June 4, 2014

CURRICULUM VITAE

Kasper Daniel Hansen

PERSONAL DATA

Web Page:	http://www.biostat.jhsph.edu/~khansen
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EDUCATION AND TRAINING

Degrees

Ph.D. 2009 University of California, Berkeley
Biostatistics with a designated emphasis in Computational and Genomic Biology
Advisor: **Sandrine Dudoit**

Cand. Scient. 2002 University of Copenhagen
Statistics
Advisor: Martin Jacobsen

B. Sc. 1998 University of Copenhagen
Statistics and mathematics

Postdoctoral Training

2009–2012 Department of Biostatistics
Johns Hopkins Bloomberg School of Public Health
Advisor: **Rafael Irizarry**

Visiting

2004–2005 Department of Biostatistics
University of California, Berkeley

PROFESSIONAL EXPERIENCE

2012–Present	Assistant Professor, Nathans-McKusick Institute of Genetic Medicine Johns Hopkins University
2012–Present	Assistant Professor, Department of Biostatistics Johns Hopkins University
2009–2012	Postdoctoral Fellow, Department of Biostatistics Johns Hopkins University
2002–2004	Research Assistant, Department of Biostatistics University of Copenhagen, Denmark.

PROFESSIONAL ACTIVITIES

Professional Memberships

American Society of Human Genetics
American Statistical Association

Project Development

2012–Present Member of the Bioconductor Technical Advisory Board.

EDITORIAL ACTIVITIES

Served as *referee* for

Annals of Applied Statistics
Bioinformatics
Biometrics
Biostatistics
BMC Bioinformatics
Genome Biology
Genome Research
International Journal of Biostatistics
Journal of the American Medical Association (JAMA)
Journal of the American Statistical Association (JASA)
Nature Biotechnology
Nature Methods
Nucleic Acids Research
PLoS Biology
PLoS Genetics
PLoS ONE
Proceedings of the National Academy of Sciences (PNAS)
RNA
Statistical Applications in Genetics and Molecular Biology

Statistics in Medicine

Review of Proposals

Joint NIH and NSF BIGDATA initiative review panel (2012)

HONORS AND AWARDS

2010	Second prize at the MGED poster competition (out of around 50)
2007	Third prize at the Computational and Genomic Biology student retreat poster competition
2007	Reshetko Family Scholarship, UC Berkeley
2005	William V. Power Top-off Graduate Award, UC Berkeley
2005	William V. Power Graduate Award, UC Berkeley

Journal Articles (peer-reviewed)

* indicates equal contributions
† indicates corresponding author (if not the senior author)

[1] Alyssa C Frazee, Sarven Sabunciyan, **Kasper D Hansen**, Irizarry, Rafael A, and Jeffrey T Leek. Differential expression analysis of RNA-seq data at single-base resolution. *Biostatistics*, 2014. In Press. doi:10.1093/biostatistics/kxt053, PMID:24398039.

[2] Martin J Aryee, Andrew E Jaffe, Hector Corrada Bravo, Christine Ladd-Acosta, Andrew P Feinberg, **Kasper D Hansen**†, and Rafael A Irizarry†. Minfi: a flexible and comprehensive Bioconductor package for the analysis of Infinium DNA methylation microarrays. *Bioinformatics*, 30(10):1363–1369, 2014. doi:10.1093/bioinformatics/btu049, PMID:24478339.

[3] **Kasper D Hansen***, Sarven Sabunciyan*, Ben Langmead, Noemi Nagy, Rebecca Curley, Georg Klein, Eva Klein, Daniel Salamon, and Andrew P Feinberg. Large-scale hypomethylated blocks associated with Epstein-Barr virus-induced B-cell immortalization. *Genome Research*, 24(2):177–184, 2014. doi:10.1101/gr.157743.113, PMID:24068705.

