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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

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)

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] L. F. Rizzardi*, **P. F. Hickey***, V. R. DiBlasi, R. Tryggvadottir, C. M. Callahan, A. Idrizi, **K. D. Hansen**†, and A. P. Feinberg†. "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.

[2] 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.

[3] 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.

[4] 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.

[5] L. Collado-Torres*, A. Nellore*, K. Kammers, S. E. Ellis, M. A. Taub, **K. D. Hansen**, A. E. Jaffe†, B. Langmead†, and J. T. Leek†. "Reproducible RNA-seq analysis using recount2". *Nature Biotechnology* 35.4 (2017), pp. 319–321. DOI: 10.1038/nbt.3838.

[6] 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.

[7] **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.

[8] **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.

[9] 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.

[10] 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†, and J. T. Leek†. "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.

[11] 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.

[12] 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.

[13] A. Nellore†, C. Wilks, **K. D. Hansen**, J. T. Leek, and B. Langmead†. "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.

[14] 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.

[15] 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.

[16] 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.

[17] A. Pacis, L. Tailleux, A. M. Morin, J. Lambourne, J. L. Maclsaac, 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†, and L. B. Barreiro†. "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.

[18] **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.

[19] 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.

[20] X. Hong*, K. Hao*, C. Ladd-Acosta*, **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. Pongracic, 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.

[21] W. Huber†, 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.

[22] **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.

[23] M. J. Ziller, **K. D. Hansen**, A. Meissner†, and M. J. Aryee†. "Coverage recommendations for methylation analysis by whole-genome bisulfite sequencing". *Nature Methods* 12.3 (2015), pp. 230–232. DOI: 10.1038/nmeth.3152.

[24] H. T. Bjornsson*†, J. S. Benjamin*, 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.

[25] **J.-P. Fortin**†, E. J. Fertig, and **K. D. Hansen**†. "shinyMethyl: interactive quality control of Illumina 450k DNA methylation arrays in R". *F1000Research* 3.175 (2014). DOI: 10.12688/f1000research.4680.1.

[26] A. C. Frazee, S. Sabunciyan, **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.

[27] M. J. Aryee, A. E. Jaffe, H. Corrada Bravo, C. Ladd-Acosta, A. P. Feinberg, **K. D. Hansen**†, and R. A. Irizarry†. "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.

[28] **K. D. Hansen***, S. Sabunciyan*, 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.

[29] M. L. Smith†, K. A. Baggerly, H. Bengtsson, M. E. Ritchie, and **K. D. Hansen**†. "illuminaio: An open source IDAT parsing tool for Illumina microarrays". *F1000Research* 264.2 (2013). DOI: 10.12688/f1000research.2-264.v1.

[30] 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.

[31] **K. D. Hansen**†, B. Langmead†, and R. A. Irizarry†. "BSmooth: from whole genome bisulfite sequencing reads to differentially methylated regions". *Genome Biology* 13 (2012), R83. DOI: 10.1186/gb-2012-13-10-r83.

[32] B. R. Herb, F. Wolschin, **K. D. Hansen**, M. J. Aryee, B. Langmead, R. Irizarry, G. V. Amdam†, and A. P. Feinberg†. "Reversible switching between epigenetic states in honeybee behavioral subcastes." *Nature Neuroscience* 15.10 (2012), pp. 1371–1373. DOI: 10.1038/nn.3218.

[33] J. Tung†, L. B. Barreiro, Z. P. Johnson, **K. D. Hansen**, V. Michopoulos, D. Toufexis, K. Michelini, M. E. Wilson, and Y. Gilad†. "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.

[34] 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.

[35] **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.

[36] **K. D. Hansen**[*], W. Timp[*], H. C. Bravo[*], S. Sabunciyan[*], B. Langmead[*], O. G. McDonald, B. Wen, H. Wu, Y. Liu, D. Diep, E. Briem, K. Zhang, R. A. Irizarry[†], and A. P. Feinberg[†]. "Increased methylation variation in epigenetic domains across cancer types". *Nature Genetics* 43.8 (2011), pp. 768–775. DOI: 10.1038/ng.865.

[37] **K. D. Hansen**, Z. Wu, R. A. Irizarry[†], and J. T. Leek[†]. "Sequencing technology does not eliminate biological variability". *Nature Biotechnology* 29.7 (2011), pp. 572–573. DOI: 10.1038/nbt.1910.

[38] A. N. Brooks, L. Yang, M. O. Duff, **K. D. Hansen**, J. W. Park, S. Dudoit, S. E. Brenner[†], and B. R. Graveley[†]. "Conservation of an RNA regulatory map between Drosophila and mammals". *Genome Research* 21.2 (2011), pp. 193–202. DOI: 10.1101/gr.108662.110.

