

Zuguang Gu

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Summary

I was a core bioinformatician responsible for a large number of projects (> 20) in German Cancer Research Center (DKFZ), National Center for Tumor Diseases (NCT) and Heidelberg University Hospital. My work was focused on systematic analysis on sequencing and array data (whole-genome sequencing, whole-exon sequencing, RNA sequencing, Whole-genome bisulfite sequencing, methylation array, ChIP sequencing).

I developed a general pipeline management system and I have implemented pipelines for data of whole genome bisulfite sequencing, RNA sequencing, ChIP sequencing and gene fusions. I have run these pipelines for more than 6,000 samples for numerous projects.

I developed many R packages for statistical analysis and data visualization. The tools are widely used in the bioinformatics community (~ 3 million downloads).

Currently I am working as a staff scientist affiliated with NCT, continuously focusing on scientific software development and being involved in [the NCT Molecular Precision Oncology Program](#).

Experience

National Center for Tumor Diseases, German Cancer Research Center (DKFZ-NCT)

Staff Scientist (permanent) 2022-present

Heidelberg Center for Personalized Oncology, German Cancer Research Center (DKFZ-HIPO)

Postdoctoral researcher 2013-2021

Education

Nanjing University, China, Ph.D. Biochemistry and Molecular Biology 2009-2012

Nanjing University, China, M.D. Biochemistry and Molecular Biology 2005-2008

Nanjing University, China, B.D. Biochemistry and Molecular Biology 2001-2005

Books¹

1. **Zuguang Gu**. [Circular Visualization in R](#).
2. **Zuguang Gu**. [ComplexHeatmap Complete Reference](#).

Journal Articles²

2022

1. **Zuguang Gu**, Daniel Hübschmann, simplifyEnrichment: an R/Bioconductor package for Clustering and Visualizing Functional Enrichment Results. *Genomics, Proteomics & Bioinformatics* 2022.

¹Online self-maintained books.

²[Google Scholar citations](#): 6411 | h-index: 21, 17 first-author papers, 4660 citations for my first-author papers, by 2022-04-22.

2. Josefine Radke, Naveed Ishaque, Randi Koll, **Zuguang Gu**, Elisa Schumann, Lina Sieverling, Sebastian Uhrig, Daniel Hübschmann, Umut H. Toprak, Cristina López, Xavier Pastor Hostench, Simone Borgoni, Dilafruz Juraeva, Fabienne Pritsch, Nagarajan Paramasivam, Gnana Prakash Balasubramanian, Matthias Schlesner, Shashwat Sahay, Marc Weniger, Debora Pehl, Helena Radbruch, Anja Osterloh, Agnieszka Korfel, Martin Misch, Julia Onken, Katharina Faust, Peter Vajkoczy, Dag Moskopp, Yawen Wang, Andreas Jödicke, Lorenz Trümper, Ioannis Anagnostopoulos, Dido Lenze, Ralf Küppers, Michael Hummel, Clemens A. Schmitt, Otmar D. Wiestler, Stephan Wolf, Andreas Unterberg, Roland Eils, Christel Herold-Mende, Benedikt Brors, ICGC MML-Seq Consortium, Reiner Siebert, Stefan Wiemann & Frank L. Heppner, [The genomic and transcriptional landscape of primary central nervous system lymphoma](#). *Nature Communication* 2022.
3. **Zuguang Gu**, Daniel Hübschmann, [Improve Consensus Partitioning via a Hierarchical Procedure](#). *Briefings in Bioinformatics* 2022.

