

Curriculum Vitae



Personal Data

Title	Dr. rer. nat.
First name	Matthias
Name	König
Current position	DFG own position QuaLiPerF, fixed-term contract until 11-2025
Current institution(s)/site(s), country	Humboldt-Universität zu Berlin, Faculty of Life Science, Institute for Biology, Institute for Theoretical Biology, Systems Medicine of the Liver Lab, Germany, https://livermetabolism.com
Identifiers	Google Scholar , Orcid , GitHub , Linkedin , ResearchGate

Qualifications and Career

Stages	Periods and Details
Degree programme	Studies of Biophysics, 2002-2008, Humboldt-Universität zu Berlin (HepatoSys, Virtual Liver), Germany
Doctorate	2015 PhD in Biophysics, Humboldt-Universität zu Berlin, Germany. Title: Computational modeling of glucose metabolism. Supervisor: Prof. Hermann-Georg Holzhütter (Charité Berlin)
Stages of academic/professional career	2021 – 2025: DFG Eigene Stelle Systems Medicine of the Liver, Faculty of Life Science, Institute for Theoretical Biology, Humboldt-Universität zu Berlin, Germany 2024 – 2025: Digital Health Professions Educator (DHPE): Charité Berlin 2016 – 2021: Junior group leader, LiSyM - Systems medicine of the liver (BMBF), Faculty of Life Science, Institute for Theoretical Biology, Humboldt-Universität zu Berlin, Germany 2008 – 2015: Scientific staff member, Institute of Biochemistry, Computational Systems Biochemistry, Charité University Hospital Berlin

Supplementary Career Information

Married, 1 child

Activities in the Research System

- 2024 – 2025 **Open Science Ambassador**, Berlin University Alliance at Humboldt-University Berlin, Faculty of Life Science
- 2024 – 2027 **Elected SED-ML editor**, Simulation Experiment Description Markup Language (SED-ML) a format for simulation setups, to ensure exchangeability and reproducibility of simulation experiments. [URL](#)
- 2023 – 2026 **Elected PEtab editor**, PEtab – a data format for specifying parameter estimation problems in systems biology. [URL](#)
- 2023 **X-Student Research Group**: Physiologically based digital twins for the treatment of hypertension with ACE inhibitors and diuretics. [URL](#)
- 2023 – 2024 **PharmVar CYP1A2 gene expert panel member** (Pharmacogene Variation Consortium). [URL](#)
- 2022 **Organizer of the 13th Computational Modeling in Biology Network (COMBINE) meeting** in Berlin. [URL](#)
- 2022 **X-Student Research Group**: Physiologically based modeling of drugs: ACE inhibitors in the treatment of high blood pressure. [URL](#)
- 2021 – 2023 **Elected SBML editor**, Systems Biology Markup Language (SBML), SBML is a software data format for describing models in biology. [URL](#)
- 2020 – 2022 **Elected SED-ML editor**. [URL](#)
- 2018 – 2020 **Elected SBML editor**. [URL](#)
- 2017 – 2019 **Elected SED-ML editor**. [URL](#)
- 2017 – 2024 **Elected COMBINE coordinator**, the COmputational Modeling in Biology NEtwork (COMBINE) is an initiative to coordinate the development of the various community standards and formats for computational models. [URL](#)

Supervision of Researchers in Early Career Phases

Over the last 5 years, 1 PhD theses, 2 Master thesis, 8 Bachelor's theses, 15 Humboldt-Internship students (HIC), and 4 Google Summer of Code (GSOC) students have been supervised. I am currently supervising 2 PhD, 1 Master, 3 Bachelor and 3 Internship projects ([group members](#)).

Bachelor (2025, [PDF](#)), Y.A. Kulanoglu, Physiologically based pharmacokinetic/pharmacodynamic modeling of the direct renin inhibitor aliskiren: Exploring the impact of hepatorenal impairment and drug-drug interactions.

Master (2024, [PDF](#)), J. Küttner, Quantitative image analysis of hepatic zonation in cytochrome P450 and steatosis using whole slide scans.

Master (2024, [PDF](#)), S. Palwankar, Enhancing Our Understanding of Enalapril's Pharmacokinetics: A Physiologically Based Modeling Approach.

Bachelor (2024, [PDE](#)), A. Hossain, A systematic overview of protein variability in CYP and UGT in the human liver.

Bachelor (2023, [PDF](#)), B. Stemmer Mallol, A physiologically based pharmacokinetic (PBPK) model of the probe drug talinolol.

PhD (2023, [PDF](#)), J. Grzegorzewski, Physiologically based pharmacokinetic (PBPK) modeling for dynamical liver function tests and CYP phenotyping.

