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CURRICULUM VITAE

Kasper Daniel Hansen

PERSONAL DATA

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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

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] Hans T Bjornsson^{*,†}, Joel S Benjamin^{*}, Li Zhang, Jacqueline Weissman, Elizabeth E Gerber, Yi-Chun Chen, Rebecca G Vaurio, Michelle C Potter, **Kasper D Hansen**, and Harry C Dietz. Histone deacetylase inhibition rescues structural and functional brain deficits in a mouse model of Kabuki syndrome. *Science Translational Medicine*, 6(256):256ra135, 2014. doi:[10.1126/scitranslmed.3009278](https://doi.org/10.1126/scitranslmed.3009278), PMID:25273096.
- [2] Jean-Philippe Fortin[†], Elana J Fertig, and **Kasper D Hansen**[†]. shinyMethyl: interactive quality control of Illumina 450k DNA methylation arrays in R. *F1000Research*, 3(175), 2014. doi:[10.12688/f1000research.4680.1](https://doi.org/10.12688/f1000research.4680.1).
- [3] Alyssa C Frazee, Sarven Sabuncuyan, **Kasper D Hansen**, Irizarry, Rafael A, and Jeffrey T Leek. Differential expression analysis of RNA-seq data at single-base resolution. *Biostatistics*, 15(3):413–426, 2014. doi:[10.1093/biostatistics/kxt053](https://doi.org/10.1093/biostatistics/kxt053), PMID:24398039.
- [4] 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](https://doi.org/10.1093/bioinformatics/btu049), PMID:24478339.
- [5] **Kasper D Hansen**^{*}, Sarven Sabuncuyan^{*}, 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](https://doi.org/10.1101/gr.157743.113), PMID:24068705.

- [6] Mike L Smith[†], Keith A Baggerly, Henrik Bengtsson, Matthew E Ritchie, 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](https://doi.org/10.12688/f1000research.2-264.v1), PMID:24701342.
- [7] Christine Ladd-Acosta, **Kasper D Hansen**, Eiríkur Briem, Falline, M Daniele, Walter E Kaufmann, and Andrew P Feinberg. Common DNA methylation alterations in multiple brain regions in autism. *Molecular Psychiatry*, 19(8):862–871, 2014. [f1000](#). doi:[10.1038/mp.2013.114](https://doi.org/10.1038/mp.2013.114), PMID:23999529.
- [8] **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](https://doi.org/10.1186/gb-2012-13-10-r83), PMID:23034175.
- [9] 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](https://doi.org/10.1038/nn.3218), PMID:22983211.
- [10] 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](https://doi.org/10.1073/pnas.1202734109), PMID:22493251.
- [11] 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](https://doi.org/10.1002/hep.25655), PMID:22331678.
- [12] **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](https://doi.org/10.1093/biostatistics/kxr054), PMID:22285995.
- [13] **Kasper D Hansen**^{*}, Winston Timp^{*}, Héctor Corrada Bravo^{*}, Sarven Sabuncian^{*}, Benjamin Langmead^{*}, Oliver G McDonald, Bo Wen, Hao Wu, Yun Liu, Dinh Diep, Eiríkur 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](https://doi.org/10.1038/ng.865), PMID:21706001.
- [14] **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](https://doi.org/10.1038/nbt.1910), PMID:21747377.
- [15] 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](https://doi.org/10.1101/gr.108662.110), PMID:20921232.

- [16] modENCODE Consortium. Identification of functional elements and regulatory circuits by Drosophila modENCODE. *Science*, 330(6012):1787–97, 2010. doi:[10.1126/science.1198374](https://doi.org/10.1126/science.1198374), PMID:[21177974](https://pubmed.ncbi.nlm.nih.gov/21177974/).
- [17] 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](https://doi.org/10.1186/gb-2010-11-8-r83), PMID:[20701754](https://pubmed.ncbi.nlm.nih.gov/20701754/).
- [18] **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](https://doi.org/10.1093/nar/gkq224), PMID:[20395217](https://pubmed.ncbi.nlm.nih.gov/20395217/).
- [19] 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](https://doi.org/10.1186/1471-2105-11-94), PMID:[20167110](https://pubmed.ncbi.nlm.nih.gov/20167110/).
- [20] **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](https://doi.org/10.1371/journal.pgen.1000525), PMID:[19543372](https://pubmed.ncbi.nlm.nih.gov/19543372/).
- [21] 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](https://doi.org/10.1371/journal.pgen.1000299), PMID:[19096707](https://pubmed.ncbi.nlm.nih.gov/19096707/).
- [22] 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](https://doi.org/10.1136/oem.2007.033506), PMID:[17681996](https://pubmed.ncbi.nlm.nih.gov/17681996/).
- [23] 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](https://doi.org/10.1080/14034940410028163), PMID:[15762028](https://pubmed.ncbi.nlm.nih.gov/15762028/).
- [24] 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](https://doi.org/10.1002/ijc.20203), PMID:[15221976](https://pubmed.ncbi.nlm.nih.gov/15221976/).
- [25] 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](https://doi.org/10.1093/aje/kwh332), PMID:[15583374](https://pubmed.ncbi.nlm.nih.gov/15583374/).

Books, Theses, Tech Reports

* indicates equal contributions

† indicates corresponding author (if not the senior author)

- [26] 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](https://doi.org/10.1101/002956).
- [27] **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/>.
- [28] **Kasper D Hansen**. *Analyses of high-throughput gene expression data*. PhD thesis, Division of Biostatistics, University of California at Berkeley, 2009.
- [29] 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/>.
- [30] 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>.
- [31] 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"). Governmental report, 2004.
- [32] **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.