

References

- Adam, Y., Samtal, C., Brandenburg, J., Falola, O., & Adebisi, E. (2021). Performing post-genome-wide association study analysis: overview, challenges and recommendations. *F1000Research*, *10*, 1002. <https://doi.org/10.12688/f1000research.53962.1>
- Alam, S. M. K., Jasti, S., Kshirsagar, S. K., Tannetta, D. S., Dragovic, R. A., Redman, C. W., Sargent, I. L., Hodes, H. C., Nauser, T. L., Fortes, T., Filler, A. M., Behan, K., Martin, D. R., Fields, T. A., Petroff, B. K., & Petroff, M. G. (2018). Trophoblast Glycoprotein (TPGB/5T4) in Human Placenta: Expression, Regulation, and Presence in Extracellular Microvesicles and Exosomes. *Reproductive Sciences (Thousand Oaks, Calif.)*, *25*(2), 185–197. <https://doi.org/10.1177/1933719117707053>
- Antúnez, C., Boada, M., González-Pérez, A., Gayán, J., Reposo Ramírez-Lorca, Francisco, J., Hernández, I., Moreno-Rey, C., Morón, F. J., Jesús López-Arrieta, Mauleón, A., Maitée Rosende-Roca, Fuensanta Noguera-Perea, Legaz-García, A., Vivancos-Moreau, L., Velasco, J. R., Escacena, L., Montserrat Alegret, Martirio Antequera-Torres, & Manzanares, S. (2011). *The membrane-spanning 4-domains, subfamily A (MS4A) gene cluster contains a common variant associated with Alzheimer's disease*. *3*(5), 33–33. <https://doi.org/10.1186/gm249>
- Aschard, H., Guillelot, V., Vilhjalmsson, B., Patel, C. J., Skurnik, D., Ye, C. J., Wolpin, B., Kraft, P., & Zaitlen, N. (2017). Covariate selection for association screening in multiphenotype genetic studies. *Nature Genetics*, *49*(12), 1789–1795. <https://doi.org/10.1038/ng.3975>
- Aschard, H., Vilhjalmsson, Bjarni J., Joshi, Amit D., Price, Alkes L., & Kraft, P. (2015). Adjusting for Heritable Covariates Can Bias Effect Estimates in Genome-Wide Association Studies. *The American Journal of Human Genetics*, *96*(2), 329–339. <https://doi.org/10.1016/j.ajhg.2014.12.021>
- Baker-Nigh, A. T., Mawuenyega, K. G., Bollinger, J. G., Ovod, V., Kasten, T., Franklin, E. E., Liao, F., Jiang, H., Holtzman, D., Cairns, N. J., Morris, J. C., & Bateman, R. J. (2016). Human Central Nervous System (CNS) ApoE Isoforms Are Increased by Age, Differentially Altered by Amyloidosis, and Relative Amounts Reversed in the CNS Compared with Plasma. *Journal of Biological Chemistry*, *291*(53), 27204–27218. <https://doi.org/10.1074/jbc.m116.721779>
- Bayat, A., Szul, P., O'Brien, A. R., Dunne, R., Hosking, B., Jain, Y., Hosking, C., Luo, O. J., Twine, N., & Bauer, D. C. (2020). VariantSpark: Cloud-based machine learning for association study of complex phenotype and large-scale genomic data. *GigaScience*, *9*(8). <https://doi.org/10.1093/gigascience/giaa077>
- Bekris, L. M., Yu, C.-E., Bird, T. D., & Tsuang, D. W. (2010). Review Article: Genetics of Alzheimer Disease. *Journal of Geriatric Psychiatry and Neurology*, *23*(4), 213–227. <https://doi.org/10.1177/0891988710383571>
- Bellenguez, C., Küçükali, F., Jansen, I. E., Kleindam, L., Moreno-Grau, S., Amin, N., Naj, A. C., Campos-Martin, R., Grenier-Boley, B., Andrade, V., Holmans, P. A., Boland, A., Damotte, V., van der Lee, S. J., Costa, M. R., Kuulasmaa, T., Yang, Q., de Rojas, I., Bis, J. C., & Yaqub, A. (2022). New insights into the genetic etiology of Alzheimer's disease and related dementias. *Nature Genetics*. <https://doi.org/10.1038/s41588-022-01024-z>