2021

4. **Zuguang Gu**, Daniel Hübschmann, [Make Interactive Complex Heatmaps in R](#). *Bioinformatics* 2021.
5. **Zuguang Gu**, Daniel Hübschmann, [spiralize: an R package for Visualizing Data on Spirals](#). *Bioinformatics* 2021
6. Marina Laplana, Matthias Bieg, Christian Faltus, Svitlana Melnik, Olga Bogatyrova, **Zuguang Gu**³, Thomas Muley, Michael Meister, Hendrik Dienemann, Esther Herpel, Christopher I Amos, Matthias Schlesner, Roland Eils, Christoph Plass, Angela Risch, [Differentially methylated regions within lung cancer risk loci are enriched in deregulated enhancers](#). *Epigenetics* 2021.
7. Ana Maia, **Zuguang Gu**, André Koch, Mireia Berdiel-Acer, Rainer Will, Matthias Schlesner, Stefan Wiemann, [IFN-beta1 secreted by breast cancer cells undergoing chemotherapy reprograms stromal fibroblasts to support tumour growth after treatment](#). *Molecular oncology* 2021.
8. Nina Hensel*, **Zuguang Gu***, Sagar*, Dominik Wieland, Katharina Jechow, Janine Kemming, Sian Llewellyn-Lacey, Emma Gostick, Oezlem Sogukpinar, Florian Emmerich, David A Price, Bertram Bengsch, Tobias Boettler, Christoph Neumann-Haefelin, Roland Eils, Christian Conrad, Ralf Bartenschlager, Dominic Grün, Naveed Ishaque, Robert Thimme, Maike Hofmann, [Memory-like HCV-specific CD8+ T cells retain a molecular scar after cure of chronic HCV infection](#). *Nature immunology* 2021. *Co-first authors.
9. **Zuguang Gu**, Matthias Schlesner, Daniel Hübschmann, [cola: an R/Bioconductor package for consensus partitioning through a general framework](#). *Nucleic acids research* 2021.
10. Daniel Hübschmann, Lea Jopp-Saile, Carolin Andresen, Stephen Krämer, **Zuguang Gu**, Christoph E Heilig, Simon Kreutzfeldt, Veronica Teleanu, Stefan Fröhling, Roland Eils, Matthias Schlesner, [Analysis of mutational signatures with yet another package for signature analysis](#). *Genes, chromosomes & cancer* 2021.
11. Elisa Espinet, **Zuguang Gu**, Charles D Imbusch, Nathalia A Giese, Magdalena Büscher, Mariam Safavi, Silke Weisenburger, Corinna Klein, Vanessa Vogel, Mattia Falcone, Jacob Insua-Rodríguez, Manuel Reitberger, Vera Thiel, Steffi O Kossi, Alexander Muckenhuber, Karnjit Sarai, Alex Y L Lee, Elyne Backx, Soheila Zarei, Matthias M Gaida, Manuel Rodríguez-Paredes, Elisa Donato, Hsi-Yu Yen, Roland Eils, Matthias Schlesner, Nicole Pfarr, Thilo Hackert, Christoph Plass, Benedikt Brors, Katja Steiger, Dieter Weichenhan, H Efsun Arda,

³The plot I made was selected as the cover image of the journal.

Ilse Rooman, Janel L Kopp, Oliver Strobel, Wilko Weichert, Martin R Sprick, Andreas Trumpp, [Aggressive PDACs Show Hypomethylation of Repetitive Elements and the Execution of an Intrinsic IFN Program Linked to a Ductal Cell of Origin](#). *Cancer discovery* 2021.

