Rebecka Jenny Jörnsten

CONTACT INFORMATION	MVH3029 *Phone:* (46) 31 772-3534 Mathematical Sciences University of Gothenburg/Chalmers *E-mail:* jornsten@chalmers.se Gothenburg, 41296, Sweden *URL:* www.math.chalmers.se/~jornsten

RESEARCH INTERESTS

Model Selection. Data integration. Systems Biology. Interface of information theory and statistics.

EDUCATION

Ph.D. in Statistics, December 2001. University of California at Berkeley
Data compression and Its Statistical Implications, with applications to the analysis of Microarray images. Advisor: Bin Yu

M.A. in Statistics, May 1998. University of California at Berkeley

M.Sc. in Engineering Physics, May 1996. Lund Institute of Technology, Lund, Sweden
Sub-pixel resolution in PIXE images. Advisor: Anders Holtsberg

PROFESSIONAL APPOINTMENTS

Professor, Mathematical Sciences, Chalmers/University of Gothenburg, June 2016 - present

Associate Professor, Mathematical Sciences, Chalmers/University of Gothenburg, January 2009 - June 2016 (Maternity leave June 2013 - October 2014)

Associate Professor with Tenure, Department of Statistics and Biostatistics, Rutgers University, July 2008 - December 2008

Assistant Professor, Department of Statistics and Biostatistics, Rutgers University, January 2002-June 2008.

Consultant, Math Center, Lucent Bell Labs, Murray Hill, New Jersey, Sep 1998, April 2000

GRANTS AND AWARDS

- Vetenskapsrådet (Swedish Research Council) Project Research Grant, "Network modeling for large-scale human cancer studies: data integration, validation and multiresolution networks." (2014-2017) PI. (5060tKr)
- Astra Zeneca: "The SciLifeLab cancer stem cell program: systems-scale analysis and prospective modeling of cancer stem cells from patients". 2014-2018. co-PI. PI is Sven Nelander. (20000tKR of which 1085tKr for co-PI)
- Knut & Alice Wallenberg foundation. "Stochastics for big data and big systems bridging local and global". 2012-2016. co-PI. PI Holger Rootzen.
- Åke Wibergs stiftelse. "Systembiologisk metodik för tumörforskning: effektiv identifiering och testning av biomarkörer och targets" Diarienr: 756194060 2012-2014 (co-PI, PI Sven Nelander, SciLife).
- Barncancerfonden. "Systematic experimental testing of in silico designed therapies and biomarkers against childhood neural tumors" Diarienr: PROJ11-057. 2012-2014 (co-PI, PI Sven Nelander, SciLife).
- Strategic Highway Research Program (SHRP 2). "Analysis of Naturalistic Driving Data - driver inattention and crash risk in rear-end collisions". 2011-2013 (co-PI, joint project with SAFER (vehicle and traffic safety center at Chalmers, Chalmers/GU Mathematical Sciences, Volvo cars).
- Vetenskapsrådet (Swedish Research Council) Project Research Grant, "Model Selection in Clustering and Multiple Testing", 2010-2012 (PI).

- Environmental Protection Agency RD-83272101-0 Bioinformatics Center grant, 2006-2008 (10%).
- National Science Foundation award DMS-0306360. "Clustering: visualization, validation and response oriented methods.", 2003-2006 (PI).
- National Science Foundation award DBI-0629346. "DNA barcode data analysis initiative: tools for a new generation of biodiversity data workshops. 2006-2007 (co-PI).
- National Science Foundation award "Eleventh New Researchers Conference in Statistics and Probability", 2008-2009 (PI).
- National Cancer Institute award "Eleventh and Twelfth New Researchers Conference in Statistics and Probability", 2008-2010 (PI).

REVIEWER OF
RESEARCH GRANTS

- Panelist National Science Foundation, Division of Mathematical Sciences, 2009
- Panelist National Cancer Institute, R13 grants, 2008-2010
- External reviewer, National Security Agency, Mathematical sciences, 2010
- External reviewer, NSERC, 2008

PUBLICATIONS:

JOURNAL PUBLICATIONS

1. Oh, Jung Hun; Thor, Maria ; Olsson, Caroline ; Skokic, Viktor; **Jrnsten, Rebecka**; Alsadius, David; Pettersson, Niclas; Steineck, Gunnar; Deasy, Joseph (2016). A factor analysis approach to investigate the relationship between radiation dose and side effects after radiotherapy from patient reported. *To appear in Methods of Information in Medicine*

2. Kling, T., Johansson, P., Sanchez, J., Marinescu, V.M., **Jörnsten, R.**, Nelander, S. (2015) Efficient exploration of pan-cancer networks by generalized covariance selection and interactive web content *Nuclear Acids Research 43(15), e98, 2015 gkv413*

