RSF Summer Institute in Social Science Genomics 2021 Reading List

Note: Readings in brackets are optional.

Topic: Using Genetic Data in Sociology

Conley, D. and Rauscher, E. (2012). “Genetic Interactions with Prenatal Social Environment: Effects on Academic and Behavioral Outcomes.” *Journal of Health and Social Behavior* 54(1).

Conley, D., Rauscher, E., Dawes, C., Magnusson P.K.E. and Siegel, M.L. (2013). “Heritability and the Equal Environments Assumption: Evidence from Multiple Samples of Misclassified Twins.” *Behavior Genetics* 43(4).

Guo, G., Fu Y., Lee, H., Cai, T. et al. (2014). “Genetic Bio-Ancestry and Social Construction of Racial Classification in Social Surveys in the Contemporary United States.” *Demography* 51(1).

Laidley, T., Domingue, B., Sinsub, P., Harris, K.M. and Conley, D., 2019. ”New evidence of skin color bias and health outcomes using sibling difference models: a research note.” *Demography*, *56*(2), pp.753-762.

Sotoudeh, R., Harris, K. M., & Conley, D. (2019). “Effects of the peer metagenomic environment on smoking behavior.” *Proceedings of the National Academy of Sciences*, *116*(33), 16302-16307.

Topic: Heritability

Falconer, D. S., & Mackay, T. F. C. (1996). “Introduction to quantitative genetics.” Essex. *UK: Longman Group*. Chapter 6. Continuous Variation.

Goldberger, A.S. (2005). “Structural Equation Models in Human Behavior Genetics.” *Identification and Inference for Econometric Models Essays in Honor of Thomas Rothenberg*, eds. DW Andrews and JS Stock. Cambridge: Cambridge University Press, 11–26.

Lynch, M., & Walsh, B. (1998). “Genetics and analysis of quantitative traits.” Chapter 4. Properties of Single Loci.

Lynch, M., & Walsh, B. (1998). “Genetics and analysis of quantitative traits.” Chapter 7. Resemblance Between Relatives.

Lynch, M., & Walsh, B. (1998). “Genetics and analysis of quantitative traits.” Chapter 19. Twins and Clones.

Polderman, T.J.C., Benyamin, B, de Leeuw, C.A, Sullivan, P.F. et al. (2015). “Meta-analysis of the heritability of human traits based on fifty years of twin studies.” *Nature Genetics* 47 (7).

Sacerdote, B. (2011). “Nature and Nurture Effects On Children’s Outcomes: What Have We Learned From Studies of Twins And Adoptees?” *Handbook of Social Economics*, Chapter 1.

Turkheimer, E. (2000). “Three laws of behavior genetics and what they mean.” *Current directions in psychological science*, *9*(5), 160-164.

[Goldberger, A.S. (1979). “Heritability.” *Economica* 46 (184).]

[Goldberger, A.S. (1991). “Expectations: Bivariate Case.” *A Course in Econometrics.* Cambridge, MA: Harvard University Press, 45-57.]

[Goldberger, A.S. (2002). “Structural Equation Models in Human Behavior Genetics.” Working paper.]

[Hill, W.G., Goddard, M.E., and Visscher, P.M. (2008). “Data and Theory Point to Mainly Additive Genetic Variance for Complex Traits.” *PLoS Genetics*, 4(2): e1000008.]

[Jencks, C. (1980). “Heredity, Environment, and Public Policy Reconsidered.” *American Sociological Review* 45 (5).]

Topic: Using Genetic Data in Psychology

Harden, K. P. (2021). “”Reports of my death were greatly exaggerated”: Behavior genetics in the postgenomic era.” *Annual Review of Psychology*, *72*, 37-60.

Topic: Molecular Genetics

[Strachan, T., A. Read, and T. Strachan. (2011). "Human molecular genetics. 4th." *New York: Garland Science*.]
Note: Reference book – not available in list of pdfs, but will be available to borrow at the Summer Institute

Topic: Social and Ethical Implications of Social-Science Genomics

Martschenko, Daphne, Sam Trejo, and Benjamin W. Domingue (2019). “Genetics and Education: Recent Developments in the Context of an Ugly History and an Uncertain Future.” *AERA Open*, 5(1), 1–15.

Martschenko, Daphne (2020). "DNA Dreams': Teacher Perspectives on the Role and Relevance of Genetics for Education." *Research in Education*, 107(1), 33–54.

