

Dr. Stefan Konigorski

Hasso Plattner Institute for Digital Engineering gGmbH
Rudolf-Breitscheid-Str. 187, 14482 Potsdam
Email: stefan.konigorski@hpi.de
Phone: +49-331-55094873
Web: www.hpi.de/lippert/team/stefan-konigorski
Linkedin: www.linkedin.com/in/stefan-konigorski



EDUCATION

- Aug 2017-Mar 2018 **HUMBOLDT UNIVERSITY OF BERLIN** Berlin, Germany
*Dr. rer. nat. in Computer Science, Department of Mathematical and Natural Sciences
(Supervisors: Prof. Marius Kloft, Prof. Tobias Pischon, Prof. Yildiz E. Yilmaz)*
Thesis: “Development and application of new statistical methods for the analysis of multiple phenotypes to investigate genetic associations with cardiometabolic traits”
- Aug 2012-Aug 2013 **UNIVERSITY OF TORONTO** Toronto, Canada
M.Sc. Biostatistics, Dalla Lana School of Public Health
- Sep 2007-Jun 2008 **UNIVERSITY OF TORONTO** Toronto, Canada
Visiting Student at the Department of Statistics, School of Graduate Studies
- Sep 2004-Jul 2011 **UNIVERSITY OF HEIDELBERG** Heidelberg, Germany
- *Dipl.-Math., Mathematics Diplom*
 - Thesis: “A Study of Dimension Reduction Techniques for Empirical Data Exploration”
 - *Psychology Diplom Cand.*

RESEARCH EXPERIENCE

- Jul 2021-present **ICAHN SCHOOL OF MEDICINE AT MOUNT SINAI** New York, USA
Adjunct Assistant Professor, Department of Genetics and Genomic Sciences
- Apr 2021-present **HASSO PLATTNER INSTITUTE FOR DIGITAL ENGINEERING & UNIVERSITY OF POTSDAM** Potsdam, Germany
Senior Researcher, Head of Digital Intervention Analytics Lab in the Digital Health - Machine Learning chair
- Build junior research group with focus on tools and methods for digital N-of-1 trials to estimate causal individual-level and population-level effects of health interventions
- Mar 2019-Jun 2021 **ICAHN SCHOOL OF MEDICINE AT MOUNT SINAI** New York, USA
Associate Scientist, Hasso Plattner Institute for Digital Health at Mount Sinai
- Lead the planning and implementation of N-of-1 trials to investigate personalized digital health interventions in a clinical context on low back pain and blood pressure
 - Apply novel statistical and machine learning models in genetic association studies and clinical risk prediction models
- Jan 2019-Mar 2021 **HASSO PLATTNER INSTITUTE FOR DIGITAL ENGINEERING & UNIVERSITY OF POTSDAM** Potsdam, Germany
Postdoctoral Scientist with Prof. Christoph Lippert, Digital Health - Machine Learning chair
- Build a platform to conduct and analyze digital N-of-1 trials, with applications to clinically meaningful use cases
 - Develop novel statistical and machine learning models to analyze N-of-1 trials with complex outcomes
 - Integrate causal inference methods in N-of-1 trials, prediction models, and machine learning models

- Develop and apply new statistical association tests of complex genotypic and phenotypic data using kernel functions and deep learning models
- Evaluate the usefulness of deep learning models for health interventions
- AI expert in the Mittelstand 4.0-Kompetenzzentrum Berlin funded by the BMWi, organizing and conducting introductory and advanced workshops on artificial intelligence for small and medium-sized companies and for other trainers.
- Supervise Master and PhD students

Mar-Dec 2018 **MAX DELBRÜCK CENTER FOR MOLECULAR MEDICINE** Berlin, Germany
Postdoctoral Scientist with Prof. Christoph Lippert, Statistical Genomics Research Group
Postdoctoral Scientist with Prof. Tobias Pischon, Molecular Epidemiology Research Group

- Analyzed genetic, transcriptomic data for associations with obesity traits and Alzheimer's disease
- Developed new kernel-based models integrating omics data for rare variant association studies
- Supervised Master students

Feb-Apr 2016 **MEMORIAL UNIVERSITY OF NEWFOUNDLAND** St. John's, Canada
Visiting Scholar with Prof. Yildiz Yilmaz, Department of Mathematics & Statistics

- Developed a new statistical causal inference approach to investigate direct genetic effects in genetic association studies including multiple phenotypes

Sep 2013-Mar 2018 **MAX DELBRÜCK CENTER FOR MOLECULAR MEDICINE** Berlin, Germany
Research Associate with Prof. Tobias Pischon, Molecular Epidemiology Research Group,
PhD student in the MDC International PhD program

- Designed and conducted genetic and transcriptomic association study with obesity traits based on RNA-Sequencing, PCR, and ELISA assays
- Analyzed whole genome sequence data and gene expression data of the Genetic Analysis Workshop 19 with focus on biological interpretation of joint statistical models
- Developed multivariate and causal inference statistical methods for the integration of multi-level biological data and powerful association tests

Apr 2012-Aug 2013 **SAMUEL LUNENFELD RESEARCH INSTITUTE** Toronto, Canada
Research Associate with Prof. Shelley Bull and Dr. Yildiz Yilmaz, Samuel Lunenfeld Research Institute, Mount Sinai Hospital