3. Barrenäs, F., Bruhn, S., **Jörnsten R.**, Langston, M., C., Nester, C., Rogers, G., Wang, H., Zhao, Y., and Benson, M. (2014) DNA methylation controls transcription factor binding in allergen-challenged CD4+ cells. *PLoS Genetics, January 2014, 10(1), e1004059.*

4. The Cancer Genome Atlas Research Network; Genome Characterization Center, Chang K, Creighton CJ, Davis C, Donehower L, Drummond J, Wheeler D, Ally A, Balasundaram M, Birol I, Butterfield YS, Chu A, Chuah E, Chun HJ, Dhalla N, Guin R, Hirst M, Hirst C, Holt RA, Jones SJ, Lee D, Li HI, Marra MA, Mayo M, Moore RA, Mungall AJ, Robertson AG, Schein JE, Sipahimalani P, Tam A, Thiessen N, Varhol RJ, Beroukhim R, Bhatt AS, Brooks AN, Cherniack AD, Freeman SS, Gabriel SB, Helman E, Jung J, Meyerson M, Ojesina AI, Pedamallu CS, Saksena G, Schumacher SE, Tabak B, Zack T, Lander ES, Bristow CA, Hadjipanayis A, Haseley P, Kucherlapati R, Lee S, Lee E, Luquette LJ, Mahadeshwar HS, Pantazi A, Parfenov M, Park PJ, Protopopov A, Ren X, Santoso N, Seidman J, Seth S, Song X, Tang J, Xi R, Xu AW, Yang L, Zeng D, Auman JT, Balu S, Buda E, Fan C, Hoadley KA, Jones CD, Meng S, Mieczkowski PA, Parker JS, Perou CM, Roach J, Shi Y, Silva GO, Tan D, Veluvolu U, Waring S, Wilkerson MD, Wu J, Zhao W, Bodenheimer T, Hayes DN, Hoyle AP, Jeffreys SR, Mose LE, Simons JV, Soloway MG, Baylin SB, Berman BP, Bootwalla MS, Danilova L, Herman JG, Hinoue T, Laird PW, Rhie SK, Shen H, Triche T, Weisenberger DJ, Carter SL, Cibulskis K, Chin L, Zhang J, Getz G, Sougnez C, Wang M; Genome Data Analysis Center, Saksena G, Carter SL, Cibulskis K, Chin L, Zhang J, Getz G, Dinh H, Doddapaneni HV, Gibbs R, Gunaratne P, Han Y, Kalra D, Kovar C, Lewis L, Morgan M, Morton D, Muzny D, Reid J, Xi L, Cho J, Dicara D, Frazer S, Gehlenborg N, Heiman DI, Kim J, Lawrence MS, Lin P, Liu Y, Noble MS, Stojanov P, Voet D, Zhang H, Zou L, Stewart C, Bernard B, Bressler R, Eakin A, Iype L, Knijnenburg T, Kramer R, Kreisberg R, Leinonen K, Lin J, Liu Y, Miller M, Reynolds SM, Rovira H, Shmulevich I, Thorsson V, Yang D, Zhang W, Amin S, Wu CJ, Wu CC, Akbani R, Aldape K, Baggerly KA, Broom B, Casasent TD, Cleland J, Creighton C, Dodda D, Edgerton M, Han L, Herbrich SM, Ju Z, Kim H, Lerner S, Li J, Liang H, Liu W, Lorenzi PL, Lu Y, Melott J, Mills GB, Nguyen L, Su X, Verhaak R, Wang W, Weinstein JN, Wong A, Yang Y, Yao J, Yao R, Yoshihara K, Yuan Y, Yung AK, Zhang N, Zheng S, Ryan M, Kane DW, Aksoy BA, Ciriello G, Dresdner G, Gao J, Gross B, Jacobsen A, Kahles A, Ladanyi M, Lee W, Lehmann KV, Miller ML, Ramirez R, Rtsch G, Reva B, Sander C, Schultz N, Senbabaoglu Y, Shen R, Sinha R, Sumer SO, Sun Y, Taylor BS, Weinhold N, Fei S, Spellman P, Benz C, Carlin D, Cline M, Craft B, Ellrott K, Goldman M, Haussler D, Ma S, Ng S, Paull E, Radenbaugh A, Salama S, Sokolov A, Stuart JM, Swatloski T, Uzunangelov V, Waltman P, Yau C, Zhu J, Hamilton SR; Sequencing Center, Getz G, Sougnez C, Abbott S, Abbott R, Dees ND, Delehaunty K, Ding L, Dooling DJ, Eldred JM, Fronick CC, Fulton R, Fulton LL, Kalicki-Veizer J, Kanchi KL, Kandoth C, Koboldt DC, Larson DE, Ley TJ, Lin L, Lu C, Magrini VJ, Mardis ER,

