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## CURRICULUM VITAE

Kasper Daniel Hansen

### PERSONAL DATA

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Mailing Address: Department of Biostatistics  
Johns Hopkins Bloomberg School of Public Health  
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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

2018 Departments of Statistics and Biology  
University of Copenhagen  
2004–2005 Department of Biostatistics  
University of California, Berkeley

## PROFESSIONAL EXPERIENCE

2018–Present	Associate Professor Department of Biostatistics Nathans-McKusick Institute of Genetic Medicine Johns Hopkins University
2012–2018	Assistant Professor Department of Biostatistics Nathans-McKusick Institute of Genetic Medicine 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

### Editorial Board Membership

Gateway advisor for the [Bioconductor Gateway](#) at F1000Research.

### Served as *referee* for

Annals of Applied Statistics  
Bioinformatics  
Biometrics  
Biostatistics  
BMC Bioinformatics  
F1000Research  
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 Communications  
Nature Ecology and Evolution  
Nature Methods  
Nature Reviews Genetics  
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)  
Israeli Science Foundation (2019)

## 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 trainees:

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

## PUBLICATIONS

### Journal Articles (peer reviewed)

\* indicates equal contributions

† indicates corresponding author(s) (if not the senior author)

**boldface** indicates a member of my lab

- [1] J. A. Fahrner<sup>†</sup>, W.-Y. Lin, R. C. Riddle, **L. Boukas**, V. B. DeLeon, S. Chopra, S. E. Lad, T. R. Luperchio, **K. D. Hansen**, and H. T. Bjornsson<sup>†</sup>. “Precocious chondrocyte differentiation disrupts skeletal growth in Kabuki syndrome mice”. *JCI Insight* (2019). DOI: [10.1172/jci.insight.129380](https://doi.org/10.1172/jci.insight.129380).
- [2] G. A. Carosso, **L. Boukas**, J. J. Augustin, H. N. Nguyen, B. L. Winer, G. H. Cannon, J. D. Robertson, L. Zhang, **K. D. Hansen**, L. A. Goff, and H. T. Bjornsson. “Precocious neuronal differentiation and disrupted oxygen responses in Kabuki syndrome”. *JCI Insight* (2019). DOI: [10.1172/jci.insight.129375](https://doi.org/10.1172/jci.insight.129375).
- [3] **L. Myint**, R. Wang, **L. Boukas**, **K. D. Hansen**, L. A. Goff, and D. G. Avramopoulos. “A screen of 1,049 schizophrenia and 30 Alzheimer’s-associated variants for regulatory potential”. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics* (2019). In Press. DOI: [10.1002/ajmg.b.32761](https://doi.org/10.1002/ajmg.b.32761).
