Bogdan Pasaniuc

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Research Interests

Computational and statistical methods for understanding genetic basis of complex traits focusing on integrative genomics, fine-mapping and heritability analyses.

Positions

2012 -	Assistant Professor, Pathology and Laboratory Medicine, Geffen School of Medicine, University of California, Los Angeles
2012 -	Assistant Professor, Human Genetics, Geffen School of Medicine, University of California, Los Angeles
2012 -	Bioinformatics IDP (executive steering committee member, chair of admission and recruiting committee), Genetics and Genomics IDP (executive steering committee member), and Jonsson Comprehensive Cancer Center (healthy and at-risk population program member), University of California, Los Angeles
2016 -	Member of editorial board, The American Journal of Human Genetics.

Education and Academic Training

2010 - 2012	Postdoctoral Fellow, Epidemiology Dept., Harvard School of Public Health and Broad Institute of Harvard and MIT
2008 - 2010	Postdoctoral Fellow, Algorithms Group, International Computer Science Institute, Berkeley, CA
2008	Ph.D. in Computer Science and Bioinformatics, University of Connecticut, Storrs, CT
2003	B.Sc. in Computer Science, "A. I. Cuza" University of Iaşi, Iaşi, Romania

Publications

50. *Colocalization of GWAS and eQTL Signals Detects Target Genes.* Hormozdiari F, van de Bunt M, Segr AV, Li X, Joo JW, Bilow M, Sul JH, Sankararaman S, Pasaniuc B, Eskin E **Am J Hum Genet.** 2016 http://dx.doi.org/10.1016/j.ajhg.2016.10.003
49. *Dissecting the genetics of complex traits using summary association statistics.* Pasaniuc B, Price AL. **Nat Rev Genet.** 2016 Nov 14. doi: 10.1038/nrg.2016.142. PMID: 27840428
48. *Improved methods for multi-trait fine mapping of pleiotropic risk loci.* Kichaev G, Roytman M, Johnson R, Eskin E, Lindstrm S, Kraft P, Pasaniuc B. **Bioinformatics**. 2016 Sep 22. pii: btw615.
47. *Contrasting the genetic architecture of 30 complex traits from summary association data.* Shi H, Kichaev G, Pasaniuc B. **Am J Hum Genet.** 2016 Jul 7;99(1):139-53. doi: 10.1016/j.ajhg.2016.05.013. PMID: 27346688. [*Genetics* highlight]
46. *Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation.* Gusev A, Shi H, Kichaev G, PRACTICAL Consortium, AAPC consortium, BPC3 consortium, Freedman M, Haiman C, Pasaniuc B. **Nat Commun.** 2016 Apr 7;7:10979. doi: 10.1038/ncomms10979. PMID: 27052111
45. *Integrative approaches for large-scale transcriptome-wide association studies.* Gusev A, Ko A, Shi H, Bhatia G, Chung W, Penninx BW, Jansen R, de Geus EJ, Boomsma DI, Wright FA, Sullivan PF, Nikkola E, Alvarez M, Civelek M, Lusis AJ, Lehtimki T, Raitoharju E, Khnen M, Seppl I, Raitakari OT, Kuusisto J, Laakso M, Price AL, Pajukanta P Pasaniuc B. **Nat Genet.** 2016 Mar;48(3):245-52. doi: 10.1038/ng.3506. Epub 2016 Feb 8. PMID: 26854917. [Nat Rev Genetics highlight]

44. *Whole-exome sequencing of over 4100 men of African ancestry and prostate cancer risk.* Rand KA, Rohland N, Tandon A, Stram A, Sheng X, Do R, Pasaniuc B, Allen A, Quinque D, Mallick S, Le Marchand L, Kaggwa S, Lubwama A; African Ancestry Prostate Cancer GWAS Consortium; ELLIPSE/GAME-ON Consortium, Stram DO, Watya S, Henderson BE, Conti DV, Reich D, Haiman CA. **Hum Mol Genet.** 2015 Nov 24. pii: ddv462. [Epub ahead of print] PMID: 26604137

43. *Prostate Cancer Susceptibility in Men of African Ancestry at 8q24.* Han Y, Rand KA, Hazelett DJ, ... , Pasaniuc B, ... , Conti DV, Henderson BE, Haiman CA. **J Natl Cancer Inst.** 2016 Jan 27;108(7). pii: djv431. doi: 10.1093/jnci/djv431. Print 2016 Jul. PMID: 26823525