- Analyzed whole genome sequence data of the Genetic Analysis Workshop 18 and EDIC study
- Performed simulation study comparing different statistical strategies and developed new approach how to adjust blood pressure for hypertension medication use

Oct 2011- Aug 2013 **UNIVERSITY OF TORONTO** Toronto, Canada
Research Associate in the Statistical Genomics Laboratory of Prof. Rafal Kustra, Department of Public Health Sciences

- Investigated dimension reduction methods for disease risk prediction
- Conducted data analysis in epigenetic study of the effect of different drug treatments on methylation expression levels at the Centre of Addiction and Mental Health (CAMH), Toronto

Apr-Aug 2007 **UNIVERSITY OF HEIDELBERG** Heidelberg, Germany
Research Assistant and Teaching Assistant in the Division of Health Psychology

Aug-Sep 2006 **MAX-PLANCK-INSTITUTE FOR HUMAN DEVELOPMENT** Berlin, Germany
Internship in the Division Adaptive Behavior and Cognition

- Planned and conducted study on the use of probability statements in judgment and decision making

ADDITIONAL EXPERIENCE

May 2019-present **HEALTH INNOVATIONS . AI UG (HAFTUNGSBESCHRÄNKT)** Berlin, Germany
Co-Founder and CEO

- Consulting companies in statistics, artificial intelligence and digital health

- Jun 2013-present **INDEPENDENT STATISTICAL CONSULTANT**
- Consulting for statistical analyses, study design planning, SAS/SPSS/AMOS programming, and for university courses and Master/PhD theses, for individuals and organizations
- Mar-Jul 2009 **HEIDELBERGER LEBENSVERSICHERUNG [LIFE INSURANCE]** Heidelberg, Germany
(LLOYDS BANKING GROUP)
Internship & Working Student in the Division Actuarial Reporting
- Performed data analysis and calculations of insurance processes

TEACHING EXPERIENCE

HASSO PLATTNER INSTITUTE FOR DIGITAL ENGINEERING & UNIVERSITY OF POTSDAM Potsdam, Germany
Lecturer in graduate courses for students in MSc programs Digital Health, Data Engineering, IT Systems Engineering, Data Science

- Master project “Adaptive digital N-of-1 trials for personalizing digital health interventions” (2022)
- “Biostatistics & Epidemiological Data Analysis using R” (2021/22)
- “N-of-1 trials and other modern study designs” (2021/22)
- “Personalized Medicine” (2021)
- “Biostatistics & Epidemiological Data Analysis using R” (2020/21)
- Master project “Digitizing and analyzing historic patient files using Deep Learning” (2020/21)
- Master project “Personalized decision support interventions to promote behavior change for people with low back pain” (2020/21)
- Master project “App-based N-of-1 trials in a clinically-relevant context for personalizing digital health interventions” (2020)
- “Theory and applications of causal inference and causal learning” (2020)
- “Personalized Medicine” (2020)
- “Data Analysis using R – Statistical Epidemiology” (2019/20)
- “Machine Learning for Precision Medicine” (2019)

UNIVERSITY OF POTSDAM & HSE UNIVERSITY (MOSCOW AND SAINT PETERSBURG) Potsdam, Germany
Lecturer in joint summer school “Debating Data. Problems and Perspectives of Digitalization” in session on

- Interpretable Data Science – Making Sense of Medical Data (2019)

BERLIN SCHOOL OF PUBLIC HEALTH & CHARITÉ UNIVERSITY HOSPITAL Berlin, Germany
Lecturer in graduate courses for students in the MSc/MPH programs Epidemiology and Public Health

- “Statistical data analysis using R” (2019-current)
- “Biostatistics II” (2016-current)
- “Molecular Epidemiology” (2016-current)
- “Statistical data analysis using SPSS” (2016-2018)
- “Multilevel Modeling” (2016)
- “SAS Programming” (2015-2018)
- “Biostatistics I” (2015-2018)

UNIVERSITY OF HEIDELBERG Heidelberg, Germany
Teaching Assistant in graduate course for students in the Diplom Program in Psychology

- “Empirical Practicum” (2007)

SCIENTIFIC GRANTS, AWARDS AND SCHOLARSHIPS

- Contributor in EU-funded Horizon 2020 INTERVENE (International consortium for integrative genomic prediction) consortium (10.4 Mio Euro, 2021-2026)
- Finalist for the Neel award in 29th annual conference of the International Genetic Epidemiology Society (IGES) 2020 in Seoul, South Korea
- Poster award (2nd prize) in 25th annual conference of the International Genetic Epidemiology Society (IGES) 2016 in Toronto, Canada
- GAW19 Travel Award for the Genetic Analysis Workshop 19, 2014, in Vienna, Austria

- Statistical Society of Canada (SSC), Student Travel Award, 2013
- School of Graduate Studies Conference Grant, University of Toronto, 2013
- University of Toronto McLaughlin Centre Training Award, 2012
- GAW18 Travel Award for the Genetic Analysis Workshop 18, 2012, in Stevenson, WA, USA
- Dalla Lana Masters Scholarship, University of Toronto, 2012-2013
- Scholarship from the Baden-Wuerttemberg Foundation for the stay at University of Toronto, 2007-2008
- Poster award (2nd prize) in 11th Congress of Empirical Practica, Department of Psychology, University of Heidelberg, Germany, 2007.

