*Curriculum Vitae*
**Dr. James Bentley Brown**

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## A.  Education
Ph.D.        Applied Science & Technology, University of California, Berkeley, 2008.
B.A.         Mathematics, University of California, Santa Cruz, 2000.

## B. Honors and Awards
Honors in Major and College Honors (GPA 4.0) Mathematics, Univ. Calif., Santa Cruz, 2000.
K99/R00 NIH Pathway to Independence Award. NHGRI. 2012-2017.

## C.  Appointments
05/05-12/08   Graduate Student Researcher, Applied Science & Technology, University of California,
              Berkeley, CA (part-time, supervised by Professor Peter Bickel)
01/06-12/07   Graduate Student Instructor, Dept. of Statistics, University of California, Berkeley, CA
12/08-09/13   Postdoctoral Fellow, Statistics, University of California, Berkeley, CA (Bickel Group)
12/09-09/13   Postdoctoral Guest Scholar, Genome Dynamics Department, Life Sciences Division, Lawrence
              Berkeley National Laboratory, Berkeley, CA (Celniker Lab)
09/13-present  Staff Scientist, Genome Dynamics Department, Life Sciences Division, LBNL, Berkeley, CA
09/14-present  Adjunct Assistant Professor, Dept. of Statistics, University of California, Berkeley, CA, USA

## D. Professional Memberships
2008-2012          Member, ENCODE Project Data Analysis Center and Analysis Working Group
2009-2012          Member, modENCODE Project Data Analysis Center and Analysis Working Group
2009-present       Member, Berkeley Drosophila Transcription Network Project
2011-present       Member, FANTOM5 Project
2012-present       Member, ENCODE3 Project Consortium Analysis Working Group
2012-present       Member, Berkeley Drosophila Genome Project
2012-present       Member, AAAS
2013-present       Member, Genetics Society of America
2014-present       Member, CHARGE Consortium
2014-present       Member, Microbes to Biomes Project
2014-present       Integrative Analysis Lead, Consortium for Environmental Omics and Toxicology
2015-present       Member, FANTOM6 Project

## E.  Invited Seminars
2011   Roslin Institute, Job talk. Statistical challenges in computational biology
2011   Center for Genomic Regulation, Barcelona, Seminar. Statistical challenges in computational biology
2011   MIT, Job talk. On mapping short read sequence data
2011   Yale, Seminar. Imputing the co-associations of genomic features
2012   Illumina, Scientific Summit. Messages from ultra-deep, tissue-specific, stranded RNA-seq
2012   European Bioinformatics Institute, Seminar. Interpreting RNA-seq and related transcriptomics data
2012   Roslin Institute, Seminar. Interpreting RNA-seq and related transcriptomics data
2012   Cold Spring Harbor, Biology of Genomes. Deep, stranded, tissue-specific RNA sequencing in
       *Drosophila melanogaster* reveals the complexity of an animal transcriptome
2013   Univ. of Mass. Medical Center. The dynamic and ecoresponsive genome of *Drosophila melanogaster*
2013   Univ. of Indiana, Bloomington. The dynamic and eco-responsive genome of *Drosophila melanogaster*
2014   KAUST, Computational Bioscience Research Center Inauguration. Lessons from the modENCODE
2015   ZENCODE Consortium planning meeting. Lessons from modENCODE
2015   Keystone Symposium, Plenary Seminar. Long Noncoding RNAs and Adaptive Responses to
       Environmental Stressors

2015    The Royal Society, Long non-coding RNAs: evolution of new epigenetic and post-transcriptional functions, Invited Plenary Seminar.

