

Nils Gehlenborg

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EDUCATION

Harvard Medical School & Broad Institute, Boston, MA, USA

Postdoctoral Training, since October 2010

University of Cambridge & European Bioinformatics Institute, Cambridge, UK

PhD in Biological Science, October 2006 - October 2010

University of Tübingen, Tübingen, Germany

MS in Bioinformatics (“Diplom”), October 2000 - March 2006

University of Washington, Seattle, WA, USA

Visiting Graduate Student in Computer Science, September 2003 - June 2004

HONORS & AWARDS

GRANTS

NIH/NHGRI K99/R00 Pathway to Independence Award, 01/2014 - 12/2018

Agilent Technologies Emerging Insights Grant (with Peter J Park), 12/2011 - 12/2012

European Molecular Biology Laboratory (EMBL) PhD Fellowship, 09/2006 - 09/2010

DAAD German Academic Exchange Service Scholarship, 10/2005 - 01/2006

Karl-Steinbuch-Scholarship, 10/2004 - 03/2005

AWARDS

Best Paper Honorable Mention (of 196 submissions) for *Domino*, IEEE InfoVis 2014, 11/2014

Best Paper Award (of 152 submissions) for *LineUp*, IEEE InfoVis 2013, 10/2013

3rd Best Paper Award (of 202 submissions) for *StratomeX*, EG/IEEE EuroVis 2012, 06/2012

Finalist, Illumina iDEA Challenge with *Seqeyes* (with Richard Park and Peter J Park), 06/2011

Best Presentation Award, 5th ISCB Student Council Symposium, 07/2009

bwcon Special Prize IT and Life Sciences 2006 for the *Mayday* Workbench, 06/2006

TRAVEL SUPPORT

Keystone Symposia Future of Science Fund Scholarship, 03/2014

Intelligent Systems for Molecular Biology (ISMB) Conference Travel Fellowship, 07/2013

Sidney Sussex College Parry-Dutton Travel Award, 10/2008

Weill-Cornell ICB NYC Computational Biology Student Meeting Travel Fellowship, 07/2008

OTHER

AAAS/Science Program for Excellence in Science, 09/2007 - 08/2008

Agilent Technologies Inc. European “Chill-Out” Program, 09/2000 - 07/2005

RESEARCH & WORK EXPERIENCE

Broad Institute, Cambridge, MA, USA

Associated Researcher, Cancer Program

- since 01/2011 Designed and implemented *Nozzle* reporting system for the high-throughput cancer genome analysis platform of *The Cancer Genome Atlas* project to generate and disseminate hundreds of analysis reports for over 20 cancer types on a monthly basis.
- Prototyping and advising on infrastructure and user interfaces for a cancer genomics portal.

Harvard Medical School, Boston, MA, USA

Research Associate, Peter J. Park Lab, Center for Biomedical Informatics

- since 10/2010 Received an *NIH/NHGRI K99/R00 Pathway to Independence* award.
- Leading *Refinery Platform* project with a team of two programmers and one PhD student to develop a web-based data analysis platform for high-throughput genomics data that combines a comprehensive data repository with analysis pipelines and visualizations tools.
- Coordinating *StratomeX* project and studying methods to support visual exploration of heterogeneous cancer genomics data sets for identification and characterization of tumor subtypes in large patient populations.
- Developed multiple visualization tools, including *UpSet* for sets and their intersections, *LineUp* for multi-attribute rankings, and *Domino* for relationships between sets.
- Researching new methods to visualize complex structural variation events in the context of functional (epi)genomics data for large patient populations.

European Bioinformatics Institute, Cambridge, UK

Predoctoral Fellow, Functional Genomics Group

- 10/2006 - 10/2010 Designed and implemented *Space Maps* visualization method for gene expression data sets with hundreds of samples (with Alvis Brazma).
- Developed information retrieval methods and visual exploration tools for large collections of transcriptomics data sets (with Alvis Brazma and Samuel Kaski).

Helsinki University of Technology, Helsinki, Finland

Visitor, Department of Information and Computer Science (now part of Aalto University)

- 04/2008 - 06/2008 Worked on supervised dimensionality reduction methods for high-dimensional gene expression data sets (with Samuel Kaski).

