# CURRICULUM VITAE
## Kasper Daniel Hansen, PhD, Cand. Scient.

## PROFESSIONAL DATA

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## EDUCATION AND TRAINING

PH.D / 2009     University of California, Berkeley
                Biostatistics, emphasis in Computational and Genomic Biology

M.SC. / 2002    University of Copenhagen, Denmark
                Statistics (full degree name: Cand. Scient.)

B.SC. / 1998    University of Copenhagen, Denmark
                Statistics and Mathematics

*POSTDOCTORAL TRAINING*

2009-2012       Department of Biostatistics, Johns Hopkins University
                Mentor: Rafael A. Irizarry.

## PROFESSIONAL EXPERIENCE

### Johns Hopkins University

Professor of Biostatistics (Primary), Johns Hopkins Bloomberg School of Public Health, 2025–present.

Professor of Genetic Medicine, Johns Hopkins School of Medicine, 2025–present.

Professor of Biomedical Engineering, Johns Hopkins School of Medicine, 2025–present.

Associate Professor of Biostatistics, Johns Hopkins Bloomberg School of Public Health, 2018–2025.

Associate Professor of Genetic Medicine, Johns Hopkins School of Medicine, 2019–2025.

Associate Professor of Biomedical Engineering, Johns Hopkins School of Medicine, 2021–2025.

Assistant Professor of Biostatistics, Johns Hopkins Bloomberg School of Public Health, 2012–2018.

Member, McKusick-Nathans Institute of Genetic Medicine, Johns Hopkins School of Medicine, 2012–2019.

Member, BDP Epigenome Sciences Cluster, Johns Hopkins University, 2023–present.

Preceptor, Predoctoral Training Program in Human Genetics and Genomics, Department of Genetic Medicine, Johns Hopkins University School of Medicine, 2012–present.

Faculty Member, Center for Computational Biology, Johns Hopkins University, 2012–present.

## Other non-JHU Professional Experience

Visiting Departments of Statistics and Biology, University of Copenhagen, Denmark, 2018.

Visiting Division of Biostatistics (Sandrine Dudoit), University of California at Berkeley, USA, 2004–2005.

Research Assistant, Department of Biostatistics, University of Copenhagen, Denmark, 2002–2004. Worked on statistical analyses of a variety of epidemiological datasets.

# PROFESSIONAL ACTIVITIES

## Society membership and leadership

Member, American Statistical Association

Member, American Society of Human Genetics.

## Participation on Advisory Panels and Boards

Elected member, Bioconductor Technical Advisory Board, 2012–present. The technical advisory board develops strategies to ensure long-term technical suitability of core infrastructure for the Bioconductor mission. This project develops open source software for computational biology; release 3.18 consisted of 3,649 packages with 42.7M cummulative distinct downloads.

Member, Generalist Repository Ecosystem Initiative Council of Councils Work Group (GREI CofC WG), National Institutes of Health.

# EDITORIAL AND OTHER PEER REVIEW ACTIVITIES

## Journal Peer Review Activities

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 Computational Biology

PLOS Genetics

PLOS ONE

Proceedings of the National Academy of Sciences (PNAS)

RNA

Statistical Applications in Genetics and Molecular Biology

Statistics in Medicine

## Journal or Other Editorial Board Membership

Gateway advisor for the Bioconductor Gateway at F1000Research. This is a ongoing collection of papers from F1000Res which are relevant to the Bioconductor project; like an ongoing special issue.