[4] Mike L Smith†, Keith A Baggerly, Henrik Bengtsson, Ritchie, Matthew E, and **Kasper D Hansen**†. illuminaio: An open source IDAT parsing tool for Illumina microarrays. *F1000Research*, 264:2, 2013. doi:10.12688/f1000research.2-264.v1, PMID:24701342.

[5] Christine Ladd-Acosta, **Kasper D Hansen**, Eirikur Briem, Falline, M Daniele, Walter E Kaufmann, and Andrew P Feinberg. Common DNA methylation alterations in multiple brain regions in autism. *Molecular Psychiatry*, 2013. In Press. f1000. doi:10.1038/mp.2013.114, PMID:23999529.

[6] **Kasper D Hansen***,†, Benjamin Langmead*,†, and Rafael A Irizarry†. BSmooth: from whole genome bisulfite sequencing reads to differentially methylated regions. *Genome Biology*, 13(10):R83, 2012. Highly accessed. doi:10.1186/gb-2012-13-10-r83, PMID:23034175.

[7] Brian R Herb*, Florian Wolschin*, **Kasper D Hansen**, Martin J Aryee, Ben Langmead, Rafael Irizarry, Gro V Amdam†, and Andrew P Feinberg†. Reversible switching between epigenetic states in honeybee behavioral subcastes. *Nature Neuroscience*, 15(10):1371–1373, 2012. doi:10.1038/nn.3218, PMID:22983211.

[8] Jenny Tung†, Luis B Barreiro, Zachary P Johnson, **Kasper D Hansen**, Vasiliki Michopoulos, Donna Toufexis, Katelyn Michelini, Wilson, Mark E, and Yoav Gilad†. Social environment is associated with gene regulatory variation in the rhesus macaque immune system. *Proceedings of the National Academy of Sciences*, 109(17):6490–6495, 2012. f1000. doi:10.1073/pnas.1202734109, PMID:22493251.

[9] Supriya Munshaw, Hyon S Hwang, Michael Torbenson, Jeffrey Quinn, **Kasper D Hansen**, Jacquie Astemborski, Shruti H Mehta, Stuart C Ray, David L Thomas, and Ashwin Balagopal. Laser captured hepatocytes show association of butyrylcholinesterase gene loss and fibrosis progression in hepatitis C-infected drug users. *Hepatology*, 56(2):544–554, 2012. doi:10.1002/hep.25655, PMID:22331678.

[10] **Kasper D Hansen**, Rafael A Irizarry, and Zhijin Wu. Removing technical variability in RNA-seq data using conditional quantile normalization. *Biostatistics*, 13(2):204–216, 2012. doi:10.1093/biostatistics/kxr054, PMID:22285995.

[11] **Kasper D Hansen***, Winston Timp*, Héctor Corrada Bravo*, Sarven Sabunciyan*, Benjamin Langmead*, Oliver G McDonald, Bo Wen, Hao Wu, Yun Liu, Dinh Diep, Eirikur Briem, Kun Zhang, Rafael A Irizarry†, and Andrew P Feinberg†. Increased methylation variation in epigenetic domains across cancer types. *Nature Genetics*, 43(8), 2011. f1000, Nat Genet, Cell. doi:10.1038/ng.865, PMID:21706001.

[12] **Kasper D Hansen**, Zhijin Wu, Rafael A Irizarry†, and Jeffrey T Leek†. Sequencing technology does not eliminate biological variability. *Nature Biotechnology*, 29(7):572–573, 2011. doi:10.1038/nbt.1910, PMID:21747377.

[13] Angela N Brooks*, Li Yang*, Michael O Duff, **Kasper D Hansen**, Jung W Park, Sandrine Dudoit, Steven E Brenner†, and Brenton R Graveley†. Conservation of an RNA regulatory map between Drosophila and mammals. *Genome Research*, 21(2):193–202, 2011. doi:10.1101/gr.108662.110, PMID:20921232.

