radiation Oncology, Düsseldorf University Hospital, Düsseldorf, Germany.
- 2008 – present Ralf Ketter, MD, Department of Neurosurgery, Saarland University Medical Center, Homburg, Germany.

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).

References

Ingo Ruczinski, PhD
Professor of Biostatistics
Department of Biostatistics
Johns Hopkins Bloomberg School of Public Health
615 North Wolfe St, Room E3618
Baltimore, MD 21205
Email: ingo@jhu.edu

Jeffrey T Leek, PhD
Professor of Biostatistics
Department of Biostatistics
Johns Hopkins Bloomberg School of Public Health
615 North Wolfe St, Room E3624
Baltimore, MD 21205
Email: jtleek@gmail.com

Rasika A Mathias, ScD
Associate Professor of Medicine
Director of Genomics, GeneSTAR Research program, General Internal Medicine
Director, Data Analysis Unit, Allergy and Clinical Immunology
Johns Hopkins University School of Medicine
5501 Hopkins Bayview Circle, 3B.79
Baltimore, MD 21224
Email: rmathias@jhmi.edu

Jörg Rahnenführer, PhD
Professor of Statistics
Department of Statistics
TU Dortmund University of Technology
Vogelpothsweg 87
Dortmund, 44227 (Germany)
Email: rahnentuehrer@statistik.tu-dortmund.de