Curriculum Vitae - Bjarni Jóhann Vilhjálmsson

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Position: Professor
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Education

- Ph.D. Computational Biology, University of Southern California, Dec. 14, 2011.
- M.Sc. (Cand. Sci.) Bioinformatics, University of Copenhagen, Feb. 28, 2006.
- B.Sc. Computer Science and Mathematics, University of Copenhagen, July 2., 2003.

Employment

- Professor, the National Centre for Register-based Research, Aarhus University, Aarhus, Denmark, since November 2020
- Senior Researcher, Bioinformatics Research Centre, Aarhus University, Aarhus, Denmark, since March 2020
- Senior Researcher, the National Centre for Register-based Research, Aarhus University, Aarhus, Denmark, October 2018 - October 2020
- Product Owner, QIAGEN, Aarhus, Denmark, March 2017 - Sept 2018 **(non-academic position)**
- Senior Bioinformatics Scientist, QIAGEN, Aarhus, Denmark, Sept 2016 - Feb 2017 **(non-academic position)**
- Postdoctoral fellow, BIRC, Aarhus University, Aarhus, Denmark, August 2014 - August 2016
- Visiting researcher, deCODE genetics, Iceland, July 2014 - August, 2014
- Postdoctoral fellow (Price group), Harvard School of Public Health, Boston, MA, May 2012 - July 2014
- Postdoctoral fellow (Nordborg lab), Gregor Mendel Institute, Vienna, Austria, Nov 2011 - April 2012
- PhD Student, University of Southern California, USA, Sept 2006 - Oct 2011

Leave from research

- 1 month of parental leave in 2010.
- 1 month of parental leave in 2013.
- 6 weeks of parental leave in 2019-2020
- 2 years and 1 month (Sept 2016 - Oct 2018) in a non-academic industry position.

Research support and honours

Ongoing Research Support

- **Lundbeck Fellow Grant - PI on a 5-year grant to develop novel statistical methods to leverage electronic health records to increase power in genetic analyses of psychiatric disorders. Informed Polygenic Scoring. 01/10/2020 -30/09/2025**

- NIMH (1R01MH122869-01) - Co-Investigator on a grant studying relapse risk after discontinuation of antidepressants during pregnancy. 01/04/2020 -31/03/2024.

Completed Research Support

- Icelandic Research Fund - Co-Investigator on a 3 year Project Grant, Population genomics of parallel evolution in Icelandic arctic charr, 01/01/2015-31/12/2017.
- Danish Council for Strategic Research - Co-Investigator on a grant studying the genetics of nitrogen fixation by rhizobium bacteria in clover plants. Forging strong links in the organic nitrogen chain. 01/01/15-31/12/19
- **The Danish Council for Independent Research - PI on an individual postdoctoral grant to develop efficient Bayesian polygenic risk prediction. 01/01/2014-31/12/2015**
- **The Danish Council for Independent Research - PI on a Sapere Aude: DFF- Research Talent Award. Identifying Confounders in Summary 01/01/2016-30/06/16**

Awards and Honours

- Program in Quantitative Genomics Student/Postdoc Travel Award, June 2013.
- Stellar Abstract Award, Program in Quantitative Genomics Conference, November 2012.
- Icelandic Chamber of Commerce Scholarship, 2011.
- **Vitterbi Fellowship, University of Southern California, 2006-2008. (Full time PhD student fellowship)**

Research

Summary of Research

In my research I have focused on developing and applying computational methods for analysing large genetic datasets. My three main contributions to research have been as follows:

1. Introduce and promote the use of mixed models in genome-wide association studies (Atwell et al., Nature 2010; Segura et al., NG 2012; Korte et al., NG 2012). These models have proven advantageous for both controlling for confounding and increasing statistical power (Vilhjalmsson and Nordborg, Nat Rev Genet 2013). Mixed models are now routinely used for conducting GWAS in population-scale datasets, such as the UK Biobank data (Loh et al., NG 2015; 2018; Jiang et al., NG 2019).
2. Develop polygenic risk scores and highlight the research and clinical potential. In Vilhjalmsson *et al.* (AJHG 2015) I proposed a more accurate method for deriving polygenic scores (LDpred), which has since become popular. Indeed, LDpred was used in several high-profile papers (Khera et al., Nat Genet 2018; Cell 2019) and was cited as a "sophisticated method" by the New York Times (G Kolata, Aug 2018).

3. I helped demonstrate the existence of genetic (parental) nurture effects in a seminal paper (Kong et al., Science, 2018) that was also highlighted by the New York Times (C Zimmer, Jan 2018).

