CURRICULUM VITAE
Kasper Daniel Hansen

PERSONAL DATA

Web Page:	http://www.hansenlab.org
Email:	khansen@jhsph.edu
Mailing Address:	Department of Biostatistics
	Johns Hopkins Bloomberg School of Public Health
	615 North Wolfe Street
	Baltimore, MD 21205-2179
Fax:	410 955-0958

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

Significant awards to students:

2014	Jean-Philippe Fortin: John van Ryzin award for best student paper submitted to ENAR.

Journal Articles (peer-reviewed)

$*$ indicates equal contributions
$\dagger$ indicates corresponding author (if not the senior author)
boldface indicates a member of my lab

[1] **Jean-Philippe Fortin** and **Kasper D Hansen**. Reconstructing A/B compartments as revealed by Hi-C using long-range correlations in epigenetic data. *Genome Biology*, 16:180, 2015. doi:10.1186/s13059-015-0741-y.
    Research highlight by Mourad and Cuvier in Genome Biology.

[2] Amy R Vandiver, Rafael A Irizarry, **Kasper D Hansen**, Luis A Garza, Arni Runarsson, Xin Li, Anna L Chien, Timothy S Wang, Sherry G Leung, Sewon Kang, and Andrew P Feinberg. Age and sun exposure-related widespread genomic blocks of hypomethylation in nonmalignant skin. *Genome Biology*, 16:80, 2015. doi:10.1186/s13059-015-0644-y, PMID:25886480.
    Highly accessed.

[3] Xiumei Hong$*$, Ke Hao$*$, Christine Ladd-Acosta$*$, **Kasper D Hansen**, Hui-Ju Tsai, Xin Liu, Xin Xu, Timothy A Thornton, Deanna Caruso, Corinne A Keet, Yifei Sun, Guoying Wang, Wei Luo, Rajesh Kumar, Ramsay Fuleihan, Anne Marie Singh, Jennifer S Kim, Rachel E Story, Ruchi S Gupta, Peisong Gao, Zhu Chen, Sheila O Walker, Tami R Bartell, Terri H Beaty, M Daniele Fallin, Robert Schleimer, Patrick G Holt, Kari Christine Nadeau, Robert A Wood, Jacqueline A Pongracic, Daniel E Weeks, and Xiaobin Wang. Genome-wide association study identifies peanut allergy-specific loci and evidence of epigenetic mediation in US children. *Nature Communications*, 6:6304, 2015. doi:10.1038/ncomms7304, PMID:25710614.

[4] Wolfgang Huber†, Vincent J Carey, Robert Gentleman, Simon Anders, Marc Carlson, Benilton S Carvalho, Héctor Corrada Bravo, Sean Davis, Laurent Gatto, Thomas Girke, Raphael Gottardo, Florian Hahne, **Kasper D Hansen**, Rafael A Irizarry, Michael Lawrence, Michael I Love, James MacDonald, Valerie Obenchain, Andrzej K Ole ś, Hervé Pagès, Alejandro Reyes, Paul Shannon, Gordon K Smyth, Dan Tenenbaum, Levi Waldron, and Martin Morgan. Orchestrating high-throughput genomic analysis with Bioconductor. *Nature Methods*, 12(2):115–121, 2015. `doi:10.1038/nmeth.3252`, `PMID:25633503`.

[5] **Jean-Philippe Fortin**, Aurélie Labbe, Mathieu Lemire, Zanke, Brent W, 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. *Genome Biology*, 15:503, 2014. `doi:10.1186/s13059-014-0503-2`, `PMID:25599564`.

[6] Michael J Ziller, **Kasper D Hansen**, Alexander Meissner†, and Martin J Aryee†. Coverage recommendations for methylation analysis by whole-genome bisulfite sequencing. *Nature Methods*, 12(3):230–232, 2015. `doi:10.1038/nmeth.3152`, `PMID:25362363`.

[7] 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`, `PMID:25273096`.

[8] **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`, `PMID:25285208`.

[9] 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*, 15(3):413–426, 2014. `doi:10.1093/biostatistics/kxt053`, `PMID:24398039`.

[10] 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`.

[11] **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`.

[12] 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`, `PMID:24701342`.

[13] 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*, 19(8):862–871, 2014. `doi:10.1038/mp.2013.114`, `PMID:23999529`.

F1000Prime recommendations.

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

[15] 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`.

[16] 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. `doi:10.1073/pnas.1202734109`, `PMID:22493251`.
  F1000Prime recommendations.

[17] 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`.

[18] **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`.

[19] **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. `doi:10.1038/ng.865`, `PMID:21706001`.
  News and Views by JP Issa in Nat Genet.
  Highlighted in Cell.
  F1000Prime recommendations.

[20] **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`.

[21] 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`.

[22] 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`.

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

[24] **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. `doi:10.1093/nar/gkq224`, `PMID:20395217`.

[25] 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. `doi:10.1186/1471-2105-11-94`, `PMID:20167110`.
Highly accessed.

[26] **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`.

[27] 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`.

[28] 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`.

[29] 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`.

[30] 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`.

[31] 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)
boldface indicates a member of my lab

[32] Alain Pacis, Ludovic Tailleux, John Lambourne, Vania Yotova, Anne Dumaine, Anne Danck-aert, Francesca Luca, Jean-Christophe Grenier, **Kasper D Hansen**, Miao Yu, Jenny Tung, Chuan He, Tomi Pastinen, Roger Pique-Regi, Yoav Gilad, and Luis B Barreiro. Bacterial Infection Remodels the DNA Methylation Landscape of Human Dendritic Cells. *bioRxiv*, 2015. `doi:10.1101/016022`.

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

[34] 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`.

[35] 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.

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

Preprints, subsequently published

* indicates equal contributions
[†] indicates corresponding author (if not the senior author)
boldface indicates a member of my lab

[37] **Jean-Philippe Fortin** and **Kasper D. Hansen**. Reconstructing A/B compartments as revealed by Hi-C using long-range correlations in epigenetic data. *bioRxiv*, 2015. Published in Genome Biology 2015. `doi:10.1101/019000`.

[38] **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. Published in Genome Biology 2014. `doi:10.1101/002956`.

[39] **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. Published in Biostatistics 2012. URL: `http://www.bepress.com/jhubiostat/paper227/`.

[40] 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. Published in BMC Bioinformatics 2010. URL: `http://www.bepress.com/ucbbiostat/paper247/`.

Citations

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.