REVIEWING ACTIVITY FOR JOURNALS, CONFERENCES & RESEARCH GRANTS

- AAAI 2021, AAAI 2020, ICML 2019, NeurIPS 2019, NeurIPS 2018, Bioinformatics, Artificial Intelligence in Medicine, PLOS Computational Biology, Genetic Epidemiology, Frontiers in Genetics, ISMB 2020, ISMB/ECCB 2019, PLOS ONE, Diabetologica, Obesity Facts, Endocrine-Related Cancer, Developmental Medicine & Child Neurology
- Carl-Zeiss-Stiftung
- BMBF (Federal Ministry of Education & Research)

MEMBERSHIP AND ACTIVITIES IN SCIENTIFIC ASSOCIATIONS

- Elected Vice Speaker of the working group human genetics of the German Association for Medical Informatics, Biometry and Epidemiology (GMDS) (2019-2022)
- International Genetic Epidemiology Society, American Society of Human Genetics, GMDS

STUDENT THESIS SUPERVISION/ CO-SUPERVISION

- Juliane Schneider, working title “Statistical methods for robust causal effect estimates in standard and adaptive n-of-1 trials” (2021-current, PhD student at HPI)
- Thomas Gärtner working title “Novel methods for time series analysis in ERP systems” (2021-current, PhD student at HPI)
- Svenja Broschag, (2021-current, MSc Epidemiology, Berlin School of Public Health, Charité Berlin)
- Marcel Schmidt, “A comparison of multiple imputation methods for missing values in diagnostic studies” (2021, MSc Epidemiology, Berlin School of Public Health, Charité Berlin)
- Nils Strelow, “Medical study collaboration and analysis platform” (2020-2021, MSc IT Systems Engineering, HPI)
- Lukas Ehrig, “FASDetect – Screening the risk of Fetal Alcohol Spectrum Disorders among ADHD patients” (2020-2021, MSc IT Systems Engineering, HPI)
- Alexander Zenner, “App-based creation of user-centric N-of-1 trials” (2020-2021, MSc IT Systems Engineering, HPI)
- Thomas Gärtner, “Statistical models to estimate causal effects of time-varying exposures on health outcomes in N-of-1 trials” (2020-2021, MSc Digital Health, HPI)
- Dr. Luca Meoli, “Exercise and Metabolism: An N-of-1 trial approach to metabolomics data”, (2020-2021, MSc Epidemiology, Berlin School of Public Health, Charité Berlin)
- Antonia Winne, “Protocol for a series of N-of-1 trials: App-based physical exercise interventions for a chronic low back pain population in Germany” (2020, MSc Digital Health, HPI)
- Pia Rautenstrauch, “seek: sequence annotations in kernel-based tests” (2019-2020, MSc Bioinformatics, University of Tübingen)
- Dr. Jana Sticht, “Genome wide association study (GWAS) of genetic variants in human leukocyte antigen (HLA) genes with autoimmune diseases in the UK Biobank” (2019-2020, MSc Epidemiology, Berlin School of Public Health, Charité Berlin)
- Theresa Hellwig, “Identifikation von Faktoren, die zur Verbesserung der Langzeitprognose bei Patienten mit Lungenkrebs führen” [Identification of factors to improve long-term prognosis of lung cancer patients] (2019-2020, MSc Epidemiology, Berlin School of Public Health, Charité Berlin, received second prize for best Master thesis at the Berlin School of Public Health)

- Julia Fiebig, “Age-period-cohort analysis of cancer risk and mortality” (2018-2019, MSc Epidemiology, Berlin School of Public Health, Charité Berlin)
- Stephanie Pape, “Comparison of the validity of biomarker tests for the differential diagnosis of Creutzfeldt-Jakob disease - a network meta-analysis” (2018-2019, MSc Epidemiology, Berlin School of Public Health, Charité Berlin)
- Dr. Iris Meier, “Infektionsrisiko der latenten Tuberkulose nach Auslandseinsatz bei medizinischem Personal” [Risk of tuberculosis infection of health workers after field assignments overseas] (2017-2019, MSc Epidemiology, Berlin School of Public Health, Charité Berlin)
- Arina Levchaeva, “Aktuelle TB Situation in der Ukraine im Zeitraum 2007-2017: deskriptive Trendanalyse anhand der öffentlich zugänglichen Sekundärdaten” [Current tuberculosis situation in the Ukraine between 2007-2017: descriptive trend analysis based on publicly available secondary data] (2017-2018, MPH Public Health, Berlin School of Public Health, Charité Berlin)
- Nina Sodogé, “Funktionelle Unabhängigkeit als Prädiktor für den Rehabilitationsverlauf in neurologischen Rehabilitationkliniken in der Schweiz [Functional independence as predictor for the rehabilitation progress in neurological rehabilitation centers in Switzerland]“ (2017-2018, MPH Public Health, Berlin School of Public Health, Charité Berlin)
- Eugenia Romo Ventura, “Dietary intake of milk and dairy products and blood concentrations of insulin-like growth factor 1 (IGF-I)” (2016-2017, MSc Epidemiology, Berlin School of Public Health, Charité Berlin)