## F. Community Service

2015          Co-organizer, Long Noncoding RNAs: From Evolution to Function (C7-2015), Keystone Symposia, Keystone, CO
2014          Community Outreach: Science at the Theater. LBNL Sponsored Theater Event. Short Talk. "Enhancing Human & Planetary Health Through Innovation"
2014-present  Associate Editor, BMC Genomics
2011-present  Reviewer, Genome Research
2011-present  Reviewer, Proceedings of the National Academy of Science
2011-present  Reviewer, BMC Genomics
2012-present  Reviewer, PLOS Computational Biology
2012-present  Reviewer, Nucleic Acids Research
2015-present  Reviewer, Translational Psychiatry (Nature Publishing Group)

## G. Teaching Experience

2006-2008   Graduate Student Instructor, Introduction to Statistics. Department of Statistics

## H.  Publications (I have published 27 peer reviewed papers. H-index 16).

Stoiber MH, May G, Duff M, Obar R, Artavanis-Tsakonas S, **Brown JB\***, Graveley BR, Celniker SE. "Extensive cross-regulation in Drosophila post-transcriptional regulatory networks". Genome Research. 2015. Provisionally Accepted. *co-senior author, corresponding author, Stoiber is Brown Lab.

**Brown JB**, Celniker SE. "Lessons from modENCODE". Annual Reviews of Genomics and Human Genetics. 2015, In Press, available online: DOI: 10.1146/annurev-genom-090413-025448

Wessel J, *et al.* "Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility". Nat Commun. 2015, (6):5897. doi: 10.1038/ncomms6897.

**Brown JB**, Boley N, Eisman R, May GE, Stoiber MH, Duff MO, Booth BW, Wen J, Park S, Suzuki AM, Wan KH, Yu C, Zhang D, Carlson JW, Cherbas L, Eads BD, Miller D, Mockaitis K, Roberts J, Davis CA, Frise E, Hammonds AS, Olson S, Shenker S, Sturgill D, Samsonova AA, Weiszmann R, Robinson G, Hernandez J, Andrews J, Bickel PJ, Carninci P, Cherbas P, Gingeras TR, Hoskins RA, Kaufman TC, Lai EC, Oliver B, Perrimon N, Graveley BR, Celniker SE. "Diversity and Dynamics of the Drosophila Transcriptome". *Nature*. 2014 Mar 16. doi: 10.1038/nature12962.

Boley N, Stoiber MH, Booth BW, Wan KH, Hoskins RA, Bickel PJ, Celniker SE, **Brown JB.** "Genome-guided transcript assembly by integrative analysis of RNA sequence data". Nat Biotechnol. 2014 Apr;32(4):341-6. doi: 10.1038/nbt.2850.

Gerstein MB, Rozowsky J, Yan KK, Wang D, Cheng C, **Brown JB\***, Davis CA, Hillier L, *et al.* "Comparative analysis of the transcriptome across distant species". Nature. 2014. (512)445-8. PMID: 25164755. *co-first author.

Alam T, Medvedeva YA, Jia H, **Brown JB**, Lipovich L, Bajic VB. "Promoter analysis reveals globally differential regulation of human long non-coding RNA and protein-coding genes". PLoS One. 2014 Oct 2;9(10):e109443. doi: 10.1371/journal.pone.0109443

Chen ZX, Sturgill D, Qu J, Jiang H, Park S, Boley N, Suzuki AM, Fletcher AR, Plachetzki DC, FitzGerald PC, Artieri CG, Atallah J, Barmina O, **Brown JB**, Blankenburg KP, Clough E, *et al.* "Comparative validation of the D. melanogaster modENCODE transcriptome annotation". Genome Res. 2014 Jul;24(7):1209-23. doi: 10.1101/gr.159384.113.

Bánfai B, Jia H, Khatun J, Wood E, Risk B, Gundling WE Jr, Kundaje A, Gunawardena HP, Yu Y, Xie L, Krajewski K, Strahl BD, Chen X, Bickel P, Giddings MC, **Brown JB\***, Lipovich L. "Long noncoding RNAs are rarely translated in two human cell lines."  Genome Res. 2012 Sep;22(9):1646-57.**\* corresponding author, co-senior author**

Fisher WW, Li JJ, Hammonds AS, **Brown JB**, Pfeiffer BD, Weiszmann R, MacArthur S, Thomas S, Stamatoyannopoulos JA, Eisen MB, Bickel PJ, Biggin MD, Celniker SE. "DNA regions bound at low occupancy by transcription factors do not drive patterned reporter gene expression in Drosophila". Proc Natl Acad Sci USA. 2012 Dec 26;109(52):21330-5. doi: 10.1073/pnas.1209589110.