In September 2016 I left academia for an industry job as a Software Product Owner, but after two years I missed the freedom to pursue exciting ideas and solve important problems. When an opportunity arose for me to establish my own research group at Aarhus University, focused on applied statistical genetics and epidemiology, I decided to rejoin academia. In October 2018 I joined the National Center for Register-based Research, Aarhus University as a senior researcher. In this role I have access to world-class collaborators and unique datasets, both large genetic datasets and linked Danish registers data. This is an exceptional opportunity to both develop novel methods that integrate multiple sources of data to decipher the etiology of psychiatric disorders and other diseases.

Orcid ID

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Citation statistics

Total citations: 7109
h-index: 24
i10-index: 31
(Obtained from google scholar on Dec 30th, 2020)

Number of publications in *Nature*, *Science*, *Nat Genet*, and *NEJM*: 10 (3 as first author)
Number of first and co-first author publications: 8
Number of senior author publications: 3
Number of peer-reviewed publications: 43

Submitted pre-prints

53. Y Ding, K Hou, K Burch, S Lapinska, F Privé, **BJ Vilhjálmsson**, S Sankararaman, B Pasaniuc. Large uncertainty in individual PRS estimation impacts PRS-based risk stratification. (Preprint on ***bioRxiv***, *doi: https://doi.org/10.1101/2020.11.30.403188*)

52. C Albiñana, J Grove, JJ McGrath, E Agerbo, NR Wray, T Werge, AD Børglum, PB Mortensen, F Privé*, **BJ Vilhjálmsson***. Leveraging both individual-level genetic data and GWAS summary statistics increases polygenic prediction of psychiatric disorders and other complex diseases. (Preprint on ***bioRxiv***, *doi: https://doi.org/10.1101/2020.11.27.401141*) (* **contributed equally**)

51. L Skotte, J Fadista, J Bybjerg-Grauholm, V Appadurai, MS Hildebrand, TF Hansen, K Banasik, J Grove, CA Climent, F Geller, CF Bjurström, **BJ Vilhjálmsson**, M Coleman, JA Damiano, R Burgess, IE Scheffer, OBV Pedersen, C Erikstrup, D Westergaard, KR Nielsen, E Sørensen, MT Bruun, X Liu, H Hjalgrim, TH Pers, PB Mortensen, O Mors, M Nordentoft, JW Dreier, A Børglum, J Christensen, DM Hougaard, A Buil, A Hviid, M Melbye, H Ullum, SF Berkovic, T Werge, B Feenstra. Genome-wide association study of febrile seizures identifies seven new loci implicating fever response and

neuronal excitability genes. (Preprint on ***medRxiv***, *doi: https://doi.org/10.1101/2020.11.18.20233916*)

50. Q Zhang, F Privé, **BJ Vilhjálmsson**, D Speed. Improved genetic prediction of complex traits from individual-level data or summary statistics. (Preprint on ***bioRxiv***, *doi: https://doi.org/10.1101/2020.06.26.172999*)

49. H Julienne, V Laville, ZR McCaw, Z He, V Guillemot, C Lasry, A Ziyatdinov, A Vaysse, P Lechat, H Ménager, W Le Goff, M-P Dube, P Kraft, I Ionita-Laza, **BJ Vilhjálmsson**, H Aschard. Multitrait genetic-phenotype associations to connect disease variants and biological mechanisms. (Preprint on ***bioRxiv***, *doi: https://doi.org/10.1101/2020.06.26.172999*)

Published articles

2020:

48.** F Privé, J Arbel, **BJ Vilhjálmsson**. LDpred2: better, faster, stronger. ***Bioinformatics, *doi: https://doi.org/10.1093/bioinformatics/btaa1029*.

47.** F Privé, K Luu, MG Blum, JJ McGrath, **BJ Vilhjálmsson**. Efficient toolkit implementing best practices for principal component analysis of population genetic data. ***Bioinformatics, *doi: https://doi.org/10.1093/bioinformatics/btaa520*.

46. E Agerbo, BB Trabjerg, AD Børglum, AJ Schork, **BJ Vilhjálmsson**, CB Pedersen, C Hakulinen, C Albiñana, DM Hougaard, J Grove, JJ McGrath, J Bybjerg-Grauholm, O Mors, O Plana-Ripoll, T Werge, NR Wray, PB Mortensen, KL Musliner. Risk of Major Depression, Polygenic Risk Score for Depression, Parental Socio-Economic Status and History of Mental Disorders: A Danish Population-Based Study. ***JAMA Psychiatry***, *in press.*

45. SD Østergaard, BB Trabjerg, TD Als, C Albiñana Climent, F Privé, **BJ Vilhjálmsson**, M Bækvad-Hansen, J Bybjerg-Grauholm, DM Hougaard, M Nordentoft, T Werge, D Demontis, PB Mortensen, AD Børglum, O Mors, E Agerbo. Polygenic Risk Score, Psychosocial Environment and the Risk of ADHD. ***Translational Psychiatry*****,** *10: 335*.

