

## **RSF Summer Institute in Social Science Genomics 2019 Reading List**

Note: Readings in brackets are optional.

### **Topic: Using Genetic Data in Psychology**

Plomin, R., DeFries, J.C., Knopik, V.S., and Neiderhiser, J.M. (2016). "Top 10 replicated findings from behavioral genetics," *Perspectives on Psychological Science* 11 (1).

Belsky, D.W., & Harden, K.P. (2019). "Phenotypic annotation: using polygenic scores to translate discoveries from genome-wide association studies from the top down," *Current Directions in Psychological Science*. Advance online publication.  
<https://doi.org/10.1177%2F0963721418807729>

McIntosh, A.M., Sullivan, P.F., & Lewis, C.M. (2019). "Uncovering the architecture of major depression," *Neuron* 102.

Reimers, M.A, Craver, C., Dozmorov, M., Bacanu, S., & Kendler, K.S. (2019). "The coherence problem: Finding meaning in GWAS complexity," *Behavior Genetics* 49 (2).

[Turkheimer, E. (2011). "Genetics and Human Agency: Comment on Dar-Nimrod and Heine (2011)," *Psychological Bulletin* 137 (5).]

[selection from Meehl, P. (1978). "Theoretical risks and tabular asterisks: Sir Karl, Sir Ronald, and the slow progress of soft psychology." *Journal of Consulting and Clinical Psychology* 46, pp. 808-813.]

[Freese, J. (2008). "Genetics and the social science explanation of individual outcomes," *American Journal of Sociology* 114 Suppl.: S1-S35]

[Harden, K.P. (2014). "Genetic influences on adolescent sexual behavior: Why genes matter for environmentally oriented researchers," *Psychological Bulletin* 140 (2).

\*\*This paper includes references to candidate gene research that is now known to be incorrect. The recommended section begins on p. 447 (heading: Implications of Genetic Influences) through the conclusion on p. 455]

### **Topic: Using Genetic Data in Sociology**

Conley, D. and Domingue, B. (2016). "The Bell Curve Revisited: Testing Controversial Hypotheses with Molecular Genetic Data," *Sociological Science* 3, 520–539.

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).

Sotoudeh, R., Harris, K.M. and Conley, D. (2019). "Metagenomic effects in human behavior: The case of adolescent smoking," to appear in *PNAS*.

Sotoudeh, R., Harris, K.M. and Conley, D. (2019). "Metagenomic effects in human behavior: The case of adolescent smoking (Supplementary Information)," to appear in *PNAS*.

### **Topic: Heritability**

Falconer, D. and T Mackay. (1996). "Continuous Variation." *Introduction to Quantitative Genetics*, 4th ed. Harlow, Essex: Longman Group Ltd, 101-107.

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.

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 year 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.

[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).]

[Kwan, JS, S Purcell, and PC Sham. (2007). "Introduction to Biometrical Genetics." *Statistical Genetics: Gene Mapping through Linkage and Association*, eds. BN Neale, MA Ferreira, SE Medland, and D Posthuma. Taylor & Francis Group, 17–42.]

### **Topic: Molecular Genetics**

[Strachan, T. and Read, A. (2011). *Human Molecular Genetics*, 4<sup>th</sup> Ed.]  
*Note: Reference book – not available in list of pdfs, but will be available to borrow at the Summer Institute*

### **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.

[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.]
- [Rietveld, C. A., Esko, T., Davies, G., Pers, et al. (2014). “Common Genetic Variants Associated with Cognitive Performance Identified Using Proxy-Phenotype Method.” *PNAS*, 111(38), 13790-4. Published online September 8. doi: 10.1073/pnas.1404623111]
- [Rietveld, C. A., Medland, S. E., Derringer, J. et al. (2013). “GWAS of 126,559 individuals identifies genetic variants associated with educational attainment.” *Science*, 340(6139): 1467–71. Published Online May 30. doi: 10.1126/science.1235488 ]
- [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: Ethical Uses of Social-Science-Genomics**

[FAQs](#) regarding Lee *et al.* (2018) “Gene discovery and polygenic prediction from a 1.1-million-person GWAS of educational attainment” *Nature Genetics*, especially Section 3 (ethical and social implications); skim the rest

Nuffield Council on Bioethics, “Summary and Recommendations” (pp. xix-xxxiii), *Genetics and Human Behavior: The Ethical Context* (2002)

