Curriculum Vitae

Personal Information

Name Michael Baudis

Workplace

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Education

2001–2003 **Postdoctoral Research Fellow**, *Pathology Department*, Stanford University, USA.

2000 **German Medical License**, State of Baden-Württemberg, Germany.

1999 **Doctor of Medicine**, *Faculty of Internal Medicine V*, University of Heidelberg, Germany.

1994–1998 **Research thesis in molecular cytogenetics**, German Cancer Research Center (DKFZ) & University of Heidelberg, Germany.

1992–1998 **Student of Medicine**, University of Heidelberg, Germany.

Employment History

2015–Present **Associate Professor of Bioinformatics**, *Department of Molecular Life Sciences, University of Zurich*, Switzerland.

2007–2015 **Research Group Leader**, *Institute of Molecular Life Sciences, University of Zurich*, Switzerland.

2006–2007 **Research Group Leader**, *Genetics Department*, RWTH Aachen University Hospital, Germany.

2003–2006 **Assistant Professor**, *Pediatric Oncology*, University of Florida, Gainesville, USA.

1998–2000 **Attending Physician**, *Faculty of Internal Medicine V*, University of Heidelberg, Germany.

Faculty positions (offered & rejected)

2013 **Associate Professor, tenured**, *Computational Oncogenomics*, Queens Univ., Kingston, Canada.

2006 **Assistant Professor, tenure track**, *Pediatric Oncology*, University of Florida, Gainesville, USA.

Long-term Research Visits

2020-02/03 Visiting Scientist, Lawrence Berkeley National Laboratory, Berkeley, U.S.A.

2018-04/06 Visiting Scientist & program participant, Kavli Institute for Theoretical Physics at UCSB, Santa Barbara, U.S.A.

Career awards & personal funding

2006–2007 Claussen-Simon-Stiftung career award

2002–2003 Dean's fellowship, Stanford University Medical School

2001–2002 Deutsche Krebshilfe, postdoctoral research stipend

Membership in Panels, Boards & Peer Review Activities

2021	Review board, ERAPerMed Joint Transnational Call 2021
2020–present	Editor in Chief, Frontiers in Genetics "Cancer Genetics and Oncogenomics"
2020–present	Member, Health 2030 Genome Center Science Council, Switzerland
2020	Reviewer, Connect Talent - Pays de la Loire, France
2020–present	Swiss Personalised Health Network (SPHN) expert panel
2019-present	Co-chair, ELIXIR hCNV Community Project
2020	Reviewer, Ontario Institute for Cancer Research Innovation Fund, Canada
2018–present	Global Alliance for Genomics and Health (GA4GH): Co-Chair "Discovery" Work Stream
2018	Vice-Chair, ERAPerMed Joint Transnational Call 2018
2017–present	Global Alliance for Genomics and Health (GA4GH) Steering Committee
2017–2018	Co-chair, GA4GH Genomic Knowledge Standards - Variant Representation
2017–present	Section editor Karger Oncology
2020	Reviewer, Wellcome Trust, United Kingdom
2016–present	Co-chair and representative, ELIXIR Beacon project
2016–2020	Swiss Personalised Health Network (SPHN): Chair WG "Bioinformatics and Data Analytics"; member expert panels
2014–2017	Co-chair, GA4GH Data Working group Metadata Task Team
2014	Reviewer, NC3Rs, United Kingdom
2014	Reviewer, Wellcome Trust, United Kingdom
2013–present	Academic editor PLoS ONE
2013	Reviewer for Fondation Recherche Medicale, France
Reviewer	BBA - Molecular Cell Research, Bioinformatics, BMC Bioinformatics, BMC Cancer, Cancer Epidemiology, Biomarkers and Prevention, Cancer Research, Clinical Cancer Research, Computational and Structural Biotechnology Journal, DATABASE - The Journal of Biological Databases and Curation, ERA-NET ERAPerMed, Experimental and Molecular Pathology, Genes Chromosomes & Cancer, Gynecologic Oncology, Haematologica, JCO Clinical Cancer Informatics, Leukemia, Molecular Oncology, Nature Communications, Nature Genetics, Nature Reports

