

CURRICULUM VITAE

Kasper Daniel Hansen

PERSONAL DATA

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EDUCATION AND TRAINING

Degrees

Ph.D. 2009 University of California, Berkeley
Biostatistics with a designated emphasis in Computational and Genomic Biology
Advisor: [Sandrine Dudoit](#)
Cand. Scient. 2002 University of Copenhagen
Statistics
Advisor: Martin Jacobsen
B. Sc. 1998 University of Copenhagen
Statistics and mathematics

Postdoctoral Training

2009–2012 Department of Biostatistics
Johns Hopkins Bloomberg School of Public Health
Advisor: [Rafael Irizarry](#)

Visiting

2004–2005 Department of Biostatistics
University of California, Berkeley

PROFESSIONAL EXPERIENCE

2012–Present Assistant Professor, Nathans-McKusick Institute of Genetic Medicine
Johns Hopkins University
2012–Present Assistant Professor, Department of Biostatistics
Johns Hopkins University
2009–2012 Postdoctoral Fellow, Department of Biostatistics
Johns Hopkins University
2002–2004 Research Assistant, Department of Biostatistics
University of Copenhagen, Denmark.

PROFESSIONAL ACTIVITIES

Professional Memberships

American Society of Human Genetics
American Statistical Association

Project Development

2012–Present Member of the Bioconductor Technical Advisory Board.

EDITORIAL ACTIVITIES

Editorial Board Membership

Guest editor for the [Bioconductor Channel](#) at F1000Research.
(This is like an editorial board membership, and not temporary, for this journal)

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 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] William T Barrington, Phillip Wulfridge, Anne E Wells, Carolina M Rojas, Selene YF Howe, Amie Perry, Kunjie Hua, Michael A Pellizzon, **Kasper D Hansen**, Brynn H Voy, Brian J Bennett, Daniel Pomp, Andrew P Feinberg, and David 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).

- [2] Marcel Ramos, Lucas Schiffer, Angela Re, Rimsha Azhar, Azfar Basunia, Carmen Rodriguez, Tiffany Chan, Phil Chapman, Sean R Davis, David Gomez-Cabrero, Aedin C Culhane, Benjamin Haibe-Kains, **Kasper D Hansen**, Hanish Kodali, Marie S Louis, Arvind S Mer, Markus Riemer, Martin Morgan, Vince Carey, and Levi 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).
- [3] Leonardo Collado-Torres*, Abhinav Nellore*, Kai Kammers, Shannon E Ellis, Margaret A Taub, **Kasper D Hansen**, Andrew E Jaffe[†], Ben Langmead[†], and Jeffrey T Leek[†]. "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).
- [4] Shijie C Zheng, Stephan Beck, Andrew E Jaffe, Devin C Koestler, **Kasper D Hansen**, Andres E Houseman, Rafael A Irizarry, and Andrew 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).
- [5] **Leslie Myint**, Andre Kleensang, Liang Zhao, Thomas Hartung, and **Kasper 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).
- [6] **Jean-Philippe Fortin**, Timothy Triche Jr, and **Kasper 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).
- [7] Joel S Benjamin, Genay Pilarowski, Giovanni Carosso, Li Zhang, J Farner, David L Huso, Loyal A Goff, Hilary Vernon, **Kasper D Hansen**, and Hans 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).
- [8] Abhinav Nellore, Andrew E Jaffe, **Jean-Philippe Fortin**, José Alquicira-Hernández, Leonardo Collado-Torres, Sirou Wang, Robert A Phillips, Nishika Karbhari, **Kasper D Hansen**, Benjamin Langmead[†], and Jeffrey 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](https://doi.org/10.1186/s13059-016-1118-6).
- [9] Shan V Andrews, Christine Ladd-Acosta, Andrew P Feinberg, **Kasper D Hansen**, and M Daniele Fallin. "Gap hunting" 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).
- [10] Xin Li, Yin Liu, Tal Salz, **Kasper D Hansen**, and Andrew 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).
- [11] Abhinav Nellore[†], Christopher Wilks, **Kasper D Hansen**, Jeffrey T Leek, and Ben 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](https://doi.org/10.1093/bioinformatics/btw177).