#### Recommended portions of same report:

- 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](http://www.nature.com/polopoly_fs/1.13861!/menu/main/topColumns/topLeftColumn/pdf/502005b.pdf)

Erika Check Hayden, "Ethics: Taboo Genetics," *Nature* 502: 26-28 (Oct. 3, 2013)  
<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>:

- Section on "Toward Trustworthy Research" (p. S6-S8), from: Erik Parens & Paul S. Appelbaum, "An Introduction to Thinking about Trustworthy Research into the Genetics of Intelligence," S2-S8
- James Tabery, "Why Is Studying the Genetics of Intelligence So Controversial?," S9-S14
- Elaine Tuttle Hansen, Stuart Gluck & Amy L. Shelton, "Obligations and Concerns of an Organization Like the Center for Talented Youth," S66-S72

### **Topic: Gene Discovery II: Winner's Curse**

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.

[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")]

### **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.

## 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.]
- [Hamer, D. H. and Sirota, L. (2000). "Beware the chopsticks gene," *Molecular Psychiatry* 5.]
- [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).]
- [Novembre, J., Johnson, T., Bryc, K., Kutalik, Z et al. (2008). "Genes mirror geography within Europe," *Nature* 456(7218).]
- [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).]
- [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]
- [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).]
- [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: 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 LDK 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: Polygenic Scores**

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).

- Vilhjálmsdóttir, 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.
- Martin, A.R., Daly, M.J. et al. (2019). "Predicting polygenic risk of psychiatric disorders." *Biological Psychiatry*.
- 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).]
- [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.]
- [Ge, T., Chen, C., Ni, Y. et al. (2019). "Polygenic prediction via Bayesian regression and continuous shrinkage priors," *Nature Communications* 10(1776).]

### **Topic: Population Genetics**

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

### **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.]

### **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).

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

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. "Missing heritability revisited"  
<https://geneticvariance.wordpress.com/2019/04/10/missing-heritability-revisited/>]

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

### **Topic: Mendelian Randomization**

Davies, N.M., Holmes, M.V. and Smith, G.D., 2018. Reading Mendelian randomisation studies: a guide, glossary, and checklist for clinicians. *BMJ* 362, p.k601.

Pingault, J.B., O'Reilly, P.F., Schoeler, T., Ploubidis, G.B., Rijdsdijk, 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, Grealley 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.
- 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.]

### **Topic: Functional Genomics and Development**

- [NOTE: All readings for this topic are optional because the lectures will focus on basics; the readings below represent recent advances.]
- [Berry, Drew. Molecular animations - [<https://www.wehi.edu.au/wehi-tv/>] Created to accurately present molecular processes and function in order educate and promote DNA science to the wider community. Also featured in *E.O.Wilson's Life on Earth (Unit 3) Genetics* (2014) FREE DIGITAL Textbook- iBooks]
- [Carvalho, C.M.B. and Lupski, J.R. (2016). "Mechanisms underlying structural variant formation in genome disorders," *Nature Reviews Genetics* 17.]
- [ENCODE Project Consortium (2012). <http://www.nature.com/encode/#/threads> (links to papers in Nature, companion papers and additional research papers) "An integrated encyclopedia of DNA elements in the human genome," *Nature* 489, 57-74.]
- [GTEx Consortium (2015). "The Genotype-Tissue Expression (GTEx) pilot analysis: multi-tissue gene regulation in humans," *Science* 348, 648-660.]

[Lek et al. (2016). "Analysis of protein-coding genetic variation in 60,706 humans," *Nature*. doi:10.1038/nature19057]

[Marchini, J. and Howie, B. (2010). "Genotype imputation for genome-wide association studies," *Nature Reviews Genetics* 11.]

[Solovieff, N., Cotsapas, C., Lee, P.H., Purcell, S.M., and Smoller, J.W. (2013). "Pleiotropy in complex traits: challenges and strategies," *Nature Reviews Genetics* 14.]

[Taudt, A., Colome-Tatche, M., and Johannes, F. (2016). "Genetic sources of population epigenetic variation," *Nature Reviews Genetics* 17.]

### **Topic: Applications in Social Science**

Barth, D., Papageorge, N. and Thom, K. (2017). "Genetic Ability, Wealth and Financial Decision-Making." Working paper.

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).]

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