McLellan MD, McMichael JF, Miller CA, O'Laughlin M, Pohl C, Schmidt H, Smith SM, Walker J, Wallis JW, Wendl MC, Wilson RK, Wylie T, Zhang Q; Data Coordinating Center, Burton R, Jensen MA, Kahn A, Pihl T, Pot D, Wan Y; Tissue Source Site, Levine DA; Biospecimen Core Resource Center, Black AD, Bowen J, Frick J, Gastier-Foster JM, Harper HA, Helsel C, Leraas KM, Lichtenberg TM, McAllister C, Ramirez NC, Sharpe S, Wise L, Zmuda E; National Cancer Institute/National Human Genome Research Institute Project Team, Chanock SJ, Davidsen T, Demchok JA, Eley G, Felau I, Ozenberger BA, Sheth M, Sofia H, Staudt L, Tarnuzzer R, Wang Z, Yang L, Zhang J; Collaborators, Omberg L, Margolin A, Raphael BJ, Vandin F, Wu HT, Leiserson MD, Benz SC, Vaske CJ, Noushmehr H, Knijnenburg T, Wolf D, Veer LV, Collisson EA, Anastassiou D, Ou Yang TH, Lopez-Bigas N, Gonzalez-Perez A, Tamborero D, Xia Z, Li W, Cho DY, Przytycka T, Hamilton M, McGuire S, Nelander S, Johansson P, <u>Jörnsten R</u>, Kling T, Sanchez J, Weinstein JN, Collisson EA, Mills GB, Shaw KR, Ozenberger BA, Ellrott K, Shmulevich I, Sander C, Stuart JM. (2013) The Cancer Genome Atlas Pan-Cancer analysis project. *Nature Genetics, 2013 Sep 26;45(10):1113-20. doi: 10.1038/ng.2764.* Published as TCGA collaborator.

5. Moreau, M.P., Bruse, S.E., **Jörnsten, R.**, Liu, Y., Brzustowicz, L.M. (2013) Chronological Changes in MicroRNA Expression in the Developing Human Brain.
PLoS One 8(4): e60480. doi:10.1371/journal.pone.0060480.

6. Gerlee, P., Schmidt, L., Monsefi, N., Kling, T., **Jörnsten, R.**, Nelander, S. (2012) Searching for Synergies: Matrix Algebraic Approaches for Efficient Pair Screening
PLoS One 8(7): e68598. doi:10.1371/journal.pone.0068598.

7. Vickhoff, B., Malmgren, H., Åström, R., Nyberg, G., Ekström, S.R., Engvall, M., Snygg, J., Nilsson, M., **Jörnsten, R.** (2013) Music structure determines heart rate variability of singers.
To appear in Frontiers, Auditory and Cognitive Neuroscience.

8. Jauhiainen, A., Nerman, O., Michailidis, G., **Jörnsten, R.** (2012) Transcriptional and metabolic data integration and modeling for pathway identification. *Biostatistics, doi: 10.1093/biostatistics/kxs016.*

9. Barrenäs, F., Couto Alves, A., Chavali, S., Coin, L, Jarvelin, M-R., **Jörnsten, R.**, Langston, M.A., Ramasamy, A., Rogers, G., Wang H., Benson, M. (2011) Highly interconnected complex disease genes are enriched for disease-associated polymorphisms. *Genome Biology 2012, 13(46), doi:10.1186/gb-2012-13-6-r46*

10. **Jörnsten, R.**, Abenius, T., Kling T., Schmidt, L., Johansson, E., Nordling, T., Nordlander, B., Sander, C., Gennemark, P., Funa, K., Nilsson, B., Lindahl, L., Nelander, S. (2011) Network modeling of the transcriptional effects of copy number aberrations in glioblastoma. *Molecular Systems Biology 7: 486 doi:10.1038/msb.2011.17*

11. Abel, F., Dalevi, D., Nethander, M., **Jörnsten, R.**, De Preter K., Vermulen, J., Stallings, R., Kogner, R., Maris, J., Nilsson, S. (2011) A 6-gene signature identifies four molecular subgroups of neuroblastoma. *Cancer Cell Int. 11(1):9*

12. Rodriguez-Saona, C.R., Polavarapu, S., Barry J.D., Pol, D., **Jörnsten, R.**, Oudemans, P.V., Liburd, O.E. (2010) Color preference, seasonality, spatial distribution and species composition of thrips (Thysanoptera: Thripidae) in northern highbush blueberries. *Crop Protection, 29(11):133-1340, Nov 2010*