Institute for Systems Biology, Seattle, WA, USA

Intern & Software Developer, Hood & Aebersold Labs

- 06/2006 - 09/2006 Developed a workflow and a *Prequips* plug-in to support an automated, directed LC-MS/MS approach for peptide identification (with Ruedi Aebersold and Bruno Domon, ETH Zürich).
- 09/2005 - 05/2006 Developed *Prequips*, an extensible software platform for integration and visualization of proteomics data from mass spectrometry experiments (with Leroy Hood and Daehee Hwang).
- Designed and implemented the *Prion Disease Database* in close collaboration with a group of systems biologists (with Leroy Hood, Daehee Hwang and Inyoul Lee).

- 07/2004 - 09/2004 Worked on an in-house pipeline for automated preprocessing and analysis of microarray data using R/Bioconductor (with Daehee Hwang and Inyoul Lee).
Built a web-based tool to create interaction networks from data in the Human Protein Reference Database (with Daehee Hwang and Inyoul Lee).

University of Tübingen, Tübingen, Germany

Research Assistant, Center for Bioinformatics

- 10/2004 - 08/2005 Designed and implemented an enhanced heatmap visualization method (with Kay Nieselt).
09/2002 - 07/2003 Developed the core software and visualization methods for *Mayday* microarray data analysis workbench (with Kay Nieselt).
06/2001 - 12/2001 Explored parallelization approaches for simulation of cellular processes (with Markus Schwehm).

University of Washington, Seattle, WA, USA

Student Researcher, Department of Computer Science and Engineering

- 01/2004 - 06/2004 Researched methods to detect secondary RNA structures in genomic sequences (with Martin Tompa).

Agilent Technologies Inc., Böblingen, Germany

Intern, Patient Monitoring Division R&D (now part of Philips Healthcare)

- 02/2001 - 03/2001 Developed a simulator for measurements from a medical device.
07/2000 - 09/2000 Developed a printer driver and queue for an embedded patient monitoring platform.

City Hospital, Waiblingen, Germany

Nursing Assistant, Department of Internal Medicine

- 08/1999 - 06/2000 Worked as a nursing assistant on a medical floor in a medium-sized hospital in fulfillment of the compulsory national service.

TEACHING AND MENTORING EXPERIENCE

Harvard Medical School, Boston, MA, USA

Research Associate, Peter J. Park Lab, Center for Biomedical Informatics

- since 05/2014 Anton Xue, high school student at Boston Latin School. *Role*: internship mentor
since 08/2013 Stefan Luger, MSc student at Johannes-Kepler University Linz. *Role*: co-advisor
06/2014 - 08/2014 Jeremy Liu, undergraduate student at Yale University. *Role*: internship mentor
07/2011 - 03/2012 Alexander Lex, PhD student at Graz University of Technology. *Role*: co-advisor
10/2010 - 03/2014 Richard Park, PhD student at Boston University. *Role*: co-mentor

University of Tübingen, Tübingen, Germany

Teaching Assistant, Department of Cognitive and Information Sciences

- 04/2005 - 07/2005 Graduate-level course "Microarray Bioinformatics" (taught by Kay Nieselt).
04/2002 - 07/2002 Undergraduate-level course "Introduction to Computer Science II - Assembler Programming" (taught by Rüdiger Loos).

University of Washington, Seattle, WA, USA

Tutor, Department of Computer Science and Engineering

04/2004 - 06/2004 Undergraduate-level course “Concepts and Tools for Software Development” (taught by Craig Chambers).