Martschenko, Daphne, and Markia Smith (2021). "Genes do not operate in a vacuum, and neither should our research." *Nature Genetics*, 53, 255–256.

Topic: Gene Discovery I: Power, Candidate Genes, GWAS

Chabris, C. F., et al. (2012). "Most Reported Genetic Associations with General Intelligence Are Probably False Positives." *Psychological Science*, 23(11), 1314–1323. doi:10.1177/0956797611435528.

Rietveld, C. A., Conley, D., Eriksson, N, Esko, T. et al. (2014). "Replicability and Robustness of Genome-Wide Association Studies for Behavioral Traits." *Psychological Science* 25 (11).

Rietveld, C. A., Conley, D., Eriksson, N, Esko, T. et al. (2014). "Replicability and Robustness of Genome-Wide Association Studies for Behavioral Traits, Supplemental Material." *Psychological Science* 25 (11).

Bayarri, M. J., Benjamin, D., Berger, J. O., and Sellke, T. M. (2016). "Rejection Odds and Rejection Ratios: A Proposal for Statistical Practice in Testing Hypotheses." *Journal of Mathematical Psychology*.

Lee, J. J., Wedow, R., Okbay, A. et al. (2018). "Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals." *Nature Genetics*, 50, 1112-1121.

Lee, J. J., Wedow, R., Okbay, A. et al. (2018). "Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals (Supplementary Information)." *Nature Genetics*, 50, 1112-1121.

Mills, M. C., Barban, N., & Tropf, F. C. (2020). "An introduction to statistical genetic data analysis." *MIT Press.*
Note: Reference book – not available in list of pdfs.

[Okbay, A et al. (2016). "Genome-wide association study identifies 74 loci associated with educational attainment." *Nature*. Published online May 11.doi:10.1038/nature17671.]

[Okbay, A et al (2016). "Genetic variants associated with subjective well-being, depressive symptoms and neuroticism identified through genome-wide analyses." *Nature Genetics*. Published online April 18.]

[Evangelou, E. and Ioannidis, J. P. A. (2013). “Meta-analysis methods for genome-wide association studies and beyond.” *Nature Reviews Genetics* 14.]

[Price, A.L, Zaitlen, N.A., Reich, D. and Patterson, N. (2010). “New approaches to population stratification in genome-wide association studies.” *Nature Reviews Genetics* 11.]

[Sham, P. C. and Purcell, S. M. (2014). “Statistical power and significance testing in large-scale genetics studies.” *Nature Reviews Genetics* 15.]

[Visscher, P. M., Wray, N.R., Zhang, Q. et al. (2017). “10 Years of GWAS Discovery: Biology, Function and Translation.” *American Journal of Human Genetics*, 101:5-22. https://doi.org/10.1016/j.ajhg.2017.06.005.]

[Mills, M.C. and Rahal, C. (2019). “A scientometric review of genome-wide association studies.” *Communications Biology,* 2(9).]

Topic: Gene Discovery II: Winner’s Curse and Stratification

Gelman, A., and Carlin, J. (2014). “Beyond Power Calculations: Assessing Type S (Sign) and Type M (Magnitude) Errors.” *Perspectives on Psychological Science*, 9(6).

Lee, J. J., Wedow, R., Okbay, A. et al. (2018). “Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals (Supplementary Information, **Section 2.4-2.6**).” *Nature Genetics*, 50, 1112-1121.

[Abdellaoui, A., Hugh-Jones, D., Yengo, L., Kemper, K. E., Nivard, M. G., Veul, L., ... & Visscher, P. M. (2019). “Genetic correlates of social stratification in Great Britain.” *Nature human behaviour*, *3*(12), 1332-1342.]

[Rietveld, C. A., Esko, T., Davies, G., Pers, et al. (2014). “Common genetic variants associated with cognitive performance identified using the proxy-phenotype method.” *PNAS*, 111(38). Supplemental Section 8 (“Correction of Effect Sizes for Winner’s Curse”).]

[Hamer, D. H. and Sirota, L. (2000). “Beware the chopsticks gene.” *Molecular Psychiatry* 5.]

[Novembre, J., Johnson, T., Bryc, K., Kutalik, Z et al. (2008). “Genes mirror geography within Europe.” *Nature* 456(7218).]