13. **Jörnsten, R.** (2009) Simultaneous subset selection via rate-distortion theory, with application to clustering and significance analysis of gene expression data. *Journal of Computational and Graphical Statistics. September 1, 2009, 18(3): 613-639. doi:10.1198/jcgs.2009.07043.*

14. **Jörnsten, R.**, and Keles, S. (2008) MIXL, Multi-level mixture modeling, with application to the analysis of multi-factor gene expression studies. *Biostatistics 9(3): 540-554.*

15. **Jörnsten, R.**, Wang, H-Y., and Ouyang, M. (2007) A Meta-data based method for DNA microarray imputation. *BMC Bioinformatics 8(109):doi:10.1186/1471-2105-8-109*

16. Goff, L.A., Davila, J., **Jörnsten, R.**, Keles, S. and Hart, R. (2007) Bioinformatic analysis of neural stem cell differentiation. *Journal of Biomolecular Techniques 18:205-212*

17. Lakshmipathy, U., Love, B., Goff, L., **Jörnsten, R.**, Graichen, R., Hart, R.P., Chesnut, J.D (2007) Micro RNA expression pattern of undifferentiated and differentiated human embryonic stem cells. *Stem Cells and Development 16:1-14*

18. Charych, E., Akum, B., Goldberg, J.S., **Jörnsten, R.J.**, Rongo, C., and Firestein, B.L. (2006) Activity-Independent Regulation of Dendrite Patterning by Postsynaptic Density Protein PSD-95. *The Journal of Neuroscience, October 4, 2006, 26(40):10164-10176;*

19. Chen, M., Lucas, K.G., Akum, B.F., Balsingam, G., Stawicki, T.M., Provost, J.M., Riefler, G.M., **Jörnsten, R.J.**, and Firestein, B.L. (2005) Novel Role for Snapin in Dendrite Patterning: Interaction with Cypin. *Molecular Biology of the Cell, Vol. 16, Issue 11, 5103-5114, November 2005.*

20. **Jörnsten, R.**, Wang H-Y., Welsh, W.J., and Ouyang, M. (2005) DNA microarray data imputation and significance analysis of differential expression. *Bioinformatics 2005 21(22):4155-4161*

21. **Jörnsten, R.** (2004) DDclust: Clustering and Classification based on the L1 data depth. *Journal of Multivariate Analysis Volume 90, Issue 1, July 2004, p. 67-89*

22. Pan, J.Z., **Jörnsten, R.**, and Hart, R.P. (2004) Screening anti-inflammatory compounds in injured spinal cord with microarrays: A comparison of bioinformatics analysis approaches. *Physiol. Genomics, 17:201-214.*

23. Freeman, W., Gaal, G., and **Jornsten, R.** (2003) A neurobiological theory of meaning in perception. Part 3. Multiple cortical areas synchronize without loss of local autonomy. *International Journal & Bifurcation & Chaos, 13(10), 2845-2856*

24. **Jörnsten, R.**, and Yu, B. (2003) Simultaneous gene clustering and subset selection for sample classification via MDL. *Bioinformatics, 2003, 19: 1100-1109.*

25. **Jörnsten, R.**, Yu, B., Wang, W., and Ramachandran, K. (2003) Microarray image compression: SLOCO and the effects of information loss. *EURASIP Signal Processing Journal, Special issue on genomic signal processing, (2003), 83/4, 859-869*

PEER-REVIEWED BOOK CHAPTERS

1. Abenius, T., **Jörnsten, R.**, Schmidth, L., Sanchez, J., Nelander, S. (2012) System scale network modeling using EPoC. *Advances in Experimental Medicine and Biology, Springer series (ICSB), Volume 736, Part 5, 617-643, DOI: 10.1007.978-1-4419-7210-1-37*

2. Lopez-Pintado, S., and **Jörnsten, R.** (2006) Functional analysis via extensions of the Band Depth. *IMS Lecture Series, Volume 54, ed. R. Liu et al, p. 103-120*

3. **Jörnsten, R.**, and Yu, B. (2004) Simultaneous clustering and subset selection via MDL. *Advances in Minimum Description Length: Theory and Applications, MIT press. P.Grunwald, IJ Myung, M. Pitt Editors. p295-322.*

4. **Jörnsten, R.**, and Yu, B. (2004) Compressing Genomic and Proteomic Array Images for Statistical Analysis. *Invited book chapter Genomic Signal Processing and Statistics. E.R. Dougherty, I. Shmulevich, J. Chen, Z.J. Wang Editors. p341-366*

5. **Jörnsten, R.**, Vardi, Y., Zhang, C-H., (2002) A Robust Clustering Method and Visualization Tool Based on Data Depth. *Statistical data analysis based on the L1norm and related methods. Y. Dodge editor. p. 353-366*