[14] modENCODE Consortium. Identification of functional elements and regulatory circuits by Drosophila modENCODE. *Science*, 330(6012):1787–97, 2010. doi:10.1126/science.1198374, PMID:21177974.

[15] Benjamin Langmead, **Kasper D Hansen**, and Jeffrey T Leek. Cloud-scale RNA-sequencing differential expression analysis with Myrna. *Genome Biology*, 11(8):R83, 2010. Highly accessed. doi:10.1186/gb-2010-11-8-r83, PMID:20701754.

[16] **Kasper D Hansen**†, Steven E Brenner, and Sandrine Dudoit. Biases in Illumina transcriptome sequencing caused by random hexamer priming. *Nucleic Acids Research*, 38(12):e131, 2010. NAR Top Article. doi:10.1093/nar/gkq224, PMID:20395217.

[17] James H Bullard*, Elizabeth Purdom*, **Kasper D Hansen**, and Sandrine Dudoit. Evaluation of statistical methods for normalization and differential expression in mRNA-Seq experiments. *BMC Bioinformatics*, 11:94, 2010. Highly accessed. doi:10.1186/1471-2105-11-94, PMID: 20167110.

[18] **Kasper D Hansen***, Liana F Lareau*, Marco Blanchette, Richard E Green, Qi Meng, Jan Rehwinkel, Fabian L Gallusser, Elisa Izaurralde, Donald C Rio, Sandrine Dudoit, and Steven E Brenner. Genome-Wide Identification of Alternative Splice Forms Down-Regulated by Nonsense-Mediated mRNA Decay in Drosophila. *PLoS Genetics*, 5(6):e1000525, 2009. doi:10.1371/journal.pgen.1000525, PMID:19543372.

[19] Albert Lee*, **Kasper D Hansen***, James Bullard*, Sandrine Dudoit, and Gavin Sherlock. Novel Low Abundance and Transient RNAs in Yeast Revealed by Tiling Microarrays and Ultra High-Throughput Sequencing Are Not Conserved Across Closely Related Yeast Species. *PLoS Genetics*, 4(12):e1000299, 2008. doi:10.1371/journal.pgen.1000299, PMID:19096707.

[20] J H Andersen†, M Harhoff, S Grimstrup, I Vilstrup, C F Lassen, L P A Brandt, A I Kryger, E Overgaard, **Kasper D Hansen**, and Sigurd Mikkelsen. Computer mouse use predicts acute pain but not prolonged or chronic pain in the neck and shoulder. *Occupational and Environmental Medicine*, 65(2):126–131, 2008. doi:10.1136/oem.2007.033506, PMID:17681996.

[21] Hella Danø†, Rune Jacobsen, **Kasper D Hansen**, Jørn Korsbø Petersen, and Elsebeth Lynge. Use of census data for construction of fertility history for Danish women. *Scandinavian Journal of Public Health*, 32:435–41, 2004. doi:10.1080/14034940410028163, PMID:15762028.

[22] Hella Danø†, **Kasper D Hansen**, Per Jensen, Jørgen Holm Petersen, Rune Jacobsen, Marianne Ewertz, and Elsebeth Lynge. Fertility pattern does not explain social gradient in breast cancer in Denmark. *International Journal of Cancer*, 111:451–6, 2004. doi:10.1002/ijc.20203, PMID:15221976.

[23] Anne-Marie Nybo Andersen†, **Kasper D Hansen**, Per Kragh Andersen†, and George Davey Smith. Advanced paternal age and risk of fetal death: a cohort study. *American Journal of Epidemiology*, 160(12):1214–22, 2004. doi:10.1093/aje/kwh332, PMID:15583374.

Books, Theses, Tech Reports

* indicates equal contributions
† indicates corresponding author (if not the senior author)

[24] Jean-Philippe Fortin, Aurelie Labbe, Mathieu Lemire, Brent W Zanke, Thomas J Hudson, Elana J Fertig, Celia MT Greenwood, and **Kasper D Hansen**†. Functional normalization of 450k methylation array data improves replication in large cancer studies. *bioRxiv*, 2014. doi:10.1101/002956.