Active Membership in Scientific Societies & Organisations

2020–present	Cancer Genomics Consortium
2018–present	International Society for Computational Biology (ISCB)
2017–present	UZH Digital Society Initiative (DSI)
2016–present	ELIXIR – European bioinformatics infrastructure network
2015–present	International Society for Biocuration (ISB)
2014–present	Global Alliance for Genomics and Health (GA4GH)
2012–present	Swiss Institute of Bioinformatics (SIB)

Publication Metrics

Web of Science J-4602-2012

Citation Indices, 2021-11-16.

h-index	26
Total Publications	113
Average citations per item	29.8
Sum of Times Cited	2803

Google Scholar qKbjZK4AAAAJ

Citation Indices, 2022-07-19.

	total	since 2017
h-index	33	23
Citations	4648	1956
i10-index	60	41

Recent & Selected Publications & Preprints

Please see the attached bibliography or *info.baudisgroup.org/publications/* for a complete list. Group members are highlighted.

2022 **Candidate targets of copy number deletion events across 17 cancer types.**, ***Huang Q***, ***Baudis M***., *bioRxiv*, **2022 Jun 30**; 2022.06.29.498080.

The GA4GH Phenopacket schema defines a computable representation of clinical data., *Jacobsen JOB*, ***Baudis M***, *Baynam GS, Beckmann JS, Beltran S, Buske OJ, Callahan TJ, Chute CG, Courtot M, Danis D, Elemento O, Essenwanger A, Freimuth RR, Gargano MA, Groza T, Hamosh A, Harris NL, Kaliyaperumal R, Lloyd KCK, Khalifa A, Krawitz PM, Köhler S, Laraway BJ, Lehväslaiho H, Matalonga L, McMurry JA, ..., Haendel MA, Robinson PN, The GAGHPMC.*, *Nature Biotechnology*, **2022**; 40(6):817.

Beacon v2 and Beacon networks: A "lingua franca" for federated data discovery in biomedical genomics, and beyond., *Rambla J*, ***Baudis M***, *Ariosa R, Beck T, Fromont LA, Navarro A*, ***Paloots R***, *Rueda M, Saunders G, Singh B, Spalding JD, Törnroos J, Vasallo C, Veal CD, Brookes AJ.*, *Hum Mutat*, **2022 Mar 17**; :.

2021 **GA4GH: International policies and standards for data sharing across genomic research and healthcare.**, *Rehm HL, Page AJH, Smith L, Adams JB, Alterovitz G, Babb LJ, Barkley MP*, ***Baudis M*** *et al.*, *Cell Genomics*, **2021/11/10 2021**; 1(2).

International federation of genomic medicine databases using GA4GH standards., *Thorogood A, Rehm HL, Goodhand P, Page AJH, Joly Y*, ***Baudis M***, *Rambla J, Navarro A et al.*, *Cell Genomics*, **2021/11/10 2021**; 1(2).

The GA4GH Variation Representation Specification: A computational framework for variation representation and federated identification., *Wagner AH, Babb L, Alterovitz G*, ***Baudis M***, *Brush M, Cameron DL, Cline M, Griffith M, Griffith OL, Hunt SE, Kreda D, Lee JM, Li S, Lopez J, Moyer E, Nelson T, Patel RY, Riehle K, Robinson PN, Rynearson S, Schuilenburg H, Tsukanov K, Walsh B, Konopko M, Rehm HL, Yates AD, Freimuth RR, Hart RK.*, *Cell Genom*, **2021 Nov 10**; 1(2):100027.

Copy number variant heterogeneity among cancer types reflects inconsistent concordance with diagnostic classifications., ***Carrio Cordo P***, ***Baudis M***., *bioRxiv*, **2021 Mar 01**; 2021.03.01.433348.