SOFTWARE

- Zenner AM, Böttinger E, **Konigorski S** (2021). StudyMe Health. <https://play.google.com/store/apps/details?id=health.studyu.me>
- Zenner AM, Strelow N, Ruether FD, Henschel F, Manaswini M, Pottbäcker F, Wernicke S, Slosarek T, Böttinger E, **Konigorski S** (2020). StudyU Health. <https://github.com/hpi-studyu/studyu>, <https://hpi.de/lippert/projects/studyu> <https://play.google.com/store/apps/details?id=health.studyu.app> <https://apps.apple.com/us/app/studyu-health/id1571991198>
- Scordialo N, Fiedler T, Wiemker V, **Konigorski S**, Probst C (2020). AAA: Animated alcohol assessment tool.
- Wieck A, Michaelis M, Danieletto M, **Konigorski S** (2020). No1: Evaluation of personalized health interventions through N-of-1 trials.
- Rautenstrauch P, Monti R, **Konigorski S**, Lippert C (2020). seak: sequence annotations in kernel-based tests. <https://github.com/HealthML/seak>.
- **Konigorski S**, Yilmaz YE. CJAMP: Copula-based joint analysis of multiple phenotypes. *R package version 0.1.1*. <https://CRAN.R-project.org/package=CJAMP>.
- **Konigorski S**, Yilmaz YE. CIEE: Estimating and testing direct effects in directed acyclic graphs using estimating equations. *R package version 0.1.1*. <https://CRAN.R-project.org/package=CIEE>.

PUBLICATION LIST – PEER-REVIEWED JOURNAL ARTICLES

- Rübsamen N, Pape S, **Konigorski S**, Zapf A, Rücker G, Karch A (2022). Diagnostic accuracy of cerebrospinal fluid and blood biomarkers for the differential diagnosis of sporadic Creutzfeldt-Jakob disease in a specialized care setting: a systematic review and (network) meta-analysis. *European Journal of Neurology*. <https://doi.org/10.1111/ene.15258>
- Wiemker V, Bunova A, Rastogi A, Neufeld M, Ferreira-Borges C, **Konigorski S**, Probst C (2022). Digital assessment tools using animation features to quantify alcohol consumption: a systematic review. *To appear in JMIR*.
- Wiemker V, Bunova A, Neufeld M, Gornyi B, Yurasova E, **Konigorski S**, Kalinina A, Kontsevaya A, Ferreira-Borges C, Probst C (2022). Pilot study to evaluate usability and acceptability of the ‘Animated Alcohol Assessment Tool’ (AAA-Tool) in Russian primary healthcare. *To appear in Digital Health*. DOI: 10.1177/20552076221074491

- Klinger JE, Ravarani CHJ, Baukman HA, Cope JL, Böttinger EP, **Konigorski S**, Schmidt MF (2021). Interaction-based feature selection algorithm outperforms polygenic risk score in predicting Parkinson's Disease status. *Frontiers in Genetics* **12**: 744557. <https://doi.org/10.3389/fgene.2021.744557>.
- Fehr J, **Konigorski S**, Olivier S, et al. (2021). Computer-aided interpretation of chest radiography reveals the spectrum of tuberculosis in rural South Africa. *npj Digital Medicine* **4**: 106. <https://doi.org/10.1038/s41746-021-00471-y>.
- Rüdiger S, **Konigorski S**, Edelman J, Zernick D, Thieme A, Lippert C (2020). Predicting the SARS-CoV-2 effective reproduction number using bulk contact data from mobile phones. *PNAS* **118(31)**: e2026731118. <https://doi.org/10.1073/pnas.2026731118>.
- Sticht J, Álvaro-Benito M, **Konigorski S** (2021). Type 1 diabetes and the HLA-region: Genetic association besides classical HLA class II genes in UK Biobank whole exome sequencing data. *Frontiers in Genetics* **12**: 1044. <https://doi.org/10.3389/fgene.2021.683946>.
- **Konigorski S** (2021). Causal inference in developmental medicine and neurology. *Developmental Medicine & Child Neurology* **63(5)**: 498. <https://doi.org/10.1111/dmcn.14813>.
- Wilkinson J, Arnold K, Murray EJ, van Smeden M, Carr K, Sippy R, de Kamps M, Beam A, **Konigorski S**, Lippert C, Gilthorpe M, Tennant P (2020). It is time to reality check the promises of machine learning-powered precision medicine. *The Lancet Digital Health* **2**: e677–80. [https://doi.org/10.1016/S2589-7500\(20\)30200-4](https://doi.org/10.1016/S2589-7500(20)30200-4).
- Piccininni M, **Konigorski S**, Rohmann JL, Kurth T (2020). Directed Acyclic Graphs and causal thinking in clinical risk prediction modeling. *BMC Medical Research Methodology* **20**: 179. <https://doi.org/10.1186/s12874-020-01058-z>.
- **Konigorski S**, Yilmaz YE, Janke J, Bergmann MM, Boeing H, Pischon T (2020). Powerful rare variant association testing in a copula-based joint analysis of multiple traits. *Genetic Epidemiology* **44**: 26–40. <https://doi.org/10.1002/gepi.22265>.
- Meier I, Schablon A, Nienhaus A, **Konigorski S** (2020). Latente Tuberkulose bei medizinischem Personal in Deutschland nach Auslandseinsatz [Latent tuberculosis infection among healthcare staff in Germany after assignments abroad]. *Pneumologie* **74**: 1–7. <https://doi.org/10.1055/a-1127-9537>.
- **Konigorski S**, Janke J, Drogan D, Bergmann MM, Hierholzer J, Kaaks R, Boeing H, Pischon T (2019). Prediction of circulating adipokine levels based on body fat compartments and adipose tissue gene expression. *Obesity Facts* **12**: 590–605. <https://doi.org/10.1159/000502117>.
- Romo Ventura E, **Konigorski S**, Rohmann S, Schneider H, Stalla GK, Pischon T, Linseisen J, Nimptsch K (2019). Association of dietary intake of milk and dairy products with blood concentrations of insulin-like growth factor 1 (IGF-I) in Bavarian adults. *European Journal of Nutrition* **59**: 1413–1420. <https://doi.org/10.1007/s00394-019-01994-7>.
- Nimptsch K, **Konigorski S**, Pischon T (2019). Diagnosis of obesity and use of obesity biomarkers in science and clinical medicine. *Metabolism: Clinical and Experimental* **92**: 61-70. <https://doi.org/10.1016/j.metabol.2018.12.006>.
- Jaeschke L, Steinbrecher A, Jeran S, **Konigorski S**, Pischon T (2018). Variability and reliability study of overall physical activity and activity intensity levels using 24h-accelerometry-assessed data. *BMC Public Health* **18(1)**: 530. <https://doi.org/10.1186/s12889-018-5415-8>.
- **Konigorski S**, Wang Y, Cigsar C, Yilmaz YE (2018). Estimating and testing direct genetic effects in directed acyclic graphs using estimating equations. *Genetic Epidemiology* **42**: 174–186. <https://doi.org/10.1002/gepi.22107>.
- **Konigorski S**, Yilmaz YE, Pischon T (2017). Comparison of single-marker and multi-marker tests in rare variant association studies of quantitative traits. *PLoS One* **12(5)**: e0178504. <https://doi.org/10.1371/journal.pone.0178504>.
- Schillert A*, **Konigorski S*** (2016). Joint analysis of multiple phenotypes - summary of results and discussions from the Genetic Analysis Workshop 19. *BMC Genetics* **17(Suppl 2)**:7. (*contributed equally). <https://doi.org/10.1186/s12863-015-0317-6>.