2020

12. Yonghe Wu*, Michael Fletcher*, **Zuguang Gu***, Qi Wang, Barbara Costa, Anna Bertoni, Ka-Hou Man, Magdalena Schlotter, Jörg Felsberg, Jasmin Mangei, Martje Barbus, Ann-Christin Gaupel, Wei Wang, Tobias Weiss, Roland Eils, Michael Weller, Haikun Liu, Guido Reifenberger, Andrey Korshunov, Peter Angel, Peter Lichter, Carl Herrmann, Bernhard Radlwimmer, [Glioblastoma epigenome profiling identifies SOX10 as a master regulator of molecular tumour subtype](#). *Nature communications* 2020. *Co-first authors.
13. Simon Raffel, Daniel Klimmeck, Mattia Falcone, Aykut Demir, Alireza Pouya, Petra Zeisberger, Christoph Lutz, Marco Tinelli, Oliver Bischel, Lars Bullinger, Christian Thiede, Anne Flörcken, Jörg Westermann, Gerhard Ehninger, Anthony D Ho, Carsten Müller-Tidow, **Zuguang Gu**, Carl Herrmann, Jeroen Krijgsveld, Andreas Trumpp, Jenny Hansson, [Quantitative proteomics reveals specific metabolic features of acute myeloid leukemia stem cells](#). *Blood* 2020.
14. Enoch B Antwi, Ada Olins, Vladimir B Teif, Matthias Bieg, Tobias Bauer, **Zuguang Gu**, Benedikt Brors, Roland Eils, Donald Olins, Naveed Ishaque, [Whole-genome fingerprint of the DNA methylome during chemically induced differentiation of the human AML cell line HL-60/S4](#). *Biology open* 2020.
15. Maike Smits, Katharina Zoldan, Naveed Ishaque, **Zuguang Gu**, Katharina Jechow, Dominik Wieland, Christian Conrad, Roland Eils, Catherine Fauvelle, Thomas F Baumert, Florian Emerich, Bertram Bengsch, Christoph Neumann-Haefelin, Maike Hofmann, Robert Thimme, Tobias Boettler, [Follicular T helper cells shape the HCV-specific CD4+ T cell repertoire after virus elimination](#). *The Journal of clinical investigation* 2020.

2019

16. Stephan M Tirier, Jeongbin Park, Friedrich Preußner, Lisa Amrhein, **Zuguang Gu**, Simon Steiger, Jan-Philipp Mallm, Teresa Krieger, Marcel Waschow, Björn Eismann, Marta Gut, Ivo G Gut, Karsten Rippe, Matthias Schlesner, Fabian Theis, Christiane Fuchs, Claudia R Ball, Hanno Glimm, Roland Eils, Christian Conrad, [Pheno-seq - linking visual features and gene expression in 3D cell culture systems](#). *Scientific reports* 2019.
17. Calvin Wing Yiu Chan, **Zuguang Gu**, Matthias Bieg, Roland Eils, Carl Herrmann, [Impact of cancer mutational signatures on transcription factor motifs in the human genome](#). *BMC medical genomics* 2019.
18. Nagarajan Paramasivam, Daniel Hübschmann, Umut H Toprak, Naveed Ishaque, Marian Neidert, Daniel Schrimpf, Damian Stichel, David Reuss, Philipp Sievers, Annkathrin Reinhardt, Annika K Wefers, David T W Jones, **Zuguang Gu**, Johannes Werner, Sebastian Uhrig, Hans-Georg Wirsching, Matthias Schick, Melanie Beverunge-Hudler, Katja Beck, Stephanie Brehmer, Steffi Urbschat, Marcel Seiz-Rosenhagen, Daniel Hänggi, Christel Herold-Mende, Ralf Ketter, Roland Eils, Zvi Ram, Stefan M Pfister, Wolfgang Wick, Michael Weller, Rachel Grossmann, Andreas von Deimling, Matthias Schlesner, Felix Sahn, [Mutational patterns and regulatory networks in epigenetic subgroups of meningioma](#). *Acta neuropathologica* 2019.
19. Verena Körber, Jing Yang, Pankaj Barah, Yonghe Wu, Damian Stichel, **Zuguang Gu**, Michael Nai Chung Fletcher, David Jones, Bettina Hentschel, Katrin Lamszus, Jörg Christian Tonn, Gabriele Schackert, Michael Sabel, Jörg Felsberg, Angela Zacher, Kerstin Kaulich, Daniel Hübschmann, Christel Herold-Mende, Andreas von Deimling, Michael Weller, Bernhard

Radlwimmer, Matthias Schlesner, Guido Reifenberger, Thomas Höfer, Peter Lichter, [Evolutionary Trajectories of IDHWT Glioblastomas Reveal a Common Path of Early Tumorigenesis Instigated Years ahead of Initial Diagnosis](#). *Cancer cell* 2019.