44. C Albiñana, **BJ Vilhjálmsson**, JJ McGrath. Families, health-registers, and biobanks – making the unmeasurable measurable. ***Biological Psychiatry***, *88: 440-441*.

43. O Plana-Ripoll, KL Musliner, S Dalsgaard, NC Momen, N Weye, MK Christensen, E Agerbo, KM Iburg, TM Laursen, PB Mortensen, CB Pedersen, LV Petersen, DF Santomauro, **BJ Vilhjálmsson**, HA Whiteford, JJ McGrath. Nature and prevalence of combinations of mental disorders and their association with excess mortality in a population-based cohort study. ***World Psychiatry***, *19: 339–349*.

42. X Liu, T Munk-Olsen, C Albiñana, **BJ Vilhjálmsson**, E Pedersen, V Schlünssen, M Bækvad-Hansen, J Bybjerg-Grauholm, M Nordentoft, A Børglum, T Werge, D Hougaard, PB Mortensen, E Agerbo. Genetic liability to major depression and risk of childhood asthma. ***Brain Behavior and Immunity*****,** *doi: https://doi.org/10.1016/j.bbi.2020.07.030*.

41.** I-J Lo, J Hill, **BJ Vilhjálmsson, J Kjems*. Linking the association between circRNAs and Alzheimer's disease progression by multi-tissue circular RNA characterization. ***RNA biology***, *doi: https://doi.org/10.1080/15476286.2020.1783487* . (* **shared corresponding authors**)

40. K Musliner, M Krebs, C Albiñana Climent, **BJ Vilhjálmsson**, E Agerbo, P Zandi, D Hougaard, M Nordentoft, A Børglum, T Werge, PB Mortensen, S Østergaard. Polygenic risk and progression to bipolar or psychotic disorders among individuals diagnosed with unipolar depression. ***The American Journal of Psychiatry***, *doi: https://doi.org/10.1176/appi.ajp.2020.19111195*.

39. K Engemann, J-C Svenning, E Agerbo, L Arge, A Børglum, A Dupont, C Erikstrup, O Hertel, D Hougaard, JJ McGrath, PB Mortensen, M Nordentoft, CE Sabel, T Sigsgaard, C Tsirogiannis, **BJ Vilhjálmsson**, T Werge, CB Pedersen, HT Horsdal. Association Between Childhood Green Space, Genetic Liability, and the Incidence of Schizophrenia. ***Schizophrenia Bulletin***, *doi: https://doi.org/10.1093/schbul/sbaa058*.

38. NC Momen, O Plana-Ripoll, E Agerbo, ME Benros, A Børglum, MK Christensen, S Dalsgaard, L Degenhardt, P de Jonge, J-C Debost, M Fenger-Grøn, JM Gunn, KM Iburg, LV Kessing, RC Kessler, TM Laursen, C Lim, O Mors, PB Mortensen, K Musliner, M Nordentoft, CB Pedersen, LV Petersen, AR Ribe, AM Roest, S Saha, AJ Schork, KM Scott, HJ Sørensen, TJ Stedman, M Vestergaard, **BJ Vilhjálmsson**, T Werge, N Weye, HA Whiteford, A Prior, JJ McGrath. Association between Mental Disorders and Subsequent Medical Conditions. ***New England Journal of Medicine***, *382: 1721-1731.*

37. F Privé, K Luu, **BJ Vilhjálmsson**, MGB Blum. Performing Highly Efficient Genome Scans for Local Adaptation with R Package pcadapt Version 4. ***Molecular Biology and Evolution***, *7:37, 2153–2154.*

36. MI Cavassim Alves, S Moeskjær, C Moslemi, B Fields, A Bachmann, **BJ Vilhjálmsson**, MH Schierup, JPW Young, SU Andersen. Symbiosis genes show a unique pattern of introgression and selection within a *Rhizobium leguminosarum* species complex. ***Microbial Genomics***, *6: doi: 10.1099/mgen.0.000351*.

35. H Julienne, P Lechat, V Guillemot, C Lasry, C Yao, R Araud, V Laville, **BJ Vilhjálmsson**, H Menager, H Aschard. JASS: Command Line and Web interface for the joint analysis of GWAS results. ***NAR Genomics and Bioinformatics***, *1, doi: https://doi.org/10.1093/nargab/lqaa003*.