- Koch SC, **Konigorski S**, Sieverding M (2014). Sexist behavior undermines women's performance in a job application situation. *Sex Roles* **70(3-4)**: 79-87. <https://doi.org/10.1007/s11199-014-0342-3>.

PUBLICATION LIST – PEER-REVIEWED CONFERENCE ARTICLES & CONTRIBUTIONS

- **Konigorski S** (2020). Incorporating electronic health record data in N-of-1 trials. <https://dx.doi.org/10.3205/20gmds332>. [Abstract]
- Kirchler M, **Konigorski S**, Schurmann C, Norden M, Meltendorf C, Kloft M, Lippert C (2020). transferGWAS: GWAS of images using deep transfer learning. In: Machine Learning for Health (ML4H) Workshop at NeurIPS 2020 [Abstract]
- **Konigorski S**, Monti R, Rautenstrauch P, Lippert C (2020). Fast kernel-based rare-variant association tests integrating variant annotations from deep learning. In: The 2020 Annual Meeting of the International Genetic Epidemiology Society. *Genetic Epidemiology* **44(5)**: 495. <https://doi.org/10.1002/gepi.22298>. [Abstract]
- **Konigorski S**, Monti R, Lippert C (2019). Kernel-based tests integrating variant effect predictions from deep learning for genetic association tests of rare variants. <https://dx.doi.org/10.3205/19gmds067>. [Abstract]
- **Konigorski S**, Khorasani S, Lippert C (2018). Integrating omics and MRI data with kernel-based tests and CNNs to identify rare genetic markers for Alzheimer's disease. In: Machine Learning for Health (ML4H) Workshop at NeurIPS 2018, arXiv:1812.00448. <https://arxiv.org/abs/1812.00448>.
- **Konigorski S**, Lippert C (2018). Kernel-based tests for very rare variants. In: The 2018 Annual Meeting of the International Genetic Epidemiology Society. *Genetic Epidemiology* **42(7)**: 711. <https://doi.org/10.1002/gepi.22163>. [Abstract]
- **Konigorski S**, Janke J, Drohan D, et al. (2018). Prediction of circulating adipokine levels by body fat compartments and adipose tissue gene expression. *Revue d'Épidémiologie et de Santé Publique* **66(5)**: S353. <https://doi.org/10.1016/j.respe.2018.05.318>. [Abstract]
- **Konigorski S**, Yilmaz YE, Pischon T (2016). Genetic association analysis based on a joint model of gene expression and blood pressure. *BMC Proceedings* **10(Suppl 7)**: 289-294. <https://doi.org/10.1186/s12919-016-0045-6>.
- **Konigorski S**, Wang Y, Cigsar C, Yilmaz YE (2016). Estimating and testing direct genetic effects in directed acyclic graphs with multiple phenotypes using estimating equations. In: The 2016 Annual Meeting of the International Genetic Epidemiology Society. *Genetic Epidemiology* **40**: 609–674. <https://doi.org/10.1002/gepi.22001>. [Abstract]
- **Konigorski S***, Yilmaz YE*, Bull SB (2014). Bivariate genetic association analysis of systolic and diastolic blood pressure by copula models. *BMC Proceedings* **8(Suppl 1)**: S72. (*contributed equally). <https://doi.org/10.1186/1753-6561-8-S1-S72>.
- **Konigorski S**, Kustra R (2012). Sparse principal component regression as a tool to detect causal regions in genetic studies. In: Abstracts from the annual meeting of the International Genetic Epidemiology Society. *Genetic Epidemiology* **36**: 720–777. <https://doi.org/10.1002/gepi.21677>. [Abstract]