6. **Jörnsten, R.**, Vardi, Y., Zhang, C-H., (2002) On the bit-plane compression of Microarray images. *Statistical Data Analysis based on the L1-norm and Related methods. Y. Dodge editor. p415-425*

7. **Jörnsten, R.**, and Yu, B., (2002) Multiterminal estimation - extensions and a geometric intepretation, Peer-reviewed extended abstract for *IEEE ISIT 2002, Lausanne, p24-29*

8. **Jornsten, R.**, Yu, B., Wang, W., Ramchandran, K. (2002) Compression of cDNA and inkjet microarray images International Conference on Image Processing (3) 961-964

9. **Jornsten, R.**, Yu, B. (2002) Compression of cDNA microarray images IEEE Int. Symposium on Biomedical Imaging, 38-41.

10. **Jornsten, R.**, Yu, B., Wang, W., Ramchandran, K. (2002) Microarray image compression and the effect of compression loss Proc. of the Workshop on Genomic Signal Processing and Statistics, GENSIPS.

11. **Jornsten, R.**, Yu, B. (2000) Comprestimation: Microarray images in abundance. Conference on Information Sciences and Systems, Princeton, 2000.

Submitted, Revised Manuscripts

1. Kling, T., Ferrarese, R., O hAilin, D., Heiland, D. H., Dai, F. P., Vasilikos, I., Weyerbrock, A., **Jörnsten, R.**, Carro, M. S., Nelander, S. (2016) Integrative modeling reveals ANXA2 as a determinant of mesenchymal transformation in glioma. Revised for *eBiomedicine*

2. Gunnar Steineck; Viktor Skokic; Fei Sjberg; Cecilia Bull; Eleftheria Alevronta; Gail Dunberger; Karin Bergmark; Ulrica Wilderng; Joseph O Deasy; **Rebecka Jrnsten** (2016). Identifying Radiation-Induced Survivorship Diseases Affecting Bowel Health. Submitted to *P*LoS One

Manuscripts, Technical reports

1. Steineck, G., Skokic, V., Bergmark, K., Bull, C., Dunberger, G., Sjöberg, F., Åvall-Lundqvist, E., Waldenström, A., **Jörnsten, R.** (2015) Late Gastro-Intestinal Toxicity after Irradiation for Gynecological Cancer 28 Atomized Symptoms in Six Distinct Groups.

2. Jauhiainen, A., Sanchez, J., Nelander, S., **Jörnsten, R.** (2015) NetCor: Network component resolution. *Manuscript, best poster paper award EMS 2015*

3. Sanchez, J., Kling, T., Nelander, S., **Jörnsten, R.** (2012) Topology-constrained differential network modeling of human cancer. *Presented at Nordstat2012 and the ISI2012-meeting, JS Licentiate thesis..*

4. Vickhoff, B., **Jörnsten, R.**, Snygg, J., Åström, R., Sommermeyer, D., Nyberg, G., Theorell, T., Nilsson, M. (2012) The Musical Score of the Body. (Kroppens Partitur) *Manuscript in preparation. Press appearances: SVT Rapport (Swedish television), P3 (Swedish radio), SvD (newspaper), Radio (SR-P3), Science Festival (Vetenskapsfestivalen 2012), "Forskning och Framsteg" (Swedish popular science journal).*

5. **Jörnsten, R.** (2007) MIXT, mixture modeling with profile transformations (online Technical report).

TEACHING: Short courses and workshops

- Guest Lecturer, short course "R for Biologists", Chalmers, Fall 2011.
- Co-organizer, short course on statistical analysis of natural driving studies (Safer - Chalmers center for vehicle and traffic safety). Spring 2011.
- Invited lecturer, NSF Statistical Genetics Short Course, Honolulu, July 2009
- Invited lecturer, Statistical Genetics Short Course, New Orleans, February 2009
- Invited lecturer, "Life after a Statistics Doctoral Program", Columbia University, April 2008.
- Lecture series sponsored by the National Institutes of Health:
- Invited lecturer, NIAMS functional genomics short course, Atlanta, March 2006
- Invited lecturer, NIDDS functional genomics short course, San Francisco, March 2006
- Rutgers Workshops: Invited lecturer, Microarray Workshop, W.M. Keck Center for Collaborative Neuroscience, Dec, 2004

CLASSROOM INSTRUCTION

- Chalmers/University of Gothenburg: Statistical Learning for Big Data, Linear Models, Survival analysis, Statistical Inference, Applied multivariate analysis. PhD courses in Bootstrap, Sparse modeling, Empirical Bayes methods.
- Rutgers University: Seminar in applied and mathematical statistics, Applied time series analysis for the Mathematical Finance master program, Statistical methods in bioinformatics, Basic statistics for research, Interpretation of Data, Regression analysis