42. *The contribution of rare variation to prostate cancer heritability.* Mancuso N*, Rohland N*, Rand K,Tandon A, Allen A, Quinque D, Mallick S, Li H, Stram A, Sheng X, Kote-Jarai Z, Easton DF, Eeles RA; PRACTICAL consortium, Le Marchand L, Lubwama A, Stram D, Watya S, Conti DV, Henderson B, Haiman C*, Pasaniuc B*, Reich D*. **Nat Genet.** 2016 Jan;48(1):30-5. doi: 10.1038/ng.3446. Epub 2015 Nov 16. PMID: 26569126

41. *Leveraging local ancestry to detect gene-by-gene interactions in genome-wide data.* Aschard H, Gusev A, Brown R, Pasaniuc B. **BMC Genet.** 2015 Oct 24;16:124. doi: 10.1186/s12863-015-0283-z. PMID: 26498930

40. *Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores.* Vilhjalmsson B, Yang J, Finucane H, Gusev A, Lindstrom S, Ripke S, Genovese G, Loh P, Bhatia G, Do R, Hayeck T, Won H, Psychiatric Genomics Consortium, DRIVE, Kathiresan S, Pato M, Pato C, Tamimi R, Stahl E, Zaitlen N, Pasaniuc B, Schierup M, De Jager P, Patsopoulos N, McCarroll S, Daly M, Purcell S, Chasman D, Neale B, Goddard M, Visscher P, Kraft P, Patterson N, Price AL. **Am J Hum Genet.** 2015 Oct 1;97(4):576-92. doi: 10.1016/j.ajhg.2015.09.001. PMID: 26430803

39. *Leveraging functional annotation data in trans-ethnic fine-mapping studies.* Kichaev G, Pasaniuc B. **Am J Hum Genet.** 2015 Aug 6;97(2):260-71. doi: 10.1016/j.ajhg.2015.06.007. Epub 2015 Jul 16. PMID: 26189819. **(Winner of the CW Cotterman award for best paper by trainee in Am J Hum Genet during 2015).**

38. *A multivariate Bernoulli model to predict DNaseI hypersensitivity status from haplotype data.* Shi H, Pasaniuc B, Lange KL. **Bioinformatics**. 2015 Jul 2. pii: btv397. [Epub ahead of print] PMID: 26139633

37. *Identification of causal genes for complex traits.* Hormozdiari F, Kichaev G, Yang WY, Pasaniuc B, Eskin E. **Bioinformatics**. 2015 Jun 15;31(12):i206-i213. doi: 10.1093/bioinformatics/btv240. PMID: 26072484 **(best paper award at ISMB 2015)**.

36. *Leveraging ancestry to improve causal variant identification in exome sequencing for monogenic disorders.* Brown R, Lee H, Eskin A, Kichaev G, Lohmueller KE, Reversade B, Nelson SF, Pasaniuc B. **Eur J Hum Genet.** 2015 Apr 22. doi: 10.1038/ejhg.2015.68. [Epub ahead of print]

35. *Partitioning heritability of regulatory and cell-type-specific variants across 11 common diseases.* Gusev A, Hong Lee S, Neale B, Trynka G, Vilhjalmsson B, Finucane H, Xu H, Zang C, Ripke S, Stahl E, Kahler AK, Hultman CM, Purcell S, McCarroll SA, Daly M, Pasaniuc B, Sullivan PF, Wray N, Raychaudhuri S, Price AL. **Am J Hum Genet.** 2014 Nov 6;95(5):535-52. doi: 10.1016/j.ajhg.2014.10.004. Epub 2014 Nov 6. PMID: 25439723 .