- Bertram, L., Lange, C., Mullin, K., Parkinson, M., Hsiao, M., Hogan, M. F., Schjeide, B. M. M., Hooli, B., DiVito, J., Ionita, I., Jiang, H., Laird, N., Moscarillo, T., Ohlsen, K. L., Elliott, K., Wang, X., Hu-Lince, D., Ryder, M., Murphy, A., & Wagner, S. L. (2008). Genome-wide Association Analysis

- Reveals Putative Alzheimer's Disease Susceptibility Loci in Addition to APOE. *The American Journal of Human Genetics*, 83(5), 623–632. <https://doi.org/10.1016/j.ajhg.2008.10.008>
- Bryja, V., Červenka, I., & Čajánek, L. (2017). The connections of Wnt pathway components with cell cycle and centrosome: side effects or a hidden logic? *Critical Reviews in Biochemistry and Molecular Biology*, 52(6), 614–637. <https://doi.org/10.1080/10409238.2017.1350135>
- Cano-Gamez, E., & Trynka, G. (2020). From GWAS to Function: Using Functional Genomics to Identify the Mechanisms Underlying Complex Diseases. *Frontiers in Genetics*, 11. <https://doi.org/10.3389/fgene.2020.00424>
- Carter, H., Hofree, M., & Ideker, T. (2013). Genotype to phenotype via network analysis. *Current Opinion in Genetics & Development*, 23(6), 10.1016/j.gde.2013.10.003. <https://doi.org/10.1016/j.gde.2013.10.003>
- Chang, C. (2022). *File format reference - PLINK 1.9*. www.cog-genomics.org. <https://www.cog-genomics.org/plink/1.9/formats>
- Chang, I. J., He, M., & Lam, C. T. (2018). Congenital disorders of glycosylation. *Annals of Translational Medicine*, 6(24). <https://doi.org/10.21037/atm.2018.10.45>
- Chen, B., Cole, J. W., & Grond-Ginsbach, C. (2017). Departure from Hardy Weinberg Equilibrium and Genotyping Error. *Frontiers in Genetics*, 8. <https://doi.org/10.3389/fgene.2017.00167>
- Chen, G., Xu, T., Yan, Y., Zhou, Y., Jiang, Y., Melcher, K., & Xu, H. E. (2017). Amyloid beta: structure, biology and structure-based therapeutic development. *Acta Pharmacologica Sinica*, 38(9), 1205–1235. <https://doi.org/10.1038/aps.2017.28>
- Chen, H.-H., Petty, L. E., Sha, J., Zhao, Y., Kuzma, A., Valladares, O., Bush, W., Naj, A. C., Gamazon, E. R., & Below, J. E. (2021). Genetically regulated expression in late-onset Alzheimer's disease implicates risk genes within known and novel loci. *Translational Psychiatry*, 11(1). <https://doi.org/10.1038/s41398-021-01677-0>
- Chen, H.-K., Ji, Z.-S., Dodson, S. E., Miranda, R. D., Rosenblum, C. I., Reynolds, I. J., Freedman, S. B., Weisgraber, K. H., Huang, Y., & Mahley, R. W. (2011). Apolipoprotein E4 Domain Interaction Mediates Detrimental Effects on Mitochondria and Is a Potential Therapeutic Target for Alzheimer Disease. *The Journal of Biological Chemistry*, 286(7), 5215–5221. <https://doi.org/10.1074/jbc.M110.151084>
- Chen, Y.-C., Hsiao, C.-J., Jung, C.-C., Hu, H.-H., Chen, J.-H., Lee, W.-C., Chiou, J.-M., Chen, T.-F., Sun, Y., Wen, L.-L., Yip, P.-K., Chu, Y.-M., Chen, C.-J., & Yang, H.-I. (2016). Performance Metrics for Selecting Single Nucleotide Polymorphisms in Late-onset Alzheimer's Disease. *Scientific Reports*, 6(1). <https://doi.org/10.1038/srep36155>
- Chimusa, E. R., Dalvie, S., Dandara, C., Wonkam, A., & Mazandu, G. K. (2018). Post genome-wide association analysis: dissecting computational pathway/network-based approaches. *Briefings in Bioinformatics*, 20(2), 690–700. <https://doi.org/10.1093/bib/bby035>