PROFESSIONAL ACTIVITIES

LEADERSHIP

Steering Committee, IEEE Symposium on Biological Data Visualization, since 10/2012

Director, International Society for Computational Biology, 01/2010 - 01/2011

Chair, Student Council of the International Society of Computational Biology, 01/2008 - 01/2009

EDITORIAL BOARDS

Associate Editor, BMC Bioinformatics, since 10/2013

CONFERENCE & WORKSHOP ORGANIZATION

Organizer, ISMB/ECCB 2013 Integrated Visualization and Computing Workshop (Berlin, Germany), 07/2013

General Chair, BioVis 2012: IEEE Symposium on Biological Data Visualization (Seattle, WA, USA), 10/2012

Organizer, ISMB 2012 Postdoc to Principal Investigator Workshop (Long Beach, CA, USA), 07/2012

General Chair, BioVis 2011: IEEE Symposium on Biological Data Visualization (Providence, RI, USA), 10/2011

Organizer, ISMB/ECCB 2011 Data Visualization & User Interfaces Workshop (Vienna, Austria), 07/2011

Poster Chair, VIZBI 2011: A Workshop on Visualizing Biological Data (Boston, MA, USA), 03/2011

Co-Chair, VIZBI 2010: EMBO Workshop on Visualizing Biological Data (Heidelberg, Germany), 03/2010

Conference Chair, 3rd ISCB Student Council Symposium (Vienna, Austria), 07/2007

Conference Chair, 2nd ISCB Student Council Symposium (Fortaleza, Brazil), 08/2006

PROGRAM COMMITTEE

16th Eurographics Conference on Visualization - Short Papers (Swansea, UK), 06/2014

ISMB/ECCB 2013 (Berlin, Germany), 07/2013

3rd Eurographics Workshop on Visual Computing in Biology and Medicine (Norrköping, Sweden), 09/2012

8th ISCB Student Council Symposium (Long Beach, CA, USA), 07/2012

14th Eurographics/IEEE Symposium on Visualization - Short Papers (Vienna, Austria), 06/2012

Art and Science Exhibition, ISMB 2010 (Boston, MA, USA), 07/2010

6th ISCB Student Council Symposium (Boston, MA, USA), 07/2010

2nd Eurographics Workshop on Visual Computing in Biology and Medicine (Leipzig, Germany), 07/2010

Visual Reflections on Science Exhibition, ISMB/ECCB 2009 (Stockholm, Sweden), 07/2009

5th ISCB Student Council Symposium (Stockholm, Sweden), 06/2009

SCAMPS PhD Symposium 2009 (Cambridge, UK), 04/2009

Visual Reflections on Science Exhibition, ISMB 2008 (Toronto, Canada), 07/2008

4th ISCB Student Council Symposium (Toronto, Canada), 07/2008

BioSysBio 2007 (Manchester, UK), 01/2007

REVIEWING

Journals: Nature Methods, Nature Biotechnology, Bioinformatics, PLoS Computational Biology, BMC Bioinformatics, BMC Genomics, Nucleic Acids Research, PLoS ONE, Proteomics, Computers & Graphics, Journal of Personalized Medicine; *Conferences*: Pacific Symposium on Biocomputing (2015), ACM SIG CHI (2013), IEEE Symposium on Biological Data Visualization (2013 - 2014), Eurographics/IEEE Symposium on Visualization (2011 - 2014); IEEE Information Visualization Conference (2010 - 2014), IEEE Visual Analytics Science and Technology Conference (2012), Asia Pacific Bioinformatics Conference (2010), British Computer Society HCI Conference (2009 - 2010)

SEMINAR, PANEL & COURSE ORGANIZATION

Co-Organizer, Panel on “Challenges in Visualizing Biological Data” at VisWeek 2010, 10/2010

Co-Organizer, EBI Interfaces Interest Group (Usability, Aesthetics, Visualization), 10/2009 - 10/2010

Co-Organizer, EBI PhD Student Lunch Seminar Series, 03/2009 - 12/2009

Organizer, Visualization Discussion Group at the EBI, 12/2007 - 09/2009

Member, Working Group on EMBL PhD Course in Molecular Systems Biology, 01/2007 - 02/2008

MEMBERSHIP

International Society for Computational Biology (ISCB) (since 2004), Institute of Electrical and Electronics Engineers (IEEE) (since 2005), American Association for the Advancement of Science (AAAS) (since 2007)