**Proposal Reviews**

U54 study section under MCST, NIH, 2025

Israeli Science Foundation, 2019

Joint NIH and NSF BIGDATA initiative review panel, 2012

# HONORS AND AWARDS

| | |
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| 2024 | BSPH "Excellence in Teaching" for Advanced Statistical Computing. |
| 2023 | R35/MIRA Outstanding Investigator Award. An R01-equivalent NIH grant awarded to a person, not a project, intended to support all NIGMS-related research from the person. |
| 2022 | JHPCE High Performer |
| 2022 | Catalyst Award, JHU |
| 2022 | Semi-finalist, President's Frontier Award, JHU |
| 2021 | Semi-finalist, President's Frontier Award, JHU |
| 2016 | Discovery Award, JHU |
| 2014 | Faculty Innovator Award, JHSPH |
| 2010 | Second prize at the MGED poster competition (out of around 50) |
| 2007 | Third prize at the omputational 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:

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| 2020 | Leandros Boukas: Charles J Epstein semi-finalist from ASHG (Highest training award in human genetics). |
| 2014 | Jean-Philippe Fortin: John van Ryzin award for best student paper submitted to ENAR (Highest training award in biostatistics). |

## 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] B Mulvey, **Y Wang**, HR Divecha, SV Bach, KD Montgomery, S Cinquemani, A Chandra, Y Du, RA Miller, JE Kleinman, SC Page, TM Hyde, K Martinowich, SC Hicks, KD Hansen, and **KR Maynard**†. "Spatially-resolved molecular sex differences at single cell resolution in the adult human hypothalamus." *Cell Reports* (2026), In press, Google scholar citations: Unknown.

[2] **G Gui***, MA Bingham*, JR Herzog, A Wong-Rolle, LW Dillon, M Goswami, E Martin, J Reeves, S Kim, A Bahrami, H Degenhardt, G Zaki, P Divakar, EC Schrom, K Calvo, CS Hourigan†, **KD Hansen**†, and C Zhao†. "Single Cell Spatial Transcriptomics Reveals Immunotherapy-Driven Bone Marrow Niche Remodeling in AML." *Scientific Advances* 11.28 (2025), eadw4871, Google scholar citations: 4. DOI: 10.1126/sciadv.adw4871.

[3] Y Li, K Jones, C Ober, AP Starling, WA Gower, LB Bacharier, A Chandran, DM Dabelea, RC Fry, DR Gold, **KD Hansen**, JB Herbstman, MF Hivert, C Keet, RL Miller, LP Jacobson, C Ladd-Acosta†, and PC for Environmental Influences. "Newborn blood DNA methylation and childhood asthma: findings from the ECHO program." *International Journal of Epidemiology* 54.3 (2025), dyaf067, Google scholar citations: Unknown. DOI: 10.1093/ije/dyaf067.

[4] P Ravichandran, P Parsana, R Keener, **DK Hansen**, and A Battle. "Aggregation of recount3 RNA-seq data improves the inference of consensus and tissue-specific gene coexpression networks." *Genome Research* 35.9 (2025), 2087–2103, Google scholar citations: 1. DOI: 10.1101/gr.280808.125.

[5] **L Boukas***, TR Luperchio*, **A Razi**, **KD Hansen**†, and HT Bjornsson†. "Neuron-specific chromatin disruption at CpG islands and aging-related regions in Kabuki syndrome mice." *Genome Research* 3 (2024), 696–710, Google scholar citations: 3. DOI: 10.1101/gr.278416.123.

[6] **K Fletez-Brant**†, Y Qiu, DU Gorkin, M Hu, and **KD Hansen**. "Removing unwanted variation between samples in Hi-C experiments." *Briefings in Bioinformatics* 25.3 (2024), bbae217, Google scholar citations: 20. DOI: 10.1093/bib/bbae217.

[7] CW Gao, WY Lin, RC Riddle, S Chopra, **L Boukas**, **KD Hansen**, HT Bjornsson, and JA Fahrner. "Growth deficiency in a mouse model of Kabuki syndrome 2 bears mechanistic similarities to Kabuki syndrome 1." *PLOS Genetics* 20.6 (2024), e1011310, Google scholar citations: 2. DOI: https://doi.org/10.1371/journal.pgen.1011310.

[8] CW Gao*, W Lin*, RC Riddle, P Kushwaha, **L Boukas**, HT Bjornsson, **KD Hansen**, and JA Fahrner. "A mouse model of Weaver syndrome displays overgrowth and excess osteogenesis reversible with KDM6A/6B inhibition." *JCI insight* 9.1 (2024), e173392, Google scholar citations: 12. DOI: 10.1172/jci.insight.173392.