Signatures of Discriminative Copy Number Aberrations in 31 Cancer Subtypes., ***Gao B***, ***Baudis M***., *Front Genet*, **2021**; 12:654887.

The Progenetix oncogenomic resource in 2021., ***Huang Q***, ***Carrio Cordo P***, ***Gao B***, ***Paloots R***, ***Baudis M***., *DATABASE*, **2021 Jul 17**.

2020 **The ELIXIR Human Copy Number Variations Community: building bioinformatics infrastructure for research.**, *Salgado D, Armean IM*, ***Baudis M***, *et al.*, *F1000Res*, **Oct 13, 2020**.

Geographic assessment of cancer genome profiling studies., ***Carrio Cordo P***, *Acheson E,* ***Huang Q***, ***Baudis M.***, *Database (Oxford)*, **2020 Jan 01**; 2020.

Minimum error calibration and normalization for genomic copy number analysis., ***Gao B***, ***Baudis M.***, *Genomics*, **2020 Sep**; 112(5):3331.

Enabling population assignment from cancer genomes with SNP2pop., ***Huang Q***, ***Baudis M.***, Sci Rep, (**2020**; 10(1):4846.

A harmonized meta-knowledgebase of clinical interpretations of somatic genomic variants in cancer., *Wagner AH, Walsh B, Mayfield G, Tamborero D, ..., Freimuth RR, Haendel M, Raca G, Madhavan S,* ***Baudis M***, *Beckmann JS, Dienstmann R, Chakravarty D, Li XS, Mockus S, Elemento O, Schultz N, Lopez-Bigas N, Lawler M, Goecks J, Griffith M, Griffith OL, Margolin AA; Variant Interpretation for Cancer Consortium.*, NatGen., (**2019**) 2020 Apr;52(4).

2019 **Leveraging European infrastructures to access 1 million human genomes by 2022.**, *Saunders G,* ***Baudis M***, *Becker R, Beltran S, Béroud C, Birney E, Brooksbank C, Brunak S, ..., Parkinson H, Rambla J, Salgado D, Steinfelder E, Swertz MA, Valencia A, Varma S, Blomberg N, Scollen S.*, Nat Rev Genet., (**2019**) , 20, pages 693–701.

Federated discovery and sharing of genomic data using Beacons., *Fiume M, Cupak M, Keenan S, Rambla J, de la Torre S, Dyke SOM, Brookes AJ, Carey K, Lloyd D, Goodhand P, Haeussler M,* ***Baudis M***, *Stockinger H, Dolman L, Lappalainen I, Törnroos J et al.*, Nat Biotechnol, (**2019**).

2018 **Registered access: authorizing data access.**, *Dyke SOM, Linden M, Lappalainen I, De Argila JR, Carey K, Lloyd D, Spalding JD, Cabili MN,..., Rätsch G, Brudno M, Boycott KM, Rehm HL,* ***Baudis M***, *Sherry ST, Kato K, Knoppers BM, Baker D and Flicek P.*, Eur J Hum Genet, (**2018**) 26:1721-1731..

segment_liftover : a Python tool to convert segments between genome assemblies., ***Gao B***, ***Huang Q*** *and* ***Baudis M.***, F1000Res, (**2018**) 7:319..

2017 **Integrated Molecular Meta-Analysis of 1,000 Pediatric High-Grade and Diffuse Intrinsic Pontine Glioma.**, *Mackay A, Burford A, Carvalho D, Izquierdo E, Fazal-Salom J, Taylor KR, Bjerke L, Clarke M, Vinci M, Nandhabalan M, ..., Pfister SM, Jones DTW, Fouladi M,* ***von Bueren AO***, ***Baudis M***, *Resnick A and Jones C.*, Cancer Cell, (**2017**) 32:520-537.e5..

2016 **CNARA: reliability assessment for genomic copy number profiles.**, ***Ai N***, ***Cai H***, *Solovan C and* ***Baudis M.***, BMC Genomics, (**2016**) 17:799..