34. *Leveraging population admixture to explain missing heritability of complex traits.* Zaitlen N, Pasaniuc B, Sakararaman S, Bhatia G, Zhang K, Gusev A, Young T, Tandon A, Pollack S, Vilhjalmsson, Assimes T, Franceschini N,. Lange LA, Patterson N, Reich D, Whitsel EA, Haiman C, Wilson J, Kooperberg C, Stram D, Reiner AP, Tang HA, Price AL. **Nat Genet.** 2014 Dec;46(12):1356-62. doi: 10.1038/ng.3139. Epub 2014 Nov 10. PMID: 25383972

33. *Spatial Localization of Recent Ancestors for Admixed Individuals.* Yang WY, Platt A, Chiang CW, Eskin E, Novembre J, Pasaniuc B. **G3: Genes, Genomes, Genetics**, 2014 Nov 3;4(12):2505-18. doi: 10.1534/g3.114.014274. PMID: 25371484

32. *Integrating functional data to prioritize causal variants in statistical fine-mapping studies.* Kichaev G, Yang WY, Lindstrom S, Hormozdiari F, Eskin E, Price AL, Kraft P, Pasaniuc B. **PloS Genetics**. Oct 30;10(10):e1004722. 2014. [Nat Genetics highlight].

31. *Identifying Causal Variants at Loci with Multiple Signals of Association.* Hormozdiari F, Kostem E, Kang EY, Pasaniuc B*, Eskin E*. **Genetics**. 2014 Aug 7. PMID: 25104515.

30. *Fast and accurate imputation of summary statistics enhances evidence of functional enrichment.* Pasaniuc B, Zaitlen N, Bhatia G, Gusev A, Pickrell JK, Hirschhorn J, Strachan DP, Patterson N, Price AL. **Bioinformatics**. 2014 Jul 1. pii: btu416.

29. *Amerindian-specific regions under positive selection harbour new lipid variants in Latinos.* Ko A, Cantor RM, Weissglas-Volkov D, Nikkola E, Reddy PM, Sinsheimer JS, Pasaniuc B, Brown R, Alvarez M, Rodriguez A, Rodriguez-Guillen R, Bautista IC, Arellano-Campos O, Muoz-Hernndez LL, Salomaa V, Kaprio J, Jula A, Jauhiainen M, Helivaara M, Raitakari O, Lehtimki T, Eriksson JG, Perola M, Lohmueller KE, Matikainen N, Taskinen MR, Rodriguez-Torres M, Riba L, Tusie-Luna T, Aguilar-Salinas CA, Pajukanta P. **Nature Communications.** June 2;5:3983. doi: 10.1038/ncomms4983. 2014

28. *A Spatial Haplotype Copying Model with Applications to Genotype Imputation.* Yang WY, F Hormozdiari F, Eskin E, Pasaniuc B. **Journal of Computational Biology** 2015 May;22(5):451-62. doi: 10.1089/cmb.2014.0151. Epub 2014 Dec 19. PMID: 25526526.

27. *IBD Genetics: Focus on (Dys) Regulation in Immune Cells and the Epithelium.* Kaser A. Pasaniuc B. **Gastroenterology** 146 (4), 896-899. 2014

26. *Enhanced methods for local ancestry assignment in sequenced admixed individuals.* Brown R. Pasaniuc B. **PLoS Computational Biology** 10 (4), e1003555, 2014

25. *Quantifying missing heritability at known GWAS loci.* Gusev A, Bhatia G, Zaitlen N, Vilhjalmsson B, Diogo D, Stahl EA, Gregersen PK, Worthington J, Klareskog L, Rayachaudhuri S, Plenge RM, Pasaniuc B, Price AL. **PLoS Genetics** 9 (12), e1003993. 2013

24. *Leveraging Multi-SNP Reads from Sequencing Data for Haplotype Inference.* Yang WY, Hormozdiari F, Wang Z, He D, Pasaniuc B, Eskin E. **Bioinformatics.** 2013 Sep 15;29(18):2245-52. doi: 10.1093/bioinformatics/btt386. Epub 2013 Jul 3.

23. *Enhanced Localization of Genetic Samples through Linkage Disequilibrium Correction.* Baran Y, Quintela I, Carracedo A, Pasaniuc B*, Halperin E*. **Am J Hum Genet**. 2013 May 29. doi:pii: S0002-9297(13)00210-3. 10.1016/j.ajhg.2013.04.023.

