

	A	B	C	D	E
1	Thesis projects for bioinformatics students: Bachelor (BA), Master (MA), Research internships (FoPra)				
2					
3	Working group/Institut (Link)	Range of Topics	BA, MA, FoPra?	Contact (Name, E-Mail)	Notes
4	Independent Max Planck Research Group "Biosocial Biology, Social Disparities, and Development" / Max Planck Institute for Human Development (https://www.mpiib-berlin.mpg.de/research/research-groups/mpig-biosocial/)	Applying omics research to social science research on health and education inequality; genome-wide DNA methylation machine learning; genome-wide association studies; polygenic scores	BA, MA, FoPra	caffington@mpiib-berlin.mpg.de	Lots of research opportunities
5	Molecular Ecology (AG Monaghan) Leibniz-IGB and FU Institute of Biology https://www.igb-berlin.de/en/profile/michael-t-monaghan	Environmental genomics, environmental microbiome, biodiversity, biomonitoring in lakes and rivers, eDNA	MA, FoPra	m.monaghan@fu-berlin.de	Field- and Laboratory components also possible
6	Bioinformatics Solution Center / Inst. Mathe-Informatik; www.bsc.fu-berlin.de , Sandro Andreotti, Chris Bielow	Workflows; Algorithmik insb. fuer Next-Generation-Sequencing und Proteomik; Qualitätskontrolle von Hochdurchsatzdaten; Implementierung und Benchmarking von Algorithmen	BA, MA, FoPra, BerPra	info@bsc.fu-berlin.de	
7	Bioinformatics in Medicine / Zuse Institute Berlin	Machine learning for analysis of omics data; network-based data integration; mathematical modelling	BA, MA, FoPra	conrad@zib.de	
8	AI in Life Sciences (AG Eils), Digital Health Center, Berlin Institute of Health at Charité, https://www.hidih.org/research/ailslab	Health data, disease risk modeling, treatment recommendation, machine learning	BA, MA, FoPra	alexandra.friedrich@bih-charite.de	
9	Algorithmische Bioinformatik (AG Reinert), FU, Institut für Informatik, http://www.mi.fu-berlin.de/en/inf/groups/abi/	algorithms for NGS analysis in the SeqAn library (www.seqan.de), algorithms for the analysis of HPLC/MS proteomics data (www.openms.de); other topics are possible; cf. https://wikis.fu-berlin.de/display/abi/BSc+and+MSc+Topics	BA, MA, FoPra	knut.reinert@fu-berlin.de	
10	Referat S.3 eScience, Bundesanstalt für Materialforschung und -prüfung	Algorithms and software development for mass spectrometry-based applications (proteomics, metaproteomics, metabolomics, chemistry); research data management; machine learning	BA, MA, FoPra	thilo.muth@bam.de	
11	AG Wolber (Computergestütztes, molekulares Wirkstoffdesign), Institut für Pharmazie, Fachbereich Biologie, Chemie, Pharmazie; https://www.bcp.fu-berlin.de/en/pharmazie/faecher/pharmazieutsche_chemie/wolber/index.html ; https://drug-design.de	Algorithmen zum computergestützten Wirkstoffdesign, Workflows für virtuelles Screening und zur Analyse von Eigenschaften von kleinen organischen Molekülen, Data mining & machine learning	BA, MA, FoPra	gerhard.wolber@fu-berlin.de	FU web page
12	https://www.mi.fu-berlin.de/en/math/groups/dibimath/index.html	Mathematical modeling, molecular networks, discrete methods for system and data analysis	BA, MA, FoPra	siebert@mi.fu-berlin.de	
13	AG Nowick (Human Biology and Primate Evolution): http://www.nowick-lab.info	Comparison of genome and transcriptome data with focus on evolution, brain and gene regulation	BA, MA, FoPra	katja.nowick@fu-berlin.de	
14	AG Szulcek, In vitro modeling systems of pulmonary diseases	Project on natural language processing in scientific literature.	MA, FoPra	robert.szulcek@charite.de	
15	AG Konietzschke: Institut für Biometrie und klinische Epidemiologie. www.biometrie-charite.de	Statistical Methods, Resampling Methods, High-Dimensional Data Analysis	MA, FoPra	frank.konietzschke@charite.de	
16	AG Stricker, FU-BCP, https://www.bcp.fu-berlin.de/en/chemie/biochemie/research-groups/stricker-group/index.html	Stammzellen im Muskuloskeletalen System; Analyse von OMICS Datensätzen aus z.B. RNA-Seq oder Histone profiling Experimenten	MA, Ma	sigmar.stricker@fu-berlin.de	
17	AG Keller, Computational and Theoretical Chemistry, http://www.chemie.fu-berlin.de/keller	Molecular-dynamics simulations, kinetic models	BA, MA, FoPra	bettina.keller@fu-berlin.de	
18	Intelligent Imaging (AG Conrad), Digital Health Center, Berlin Institute of Health at Charité, https://www.bihealth.org/en/research/research-group/conrad-lab-intelligent-imaging	single cell sequencing, spatial transcriptomics, high content screening, machine learning	BA, MA, FoPra	christian.conrad@bih-charite.de	
19	Bioinformatics Unit (MF1), Robert Koch Institute, https://www.rki.de/DE/Content/Forsch/Forschungsmethoden/Bioinformatik/Bioinformatik.html	Group working on the Statistical and Bioinformatic analysis of sequencing/omics data, with a focus on: * bioinformatics workflow management systems, real-time nanopore sequencing (or real-time pathogen detection) (HoelzerM) * Machine Learning and Statistics, outbreak detection and pathogen evolution (RichardH) * Genomic surveillance of pathogens (FuchsS). cf https://rki-mf1.github.io/projects/	BA, MA, FoPra	{RichardH,FuchsS,HoelzerM}@rki.de	
20	AG Mathematical Modelling of Cellular Processes (Wolf lab), MDC Berlin & FU Berlin, https://www.mdc-berlin.de/wolf	Computational Systems Biology and System Medicine, computational modeling, data analysis	MA, FoPra	iana.wolf@mdc-berlin.de	
21	Systems Biology of Infectious Diseases (AG Buchauer), Department of Infectious Diseases and Intensive Care, Charité, https://libuchauer.github.io	Computational method and software development for single cell omics data and flow cytometry data; high-dimensional data analysis (single cell omics, bulk RNAseq, spatial omics, flow cytometry) in translational collaboration projects with infectious disease/vaccine/immunology researchers and clinicians	BA,MA, FoPra	Lisa.buchauer@charite.de	
22	Computational and Developmental Biology (AG Mittnenzweig), Berlin Institute of Medical Systems Biology, Max Delbrück Center, https://www.mdc-berlin.de/de/mittnenzweig	Machine learning and data analysis of single-cell omics data (single-cell multiomics, spatial transcriptomics) Single-cell regulatory genomics - understanding the enhancer code controlling development Evolutionary models of embryonic development Computational method and software development for time-resolved imaging and single-cell omics data	BA, MA, FoPra	markus.mittnenzweig@mdc-berlin.de	