[9] A Kuo, **KD Hansen**, and SC Hicks. "Quantification and statistical modeling of droplet-based single-nucleus RNA-sequencing data." *Biostatistics* 25.3 (2024), 801–817, Google scholar citations: 10. DOI: 10.1093/biostatistics/kxad010.

[10] M Majumder[†], JT Leek, **K D Hansen**, **A Razi**, and AL McGuire. "Large-scale genotype prediction from RNA sequence data necessitates a new ethical and policy framework." *Nature Genetics* 56.8 (2024), 1537–1540, Google scholar citations: 1. DOI: 10.1038/s41588-024-01825-4.

[11] EK Lo[*], BM Mears[*], HC Maurer, A Idrizi, **KD Hansen**, ED Thompson, RH Hruban, KP Olive, and AP Feinberg. "Comprehensive DNA Methylation Analysis Indicates That Pancreatic Intraepithelial Neoplasia Lesions Are Acinar-Derived and Epigenetically Primed for Carcinogenesis." *Cancer Research* 83.11 (2023), 1905–1916, Google scholar citations: 24. DOI: 10.1158/0008-5472.CAN-22-4052.

[12] SK Maden, B Walsh, K Ellrott, **KD Hansen**, R Thompson, and A Nellore. "recountmethylation enables flexible analysis of public blood DNA methylation array data." *Bioinformatics Advances* 3.1 (2023), vbad020, Google scholar citations: DOI: 10.1093/bioadv/vbad020.

[13] A Morin[*], EE Thompson[*], BA Helling[*], LE Shorey-Kendrick, P Faber, T Gebretsadik, LB Bacharier, M Kattan, GT O'Connor, K Rivera-Spoljaric, RA Wood, KC Barnes, RA Mathias, MC Altman, **KD Hansen**, CT McEvoy, ER Spindel, T Hartert, DJ Jackson, JE Gern, CG McKennan[†], C Ober[†], program collaborators for Environmental Influences, C Respiratory, and nvironmental Workgroup. "A functional genomics pipeline to identify high-value asthma and allergy CpGs in the human methylome." *The Journal of Allergy and Clinical Immunology* 151.6 (2023), 1609–1621, Google scholar citations: 25. DOI: 10.1016/j.jaci.2022.12.828.

[14] LM Weber, A Saha, A Datta, **KD Hansen**, and SC Hicks. "nnSVG for the scalable identification of spatially variable genes using nearest-neighbor Gaussian processes." *Nature Communications* 14 (2023), 4059, Google scholar citations: 103. DOI: 10.1038/s41467-023-39748-z.

[15] P Wulfridge[*], A Davidovich[*], AC Salvador[*], GC Manno, R Tryggvadottir, A Idrizi, MN Huda, BJ Bennett, LG Adams, **KD Hansen**[†], DW Threadgill[†], and AP Feinberg[†]. "Precision pharmacological reversal of strain-specific diet-induced metabolic syndrome in mice informed by epigenetic and transcriptional regulation." *PLOS Genetics* 19.10 (2023), e1010997, Google scholar citations: 2. DOI: 10.1371/journal.pgen.1010997.

[16] **SC Zheng**, G Stein-O'Brien, **L Boukas**, LA Goff[†], and **KD Hansen**[†]. "Pumping the brakes on RNA velocity by understanding and interpreting RNA velocity estimates." *Genome Biology* 24.1 (2023), 246, Google scholar citations: 74. DOI: 10.1186/s13059-023-03065-x.

[17] A Arneson, A Haghani, MJ Thompson, M Pellegrini, SB Kwon, H Vu, E Maciejewski, M Yao, CZ Li, AT Lu, M Morselli, L Rubbi, B Barnes, **KD Hansen**, W Zhou, CE Breeze, J Ernst[†], and S Horvath[†]. "A mammalian methylation array for profiling methylation levels at conserved sequences." *Nature Communications* 13.1 (2022), 783, Google scholar citations: 221. DOI: 10.1038/s41467-022-28355-z.