22. *Using Extended Genealogy to Estimate Components of Heritability for 23 Quantitative and Dichotomous Traits.* Zaitlen N, Kraft P, Patterson N, Pasaniuc B, Bhatia G, Pollack S, Price AL. **PLoS Genetics**. 2013 May;9(5):e1003520. doi: 10.1371/journal.pgen.1003520. Epub 2013 May 30

21. *Analysis of Latino populations from GALA and MEC studies reveals genomic loci with biased local ancestry estimation.* Pasaniuc B*, Sankararaman S*, Torgerson D, Gignoux C, Eng C, Rodriguez-Cintron W, Chapela R, Ford JG, Avila PC, Rodriguez-Santana J, Chen GK, Le Marchand L, Henderson B, Reich D, Haiman C, Burchard EG, Halperin E. **Bioinformatics**. 2013 Jun 1;29(11):1407-15. doi: 10.1093/bioinformatics/btt166. Epub 2013 Apr 9.

20. *Using population admixture to help complete maps of the human genome.* Genovese G, Handsaker RE, Li H, Altemose N, Lindgren AM, Chambert K, Pasaniuc B Price AL, Reich D, Morton CC, Pollak MR, Wilson JG, McCarroll SA. **Nat Genetics**,. 2013 Feb 24. doi: 10.1038/ng.2565.

19. *Extremely low-coverage sequencing and imputation increases power for genome-wide association studies.* Pasaniuc B, Rohland N, McLaren PJ, Garimella K, Zaitlen N, Li, H, Gupta N, Neale B, Daly M, Sklar P, Sullivan P, Bergen S, Moran J, Hultman C, Lichtenstein P, Magnusson P, Purcell S, Haas DW, Liang L, Sunyaev S, Patterson N, de Bakker PIW, Reich D, Price AL. **Nat Genetics**, 2012 May 20;44(6):631-5. doi: 10.1038/ng.2283. **(recommended by the Faculty of 1000)**.

18. *Informed conditioning on clinical covariates increases power in case-control association studies.* Zaitlen N, Lindstrom S, Pasaniuc B, Cornelis M, Genovese G, Pollack S, Barton A, Bowden D, Eyre S, Freedman B, Friedman D, Field J, Groop L, Haugen A, Henderson BE, Hicks PJ, Hocking L, Kolonel L, Landi MT, Langefeld CD, Marchand L, Meister M, Morgan AW, Raji OY, Risch A, Scherf D, Steer S, Warshaw M, Waters KM, Wilson AG, Wordsworth P, Zienolddiny S, Haiman C, Hunter DJ, Plenge RM, Worthington J, Christiani D, Schaumberg DA, Chasman DI, Altshuler D, Voight B, Kraft P, Patterson N, Price AL. **PLoS Genetics**, 2012.

17. *Effective analysis of case-control association studies with known genetic effects.* Zaitlen N, Pasaniuc B, Patterson N, Voight B., Groop L, Altshuler D, Henderson BE, Kolonel LN, Marchand L, Waters K, Haiman CA, Stranger BE, Dermitzakis ET, Kraft P, Price AL. **Bioinformatics**, 2012.

