

## Coming Soon: INQuery

INQuery is a web-based user interface enabling access of data including phenotypes and genotypes associated with GWAS studies to qualified investigators. Harmonized phenotypes and genotypes (genome build hg37) will be available for all GWAS datasets housed in NIAGADS. In addition, information on the availability of a sample stored at NCRAD for request is provided. The database enables users to query a set of samples based on a particular phenotype/genotype of interest to determine if there is a sample available at NCRAD for further analysis. We will release INQuery by the fall of 2017.

Query for a set of samples based on genotype and phenotype:

1. Filter for subjects based on phenotype
2. Search for genotypes
3. See if NCRAD has a sample available for the subjects of interest

The screenshot shows the NIAGADS INQuery web interface. The top navigation bar includes the NIAGADS logo and the text 'INQuery'. Below the navigation bar, there are options for 'Allowed Dataset: ALL' and 'Logged in as apa'. The main interface is divided into several sections:

- Left Panel:** A sidebar with a search bar and a list of fields to filter by. A yellow box labeled '1' highlights the 'NIAGADS\_Pheno\_View\_Sample.sex (varchar) Filter' option.
- Top Center:** A 'Query By' section with radio buttons for 'By SNP' (selected) and 'By Position'. A yellow box labeled '2' highlights the 'By SNP' option.
- Markers:** A text input field containing 'rs709830' and a 'Find Genotypes' button. A yellow box labeled '3' highlights the 'Markers' section.
- Table:** A data table with columns: subject\_id, niagads\_dat..., ncrad\_sampl..., cohort, dx, sex, apoe, autopsy, and rs709830. The table contains multiple rows of data for subject NG00022.
- Filter Dialog:** A yellow dialog box is open over the table, showing the filter criteria: 'NIAGADS\_Pheno\_View\_Sample.sex = M'. An 'Apply' button is visible.

New Datasets available at <https://www.niagads.org/datasets>

**NG00053: IGAP Summary Statistics, ADGC Subset—**  
Lambert et al. (2013)

PI: Dr. Gerard Schellenberg, U of Pennsylvania

These data are summary statistics generated for the International Genomics of Alzheimer's Project (IGAP) meta-analysis of Genome-Wise Association data in Alzheimer's Disease. This dataset contains the ADGC subset of the data analyzed in Stage 1 of the meta-analysis.

**NG00056: Transethnic GWAS for AD Summary**  
**Statistics—**Jun et al. (2017)

PI: Dr. Lindsay Farrer, Boston University

These data are summary statistics generated from a transethnic GWAS analysis obtained from cohorts including European, African American, Japanese, and Israeli Arab Ancestries.

Visit the NIAGADS website at <http://www.niagads.org>.  
Contact us with questions at [niagads@upenn.edu](mailto:niagads@upenn.edu).