[18] JR Hu[*], **L Myint**[*], AS Levery, J Coresh, LA Inker, ME Grams, E Guallar, **KD Hansen**, EP Rhee, and T Shafi. "A metabolomics approach identified toxins associated with uremic symptoms in advanced chronic kidney disease." *Kidney International* 101.2 (2022), 369–378, Google scholar citations: 19. DOI: 10.1016/j.kint.2021.10.035.

[19] MC Schatz[†], AA Philippakis[†], E Afgan, E Banks, VJ Carey, RJ Carroll, A Culotti, K Ellrott, J Goecks, RL Grossman, IM Hall, **KD Hansen**, J Lawson, JT Leek, AO Luria, S Mosher, M Morgan, A Nekrutenko, BD O'Connor, K Osborn, B Paten, C Patterson, FJ Tan, CO Taylor, J Vessio, L Waldron, T Wang, K Wuichet, and A Team. "Inverting the model of genomics data sharing with the NHGRI Genomic Data Science Analysis, Visualization, and Informatics Lab-space." *Cell Genomics* 2.1 (2022), 100085, Google scholar citations: 143. DOI: 10.1016/j.xgen.2021.100085.

[20] **Y Wang**, SC Hicks, and **KD Hansen**. "Addressing the mean-correlation relationship in co-expression analysis." *PLOS Comp Bio* 3 (2022), e1009954, Google scholar citations: 20. DOI: 10.1371/journal.pcbi.1009954.

[21] **SC Zheng**, G Stein-O'Brien, JJ Augustin, J Slosberg, GA Carosso, B Winer, G Shin, HT Bjornsson, LA Goff[†], and **KD Hansen**[†]. "Universal prediction of cell cycle position using transfer learning." *Genome Biology* 23.1 (2022), 41, Google scholar citations: 125. DOI: 10.1186/s13059-021-02581-y.

[22] JJ Credle, ML Robinson, J Gunn, D Monaco, B Sie, A Tchir, J Hardick, X Zheng, K Shaw-Saliba, RE Rothman, SH Eshleman, A Pekosz, **K Hansen**, H Mostafa, M Steinegger, and HB Larman. "Highly multiplexed oligonucleotide probe-ligation testing enables efficient extraction-free SARS-CoV-2 detection and viral genotyping." *Modern Pathology* 34.6 (2021), 1093–1103, Google scholar citations: 18. DOI: 10.1038/s41379-020-00730-5k.

[23] TR Luperchio[*], **L Boukas**[*], L Zhang, GO Pilarowski, J Jiang, A Kalinousky, **KD Hansen**[†], and HT Bjornsson[†]. "Leveraging the Mendelian disorders of the epigenetic machinery to systematically map functional epigenetic variation." *eLife* 10 (2021), e65884, Google scholar citations: 21. DOI: 10.7554/eLife.65884.

[24] SK Maden, RF Thompson, **KD Hansen**[†], and A Nellore[†]. "Human methylome variation across Infinium 450K data on the Gene Expression Omnibus." *NAR Genomics and Bioinformatics* 3.2 (2021), lqab025, Google scholar citations: 23. DOI: 10.1093/nargab/lqab025.

[25] LF Rizzardi[*], **PF Hickey**, A Idrizi, R Tryggvadottir, CM Callahan, KE Stephens, SD Taverna, H Zhang, S Ramazanoglu, GTEx Consortium, **KD Hansen**[†], and AP Feinberg[†]. "Human brain region-specific variably methylated regions are enriched for heritability of distinct neuropsychiatric traits." *Genome Biology* 22 (2021), 116, Google scholar citations: 30. DOI: 10.1186/s13059-021-02335-w.