Yip KY, Cheng C, Bhardwaj N, **Brown JB**, Leng J, Kundaje A, Rozowsky J, Birney E, Bickel P, Snyder M, Gerstein M. "Classification of human genomic regions based on experimentally determined binding sites of more than 100 transcription-related factors." Genome Biol. 2012 Sep 5;13(9):R48.

Dong X, Greven MC, Kundaje A, Djebali S, **Brown JB**, Cheng C, Gingeras TR, Gerstein M, Guigó R, Birney E, Weng Z. "Modeling gene expression using chromatin features in various cellular contexts." Genome Biol. 2012 Sep 5;13(9):R53.

Smibert P, Miura P, Westholm JO, Shenker S, May G, Duff MO, Zhang D, Eads BD, Carlson J, **Brown JB**, Eisman RC, Andrews J, Kaufman T, Cherbas P, Celniker SE, Graveley BR, Lai EC. "Global patterns of tissue-specific alternative polyadenylation in Drosophila." Cell Rep. 2012 Mar 29;1(3):277-89.

Landt SG, Marinov GK, Kundaje A, Kheradpour P, Pauli F, Batzoglou S, Bernstein BE, Bickel P, **Brown JB**, Cayting P, Chen Y, Desalvo G, Epstein C, Fisher-Aylor KI, Euskirchen G, Gerstein M, Gertz J, Hartemink AJ, Hoffman MM, Iyer VR, Jung YL, Karmakar S, et al. "ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia." Genome Res. 2012 Sep;22(9):1813-31.

Derrien T, Johnson R, Bussotti G, Tanzer A, Djebali S, Tilgner H, Guernec G, Martin D, Merkel A, Knowles DG, Lagarde J, Veeravalli L, Ruan X, Ruan Y, Lassmann T, Carninci P, **Brown JB**, Lipovich L, Gonzalez JM, Thomas M, Davis CA, Shiekhattar R, et al.The GENCODE v7 catalog of human long noncoding RNAs: Analysis of their gene structure, evolution, and expression." Genome Res. 2012 Sep;22(9):1775-89.

ENCODE Project Consortium. "An integrated encyclopedia of DNA elements in the human genome." Nature. 2012 Sep 6;489(7414):57-74. doi: 10.1038/nature11247.

Atherton J, Boley N, **Brown JB**, Ogawa N, Davidson SM, Eisen MB, Biggin MD, Bickel P. "A model for sequential evolution of ligands by exponential enrichment (SELEX) data."  Ann. Appl. Stat. 2012. Volume 6, Number 3: 928-949.

Graveley BR, *et al*. "The developmental transcriptome of Drosophila melanogaster". Nature. 2011. 471(7339):473-9.

The ENCODE Project Consortium. A User's Guide to the Encyclopedia of DNA Elements (ENCODE). PLoS Biol. 2011. 9(4): e1001046.

Li Q, **Brown JB**, Huang H, Bickel PJ. "Measuring Reproducibility of High-Throughput Experiments." Ann. Appl. Stat. 2011. 5(3):1752-1779.

Li JJ, Jiang CR, **Brown JB**, Huang H, Bickel PJ. "Sparse linear modeling of next-generation mRNA sequencing (RNA-Seq) data for isoform discovery and abundance estimation." Proc Natl Acad Sci U S A. 2011 Dec 13;108(50):19867-72.

Hoskins RA*, Landolin JM*, **Brown JB***, Sandler JE, Takahashi H, Lassmann T, Yu C, Booth BW, Zhang D, Wan KH, Yang L, Boley N, Andrews J, Kaufman TC, Graveley BR, Bickel PJ, Carninci P, Carlson JW, Celniker SE. Genome-wide analysis of promoter architecture in Drosophila melanogaster. Genome Research, 2010, 21(2):182-92.  *contributed equally to this work

Bickel PJ, Boley N, **Brown JB**, Huang H, and Zhang NR. "Subsampling methods for genomic inference." Ann. Appl. Stat. 2010. 4(4):1660-1697.