- [4] P. Wulfridge, B. Langmead, A. P. Feinberg, and **K. D. Hansen**. “Analyzing whole genome bisulfite sequencing data from highly divergent genotypes”. *Nucleic Acids Research* (2019). In Press. DOI: [10.1093/nar/gkz674](https://doi.org/10.1093/nar/gkz674).
- [5] **L. Myint**, D. G. Avramopoulos, L. A. Goff, and **K. D. Hansen**. “Linear models enable powerful differential activity analysis in massively parallel reporter assays”. *BMC Genomics* 20 (2019), p. 209. DOI: [10.1186/s12864-019-5556-x](https://doi.org/10.1186/s12864-019-5556-x).
- [6] **L. Boukas**, J. M. Havrilla, **P. F. Hickey**, A. R. Quinlan, H. T. Bjornsson<sup>†</sup>, and **K. D. Hansen**<sup>†</sup>. “Coexpression patterns define epigenetic regulators associated with neurological dysfunction”. *Genome Research* 29.4 (2019). In press, pp. 532–542. DOI: [10.1101/gr.239442.118](https://doi.org/10.1101/gr.239442.118).
- [7] L. F. Rizzardi<sup>\*</sup>, **P. F. Hickey**<sup>\*</sup>, V. R. DiBlasi, R. Tryggvadottir, C. M. Callahan, A. Idrizi, **K. D. Hansen**<sup>†</sup>, and A. P. Feinberg<sup>†</sup>. “Neuronal brain region-specific DNA methylation and chromatin accessibility are associated with neuropsychiatric disease heritability”. *Nature Neuroscience* 22.2 (2019), pp. 307–316. DOI: [10.1038/s41593-018-0297-8](https://doi.org/10.1038/s41593-018-0297-8).
- [8] V. Gaysinskaya, B. F. Miller, C. De Luca, G. W. van der Heijden, **K. D. Hansen**, and A. Bortvin. “Transient reduction of DNA methylation at the onset of meiosis in male mice”. *Epigenetics & Chromatin* 11.1 (2018), p. 15. DOI: [10.1186/s13072-018-0186-0](https://doi.org/10.1186/s13072-018-0186-0).
- [9] W. T. Barrington, P. Wulfridge, A. E. Wells, C. M. Rojas, S. Y. Howe, A. Perry, K. Hua, M. A. Pellizzon, **K. D. Hansen**, B. H. Voy, B. J. Bennett, D. Pomp, A. P. Feinberg, and D. W. Threadgill. “Improving metabolic health through precision dietetics in mice”. *Genetics* 208.1 (2018), pp. 399–417. DOI: [10.1534/genetics.117.300536](https://doi.org/10.1534/genetics.117.300536).
- [10] M. Ramos, L. Schiffer, A. Re, R. Azhar, A. Basunia, C. Rodriguez, T. Chan, P. Chapman, S. R. Davis, D. Gomez-Cabrero, A. C. Culhane, B. Haibe-Kains, **K. D. Hansen**, H. Kodali, M. S. Louis, A. S. Mer, M. Riester, M. Morgan, V. Carey, and L. Waldron. “Software for the Integration of Multiomics Experiments in Bioconductor”. *Cancer Research* 77.21 (2017), e39–e42. DOI: [10.1158/0008-5472.CAN-17-0344](https://doi.org/10.1158/0008-5472.CAN-17-0344).
- [11] L. Collado-Torres<sup>\*</sup>, A. Nellore<sup>\*</sup>, K. Kammers, S. E. Ellis, M. A. Taub, **K. D. Hansen**, A. E. Jaffe<sup>†</sup>, B. Langmead<sup>†</sup>, and J. T. Leek<sup>†</sup>. “Reproducible RNA-seq analysis using recount2”. *Nature Biotechnology* 35.4 (2017), pp. 319–321. DOI: [10.1038/nbt.3838](https://doi.org/10.1038/nbt.3838).