[Sohail, M., Maier, R.M., Ganna, A., Bloemendal, A., Martin, A.R., Turchin, M.C. et al. (2019). "Polygenic adaptation on height is overestimated due to uncorrected stratification in genome-wide association studies." *eLife,* 8. DOI: 10.7554/eLife.39702.]

[Berg, J. J., Harpak, A. H., Sinnott-Armstrong, N. et al. (2019). “Reduced signal for polygenic adaptation of height in UK Biobank.” *eLife*, 8. DOI: 10.7554/eLife.39725.]

Topic: Quality Control of Genomic Data

Okbay, A., Beauchamp, J. P., Fontana, M. A., Lee, et al. (2016). “Genome-wide association study identifies 74 loci associated with educational attainment.” *Nature*. Supplemental Section 1.5 (“Quality Control”).

Winkler, T. W., et al. (2014). “Quality control and conduct of genome-wide association meta-analyses.” *Nature Protocols*, 9(5): 1192–1212.

[Deelen, P., Bonder, M. J., van der Velde, K. J., Westra, H. J., Winder, E., Hendriksen, D., ... & Swertz, M. A. (2014). “Genotype harmonizer: automatic strand alignment and format conversion for genotype data integration.” *BMC research notes*, *7*(1), 1-4.]

[Marchini, J., & Howie, B. (2010). “Genotype imputation for genome-wide association studies.” *Nature Reviews Genetics*, *11*(7), 499-511.]

Topic: LD Score Regression and Stratification

Bulik-Sullivan, B., Loh, P, Finucane H.K., Ripke, S. et al. (2015). “LD Score regression distinguishes confounding from polygenicity in genome-wide association studies.” *Nature Genetics* 47(3).

Lee, J. J., Wedow, R., Okbay, A. et al. (2018). “Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals.” *Nature Genetics*, 50, 1112-1121. **Supplementary Information, Section 2**.

Evans, L. M., Tahmasbi, R., Vrieze, S. I. et al. (2018). “Comparison of methods that use whole genome data to estimate the heritability and genetic architecture of complex traits.” *Nature Genetics*, 50, 737-745. **Table 1**.

[Evans, L. M., Tahmasbi, R., Vrieze, S. I. et al. (2018). “Comparison of methods that use whole genome data to estimate the heritability and genetic architecture of complex traits.” *Nature Genetics*, 50, 737-745.]

[Loh, P., Tucker, G., Bulik-Sullivan, B., VIljalmas, et al. (2015). “Efficient Bayesian mixed-model analysis increases association power in large cohorts.” *Nature Genetics* 47(3).]

[Price, A. L., Patterson, N. J., Plenge, R. M., Weinblatt, M.E. (2006). “Principal components analysis corrects for stratification in genome-wide association studies.” *Nature Genetics* 38(8).]

[Yang, J., Zaitlen, N. A., Goddard, M. E., Visscher, P. M., & Price, A. L. (2014). “Advantages and pitfalls in the application of mixed-model association methods.” *Nature Genetics* 46(2).]

[Lee, J. J., McGue, M., Iacono, W. G., and Chow, C. C. (2018). "The accuracy of LD Score regression as an estimator of confounding and genetic correlations in genome-wide association studies." *Genetic Epidemiology*, 42(8).]

Topic: Genetic Correlation and Partitioning

Bulik-Sullivan, B., Finucane, H. K., Anttila, Y., Gusev, A., et al. (2015). “An atlas of genetic correlations across human diseases and traits.” *Nature Genetics* 47(11).

Finucane, H. K., Bulik-Sullivan, B, Gusev, A., Trynka, G. et al. (2015). “Partitioning heritability by functional annotation using genome-wide association summary statistics.” *Nature Genetics* 47(11).

Okbay, A., Beauchamp, J. P., Fontana, M. A., Lee, et al. (2016). “Genome-wide association study identifies 74 loci associated with educational attainment.” *Nature*. Supplemental Section 3 (“Genetic Overlap”).

Neale Lab blog posts: http://www.nealelab.is/blog

[Lee, S. H., Yang, J., Goddard, M. E., VIsscher, P. M. and Wray N.R. (2012). “Estimation of pleiotropy between complex diseases using SNP-derived genomic relationships and restricted maximum likelihood.” *Bioinformatics* 28(19).]

[Yang, J., Manolio, T. A., Pasquale, L. R., Boerwinkle, E. et al. (2011). “Genome partitioning of genetic variation for complex traits using common SNPs.” *Nature Genetics* 43(6).]

