

An Examination of the Genetic Architecture of Alcohol Withdrawal

Pamela Romero ^{1,4}, Kathleen Bucholz PhD ², Andrew C. Heath PhD ², Chelsie Benca PhD ¹, Valerie S. Knopik PhD³, Rohan Palmer PhD ¹



¹ Behavioral Genetics of Addiction Lab, Emory University, Atlanta GA
² Midwest Alcohol Research Center, Washington University, St. Louis MO
³ Human Development and Family Studies, Purdue University, West Lafayette, IN
⁴ Emory College



BACKGROUND:

- Alcohol is the most abused drug in the United States, but alcohol dependence (AD) remains poorly understood because of its heterogeneous and polygenic features.
- The emergence of a negative emotional state when a person is unable to access alcohol (i.e., withdrawal) is a key motivational factor that may provide insight into the effects of chronic use.
 - Approximately 27% of alcohol dependence individuals meet criteria of alcohol withdrawal (AW).
 - Studies suggest AW is under genetic influence (Levey et al. 2014, Palmer et al., 2015, Wang et al. 2012), but no specific loci have been found that survive correction (Bonferroni p-value threshold $p < 5 \times 10^{-8}$) for multiple testing.
 - Integrative whole genome-methods (see Figure 1 (right side) are anticipated to aid in overcoming this limitation (Palmer et al., 2012).

OBJECTIVES:

- The goal of this project is to identify genetic loci, genes, and an optimal gene set involved in AW. We intend to:
 - Confirm candidate genes derived from previous literature and experimental studies.
 - Identify novel loci through whole-genome analysis.

SAMPLE DESCRIPTION

- Mean age: 37.37 (range 7-88); 50% female.
- Withdrawal symptoms assessed using the Semi-structured Assessment for the Genetics of Alcoholism (Bucholz et al., 1994).

Table 1. Summary Statistics for Withdrawal Symptoms in combined sample

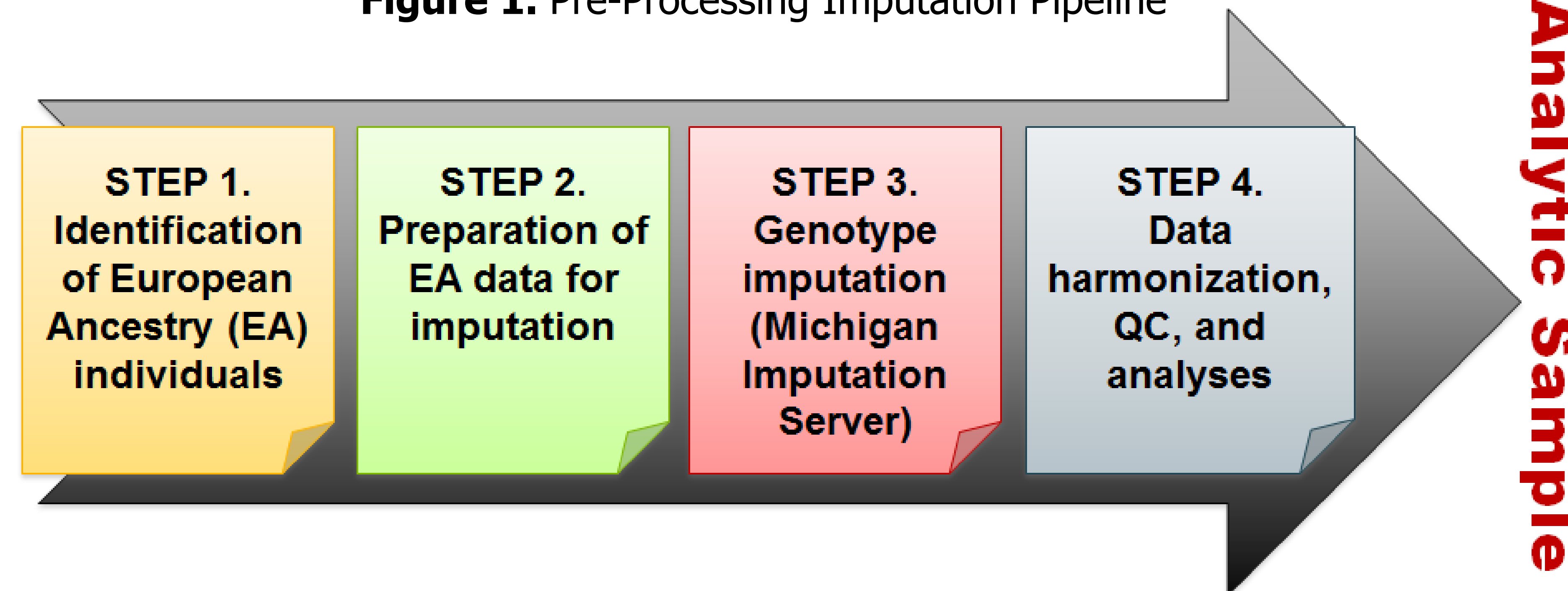
Symptoms	Symptoms		
	No	Yes	Total N
Shakes	2617	749	3366
No Sleep	2488	875	3363
Anxious / Depressed	2171	1192	3363
Sweats	2610	754	3364
Heart Beating Quickly	2679	683	3362
Nausea	2884	479	3363
Physically Weak	2453	910	3363
Headache	2725	639	3364
Hallucinations	3110	255	3365