- [12] S. C. Zheng, S. Beck, A. E. Jaffe, D. C. Koestler, **K. D. Hansen**, A. E. Houseman, R. A. Irizarry, and A. E. Teschendorff. “Correcting for cell-type heterogeneity in epigenome-wide association studies: revisiting previous analyses”. *Nature Methods* 14.3 (2017), pp. 216–217. DOI: [10.1038/nmeth.4187](https://doi.org/10.1038/nmeth.4187).
- [13] **L. Myint**, A. Kleensang, L. Zhao, T. Hartung, and **K. D. Hansen**. “Joint bounding of peaks across samples improves differential analysis in mass spectrometry-based metabolomics”. *Analytical Chemistry* 89.6 (2017), pp. 3517–3523. DOI: [10.1021/acs.analchem.6b04719](https://doi.org/10.1021/acs.analchem.6b04719).
- [14] **J.-P. Fortin**, T. Triche Jr, and **K. D. Hansen**. “Preprocessing, normalization and integration of the Illumina HumanMethylationEPIC array with minfi”. *Bioinformatics* 33.4 (2017), pp. 558–560. DOI: [10.1093/bioinformatics/btw691](https://doi.org/10.1093/bioinformatics/btw691).
- [15] J. S. Benjamin, G. Pilarowski, G. Carosso, L. Zhang, J. Farner, D. L. Huso, L. A. Goff, H. Vernon, **K. D. Hansen**, and H. T. Bjornsson. “A ketogenic diet rescues hippocampal memory defects in a mouse model of Kabuki syndrome”. *Proceedings of the National Academy of Sciences* 114.1 (2017), pp. 125–130. DOI: [10.1073/pnas.1611431114](https://doi.org/10.1073/pnas.1611431114).
- [16] A. Nellore, A. E. Jaffe, **J.-P. Fortin**, J. Alquicira-Hernández, L. Collado-Torres, S. Wang, R. A. Phillips, N. Karbhari, **K. D. Hansen**, B. Langmead<sup>†</sup>, and J. T. Leek<sup>†</sup>. “Human splicing diversity and the extent of unannotated splice junctions across human RNA-seq samples on the Sequence Read Archive”. *Genome Biology* 17 (2016), p. 266. DOI: [10.1186/s13059-016-1118-6](https://doi.org/10.1186/s13059-016-1118-6).
- [17] S. V. Andrews\*, C. Ladd-Acosta\*, A. P. Feinberg, **K. D. Hansen**, and M. D. Fallin. “Gap hunting” to to characterize clustered probe signals in Illumina methylation array data”. *Epigenetics and Chromatin* 9 (2016), p. 56. DOI: [10.1186/s13072-016-0107-z](https://doi.org/10.1186/s13072-016-0107-z).
- [18] X. Li, Y. Liu, T. Salz, **K. D. Hansen**, and A. P. Feinberg. “Whole genome analysis of the methylome and hydroxymethylome in normal and malignant lung and liver”. *Genome Research* 26.12 (2016), pp. 1730–1741. DOI: [10.1101/gr.211854.116](https://doi.org/10.1101/gr.211854.116).
- [19] A. Nellore<sup>†</sup>, C. Wilks, **K. D. Hansen**, J. T. Leek, and B. Langmead<sup>†</sup>. “Rail-dbGaP: analyzing dbGaP-protected data in the cloud with Amazon Elastic MapReduce”. *Bioinformatics* 32.16 (2016), pp. 2551–2553. DOI: [10.1093/bioinformatics/btw177](https://doi.org/10.1093/bioinformatics/btw177).
- [20] L. Gatto, **K. D. Hansen**, M. R. Hoopmann, H. Hermjakob, O. Kohlbacher, and A. Beyer. “Testing and validation of computational methods for mass spectrometry”. *Journal of Proteome Research* 15.3 (2016), pp. 809–814. DOI: [10.1021/acs.jproteome.5b00852](https://doi.org/10.1021/acs.jproteome.5b00852).
- [21] A. R. Vandiver, A. Idrizi, L. Rizzardi, A. P. Feinberg, and **K. D. Hansen**. “DNA methylation is stable during replication and cell cycle arrest”. *Scientific Reports* 5 (2015), p. 17911. DOI: [10.1038/srep17911](https://doi.org/10.1038/srep17911).
- [22] L. Kannan, M. Ramos, A. Re, N. El-Hachem, Z. Safikhani, D. M. A. Gendoo, S. Davis, D. Gomez-Cabrero, R. Castelo, **K. D. Hansen**, V. J. Carey, M. Morgan, A. C. Culhane, B. Haibe-Kains, and L. Waldron. “Public data and open source tools for multi-assay genomic investigation of disease.” *Briefings in Bioinformatics* 17.4 (2016), pp. 603–615. DOI: [10.1093/bib/bbv080](https://doi.org/10.1093/bib/bbv080).