[25] **Kasper D Hansen**, Rafael A Irizarry, and Zhijin Wu†. Removing technical variability in RNA-seq data using conditional quantile normalization. Working Paper 227, Johns Hopkins, Dept of Biostatistics, 2011. URL: http://www.bepress.com/jhubiostat/paper227/.

[26] **Kasper D Hansen**. *Analyses of high-throughput gene expression data*. PhD thesis, Division of Biostatistics, University of California at Berkeley, 2009.

[27] James H Bullard*, Elizabeth A Purdom*, **Kasper D Hansen**, Steffen Durinck, and Sandrine Dudoit. Statistical Inference in mRNA-Seq: Exploratory Data Analysis and Differential Expression. Working Paper 247, U.C. Berkeley, Division of Biostatistics, 2009. URL: http://www.bepress.com/ucbbiostat/paper247/.

[28] Henrik Bengtsson†, Ken Simpson, James Bullard, and **Kasper D Hansen**. aroma.affymetrix: A generic framework in R for analyzing small to very large Affymetrix data sets in bounded memory. Technical Report 745, Department of Statistics, University of California, Berkeley, 2008. URL: http://statistics.berkeley.edu/25.

[29] Kirsten Schultz-Larsen, Svend Kreiner, Susanne Hanning, Nina Støvring, **Kasper D Hansen**, and Susie Lendal. Den danske ældrepleje under forandring ("An evaluation of the quality of the danish elder care"). Govermental report, 2004.

[30] **Kasper D Hansen** and Ernst Hansen. *Opgaver i videregående sandsynlighedsregning ("Exercises in Advanced Probability")*. University of Copenhagen (HCØ Tryk), 2000.

Google Scholar Citations

profile (link)

Software

Bioconductor

affxparser A package for parsing output files from Affymetrix microarrays using the Affymetrix Fusion SDK.

bsseq A package for analyzing whole-genome bisulfite sequencing data.

bumphunter A package implementing a general backend for the bumphunter approach.

cqn A package for normalizing RNA-seq data using the CQN algorithm.

Genominator A package implementing a SQLite based backend for genomic data, including sequencing and microarrays.

illuminaio A package for parsing output for Illumina microarrays. This package is not yet in Bioconductor release.

minfi A package for analysing Illumina's 450k DNA methylation microarray.

Rgraphviz A package for visualizing graphs using the Graphviz toolkit.

Other

Myrna Myrna is a cloud computing tool for calculating differential gene expression in large RNA-seq datasets. Myrna uses Bowtie for short read alignment and R/Bioconductor for interval calculations, normalization, and statistical testing. These tools are combined in an automatic, parallel pipeline that runs in the cloud (Elastic MapReduce in this case) on a local Hadoop cluster, or on a single computer, exploiting multiple computers and CPUs wherever possible.

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Kasper Daniel Hansen

Part II

TEACHING

Advisees

Jean-Philippe Fortin, Department of Biostatistics, SPH, 2013–present.
Kipper Fletez-Brant, Institute of Genetic Medicine, SOM, 2014–present.

Academic Advisees

Leslie Myint, Department of Biostatistics, SPH, 2013–present.

Thesis Committee

Joel Benjamin, Institute of Genetic Medicine, SOM, 2012.
Alyssa Frazee, Department of Biostatistics, SPH, 2012.
Christine M. Dejea, Department of Molecular Microbiology and Immunology, SPH, 2013.

Preliminary Oral Participation

Alyssa Frazee, Department of Biostatistics, SPH, 2012.

Comprehensive Exam

Genevieve Stein-O'Brien, Institute of Genetic Medicine, SOM, 2013.

Special Studies

Dan Jiang, Department of Biostatistics, SPH, 2013.
Leslie Myint, Department of Biostatistics, SPH, 2013–2014.