Variables	Other Alcohol Measures					
	No	Yes	Total N	Min	Median	Mean
Ever Drink	238	4141	4379			
Drink to Avoid Symptoms	347	931	1278			
2+ Symptoms at a time						
				Min	Median	Mean
Age Regularly Drinking	5	18	19.16	65	298	4142
Age First Drunk	2	16	17.45	68	347	4075
Max Drinks in 24 hrs	0	15	21.34	274	299	4123

PROCEDURAL STEPS:

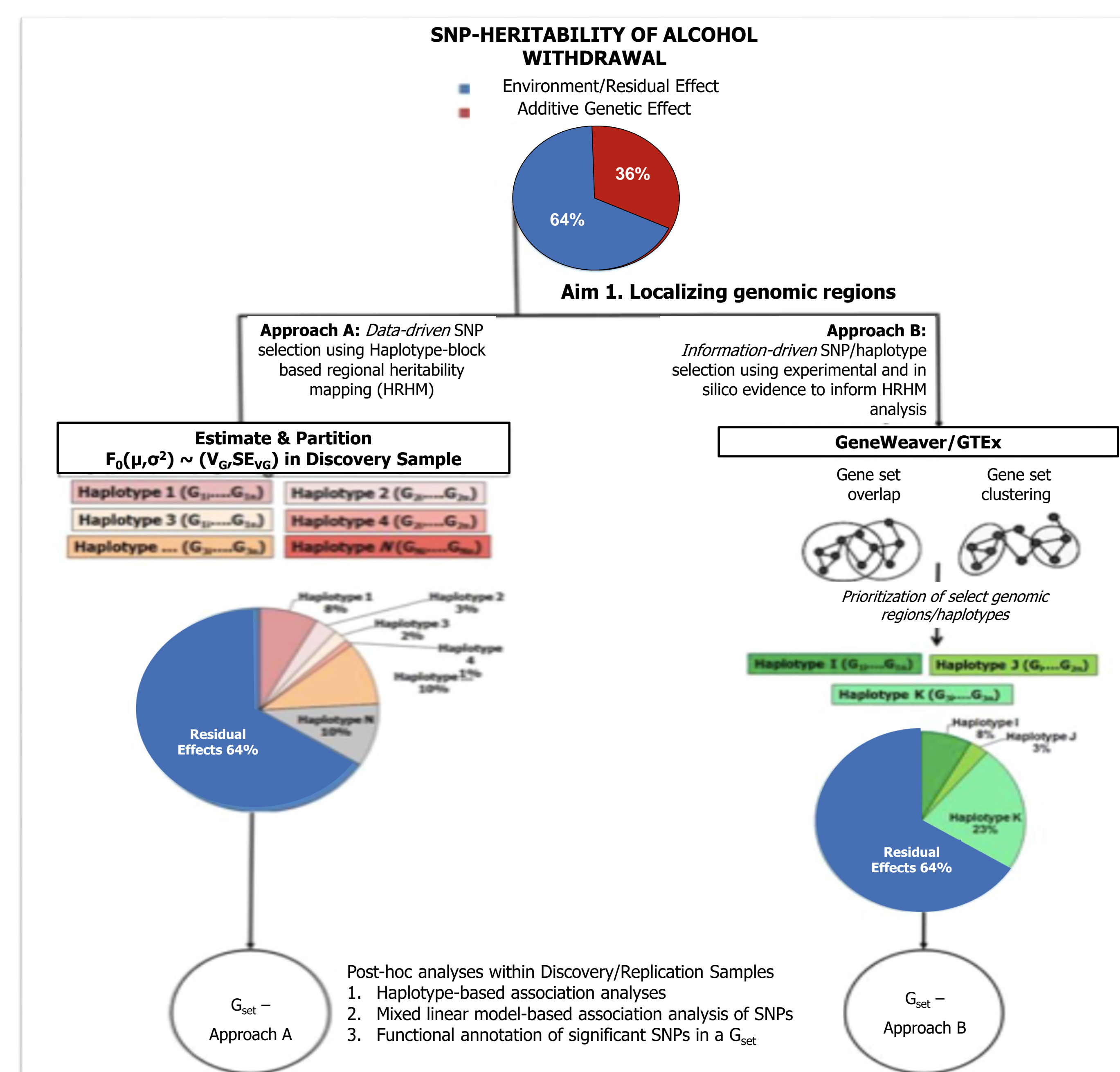
- Integrate several assessments from the Collaborative Study on the Genetics of Alcoholism (COGA) to form a single dataset (discovery sample).
- Impute genomic data using the 1000 Genomes Project as a reference (see Figure 1).