PUBLICATION LIST – PREPRINTS

- Kirchler M, **Konigorski S**, Norden M, Meltendorf C, Kloft M, Schurmann C, Lippert C (2021). transferGWAS: GWAS of images using deep transfer learning. *bioRxiv* 2021.10.22.465430. <https://doi.org/10.1101/2021.10.22.465430>.
- Zenner AM, Böttinger E, **Konigorski S** (2021). StudyMe: a new mobile app for user-centric N-of-1 Trials. *arXiv:2108.00320*. <http://arxiv.org/abs/2108.00320>.
- Klinger JE, Ravarani CNJ, Baukman HA, Cope JL, Böttinger EP, **Konigorski S**, Schmidt MF (2021). Interaction-based feature selection algorithm outperforms polygenic risk score in

predicting Parkinson's Disease status. *medRxiv* 2021.07.20.21260848. <https://doi.org/10.1101/2021.07.20.21260848>.

- Monti R, Rautenstrauch P, Ghanbari M, James AR, Ohler U*, **Konigorski S***, Lippert C* (2021). Identifying interpretable gene-biomarker associations with functionally informed kernel-based tests in 190,000 exomes. *bioRxiv* 2021.05.27.444972. <https://doi.org/10.1101/2021.05.27.444972>.
- RübSamen N, Pape S, **Konigorski S**, Zapf A, Rucker G, Karch A (2021). Diagnostic accuracy of cerebrospinal fluid and blood biomarkers for the differential diagnosis of sporadic Creutzfeldt-Jakob disease in a specialized care setting: a systematic review and (network) meta-analysis. *medRxiv* 2021.03.25.21254312. <https://doi.org/10.1101/2021.03.25.21254312>.
- **Konigorski S**, Wernicke S, Slosarek T, Zenner AM, Strelow N, Ruether FD, Henschel F, Manaswini M, Pottbäcker F, Edelman JA, Owoyele B, Danieletto M, Golden E, Zweig M, Nadkarni G, Böttinger E (2020). StudyU: a platform for designing and conducting innovative digital N-of-1 trials. *arXiv*:2012.14201. <https://arxiv.org/abs/2012.14201>.
- Fehr J, **Konigorski S**, Olivier S, et al. (2020). Computer-aided interpretation of chest radiography to detect TB in rural South Africa. *medRxiv*:2020.09.04.20188045. <https://doi.org/10.1101/2020.09.04.20188045>. (now published in *npj Digital Medicine*, see above)
- Rüdiger S, **Konigorski S**, Edelman J, Zernick D, Thieme A, Lippert C (2020). Forecasting the SARS-CoV-2 effective reproduction number using bulk contact data from mobile phones. *medRxiv*:2020.10.02.20188136. <https://doi.org/10.1101/2020.10.02.20188136> (now published in PNAS, see above)
- Piccininni M, **Konigorski S**, Rohmann JL, Kurth T (2020). Directed Acyclic Graphs and causal thinking in clinical risk prediction modeling. *arXiv*:2002.09414. <https://arxiv.org/abs/2002.09414>. (now published in *BMC Medical Research Methodology*, see above)

PUBLICATION LIST – PEER-REVIEWED BOOK CHAPTERS

- **Konigorski S**, Glicksberg BS (2021). *Using C-JAMP to investigate epistasis and pleiotropy*. In: Wong KC (eds) *Epistasis. Methods in Molecular Biology*, vol 2212. Springer, New York, NY. <https://doi.org/10.1007/978-1-0716-0947-7>.
- Fehr J, **Konigorski S**, Lippert C (2020). *Data Science für Digitale Medizin. [Data science for digital medicine]*. In: Matusiewicz D, Henningsen M, Ehlers J (eds). *Digitale Medizin – Kompendium für Studium und Praxis. [Digital Medicine – A textbook for students and professionals]*. Medizinisch Wissenschaftliche Verlagsgesellschaft, Berlin. <https://www.mwv-berlin.de/produkte/!/title/digitale-medizin/id/673>.
- Fehr J, **Konigorski S**, Lippert C. (2020) *Bias and Fairness*. In: DEL7.3: Data and artificial intelligence assessment methods (DAISAM) reference, FG-AI4H-I-035, Geneva, Switzerland.