[Gazal, S., Loh, P. R., Finucane, H. K., Ganna, A., Schoech, A., Sunyaev, S. et al. (2018). "Functional architecture of low-frequency variants highlights strength of negative selection across coding and non-coding annotations." *Nature Genetics*, 50.]

[Gazal, S., Marquez-Luna, C., Finucane, H.K. and Price, A.L. (2018). "Reconciling S-LDSC and LDAK models and functional enrichment estimates." *bioRxiv*, https://doi.org/10.1101/256412.]

[Brown, B. C., Asian Genetic Epidemiology Network Type 2 Diabetes Consortium, Ye, C. J., Price, A. L. and Zaitlen, N. (2016). "Transethnic Genetic-Correlation Estimates from Summary Statistics." *American Journal of Human Genetics*, 99(1).]

[van Reenan, W., Peyrot, W.J., et al. (2019). "Genetic correlations of polygenic disease traits-from theory to practice." *Nature Reviews.*]

Topic: Responsibly Communicating Social-Science Genomics

FAQs for: Becker et al. (2021), "Resource profile and user guide of the Polygenic Index Repository." *Nature Human Behavior* (in press), available at https://www.biorxiv.org/content/biorxiv/early/2021/05/10/2021.05.08.443158/DC5/embed/media-5.pdf?download=true.

- Skim the whole thing to get a sense of the content and structure, but carefully read FAQs 1.4–1.6 & 3.1–3.7

FAQs for: Turley et al. (2021), "Multi-ancestry meta-analysis yields novel genetic discoveries and ancestry-specific associations." *bioRxiv,* available at https://www.biorxiv.org/content/biorxiv/early/2021/04/24/2021.04.23.441003/DC1/embed/media-1.pdf?download=true.

- Skim the whole thing to get a sense of the content and structure, but carefully read FAQs 2.6–2.9, 4.3 & 5.1–5.7

Broad Communications, "Perspectives on the complex genetics of same-sex sexual behavior." a Broad Institute website devoted to discussion of Ganna et al. (2019), "Large-scale GWAS reveals insights into the genetic architecture of same-sex sexual behavior." *Science*, https://www.broadinstitute.org/news/perspectives-complex-genetics-same-sex-sexual-behavior.

- Read the webpage and at least a few of the critical "Broadminded blog" commentaries on the study linked at the bottom (and also in the right-hand side bar)
- In the right-hand side bar, view at least a few of the 5 brief videos by senior author Ben Neale
- In the right-hand side bar, click the link to a separate website (https://geneticsexbehavior.info) devoted to the study; browse the FAQs there and watch the animated video

Browse the Hastings Center repository of FAQs for a variety of social-science genomics studies and read at least one of relevance to you (e.g., a study of a phenotype you're interested in): https://www.thehastingscenter.org/genomics-research-index/

Turley et al. (2021), "Challenges with embryo selection using polygenic scores." *New England Journal of Medicine* (in press)

[Nuffield Council on Bioethics, *Genetics and Human Behavior: The Ethical Context* (2002)
- Summary and Recommendations, pp. xix–xxxiii
- Ch. 2, Historical Context, pp. 13-22
- Ch. 12: Determinism, pp. 121-130
- Ch. 13: Selecting & Changing Behavioural Traits, pp. 133-156
- Ch. 14: Legal Responsibility, pp. 149-171
- Ch. 15: Testing & Selection in Employment, Education, & Insurance, pp. 175-188]

[Nature editorial, "Dangerous Work." *Nature* 502: 5-6 (Oct. 3, 2013), http://www.nature.com/polopoly_fs/1.13861!/menu/main/topColumns/topLeftColumn/pdf/502005b.pdf.]

[Hayden, E. C. (2013). "Ethics: Taboo genetics." *Nature News*, *502*(7469), 26. Available at http://www.nature.com/news/ethics-taboo-genetics-1.13858.]

[Selections from Special Report, "The Genetics of Intelligence: Ethics and the Conduct of Trustworthy Research." *Hastings Center Report* 45(S1): S2-S72, (Sept.-Oct. 2015, Erik Parens & Paul S. Appelbaum eds.). https://onlinelibrary.wiley.com/toc/1552146x/45/S1]

Parens, E., & Appelbaum, P. S. (2015). "An introduction to thinking about trustworthy research into the genetics of intelligence."