Figure 1. Pre-Processing Imputation Pipeline



- Identify 'a priori' genomic loci and genes using curated databases (GeneWeaver and PubMed literature Review); excluding association-type studies.
- Apply two main computational methods to observe pattern trait-locus patterns and to test the identified gene sets.
 - Family-based genomewide association analysis and genomic-relatedness maximum likelihood analysis. All analyses will account for variation in ancestral background, age, and gender.
 - Jaccard Similarity will be used to compare "top" SNPs from the GWA analysis to the information-driven gene set.
- Epistatic interactions will also be explored.

Figure 2. Data Analysis Pipeline



EXAMPLE GENE LIST:

- These six genes have been associated with delirium tremens (DT) (Baker 2012).
- It will be contrasted with many other gene-sets.
- In this example, only 1/6 genes overlap with 17 other gene-sets identified.

Table 2. Example Gene-set

Gene Name	System
ALDH2	Glutamate Decarboxylase
DBH	GABA receptors
DRD2	Neurotransmitter Agents
NPY	cortical excitability and stress response
SLC6A3	DA transporter
SLC6A4	SER transporter

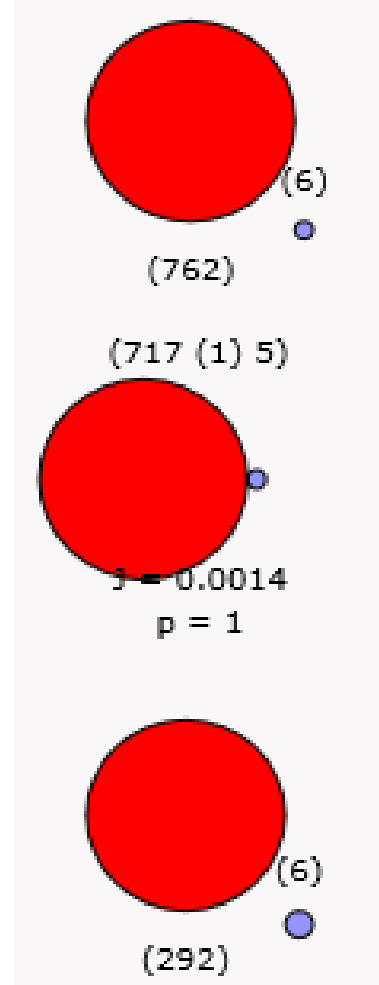


Figure 3. Gene-set Intersection graph

LIMITATIONS

- Power for the current analyses are limited by sample size, however we seek to minimize this by controlling for confounders, in particular ancestry, by using ancestral principal components based on the six major super populations.
- A priori gene set analyses are primarily based on study results reported to the GeneWeaver ontological engine, which we hope to supplement using a PUBMED search with the following parameters:
 - Date of Publication since 1970.
 - Text contains:
 - "alcohol withdrawal" AND "genetic"
 - "alcohol withdrawal" AND "GWAS"
 - "alcohol withdrawal" AND "candidate gene"

ACKNOWLEDGEMENTS

Grant funding: This body of work is supported by grants from the National Institute on Alcohol Abuse and Alcoholism (K01AA021113 awarded to PI Rohan Palmer and P60AA11998 awarded to Andrew Heath) and the National Institute on Drug Abuse (DP1DA042103 awarded to Rohan Palmer). Funding support for collection of datasets and samples in the Collaborative Study on the Genetics of Alcoholism (COGA) was provided by U10AA008401).