Classroom Instruction - Principal Instructor

140.688.01 Statistics for Genomics, 2014.

Classroom Instruction - Invited Guest Lecturer (JHU)

ME:260.710	Epigenetics, 2014.
ME:260.710	Epigenetics, 2013.
140.688.01	Statistics for Genomics, 2012.
140.778.01	Advanced Statistical Computing, 2012.

RESEARCH GRANT PARTICIPATION

Ongoing Research Support

Statistical methods for analysis of metabolomics data generated from a LC-MS instrument
JHU Faculty Innovation.
Principal Investigator: Kasper Daniel Hansen.
May 2014–May 2015, Direct costs: $30,000.
Responsibility: Principal Investigator (20%)

Strategic mapping of tissue and population methylation for mental health research
NIH U01 MH104393-01
Principal Investigator: Andrew P. Feinberg.
3 years, ending 2016. Direct costs: $2,072,969.
Responsibility: Co-investigator (10%)

Completed

Workshops and Short Courses

Statistical Methods for Next Generation Sequencing.
ENAR Washington, D.C.. 2012.

Computational Statistics for Genome Biology.
Brixen, Italy. 2011.

High throughput sequence analysis tools and approaches with Bioconductor.
FHCRC, Seattle, USA. 2009.

Statistical analysis of gene expression data with R and Bioconductor.
University of Copenhagen, Denmark. 2009.

R for (computational) biologists.
University of California, Berkeley, USA. 2008.

III International Course on Microarray Data Analysis.
Valencia, Spain. 2007.

Statistical Analysis of Microarray Expression Data with R and Bioconductor.

University of Copenhagen, Denmark. 2007.

I Course on Microarray Data Analysis.
Valencia, Spain. 2005.

Statistical Computing with R.
University of Copenhagen. 2004.

ACADEMIC SERVICE

Institute of Genetic Medicine

Member, Joint High Performance Computing Exchange Oversight Committee (2012 – present).

PRESENTATIONS

Scientific Meetings

1 Functional Normalization. *3rd Annual Infinium HumanMethylation450 Array Workshop (London, UK).* 2014.

2 A genome-wide look at DNA methylation. *Statistical Data Integration Challenges in Computational Biology: Regulatory Networks and Personalized Medicine at BIRS (Banff, Canada).* 2013.

3 Statistical modeling of epigenomewide data. *Joint Statistical Meetings (Montreal, Canada).* 2013.

4 A genome-wide look at DNA methylation. *BioC2013, Bioconductor Annual Meeting (FHCRC, USA).* 2013.

5 Using minfi to identify differentially methylated regions with the 450K array. *2nd Annual Infinium HumanMethylation450 Array Workshop (London, UK).* 2013.

6 Analysis of shotgun bisulfite sequencing of cancer samples. *Statistical Analysis of Genomic Data (CSHL, USA).* 2011.

7 Loss of stability of epigenetic domains across cancer types. *Copenhagenomics (Copenhagen, Denmark).* 2011.

8 Analysis of shotgun bisulfite sequencing of cancer samples. *Statistical Challenges and Biomedical Applications of Deep Sequencing Data (Ascona, Switzerland).* 2011.

9 Aspects of RNA-Seq data: computations, variance and bias. *DIMACS Workshop on Next Generation Sequencing at Rutgers (New Jersey, USA).* 2010.

10 Biases and variation in RNA-Seq. *Statistical Genomics in Biomedical Research workshop at BIRS (Banff, Canada).* 2010.

11 RNA-Seq: Sequencing the Transcriptome. *High throughput sequence analysis tools and approaches with Bioconductor (FHCRC, USA)*. 2009.

12 Biases in Illumina transcriptome sequencing caused by random hexamer priming. *Gene expression based on sequencing technologies workshop (Copenhagen, Denmark)*. 2009.