Bachelor (2022, [PDE](#)), H. Pujol, A physiologically based model of pravastatin - The role of genotypes and hepatic or renal impairment on the pharmacokinetics of pravastatin.

Bachelor (2021, [PDF](#)), S. Balci, Computational modelling of omeprazole - pharmacokinetics and pharmacodynamics.

Bachelor (2021, [PDF](#)), A. Köller, A physiologically based model of indocyanine green liver function tests - Effects of physiological factors, hepatic disease and hepatic surgery.

Bachelor (2020, [PDF](#)), F. Bartsch, Computational Modelling of Simvastatin - Effects on HMG-CoA Reductase Activity and Cholesterol.

Bachelor (2020, [PDF](#)), Y. Duport, Computational Modelling of Midazolam Clearance: Effect of Inhibitors and Inducers.

Scientific Results

Category A (ten selected publications, total: 69, HF 24, [Google Scholar](#) 02/25)

1. König M, Bulik S, Holzhütter HG (2012). *Quantifying the Contribution of the Liver to the Homeostasis of Plasma Glucose: A Detailed Kinetic Model of Hepatic Glucose Metabolism Integrated with the Hormonal Control by Insulin, Glucagon and Epinephrine*; PLoS Comput Biol. 2012 Jun;8(6). doi: [10.1371/journal.pcbi.1002577](https://doi.org/10.1371/journal.pcbi.1002577) (IF: 4.0)
2. Berndt N, Bulik S, Wünsch T, König M, Stockmann M, Meierhofer D, Holzhütter HG (2018). *HEPATOKIN1 is a biochemistry-based model of liver metabolism for applications in medicine and pharmacology*. Nat Commun. 2018 Jun 19;9(1):2386. doi: [10.1038/s41467-018-04720-9](https://doi.org/10.1038/s41467-018-04720-9). (IF: 15.4)
3. Gille C, Bölling C, Hoppe A, Bulik S, Hoffmann S, Hübner K, Karlstädt A, Ganeshan R, König M, Rother K, Weidlich M, Behre J, Holzhütter HG. *HepatoNet1: a comprehensive metabolic reconstruction of the human hepatocyte for the analysis of liver physiology*. Mol Syst Biol. 6 (2010), p. 411. doi: [10.1038/msb.2010.62](https://doi.org/10.1038/msb.2010.62) (IF: 8.8)
4. Grzegorzewski J, Brandhorst J, König M. *Physiologically based pharmacokinetic (PBPK) modeling of the role of CYP2D6 polymorphism for metabolic phenotyping with dextromethorphan*. Front Pharmacol. 2022 Oct 24;13:1029073. doi: [10.3389/fphar.2022.1029073](https://doi.org/10.3389/fphar.2022.1029073). (IF: 5.4)
5. Köller A, Grzegorzewski J, Tautenhahn HM, König M. *Prediction of survival after hepatectomy using a physiologically based pharmacokinetic model of indocyanine green liver function tests*. Front. Physiol., 2021 Nov 22. doi: [10.3389/fphys.2021.730418](https://doi.org/10.3389/fphys.2021.730418). (IF: 3.9)
6. Maheshvare MD., Raha S., König M.*, and Pal D.* (* equal contribution). *A pathway model of glucose-stimulated insulin secretion in the pancreatic β-cell*. Front. Endocrinol. 2023 Aug 2. 14:1185656. doi:[10.3389/fendo.2023.1185656](https://doi.org/10.3389/fendo.2023.1185656) (IF: 3.9)
7. Keating SM, Waltemath D, König M, ..., Hucka M, and SBML Community members. *SBML Level 3: an extensible format for the exchange and reuse of biological models*. Mol Syst Biol. 2020;16(8):e9110. doi: [10.15252/msb.20199110](https://doi.org/10.15252/msb.20199110). (IF: 8.8)
8. Somogyi ET, Bouteiller JM, Glazier JM, König M, Medley JK, Swat MH, Sauro HM. *libRoadRunner: a high performance SBML simulation and analysis library*. Bioinformatics 31 (20 2015), pp. 3315–3321. doi: [10.1093/bioinformatics/btv363](https://doi.org/10.1093/bioinformatics/btv363). (IF: 6.0)
9. Grzegorzewski J, Brandhorst J, Green K, Eleftheriadou D, Duport Y, Barthorscht F, Köller A, Ke DYJ, De Angelis S, König M. *PK-DB: pharmacokinetics database for individualized and stratified computational modeling*. Nucleic Acids Res. 2021 Jan 8;49(D1):D1358-D1364. doi: [10.1093/nar/gkaa990](https://doi.org/10.1093/nar/gkaa990). (IF: 14.1)
10. Albadry M, Kuettner J, Grzegorzewski J, Dirsch O, Kindler E, Klopflisch R, Liska V, Moulisova V, Nickel S, Palek R, Rosendorf J, Saalfeld S, Settmacher U, Tautenhahn HM, König M*, U. Dahmen* (*equal contribution). *Cross-Species Variability in Lobular Geometry and Cytochrome P450 Hepatic Zonation: Insights into CYP1A2, CYP2E1, CYP2D6 and CYP3A4*. Front Pharmacol. 2024 May 16;15:1404938. doi:[10.3389/fphar.2024.1404938](https://doi.org/10.3389/fphar.2024.1404938). (IF: 5.4)