Tabery, J. (2015). "Why is studying the genetics of intelligence so controversial?."

Hansen, E. T., Gluck, S., & Shelton, A. L. (2015). "Obligations and Concerns of an Organization Like the Center for Talented Youth." *Hastings Center Report*, *45*(S1), S66-S72.

Topic: Polygenic Indices

Daetwyler, H.D., Villaneuva, B., and Woolliams, J.A. (2008). "Accuracy of Predicting the Genetic Risk of Disease Using a Genome-Wide Approach." *PLoS One* 3(10).

Vilhjálmsson, B.J., Yang J., Finucane, H.K., Gusev, A. et al. (2015). "Modeling linkage disequilibrium increases accuracy of polygenic risk scores." *The American Journal of Human Genetics* 97(4).

Martin, A.R., Kanai, M. et al. (2019). "Clinical use of current polygenic risk scores may exacerbate health disparities." *Nature Genetics* (51), pp. 584-591.

Mostafavi, H., Harpak, A., Agarwal, I., Conley, D., Pritchard, J. K., & Przeworski, M. (2020). “Variable prediction accuracy of polygenic scores within an ancestry group.” *Elife*, *9*, e48376.

Lee, J.J., Wedow, R., Okbay, A. et al. (2018). “Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals.” *Nature Genetics*, 50, 1112-1121. **Supplementary Information, Section 6**.

de Vlaming, R., Okbay, A. Rietveld, C.A. et al. (2017). “Meta-GWAS Accuracy and power calculator shows that hiding heritability is partially due to imperfect genetic correlations across studies.” *PLOS Genetics*, 13(1): e1006495.

[Dudbridge, F. (2013). "Power and predictive accuracy of polygenic risk scores." *PLoS Genet* 9(3).]

[Ge, T., Chen, C., Ni, Y. et al. (2019). “Polygenic prediction via Bayesian regression and continuous shrinkage priors.” *Nature Communications* 10(1776).]

[Lloyd-Jones, L. R., Zeng, J., Sidorenko, J., Yengo, L., Moser, G., Kemper, K. E., ... & Visscher, P. M. (2019). “Improved polygenic prediction by Bayesian multiple regression on summary statistics.” *Nature communications*, *10*(1), 1-11.]

[Wray, N. R., Yang, J., Hayes, B. J, Price, A. L. et al. (2013). “Pitfalls of predicting complex traits from SNPs.” *Nature Reviews Genetics* 14.]

Topic: Population Genetics

Lee, J.J. (2019). “Psychology 5135: Class Notes on Genetics.” Sections 1 and 4.

[Kondrashov, Alexey S. (2018). “Through Sex, Nature Is Telling Us Something Important.” *Trends in Genetics*, 34(5), 352-361.]

[Sella, Guy, and Nicholas H. Barton (2019). “Thinking About the Evolution of Complex Traits in the Era of Genome-Wide Association Studies.” *Annual Review of Genomics and Human Genetics*, 20, 461–93.]

[Zeng, Jian (2021). “Widespread signatures of natural selection across human complex traits and functional genomic categories.” *Nature Communications*, 12, 1164.]

Diverse Ancestry, Admixed Populations, and Eurocentric Bias

Popejoy, A. B., & Fullerton, S. M. (2016). “Genomics is failing on diversity.” *Nature News*, *538*(7624), 161.

Peterson, R. E., Kuchenbaecker, K., Walters, R. K., Chen, C. Y., Popejoy, A. B., Periyasamy, S., ... & Duncan, L. E. (2019). “Genome-wide association studies in ancestrally diverse populations: opportunities, methods, pitfalls, and recommendations.” *Cell*, *179*(3), 589-603.

Martin, A. R., Kanai, M., Kamatani, Y., Okada, Y., Neale, B. M., & Daly, M. J. (2019). “Clinical use of current polygenic risk scores may exacerbate health disparities.” *Nature genetics*, *51*(4), 584-591.

[Atkinson, E. G., Maihofer, A. X., Kanai, M., Martin, A. R., Karczewski, K. J., Santoro, M. L., ... & Neale, B. M. (2021). “Tractor uses local ancestry to enable the inclusion of admixed individuals in GWAS and to boost power.” *Nature Genetics*, *53*(2), 195-204.]

Topic: Assortative Mating

Yengo et al. (2018). “Imprint of Assortative Mating on the Human Genome.” *Nature Human Behavior*. 2: 948-954.