Aswani A, Keränen S, **Brown J**, Fowlkes C, Knowles DW, Biggin MD, Bickel P and Tomlin CJ. "Nonparametric identification of regulatory interactions from spatial and temporal gene expression data." BMC Bioinformatics. 2010. 11:413

MacArthur S, Li XY, Li J, **Brown JB**, Chu HC, Zeng L, Grondona BP, Hechmer A, Simirenko L, Keränen SV, Knowles DW, Stapleton M, Bickel P, Biggin MD, Eisen MB. Developmental roles of 21 Drosophila transcription factors are determined by quantitative differences in binding to an overlapping set of thousands of genomic regions. Genome Biology. 2009. 10(7):R80

The ENCODE Project Consortium. "Identification and analysis of functional elements in 1% of the human

genome by the ENCODE pilot project." Nature. 2007. 447(7146):799-816.

Margulies EH, *et al*. Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. Genome Research. 2007. 17(6):760-74.


## I. Book Chapters

Xiong H, **Brown JB**, Boley N, Bickel PJ, Huang H. 2014. DE-FPCA: Testing Gene Differential Expression and Exon Usage through Functional Principal Component Analysis. In S. Datta and D. Nettleton, editors, "Statistical Analysis of Next Generation Sequence Data (Frontiers in Probability and Statistical Science)." Springer. New York. (ISBN-13: 978‑3319072111 ISBN-10: 3319072110)


## J.  Grant Support (current)

DE-AC02-05CH11231 14-200 LDRD (Brown, JB)          10/01/13 – 09/30/16
Department of Energy/LBNL
*Reinventing preclinical and environmental testing paradigms*
The long-term goal of this laboratory-directed research and development project is to reduce the costs of drug development and biological risk assessment by developing new approaches to translating genomes through functional studies on complex populations, including techniques in experimental design, dimension reduction, and data integration.


R00 HG006698-01    Brown    9/17/2015-9/16/2017          NIH NHGRI
**Nonparametric methods for functional and translational genomics**
This application for a Pathway to Independence Award (K99/R00) includes a 2-year mentoring phase at University of California Berkeley with Doctors Peter Bickel, Susan Celnicker (Lawrence Berkeley National Laboratory), and Ewan Birney (European Bioinformatics Institute) followed by three years of independent research support. Dr. Brown proposes to develop statistical methods and tools for the characterization of functional elements of the genome encompassing steps in the genomics pipeline from base-calling to integrative analysis. Dr. Brown's long term research career goal is the study of genetic elements and how they direct and coordinate phenotype in humans.
Total Funding: $103,000 per year for two years (K99), $250,000 per year for 3 additional years (R00)
Role: PI


U01 HG007031      Bickel  7/1/2012 – 6/30/15               NIH/NHGRI
**Removing Statistical Bottle-Necks in Data Analysis for the Encode Consortium**
The goal for this project is applying high-throughput bioinformatics and statistical techniques to interrogate all consortium data, per the direction of the AWG. However, as the dimensionality of the data increases geometrically, existing tools for integrative analysis will become less useful and new techniques and software will need to be developed.
Role: Key Personnel


Additional grants on which I am key personnel:


P01 GM099655-01    Biggin  12/1/11 - 11/30/16    NIH/NIGMS
**Quantitative Modeling of Transcriptional Information in the Drosophila Genome**
This Program Project will integrate computational modeling and wet laboratory methods to learn how genomic sequence information is read by transcription factors to produce patterns of gene expression within the context of regulatory networks in developing embryos to support the belief that only quantitative, predictive mathematical models that have been validated experimentally can provide the rigorous understanding required. Our project will provide uniquely detailed datasets and modeling strategies for studying the developmental control of transcription, including extensive experimental testing and validation of the models predictions.