
Abstract/Session Information for Program Number 1862W

Session Information

Session Title: Statistical Genetics and Genetic Epidemiology **Session Type:** Poster

Session Location: Exhibit Hall, Level 1, Convention Center **Session Time:** Wed 10:00AM-4:30PM

Abstract Information

Program Number: 1862W **Presentation Time:** Wed, Oct 23, 2013, 11:30AM-12:30PM

Keywords: Statistical Genetics and Genetic Epidemiology, KW086 - identification of disease genes, KW080 - genome-wide association, KW008 - bioinformatics, KW100 - mapping complex traits, KW075 - genetic mapping

Abstract Content

IBD Mapping of Autism Microarray Data. *G. Povysil, S. Hochreiter* Institute of Bioinformatics, Johannes Kepler University Linz, Linz, Austria.

Identity by descent (IBD) between two individuals means that their alleles are identical because they were inherited from a common ancestor. This information can be used via IBD mapping to increase the power of association analysis by grouping single nucleotide variants (SNVs) based on IBD. The basic principle of IBD mapping is to look for segments of DNA that are shared identical by descent more often among cases than controls.

HapFABIA is a biclustering algorithm that was originally designed to extract short IBD segments that are present in multiple individuals from large sequencing data using only rare variants. In this setting we used HapFABIA on SNP microarray data from the Autism Genetics Resource Exchange (AGRE) to look for IBD segments that are shared more often by cases than controls.

We found several IBD segments that were almost exclusively shared by cases. Some of these map to genes that have been previously associated with autism. Further analyses are needed to confirm or dismiss these results.

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