Robinson et al. (2017). “Genetic Evidence of Assortative Mating in Humans.” *Nature Human Behavior*. 1:0016.

Nordsletten et al. (2016). “Patterns of Nonrandom Mating Within and Across 11 Major Psychiatric Disorders.” *JAMA Psychiatry* 73(4):354-61.

[Tenesa et al. (2015). “Genetic determination of height-mediated mate choice.” *Genome Biology*: 16:269.]

[Crow J. F., and Kimura M. (2011). “Correlation between relatives and assortative mating.” *An Introduction to Population Genetics Theory*, Chapter 4.]

[Border, R., O’Rourke, S., de Candia, T., Goddard, M. E., Visscher, P. M., Yengo, L., ... & Keller, M. C. (2021). “Assortative mating biases marker-based heritability estimators.” *bioRxiv*.]

Topic: Gene-Environment Interactions

Duncan, L.E., and Keller, M.C. (2011). "A critical review of the first 10 years of candidate gene-by-environment interaction research in psychiatry." *American Journal of Psychiatry* 168 (10).

Keller, M.C. (2013). "Gene × environment interaction studies have not properly controlled for potential confounders: the problem and the (simple) solution." *Biological Psychiatry* 75 (1).

Schmitz, L., & Conley, D. (2017). "Modeling gene-environment interactions with quasi-natural experiments." *Journal of personality*, *85*(1), 10-21.

[Barcellos, S. H., Carvalho, L., & Turley, P. (2021). "The Effect of Education on the Relationship between Genetics, Early-Life Disadvantages, and Later-Life SES (No. w28750)." *National Bureau of Economic Research*.]

[Caspi A., McClay, J., Moffitt, T.E., Mill, J. et al. (2002). "Role of genotype in the cycle of violence in maltreated children." *Science* 297 (5582).]

[Caspi, A, Sugden, K., Moffitt T.E., Taylor A., et al. (2003). "Influence of life stress on depression: moderation by a polymorphism in the 5-HTT gene." *Science* 301 (5631).]

[Dick, D.M., Agrawal, A. Keller, M.C., Adkins A., et al. (2015). "Candidate gene–environment interaction research reflections and recommendations." *Perspectives on Psychological Science* 10 (1).]

[Lee, J.J., Wedow, R., Okbay, A. et al. (2018). "Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals." *Nature Genetics*, 50, 1112-1121. **Supplementary Information, Section 3**.]

Topic: Gene-Environment Correlation and Genetic Nurture

Young, A. "Heritability estimation: what is heritability?" https://geneticvariance.wordpress.com/2017/09/28/heritability-estimation-what-is-heritability-i/.

Young, A. "Heritability estimation: the central problem" https://geneticvariance.wordpress.com/2017/10/09/heritability-estimation-the-central-problem-ii/.

[Young, A. "Relatedness disequilibrium regression explained" https://geneticvariance.wordpress.com/2018/08/13/relatedness-disequilibrium-regression-explained/.]

Young, A. (2018). "Relatedness disequilibrium regression estimates heritability without environmental bias." *Nature Genetics* 50 (9), 1304-1310.

[Kong, A. Thorleifsson, G., Frigge, M.L. et al. (2018). “The nature of nurture: Effects of parental genotypes.” *Science* 359, 424-428.]

[Young, A. I. (2019). “Solving the missing heritability problem.” *PLoS genetics*, *15*(6), e1008222.]

[Young, A. I., Benonisdottir, S., Przeworski, M., & Kong, A. (2019). “Deconstructing the sources of genotype-phenotype associations in humans.” *Science*, *365*(6460), 1396-1400.]

Topic: Mendelian Randomization

Davies, N. M., Holmes, M. V., & Smith, G. D. (2018). “Reading Mendelian randomisation studies: a guide, glossary, and checklist for clinicians.” *Bmj*, *362*.

Pingault, J.B., O’Reilly, P.F., Schoeler, T., Ploubidis, G.B., Rijsdijk, F. and Dudbridge, F. (2018). “Using genetic data to strengthen causal inference in observational research.” *Nature Reviews Genetics*, p.1.

Bowden, J., Davey Smith, G., and Burgess, S. (2015). "Mendelian randomization with invalid instruments: effect estimation and bias detection through Egger regression." *International Journal of Epidemiology* 44:2, 512-525.