13 Investigating RNA-Seq data. *Statistical and Computational Challenges in Next-Generation Sequencing workshop (Berkeley, USA)*. 2008.

14 Modeling splice-junction arrays. *Joint Statistical Meetings (Colorado, USA)*. 2008.

Invited Seminars

15 Statistical analysis of epigenomewide data. *University of Pittsburgh and Carnegie-Mellon University (Pittsburgh, USA)*. 2014.

16 Analysis of whole-genome bisulfite sequencing data. *Johns Hopkins University (Baltimore, USA)*. 2013.

17 The structure of epigenetic changes in cancer as revealed by whole-genome shotgun bisulfite sequencing. *New York University (New York, USA)*. 2012.

18 Epigenetic changes in cancer revealed by whole-genome shotgun bisulfite sequencing. *Dana-Farber Cancer Institute (Boston, USA)*. 2012.

19 Epigenetic changes in cancer revealed by whole-genome shotgun bisulfite sequencing. *University of Michigan (Michigan, USA)*. 2012.

20 Epigenetic changes in cancer revealed by whole-genome shotgun bisulfite sequencing. *Johns Hopkins University (Baltimore, USA)*. 2012.

21 The structure of epigenetic changes in cancer as revealed by whole-genome shotgun bisulfite sequencing. *Johns Hopkins University (Baltimore, USA)*. 2012.

22 Epigenetic changes in cancer revealed by whole-genome shotgun bisulfite sequencing. *University of British Columbia (Vancouver, Canada)*. 2012.

23 Analysis of whole-genome shotgun bisulfite sequencing data. *University of Pennsylvania (Philadelphia, USA)*. 2012.

24 Increased methylation variation across cancer types. *Cancer Research UK (Cambridge, UK)*. 2012.

25 Epigenetic changes in cancer revealed by whole-genome shotgun bisulfite sequencing. *European Bioinformatics Institute (Hinxton, UK)*. 2012.

26 The structure of epigenetic changes in cancer as revealed by whole-genome shotgun bisulfite sequencing. *Pacific Biosciences (Menlo Park, USA)*. 2012.

27 Analysis of shotgun bisulfite sequencing of cancer samples. *Seminar in Applied Mathematics and Statistics (Copenhagen, Denmark)*. 2011.

28 Biological variation in high-throughput RNA sequencing experiments. *Young Investigator Symposium at Johns Hopkins (Baltimore, USA)*. 2010.

29 The use of random priming induces global biases in Illumina transcriptome sequencing. *(NIH, USA)*. 2010.

30 Biases in Illumina RNA-Seq due to random priming. *University of Chicago (Chicago, USA)*. 2009.

31 Biases in Illumina RNA-Seq. *Johns Hopkins University (Baltimore, USA)*. 2009.

32 RNA-Seq: Sequencing the transcriptome. *Using Bioconductor for ChIP-Seq experiments workshop (FHCRC, USA)*. 2008.

33 RNA-Seq: Sequencing the transcriptome. *Walter and Eliza Hall Institute of Medical Research (WEHI) (Melbourne, Australia)*. 2008.

Posters

34 *minfi: Finding differentially methylated regions using the 450k array*,
Epigenomics of Common Disease, Baltimore, USA (2012)

35 *The structure of DNA methylation in normal tissues*,
Epigenomics of Common Disease, Baltimore, USA (2012)

36 *Generalized loss of stability of epigenetic domains across cancers*,
Statistical Methods for Very Large Datasets, Baltimore, USA (2011)

37 *Generalized loss of stability of epigenetic domains across cancers*,
Biology of Genomes, CSHL, USA (2011)

38 *Biases in Illumina transcriptome sequencing caused by random hexamer priming*,
MGED, ISMB satellite meeting, Boston, USA (2010)

39 *Biases in Illumina transcriptome sequencing caused by random hexamer priming*,
HIT-Seq, ISMB satellite meeting, Boston, USA (2010)