- [23] A. Pacis, L. Tailleux, A. M. Morin, J. Lambourne, J. L. MacIsaac, V. Yotova, A. Dumaine, A. Danckaert, F. Luca, J.-C. Grenier, **K. D. Hansen**, B. Gicquel, M. Yu, A. Pai, C. He, J. Tung, T. Pastinen, M. S. Kobor, R. Pique-Regi, Y. Gilad<sup>†</sup>, and L. B. Barreiro<sup>†</sup>. “Bacterial infection remodels the DNA methylation landscape of human dendritic cells”. *Genome Research* 25.12 (2015), pp. 1801–1811. DOI: [10.1101/gr.192005.115](https://doi.org/10.1101/gr.192005.115).
- [24] **J.-P. Fortin** and **K. D. Hansen**. “Reconstructing A/B compartments as revealed by Hi-C using long-range correlations in epigenetic data”. *Genome Biology* 16 (2015), p. 180. DOI: [10.1186/s13059-015-0741-y](https://doi.org/10.1186/s13059-015-0741-y).
- [25] A. R. Vandiver, R. A. Irizarry, **K. D. Hansen**, L. A. Garza, A. Runarsson, X. Li, A. L. Chien, T. S. Wang, S. G. Leung, S. Kang, and A. P. Feinberg. “Age and sun exposure-related widespread genomic blocks of hypomethylation in nonmalignant skin”. *Genome Biology* 16 (2015), p. 80. DOI: [10.1186/s13059-015-0644-y](https://doi.org/10.1186/s13059-015-0644-y).
- [26] X. Hong<sup>\*</sup>, K. Hao<sup>\*</sup>, C. Ladd-Acosta<sup>\*</sup>, **K. D. Hansen**, H.-J. Tsai, X. Liu, X. Xu, T. A. Thornton, D. Caruso, C. A. Keet, Y. Sun, G. Wang, W. Luo, R. Kumar, R. Fuleihan, A. M. Singh, J. S. Kim, R. E. Story, R. S. Gupta, P. Gao, Z. Chen, S. O. Walker, T. R. Bartell, T. H. Beaty, M. D. Fallin, R. Schleimer, P. G. Holt, K. C. Nadeau, R. A. Wood, J. A. Pongratic, D. E. Weeks, and X. Wang. “Genome-wide association study identifies peanut allergy-specific loci and evidence of epigenetic mediation in US children.” *Nature Communications* 6 (2015), p. 6304. DOI: [10.1038/ncomms7304](https://doi.org/10.1038/ncomms7304).
- [27] W. Huber<sup>†</sup>, V. J. Carey, R. Gentleman, S. Anders, M. Carlson, B. S. Carvalho, H. C. Bravo, S. Davis, L. Gatto, T. Girke, R. Gottardo, F. Hahne, **K. D. Hansen**, R. A. Irizarry, M. Lawrence, M. I. Love, J. MacDonald, V. Obenchain, A. K. Oleś, H. Pagès, A. Reyes, P. Shannon, G. K. Smyth, D. Tenenbaum, L. Waldron, and M. Morgan. “Orchestrating high-throughput genomic analysis with Bioconductor”. *Nature Methods* 12.2 (2015), pp. 115–121. DOI: [10.1038/nmeth.3252](https://doi.org/10.1038/nmeth.3252).
- [28] **J.-P. Fortin**, A. Labbe, M. Lemire, B. W. Zanke, T. J. Hudson, E. J. Fertig, C. M. Greenwood, and **K. D. Hansen**. “Functional normalization of 450k methylation array data improves replication in large cancer studies”. *Genome Biology* 15 (2014), p. 503. DOI: [10.1186/s13059-014-0503-2](https://doi.org/10.1186/s13059-014-0503-2).
- [29] M. J. Ziller, **K. D. Hansen**, A. Meissner<sup>†</sup>, and M. J. Aryee<sup>†</sup>. “Coverage recommendations for methylation analysis by whole-genome bisulfite sequencing”. *Nature Methods* 12.3 (2015), pp. 230–232. DOI: [10.1038/nmeth.3152](https://doi.org/10.1038/nmeth.3152).
- [30] H. T. Bjornsson<sup>\*†</sup>, J. S. Benjamin<sup>\*</sup>, L. Zhang, J. Weissman, E. E. Gerber, Y.-C. Chen, R. G. Vaurio, M. C. Potter, **K. D. Hansen**, and H. C. Dietz. “Histone deacetylase inhibition rescues structural and functional brain deficits in a mouse model of Kabuki syndrome.” *Science Translational Medicine* 6.256 (2014), 256ra135. DOI: [10.1126/scitranslmed.3009278](https://doi.org/10.1126/scitranslmed.3009278).
- [31] **J.-P. Fortin**<sup>†</sup>, E. J. Fertig, and **K. D. Hansen**<sup>†</sup>. “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).
- [32] A. C. Frazee, S. Sabuncuyan, **K. D. Hansen**, R. A. Irizarry, and J. T. Leek. “Differential expression analysis of RNA-seq data at single-base resolution.” *Biostatistics* 15.3 (2014), pp. 413–426. DOI: [10.1093/biostatistics/kxt053](https://doi.org/10.1093/biostatistics/kxt053).