16. *Fast and accurate inference of local ancestry in Latino populations.* Baran Y*, Pasaniuc B*, Sankararaman S*, Torgerson D, Gignoux C, Eng C, Rodriguez-Cintron W, Chapela R, Ford JG, Avila PC, Rodriguez-Santana J, Burchard EG, Halperin E. **Bioinformatics**, 2012.
15. *Admixture Mapping Identifies Loci on 6q25 and 11p15 Associated with Breast Cancer Risk in US Latinas.* Fejerman L, Chen G, Huntsman S, Hu D, Williams A, Pasaniuc B, John E, Via M, Gignoux C, Ingles S, Marchand L, Kolonel L, Torres-Meja G, Prez-Stable E, Burchard EG, Eng C, Henderson BE, Haiman C, Ziv E. . **Human Molecular Genetics** 2012 Jan 19. doi:10.1093/hmg/ddr617.
14. *New approaches to disease mapping in admixed populations.* Seldin MF*, Pasaniuc B*, Price AL*. **Nat Rev Genetics**, 2011 Jun 28. doi:10.1038/nrg3002.
13. *Enhanced statistical tests for GWAS in admixed populations: assessment using African Americans from CARe and a Breast Cancer Consortium.* Pasaniuc B, Zaitlen N, Lettre G, Chen GK, Tandon A, Kao WH, Ruczinski I, Fornage M, Siscovick DS, Zhu X, Larkin E, Lange LA, Cupples LA, Yang Q, Akylbekova EL, Musani SK, Divers J, Mychaleckyj J, Li M, Papanicolaou GJ, Millikan RC, Ambrosone CB, John EM, Bernstein L, Zheng W, Hu JJ, Ziegler RG, Nyante SJ, Bandera EV, Ingles SA, Press MF, Chanock SJ, Deming SL, Rodriguez-Gil JL, Palmer CD, Buxbaum S, Ekunwe L, Hirschhorn JN, Henderson BE, Myers S, Haiman CA, Reich D, Patterson N, Wilson JG, Price AL. **PLoS Genetics.** 2011 Apr;7(4):e1001371. Epub 2011 Apr 21.
12. *Genome-wide comparison of African-ancestry populations from CARe and other cohorts reveals signals of natural selection.* Bhatia G, Patterson N, Pasaniuc B, Zaitlen N, Genovese G, Pollack S, Mallick S, Myers S, Tandon A, Spencer C, Palmer C, Adebowale A, Akylbekova E, Cupples LA, Divers J, Fornage M, Kao L, Lange L, Li M, Musani S, Mychaleckyuj J, Ogunniyi A, Papanicolaou G, Rotimi C, Rotter J, Ruczinzki I, Salako B, Siscovick S, Tayo B, Yahg Q, McCarrol S, Sabeti P, Lettre G, De Jagger P, Hirschhorn J, Zhu X, Cooper R, Reich D, Wilson JG, Price AL. **Am J Hum Genet.** 2011
11. *Combining effects from rare and common genetic variants in an exome-wide association study of sequence data.* Aschard H, Qiu W, Pasaniuc B, Zaitlen N, Cho M and Carey V. **BMC Proceedings** 2011, 5(Suppl 9):S44
10. *Inhibition of activated pericentromeric SINE/Alu repeat transcription in senescent human adult stem cells reinstates self-renewal.* Wang J, Geesman G, Hostikka S, Atallah M, Blackwell B, Lee E, Cook P, Pasaniuc B, Shariat G, Halperin E, Dobke M, Rosenfield MG, Jordan IK, Lunyak VV. **Cell Cycle.** 2011, Sept 1; 10:17
9. *Accurate Estimation of Expression Levels of Homologous Genes in RNA-seq Experiments.* Pasaniuc B, Zaitlen N, Halperin E. **Journal of Computational Biology.** 2011 Mar;18(3):459-68.
8. *Genotyping common and rare variation using overlapping pool sequencing.* He D, Zaitlen N, Pasaniuc B, Eskin E, Halperin E. **BMC Bioinformatics.** 2011, 12(Suppl 6):S2
7. *Optimal Testing of Digital Microfluidic Biochips.* Pasaniuc B, Garfinkel R, Mandoiu I, Zelikovsky A. **INFORMS Journal on computing.** 2011.
6. *A Generic Coalescent-based Framework for the Selection of a Reference Panel for Imputation.* Pasaniuc B, Avinery, R, Gur T, Skibola CF, Brooks PM, Halperin E. **Genetic Epidemiology.** 2010 Dec;34(8):773-82.
5. *Leveraging genetic variability across populations for the identification of causal variants.* Zaitlen N*, Pasaniuc B*, Gur T, Ziv E, Halperin E. **Am J Hum Genet.** 2010 Jan;86(1):23-33.
4. *Imputation-Based Local Ancestry Inference in Admixed Populations.* Pasaniuc B, Kennedy J, Mandoiu I. **Proc. 5th International Symposium on Bioinformatics Research and Applications**, pp. 221-233, 2009.
3. *Inference of locus-specific ancestry in closely related populations.* Pasaniuc B*, Sankararaman S*, Kimmel G, Halperin E. **Bioinformatics** (special edition of ISMB 2009). 2009 Jun 15;25(12):i213-21.
2. *Genotype error detection using Hidden Markov Models of haplotype diversity.* Kennedy J, Mandoiu I, Pasaniuc B. **Journal of Computational Biology.** 2008 Nov;15(9):1155-71.
1. *Highly scalable genotype phasing by entropy minimization.* Gusev A, Mandoiu II, Pasaniuc B. **IEEE/ACM Transactions on Computational Biology and Bioinformatics.** 2008 Apr-Jun;5(2):252-61. (conference version: *Highly scalable genotype phasing by entropy minimization.* Pasaniuc B, Mandoiu I. **Conf Proc IEEE Eng Med Biol Soc.** 2006;1:3482-6.)