PRESENTATIONS

INVITED TALKS

1. TBD, Gordon Research Conference on Visualization in Science and Education, Lewiston, ME, USA (08/2015)
2. “Guided Visual Exploration of Patient Stratifications in Cancer Genomics”, Beyond the Genome: Cancer Genomics, Boston, MA, USA (10/2014)
3. “Visual Exploration of Clinical and Genomic Data for Patient Stratification”, Simons Foundation/New York Bioinformatics User Group Biotech Symposium, New York, NY, USA (09/2014)
4. “The Impact of the ISCB Student Council”, 10th ISCB Student Council Symposium, Boston, MA, USA (07/2014)
5. “A Primer on Visualization for Insight and Communication”, Gordon Research Seminar on Marine Microbes, Waltham, MA, USA (06/2014)
6. “Building an Integrative Data Visualization Platform: Challenges and Insights”, Broad Institute Computational Biology and Bioinformatics Meeting, Cambridge, MA, USA (05/2014)
7. “Integrated Analysis and Visualization of Large-Scale Biological Data with the Refinery Platform”, Bio-IT World Expo 2014, Boston, MA, USA (04/2014)
8. “A Little Data - Challenges and Opportunities in Building Visualization Tools for Biomedical Scientists”, Harvard School of Engineering and Applied Sciences, Cambridge, MA, USA (02/2014)
9. “Visual Analysis of Cancer Genomics Data for Subtype Exploration”, Worcester Polytechnic Institute, Worcester, MA, USA (11/2013)
10. “Tumor Subtype Exploration through Visual Integration”, British Columbia Genome Science Centre, Vancouver, BC, Canada (09/2013)
11. “Visual Exploration of Cancer Genomics Data for Identification and Characterization of Tumor Subtypes”, BioIT World Expo 2013, Boston, USA (04/2013)

12. “Visualization and Analysis of Large (Epi)Genomics Data Sets with Refinery”, University of Tokyo, Tokyo, Japan (02/2013)
13. “Data Analysis & Visualization for The Cancer Genome Atlas”, Graz University of Technology, Graz, Austria (03/2012)
14. “Exploration and Visualization of Transcriptomics Data”, Harvard Medical School, Boston, MA, USA (06/2010)
15. “Exploration and Visualization of Transcriptomics Data”, Broad Institute of MIT and Harvard, Cambridge, MA, USA (06/2010)
16. “Exploration and Visualization of Transcriptomics Data”, The Jackson Laboratory, Bar Harbor, ME, USA (05/2010)
17. “Exploration and Visualization of Transcriptomics Data”, Sage Bionetworks, Seattle, WA, USA (05/2010)
18. “Exploration and Visualization of Transcriptomics Data”, Institute for Systems Biology, Seattle, WA, USA (05/2010)
19. “Visual Exploration of Large Gene Expression Data Sets with Space Maps”, University of Leeds – School of Computing, Leeds, UK (03/2010)
20. “Exploring Biological High-Throughput Data”, Netherlands Bioinformatics Centre – RSG BioCafé, Utrecht, The Netherlands (10/2009)

SELECTED ORAL PRESENTATIONS

1. “Refinery Platform - Integrating Visualization and Analysis of Large-Scale Biological Data”, Bioinformatics Open Source Conference (BOSC) 2013, Berlin, Germany (07/2013)
2. “Visual Exploration for Cancer Subtype Analysis”, *ISMB/ECCB 2013*, Berlin, Germany (07/2013)
3. “Supporting Subtype Characterization Through Integrative Visualization of Cancer Genomics Data Sets”, *1st Annual The Cancer Genome Atlas (TCGA) Scientific Symposium*, National Harbor, MD, USA (11/2011)
4. “Introduction to Firehose: The Broad GDAC Pipeline” (presented with M Noble), *3rd National Cancer Institute Translational Science Meeting*, Washington DC, USA (07/2011)
5. “Broad/Harvard GDAC Analysis Pipeline”, *The Cancer Genome Atlas Consortium Meeting*, Washington DC, USA (04/2011)
6. “Visualization of Large Microarray Experiments with Space Maps”, *5th ISCB Student Council Symposium*, Stockholm, Sweden (06/2009) **Best Presentation Award**
7. “Visualization of Large Microarray Experiments with Space Maps”, *SCAMPS PhD Symposium 2009*, Cambridge, UK (04/2009)
8. “Interfaces for Visualization and Exploration of Functional Genomics Data Warehouses”, *VisWeek Doctoral Colloquium*, Columbus, OH, USA (10/2008)