[26] C Wilks, **SC Zheng**, **FY Chen**, R Charles, B Solomon, JP Ling, EL Imada, D Zhang, L Joseph, JT Leek, AE Jaffe, A Nellore, L Collado-Torres, **KD Hansen**[†], and B Langmead[†]. "recount3: summaries and queries for large-scale RNA-seq expression and splicing." *Genome Biology* 22.1 (2021), 323, Google scholar citations: 243. DOI: 10.1186/s13059-021-02533-6.

[27] **L Boukas**, HT Bjornsson[†], and **KD Hansen**[†]. "Promoter CpG density predicts downstream gene loss-of-function intolerance." *AJHG* 107.3 (2020), 487–498, Google scholar citations: 18. DOI: 10.1016/j.ajhg.2020.07.014.

[28] OM de Goede, DC Nachun, NM Ferraro, MJ Gloudemans, AS Rao, C Smail, TY Eulalio, F Aguet, B Ng, J Xu, AN Barbeira, SE Castel, S Kim-Hellmuth, Y Park, AJ Scott, BJ Strober, GTEx Consortium, CD Brown, X Wen, IM Hall, A Battle, T Lappalainen, HK Im, KG Ardlie, S Mostafavi, T Quertermous, K Kirkegaard, and SB Montgomery. "Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease." *Cell* 184.10 (2020), 2633–2648.e19, Google scholar citations: 195. DOI: 10.1016/j.cell.2021.03.050. KD Hansen is a member of eGTEx.

[29] GTEx Consortium. "The GTEx Consortium atlas of genetic regulatory effects across human tissues." *Science* 369 (2020), 1318–1339, Google scholar citations: 4623. DOI: 10.1126/science.aaz1776.
KD Hansen is a member of eGTEx.

[30] L Jiang, M Wang, S Lin, R Jian, X Li, J Chan, G Dong, H Fang, AE Robinson, GTEx Consortium, and MP Snyder. "A quantitative proteome map of the human body." *Cell* 183.1 (2020), 269–283.e19, Google scholar citations: 496. DOI: 10.1016/j.cell.2020.08.036.
KD Hansen is a member of eGTEx.

[31] I Lee, R Razaghi, T Gilpatrick, M Molnar, A Gershman, N Sadowski, FJ Sedlazeck, **KD Hansen**, JT Simpson, and W Timp. "Simultaneous profiling of chromatin accessibility and methylation on human cell lines with nanopore sequencing." *Nature Methods* 17.12 (2020), 1191–1199, Google scholar citations: 222. DOI: 10.1038/s41592-020-01000-7.

[32] **L Myint**, R Wang, **L Boukas**, **KD Hansen**, LA Goff, and DG 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* 183.1 (2020), 61–73, Google scholar citations: 52. DOI: 10.1002/ajmg.b.32761.

[33] M Oliva, M Muñoz-Aguirre, S Kim-Hellmuth, V Wucher, ADH Gewirtz, DJ Cotter, P Parsana, S Kasela, B Balliu, A Viñuela, SE Castel, P Mohammadi, F Aguet, Y Zou, EA Khramtsova, AD Skol, D Garrido-Martín, F Reverter, A Brown, P Evans, ER Gamazon, A Payne, R Bonazzola, AN Barbeira, AR Hamel, A Martinez-Perez, JM Soria, GTEx Consortium, BL Pierce, M Stephens, E Eskin, ET Dermitzakis, AV Segrè, HK Im, BE Engelhardt, KG Ardlie, SB Montgomery, AJ Battle, T Lappalainen, R Guigó, and BE Stranger. "The impact of sex on gene expression across human tissues." *Science* 369.6509 (2020), eaba3066, Google scholar citations: 1095. DOI: 10.1126/science.aba3066.
KD Hansen is a member of eGTEx.

[34] S Rajagopalan[*†], B Park[*], R Palanivel, V Vinayachandran, JA Deiuliis, RS Gangwar, LM Das, J Yin, Y Choi, S Al-Kindi, MK Jain, **KD Hansen**, and S Biswal[†]. "Metabolic effects of air pollution exposure and reversibility." *The Journal of Clinical Investigation* 130.11 (2020), 6034–6040, Google scholar citations: 86. DOI: 10.1172/JCI137315.