34. N Shah, T Wakabayashi, Y Kawamura, C Skovbjerg, M-Z Wang, Y Mustamin, Y Isomura, V Gupta, H Jin, T Mun, N Sandal, F Azuma, E Fukai, Ü Seren, S Kusakabe, Y Kikuchi, S Nitanda, T Kumaki, M Hashiguchi, H Tanaka, A Hayashi, M Sønderkær, K Nielsen, K Schneeberger, **BJ Vilhjálmsson**, R Akashi, J Stougaard, S Sato, M Schierup, SU Andersen. Extreme genetic signatures of local adaptation during *Lotus japonicus* colonization of Japan. ***Nature Communication***, *11: 253.*

2019:

33. F Privé, **BJ Vilhjálmsson**, H Aschard, MG Blum. Making the most of Clumping and Thresholding for polygenic scores. ***American Journal of Human Genetics***, *105: 1213-1221.*

*__32.__ **BJ Vilhjálmsson**, F Privé. Headaches and Polygenic Scores. ***Neurology: Genetics***, *5: e368.*

31. HT Horsdal, E Agerbo, JJ McGrath, **BJ Vilhjálmsson**, S Antonsen, AM Closter, A Timmermann, J Grove, P Mok, RT Webb, CE Sabel, O Hertel, T Sigsgaard, C Erikstrup, DM Hougaard, T Werge, M Nordentoft, A Børglum, O Mors, PB Mortensen, J Brandt, C Geels and CB Pedersen. Association of Childhood Exposure to Nitrogen Dioxide and Polygenic Risk Score for Schizophrenia With the Risk of Developing Schizophrenia. ***JAMA Network***, *2: e1914401.*

30. S Besenbacher, T Mailund, **BJ Vilhjálmsson**, MH Schierup. Association Mapping and Disease: Evolutionary Perspectives. ***Evolutionary Genomics***, *533-553*.

29. D Duszynska, **BJ Vilhjálmsson**, R Castillo Bravo, S Swamidatta, TE Younger, MTA Donoghue A Comte; M Nordborg, TF Sharbel, G Brychkova, PC McKeown; C Spillane. Transgenerational effects of inter-ploidy cross direction on reproduction and seed development in Arabidopsis thaliana F1 hybrid triploids. ***Plant Reproduction***, *doi:10.1007/s00497-019-00369-6*.

2018:

28. A Kong, G Thorleifsson, ML Frigg, **BJ Vilhjálmsson**, AI Young, TE Thorgeirsson, S Benonisdottir, A Oddsson, BV Halldorsson, G Masson, D Gudbjartsson, A Helgason, G Bjornsdottir, U Thorsteinsdottir, K Stefansson. The nature of nurture: Effects of parental genotypes. ***Science***, *359:424-428*.

- *More than 200 citations.*
- *Featured in a New York Times article by C Zimmer.*

27. J Zheng, T Richardson, L Millard, G Hemani, C Raistrick, **BJ Vilhjálmsson**, P Haycock, T Gaunt. PhenoSpD: an atlas of phenotypic correlations and a multiple testing correction for the human phenome. ***GigaScience***, *7:giy090*.

2017:

26. H Aschard, V Guillemot, **BJ Vilhjálmsson**, CJ Patel, D Skurnik, J Yu, B Wolpin, P Kraft, N Zaitlen. Covariate selection for association screening in multi-phenotype genetic studies. ***Nature Genetics***, *49:1789-1795*.

2016:

25. G Athanasiadis, J Cheng, **BJ Vilhjálmsson**, FG Jørgensen, TD Als, S Le Hellard, T Espeseth, PF Sullivan, CM Hultman, PC Kjærgaard, MH Schierup, and T Mailund. Nationwide Genomic Study in Denmark Reveals Remarkable Population Homogeneity. ***Genetics***, *204:711-722*.

24. H Aschard, **BJ Vilhjálmsson**, A Joshi, AL Price, P Kraft. Response to Day et al. ***American Journal of Human Genetics***, *98: 394-395*.

2015:

*__23.__ **BJ Vilhjálmsson**, J Yang, H Finucane, A Gusev, S Lindström, S Ripke, G Genovese, P-R Loh, G Bhatia, R Do, M Pato, C Pato, T Hayeck, H-H Won, Schizophrenia Working Group of the PGC, the Discovery, Biology, and Risk of Inherited Variants in Breast Cancer (DRIVE) study, S Kathiresan, M Pato, C Pato, R Tamimi, E Stahl, N Zaitlen, B Pasaniuc, MH Schierup, P De Jager, N Patsopoulos, S McCarroll, M Daly, S Purcell, D Chasman, B Neale, M Goddard, P Visscher, P Kraft, N Patterson, AL Price. Modeling linkage disequilibrium increases accuracy of polygenic risk scores. ***American Journal of Human Genetics***, *97: 576-592*.