PEDAGOGICAL COURSES

- HEP201, 5hsp, Supervision in Postgraduate Programmes. Fall 2011.
- HEP101, 5hsp, Teaching and Learning in Higher Education. Fall 2014.
  Essay: "A personal reflection on the use of the inverted classroom in science education".
- HEP102, 5hsp, Teaching and learning in Higher Education 2: Discipline Specific Pedagogic. Spring 2015.
- HEP103, 5hsp, Teaching and Learning in Higher Education 3: Applied Analysis, Spring 2014.
  Essay: "An elaborate reflection of the role of gender in higher education."

PH.D. STUDENTS

- Jose Sanchez, 2009-2014. *Network models with applications to genomic data: generalization, validation and uncertainty assessment.* Current position: Bioinformatician, Sahlgrenska.
- Jonatan Kallus 2014-present. Tentative title of thesis: *Model selection and validation challenges in high-dimensional biology.*
- Teresia Kling, 2010-2015. (co-advisor, main advisor Sven Nelander). Tentative title of thesis: *System-scale modeling of cancer.* Will defend on October 23rd 2015.
- Alexandra Jauhainen (co-advisor, main advisor Olle Nerman). *Statistics in gene expression, metabolomics, and comparative genomics in evolution.* Degree conferred September 2010. Positions: postdoctoral researcher, Department of Statistics, University of Michigan (2010), postdoctoral researcher, Karolinska Institute, (2011-2014), senior analyst, Astra Zeneca, (2015-present). .
- Patrik Johansson. 2012-present. (co-advisor, main advisor Sven Nelander).
- Satishkumar Baskaran, 2012-present. (co-advisor, main advisor Sven Nelander).

MASTER STUDENTS (S-SUPERVISOR, E-EXAMINER)

- Sebastian Franzn, 2016-present, *Multi-resolution network modeling* (s)
- Filip Birve, 2016-present, *Joint community detection* (s)
- Emilio Jorge, 2016-present, *Solving tasks using multi-agent reinforcement learning* (e)
- Ludvig Vikstrm, 2016-present, *Capital Pricing Asset Model - analysis of AP data* (e)
- Oskar Lilja, 2015-2016, *Clustering cancer tumor data using deep learning techniques* (s)
- Maja Fahln, 2015-2016, *Multi-layer latent modeling of cancer data* (s)
- Sofia Hjalmarsson, 2015-2016 *Modeling hospital log data: sensitivity analysis* (s)
- Sebastian Anerud, 2014-2015. *Discovery of subgroup dynamics in Glioblastome multiforme* (s)
- Susanne Pettersson, 2014-2015. *Inference of gene regulatory networks and master regulators of disease* (s)
- Linus Lundin, 2013-2016. *Musical therapy for Parkinson patients.* (s)
- Johanna Svensson, 2013-2014. *Application of Ensemble Methods on Prediction of Stock Returns* Current position, analyst at 2nd AP fund (s)

- Patrik Johansson, 2011-2012. *Integrated modeling of DNA methylation, mRNA and microRNA expression profiles in human cancer.* (s) Current position, PhD student at the Nelander lab, Uppsala University.
- Viktor Skokic. 2011-2012. *An investigation of self assessed quality of life among long term testicular cancer survivors and it's relation to chemotherapy.* (s) Current position, analyst with Prof. Gunnar Steineck, Oncology, Karolinska Institute.
- Johanna Sigmundsdottir 2011-2012. *Joint segmentation modeling of epilepsy episodes and physiological response to music.* (s)
- Tobias Abenius (secondary advisor), 2009-2010 *Endogenous perturbation analysis of cancer.*
- Eric Burlow, 2010. *Sparse logistic regression modeling with applications to internet advertisement.* (s)
- Owen Martin, 2007. (s)
- Diane Richardson, 2006. Current position, Project Director - Research, Pharmacoeconomics and Outcomes Research, Thomas Jefferson University (s)

Ph.D. Committee
- Opponent for Rezvan Ehsani, NTNU, September 2016
- Kerstin Johnsson, Lund, September 2016
- Harriet Melenius, Uppsala University, October 2015
- Francesco Gatto, Chalmers, September 2015
- Kristoffer Hellton, University of Oslo, February 2015
- Ying Li, SLU, December 2014
- Szilard Nemes, Sahlgrenska Academy, degree conferred December 2012.
- P.O. Lindberg, Transport Research, Royal Institute of technology, conferred June 2012.
- Opponent for Mattias Landfors, Statistics, Umeå University, conferred April 2012
- Xia Shen, Genetics, Uppsala University, conferred April 2012
- Loyal Goff, Molecular and Cell Biology, Rutgers, conferred April 2008
- Weihua Tang, Statistics, Rutgers, conferred May 2006
- Susanna Eyheramendy, Statistics, Rutgers, conferred May 2004

