

# Nils Gehlenborg

## List of Publications by Year in descending order

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86  
papers

36,701  
citations

66343

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53230

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124  
all docs

124  
docs citations

124  
times ranked

54946  
citing authors

#	ARTICLE	IF	CITATIONS
1	ThreadStates: State-based Visual Analysis of Disease Progression. IEEE Transactions on Visualization and Computer Graphics, 2022, 28, 238-247.	4.4	10
2	Gosling: A Grammar-based Toolkit for Scalable and Interactive Genomics Data Visualization. IEEE Transactions on Visualization and Computer Graphics, 2022, 28, 140-150.	4.4	24
3	MITI minimum information guidelines for highly multiplexed tissue images. Nature Methods, 2022, 19, 262-267.	19.0	37
4	Effective Communication of Personalized Risks and Patient Preferences During Surgical Informed Consent Using Data Visualization: Qualitative Semistructured Interview Study With Patients After Surgery. JMIR Human Factors, 2022, 9, e29118.	2.0	6
5	Viv: multiscale visualization of high-resolution multiplexed bioimaging data on the web. Nature Methods, 2022, 19, 515-516.	19.0	21
6	The 4D Nucleome Data Portal as a resource for searching and visualizing curated nucleomics data. Nature Communications, 2022, 13, 2365.	12.8	49
7	User-Centric Process of Designing a Molecular & Cellular Query Interface for Biomedical Research. Proceedings of the Design Society, 2022, 2, 221-230.	0.8	0
8	International electronic health record-derived post-acute sequelae profiles of COVID-19 patients. Npj Digital Medicine, 2022, 5, .	10.9	17
9	OUP accepted manuscript. Bioinformatics, 2021, 37, i59-i66.	4.1	1
10	What Every Reader Should Know About Studies Using Electronic Health Record Data but May Be Afraid to Ask. Journal of Medical Internet Research, 2021, 23, e22219.	4.3	61
11	International Changes in COVID-19 Clinical Trajectories Across 315 Hospitals and 6 Countries: Retrospective Cohort Study. Journal of Medical Internet Research, 2021, 23, e31400.	4.3	19
12	International Analysis of Electronic Health Records of Children and Youth Hospitalized With COVID-19 Infection in 6 Countries. JAMA Network Open, 2021, 4, e2112596.	5.9	33
13	Multinational characterization of neurological phenotypes in patients hospitalized with COVID-19. Scientific Reports, 2021, 11, 20238.	3.3	10
14	Guidelines for reporting single-cell RNA-seq experiments. Nature Biotechnology, 2020, 38, 1384-1386.	17.5	27
15	P<sc>eax</sc>: Interactive Visual Pattern Search in Sequential Data Using Unsupervised Deep Representation Learning. Computer Graphics Forum, 2020, 39, 167-179.	3.0	20
16	International electronic health record-derived COVID-19 clinical course profiles: the 4CE consortium. Npj Digital Medicine, 2020, 3, 109.	10.9	128
17	Making Tools that People Will Use: User-Centered Design in Computational Biology Research. , 2020, , .		0
18	Tasks, Techniques, and Tools for Genomic Data Visualization. Computer Graphics Forum, 2019, 38, 781-805.	3.0	61