- *More than 500 citations*
- *Highlighted in a Best of AJHG 2015 and 2016 reprint.*

- *Cited as a "sophisticated new algorithm" in an Aug 13th, 2018 New York Times article by G Kolata.*

22.** H Aschard*, **BJ Vilhjálmsson, A Joshi, AL Price, P Kraft. Adjusting for heritable covariates can bias effect estimates in genome-wide association studies. ***American Journal of Human Genetics***, *96:329-339*. (*** equal contributions**)

- *More than 150 citations.*

21. E Agerbo, PF Sullivan, **BJ Vilhjálmsson**, CB Pedersen, O Mors, AD Børglum, DM Hougaard, MV Hollegaard, S Meier, S Ripke, NR Wray, PB Mortensen. Polygenic Risk Score, Parental Socioeconomic Status, Family History of Psychiatric Disorders and the Risk of Schizophrenia: A Danish Population-Based Study. ***JAMA Psychiatry***, *72: 635-641.*

20. MJ Dubin, P Zhang, D Meng, M-S Remigereau, EJ Osborne, FP Casale, P Drewe, A Kahles, **BJ Vilhjálmsson**, J Jagoda, S Irez, V Voronin, Q Song, Q Long, G Rätsch, O Stegle, RM Clark, M Nordborg. DNA methylation variation in Arabidopsis has a genetic basis and shows evidence of local adaptation. ***eLife***, *4:e05255.*

19. T Hayeck, NA Zaitlen, P-R Loh, **BJ Vilhjálmsson**, S Pollack, A Gusev, J Yang, G-B Chen, ME Goddard, PM Visscher, N Patterson, AL Price. Mixed model with correction for case-control ascertainment increases association power. ***American Journal of Human Genetics***, *96: 720-730.*

18. P-R Loh, G Tucker, BK Bulik-Sullivan, **BJ Vilhjálmsson**, HK Finucane, RM Salem, DI Chasman, PM Ridker, BM Neale, B Berger, N Patterson, AL Price. Efficient Bayesian mixed model analysis increases association power in large cohorts. ***Nature Genetics***, *47:284-290.*

- *More than 600 citations.*

2014:

17. H Aschard, **BJ Vilhjálmsson**, N Greliche, P-E Morange, D-A Trégouët, P Kraft. Maximizing the Power in Genome-wide Association Studies of Principal Components from Correlated Phenotypes. ***American Journal of Human Genetics***, *94:1-15.*

16. N Zaitlen, B Pasaniuc, S Sankararam, G Bhatia, J Zhang, A Gusev, T Young, A Tandon, S Pollack, **BJ Vilhjálmsson**, TL Assimes, SI Berndt, WJ Blot, S Chanock, N Franceschini, PG Goodman, J He, AJM Hennis, A Hsing, SA Ingles, W Isaacs, RA Kittles, EA Klein, LA Lange, B Nemesure, N Patterson, D Reich, BA Rybicki, JL Stanford, VL Stevens, SS Strom, EA Whitsel, JS Witte, J Xu, C Haiman, JG Wilson, C Kooperberg, D Stram, AP Reiner, H Tang, AL Price. Leveraging population admixture to characterize the heritability of complex traits. ***Nature Genetics***, *46:1356-1362.*

15. A Gusev, SH Lee, G Trynka, H Finucane, **BJ Vilhjálmsson**, H Xu, C Zang, S Ripke, B Bulik-Sullivan, E Stahl, Schizophrenia Working Group of the Psychiatric Genomics Consortium, SWE-SCZ Consortium, AK Kahler, CM Hultman, SM Purcell, SA McCarroll, M Daly, B Pasaniuc, PF Sullivan, B Neale, NR Wray, S Raychaudhuri, AL Price. Partitioning Heritability of Regulatory and Cell-Type-Specific Variants across 11 Common Diseases. ***American Journal of Human Genetics***, *95:535-552.*

- *More than 400 citations.*

14. MW Horton, N Bodenhausen, K Beilsmith, D Meng, BD Muegge, S Subramanian, MM Vetter, **BJ Vilhjálmsson**, M Nordborg, JI Gordon, J Bergelson. Genome-wide association study of Arabidopsis thaliana leaf microbial community. ***Nature Communications***, *5:5320*.

13. BZ He, MZ Ludwig, DA Dickerson, L Barse, B Arun, **BJ Vilhjálmsson**, S-Y Park, NA Tamarina, SB Selleck, PJ Wittkopp, GI Bell, M Kreitman. Effect of genetic variation in a Drosophila model of diabetes-associated misfolded human proinsulin. ***Genetics***, *196:557-567*.

- *Cover feature.*

2013:

*__12.__ **BJ Vilhjálmsson** and M Nordborg. The nature of confounding in genome-wide association studies. ***Nature Reviews Genetics***, *14:1-2*.

11. A Gusev, G Bhatia, N Zaitlen, **BJ Vilhjálmsson**, D Diogo, EA Stahl, PK Gregersen, JWorthington, L Klareskog, S Raychaudhuri, RM Plenge, B Pasaniuc, AL Price. Quantifying missing heritability at known GWAS loci. ***PLoS Genetics***, *9:e1003993*.