PUBLICATION LIST – THESES

- **Konigorski S** (2018). *Development and application of new statistical methods for the analysis of multiple phenotypes to investigate genetic associations with cardiometabolic traits*. PhD Thesis. Humboldt-Universität zu Berlin, Mathematisch-Naturwissenschaftliche Fakultät. <http://dx.doi.org/10.18452/19132>.
- **Konigorski S** (2011). *A study of dimension reduction techniques for empirical data exploration*. Diplom Thesis. Ruprecht-Karls-Universität Heidelberg, Fakultät für Mathematik und Informatik.

LIST OF SCIENTIFIC PRESENTATIONS

- Konigorski S (2022). *AI for an automated digital health intervention app*. Invited talk at the AIDHeal Symposium in Berlin, Germany (virtual seminar).

- Konigorski S (2021). *Causal inference in clinical risk prediction models*. Invited talk at the biotx Beyond seminar series in Berlin, Germany (virtual seminar). <https://www.youtube.com/watch?v=PjcTkACoC18>
- Konigorski S (2021). *Digital N-of-1 trials – Connecting personalized medicine & population-level studies?*. Invited talk at the Berlin Epidemiological Methods Colloquium in Berlin, Germany (virtual seminar). <https://www.youtube.com/watch?v=KaGearXQkI>
- Konigorski S (2021). *Digital N-of-1 trials using the StudyU platform*. Invited talk at the ‘Versorgungsforschung in Brandenburg’ [Health services research in Brandenburg] Colloquium at the Medizinische Hochschule Brandenburg in Berlin, Germany (virtual seminar).
- Konigorski S (2020). *Personalizing health interventions using a platform for digital N-of-1 trials*. Invited talk at the HPI Colloquium in Potsdam, Germany (virtual seminar).
- Konigorski S (2020). *Incorporating electronic health record data in N-of-1 trials*. Accepted poster at joint conference of the GMDS & CEN-IBS 2020 in Berlin, Germany (virtual conference).
- Konigorski S, Piccininni M, Rohmann J, Kurth T (2020). *Improving clinical risk prediction models through causal inference*. Accepted talk at the 30th International Biometric Conference (IBC) 2020 in Seoul, South Korea (virtual conference).
- Konigorski S (2020). *Incorporating electronic health records in N-of-1 trials*. Accepted poster at the 30th International Biometric Conference (IBC) 2020 in Seoul, South Korea (virtual conference).
- Konigorski S, Monti R, Rautenstrauch P, Lippert C (2020). *Fast Kernel-based Rare-Variant Association Tests Integrating Variant Annotations from Deep Learning*. Talk given (finalist for Neel award) at the 31st annual conference of the International Genetic Epidemiology Society (IGES) 2020 in Seoul, South Korea (virtual conference).
- Konigorski S (2020). *Einführung in Künstliche Intelligenz und Anwendungspotenziale für KMUs. [Introduction to AI and the potential of applications for SMEs]*. Invited talk to the research committee of the Chamber of Commerce and Industry [Industrie- und Handelskammer] in Gera, Germany.
- Konigorski S (2020). *N-of-1 trials: an old concept for modern clinical studies?* Invited talk in the Epidemiologie Seminar [epidemiology seminar] at the University of Münster, Germany.
- Konigorski S (2020). *KI-Erweiterung der Kompetenzzentren Mittelstand 4.0 [AI-Extension of the competence centers of the initiative „Mittelstand 4.0“]*. Invited talk at the Social-AI lecture series at the University of Potsdam, Germany.
- Konigorski S (2019). *N-of-1 trials for personalized medicine and to evaluate treatments*. Invited keynote talk at the Expert Forum on “AI in Minimally Invasive Surgery & Treatment” of the UK Science and Innovation Network (SIN), 2019, Berlin, Germany.
- Konigorski S (2019). *N-of-1 trials for personalized medicine*. Invited talk at the 4th Future Medicine Conference, 2019, Berlin, Germany.
- Konigorski S, Monti R, Lippert C (2019). *Kernel-based tests integrating variant effect predictions from deep learning for genetic association tests of rare variants*. Talk given in the 64th annual conference of the German Association for Medical Informatics, Biometry and Epidemiology (GMDS), 2019, Dortmund, Germany.
- Konigorski S (2019). *Integrating omics data with kernel-based tests in genetic association studies of rare variants*. Talk given in the workshop “Biometrische Aspekte der Genomanalyse VIII” of the GMDS, the DGEpi and the IBS-DR, 2019, Lübeck, Germany.
- Konigorski S (2018). *Using RNA-Seq, copulas and Mendelian randomization to investigate obesity biology*. Invited Talk at Lady Davis Research Institute, Jewish General Hospital and McGill University in Montréal, Canada.
- Konigorski S, Khorasani S, Lippert C (2018). *Integrating omics and MRI data with kernel-based tests and CNNs to identify rare genetic markers for Alzheimer's disease*. Paper presented at the ML4H (Machine Learning for Health) workshop at the 32nd Conference on Neural Information Processing Systems 2018 in Montréal, Canada.