#	ARTICLE	IF	CITATIONS
19	Pattern-Driven Navigation in 2D Multiscale Visualizations with Scalable Insets. IEEE Transactions on Visualization and Computer Graphics, 2019, 26, 1-1.	4.4	11
20	Lineage: Visualizing Multivariate Clinical Data in Genealogy Graphs. IEEE Transactions on Visualization and Computer Graphics, 2019, 25, 1543-1558.	4.4	23
21	HiPiler: Visual Exploration of Large Genome Interaction Matrices with Interactive Small Multiples. IEEE Transactions on Visualization and Computer Graphics, 2018, 24, 522-531.	4.4	37
22	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. Cell, 2018, 173, 400-416.e11.	28.9	2,277
23	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	28.9	1,670
24	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. Cell, 2018, 173, 291-304.e6.	28.9	1,718
25	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	28.9	272
26	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. Cell Reports, 2018, 23, 282-296.e4.	6.4	333
27	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	6.4	801
28	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. Cell Systems, 2018, 6, 271-281.e7.	6.2	605
29	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	16.8	750
30	Visual Pattern-Driven Exploration of Big Data. , 2018, 2018, .		2
31	SATORI: a system for ontology-guided visual exploration of biomedical data repositories. Bioinformatics, 2018, 34, 1200-1207.	4.1	10
32	HiGlass: web-based visual exploration and analysis of genome interaction maps. Genome Biology, 2018, 19, 125.	8.8	950
33	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. Cancer Cell, 2017, 31, 181-193.	16.8	532
34	Integrated Molecular Characterization of Uterine Carcinosarcoma. Cancer Cell, 2017, 31, 411-423.	16.8	309
35	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. Cell Reports, 2017, 18, 2780-2794.	6.4	416
36	UpSetR: an R package for the visualization of intersecting sets and their properties. Bioinformatics, 2017, 33, 2938-2940.	4.1	2,255

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37	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , 2017, 32, 204-220.e15.	16.8	642
38	Interactive visual exploration and refinement of cluster assignments. <i>BMC Bioinformatics</i> , 2017, 18, 406.	2.6	17
39	From Visual Exploration to Storytelling and Back Again. <i>Computer Graphics Forum</i> , 2016, 35, 491-500.	3.0	47
40	AVOCADO: Visualization of Workflowâ€œDerived Data Provenance for Reproducible Biomedical Research. <i>Computer Graphics Forum</i> , 2016, 35, 481-490.	3.0	32
41	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. <i>Cell</i> , 2016, 164, 550-563.	28.9	1,695
42	METHODS TO ENHANCE THE REPRODUCIBILITY OF PRECISION MEDICINE. , 2016, , .		2
43	METHODS TO ENHANCE THE REPRODUCIBILITY OF PRECISION MEDICINE. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2016, 21, 180-182.	0.7	6
44	Temporal data. <i>Nature Methods</i> , 2015, 12, 97-97.	19.0	3
45	Genomic Classification of Cutaneous Melanoma. <i>Cell</i> , 2015, 161, 1681-1696.	28.9	2,562
46	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015, 372, 2481-2498.	27.0	2,582
47	Response to "Plotting intersections" by Lentini. <i>Nature Methods</i> , 2015, 12, 281-281.	19.0	1
48	The Molecular Taxonomy of Primary Prostate Cancer. <i>Cell</i> , 2015, 163, 1011-1025.	28.9	2,435
49	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. <i>Cell</i> , 2015, 163, 506-519.	28.9	1,485
50	Domino: Extracting, Comparing, and Manipulating Subsets Across Multiple Tabular Datasets. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2014, 20, 2023-2032.	4.4	53
51	UpSet: Visualization of Intersecting Sets. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2014, 20, 1983-1992.	4.4	1,549
52	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. <i>Cell</i> , 2014, 159, 676-690.	28.9	2,318
53	Characterization of HPV and host genome interactions in primary head and neck cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 15544-15549.	7.1	317
54	Guided visual exploration of genomic stratifications in cancer. <i>Nature Methods</i> , 2014, 11, 884-885.	19.0	20