[Scholder, S.V.H.K., Smith G.D., Lawlor, D.A., Propper, C. et al. (2015). "Genetic markers as instrumental variables." *Journal of Health Economics* 45, 131-148.]

[Tyrrell, Jessica, et al. (2016) "Height, body mass index, and socioeconomic status: Mendelian randomisation study in UK Biobank." *British Medical Journal* 352: i582.]

[O’Connor, L.J. and Price, A.L. (2018). “Distinguishing genetic correlation from causation across 52 diseases and complex traits.” *Nature Genetics* 50, 1728-1734.]

[Verbanck M., Chen C. Y., Neale B. and Do R. (2018). “Detection of widespread horizontal pleiotropy in causal relationships inferred from Mendelian randomization between complex traits and diseases.” *Nature Genetics* 50(5), 693-698.]

Topic: Epigenetics and Social Science

Zimmer, Carl. “Growing Pains for Field of Epigenetics as Some Call for Overhaul.” *NY Times*. July 1, 2016. https://www.nytimes.com/2016/07/02/science/epigenetic-marks-dna-genes.html?action=click&module=RelatedLinks&pgtype=Article.

Carey, Benedict. “Can We Really Inherit Trauma?” *NY Times*. December 10, 2018. https://www.nytimes.com/2018/12/10/health/mind-epigenetics-genes.html.

Birney E, Smith GD, Greally JM (2016). “Epigenome-wide Association Studies and the Interpretation of Disease -Omics.” *PLoS Genetics* 12(6): e1006105.

van Otterdijk, S. D., and Michels, K. B. (2016). “Transgenerational epigenetic inheritance in mammals: how good is the evidence?” *The FASEB Journal*, 30(7), 2457-2465.

Hüls, A., & Czamara, D. (2020). “Methodological challenges in constructing DNA methylation risk scores.” *Epigenetics*, 15(1-2), 1-11.

Evans, L., Engelman, M., Mikulas, A., & Malecki, K. (2021). “How are social determinants of health integrated into epigenetic research? A systematic review*.” Social Science & Medicine*, 113738.

Horvath, S., and Raj, K. (2018). “DNA methylation-based biomarkers and the epigenetic clock theory of ageing.” *Nature Reviews Genetics*, 19: 371-384. **[students: please read to the top of page 376.]

[Heard, E., and Martienssen, R. A. (2014). “Transgenerational epigenetic inheritance: Myths and mechanisms.” *Cell*, 157(1), 95–109.]

[Heijmans, B. T. and Mill J. (2012). “Commentary: The seven plagues of epigenetic epidemiology.” *International Journal of Epidemiology* 41(1), 74-78.]

[Horsthemke, B. (2010). Epigenetics. In F. Vogel, A. G. Motulsky, M. R. Speicher, & S. E. Antonarakis, “Human Genetics: Problems and Approaches” (pp. 299–318). Berlin, Germany: Springer.]

[Bell, C. G., Lowe, R., Adams, P. D., Baccarelli, A. A., Beck, S., Bell, J. T., ... & Rakyan, V. K. (2019). “DNA methylation aging clocks: challenges and recommendations.” *Genome Biology*, 20(1), 1-24.]

[Field, A. E., Robertson, N. A., Wang, T., Havas, A., Ideker, T., & Adams, P. D. (2018). “DNA methylation clocks in aging: categories, causes, and consequences.” *Molecular Cell*, 71(6), 882-895.]

Topic: Genomic Structural Equation Modeling

Grotzinger A. D., Rhemtulla M., de Valming R., Ritchie, S. J., Mallard, T. T., Hill W. D., Ip, H. F., Marioni, R. E., McIntosh, A. M., Deary, I. J., Koellinger, P. D., Harden, K. P., Nivard, M. G. and Tucker-Drob, E. M. (2019). “Genomic structural equation modelling provides insights into the multivariate genetic architecture of complex traits." *Nature Human Behaviour* 3*,* 513–525.

Grotzinger, A. D., Mallard, T. T., Akingbuwa, W. A., Ip, H. F., Adams, M. J., Lewis, C. M., ... & Schizophrenia Working Group of the Psychiatric Genetics Consortium. (2020). "Genetic architecture of 11 major psychiatric disorders at biobehavioral, functional genomic, and molecular genetic levels of analysis." medRxiv.

Boker, S. M., & McArdle, J. J. (2005). "Path analysis and path diagrams." *Encyclopedia of statistics in behavioral science*.