2015 **arrayMap 2014: an updated cancer genome resource.**, ***Cai H***, ***Gupta S***, ***Rath P***, ***Ai N*** *and* ***Baudis M.***, Nucleic Acids Res, (**2015**) 43:D825-30..

A Biobank Supporting Rare Disease Research In Dermatopathology. Our Experience In Establishing A Biobank., *Beleut M, Seclaman E,* ***Baudis M***, *Nicula A and Solovan C.*, RoJCED, (**2015**) 2:202-206..

2014 **Chromothripsis-like patterns are recurring but heterogeneously distributed features in a survey of 22,347 cancer genome screens.**, ***Cai H***, ***Kumar N***, *Bagheri HC, von Mering C, Robinson MD and* ***Baudis M.***, BMC Genomics, (**2014**) 15:82..

Progenetix: 12 years of oncogenomic data curation., ***Cai H***, ***Kumar N***, ***Ai N***, ***Gupta S***, ***Rath P*** *and* ***Baudis M.***, Nucleic Acids Res, (**2014**) 42:D1055-62..

Selected Reviews

2020 **DNA Copy Number Changes in Diffuse Large B Cell Lymphomas.**, *Cascione L, Aresu L,* ***Baudis M***, *Bertoni F.*, *Front Oncol*, **2020**; 10:584095.

2018 **Mountains and Chasms: Surveying the Oncogenomic Publication Landscape.**, *Carrio-Cordo P,* ***Baudis M.***, *Oncology*, **2018 Oct 26**; 2018:1.

2009 **Translocations involving 8q24 in Burkitt lymphoma and other malignant lymphomas: a historical review of cytogenetics in the light of todays knowledge.**, *Boerma EG, Siebert R, Kluin PM,* ***Baudis M.***, *Leukemia*, **2009 Feb**; 23(2):225.

Online Resources

2018–present **SchemaBlocks – An Initiative of the Global Alliance for Genomics and Health**, *schemablocks.org*.

2017–present **Beacon$^+$ – A forward looking genome beacon**, *beacon.progenetix.org*.

2012–present **arrayMap – A reference resource for genomic copy number imbalances in human malignancies**, *arraymap.org*.

2012–2018 **Diffuse Intrinsic Pontine Glioma (DIPG) Genomics Repository**, *dipg.progenetix.org*.

2000–present **Progenetix - Genomic copy number aberrations in cancer**, *progenetix.org*.

Oral Presentations

Please see *info.baudisgroup.org/presentations/* ... for a list.

Research

The majority of my research is centered around the computational analysis of human genome data, both for the exploration of genetic diseases and, as main focus, the exploration of cancer genome "landscapes". Originally starting out from experimental molecular cytogenetics and clinical oncology, I realised that the heterogeneity of cancer genomes requires the systematic collection and meta-analysis of whole genome datasets, in formats accessible to computational data mining. This interest has continuously expanded, including areas of data annotations, genomic data formats, data schemas and exchange protocols and research epistemology.

Past Research

Genomic Variations in Human Cancers - Analysis & Resources.

Starting with my thesis project in lymphoma genomics at the German Cancer Research Center, I have been fascinated by the extent and patterning of structural genome mutations in cancer, an their correlation with histopathological subtypes andclinical parameters. Early projects in Heidelberg and Stanford applied molecular "wet lab" technologies to the study of leukemias and lymphomas, with focus on genomic profiling and functional analysis of fusion genes and effects of activated oncogenes such as ABCB1 (Baudis *et al.*, 2006). In parallel I became interested in the comparative analysis of genomic variation profiles across cancer entities and established in 2001 the *progenetix.net* online resource for copy number variation profiling data in cancer. The oncogenomic data collections served as the basis for the quantitative exploration of cancer specific structural variations as well as for the computational analysis of genomic phenomena such as Chromothripsis.

Defining Cancer Entities: Collaborative studies.