For a full list of publications and preprints see: <https://livermetabolism.com/publications/>

Category B (ten selected research outcomes)

1. Preprint: Gerhäuser S, Lambers L, Mandl L, Franquinet J, Ricken T, **König M.** *Simulation of zonation-function relationships in the liver using coupled multiscale models: Application to drug-induced liver injury.* bioRxiv. doi:[10.1101/2024.03.26.586870](https://doi.org/10.1101/2024.03.26.586870)
2. Preprint: Stemmer Mallol B, Grzegorzewski J, **König M.** *Insights into Intestinal P-glycoprotein Function using Talinolol: A PBPK Modeling Approach.* bioRxiv doi: [10.1101/2023.11.21.568168](https://doi.org/10.1101/2023.11.21.568168)
3. Preprint: Küttner J, Grzegorzewski J, Tautenhahn HM, **König M.** *A physiologically based pharmacokinetic model for CYP2E1 phenotyping via chlorzoxazone.* bioRxiv doi: [10.1101/2023.04.12.536571](https://doi.org/10.1101/2023.04.12.536571)
4. Preprint: Bartsch F, Grzegorzewski J, Pujol H, Tautenhahn HM, **König M.** *Simvastatin therapy in different subtypes of hypercholesterolemia - a physiologically based modelling approach.* medRxiv. doi: [10.1101/2023.02.01.23285358](https://doi.org/10.1101/2023.02.01.23285358)
5. Database: *PK-DB: pharmacokinetics database for individualized and stratified computational modeling.* <https://pk-db.com>, described in [10.1093/nar/gkaa990](https://doi.org/10.1093/nar/gkaa990)
6. Software: SBML4Humans - SBML simulation made easy. <https://sbml4humans.de>
7. Software: sbmlutils - Python utilities for SBML. [10.5281/zenodo.597149](https://doi.org/10.5281/zenodo.597149)
8. Software: cysbml - Cytoscape 3 app for SBML. [10.5281/zenodo.597154](https://doi.org/10.5281/zenodo.597154)
9. Software: roadrunner - High-performance simulator for SBML. Contributor to libRoadRunner <https://github.com/sys-bio/roadrunner/>
10. Software: COBRApy - COBRA python package. Contributor to COBRApy <https://github.com/opencobra/cobrapy/>

Academic Distinctions

- 2023 **Michael Stifel Price** to promote interdisciplinary, data-driven research
2015 **Scholarship Google Summer of Code** to develop SBML
2005 **Scholarship Studienstiftung des Deutschen Volkes**

Funding (last five years)

- 2024 – 2025 AlgoNomy - Algorithmic Regulation Before Medical Liability - Advancing Doctor-Patient Autonomy in AI-Driven Healthcare (Circle U. - European University Alliance, 10T€ seed funding)
- 2024 – 2027 SPP2311 - SimLivA - SIMulation supported LIVer Assessment for donor organs (DFG, 219T€)
- 2023 – 2026 AI and Simulation for Tumor Liver Assessment (ATLAS) (BMBF-Project Computational Life Sciences – KI-Methoden für die Systemmedizin, Project number: 031L0304B, 311T€)
- 2023 X-Student Research Group - Physiologically based digital twins for the treatment of hypertension with ACE inhibitors and diuretics (DFG, 1.5T€)
- 2022 X-Student Research Group - Physiologically based modeling of drugs: ACE inhibitors in the treatment of high blood pressure (DFG, 1.5T€)
- 2021 – 2025 FOR5151 - QuaLiPerF - Quantifying Liver Perfusion-Function Relationship in Complex Resection – A Systems Medicine Approach (DFG, 425T€)
- 2021 – 2024 SPP2311 - SimLivA - SIMulation supported LIVer Assessment for donor organs (DFG, co-applicant, no own funding)
- 2020 – 2021 EOSC-Life Reproducible simulation studies for COVID-19 (EU Horizon, 25T€)
- 2016 – 2021 LiSyM – Systems Medicine of the Liver – Junior group, Computational modeling of dynamical liver function tests (BMBF, 723T€)