Select Presentations
- Invited speaker, Third International Conference on Computational Biomedicine (CBM 2016), Florida, February 2016
- Invited speaker, Karolinska, October 2015
- Invited speaker, SciLifeLab Day, October 2015
- Invited speaker, Data Science Workshop, Stockholm, December 2014.
- Invited speaker, LinStat, September 2014
- Keynote speaker, Sonja Kovalevska dagarna, Umeå, Nov 2012.
- Keynote speaker, Nordstat, June 2012
- Invited speaker, Karolinska Institute, May 2012
- Invited speaker, Stockholm University, April 2012
- Invited speaker, Uppsala University, February 2012
- Invited speaker, JSM Vancouver, August 2010
- Invited speaker, FMS Spring conference, March 2009.

- Invited speaker, Biostatistics Day, Rutgers University, April 2008
- Invited panelist, Columbia symposium on Careers in Statistics, April, 2008
- Invited speaker, ENAR 2008
- Invited speaker, University of Bergen, January 4, 2008
- Invited speaker, Section for Statistical Genetics, UAB, Oct 2007
- Discussant, ISI-Bernouilli, August 2007
- Invited speaker, JSM, August 2007
- Invited speaker, PICASSO seminar, Princeton, April 2007
- Invited speaker, NISS, April 2007
- Invited speaker, NYU Biostatistics seminar, November 2006
- Invited speaker, Computational Genomics meeting, Banff, July 2006
- Invited speaker, Interface, Pasadena, May 2006
- Invited speaker, UMDNJ, biostatistics seminar, May 2006
- Selected presenter, 8th annual conference on computational genomics, MIT, Nov 2005
- Invited speaker, Yale university, Biostatistics seminar, Nov 2005
- Invited speaker, Barcode of Life - data analysis working group meeting, Paris, Oct 2005
- Invited speaker, UAB genomics workshop, Mohonk, September 2005
- Invited speaker, Mount Sinai, Statistics seminar, May 2005
- Invited speaker, U. Wisconsin, Biostatistics seminar series, April 2005
- Invited speaker, PSU Department of Statistics, Jan 2005
- Invited speaker, First annual Central New Jersey systems biology symposium, Institute for advance sciences, Princeton, Sep 2004
- Invited speaker, Joint statistical meetings, Toronto Aug 2004.
- Invited speaker, Department of Biostatistics, Karolinska institutet, Stockholm, Aug 2004
- Invited speaker, Infocast symposium on microarray data analysis, June 2004

EDITORIAL
ACTIVITIES:

- Editor for Journals of Statistical Software 2011-2013, 2015-present
- AE for Scandinavian Journal of Statistics 2011-2013

REFEREE FOR

Bioinformatics, Biometrics, BMC Bioinformatics, Drug Discovery Today, EURASIP Journal of Signaling Processing, IEEE Transactions on Computational Biology and Bioinformatics, IEEE Transactions on Medical Imaging, IEEE Transactions on Signal Processing, Journal of the American Statistical Association, Journal of Computational and Graphical Statistics, Journal of Multivariate Analysis, Pattern Recognition Letters, PLoS Genetics, RECOMB, Statistical Applications in Genetics and Molecular Biology, Scandinavian Journal of Statistics, Technometrics

SERVICE: SCIENTIFIC LEADERSHIP, ADMINISTRATION
- Chair, Cramer Society, 2016-present
- Committee member for the development of new program Data Science, 2015-present
- Institutionsrådet, 2011-present
- External review board for graduate education accreditation, Skövde University, 2010
- Graduate Curriculum committee, 2002-2009
- Acting director of the Office for Statistical Consulting, July 2007-June 2008
- Seminar chair, 2006-2007
- Department website committee, 2003-2005, 2007
- Search committee, 2003-2005, 2007
- Computing committee, 2003-2006
- Biostatistics committee, 2003-2006
- Graduate student admissions committee, 2004

SERVICE TO THE PROFESSION
- External reviewer of applications for tenure track hiring, Uppsala, 2016
- External reviewer of applications for lektor position, Linköping University, 2016
- Tenure review committee, Northwestern University, February 2013
- External committee member for associate professorship hiring, University of Oslo, 2011.
- Member, IMS - committee Special Lecture series, 2009-2011.
- Participating faculty, Master's program in Mathematical Finance, Rutgers University, 2007-2009
- Chair, IMS - New Researchers Conference Committee, 2007-2009, (applied and managed funding, reporting to funding agencies, coordination and organization of event).
- Session organizer, IMS-Bernoulli society meeting, Aug 2007
- Member, IMS - New Researchers Conference Committee, 2006-2008
- Session organizer, Classification of Society of North America, May 2006
- Organizer of the DIMACS meeting for the data analysis working group, Barcode of Life, Sept. 2005
- Member of the steering committee for the Barcode of Life data analysis working group, 2005-2006
- Co-organizer of the Rutgers Microarray workshop, Dec 2004
- Outreach: Rutgers faculty traveling seminar, visiting high schools and policy makers, 2004.