[39] B. Langmead, **K. D. Hansen**, and J. T. Leek. "Cloud-scale RNA-sequencing differential expression analysis with Myrna." *Genome Biology* 11.8 (2010), R83. DOI: 10.1186/gb-2010-11-8-r83.

[40] **K. D. Hansen**[†], 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.

[41] J. H. Bullard[*], E. Purdom[*], **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.

[42] **K. D. Hansen**[*], L. F. Lareau[*], 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.

[43] A. Lee[*], **K. D. Hansen**[*], J. Bullard[*], 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.

[44] J. H. Andersen[†], 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.

[45] H. Danø[†], 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.

[46] H. Danø†, **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.

[47] A.-M. Nybo Andersen†, **K. D. Hansen**, P. K. Andersen, and G. Davey Smith. "Advanced paternal age and risk of fetal death: a cohort study". *American Journal of Epidemiology* 160.12 (2004), pp. 1214–22. DOI: 10.1093/aje/kwh332.

Journal Articles, Consortia member (peer reviewed)

[48] eGTEx Project. "Enhancing GTEx by bridging the gaps between genotype, gene expression, and disease". *Nature Genetics* 12 (2017), pp. 1664–1670. DOI: 10.1038/ng.3969.

[49] A. Saha, Y. Kim, A. D. H. Gewirtz, B. Jo, C. Gao, I. C. McDowell, GTEx Consortium, B. E. Engelhardt, and A. Battle. "Co-expression networks reveal the tissue-specific regulation of transcription and splicing". *Genome Research* 27.11 (2017), pp. 1843–1858. DOI: 10.1101/gr.216721.116.

[50] F. Yang, J. Wang, GTEx Consortium, B. L. Pierce, and L. S. Chen. "Identifying cis-mediators for trans-eQTLs across many human tissues using genomic mediation analysis". *Genome Research* 27.11 (2017), pp. 1859–1871. DOI: 10.1101/gr.216754.116.

[51] X. Li, Y. Kim, E. K. Tsang, J. R. Davis, F. N. Damani, C. Chiang, G. T. Hess, Z. Zappala, B. J. Strober, A. J. Scott, A. Li, A. Ganna, M. C. Bassik, J. D. Merker, GTEx Consortium, Laboratory, Data Analysis & Coordinating Center (LDACC)—Analysis Working Group, Statistical Methods groups—Analysis Working Group, Enhancing GTEx (eGTEx) groups, NIH Common Fund, NIH/NCI, NIH/NHGRI, NIH/NIMH, NIH/NIDA, Biospecimen Collection Source Site—NDRI, Biospecimen Collection Source Site—RPCI, Biospecimen Core Resource—VARI, Brain Bank Repository—University of Miami Brain Endowment Bank, Leidos Biomedical—Project Management, ELSI Study, Genome Browser Data Integration & Visualization—EBI, Genome Browser Data Integration & Visualization—UCSC Genomics Institute, University of California Santa Cruz, I. M. Hall, A. Battle, and S. B. Montgomery. "The impact of rare variation on gene expression across tissues". *Nature* 550.7675 (2017), pp. 239–243. DOI: 10.1038/nature24267.

[52] M. H. Tan, Q. Li, R. Shanmugam, R. Piskol, J. Kohler, A. N. Young, K. I. Liu, R. Zhang, G. Ramaswami, K. Ariyoshi, A. Gupte, L. P. Keegan, C. X. George, A. Ramu, N. Huang, E. A. Pollina, D. S. Leeman, A. Rustighi, Y. P. S. Goh, GTEx Consortium, Laboratory, Data Analysis & Coordinating Center (LDACC)—Analysis Working Group, Statistical Methods groups—Analysis Working Group, Enhancing GTEx (eGTEx) groups, NIH Common Fund, NIH/NCI, NIH/NHGRI, NIH/NIMH, NIH/NIDA, Biospecimen Collection Source Site—NDRI, Biospecimen Collection Source Site—RPCI, Biospecimen Core Resource—VARI, Brain Bank Repository—University of Miami Brain Endowment Bank, Leidos Biomedical—Project Management, ELSI Study, Genome Browser Data Integration & Visualization—EBI, Genome Browser Data Integration & Visualization—UCSC Genomics Institute, University of California Santa Cruz, A. Chawla, G. Del Sal, G. Peltz, A. Brunet, D. F. Conrad, C. E. Samuel, M. A. O'Connell, C. R. Walkley, K. Nishikura, and J. B. Li. "Dynamic landscape and regulation of RNA editing in mammals". *Nature* 550.7675 (2017), pp. 249–254. DOI: 10.1038/nature24041.