[35] **L Boukas**, JM Havrilla, **PF Hickey**, AR Quinlan, HT Bjornsson[†], and **KD Hansen**[†]. "Co-expression patterns define epigenetic regulators associated with neurological dysfunction." *Genome Research* 29.4 (2019), 532–542, Google scholar citations: 60. DOI: 10.1101/gr.239442.118.

[36] GA Carosso, **L Boukas**, JJ Augustin, HN Nguyen, BL Winer, GH Cannon, JD Robertson, L Zhang, **KD Hansen**, LA Goff, and HT Bjornsson. "Precocious neuronal differentiation and disrupted oxygen responses in Kabuki syndrome." *JCI Insight* 4.20 (2019), 129375, Google scholar citations: 57. DOI: 10.1172/jci.insight.129375.

[37] JA Fahrner[†], WY Lin, RC Riddle, **L Boukas**, VB DeLeon, S Chopra, SE Lad, TR Luperchio, **KD Hansen**, and HT Bjornsson[†]. "Precocious chondrocyte differentiation disrupts skeletal growth in Kabuki syndrome mice." *JCI Insight* 4.20 (2019), 129380, Google scholar citations: 41. DOI: 10.1172/jci.insight.129380.

[38] DU Gorkin[*], Y Qiu[*], M Hu[*†], **K Fletez-Brant**, T Liu, AD Schmitt, A Noor, J Chiou, KJ Gaulton, J Sebat, Y Li, **KD Hansen**, and B Ren[†]. "Common DNA sequence variation influences 3-dimensional conformation of the human genome." *Genome Biology* 20 (2019), 255, Google scholar citations: 98. DOI: 10.1186/s13059-019-1855-4.

[39] **L Myint**, DG Avramopoulos, LA Goff, and **KD Hansen**. "Linear models enable powerful differential activity analysis in massively parallel reporter assays." *BMC Genomics* 20 (2019), 209, Google scholar citations: 68. DOI: 10.1186/s12864-019-5556-x.

[40] LF Rizzardi[*], **PF Hickey**[*], VR DiBlasi, R Tryggvadottir, CM Callahan, A Idrizi, **KD Hansen**[†], and AP Feinberg[†]. "Neuronal brain region-specific DNA methylation and chromatin accessibility are associated with neuropsychiatric disease heritability." *Nature Neuroscience* 22.2 (2019), 307–316, Google scholar citations: 162. DOI: 10.1038/s41593-018-0297-8.

[41] P Wulfridge, B Langmead, AP Feinberg, and **KD Hansen**. "Analyzing whole genome bisulfite sequencing data from highly divergent genotypes." *Nucleic Acids Research* 47.19 (2019), e117, Google scholar citations: 38. DOI: 10.1093/nar/gkz674.

[42] WT Barrington, P Wulfridge, AE Wells, CM Rojas, SY Howe, A Perry, K Hua, MA Pellizzon, **KD Hansen**, BH Voy, BJ Bennett, D Pomp, AP Feinberg, and DW Threadgill. "Improving metabolic health through precision dietetics in mice." *Genetics* 208.1 (2018), 399–417, Google scholar citations: 68. DOI: 10.1534/genetics.117.300536.

[43] V Gaysinskaya, BF Miller, C De Luca, GW van der Heijden, **KD Hansen**, and A Bortvin. "Transient reduction of DNA methylation at the onset of meiosis in male mice." *Epigenetics & Chromatin* 11.1 (2018), 15, Google scholar citations: 64. DOI: 10.1186/s13072-018-0186-0.

[44] JS Benjamin, G Pilarowski, G Carosso, L Zhang, J Farner, DL Huso, LA Goff, H Vernon, **KD Hansen**, and HT 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), 125–130, Google scholar citations: 135. DOI: 10.1073/pnas.1611431114.

