Combined Analysis of Psychiatric Studies (CAPS)

In 2014, the CAPS project published the results of the 2012 reanalysis of a group of datasets from the NRGR as well as of a set of new SNP genotypes for 47 pedigrees in the Schizophrenia collection. All datasets are available for download by authorized investigators in the Download Data section of www.nimhgenetics.org.

Results were published in the following papers, which are included in the results file folder of this download:

- Vieland VJ, Walters KA, Lehner T, Azaro M, Tobin K, Huang Y, et al. Revisiting schizophrenia linkage data in the NIMH Repository: reanalysis of regularized data across multiple studies. *Am J Psychiatry*, 2014 Mar 1;171(3):350-9.
- Walters KA, Huang Y, Azaro M, Tobin K, Lehner T, Brzustowicz LM, et al. Meta-analysis of repository data: impact of data regularization on NIMH schizophrenia linkage results. *PLoS One*, 2014;9(1):e84696.

    Linkage Results: Kelvin uses the Bayesian technique of sequential updating to accumulate evidence across multiple, potentially highly heterogeneous, sets of data. We provide static (tif) and dynamic (grx) views of the linkage results. Omnibus results [see files ppl_sz.tif and ppl_sz.grx] are based on all families. Additionally, the results can be viewed separately by study [see files ppl_sz_dataset.tif and ppl_sz_dataset.grx], as well as by ethnic [see files ppl_sz_ethnic.tif and ppl_sz_ethnic.grx] or clinical groups (families with or without schizoaffective disorder) [see files ppl_sz_famtype.tif and ppl_sz_famtype.grx].

    GRX files can be viewed and customized using Kelviz.

- Vieland VJ, Walters KA, Azaro M, Brzustowicz LM, Lehner T. The value of regenotyping older linkage data sets with denser marker panels. *Hum Hered*, 2014;78:9-16.

    Linkage analysis can help determine regions of interest in whole genome sequence studies. However, many linkage studies rely on older microsatellite (MSAT) panels. We set out to determine whether results would change if we regenotyped families using a dense map of SNPs. Because our genotyping budget was limited, we chose a single set of families for this study, in part based on a phenotype of particular interest. Specifically, we focus on the Hispanic American SZ sample originally collected by Escamilla and colleagues in 2003 and 2005 as reported in [1, 2], and the complete subset of families (n=47) from this data set that had at least one case of strictly defined SZ as well as at least one case of schizophrenia with a strong affective component.

    In the process of combining the new SNPs with the older MSAT data, we also explored alternative ways to select subsets of SNPs to include in the map in order to maximize information content while minimizing marker-to-marker LD.

    1. Escamilla, M.A., et al., A genome-wide scan for schizophrenia and psychosis susceptibility loci in families of Mexican and Central American ancestry. American journal of medical genetics. Part B, Neuropsychiatric genetics : the official publication of the International Society of Psychiatric Genetics, 2007. 144B(2): p. 193-9.
    2. Escamilla, M., et al., A schizophrenia gene locus on chromosome 17q21 in a new set of families of Mexican and central american ancestry: evidence from the NIMH Genetics of schizophrenia in latino populations study. The American journal of psychiatry, 2009. 166(4): p. 442-9.