Participation in academic self-governance

2025	EP PerMed Training on Scientific Integrity (Training). Framed in the EP PerMed strategy to support the research community on Ethical Legal and Social Aspects (ELSA) of personalised medicine, this training action explored critical issues related to scientific integrity in personalised medicine related research, including: most significant guidelines of the European Code of Conduct; key principles of research integrity; crucial procedures of good research practice; the ethical way of disseminating, communicating & exploiting the research results; the Ethics Compliance under Horizon Europe.
2024 – 2025	Digital Health Professions Educator (DHPE) at Charité Berlin. The 'Digital Health Professions Educator' certificate programme is part of the 'HEDS: Digital Strengths for Action and Decision-Making' project. Goals: The further development of one's own teaching and/or that of the institution in the area of future-oriented teaching and learning scenarios. Faculty development in the area of digital teaching in healthcare degree programmes.
2024 – 2025	Open Science Ambassador, Berlin University Alliance (BUA, 4T€) The BUA Open Science Ambassadors were appointed by the deans of the Berlin University Alliance partners at the end of an application process. The 23 ambassadors will campaign for open science standards at the institutions. As ambassador at the Faculty of Life Science I promote reproducible and open science.
2023	Development of Open Science Concept as part of Eleven Strategies for Making Reproducible Research and Open Science Training the Norm at Research Institutions. eLife (2023) 12:e89736. doi: 10.7554/eLife.89736 .

Teaching

04/2024	- Theory, tools and methods in biology
09/2024 Humboldt-Univ ersität zu Berlin (HU)	I led the pharmacokinetic modeling submodule, covering drug distribution, clearance, and elimination, using compartmental and PBPK models. The course included pharmacodynamics, drug interactions, and clinical applications, with materials available at GitHub .
04/2023	- Theory, tools and methods in biology
09/2023 HU	see above
04/2023 09/2023 Berlin University Alliance (BUA)	- X-Student Research Group: Physiologically based digital twins for the treatment of hypertension with ACE inhibitors and diuretics This X-Student Research Group focused on PBPK modeling of hydrochlorothiazide (diuretic) and lisinopril (ACE inhibitor), essential for hypertension treatment. Students explored drug absorption, distribution, metabolism, and elimination (ADME) through lectures, tutorials, and hands-on modeling. Designed for STEM students (biology, computer science, medicine) with basic Python skills, the project provided practical experience in computational pharmacokinetics and interdisciplinary research. With the X-Student Research Groups , the Berlin University Alliance supports research teams consisting of young researchers and students in project based learning. The goal is to involve students in current research projects of the

alliance partners and to enable them to participate in (cutting-edge) research already during their studies.

- 10/2022 – **X-Student Research Group: Physiologically based modeling of drugs: ACE inhibitors in the treatment of high blood pressure**
03/2023 BUA
- Physiological-based pharmacokinetics model of the ACE inhibitors. The models will study the absorption (GI tract), distribution (systemic circulation), metabolism (liver) and elimination (kidneys and liver) of the ACE inhibitors lisinopril and ramipril. Organs and plasma volumes are connected via the blood flow (Q). A key challenge in treating people is to understand the pharmacokinetics of a given drug, i.e., how it is absorbed, distributed, metabolized and eliminated by the body, and the pharmacodynamics of the drug, i.e., how the substance is affecting the body. Physiological-based pharmacokinetics (PBPK) models are computational models which allow the study of the pharmacokinetics and pharmacodynamics of drugs *in silico*. Within this X-Student Research Group we developed together with the students PBPK models of ACE inhibitors. The methodical approach was a combination of lectures, tutorials, and practical work by the students. The research project was aimed at a maximum of 15 students primarily for students with STEM (science, technology, engineering, math) background including biological, informatic and medical students.
- 10/2021 – **Important models of quantitative biology from the literature**
03/2022 HU
- This course discusses, implements and analyzes important models in quantitative biology. The course covers Boolean and ordinary differential equation models from metabolism and signaling.
- 10/2020 – **Important models of quantitative biology from the literature**
03/2021 HU
- see above
- 10/2019 – **Models of cellular processes**
03/2020 HU
- This course introduces, implements and analyzes models of cellular processes. The lecture covers constraint-based models, Boolean models and ordinary differential equation models from metabolism and signaling. Methods such as parameter optimisation, stochastic models and sensitivity analysis are introduced.
- 10/2019 – **Important models of quantitative biology from the literature**
03/2020 HU
- see above
- 10/2018 – **Important models of quantitative biology from the literature**
03/2019 HU
- see above

Matthias König,
Berlin, 28 February 2025