2018

20. Naveed Ishaque, Mohammed L Abba, Christine Hauser, Nitin Patil, Nagarajan Paramasivam, Daniel Huebschmann, Jörg Hendrik Leupold, Gnana Prakash Balasubramanian, Kortine Kleinheinz, Umut H Toprak, Barbara Hutter, Axel Benner, Anna Shavinskaya, Chan Zhou, **Zuguang Gu**, Jules Kerssemakers, Alexander Marx, Marcin Moniuszko, Mirosław Kozłowski, Joanna Reszec, Jacek Niklinski, Jürgen Eils, Matthias Schlesner, Roland Eils, Benedikt Brors, Heike Allgayer, [Whole genome sequencing puts forward hypotheses on metastasis evolution and therapy in colorectal cancer](#). *Nature communications* 2018.
21. **Zuguang Gu**, Roland Eils, Matthias Schlesner, Naveed Ishaque, [EnrichedHeatmap: an R/Bioconductor package for comprehensive visualization of genomic signal associations](#). *BMC genomics* 2018.

2017

22. Daniel B Lipka, Tania Witte, Reka Toth, Jing Yang, Manuel Wiesenfarth, Peter Nöllke, Alexandra Fischer, David Brocks, **Zuguang Gu**, Jeongbin Park, Brigitte Strahm, Marcin Wlodarski, Ayami Yoshimi, Rainer Claus, Michael Lübbert, Hauke Busch, Melanie Boerries, Mark Hartmann, Maximilian Schönung, Umut Kilik, Jens Langstein, Justyna A Wierzbinska, Caroline Pabst, Swati Garg, Albert Catalá, Barbara De Moerloose, Michael Dworzak, Henrik Hasle, Franco Locatelli, Riccardo Masetti, Markus Schmugge, Owen Smith, Jan Stary, Marek Ussowicz, Marry M van den Heuvel-Eibrink, Yassen Assenov, Matthias Schlesner, Charlotte Niemeyer, Christian Flotho, Christoph Plass, [RAS-pathway mutation patterns define epigenetic subclasses in juvenile myelomonocytic leukemia](#). *Nature communications* 2017.
23. Paul A Northcott, Ivo Buchhalter, A Sorana Morrissy, Volker Hovestadt, Joachim Weischenfeldt, Tobias Ehrenberger, Susanne Gröbner, Maia Segura-Wang, Thomas Zichner, Vasilisa A Rudneva, Hans-Jörg Warnatz, Nikos Sidiropoulos, Aaron H Phillips, Steven Schumacher, Kortine Kleinheinz, Sebastian M Waszak, Serap Erkek, David T W Jones, Barbara C Worst, Marcel Kool, Marc Zapatka, Natalie Jäger, Lukas Chavez, Barbara Hutter, Matthias Bieg, Nagarajan Paramasivam, Michael Heinold, **Zuguang Gu**, Naveed Ishaque, Christina Jäger-Schmidt, Charles D Imbusch, Alke Jugold, Daniel Hübschmann, Thomas Risch, Vyacheslav Amstislavskiy, Francisco German Rodriguez Gonzalez, Ursula D Weber, Stephan Wolf, Giles W Robinson, Xin Zhou, Gang Wu, David Finkelstein, Yanling Liu, Florence M G Cavalli, Betty Luu, Vijay Ramaswamy, Xiaochong Wu, Jan Koster, Marina Ryzhova, Yoon-Jae Cho, Scott L Pomeroy, Christel Herold-Mende, Martin Schuhmann, Martin Ebinger, Linda M Liau, Jaume Mora, Roger E McLendon, Nada Jabado, Toshihiro Kumabe, Eric Chuah, Yussanne Ma, Richard A Moore, Andrew J Mungall, Karen L Mungall, Nina Thiessen, Kane Tse, Tina Wong, Steven J M Jones, Olaf Witt, Till Milde, Andreas Von Deimling, David Capper, Andrey Korshunov, Marie-Laure Yaspo, Richard Kriwacki, Amar Gajjar, Jinghui Zhang, Rameen Beroukhim, Ernest Fraenkel, Jan O Korbel, Benedikt Brors, Matthias Schlesner, Roland Eils, Marco A Marra, Stefan M Pfister, Michael D Taylor, Peter Lichter, [The whole-genome landscape of medulloblastoma subtypes](#). *Nature* 2017.
24. Marcus Winter, Loreen Thürmann, **Zuguang Gu**, Gerrit Schüürmann, Gunda Herberth, Denise Hinz, Martin von Bergen, Hauke Harms, Sven Olek, Stefan Röder, Michael Borte, Roland Eils, Irina Lehmann, Saskia Trump, [The benzene metabolite 1,4-benzoquinone](#)