WORKSHOPS

1. “Strategies for Visualizing Data” (with B Wong, Broad Institute), half-day workshop at *Broad Institute*, Cambridge, MA, USA (07/2014)
2. “Visualization in Biology: From the Basics to Big Data”, half-day workshop at *BioIT World 2014*, Boston, USA (04/2014)
3. “Visualization in Biology: From the Basics to Big Data”, half-day workshop at *Big Data in Pharma 2013*, Boston, MA, USA (09/2013)
4. “Visual Strategies for Exploring and Explaining Scientific Data” (with B Wong, Broad Institute), half-day workshop at *Broad Institute*, Cambridge, MA, USA (05/2013)

5. “Visualization in Biology: From the Basics to Big Data”, half-day workshop at *BioIT World 2013*, Boston, USA (04/2013)
6. “StratomeX and enRoute: Integrative Visualization with Caleydo” (with A Lex, Harvard University), half-day tutorial at *VIZBI 2013*, Cambridge, MA, USA (03/2013)
7. “Introduction to Biological Information Visualization” (with J Kennedy, Edinburgh Napier University), half-day workshop at *University of Tokyo*, Tokyo, Japan (02/2013)
8. “Visualization in Biology: From the Basics to Big Data”, half-day workshop at *Molecular Med Tri-Con 2013*, San Francisco, CA, USA (02/2013)
9. “Visualization in Biology: From the Basics to Big Data”, half-day workshop at *BioIT World 2012*, Boston, MA, USA (04/2012)
10. “Data Visualization”, Presentation in *Data Visualization and User Interfaces Workshop at ISMB/ECCB 2011*, Vienna, Austria (07/2011)
11. “Visualization of Large-Scale Biological Data” (with M Meyer, Harvard University), half-day workshop at *BioIT World 2011*, Boston, MA, USA (04/2011)
12. “Visualization of Large-Scale Biological Data” (with K Nieselt, University of Tübingen), half-day workshop at *BioIT World Europe 2010*, Hanover, Germany (10/2010)

PUBLICATIONS

MANUSCRIPTS IN PREPARATION

1. **N Gehlenborg**, SJ Ho Sui, I Sytchev, R Park, P Haseley, S Luger, A Xue, J Liu, M Streit, W Hide, PJ Park, “Refinery: a web-based platform for interpretation of large-scale (epi)genomics data analyses”.
2. SJ Ho Sui*, S Das*, **N Gehlenborg**, ME Merrill, I Sytchev, RW Park, J Hutchinson, S Corlosquet, P Haseley, T Hansen, O Hofmann, PJ Park, W Hide, “A Stem Cell Commons for the Harvard Stem Cell Institute”.

MANUSCRIPTS UNDER REVIEW

1. The Cancer Genome Atlas Network, incl. **N Gehlenborg**, “Comprehensive Genomic Characterization of Head and Neck Squamous Cell Carcinomas”. Revision under review at *Nature*.
2. The Cancer Genome Atlas Network, incl. **N Gehlenborg**, “Comprehensive and Integrative Genomic Characterization of Diffuse Lower Grade Gliomas”. Under review at *New England Journal of Medicine*.

JOURNAL & CONFERENCE PAPERS

1. The Cancer Genome Atlas Network, incl. **N Gehlenborg**, “Integrated Genomic Characterization of Papillary Thyroid Carcinoma”. To appear in *Cell*.
2. M Parfenov*, CS Pedamallu*, **N Gehlenborg**, SS Freeman, L Danilova, CA Bristow, S Lee, A Hadjipanayis, E Ivanova, MD Wilkerson, A Protopopov, L Yang, S Seth, X Song, J Tang, X Ren, J Zhang, A Pantazi, N Santoso, AW Xu, H Mahadeshwar, DA Wheeler, RI Haddad, J Jung, AI Ojesina, N Isaeva, WG Yarbrough, DN Hayes, JR Grandis, AK El-Naggar, M Meyerson, PJ Park, L Chin, JG Seidman, PS Hammerman**, R Kucheralapati**, TCGA Network, “Characterization of HPV and Host-Genome Interactions in Primary Head and Neck Cancers”. To appear in *Proceedings of the National Academy of Sciences USA*.
3. A Lex, **N Gehlenborg**, H Strobel, R Vuillemot and H Pfister, “UpSet: Visualization of Intersecting Sets”. To appear in *IEEE Transactions on Visualization and Computer Graphics (Proceedings of InfoVis ’14)*.
4. S Gratzl, **N Gehlenborg**, A Lex, H Pfister and M Streit, “Domino: Extracting, Comparing, and Manipulating Subsets across Multiple Tabular Datasets”. To appear in *IEEE Transactions on Visualization and Computer Graphics (Proceedings of InfoVis ’14)*. **IEEE InfoVis 2014 Best Paper Honorable Mention**