- [33] M. J. Aryee, A. E. Jaffe, H. Corrada Bravo, C. Ladd-Acosta, A. P. Feinberg, **K. D. Hansen**<sup>†</sup>, and R. A. Irizarry<sup>†</sup>. “Minfi: a flexible and comprehensive Bioconductor package for the analysis of Infinium DNA methylation microarrays.” *Bioinformatics* 30.10 (2014), pp. 1363–1369. DOI: [10.1093/bioinformatics/btu049](https://doi.org/10.1093/bioinformatics/btu049).
- [34] **K. D. Hansen**<sup>\*</sup>, S. Sabunciyan<sup>\*</sup>, B. Langmead, N. Nagy, R. Curley, G. Klein, E. Klein, D. Salamon, and A. P. Feinberg. “Large-scale hypomethylated blocks associated with Epstein-Barr virus-induced B-cell immortalization.” *Genome Research* 24.2 (2014), pp. 177–184. DOI: [10.1101/gr.157743.113](https://doi.org/10.1101/gr.157743.113).
- [35] M. L. Smith<sup>†</sup>, K. A. Baggerly, H. Bengtsson, M. E. Ritchie, and **K. D. Hansen**<sup>†</sup>. “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).
- [36] C. Ladd-Acosta, **K. D. Hansen**, E. Briem, M. D. Falline, W. E. Kaufmann, and A. P. Feinberg. “Common DNA methylation alterations in multiple brain regions in autism”. *Molecular Psychiatry* 19.8 (2014), pp. 862–871. DOI: [10.1038/mp.2013.114](https://doi.org/10.1038/mp.2013.114).
- [37] **K. D. Hansen**<sup>†</sup>, B. Langmead<sup>†</sup>, and R. A. Irizarry<sup>†</sup>. “BSmooth: from whole genome bisulfite sequencing reads to differentially methylated regions”. *Genome Biology* 13 (2012), R83. DOI: [10.1186/gb-2012-13-10-r83](https://doi.org/10.1186/gb-2012-13-10-r83).
- [38] B. R. Herb, F. Wolschin, **K. D. Hansen**, M. J. Aryee, B. Langmead, R. Irizarry, G. V. Amdam<sup>†</sup>, and A. P. Feinberg<sup>†</sup>. “Reversible switching between epigenetic states in honeybee behavioral subcastes.” *Nature Neuroscience* 15.10 (2012), pp. 1371–1373. DOI: [10.1038/nn.3218](https://doi.org/10.1038/nn.3218).
- [39] J. Tung<sup>†</sup>, L. B. Barreiro, Z. P. Johnson, **K. D. Hansen**, V. Michopoulos, D. Toufexis, K. Michelini, M. E. Wilson, and Y. Gilad<sup>†</sup>. “Social environment is associated with gene regulatory variation in the rhesus macaque immune system.” *Proceedings of the National Academy of Sciences* 109.17 (2012), pp. 6490–6495. DOI: [10.1073/pnas.1202734109](https://doi.org/10.1073/pnas.1202734109).
- [40] S. Munshaw, H. S. Hwang, M. Torbenson, J. Quinn, **K. D. Hansen**, J. Astemborski, S. H. Mehta, S. C. Ray, D. L. Thomas, and A. Balagopal. “Laser captured hepatocytes show association of butyrylcholinesterase gene loss and fibrosis progression in hepatitis C-infected drug users.” *Hepatology* 56.2 (2012), pp. 544–554. DOI: [10.1002/hep.25655](https://doi.org/10.1002/hep.25655).
- [41] **K. D. Hansen**, R. A. Irizarry, and Z. Wu. “Removing technical variability in RNA-seq data using conditional quantile normalization.” *Biostatistics* 13.2 (2012), pp. 204–216. DOI: [10.1093/biostatistics/kxr054](https://doi.org/10.1093/biostatistics/kxr054).
- [42] **K. D. Hansen**<sup>\*</sup>, W. Timp<sup>\*</sup>, H. C. Bravo<sup>\*</sup>, S. Sabunciyan<sup>\*</sup>, B. Langmead<sup>\*</sup>, O. G. McDonald, B. Wen, H. Wu, Y. Liu, D. Diep, E. Briem, K. Zhang, R. A. Irizarry<sup>†</sup>, and A. P. Feinberg<sup>†</sup>. “Increased methylation variation in epigenetic domains across cancer types”. *Nature Genetics* 43.8 (2011), pp. 768–775. DOI: [10.1038/ng.865](https://doi.org/10.1038/ng.865).
- [43] **K. D. Hansen**, Z. Wu, R. A. Irizarry<sup>†</sup>, and J. T. Leek<sup>†</sup>. “Sequencing technology does not eliminate biological variability”. *Nature Biotechnology* 29.7 (2011), pp. 572–573. DOI: [10.1038/nbt.1910](https://doi.org/10.1038/nbt.1910).
- [44] A. N. Brooks, L. Yang, M. O. Duff, **K. D. Hansen**, J. W. Park, S. Dudoit, S. E. Brenner<sup>†</sup>, and B. R. Graveley<sup>†</sup>. “Conservation of an RNA regulatory map between *Drosophila* and mammals”. *Genome Research* 21.2 (2011), pp. 193–202. DOI: [10.1101/gr.108662.110](https://doi.org/10.1101/gr.108662.110).