[45] L Collado-Torres[*], A Nellore[*], K Kammers, SE Ellis, MA Taub, **KD Hansen**, AE Jaffe[†], B Langmead[†], and JT Leek[†]. "Reproducible RNA-seq analysis using recount2." *Nature Biotechnology* 35.4 (2017), 319–321, Google scholar citations: 446. DOI: 10.1038/nbt.3838.

[46] eGTEx Project. "Enhancing GTEx by bridging the gaps between genotype, gene expression, and disease." *Nature Genetics* 12 (2017), 1664–1670, Google scholar citations: Unknown. DOI: 10.1038/ng.3969.
KD Hansen is a member of eGTEx.

[47] **JP Fortin**, T Triche Jr, and **KD Hansen**. "Preprocessing, normalization and integration of the Illumina HumanMethylationEPIC array with minfi." *Bioinformatics* 33.4 (2017), 558–560, Google scholar citations: 916. DOI: 10.1093/bioinformatics/btw691.

[48] GTEx Consortium, A Battle, CD Brown, BE Engelhardt, and SB Montgomery. "Genetic effects on gene expression across human tissues." *Nature* 550.7675 (2017), 204–213, Google scholar citations: 3956. DOI: 10.1038/nature24277.
KD Hansen is a member of eGTEx.

[49] X Li, Y Kim, EK Tsang, JR Davis, FN Damani, C Chiang, GT Hess, Z Zappala, BJ Strober, AJ Scott, A Li, A Ganna, MC Bassik, JD Merker, GTEx Consortium, IM Hall, A Battle, and SB Montgomery. "The impact of rare variation on gene expression across tissues." *Nature* 550.7675 (2017), 239–243, Google scholar citations: Unknown. DOI: 10.1038/nature24267.
KD Hansen is a member of eGTEx.

[50] **L Myint**, A Kleensang, L Zhao, T Hartung, and **KD Hansen**. "Joint bounding of peaks across samples improves differential analysis in mass spectrometry-based metabolomics." *Analytical Chemistry* 89.6 (2017), 3517–3523, Google scholar citations: 17. DOI: 10.1021/acs.analchem.6b04719.

[51] M Ramos, L Schiffer, A Re, R Azhar, A Basunia, C Rodriguez, T Chan, P Chapman, SR Davis, D Gomez-Cabrero, AC Culhane, B Haibe-Kains, **KD Hansen**, H Kodali, MS Louis, AS 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, Google scholar citations: 129. DOI: 10.1158/0008-5472.CAN-17-0344.

[52] A Saha, Y Kim, ADH Gewirtz, B Jo, C Gao, IC McDowell, GTEx Consortium, BE Engelhardt, and A Battle. "Co-expression networks reveal the tissue-specific regulation of transcription and splicing." *Genome Research* 27.11 (2017), 1843–1858, Google scholar citations: 207. DOI: 10.1101/gr.216721.116.
KD Hansen is a member of eGTEx.

[53] MH Tan, Q Li, R Shanmugam, R Piskol, J Kohler, AN Young, KI Liu, R Zhang, G Ramaswami, K Ariyoshi, A Gupte, LP Keegan, CX George, A Ramu, N Huang, EA Pollina, DS Leeman, A Rustighi, YPS Goh, GTEx Consortium, A Chawla, G Del Sal, G Peltz, A Brunet, DF Conrad, CE Samuel, MA O'Connell, CR Walkley, K Nishikura, and JB Li. "Dynamic landscape and regulation of RNA editing in mammals." *Nature* 550.7675 (2017), 249–254, Google scholar citations: 682. DOI: 10.1038/nature24041.
KD Hansen is a member of eGTEx.