5. M Streit*, A Lex*, S Gratzl, C Partl, D Schmalstieg, H Pfister, PJ Park** and N Gehlenborg**, “Guided Visual Exploration of Genomic Stratifications in Cancer”. *Nature Methods* 11:884–885 (2014).
6. JWK Ho*, YL Jung*, Tao Liu*, BH Alver, S Lee, K Ikegami, K-A Sohn, A Minoda, MY Tolstorukov, A Apert, SCJ Parker, T Gu, A Kundaje, NC Riddle, E Bishop, TA Egelhofer, SS Hu, AA Alekseyenko, A Rechtsteiner, D Asker, JA Belsky, SK Bowman, QB Chen, RAJ Chen, DS Day, Y Dong, AC Dose, X Duan, CB Epstein, S Ercan, EA Feingold, F Ferrari, J M Garrigues, N Gehlenborg, PJ Good, P Haseley, D He, M Herrmann, MM Hoffman, TE Jeffers, PV Kharchenko, PK Zwierz, CV Kotwaliwale, N Kumar, SA Langley, EN Larschan, I Latorre, MW Libbrecht, X Lin, R Park, MJ Pazin, HN Pham, A Plachetka, B Qin, YB Schwartz, N Shores, P Stempor, A Vielle, C Wang, CM Whittle, H Xue, RE Kingston, JH Kim, BE Bernstein, AF Dernburg, V Pirrotta, MI Kuroda, WS Noble, TD Tullius, M Kellis, DM MacAlpine, S Strome, SCR Elgin, XS Liu, JD Lieb, J Ahringer, GH Karpen and PJ Park, “Comparative analysis of metazoan chromatin organization”. *Nature* 512:449–452, 2014.
7. CF Davis*, CJ Ricketts*, M Wang*, L Yang*, AD Cherniack, H Shen, C Buhay, H Kang, SC Kim, CC Fahey, KE Hacker, G Bhanot, DA Gordenin, A Chu, PH Gunaratne, MBiehl, S Seth, BA Kaipparettu, CA Bristow, LA Donehower, EM Wallen, AB Smith, SK Tickoo, P Tamboli, V Reuter, LS Schmidt, JJ Hsieh, TK Choueiri, AA Hakimi, The Cancer Genome Atlas Research Network incl. N Gehlenborg, L Chin, M Meyerson, R Kucherlapati, WY Park, AG Robertson, PW Laird, EP Henske, DJ Kwiatkowski, PJ Park, M Morgan, B Shuch, DMuzny, DA Wheeler, WM Linehan, RA Gibbs, WK Rathmell**, CJ Creighton**, “The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma”, *Cell*. Published online ahead of print.
8. KA Hoadley*, C Yau*, DM Wolf*, AD Cherniack*, D Tamborero, S Ng, MDM Leiserson, B Niu, MD McLellan, V Uzunangelov, J Zhang, C Kandoth, R Akbani, H Shen, L Omberg, A Chu, AA Margolin, LJ van’t Veer, N Lopez-Bigas, PW Laird, BJ Raphael, L Ding, AG Robertson, LA Byers, GB Mills, JN Weinstein, C Van Waes, Z Chen, EA Collisson, The Cancer Genome Atlas Network incl. N Gehlenborg, CC Benz, CM Perou, JM Stuart, “Multi-platform integration of 12 cancer types reveals cell-of-origin classes with distinct molecular signatures”, *Cell*. Published online ahead of print.