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- [46] **K. D. Hansen**<sup>†</sup>, S. E. Brenner, and S. Dudoit. “Biases in Illumina transcriptome sequencing caused by random hexamer priming”. *Nucleic Acids Research* 38.12 (2010), e131. DOI: [10.1093/nar/gkq224](https://doi.org/10.1093/nar/gkq224).
- [47] J. H. Bullard<sup>\*</sup>, E. Purdom<sup>\*</sup>, **K. D. Hansen**, and S. Dudoit. “Evaluation of statistical methods for normalization and differential expression in mRNA-Seq experiments”. *BMC Bioinformatics* 11 (2010), p. 94. DOI: [10.1186/1471-2105-11-94](https://doi.org/10.1186/1471-2105-11-94).
- [48] **K. D. Hansen**<sup>\*</sup>, L. F. Lareau<sup>\*</sup>, M. Blanchette, R. E. Green, Q. Meng, J. Rehwinkel, F. L. Gallusser, E. Izaurralde, D. C. Rio, S. Dudoit, and S. E. Brenner. “Genome-Wide Identification of Alternative Splice Forms Down-Regulated by Nonsense-Mediated mRNA Decay in *Drosophila*”. *PLoS Genetics* 5.6 (2009), e1000525. DOI: [10.1371/journal.pgen.1000525](https://doi.org/10.1371/journal.pgen.1000525).
- [49] A. Lee<sup>\*</sup>, **K. D. Hansen**<sup>\*</sup>, J. Bullard<sup>\*</sup>, S. Dudoit, and G. 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 (2008), e1000299. DOI: [10.1371/journal.pgen.1000299](https://doi.org/10.1371/journal.pgen.1000299).
- [50] J. H. Andersen<sup>†</sup>, M. Harhoff, S. Grimstrup, I. Vilstrup, C. F. Lassen, L. P. A. Brandt, A. I. Kryger, E. Overgaard, **K. D. Hansen**, and S. Mikkelsen. “Computer mouse use predicts acute pain but not prolonged or chronic pain in the neck and shoulder.” *Occupational and Environmental Medicine* 65.2 (2008), pp. 126–131. DOI: [10.1136/oem.2007.033506](https://doi.org/10.1136/oem.2007.033506).
- [51] H. Danø<sup>†</sup>, R. Jacobsen, **K. D. Hansen**, J. K. Petersen, and E. Lynge. “Use of census data for construction of fertility history for Danish women.” *Scandinavian Journal of Public Health* 32 (2004), pp. 435–41. DOI: [10.1080/14034940410028163](https://doi.org/10.1080/14034940410028163).
- [52] H. Danø<sup>†</sup>, **K. D. Hansen**, P. Jensen, J. H. Petersen, R. Jacobsen, M. Ewertz, and E. Lynge. “Fertility pattern does not explain social gradient in breast cancer in Denmark.” *International Journal of Cancer* 111 (2004), pp. 451–6. DOI: [10.1002/ijc.20203](https://doi.org/10.1002/ijc.20203).
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## Journal Articles, Consortia member (peer reviewed)

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\* indicates equal contributions

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## PRACTICE ACTIVITIES

### Software - Bioconductor Project

[affxparser](#) A package for parsing output files from Affymetrix microarrays using the Affymetrix Fusion SDK.

[bnbc](#) A package to normalize and remove unwanted variation in Hi-C data.

[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.

[mpr](#) A package to analysis massively parallel reporter assays (MPRA).

[Rgraphviz](#) A package for visualizing graphs using the Graphviz toolkit.

[yamss](#) A package for analyzing MS-based metabolomics experiments.

## Software - 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.