- Christiansen, M. K., Larsen, S. B., Nyegaard, M., Neergaard-Petersen, S., Ajjan, R., Würtz, M., Grove, E. L., Hvas, A.-M., Jensen, H. K., & Kristensen, S. D. (2017). Coronary artery disease-associated genetic variants and biomarkers of inflammation. *PLOS ONE*, 12(7), e0180365. <https://doi.org/10.1371/journal.pone.0180365>
- Coleman, J. R. I., Euesden, J., Patel, H., Folarin, A. A., Newhouse, S., & Breen, G. (2015). Quality control, imputation and analysis of genome-wide genotyping data from the Illumina HumanCoreExome microarray. *Briefings in Functional Genomics*, 15(4), 298–304. <https://doi.org/10.1093/bfgp/elv037>

- Couronné, R., Probst, P., & Boulesteix, A.-L. (2018). Random forest versus logistic regression: a large-scale benchmark experiment. *BMC Bioinformatics*, *19*(1). <https://doi.org/10.1186/s12859-018-2264-5>
- de los Campos, G., Grueneberg, A., Funkhouser, S., Pérez-Rodríguez, P., & Samaddar, A. (2022). Fine mapping and accurate prediction of complex traits using Bayesian Variable Selection models applied to biobank-size data. *European Journal of Human Genetics*, 1–8. <https://doi.org/10.1038/s41431-022-01135-5>
- Deane, R., Sagare, A., Hamm, K., Parisi, M., Lane, S., Finn, M. B., Holtzman, D. M., & Zlokovic, B. V. (2008). apoE isoform-specific disruption of amyloid β peptide clearance from mouse brain. *Journal of Clinical Investigation*, *118*(12), 4002–4013. <https://doi.org/10.1172/jci36663>
- Efthymiou, A. G., & Goate, A. M. (2017). Late onset Alzheimer’s disease genetics implicates microglial pathways in disease risk. *Molecular Neurodegeneration*, *12*(1). <https://doi.org/10.1186/s13024-017-0184-x>
- Genomic Variants in Human Genome (Build 36: Mar. 2006, hg18): 800 kbp from chr7:71,890,181..72,690,180.* (n.d.). Dgv.tcag.ca. Retrieved November 25, 2022, from http://dgv.tcag.ca/gb2/gbrowse/dgv2_hg18/
- Hail. (2020). Hail.is. <https://hail.is/>
- Hellwege, J. N., Keaton, J. M., Giri, A., Gao, X., Velez Edwards, D. R., & Edwards, T. L. (2017). Population Stratification in Genetic Association Studies. *Current Protocols in Human Genetics*, *95*(1), 1.22.1–1.22.23. <https://doi.org/10.1002/cphg.48>
- Isik, A. T. (2010). Late onset Alzheimer’s disease in older people. *Clinical Interventions in Aging*, 307. <https://doi.org/10.2147/cia.s11718>
- Jansen, I. E., Savage, J. E., Watanabe, K., Bryois, J., Williams, D. M., Steinberg, S., Sealock, J., Karlsson, I. K., Hägg, S., Athanasiu, L., Voyle, N., Proitsi, P., Witoelar, A., Stringer, S., Aarsland, D., Almdahl, I. S., Andersen, F., Bergh, S., Bettella, F., & Bjornsson, S. (2019). Genome-wide meta-analysis identifies new loci and functional pathways influencing Alzheimer’s disease risk. *Nature Genetics*, *51*(3), 404–413. <https://doi.org/10.1038/s41588-018-0311-9>
- Jeong, W., & Jho, E. (2021). Regulation of the Low-Density Lipoprotein Receptor-Related Protein LRP6 and Its Association With Disease: Wnt/ β -Catenin Signaling and Beyond. *Frontiers in Cell and Developmental Biology*, *9*. <https://doi.org/10.3389/fcell.2021.714330>
- Jiang, Q., Lee, C. Y. D., Mandrekar, S., Wilkinson, B., Cramer, P., Zelcer, N., Mann, K., Lamb, B., Willson, T. M., Collins, J. L., Richardson, J. C., Smith, J. D., Comery, T. A., Riddell, D., Holtzman, D. M., Tontonoz, P., & Landreth, G. E. (2008). ApoE Promotes the Proteolytic Degradation of A β . *Neuron*, *58*(5), 681–693. <https://doi.org/10.1016/j.neuron.2008.04.010>