An important aspect of my group's research activities is the support of cancer genome data analysis projects in specific disease entities, as part of joint projects with international collaborators. These projects make use of synergies arising from the collaborators' expertise in biology and clinics of the respective cancer entities, and my group's established resources and experience in the analysis of cancer genome data, such as a SNF/UEFISCDI supported Swiss-Romanian study into the biology and genomics of inflammatory and malignant T-cell dependent skin diseases; and a long term collaborative project with the Institute of Cancer Research U.K. (Chris Jones) aggressive childhood brain tumours. Additional projects have targeted neuroblastoma pathology, primitive neurooectodermal brain tumours, various epithelial neoplasias and hematologic malignancies and in dynamic genome changes in cell line models.

Algorithms and Tools for Genomic Data.

Here, we have published various methods and tools for genomic data processing, such as for the stratification of population backgrounds from noisy cancer profiling data; methods for quality control and calibration of genomic profiling data from heterogeneous data collections; a tool for the co-occurrence analysis of individual CNVs; and a software package for the efficient translation of genomic coordinates between data mapped to different reference genomes.

Ongoing Activities and Future Directions

Defining cancer: Patterns, Pathways, Populations.

While the understanding of individual genomic alterations in many cancer entities has considerably increased, main challenges are represented through the overall genomic heterogeneity in the majority of neoplasias as well as the complexity of possible interactions between acquired mutations and inherited genomic variability. Here, current and future research projects target areas of cancer classification, e.g. through AI-driven evaluation of mutational signatures with disease concepts (e.g. Gao & Baudis, 2020); correlations between population-specific genome patterns (e.g. Huang *et al.*, 2020) and structural genome variations; and the comparative analysis of mutational signatures in cancer cell lines with respect to their type-specific representation of genomic alterations in native tumors.

Additionally to the work on genomic variation data, based on our extensively curated data of genomic profiling studies we have started to address questions of data provenance and research epistemology, e.g. the globally uneven distribution of molecular studies into the origins and pathways of cancer. Together with the data-driven exploration of population backgrounds and somatic mutation patterns, this fascinating area now is leading us to further evaluate connections between geographic origin, population background and disease biology, but also to inform researchers and policy makers more efficiently about "blind spots" in our knowledge of cancer genomics.

Summary The complexity of cancer genome landscapes constitutes a challenging and exciting field of research, which is becoming increasingly accessible due to growing expanding data and new computational methods. The combination of advancements in disease concepts with the integrative analyses of inherited genomic variations, somatic mutation patterns and structured metadata provides exciting research opportunities, with my group being well positioned at the intersection of these areas.

Reference resources for cancer genome datasets.

Based on the original Progenetix online resource, my group maintains the internationally largest resource for curated copy number variation (CNV) data in cancer. The Progenetix project is one of the reference resources in recently launched ELIXIR *hCNV* implementation studies and - through the Beacon+ project on top of the database - has been essential in driving the development of the GA4GH Beacon project and several data schemas in the GA4GH ecosystem. The resource has become increasingly embedded in Swiss, European and International development projects, such as serving as driver for developing data exchange standards for the Global Alliance for Genomics and Health and their adoption through e.g. the Swiss Personalized Health Network (SPHN).

While the focus of the Progenetix resource traditionally has been on cancer CNV data, increasingly "precise" sequence variants have been integrated into the resource environment, originally to develop schemas and methodologies for the Beacon project. With more such data becoming available from integrated genome profiling studies and repositories, we intend to expand the availability and representation of "beyond CNV" mutation data, with a focus on datasets were both CNV and SNV/INDEL annotations are available. Another point for such data integration efforts will be in cancer cell lines, where a large amount of external mapped variant data is available and can be cross-referenced with directly processed CNV profiling experiments. Also, we are currently in the preparative phase for a research project into data mining from scientific literature (collaboration with Prof. Patrick Ruch, Uni Geneve) where machine learning based text analysis methods will be used on an expert-annotated corpus of scientific studies.