9. The Cancer Genome Atlas Network, incl. N Gehlenborg, “Comprehensive Molecular Characterization of Gastric Adenocarcinoma”, *Nature*. Published online ahead of print.
10. The Cancer Genome Atlas Network, incl. N Gehlenborg, “Comprehensive Molecular Profiling of Lung Adenocarcinoma”, *Nature*. Published online ahead of print.
11. A Lex and N Gehlenborg, “Points of View: Sets and Intersections”, *Nature Methods* 11:779 (2014). Invited editorial.
12. S Carpendale, M Chen, D Evanko, N Gehlenborg, C Görg, L Hunter, F Rowland, M-A Storey and H Strobel, “Ontologies in Biological Data Visualization”, *IEEE Computer Graphics and Applications* 34:8–15 (2014). **Featured in IEEE Computer in May 2014**
13. The Cancer Genome Atlas Network, incl. N Gehlenborg, “Comprehensive Molecular Characterization of Urothelial Bladder Carcinoma”, *Nature* 507:315–322 (2014).
14. M Streit and N Gehlenborg, “Points of View: Bar Charts and Box Plots”, *Nature Methods* 11:117 (2014). Invited editorial.
15. SJ Ho Sui, ME Merrill, N Gehlenborg, P Haseley, I Sytchev, RW Park, P Rocca-Serra, S Corlosquet, A Gonzalez-Beltran, E Maguire, O Hofmann, PJ Park, S Das, SA Sansone, W Hide, “The Stem Cell Commons: an exemplar for data integration in the biomedical domain driven by the ISA framework”, *AMIA Summits Translational Science Proceedings* 2013:70 (2013). Extended abstract.
16. S Gratzl, A Lex, N Gehlenborg, H Pfister and M Streit, “LineUp: Visual Analysis of Multi-Attribute Rankings”, *IEEE Transactions on Visualization and Computer Graphics* 19:2277–2286 (2013). **IEEE InfoVis 2013 Best Paper Award and featured in IEEE Computing Now, Harvard SEAS News, Forbes, Scientific Computing, Der Standard**
17. CW Brennan, RG Verhaak, A McKenna, B Campos, H Nounshmehr, SR Salama, S Zheng, D Chakravarty, JZ Sanborn, SH Berman, R Beroukhim, B Bernard, CJ Wu, G Genovese, I Shmulevich, J Barnholtz-Sloan, L Zou, R Vegesna, SA Shukla, G Ciriello, WK Yung, W Zhang, C Sougnez, T Mikkelsen, K Aldape, DD