* denotes equal contribution.

Grants

- STOP CANCER I.C.O.N. Seed Grant (PI:Pasaniuc), 2014.
- NIH/NCI R03 CA162200 (PI:Pasaniuc). 09/2012-09/2014. Metrics and methods for cross-population fine mapping.
- NIH/NCI R21 CA182821(PI:Lindstroem, Role:PI of subcontract). 08/2014-08/2016. Prioritizing Follow-up of GWAS Loci Using Genetic and Functional Annotation Data.
- NIH/NCI U01 CA182821(PI:Lindstroem, Role:PI of subcontract). 08/2015-08/2018. Quantifying and Characterizing the shared genetic contribution to common cancers.
- NIH/NCI U01 CA188392 (PI:Schumacker, Role:PI of subcontract). 09/2014-06/2017. Imputation-based Approach to Identify Low Frequency Variants in Prostate Cancer.
- NIH/NHLBI R01 HL095056 (PI:Pajukanta, Role:Co-I). 04/2015-04/2020. Genetics of High Serum Triglycerides and Related Metabolic Traits in Mexicans.
- NIH/NIGMS R01 GM053275 (PI:Lange, Role:Co-I). 03/2013-03/2022. Statistical methods for gene mapping.
- NIH/NCI R01 MH107250 (PI:Bearden, Role:Co-I). 08/2015-08/2018. Genetic Risk for Developmental Expression of Neuropsychiatric Intermediate Traits.

Software

- TWAS: Transcriptome-wide associaiton studies through gene expression imputation. `http://bogdan.bioinformatics.u`
- HESS: SNP heritability estimation from GWAS summary data. `http://bogdan.bioinformatics.ucla.edu/software/h`
- ImpG: imputation from summary association statistics from large-scale genome-wide association data. `http://bogdan.bioinformatics.ucla.edu/software/impg/`
- Lanc-CSV: local ancestry inference using continental specific variants. `http://bogdan.bioinformatics.ucla.edu/software/lanccsv/`
- PAINTOR: fine-mapping for causal variants using functional and GWAS data. `http://bogdan.bioinformatics.ucla.edu/software/paintor/`
- MIXSCORE: disease scoring (combining case-only admixture and case-control SNP association signals) in admixed populations such as African Americans. `http://www.hsph.harvard.edu/faculty/alkes-price/files/mixscore-1.0.tar.gz`.
- SEQ-EM: inference of homologous gene expression levels using short read sequencing. `http://www.icsi.berkeley.edu/~heran/cozygene/software/seqem.html`.
- MULTIPOP: software package for designing follow up fine mapping studies over multiple populations `http://multipop.icsi.berkeley.edu/multipop`.
- LAMP/LAMP-LD: Local Ancestry in adMixed Populations, sofware package for inferring the locus-specific ancestry in recently admixed populations. `http://lamp.icsi.berkeley.edu/lamp`.
- GEDI-ADMX: Software for inferring locus specific ancestry in recently admixed populations based on genotype imputation accuracy. `http://dna.engr.uconn.edu/~software/GEDI-ADMX`.
- GEDI: Genotype error detection in whole-genome SNP genotype data, recovery of missing SNP genotypes and imputation of genotypes at untyped SNPs based on reference haplotypes `http://dna.engr.uconn.edu/~software/GEDI`.
- ENT: Highly scalable genotype phasing algorithm based on entropy minimization capable of phasing both unrelated and related genotypes coming from complex pedigrees `http://dna.engr.uconn.edu/~software/ent`.

Other Contributions

- Reviewer for Nature Genetics, Nature Methods, Nature Communications, PloS Genetics, American Journal of Human Genetics, IEEE/ACM Transactions on Computational Biology and Bioinformatics, Bioinformatics, BMC Bioinformatics, Journal of Computational Biology, RECOMB (Int. Conf. on Research in Computational Molecular Biology), ISMB (Int. Conf. on Intelligent Systems for Molecular Biology).
- Ad-hoc fellowship reviewer for the Wellcome Trust and Royal Society.
- Program Committee member: ISMB 2013, 2015, RECOMB-seq 2012, ISBRA 2012,2013,2015 and ICCABS 2012.

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