- Johnson, E. O., Hancock, D. B., Levy, J. L., Gaddis, N. C., Saccone, N. L., Bierut, L. J., & Page, G. P. (2013). Imputation across genotyping arrays for genome-wide association studies: assessment of bias and a correction strategy. *Human Genetics*, *132*(5), 509–522. <https://doi.org/10.1007/s00439-013-1266-7>
- Kaur, S., Ali, A., Ahmad, U., Siahbalaee, Y., Pandey, A. K., & Singh, B. (2019). Role of single nucleotide polymorphisms (SNPs) in common migraine. *The Egyptian Journal of Neurology, Psychiatry and Neurosurgery*, *55*(1). <https://doi.org/10.1186/s41983-019-0093-8>
- Kawabori, M., Kacimi, R., Kauppinen, T., Calosing, C., Kim, J. Y., Hsieh, C. L., Nakamura, M. C., & Yenari, M. A. (2015). Triggering Receptor Expressed on Myeloid Cells 2 (TREM2) Deficiency Attenuates Phagocytic Activities of Microglia and Exacerbates Ischemic Damage in Experimental Stroke. *Journal of Neuroscience*, *35*(8), 3384–3396. <https://doi.org/10.1523/jneurosci.2620-14.2015>

- Kleinberger, G., Yamanishi, Y., Suárez-Calvet, M., Czirr, E., Lohmann, E., Cuyvers, E., Struyfs, H., Pettkus, N., Wenninger-Weinzierl, A., Mazaheri, F., Tahirovic, S., Lleó, A., Alcolea, D., Fortea, J., Willem, M., Lammich, S., Molinuevo, J. L., Sánchez-Valle, R., Antonell, A., & Ramirez, A. (2014). TREM2 mutations implicated in neurodegeneration impair cell surface transport and phagocytosis. *Science Translational Medicine*, *6*(243). <https://doi.org/10.1126/scitranslmed.3009093>
- Kraft, P., Zeggini, E., & Ioannidis, J. P. A. (2009). Replication in Genome-Wide Association Studies. *Statistical Science*, *24*(4), 561–573. <https://doi.org/10.1214/09-sts290>
- Ku, C. S., Loy, E. Y., Pawitan, Y., & Chia, K. S. (2010). The pursuit of genome-wide association studies: where are we now? *Journal of Human Genetics*, *55*(4), 195–206. <https://doi.org/10.1038/jhg.2010.19>
- Lee, S., Abecasis, Gonçalo R., Boehnke, M., & Lin, X. (2014). Rare-Variant Association Analysis: Study Designs and Statistical Tests. *The American Journal of Human Genetics*, *95*(1), 5–23. <https://doi.org/10.1016/j.ajhg.2014.06.009>
- Li, B., Liu, D. J., & Leal, S. M. (2013). Identifying rare variants associated with complex traits via sequencing. *Current Protocols in Human Genetics / Editorial Board, Jonathan L. Haines ... [et Al.]*, *0 1*. <https://doi.org/10.1002/0471142905.hg0126s78>
- Li, Y., Willer, C., Sanna, S., & Abecasis, G. (2009). Genotype Imputation. *Annual Review of Genomics and Human Genetics*, *10*(1), 387–406. <https://doi.org/10.1146/annurev.genom.9.081307.164242>
- Lindh, M., Blomberg, M., Jensen, M., Basun, H., Lannfelt, L., Engvall, B., Scharnagel, H., März, W., Wahlund, L.-O., & F. Cowburn, R. (1997). Cerebrospinal fluid apolipoprotein E (apoE) levels in Alzheimer's disease patients are increased at follow up and show a correlation with levels of tau protein. *Neuroscience Letters*, *229*(2), 85–88. [https://doi.org/10.1016/s0304-3940\(97\)00429-1](https://doi.org/10.1016/s0304-3940(97)00429-1)
- Livingston, G., Huntley, J., Sommerlad, A., Ames, D., Ballard, C., Banerjee, S., Brayne, C., Burns, A., Cohen-Mansfield, J., Cooper, C., Costafreda, S. G., Dias, A., Fox, N., Gitlin, L. N., Howard, R., Kales, H. C., Kivimäki, M., Larson, E. B., Ogunniyi, A., & Orgeta, V. (2020). Dementia prevention, intervention, and care: 2020 report of the Lancet Commission. *The Lancet*, *396*(10248), 413–446.