Summary Progenetix and associated resources will play an increasing role for collaborative studies and increase the recognition of UZH in bioinformatics and cancer genomics, particularly through the integration with leading European and international initiatives

Genomic Data Standards.

The availability of genomic data becomes increasingly important in the areas of cancer research, rare diseases, genetic predisposition and risk evaluation and pharmaco-genomics. For many research and clinical applications the access to single databases and knowledge repositories is not sufficient, especially with view on inter-population heterogeneity; nor can it be sufficient for a deep understanding of complex mutation landscapes encountered in most human malignancies. Efforts to enable distributed ("federated") data access over a large number of heterogeneous, international genomic data resources have become increasingly relevant. Since 2014, the Global Alliance for Genomics and Health (GA4GH) has become the main community and standard defining organization at the intersection of "genomics and health", including covering areas as ethics and security recommendations as well as genomic data formats, schemas and protocols for exchange of genomic data and structured biomedical annotations. On the European level the organization most relevant for large-scale biological data sharing and processing is ELIXIR, the European bioinformatics network organization with the Swiss Institute of Bioinformatics as its Swiss node. In Switzerland, the need for shared data and compute services for biomedical data has found its expression in the foundation of the Swiss Personalized Health Network (SPHN).

I have been involved with GA4GH since its foundation in 2014 and have (co-)led a number of GA4GH projects since then, e.g. the Data Working Group's *Metadata Task Team*, the *Variant Representation* group of the Genomic Knowledge Standards work stream and also participated in the Genomic Knowledge Standards workgroup, e.g. in the development of the *Phenopackets* standard. Since 2016 I have been a member of the GA4GH steering committee and - as co-lead of the Discovery work stream - have been responsible for the *Beacon* genomic data discovery standard and the creation of the *SchemaBlocks* initiative (schemablocks.org). Also, I have co-lead the successful integration of SPHN as a GA4GH "driver project" and represent this Swiss initiative towards GA4GH. The participation in GA4GH related activities has lad to a number of resource ongoing development and research projects, for example into the use of ontologies for cancer classifications or into the development of genome variation annotation resources for clinical use cases.

Going forward, I will continue to use my leadership role in GA4GH and ELIXIR projects to work on the development and implementation of international standards for federated access to genomic and knowledge resources, e.g. through the upcoming *Beacon v2* standard and its use in networked resources, as part of several ELIXIR projects. Additionally, as the lead of a collaborative European project for structural genome variation data which starts this year, I will work on the standardization, exchange and analysis of copy number variation data within a network of partners from five European countries.

Summary Research into genomic data exchange formats and protocols as well as their implementation in international, European and Swiss resource and research projects represents an exciting area in bioinformatics and data science. Leadership roles in GA4GH and ELIXIR projects provides opportunities to shape research and resource policies and technologies, for an unprecedented scale of analysis into disease mechanisms especially in rare diseases and cancer.

Teaching

Focus of Teaching Activities

The main focus of my teaching is in the area of bioinformatics and especially its application to biomedical research. Specific topics which I want to bring to the students' attention - and hopefully generate original interest and excitement for - are from diverse areas as the study of high-throughput genome data, techniques used for data curation and structured knowledge annotation, and the latest developments biomedical data exchange through knowledge resources, common data standards and the efficient application of data mining techniques in biomedical research and clinical applications.

Apart from aspects of processing and curation of biomedical data, an increasingly important topic has been the teaching of concepts related to data privacy and security in the context of human data, especially when related to the area of *precision medicine* or *personalized health*. Here, my own background in medicine and my involvement with leading international data sharing initiatives has served as a foundation to engage students in a discourse about risks and benefits from genomic and other personal data generation and exchange, and to increase their interests in the technological issues as well as ethical aspects of a rapidly developing field.