[McArdle, J. J., & Kadlec, K. M. (2013). "Structural equation models." *The Oxford handbook of quantitative methods*, *2*, 295-337.]

[Rodgers, J. L. (2010). "The epistemology of mathematical and statistical modeling: a quiet methodological revolution." *American Psychologist*, *65*(1), 1.]

Topic: Applications in Social Science

Barth, D., Papageorge, N. W., & Thom, K. (2017). "Genetic ability, wealth, and financial decision-making." IZA Discussion Paper No. 10567, Available at SSRN: https://ssrn.com/abstract=2923653

Barcellos, S.H., Carvalho, L, and Turley, P.T. (2018). "Education can reduce health differences related to genetic risk of obesity." *PNAS,* 115(42), E9765-E9772.

DiPrete, T.A., Burik, C.A.P. and Koellinger, P.D. (2018). "Genetic instrumental variable regression: Explaining socioeconomic and health outcomes in nonexperimental data." *PNAS,* 115 (22) E4970-E4979.

DiPrete, T.A., Burik, C.A.P. and Koellinger, P.D. (2018). "Genetic instrumental variable regression: Explaining socioeconomic and health outcomes in nonexperimental data (Supporting Information)." *PNAS,* 115 (22) E4970-E4979.

Rietveld, C. A., Medland, S.E., Derringer, J., Yang, J. et al. (2013). "GWAS of 126,559 individuals identifies genetic variants associated with educational attainment." *Science*, 340(6139). **Supplemental Section 8** ("Using a polygenic score as a control variable in a randomized experiment").

[Belsky D. W., Domingue B. D., Weedow R., Arseneault L., Boardman J., Caspi A., Conley D. C., Fletcher J., Freese J., Herd P., Moffitt T. E., Poulton R., Sicinski K., Wertz J. and Harris K. M. (2018). "Genetic analysis of social-class mobility in five longitudinal studies." *Proceedings of the National Academy of Sciences*, 115(31):E7275-E7284.]

[Belsky D. W., Moffitt T. E., Corcoran D. L., Domingue B., Harrington H. L., Hogan S., Houts R., Ramrakha S., Sugden K., Williams B., Poulton R. and Caspi A. (2016). “The genetics of success: How SNPs associated with educational attainment relate to life course development.” *Psychological Science* 27(7): 957-972.]

[Benjamin, D.J., Cesarini, D., van der Loos, M.J.H., Dawes, C.T., et al. (2012). “The genetic architecture of economic and political preferences.” *PNAS,* 109 (21).]

[Biroli, P. (2015). “Genetic and Economic Interaction in Health Formation: The Case of Obesity.” https://sites.google.com/site/pietrobiroli/research (second link in Working Papers).]

[Cesarini, D., Johannesson, M, and Oskarsson, S. (2014). “Pre-Birth Factors, Post-Birth Factors, and Voting: Evidence from Swedish Adoption Data.” *American Political Science Review* 108 (1).]

[Houmark, M. A., Ronda, V., & Rosholm, M. (2020). “The Nurture of Nature and the Nature of Nurture: How Genes and Investments Interact in the Formation of Skills (No. 13780).” IZA Discussion Paper No. 13780, Available at SSRN: https://papers.ssrn.com/sol3/papers.cfm?abstract_id=3708642]

[Papageorge, N. W., & Thom, K. (2020). “Genes, education, and labor market outcomes: evidence from the health and retirement study.” *Journal of the European Economic Association*, *18*(3), 1351-1399.]

[Sanz-de-Galdeano, A., & Terskaya, A. (2019). “Sibling Differences in Educational Polygenic Scores: How Do Parents React?”. IZA Discussion Paper No. 12375, Available at SSRN: https://papers.ssrn.com/sol3/papers.cfm?abstract_id=3401143]

Topic: Computing in Social Science Genomics

“Introduction to the Linux Command Line.” https://cscar.research.umich.edu/wp-content/uploads/sites/5/2016/09/Intro-to-Command-Line.pdf .

“ldsc wiki.” https://github.com/bulik/ldsc/wiki .

"ldpred wiki" https://github.com/bvilhjal/ldpred/wiki/Q-and-A .

[Gentzkow, M. and Shapiro, J. (2014). “Code and Data for the Social Sciences: A Practitioner’s Guide,” University of Chicago mimeo, http://web.stanford.edu/~gentzkow/research/CodeAndData.pdf]