reduces regulatory T-cell function: A potential mechanism for tobacco smoke-associated atopic dermatitis. *The Journal of allergy and clinical immunology* 2017.

2016

25. Federico Vita, Cosimo Taiti, Antonio Pompeiano, **Zuguang Gu**, Emilio Lo Presti, Larisa Whitney, Michele Monti, Giuseppe Di Miceli, Dario Giambalvo, Paolo Ruisi, Lorenzo Guglielminetti, Stefano Mancuso, [Aromatic and proteomic analyses corroborate the distinction between Mediterranean landraces and modern varieties of durum wheat](#). *Scientific reports* 2016.
26. Saskia Trump, Matthias Bieg, **Zuguang Gu**, Loreen Thürmann, Tobias Bauer, Mario Bauer, Naveed Ishaque, Stefan Röder, Lei Gu, Gunda Herberth, Christian Lawerenz, Michael Borte, Matthias Schlesner, Christoph Plass, Nicolle Diessl, Markus Eszlinger, Oliver Mücke, Horst-Dietrich Elvers, Dirk K Wissenbach, Martin von Bergen, Carl Herrmann, Dieter Weichenhan, Rosalind J Wright, Irina Lehmann, Roland Eils, [Prenatal maternal stress and wheeze in children: novel insights into epigenetic regulation](#). *Scientific reports* 2016.
27. **Zuguang Gu**⁴, Roland Eils, Matthias Schlesner, [Complex heatmaps reveal patterns and correlations in multidimensional genomic data](#). *Bioinformatics (Oxford, England)* 2016.
28. **Zuguang Gu**, Roland Eils, Matthias Schlesner, [HilbertCurve: an R/Bioconductor package for high-resolution visualization of genomic data](#). *Bioinformatics (Oxford, England)* 2016.
29. **Zuguang Gu**, Roland Eils, Matthias Schlesner, [gtrellis: an R/Bioconductor package for making genome-level Trellis graphics](#). *BMC bioinformatics* 2016.
30. Tobias Bauer, Saskia Trump, Naveed Ishaque, Loreen Thürmann, Lei Gu, Mario Bauer, Matthias Bieg, **Zuguang Gu**, Dieter Weichenhan, Jan-Philipp Mallm, Stefan Röder, Gunda Herberth, Eiko Takada, Oliver Mücke, Marcus Winter, Kristin M Junge, Konrad Grützmann, Ulrike Rolle-Kampczyk, Qi Wang, Christian Lawerenz, Michael Borte, Tobias Polte, Matthias Schlesner, Michaela Schanne, Stefan Wiemann, Christina Geörg, Hendrik G Stunnenberg, Christoph Plass, Karsten Rippe, Junichiro Mizuguchi, Carl Herrmann, Roland Eils, Irina Lehmann, [Environment-induced epigenetic reprogramming in genomic regulatory elements in smoking mothers and their children](#). *Molecular systems biology* 2016.