While originally mostly focussed on the teaching of graduate courses and seminars through the Zurich Life Sciences Graduate School and the direct exchange with graduate students working on research projects, over the last several years I have increasingly focussed on early career students, with the goal to enable them to gain or improve increasingly relevant bioinformatics skills and with the hope to awake their fascination for the different areas of computational data analysis in life sciences.

Organization of Lectures & Courses

2018 - **UZH BIO392**, *Bioinformatics of Sequence Variation*, Block Course.

The *Bioinformatics of Sequence Variation* course was introduced to provide a "hands on" approach to the exciting area of bioinformatic analysis of genomic and related data, such as the output from high-throughput sequencing and array based molecular analyses. It is aimed at life science students with interest, but limited experience in low-level computational approaches and is balanced between the teaching of basic concepts of code and data warehousing as well as some biomedical background in areas where sequence analyses are important.

2017 - **UZH BIO390**, *Introduction to Bioinformatics*, Lecture Series.

With the support of colleagues from the University of Zurich and other institutions, in 2018 I've created the *Introduction to Bioinformatics* module to introduce undergraduate students in life sciences to the field of bioinformatics and the application of bioinformatic methods and techniques in biology and related areas, especially biomedical research. The module was designed as a lecture series, in which - in addition to a general introduction and overview of the area - individual specialists present the use of bioinformatics, biostatistics and computational biology in their research and application areas such as clinical analytics.

Starting with a set of 55 registered participants in 2017, the attendance has constantly grown to currently 120 attendants (2020). Aside for being part of the life sciences undergraduate curriculum, the BIO390 module has become part graduate programs such as in Biochemistry.

2012 - **UZH BIO612**, *Zurich Seminars in Bioinformatics*, Seminar Series.

The *Zurich Seminars in Bioinformatics* were originally created to allow graduate students of affiliated groups - originally the von Mering, Robinson and Baudis teams - at the UZH to present the progress of their respective projects, and to facilitate networking between research groups. Over the years, this year-round seminar series has become well received forum for members from UZH research groups as well as from other institutions in the area, with participants from FGCZ, ETHZ, USZ and external visitors. Importantly, the seminar series offers a forum for junior bioinformatics researchers "embedded" in wet-lab or medical research projects to discuss their work.

Participation in Courses

Ongoing **UZH BIO614**, *DMLS Research Progress Reports*.

UZH BIO616, *Seminar in Molecular Life Sciences*.

UZH BIO259, *Research Internship in Molecular and Cellular Biology*.

Graduate Schools & Courses

Since 2008 I have been a member of the *Life Sciences Zurich Graduate School*, the organization for PhD programs in biology and related sciences shared among UZH and ETHZ. Specifically, I have been part of the *Cancer Biology*, *Systems Biology* and *Molecular Life Sciences* programs in all of which former or current PhD candidates from my group have participated. Additionally I have been involved in the supervision of students from other LSZGS programs. I regularly contribute to the organization of the LSZGS through participation in selection- and interview committees and have also contributed to its outreach activities, e.g. through providing software for visualization of student participation and international reach. In the different programs, my main interest is in improving the use of bioinformatics and data science methods in the projects of the participants, and on the other hand to increase the understanding of medical and genomic components of studies by participants with a more "systems" or computational background.

Apart from the LSZGS programs I am one of the members of the new program in *Data Science* of the MNF. Also, outside my teaching assignments and activities at the University of Zurich I have taught both undergraduate and graduate lectures and courses at the ETHZ. Also, I have led graduate student activities through the Swiss Institute of Bioinformatics and have previously been the head of a selection committee there. Starting in 2021

Supervision of Graduate Students and Researchers

2022 - **Ms. Feifei Xia**, *PhD cand. in Data Science, ZHAW*, head of committee.

2021 - **Ms. Hangjia Zhang**, *PhD cand. in Molecular Life Sciences, LSZGS*, supervisor.

2020 - **Ms. Ziying Yang**, *PhD cand. in Molecular Life Sciences, LSZGS*, supervisor.