- Bigner, EG Van Meir, M Prados, A Sloan, KL Black, J Eschbacher, G Finocchiaro, W Friedman, DW Andrews, A Guha, M Iacocca, BP O'Neill, G Foltz, J Myers, DJ Weisenberger, R Penny, R Kucherlapati, CM Perou, DN Hayes, R Gibbs, M Marra, GB Mills, E Lander, P Spellman, R Wilson, C Sander, J Weinstein, M Meyerson, S Gabriel, PW Laird, D Haussler, G Getz, L Chin, The Cancer Genome Atlas Network, incl. **N Gehlenborg**, "The somatic genomic landscape of glioblastoma", *Cell* 155:462-77 (2013).
18. J de Ridder*, T Abeel*, M Michaut, VP Satagopam and **N Gehlenborg**, "Don't Wear Your New Shoes (Yet): Taking the Right Steps to Become a Successful Principal Investigator", *PLoS Computational Biology* 9:e1002834 (2013). Workshop report.
 19. The Cancer Genome Atlas Network, incl. **N Gehlenborg**, "The Cancer Genome Atlas Pan-Cancer analysis project", *Nature Genetics* 45:1113-1120 (2013).
 20. **N Gehlenborg**, MS Noble, G Getz, L Chin and PJ Park, "Nozzle: a report generation toolkit for data analysis pipelines", *Bioinformatics* 29:1089-1091 (2013).
 21. The Cancer Genome Atlas Network, incl. **N Gehlenborg**, "Comprehensive molecular characterization of clear cell renal cell carcinoma", *Nature* 499:43-49 (2013).
 22. L Yang, LJ Luquette, **N Gehlenborg**, R Xi, PS Haseley, C-H Hsieh, C Zhang, X Ren, A Protopopov, L Chin, R Kucherlapati, C Lee, PJ Park and The Cancer Genome Atlas Network, "Diverse mechanisms of somatic structural variations in human cancer genomes", *Cell* 153:919-929 (2013).
 23. **N Gehlenborg** and B Wong, "Points of View: Power of the Plane". *Nature Methods* 9:935 (2012). Invited editorial.
 24. **N Gehlenborg** and B Wong, "Points of View: Into the Third Dimension". *Nature Methods* 9:851 (2012). Invited editorial.
 25. **N Gehlenborg** and B Wong, "Points of View: Mapping Quantitative Data to Color". *Nature Methods* 9:769 (2012). Invited editorial.
 26. **N Gehlenborg** and B Wong, "Points of View: Integrating Data". *Nature Methods* 9:315 (2012). Invited editorial.
 27. **N Gehlenborg** and B Wong, "Points of View: Heat maps". *Nature Methods* 9:213 (2012). Invited editorial.
 28. **N Gehlenborg** and B Wong, "Points of View: Networks". *Nature Methods* 9:115 (2012). Invited editorial.
 29. The Cancer Genome Atlas Network, incl. **N Gehlenborg**, "Comprehensive molecular portraits of human breast tumours". *Nature* 490:61-70 (2012).
 30. The Cancer Genome Atlas Network, incl. **N Gehlenborg**, "Comprehensive genomic characterization of squamous cell lung cancers". *Nature* 489:519-525 (2012).
 31. The Cancer Genome Atlas Network, incl. **N Gehlenborg**, "Comprehensive molecular characterization of human colon and rectal cancer". *Nature* 487:330-337 (2012).
 32. A Lex, M Streit, H-J Schulz, C Partl, D Schmalstieg, PJ Park, **N Gehlenborg**, "StratomeX: Visual Analysis of Large-Scale Heterogeneous Genomics Data for Cancer Subtype Characterization". *Computer Graphics Forum (Proceedings of EuroVis 2012)* 31:1175-1184 (2012). **EuroVis 2012 3rd Best Paper Award**
 33. J Caldas*, **N Gehlenborg***, E Kettunen, A Faisal, M Rönty, AG Nicholson, S Knuutila, A Brazma and S Kaski, "Data-Driven Information Retrieval in Heterogeneous Collections of Transcriptomics Data Links SIM2s to Malignant Pleural Mesothelioma", *Bioinformatics* 28:246-253 (2012).
 34. **N Gehlenborg**, SI O'Donoghue, NS Baliga, A Goesmann, MA Hibbs, H Kitano, O Kohlbacher, H Neuweger, R Schneider, D Tenenbaum and AC Gavin, "Visualization of Omics Data for Systems Biology", *Nature Methods* 7:S56-S68 (2010).
 35. SI O'Donoghue, AC Gavin, **N Gehlenborg**, DS Goodsell, JK Hériché, CB Nielsen, C North, AJ Olson, JB Procter, DW Shattuck, T Walter and B Wong, "Visualizing biological data - now and in the future", *Nature Methods* 7:S2-S4 (2010). Commentary.

36. J Peltonen, H Aidos, **N Gehlenborg**, A Brazma and S Kaski, “An Information Retrieval Perspective on Visualization of Gene Expression Data with Ontological Annotation”, *Proceedings of the IEEE 2010 International Conference on Acoustics, Speech, and Signal Processing (ICASSP 2010)*, 2178 - 2181 (2010).
37. **N Gehlenborg***, D Hwang*, IY Lee*, H Yoo, B Petritis, D Baxter, R Pitstick, B Marzolf, SJ DeArmond, GA Carlson and LE Hood, “The Prion Disease Database: A Comprehensive Transcriptome Resource for Systems Biology Research in Prion Diseases”, *Database* **2009**:bap011 (2009).
38. **N Gehlenborg** and A Brazma, “Visualization of Large Microarray Experiments with Space Maps”, *BMC Bioinformatics* **10**(Suppl 13):O7 (2009). Extended abstract.
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