2015

31. Jenny Wegert, Naveed Ishaque, Romina Vardapour, Christina Geörg, **Zuguang Gu**, Matthias Bieg, Barbara Ziegler, Sabrina Bausenwein, Nasenien Nourkami, Nicole Ludwig, Andreas Keller, Clemens Grimm, Susanne Kneitz, Richard D Williams, Tas Chagtai, Kathy Pritchard-Jones, Peter van Sluis, Richard Volckmann, Jan Koster, Rogier Versteeg, Tomas Acha, Maureen J O'Sullivan, Peter K Bode, Felix Niggli, Godelieve A Tytgat, Harm van Tinteren, Marry M van den Heuvel-Eibrink, Eckart Meese, Christian Vokuhl, Ivo Leuschner, Norbert Graf, Roland Eils, Stefan M Pfister, Marcel Kool, Manfred Gessler, [Mutations in the SIX1/2 pathway and the DROSHA/DGCR8 miRNA microprocessor complex underlie high-risk blastemal type Wilms tumors](#). *Cancer cell* 2015.
32. Lei Gu, Sandra C Frommel, Christopher C Oakes, Ronald Simon, Katharina Grupp, Cristina Y Gerig, Dominik Bär, Mark D Robinson, Constance Baer, Melanie Weiss, **Zuguang Gu**, Matthieu Schapira, Ruprecht Kuner, Holger Sülthmann, Maurizio Provenzano, Marie-Laure Yaspo, Benedikt Brors, Jan Korbel, Thorsten Schlomm, Guido Sauter, Roland Eils, Christoph Plass, Raffaella Santoro, [BAZ2A \(TIP5\) is involved in epigenetic alterations in prostate cancer and its overexpression predicts disease recurrence](#). *Nature genetics* 2015.

⁴It has 2838 Google Scholar citations, by 2022-04-22.

2014

33. **Zuguang Gu**⁵, Lei Gu, Roland Eils, Matthias Schlesner, Benedikt Brors, [circlize Implements and enhances circular visualization in R](#). *Bioinformatics (Oxford, England)* 2014.

2013

34. **Zuguang Gu**, Jin Wang, [CePa: an R package for finding significant pathways weighted by multiple network centralities](#). *Bioinformatics (Oxford, England)* 2013.

2012

35. Chenfeng He, Ying-Xin Li, Guangxin Zhang, **Zuguang Gu**, Rong Yang, Jie Li, Zhi John Lu, Zhi-Hua Zhou, Chenyu Zhang, Jin Wang, [MiRmat: mature microRNA sequence prediction](#). *PloS one* 2012.
36. **Zuguang Gu**, Jialin Liu, Kunming Cao, Junfeng Zhang, Jin Wang, [Centrality-based pathway enrichment: a systematic approach for finding significant pathways dominated by key genes](#). *BMC systems biology* 2012.
37. **Zuguang Gu**, Chenyu Zhang, Jin Wang, [Gene regulation is governed by a core network in hepatocellular carcinoma](#). *BMC systems biology* 2012.

2011

38. **Zuguang Gu**, Jie Li, Song Gao, Ming Gong, Junling Wang, Hua Xu, Chenyu Zhang, Jin Wang, [InterMitoBase: an annotated database and analysis platform of protein-protein interactions for human mitochondria](#). *BMC genomics* 2011.

2010

39. Lingyun Zhu, Qiang Wang, Lin Zhang, Zhixiang Fang, Fang Zhao, Zhiyuan Lv, **Zuguang Gu**, Junfeng Zhang, Jin Wang, Ke Zen, Yang Xiang, Dongjin Wang, Chen-Yu Zhang, [Hypoxia induces PGC-1-alpha expression and mitochondrial biogenesis in the myocardium of TOF patients](#). *Cell research* 2010.