10. Q Long, FA Rabanal, D Meng, CD Huber, A Farlow, A Platzer, Q Zhang, **BJ Vilhjálmsson**, A Korte, V Nizhynska, V Voronin, Ü Seren, L Sedman, I Hellmann, M Nordborg. Massive genomic variation and strong selection in Arabidopsis thaliana lines from Sweden. ***Nature Genetics***, *45:884-890*.

9. S Beleza, NA Johnson, SI Candille, DM Absher, MA Coram, J Lopes, J Campos, II Araújo, TM Anderson, **BJ Vilhjálmsson**, M Nordborg, A Correia e Silva, MD Shriver, J Rocha, GS Barsh, H Tang. Genetic architecture of skin and eye color in an African-European admixed population. ***PLoS Genetics***, *9: e1003372*.

- *Cover feature.*

8. Q Long, Q Zhang, **BJ Vilhjálmsson**, Ü Seren, P Forai, M Nordborg. JAWAMix5: an outof-core HDF5-based java implementation of whole-genome association studies using mixed models. ***Bioinformatics***, *29:1220-1222*.

2012:

__7.__ V Segura, **BJ Vilhjálmsson***, A Platt, A Korte, Ü Seren, Q Long, and M Nordborg (2012). Multilocus mixed model for genome-wide association studies in structured populations. ***Nature Genetics***, *44:825-830*. (* **contributed equally**)

- *More than 500 citations.*

__6.__ A Korte, **BJ Vilhjálmsson***, V Segura*, A Platt, Q Long, and M Nordborg (2012). A mixed model for genome-wide association studies of correlated traits in structured populations. ***Nature Genetics*** *44:1066-1071*. (* **contributed equally**)

- *More than 300 citations.*

5.** Ü Seren*, **BJ Vilhjálmsson, MW Horton, D Meng, P Forai, YS Huang, Q Long, V Segura, and M Nordborg. GWAPP: A web application for genome-wide association studies in A. thaliana. ***Plant Cell***, *24:4793-4805*. (*** contributed equally**)

4. MW Horton, AM Hancock, YS Huang, C Toomajian, S Atwell, A Auton, NW Muliyati, A Platt, FG Sperone, **BJ Vilhjálmsson**, M Nordborg, JO Borevitz, J Bergelson (2012). Genome-wide patterns of genetic variation in worldwide Arabidopsis thaliana accessions from the RegMap panel. ***Nature Genetics***, *44:212-216*.

- *More than 400 citations.*

2011:

3. YS Huang, M Horton, **BJ Vilhjálmsson**, Ü Seren, D Meng, C Meyer, MA Amer, JO Borevitz, J Bergelson, and M Nordborg (2011). Analysis and visualization of Arabidopsis thaliana GWAS using web 2.0 technologies. ***Database***, *2011:bar014*.

2010:

2.** S Atwell*, YS Huang*, **BJ Vilhjálmsson, G Willems*, M Horton, Y Li, D Meng, A Platt, AM Tarone, TT Hu, R Jiang, NW Muliyati, X Zhang, MA Amer, I Baxter, B Brachi, J Chory, C Dean, M Debieu, J De Meaux, JR Ecker, N Faure, JM Kniskern, JDG Jones, T Michael, A Nemri, F Roux, DE Salt, C Tang, M Todesco, MB Traw, D Weigel, P Marjoram, JO Borevitz, J Bergelson, M Nordborg. Genome-wide association study of 107 phenotypes in Arabidopsis thaliana inbred lines. ***Nature,*** *465:627-631*. (*** contributed equally**)

- *More than 1400 citations.*

1. A Platt, **BJ Vilhjálmsson**, M Nordborg (2010). Conditions Under Which Genome-wide Association Studies Will be Positively Misleading. Genetics 186:1045-1052.

Other scientific publications

F Privé, **BJ Vilhjálmsson**, H Aschard. Fitting penalized regressions on very large genetic data using snpnet and bigstatsr. (2020) ***bioRxiv***, *doi: https://doi.org/10.1101/2020.10.30.362079*

F Lescai, **BJ Vilhjálmsson**, A-M Hein, T Rask, RG Madsen, D Kamaev, MM Johansen, L Husted, R Samara, J-N Billaud, E Lader, A Materna, L Schauser and M Simonsen (2018). QIAseq Targeted Panels: accurately identify genetic variants with ease. An online application note

G Bhatia, A Gusev, P-R Loh, HK Finucane, **BJ Vilhjálmsson**, S Ripke, Schizophrenia Working Group of the Psychiatric Genomics Consortium, S Purcell, E Stahl, M Daly, TR de Candia, SH Lee, N Wray, BM Neale, MC Keller, NA Zaitlen, B Pasaniuc, N Patterson, J Yang, AL Price. Subtle stratification confounds estimates of heritability from rare variants. (2016) ***bioRxiv*** *doi: https://doi.org/10.1101/048181*

BJ Vilhjálmsson (2011). Mapping complex traits in structured populations. PhD dissertation, University of Southern California. Committee: Magnus Nordborg (chair), Sergey Nuzhdin, Paul Marjoram, Fengzhu Sun, and David Conti.