[53] GTEx Consortium, Laboratory, Data Analysis & Coordinating Center (LDACC)—Analysis Working Group, Statistical Methods groups—Analysis Working Group, Enhancing GTEx (eGTEx) groups, NIH Common Fund, NIH/NCI, NIH/NHGRI, NIH/NIMH, NIH/NIDA, Biospecimen Collection Source Site—NDRI, Biospecimen Collection Source Site—RPCI, Biospecimen Core Resource—VARI, Brain Bank Repository—University of Miami Brain Endowment Bank, Leidos Biomedical—Project Management, ELSI Study, Genome Browser Data Integration & Visualization—EBI, Genome Browser Data Integration & Visualization—UCSC Genomics Institute, University of California Santa Cruz, Lead analysts: Laboratory, Data Analysis & Coordinating Center (LDACC): NIH program management: Biospecimen collection: Pathology: eQTL manuscript working group: A. Battle, C. D. Brown, B. E. Engelhardt, and S. B. Montgomery. "Genetic effects on gene expression across human tissues". *Nature* 550.7675 (2017), pp. 204–213. DOI: 10.1038/nature24277.

[54] T. Tukiainen, A.-C. Villani, A. Yen, M. A. Rivas, J. L. Marshall, R. Satija, M. Aguirre, L. Gauthier, M. Fleharty, A. Kirby, B. B. Cummings, S. E. Castel, K. J. Karczewski, F. Aguet, A. Byrnes, GTEx Consortium, Laboratory, Data Analysis & Coordinating Center (LDACC)—Analysis Working Group, Statistical Methods groups—Analysis Working Group, Enhancing GTEx (eGTEx) groups, NIH Common Fund, NIH/NCI, NIH/NHGRI, NIH/NIMH, NIH/NIDA, Biospecimen Collection Source Site—NDRI, Biospecimen Collection Source Site—RPCI, Biospecimen Core Resource—VARI, Brain Bank Repository—University of Miami Brain Endowment Bank, Leidos Biomedical—Project Management, ELSI Study, Genome Browser Data Integration & Visualization—EBI, Genome Browser Data Integration & Visualization—UCSC Genomics Institute, University of California Santa Cruz, T. Lappalainen, A. Regev, K. G. Ardlie, N. Hacohen, and D. G. MacArthur. "Landscape of X chromosome inactivation across human tissues". *Nature* 550.7675 (2017), pp. 244–248. DOI: 10.1038/nature24265.

[55] modENCODE Consortium. "Identification of functional elements and regulatory circuits by Drosophila modENCODE". *Science* 330.6012 (2010), pp. 1787–97. DOI: 10.1126/science.1198374.

Preprints (not peer reviewed)

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

[56] **L. Myint**, R. Wang, **L. Boukas**, **K. D. Hansen**, L. A. Goff, and D. G. Avramopoulos. "Testing the regulatory consequences of 1,049 schizophrenia associated variants with a massively parallel peporter assay". *bioRxiv* (2018). Preprint, p. 447557. DOI: 10.1101/447557.

[57] **L. Boukas**, J. M. Havrilla, A. R. Quinlan, H. T. Bjornsson, and **K. D. Hansen**. "Co-expression patterns define epigenetic regulators associated with neurological dysfunction". *bioRxiv* (2018). Preprint, p. 219097. DOI: 10.1101/219097.

[58] **K. Fletez-Brant**, Y. Qiu, D. U. Gorkin, M. Hu, and **K. D. Hansen**. "Removing unwanted variation between samples in Hi-C experiments". *bioRxiv* 214361 (2017). Preprint. DOI: 10.1101/214361.

[59] **L. Myint**, D. G. Avramopoulos, L. A. Goff, and **K. D. Hansen**. "Linear models enable powerful differential activity analysis in massively parallel reporter assays". *bioRxiv* 196394 (2017). Preprint. DOI: 10.1101/196394.

[60] P. Wulfridge, B. Langmead, A. P. Feinberg, and **K. D. Hansen**. "Choice of reference genome can introduce massive bias in bisulfite sequencing data". *bioRxiv* 076844 (2016). Preprint. DOI: 10.1101/076844.

[61] S. C. Zheng, S. Beck, A. E. Jaffe, D. C. Koestler, **K. D. Hansen**, A. E. Houseman, R. A. Irizarry, M. Widschwendter, and A. E. Teschendorff. "Correcting For Cell-Type Heterogeneity In Epigenome-Wide Association Studies: Premature Analyses And Conclusions". *bioRxiv* 121533 (2017). Preprint. DOI: 10.1101/121533.

Books, Theses, Editorials, Abandoned Preprints (not peer reviewed)

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

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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.

mpra 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.