- [12] Laurent Gatto, **Kasper D Hansen**, Michael R Hoopmann, Henning Hermjakob, Oliver Kohlbacher, and Andreas 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).
- [13] Amy R Vandiver, Adrian Idrizi, Lindsay Rizzardi, Andrew P Feinberg, and **Kasper 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).
- [14] Lavanya Kannan, Marcel Ramos, Angela Re, Nehme El-Hachem, Zhaleh Safikhani, Deena M A Gendoo, Sean Davis, David Gomez-Cabrero, Robert Castelo, **Kasper D Hansen**, Vincent J Carey, Martin Morgan, Aedin C Culhane, Benjamin Haibe-Kains, and Levi 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).
- [15] Alain Pacis, Ludovic Tailleux, Alexander M Morin, John Lambourne, Julia L Maclsaac, Vania Yotova, Anne Dumaine, Anne Danckaert, Francesca Luca, Jean-Christophe Grenier, **Kasper D Hansen**, Brigitte Gicquel, Miao Yu, Athma Pai, Chuan He, Jenny Tung, Tomi Pastinen, Michael S Kobor, Roger Pique-Regi, Yoav Gilad[†], and Luis 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](https://doi.org/10.1101/gr.192005.115).
- [16] **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 (2015), p. 180. DOI: [10.1186/s13059-015-0741-y](https://doi.org/10.1186/s13059-015-0741-y).
- [17] 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 (2015), p. 80. DOI: [10.1186/s13059-015-0644-y](https://doi.org/10.1186/s13059-015-0644-y).
- [18] 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 (2015), p. 6304. DOI: [10.1038/ncomms7304](https://doi.org/10.1038/ncomms7304).
- [19] 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 Oleś, 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 (2015), pp. 115–121. DOI: [10.1038/nmeth.3252](https://doi.org/10.1038/nmeth.3252).

- [20] **Jean-Philippe Fortin**, Aurélie 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”. *Genome Biology* 15 (2014), p. 503. DOI: [10.1186/s13059-014-0503-2](https://doi.org/10.1186/s13059-014-0503-2).
- [21] 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 (2015), pp. 230–232. DOI: [10.1038/nmeth.3152](https://doi.org/10.1038/nmeth.3152).
- [22] 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 (2014), 256ra135. DOI: [10.1126/scitranslmed.3009278](https://doi.org/10.1126/scitranslmed.3009278).
- [23] **Jean-Philippe Fortin**[†], Elana J Fertig, and **Kasper D Hansen**[†]. “shinyMethyl: interactive quality control of Illumina 450k DNA methylation arrays in R”. *F1000Research* 3.175 (2014). DOI: [10.12688/f1000research.4680.1](https://doi.org/10.12688/f1000research.4680.1).
- [24] Alyssa C Frazee, Sarven Sabuncian, **Kasper D Hansen**, Rafael A Irizarry, and Jeffrey 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).
- [25] 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 (2014), pp. 1363–1369. DOI: [10.1093/bioinformatics/btu049](https://doi.org/10.1093/bioinformatics/btu049).
- [26] **Kasper D Hansen**^{*}, Sarven Sabuncian^{*}, 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 (2014), pp. 177–184. DOI: [10.1101/gr.157743.113](https://doi.org/10.1101/gr.157743.113).
- [27] Mike L Smith[†], Keith A Baggerly, Henrik Bengtsson, Matthew E Ritchie, and **Kasper D Hansen**[†]. “illuminaio: An open source IDAT parsing tool for Illumina microarrays”. *F1000Research* 264.2 (2013). DOI: [10.12688/f1000research.2-264.v1](https://doi.org/10.12688/f1000research.2-264.v1).
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- [29] **Kasper D Hansen**^{*,†}, Benjamin Langmead^{*,†}, and Rafael 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](https://doi.org/10.1186/gb-2012-13-10-r83).
- [30] 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 (2012), pp. 1371–1373. DOI: [10.1038/nn.3218](https://doi.org/10.1038/nn.3218).