BJ Vilhjálmsson (2006). Predicting a new type of solvent exposure. Masters thesis, University of Copenhagen. Advisors: Thomas Hamelryck and Anders Krogh.

Scientific Software

- **LDpred**, A set of Python scripts that implement the LDpred Gibbs sampler and other methods for calculating polygenic risk scores.
- **TheHonestGene.org**, A open-source web-framework for inferring individual ancestry and calculating polygenic risk scores. The code repository can be found on github.
- **GWAPP**, A web application for conducting genome-wide association studies in A. thaliana. Developed in collaboration with Ümit Seren. Website: http://gwas.gmi.oeaw.ac.at. Public code repository: https://github.com/timeu/GWAPP.
- **mixmogam**, A set of Python scripts that implement efficient mixed models for conducting genome-wide association mapping and estimating heritability in A. thaliana and other organisms. The proprietary SNP & Variation Suite 7 from Golden Helix relies mixmogam for mixed models implementation.

Other media

- My work on polygenic scores was highlighted in a New York Times article by G Kolata, August 2018.
- Work on the genetics of parental nurture was featured in a New York Times article by C Zimmer, Jan 2018.
- Interview at the annual American Society of Human Genetics meeting on my research at QIAGEN, October 2017
- An interview for videnskab.dk; 14. March, 2016.
- An interview for Rømer; 17. March, 2016.
- An interview for videnskab.dk; 24. March, 2014. This interview was picked up by Berlingske, ScienceNordic, and forskning.no.
- **BJ Vilhjálmsson** (2013). Erfðafræðibyltingin er tækifæri fyrir Ísland. Morgunblaðið, (an Icelandic newspaper), 12. April, 2013.

Selected invited talks and oral presentations

- The Promise of Polygenic Risk Scores: Perspective and Applications. **Invited talk** by Illumina, World Congress of Psychiatric Disorders, Oct 2020..
- Quantifying Population Stratification in GWAS Summary Statistics. **Invited talk** by Professor Naomi Wray at the University of Queensland, Australia, April 2019.
- Immuno-Oncology Applications (QIAGEN). **Platform presentation** at the Festival of Genomics, London, January 2018.

- Joint GWAS Meta Analysis. **Invited speaker** at a workshop titled "Functional Analysis of Sequence Variants in HBOC Genes", NCI, Amsterdam, Netherlands, June 2017.
- Joint GWAS Meta Analysis. **Selected for platform presentation at ASHG 2016**, Vancouver, Canada, October 2016.
- Joint GWAS Meta Analysis. **Invited talk** by Prof. Hugues Aschard at the Pasteur Institute, Paris, France, October 2016.
- Genomic Prediction in Medicine. **Invited speaker** at the 4'th annual workshop titled "Phenotype Prediction Using Genomic Data" at University of Florida, USA. Gene, August 2016.
- Bayesian Polygenic Risk Scores for Everyone. **Invited speaker** at Gene Environment Interactions in Mental Health, Novo Nordisk Foundation, Copenhagen, March 2016.
- Developing Internationalization in Research. **Invited speaker** at an event for Sapere Aude: DFF-Research Talent grant holders. Copenhagen, January 2016.
- **Keynote speaker** at a conference on Medical population genetics and GWAS mega-analysis for complex diseases. The African Institute for Mathematical Sciences, Cape Town, South Africa, April 2015.
- Predicting Disease Risk from Whole Genome Data. **Invited speaker**, iSEQ seminar, Aarhus University, November 2014.
- Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores for Schizophrenia and other Diseases. World Congress of Psychiatric Genetics, Denmark, October 2014. Abstract **selected for oral presentation**
- Efficient genetic risk prediction in large samples. **Invited speaker**, Bertinoro Computational Biology (meeting), Italy, October 2014.
- More Accurate Polygenic Risk Scores. **Invited talk** by Professor Douglas Easton, Strangeways Research Laboratories, University of Cambridge, July 2014.
- Modeling linkage disequilibrium increases accuracy of polygenic risk scores. **Oral presentation**, The Broad Institute of MIT and Harvard, June 2014.
- Polygenic risk prediction using summary statistics. **Invited talk** by Professor Oluf B. Pedersen, Novo Nordisk Foundation Center for Basic Metabolic Research, University of Copenhagen, December 2012.
- Polygenic risk prediction using summary statistics. Program in Quantitative Genomics Conference, Harvard School of Public Health, November 2012. **Abstract selected for oral presentation.**
- Genome-wide association studies of correlated traits in structured populations. **Invited talk** by Professor Peter Donnelly, Wellcome Trust Centre for Human Genetics, Oxford University, June 2012.