- Mahley, Robert W., & Huang, Y. (2012). Apolipoprotein E Sets the Stage: Response to Injury Triggers Neuropathology. *Neuron*, *76*(5), 871–885. <https://doi.org/10.1016/j.neuron.2012.11.020>
- Marees, A. T., de Kluiver, H., Stringer, S., Vorspan, F., Curis, E., Marie-Claire, C., & Derks, E. M. (2018). A tutorial on conducting genome-wide association studies: Quality control and statistical analysis. *International Journal of Methods in Psychiatric Research*, *27*(2), e1608. <https://doi.org/10.1002/mpr.1608>
- Mbatchou, J., Barnard, L., Backman, J., Marcketta, A., Kosmicki, J. A., Ziyatdinov, A., Benner, C., O'Dushlaine, C., Barber, M., Boutkov, B., Habegger, L., Ferreira, M., Baras, A., Reid, J., Abecasis, G., Maxwell, E., & Marchini, J. (2021). Computationally efficient whole-genome regression for quantitative and binary traits. *Nature Genetics*, *53*(7), 1097–1103. <https://doi.org/10.1038/s41588-021-00870-7>
- Medway, C., Shi, H., Bullock, J., Black, H., Brown, K., Vafadar-isfahani, B., Matharoo-ball, B., Ball, G., Rees, R., Kalsheker, N., & Morgan, K. (2010). Using In silico LD clumping and meta-analysis of genome-wide datasets as a complementary tool to investigate and validate new candidate biomarkers in Alzheimer's disease. *International Journal of Molecular Epidemiology and Genetics*, *1*(2), 134–144. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3076759/>

- Miao, L., Yin, R.-X., Pan, S.-L., Yang, S., Yang, D.-Z., & Lin, W.-X. (2018). BCL3-PVRL2-TOMM40 SNPs, gene-gene and gene-environment interactions on dyslipidemia. *Scientific Reports*, *8*(1). <https://doi.org/10.1038/s41598-018-24432-w>
- Moreno-Grau, S., Hernández, I., Heilmann-Heimbach, S., Ruiz, S., Rosende-Roca, M., Mauleón, A., Vargas, L., Rodríguez-Gómez, O., Alegret, M., Espinosa, A., Ortega, G., Aguilera, N., Abdelnour, C., Initiative, A. D. N., Gil, S., Maier, W., Sotolongo-Grau, O., Tárraga, L., Ramirez, A., & López-Arrieta, J. (2018). Genome-wide significant risk factors on chromosome 19 and the APOE locus. *Oncotarget*, *9*(37). <https://doi.org/10.18632/oncotarget.25083>
- Naj, A. C. (2019). Genotype Imputation in Genome-Wide Association Studies. *Current Protocols in Human Genetics*, *102*(1). <https://doi.org/10.1002/cphg.84>
- Panagiotou, O. A., Willer, C. J., Hirschhorn, J. N., & Ioannidis, J. P. A. (2013). The Power of Meta-Analysis in Genome-Wide Association Studies. *Annual Review of Genomics and Human Genetics*, *14*(1), 441–465. <https://doi.org/10.1146/annurev-genom-091212-153520>
- Pavone, P., Polizzi, A., Marino, S. D., Corsello, G., Falsaperla, R., Marino, S., & Ruggieri, M. (2020). West syndrome: a comprehensive review. *Neurological Sciences*, *41*(12), 3547–3562. <https://doi.org/10.1007/s10072-020-04600-5>
- PLINK: Whole genome data analysis toolset. (2017). zdz.bwh.harvard.edu. <https://zdz.bwh.harvard.edu/plink/anal.shtml#glm>