My research program centers on model selection problems that arise in the analysis of high-dimensional data, primarily with applications to genomic studies. I am also interested in developing general clustering methodology, using flexible mixture models or nonparametric techniques such as data depth. I enjoy collaborative research, which often serves as a source of inspiration for methodology research. My collaborative projects range from data integration in systems biology, modeling of naturalistic driving studies for traffic safety, analysis of pest populations in North-American blueberry fields; and, most recently, analysis of music as a therapeutic aid for parkinson and stroke patients.

A. STATISTICAL MODELING OF HIGH-DIMENSIONAL BIOLOGICAL DATA.

With Sven Nelander's group (Uppsala SciLifeLab and Sahlgrenska-CMR/Wallenberg lab) I investigate system scale network models for human cancer. We recently published a paper in MSB, integrating mRNA expression data with DNA copy-number to construct network models whose structure can be summarized as prognostic scores (predicting patient survival). We are currently working to extend this to include even more data types, e.g. methylation, microRNA data and SNPs. Another research track we are pursuing is experimental planning in systems biology.
With Mikael Benson's group (Linköping University, Center for Individualized Medicine), I also work on data integration problems geared at identifying biomarkers (disease-drivers), here focusing on allergy.

(A.i) Gerlee, P., Schmidt, L., Monsefi, N., Kling, T., **Jörnsten, R.**, Nelander, S. (2011) Efficient experimental screening: fast, system-scale discovery of synergistic target pairs. To be submitted to Molecular Systems Biology.

(A.ii) **Jörnsten, R.**, Abenius, T., Kling T., Schmidt, L., Johansson, E., Nordling, T., Nordlander, B., Sander, C., Gennemark, P., Funa, K., Nilsson, B., Lindahl, L., Nelander, S. (2011) Network modeling of the transcriptional effects of copy number aberrations in glioblastoma. Molecular Systems Biology 7: 486 doi:10.1038/msb.2011.17

(A.iii) Abenius, T., **Jörnsten, R.**, Schmidth, L., Nelander, S. (2011) System scale network modeling using EPoC. Proceedings of the 11th ICSB, to be published in the Springer series Advances in Experimental Medicine and Biology.

(A.iv) (C.ii) Barrenäs, F., Couto Alves, A., Chavali, S., Coin, L, Jarvelin, M-R., **Jörnsten, R.**, Langston, M.A., Ramasamy, A., Rogers, G., Wang H., Benson, M. (2011) Highly interconnected complex disease genes are enriched for disease-associated polymorphisms. Under revision for Genome Biology.

B. MODEL SELECTION IN PATHWAY MODELING, CLUSTERING AND CLASSIFICATION.

My second research agenda centers on model selection. I am particularly interested in integrating information theory and data coding techniques into statistical model selection. Together with former student, Alexandra Jauhianen (now a post-doc at Karolinska Institutet), the coding-based model selection framework I introduced in a JCGS article in 2009 is extended to integrate mRNA and metabolic data for the identification of pathways that are "activated" under certain experimental conditions. With my student Jose Sanchez I also work at extending the flexible mixture model framework (MIXL and MIXT) for variable selection in clustering. We call this problem "dynamical clustering", referring to the fact that clustering is dependent on the variables or features included in the analysis (manuscript in preparation).

(B.i) Jauhianen, A., Nerman, O., Michailidis, G., **Jörnsten, R.** (2011) Transcriptional and metabolic data integration and modeling for pathway identification. Submitted to Biostatistics.

(B.ii) **Jörnsten, R.** (2009) Simultaneous subset selection via rate-distortion theory, with application to clustering and significance analysis of gene expression data. Journal of Computational and Graphical Statistics. September 1, 2009, 18(3): 613-639. doi:10.1198/jcgs.2009.07043.

(B.iii) **Jörnsten, R.** (2007) MIXT, mixture modeling with profile transformations. Technical report.

(B.iv) **Jörnsten, R.**, and Keles, S. (2008) MIXL, Multi-level mixture modeling, with application to the analysis of multi-factor gene expression studies. Biostatistics 9(3): 540-554.