Working papers and preprints

1. **Zuguang Gu**, Daniel Hübschmann, [pkgndep: a tool for analyzing dependency heaviness of R packages](#). *bioRxiv* 2022.

Software

*R Programming Language*⁶

Data visualization

circlize: Circular visualization in R, *published on Bioinformatics*. It has been a major software for making circular visualization, and it has been widely applied not only in Bioinformatics, but also in varieties of other research topics such as climate changes, migration flows, information science, environment science [and more](#). It has been downloaded more than 1 million times.

⁵It has 1529 Google Scholar citations, by 2022-04-22.

⁶My R packages have been downloaded > 3 million times, and gained > 2300 GitHub stars. I am also an active and responsible maintainer of all my R packages. I have answered > 1000 questions from users on GitHub and by email.

ComplexHeatmap: Flexibly arrange multiple heatmaps and self-define annotation graphics, *published on Bioinformatics*. It has been a major software for making heatmaps for Bioinformatics studies. It has been introduced in [text books](#) also in [YouTube videos](#). It has been downloaded more than 500 thousand times.

spiralize: Visualize data on spirals, *published on Bioinformatics*.

InteractiveComplexHeatmap: Make interactive complex heatmaps, *published on Bioinformatics*.

EnrichedHeatmap: Visualize the enrichment of genomic signals on specific target regions, *published on BMC Genomics*.

HilbertCurve: Making 2D Hilbert Curve, *published on Bioinformatics*.

gtrellis: Genome-level trellis layout, *published on BMC Bioinformatics*.

Statistical analysis

simplifyEnrichment: Simplify functional enrichment results, manuscript under review.

cola: A Framework for Consensus Partitioning, *published on Nucleic Acids Research and Briefings in Bioinformatics*.

rGREAT: Client of GREAT analysis.

CePa: Centrality-based pathway enrichment, *published on Bioinformatics*.

Software engineering

pkgndep: Analyzing Dependency Heaviness of R Packages.

Utility tools

bsub: Submitter and monitor of LSF cluster.

GlobalOptions: Setting global options in R.

GetOptLong: Wrapper of the Perl module Getopt::Long, also provides a simple variable interpolation in R.

Perl Programming Language

rhydrogen: Translate comments to documentations in R.

Microarray::GEO::SOFT: Reading microarray data in SOFT format from GEO database.

Statistics::Multtest: Control false discovery rate in multiple test problem.

List::Vectorize: Functions to make vectorized calculation easy.

ngspipeline: NGS pipeline maker.

Teaching

Heidelberg University | German Cancer Research Center

1. As a teaching assistant for Perl programming course (for undergraduate students) in 2014.
2. Prepared practicing materials for RNASeq course (for master students) in 2017 and 2018.
3. Gave lectures on the topic of clustering (for master students) in 2018.
4. Supervised two intern students (2015 and 2017) and one master student (2018).

Online workshop

5. Gave lectures on the topic of gene set enrichment analysis on [physalia-courses](#) in May 2022.

Conferences

1. circlize: circular visualization in R, poster presentation in [useR! 2015](#), Aalborg, Denmark.
2. Make interactive complex heatmaps, poster presentation in [Bioconductor conference 2021](#), online conference. *Awarded as Best Innovative poster ideas.*
3. spiralize: an R package for visualizing data on spirals, contributed talk in [Bioconductor Asia 2021](#), online conference.
4. On the heaviness of package dependencies, contributed talk in [useR! 2022](#), online conference.
5. cola: a general framework for consensus partitioning, package demo in [Bioconductor conference 2022](#), online conference.

Professional Service

Manuscripts reviewed for *Bioinformatics* (7), *PLoS Computational Biology* (1), *BMC Bioinformatics* (3), *BMC Genomics* (2), *Frontiers in Genetics* (1), *Journal of Computational and Graphical Statistics* (1), *F1000Research* (1).