- Purcell, S., Neale, B., Todd-Brown, K., Thomas, L., Ferreira, Manuel A. R., Bender, D., Maller, J., Sklar, P., de Bakker, Paul I. W., Daly, Mark J., & Sham, Pak C. (2007). PLINK: A Tool Set for Whole-Genome Association and Population-Based Linkage Analyses. *American Journal of Human Genetics*, *81*(3), 559–575. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1950838/>
- Ramstetter, M. D., Shenoy, S. A., Dyer, T. D., Lehman, D. M., Curran, J. E., Duggirala, R., Blangero, J., Mezey, J. G., & Williams, A. L. (2018). Inferring Identical-by-Descent Sharing of Sample Ancestors Promotes High-Resolution Relative Detection. *American Journal of Human Genetics*, *103*(1), 30–44. <https://doi.org/10.1016/j.ajhg.2018.05.008>
- Reed, E., Nunez, S., Kulp, D., Qian, J., Reilly, M. P., & Foulkes, A. S. (2015). A guide to genome-wide association analysis and post-analytic interrogation. *Statistics in Medicine*, *34*(28), 3769–3792. <https://doi.org/10.1002/sim.6605>
- Ridge, P. G., Mukherjee, S., Crane, P. K., & Kauwe, J. S. K. (2013). Alzheimer’s Disease: Analyzing the Missing Heritability. *PLoS ONE*, *8*(11), e79771. <https://doi.org/10.1371/journal.pone.0079771>
- Schaid, D. J., Chen, W., & Larson, N. B. (2018). From genome-wide associations to candidate causal variants by statistical fine-mapping. *Nature Reviews Genetics*, *19*(8), 491–504. <https://doi.org/10.1038/s41576-018-0016-z>
- Selkoe, D. J., & Hardy, J. (2016). The amyloid hypothesis of Alzheimer’s disease at 25 years. *EMBO Molecular Medicine*, *8*(6), 595–608. <https://doi.org/10.15252/emmm.201606210>
- Shapshak, P. (2012). Single nucleotide polymorphisms (SNPs) for genome wide association studies (GWAS) and molecule of the month Nitric Oxide Synthase, multiple interactive pathways for three similar genes, Nitric Oxide Synthase-1, -2, -3 (NOS-1, -2, -3). *Bioinformatics*, *8*(11), 496–497. <https://doi.org/10.6026/97320630008496>
- Spires-Jones, Tara L., & Hyman, Bradley T. (2014). The Intersection of Amyloid Beta and Tau at Synapses in Alzheimer’s Disease. *Neuron*, *82*(4), 756–771. <https://doi.org/10.1016/j.neuron.2014.05.004>
- Statistical analysis for genome-wide association study. (2015). *Journal of Biomedical Research*. <https://doi.org/10.7555/jbr.29.20140007>

- Stephan, J., Stegle, O., & Beyer, A. (2015). A random forest approach to capture genetic effects in the presence of population structure. *Nature Communications*, 6(1). <https://doi.org/10.1038/ncomms8432>
- Tam, V., Patel, N., Turcotte, M., Bossé, Y., Paré, G., & Meyre, D. (2019). Benefits and limitations of genome-wide association studies. *Nature Reviews Genetics*, 20(8), 467–484. <https://doi.org/10.1038/s41576-019-0127-1>
- Teng, Z., Guo, Z., Zhong, J., Cheng, C., Huang, Z., Wu, Y., Tang, S., Luo, C., Peng, X., Wu, H., Sun, X., & Jiang, L. (2017). ApoE Influences the Blood-Brain Barrier Through the NF- κ B/MMP-9 Pathway After Traumatic Brain Injury. *Scientific Reports*, 7(1). <https://doi.org/10.1038/s41598-017-06932-3>