2020 - **Mr. Max Verbiest**, *PhD cand. in Data Science, ZHAW*, head of committee.

2020 - **Ms. Elena Cabello**, *PhD cand. in Molecular Genetics, LSZGS*, member of committee.

2019 - **Ms. Rahel Paloots**, *PhD cand. in Molecular Life Sciences, LSZGS*, supervisor.

2017 - **Ms. Cécile Mingard**, *PhD cand. in Molecular and Translational Biomedicine, ETHZ & LSZGS*, member of committee.

2017 - **Ms. Qingyao Huang**, *PhD cand. in Molecular Life Sciences, LSZGS*, supervisor, defence July 2021.

2017 - **Ms. Marie Ghraichy**, *PhD cand. in Microbiology and Immunology, USZ & LSZGS*, member of committee.

2017-2021 **Ms. Paula Carrio-Cordo**, *PhD in Molecular Life Sciences, LSZGS*, supervisor.

2016-2021 **Mr. Bo Gao**, *PhD cand. in Molecular Life Sciences*, supervisor, expected defence August 2021.

2016-2021 **Katharina Holste-Benischke, PhD**, *PhD in Cancer Biology, LSZGS*, member of committee.

2016-2018 **Valdemar Priebe, PhD**, *PhD in Biology, Faculté des Sciences et Medecine, Université de Lausanne* , member of committee.

2016 **Ms. Linda Grob**, *MSc. in Computational Biology and Bioinformatics ETHZ*, supervisor of thesis.

2015 **Ms. Yuyu Liu**, *MSc. Biology Université de Pierre et Marie Curie Paris*, supervisor of thesis.

2014-2019 **Ms. Ni Ai**, *PhD cand. in Systems Biology, LSZGS*, supervisor.

2013-2017 **Ms. Saumya Gupta**, *PhD cand. in Systems Biology, LSZGS*, supervisor.

2012 **Dr. med. André von Büren**, *post-doc*.

2012 **Ms. Saumya Gupta**, *MSc. in Computational Biology and Bioinformatics ETHZ & UZH*, supervisor of thesis.

2011-2012 **Mr. Kamal Kishore**, *MSc. in Molecular Life Sciences & UZH*, supervisor.

2009-2014 **Haoyang Cai, PhD**, *PhD in Cancer Biology, LSZGS & post-doc*, supervisor.

2008-2012 **Nitin Kumar, PhD**, *PhD in Cancer Biology, LSZGS & post-doc*, supervisor.

Bibliography

Publications - Original Articles & Reviewed Proceedings

Please see *info.baudisgroup.org/publications/* ... for an updated list.

2022 **Candidate targets of copy number deletion events across 17 cancer types.**, ***Huang Q***, ***Baudis M***., *bioRxiv*, **2022 Jun 30**; 2022.06.29.498080.

The GA4GH Phenopacket schema defines a computable representation of clinical data., *Jacobsen JOB*, ***Baudis M***, *Baynam GS, Beckmann JS, Beltran S, Buske OJ, Callahan TJ, Chute CG, Courtot M, Danis D, Elemento O, Essenwanger A, Freimuth RR, Gargano MA, Groza T, Hamosh A, Harris NL, Kaliyaperumal R, Lloyd KCK, Khalifa A, Krawitz PM, Köhler S, Laraway BJ, Lehväslaiho H, Matalonga L, McMurry JA, ..., Haendel MA, Robinson PN, The GAGHPMC.*, *Nature Biotechnology*, **2022**; 40(6):817.

Beacon v2 and Beacon networks: A "lingua franca" for federated data discovery in biomedical genomics, and beyond., *Rambla J*, ***Baudis M***, *Ariosa R, Beck T, Fromont LA, Navarro A*, ***Paloots R***, *Rueda M, Saunders G, Singh B, Spalding JD, Törnroos J, Vasallo C, Veal CD, Brookes AJ.*, *Hum Mutat*, **2022 Mar 17**; :.

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