- Konigorski S, Lippert C (2018). *Kernel-based tests for very rare variants*. Poster presented at the 27th annual conference of the International Genetic Epidemiology Society (IGES) 2016 in San Diego, USA.
- Konigorski S, Janke J, Patone G, et al. (2018). *Identification of novel genes whose expression in adipose tissue is causally associated with obesity traits*. Poster presented at the 68th annual meeting of the American Society of Human Genetics (ASHG) 2018 in San Diego, USA.
- Konigorski S, Janke J, Drohan D, et al. (2018). *Prediction of circulating adipokine levels by body fat compartments and adipose tissue gene expression*. Poster presented at the European Congress of Epidemiology “Crises, epidemiological transitions and the role of epidemiologists” in Lyon, France.
- Konigorski S. (2017). *Prediction of circulating adipokine levels based on body fat compartments and adipose tissue gene expression*. Invited talk in the epidemiology seminar in the German Institute of Human Nutrition Potsdam-Rehbrücke, Nuthetal, Germany.
- Konigorski S, Wang Y, Cigsar C, Yilmaz YE (2017). *Inferring direct genetic effects using the estimating equations method*. Talk given at the Herbstworkshop 2017 “Statistical Models for Prediction and Causal Inference” organized by DGEpi, GMDS, IBS-DR in Braunschweig, Germany.
- Konigorski S. (2016). *Methods for genetic association studies with multiple phenotypes*. Invited talk in the pharmacogenomics seminar in the Centre for Addiction and Mental Health (CAMH) in Toronto, Canada.
- Konigorski S, Wang Y, Cigsar C, Yilmaz YE (2016). *Estimating and testing direct genetic effects in directed acyclic graphs with multiple phenotypes using estimating equations*. Poster presented at the 25th annual conference of the International Genetic Epidemiology Society (IGES) 2016 in Toronto, Canada.
- Konigorski S, Yilmaz YE, Pischon T (2016). *Single-marker tests using a new joint modeling approach of multiple traits outperform current single- and multi-marker tests in rare variant association studies*. Poster presented at the 66th annual meeting of the American Society of Human Genetics (ASHG) 2016, Vancouver, Canada.
- Konigorski S, Yilmaz YE, Pischon T (2016). *A comparison of association tests for the analysis of rare genetic variants*. Poster presented at the FMP/MDC retreat 2016, Berlin, Germany.
- Konigorski S (2016). *Association analysis of rare genetic variants with multiple traits*. Talk given in the Wollenberger Seminar, Max-Delbrück-Center for Molecular Medicine in the Helmholtz Association, Berlin, Germany.
- Konigorski S, Yilmaz YE, Pischon T (2015). *Multivariate Modelle mit Copula Funktionen zur Integration von biologischen Daten für genetische Assoziationsstudien* [Multivariate models based on copula functions to integrate biological data for genetic association studies]. Poster presented at the 10th Annual Meeting of the German Society for Epidemiology (DGepi), 2015, Potsdam, Germany.
- Konigorski S, Yilmaz YE, Pischon T (2015). *C-JAMP (Copula-based Joint Analysis of Multiple Phenotypes): A joint statistical model integrating multi-level biological data for genetic association analysis based on copula functions*. Talk given at the 8th conference of the Eastern Mediterranean Region of the International Biometric Society (EMR-IBS), 2015, Nevsehir, Turkey.
- Konigorski S, Yilmaz YE, Pischon T (2015). *A joint statistical model integrating multi-level biological data for genetic association analysis*. Talk given in the workshop “Biometrische Aspekte der Genomanalyse VI” [Biometrical aspects of genome analysis VI] of the GMDS, the DGEpi and the IBS-DR, 2015, Heidelberg, Germany.
- Konigorski S, Yilmaz YE, Pischon T (2014). *Genetic association analysis based on a joint model of gene expression and blood pressure*. Paper and Poster presented at the Genetic Analysis Workshop 19, 2014, in Vienna, Austria.
- Konigorski S (2013). *Epigenetic measures*. Tutorial given in the course “Advanced topics in genome-wide association (GWA) studies” at the Ontario Institute for Cancer Research, Toronto, Canada.

- Konigorski S, Yilmaz YE, Bull SB (2013). *A censored regression method to adjust for medication effects in genetic analysis of a quantitative trait when the treatment received depends on the trait*. Talk given at the 41st Annual Meeting of the Statistical Society of Canada, 2013, in Edmonton, AB, Canada.
- Chen S, Konigorski S, Lin D, Lu Z, Teterina A (2013). *Spatial and temporal variations of noise levels in Toronto*. Poster presented at the 41st Annual Meeting of the Statistical Society of Canada, 2013, in Edmonton, AB, Canada.
- Konigorski S, Kustra R (2012). *Sparse principal component regression as a tool to detect causal regions in genetic studies*. Poster presented at the 21st annual conference of the International Genetic Epidemiology Society (IGES) 2012 in Stevenson, WA, USA.
- Konigorski S, Yilmaz YE, Bull SB (2012). *Bivariate genetic association analysis of systolic and diastolic blood pressure by copula models*. Paper and Poster presented at the Genetic Analysis Workshop 18, 2012, in Stevenson, WA, USA.
- Konigorski S, Kustra R (2012). *Detecting causal loci regions in genetic studies with sparse PCA*. Poster presented at the Canadian Human and Statistical Genetics Meeting 2012, Niagara-on-the-Lake, ON, Canada.
- Konigorski S, Shim G, Weisang S (2007). *An intercultural comparison of Germany, Japan, Korea on subjective well-being and fear of death*. Poster presented at the 11th Congress of Empirical Practica, Department of Psychology, University of Heidelberg, Germany.

REFERENCES AVAILABLE UPON REQUEST.