REFERENCES

- Becker, H. C. (2000). Animal models of alcohol withdrawal. *Alcohol Research & Health: The Journal of the National Institute on Alcohol Abuse and Alcoholism*, 24(2), 105-113. Retrieved from <http://www.ncbi.nlm.nih.gov/pubmed/11199277>
- Bucholz, SEMI STRUCTURED ASSESSMENT FOR THE GENETICS OF ALCOHOLISM (SSAGA). (1994). Retrieved from https://niaaagenetics.org/coga_instruments/phase1/ssaga/ssaga.pdf
- Carlson, R. W., Kumar, N. N., Wong-McKinstry, E., Ayyagari, S., Puri, N., Jackson, F. K., & Shashikumar, S. (2012). Alcohol Withdrawal Syndrome. *Critical Care Clinics*. <https://doi.org/10.1016/j.ccc.2012.07.004>
- Levey, D. F., Le-Niculescu, H., Frank, J., Ayalew, M., Jain, N., Kiriln, B., ... Niculescu, A. B. (2014). Genetic risk prediction and neurobiological understanding of alcoholism. *Translational Psychiatry*, 4(5), e391. <https://doi.org/10.1038/tp.2014.29>
- Palmer, R., McGeary, J., Francazio, S., Raphael, B., Lander, A., Heath, A., & Knopik, V. (2012). The Genetics of Alcohol Dependence: Advancing Towards Systems-based Approaches. *Drug and Alcohol Dependence*, 125(3), 179-191. <http://doi.org/10.1016/j.drugalcdep.2012.07.005>
- Wang, K.-S., Liu, X., Zhang, Q., Wu, L.-Y., & Zeng, M. (2012). Genome-wide association study identifies 5q21 and 9p24.1 (KDM4C) loci associated with alcohol withdrawal symptoms. *Journal of Neural Transmission*, 119(4), 425-433. <https://doi.org/10.1007/s00702-011-0729-z>
- Zuo, L., Zhang, C. K., Sayward, F. G., Cheung, K.-H., Wang, K., Krystal, J. H., ... Luo, X. (2015). Gene-based and pathway-based genome-wide association study of alcohol dependence. *Shanghai Arch Psychiatry, Shanghai Archives of Psychiatry*, 27(2), 111-118. Retrieved from <http://dx.doi.org/10.11919/j.issn.1002-0829.215031>
- Erich J. Baker, Jeremy J. Jay, Jason A. Bubier, Michael A. Langston, and Elissa J. Chesler. *GeneWeaver: a web-based system for integrative functional genomics*. *Nucl. Acids Res.* (2012) 40(D1): D1067-D1076