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55	Comparative analysis of metazoan chromatin organization. <i>Nature</i> , 2014, 512, 449-452.	27.8	363
56	Bar charts and box plots. <i>Nature Methods</i> , 2014, 11, 117-117.	19.0	68
57	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. <i>Cancer Cell</i> , 2014, 26, 319-330.	16.8	665
58	Sets and intersections. <i>Nature Methods</i> , 2014, 11, 779-779.	19.0	80
59	Ontologies in Biological Data Visualization. <i>IEEE Computer Graphics and Applications</i> , 2014, 34, 8-15.	1.2	19
60	The Somatic Genomic Landscape of Glioblastoma. <i>Cell</i> , 2013, 155, 462-477.	28.9	3,979
61	Nozzle: a report generation toolkit for data analysis pipelines. <i>Bioinformatics</i> , 2013, 29, 1089-1091.	4.1	19
62	LineUp: Visual Analysis of Multi-Attribute Rankings. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2013, 19, 2277-2286.	4.4	221
63	Diverse Mechanisms of Somatic Structural Variations in Human Cancer Genomes. <i>Cell</i> , 2013, 153, 919-929.	28.9	308
64	Don't Wear Your New Shoes (Yet): Taking the Right Steps to Become a Successful Principal Investigator. <i>PLoS Computational Biology</i> , 2013, 9, e1002834.	3.2	3
65	Data-driven information retrieval in heterogeneous collections of transcriptomics data links SIM2s to malignant pleural mesothelioma. <i>Bioinformatics</i> , 2012, 28, 246-253.	4.1	13
66	Heat maps. <i>Nature Methods</i> , 2012, 9, 213-213.	19.0	84
67	Networks. <i>Nature Methods</i> , 2012, 9, 115-115.	19.0	10
68	Power of the plane. <i>Nature Methods</i> , 2012, 9, 935-935.	19.0	6
69	Integrating data. <i>Nature Methods</i> , 2012, 9, 315-315.	19.0	6
70	Into the third dimension. <i>Nature Methods</i> , 2012, 9, 851-851.	19.0	11
71	Mapping quantitative data to color. <i>Nature Methods</i> , 2012, 9, 769-769.	19.0	19
72	StratomeX: Visual Analysis of Large-scale Heterogeneous Genomics Data for Cancer Subtype Characterization. <i>Computer Graphics Forum</i> , 2012, 31, 1175-1184.	3.0	74

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73	Visualization of omics data for systems biology. <i>Nature Methods</i> , 2010, 7, S56-S68.	19.0	548
74	Visualizing biological data—now and in the future. <i>Nature Methods</i> , 2010, 7, S2-S4.	19.0	115
75	An information retrieval perspective on visualization of gene expression data with ontological annotation. , 2010, , .		1
76	The Prion Disease Database: a comprehensive transcriptome resource for systems biology research in prion diseases. <i>Database: the Journal of Biological Databases and Curation</i> , 2009, 2009, bap011.	3.0	18
77	A systems approach to prion disease. <i>Molecular Systems Biology</i> , 2009, 5, 252.	7.2	230
78	Prequips—an extensible software platform for integration, visualization and analysis of LC-MS/MS proteomics data. <i>Bioinformatics</i> , 2009, 25, 682-683.	4.1	12
79	Probabilistic retrieval and visualization of biologically relevant microarray experiments. <i>Bioinformatics</i> , 2009, 25, i145-i153.	4.1	41
80	Visualization of large microarray experiments with space maps. <i>BMC Bioinformatics</i> , 2009, 10, .	2.6	5
81	Probabilistic retrieval and visualization of biologically relevant microarray experiments. <i>BMC Bioinformatics</i> , 2009, 10, .	2.6	9
82	An Integrated, Directed Mass Spectrometric Approach for In-depth Characterization of Complex Peptide Mixtures. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 2138-2150.	3.8	127
83	Ten Simple Rules for Organizing a Scientific Meeting. <i>PLoS Computational Biology</i> , 2008, 4, e1000080.	3.2	23
84	Highlights from the Third International Society for Computational Biology Student Council Symposium at the Fifteenth Annual International Conference on Intelligent Systems for Molecular Biology. <i>BMC Bioinformatics</i> , 2007, 8, .	2.6	7
85	Mayday—a microarray data analysis workbench. <i>Bioinformatics</i> , 2006, 22, 1010-1012.	4.1	47
86	A Framework for Visualization of Microarray Data and Integrated Meta Information. <i>Information Visualization</i> , 2005, 4, 164-175.	1.9	19