Academic supervision

Postdocs

- Florian Privé, postdoc, National Center for Register-based Research, Aarhus University, since Oct 2019.

- Zhihong Zhu, postdoc, National Center for Register-based Research, Aarhus University, since Aug 2020.

PhD students (main supervisor)

- Emil M Pedersen, National Centre for Register-based Research, Aarhus University, since Dec 2019. (Research Assistant Dec 2018-Nov 2019)
- Clara Albiñana, National Centre for Register-based Research, Aarhus University, since Dec 2019. (Research Assistant Dec 2018-Nov 2019)

PhD students (co-supervisor)

- Arnor Ingi Sigurdsson, PhD student (external co-supervisor), NNF Centre for Basic Metabolic Research, University of Copenhagen, since Februar 2020.
- Petar V Todorov, PhD student (external co-supervisor), NNF Centre for Basic Metabolic Research, University of Copenhagen, since August 2019.
- IJu Lo, PhD student (primary supervisor until Oct. 2018), QIAGEN and Aarhus University, since August 2017.
- Asger Bachmann, PhD student (co-supervisor until August 2016, interrupted by move to QIAGEN), Aarhus University, August 2015-August 2016.

MSc students

- Muna Hasan Mohamed, Bioinformatics student, Aarhus University, Feb-Jun 2019.
- Kristian Andersen-Møller, Bioinformatics student (project and thesis advisor), Aarhus University, Jan-Dec 2016.

BSc students

- Jette Steinbach, Statistics student, Aarhus University, Jan-June 2016.
- Simon Drue, Statistics student, Aarhus University, Jan-June 2016.

Research Assistants

- Emil M Pedersen, National Centre for Register-based Research, Aarhus University, Dec 2018-Nov 2019 (a PhD student as of Dec 2019)
- Clara Albiñana, National Centre for Register-based Research, Aarhus University, since Dec 2019. Dec 2018-Nov 2019 (a PhD student as of Dec 2019).
- Meindert J Witteveen, since Nov 2020.

Teaching experience

I have contributed to, taught and organized several courses, all of which have focused on statistics, statistical genetics, and bioinformatics. This includes a Bioinformatics masters course titled “Genome Variation and Human Health”, which I organized and taught together with Prof. Søren Besenbacher in 2015 and 2016. In addition I organized a Bioinformatics journal club (Oct 2014 - June 2016), and currently a Statistical Genetics journal club (since Nov 2018), for which students

can get credit. While at Harvard T H Chan School of Public Health (HSPH) I also organized a Program in Quantitative Genetics seminar series (Sept 2013 - Jun 2014). In 2015 I completed the teacher training program (adjunktkursus) offered by Aarhus University (modules 1-4), and I am currently participating in a PhD supervision course.

Management experience

- Established a Statistical Genetics research group at NCRR focusing on developing and applying statistical methods that combine genetics and register data to study psychiatric disorders. Since Oct. 2018, I have secured more than 10 million DKK in research funding, recruited 2 PhD students, 2 postdocs and 1 research assistant.
- As a Product Owner at QIAGEN I was responsible for the software development of the Biomedical Workbench and leading a team of 8 developers from March 2017 - April 2018. Between May 2018 - Sep 2018, I also took on the software development responsibilities of the Genomics Workbench, leading a team of 16 developers.
- I completed several QIAGEN management courses.

Academic services

- Editorial Board member at *Genes* (ISSN 2073-4425) and *Frontiers in Genetics* (ISSN 1664-8021).
- Reviewed articles for Nature Genetics; Nature Reviews Genetics; Nature Methods; Nature Communications; F1000 Research; PLoS Genetics; JAMA Psychiatry; Biological Psychiatry; Annals of Neurology; Bioinformatics; PLoS Computational Biology; Genetics, Theoretical Population Biology; Molecular Ecology; BMC Genetics; Statistics in Medicine; Evolution, Medicine, and Public Health; Entropy; ISMB (2016-2017); PLoS One; Pacific Symposium on Biocomputing (2013-2017); RECOMB Genetics (2018).
- A member of the program committee for Pacific Symposium on Biocomputing 2013-2017 and RECOMB Genetics (2018).
- A member of the American Society of Human Genetics (2012-2018), International Society of Psychiatric Genetics (2013-2015, 2018-), the International Society of Computational Biology (2011-2016), and the Genetics Society of America (2010-2016).