[54] T Tukiainen, AC Villani, A Yen, MA Rivas, JL Marshall, R Satija, M Aguirre, L Gauthier, M Fleharty, A Kirby, BB Cummings, SE Castel, KJ Karczewski, F Aguet, A Byrnes, GTEx Consortium, T Lappalainen, A Regev, KG Ardlie, N Hacohen, and DG MacArthur. "Landscape of X chromosome inactivation across human tissues." *Nature* 550.7675 (2017), 244–248, Google scholar citations: Unknown. DOI: 10.1038/nature24265.
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[55] F Yang, J Wang, GTEx Consortium, BL Pierce, and LS Chen. "Identifying cis-mediators for trans-eQTLs across many human tissues using genomic mediation analysis." *Genome Research* 27.11 (2017), 1859–1871, Google scholar citations: 80. DOI: 10.1101/gr.216754.116.
KD Hansen is a member of eGTEx.

[56] SC Zheng, S Beck, AE Jaffe, DC Koestler, **KD Hansen**, AE Houseman, RA Irizarry, and AE Teschendorff. "Correcting for cell-type heterogeneity in epigenome-wide association studies: revisiting previous analyses." *Nature Methods* 14.3 (2017), 216–217, Google scholar citations: 77. DOI: 10.1038/nmeth.4187.

[57] SV Andrews[*], C Ladd-Acosta[*], AP Feinberg, **KD Hansen**, and MD Fallin. "Gap hunting" to to characterize clustered probe signals in Illumina methylation array data." *Epigenetics and Chromatin* 9 (2016), 56, Google scholar citations: 86. DOI: 10.1186/s13072-016-0107-z.

[58] L Gatto, **KD Hansen**, MR Hoopmann, H Hermjakob, O Kohlbacher, and A Beyer. "Testing and validation of computational methods for mass spectrometry." *Journal of Proteome Research* 15.3 (2016), 809–814, Google scholar citations: 44. DOI: 10.1021/acs.jproteome.5b00852.

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## Books or Monographs

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

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## Articles, Editorials and Other Publications Not Peer Reviewed

* indicates equal contributions
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## Citation databases

Google Scholar: profile (link)

ORCID: 0000-0003-0086-0687 (link)

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# PRACTICE ACTIVITIES

## Media Dissemination

"scRNA-seq: oh, the joys" by Vivien Marx. Nature Methods 2024, 21:750–753. DOI: 10.1038/s41592-024-02263-0 (link).

## Software and Other Product Development

The total cumulative downloads for all my software is approximately **4.3 million** downloads (calculated from the combination of download statistics from Bioconductor, CRAN and conda), per 28th of April 2024.

affxparser An R/Bioconductor package for parsing output files from Affymetrix microarrays using the Affymetrix Fusion SDK.
Total downloads: 368,429

bnbc An R/Bioconductor package to normalize and remove unwanted variation in Hi-C data.
Total downloads: 32,844

bsseq An R/Bioconductor package for analyzing whole-genome bisulfite sequencing data.
Total downloads: 257,146

bumphunter An R/Bioconductor package implementing a general backend for the bumphunter approach.
Total downloads: 449,128

cqn An R/Bioconductor package for normalizing RNA-seq data using the CQN algorithm.
Total downloads: 84,422

Genominator An R/Bioconductor package implementing a SQLite based backend for genomic data, including sequencing and microarrays.
Total downloads: 50,974

illuminaio An R/Bioconductor package for parsing output for Illumina microarrays.
Total downloads: 471,949

minfi An R/Bioconductor package for analysing Illumina's 450k DNA methylation microarray.
Total downloads: 863,314

mpra An R/Bioconductor package to analysis massively parallel reporter assays (MPRA).
Total downloads: 41,699

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.
Total downloads: Unknown

Rgraphviz An R/Bioconductor package for visualizing graphs using the Graphviz toolkit.
Total downloads: 1,597,149

spqn An R/Bioconductor package for addressing the mean-correlation relationship in RNA-seq data.
Total downloads: 22,404

tricycle An R/Bioconductor package for estimating cell cycle position from single-cell RNA-seq data.
Total downloads: 12,164

yamss An R/Bioconductor package for analyzing MS-based metabolomics experiments.
Total downloads: 30,872