- Tiwari, S., Atluri, V., Kaushik, A., Yndart, A., & Nair, M. (2019). Alzheimer's disease: pathogenesis, diagnostics, and therapeutics. *International Journal of Nanomedicine*, Volume 14, 5541–5554. <https://doi.org/10.2147/ijn.s200490>
- Tokuda, T., Calero, M., Matsubara, E., Vidal, R., Kumar, A., Permanne, B., Zlokovic, B., Smith, J. D., Ladu, M. J., Rostagno, A., Frangione, B., & Ghiso, J. (2000). Lipidation of apolipoprotein E influences its isoform-specific interaction with Alzheimer's amyloid beta peptides. *The Biochemical Journal*, 348 Pt 2(Pt 2), 359–365. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1221074/>
- Turner, S., Armstrong, L. L., Bradford, Y., Carlson, C. S., Crawford, D. C., Crenshaw, A. T., de Andrade, M., Doheny, K. F., Haines, J. L., Hayes, G., Jarvik, G., Jiang, L., Kullo, I. J., Li, R., Ling, H., Manolio, T. A., Matsumoto, M., McCarty, C. A., McDavid, A. N., & Mirel, D. B. (2011). Quality Control Procedures for Genome-Wide Association Studies. *Current Protocols in Human Genetics*, 68(1), 1.19.1–1.19.18. <https://doi.org/10.1002/0471142905.hg0119s68>
- Uffelmann, E., Huang, Q. Q., Munung, N. S., de Vries, J., Okada, Y., Martin, A. R., Martin, H. C., Lappalainen, T., & Posthuma, D. (2021). Genome-wide association studies. *Nature Reviews Methods Primers*, 1(1). <https://doi.org/10.1038/s43586-021-00056-9>
- van Harten, A. C., Jongbloed, W., Teunissen, C. E., Scheltens, P., Veerhuis, R., & van der Flier, W. M. (2017). CSF ApoE predicts clinical progression in nondemented APOE ϵ 4 carriers. *Neurobiology of Aging*, 57, 186–194. <https://doi.org/10.1016/j.neurobiolaging.2017.04.002>
- Vergara, C., Parker, M. M., Franco, L., Cho, M. H., Valencia-Duarte, A. V., Beaty, T. H., & Duggal, P. (2018). Genotype Imputation Performance of Three Reference Panels Using African Ancestry Individuals. *Human Genetics*, 137(4), 281–292. <https://doi.org/10.1007/s00439-018-1881-4>
- Verghese, P. B., Castellano, J. M., Garai, K., Wang, Y., Jiang, H., Shah, A., Bu, G., Frieden, C., & Holtzman, D. M. (2013). ApoE influences amyloid- (A) clearance despite minimal apoE/A association in physiological conditions. *Proceedings of the National Academy of Sciences*, 110(19), E1807–E1816. <https://doi.org/10.1073/pnas.1220484110>
- Visscher, P. M., Wray, N. R., Zhang, Q., Sklar, P., McCarthy, M. I., Brown, M. A., & Yang, J. (2017). 10 Years of GWAS Discovery: Biology, Function, and Translation. *The American Journal of Human Genetics*, 101(1), 5–22. <https://doi.org/10.1016/j.ajhg.2017.06.005>
- Wadhvani, A. R., Affaneh, A., Van Gulden, S., & Kessler, J. A. (2019). Neuronal apolipoprotein E4 increases cell death and phosphorylated tau release in alzheimer disease. *Annals of Neurology*, 85(5), 726–739. <https://doi.org/10.1002/ana.25455>
- Wang, M. H., Cordell, H. J., & Van Steen, K. (2019). Statistical methods for genome-wide association studies. *Seminars in Cancer Biology*, 55, 53–60. <https://doi.org/10.1016/j.semcan.2018.04.008>