- [31] Jenny Tung[†], Luis B Barreiro, Zachary P Johnson, **Kasper D Hansen**, Vasiliki Michopoulos, Donna Toufexis, Katelyn Michelini, Mark E Wilson, 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 (2012), pp. 6490–6495. DOI: [10.1073/pnas.1202734109](https://doi.org/10.1073/pnas.1202734109).
- [32] 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 (2012), pp. 544–554. DOI: [10.1002/hep.25655](https://doi.org/10.1002/hep.25655).
- [33] **Kasper D Hansen**, Rafael A Irizarry, and Zhijin 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).
- [34] **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), pp. 768–775. DOI: [10.1038/ng.865](https://doi.org/10.1038/ng.865).
- [35] **Kasper D Hansen**, Zhijin Wu, Rafael A Irizarry[†], and Jeffrey T Leek[†]. “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).
- [36] 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 (2011), pp. 193–202. DOI: [10.1101/gr.108662.110](https://doi.org/10.1101/gr.108662.110).
- [37] Benjamin Langmead, **Kasper D Hansen**, and Jeffrey 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](https://doi.org/10.1186/gb-2010-11-8-r83).
- [38] **Kasper D Hansen**[†], Steven E Brenner, and Sandrine 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).
- [39] 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 (2010), p. 94. DOI: [10.1186/1471-2105-11-94](https://doi.org/10.1186/1471-2105-11-94).
- [40] **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 (2009), e1000525. DOI: [10.1371/journal.pgen.1000525](https://doi.org/10.1371/journal.pgen.1000525).
- [41] 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 (2008), e1000299. DOI: [10.1371/journal.pgen.1000299](https://doi.org/10.1371/journal.pgen.1000299).

- [42] 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 (2008), pp. 126–131. DOI: [10.1136/oem.2007.033506](https://doi.org/10.1136/oem.2007.033506).
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- [44] 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 (2004), pp. 451–6. DOI: [10.1002/ijc.20203](https://doi.org/10.1002/ijc.20203).
- [45] 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 (2004), pp. 1214–22. DOI: [10.1093/aje/kwh332](https://doi.org/10.1093/aje/kwh332).

Journal Articles, Consortia member (peer reviewed)

* indicates equal contributions

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

boldface indicates a member of my lab

- [46] 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](https://doi.org/10.1038/ng.3969).
- [47] Ashis Saha, Yungil Kim, Ariel D H Gewirtz, Brian Jo, Chuan Gao, Ian C McDowell, GTEx Consortium, Barbara E Engelhardt, and Alexis 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](https://doi.org/10.1101/gr.216721.116).
- [48] Fan Yang, Jiebiao Wang, GTEx Consortium, Brandon L Pierce, and Lin 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](https://doi.org/10.1101/gr.216754.116).
- [49] Xin Li, Yungil Kim, Emily K Tsang, Joe R Davis, Farhan N Damani, Colby Chiang, Gaelen T Hess, Zachary Zappala, Benjamin J Strober, Alexandra J Scott, Amy Li, Andrea Ganna, Michael C Bassik, Jason 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, Ira M Hall, Alexis Battle, and Stephen B Montgomery. “The impact of rare variation on gene expression across tissues”. *Nature* 550.7675 (2017), pp. 239–243. DOI: [10.1038/nature24267](https://doi.org/10.1038/nature24267).

- [50] Meng How Tan, Qin Li, Raghuvaran Shanmugam, Robert Piskol, Jennefer Kohler, Amy N Young, Kaiwen Ivy Liu, Rui Zhang, Gokul Ramaswami, Kentaro Ariyoshi, Ankita Gupte, Liam P Keegan, Cyril X George, Avinash Ramu, Ni Huang, Elizabeth A Pollina, Dena S Lee-man, Alessandra Rustighi, Y P Sharon 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, Ajay Chawla, Giannino Del Sal, Gary Peltz, Anne Brunet, Donald F Conrad, Charles E Samuel, Mary A O’Connell, Carl R Walkley, Kazuko Nishikura, and Jin Billy Li. “Dynamic landscape and regulation of RNA editing in mammals”. *Nature* 550.7675 (2017), pp. 249–254. DOI: [10.1038/nature24041](https://doi.org/10.1038/nature24041).
- [51] 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: Alexis Battle, Christopher D Brown, Barbara E Engelhardt, and Stephen B Montgomery. “Genetic effects on gene expression across human tissues”. *Nature* 550.7675 (2017), pp. 204–213. DOI: [10.1038/nature24277](https://doi.org/10.1038/nature24277).
- [52] Taru Tukiainen, Alexandra-Chloé Villani, Angela Yen, Manuel A Rivas, Jamie L Marshall, Rahul Satija, Matt Aguirre, Laura Gauthier, Mark Fleharty, Andrew Kirby, Beryl B Cummings, Stephane E Castel, Konrad J Karczewski, François Aguet, Andrea 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, Tuuli Lappalainen, Aviv Regev, Kristin G Ardlie, Nir Hacohen, and Daniel G MacArthur. “Landscape of X chromosome inactivation across human tissues”. *Nature* 550.7675 (2017), pp. 244–248. DOI: [10.1038/nature24265](https://doi.org/10.1038/nature24265).
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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.

[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.