- Wang, T., Xue, X., Xie, X., Ye, K., Zhu, X., & Elston, R. C. (2018). Adjustment for Covariates Using Summary Statistics in GWAS analysis. *Genetic Epidemiology*, *42*(8), 812–825. <https://doi.org/10.1002/gepi.22148>
- Wang, Y., Cella, M., Mallinson, K., Ulrich, Jason D., Young, Katherine L., Robinette, Michelle L., Gilfillan, S., Krishnan, Gokul M., Sudhakar, S., Zinselmeier, Bernd H., Holtzman, David M., Cirrito, John R., & Colonna, M. (2015). TREM2 Lipid Sensing Sustains the Microglial Response in an Alzheimer's Disease Model. *Cell*, *160*(6), 1061–1071. <https://doi.org/10.1016/j.cell.2015.01.049>
- Webster, J. A., Gibbs, J. R., Clarke, J., Ray, M., Zhang, W., Holmans, P., Rohrer, K., Zhao, A., Marlowe, L., Kaleem, M., McCorquodale, D. S., Cuello, C., Leung, D., Bryden, L., Nath, P., Zismann, V. L., Joshipura, K., Huentelman, M. J., Hu-Lince, D., & Coon, K. D. (2009). Genetic control of human brain transcript expression in Alzheimer disease. *American Journal of Human Genetics*, *84*(4), 445–458. <https://doi.org/10.1016/j.ajhg.2009.03.011>
- White, M. J., Yaspan, B. L., Veatch, O. J., Goddard, P., Risse-Adams, O. S., & Contreras, M. G. (2019). Strategies for Pathway Analysis using GWAS and WGS Data. *Current Protocols in Human Genetics*, *100*(1), e79. <https://doi.org/10.1002/cphg.79>
- Xu, C., Tachmazidou, I., Walter, K., Ciampi, A., Zeggini, E., & Greenwood, C. M. T. (2014). Estimating Genome-Wide Significance for Whole-Genome Sequencing Studies. *Genetic Epidemiology*, *38*(4), 281–290. <https://doi.org/10.1002/gepi.21797>
- Xue, A., Wu, Y., Zhu, Z., Zhang, F., Kemper, K. E., Zheng, Z., Yengo, L., Lloyd-Jones, L. R., Sidorenko, J., Wu, Y., McRae, A. F., Visscher, P. M., Zeng, J., & Yang, J. (2018). Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes. *Nature Communications*, *9*(1). <https://doi.org/10.1038/s41467-018-04951-w>
- Yamazaki, Y., Painter, M. M., Bu, G., & Kanekiyo, T. (2016). Apolipoprotein E as a Therapeutic Target in Alzheimer's Disease: A Review of Basic Research and Clinical Evidence. *CNS Drugs*, *30*(9), 773–789. <https://doi.org/10.1007/s40263-016-0361-4>
- Zhao, Y., Wu, X., Li, X., Jiang, L.-L., Gui, X., Liu, Y., Sun, Y., Zhu, B., Piña-Crespo, J. C., Zhang, M., Zhang, N., Chen, X., Bu, G., An, Z., Huang, T. Y., & Xu, H. (2018). TREM2 Is a Receptor for β -Amyloid that Mediates Microglial Function. *Neuron*, *97*(5), 1023-1031.e7. <https://doi.org/10.1016/j.neuron.2018.01.031>
- Zhou, Q., Zhao, F., Lv, Z., Zheng, C., Zheng, W., Sun, L., Wang, N., Pang, S., de Andrade, F. M., Fu, M., He, X., Hui, J., Jiang, W., Yang, C., Shi, X., Zhu, X., Pang, G., Yang, Y., Xie, H., & Zhang, W. (2014). Association between APOC1 Polymorphism and Alzheimer's Disease: A Case-Control Study and Meta-Analysis. *PLoS ONE*, *9*(1), e87017. <https://doi.org/10.1371/journal.pone.0087017>