

## **WAGER 2.0.5 Release**

Release Date: 6th November, 2009 (5pm)

The following enhancements have been incorporated into this release:

### **Study Manager**

- The summary statistics shown on the Study Manager Study Home page now reflect the number of participants that have a status of 'Ineligible'.
- The extraction of genotypic data can now be controlled using genotypic data specific permissions.
- The ability to store binary files, such as images, with each subject has been added to Study Manager.
- The data dictionary fields are now sorted by field name whenever the data dictionary fields are provided for download from WAGER.
- Additional summary SNP data has been added to the 'Search Markers' screen.
- The biospecimen counts in Study manager have also been updated to reflect subjects that have a status of 'withdrawn'.

### **Data Analysis**

- The data access restriction within Data Analysis that only allowed users to see those fields that were part of a specified fieldset, even when they were a member of another security group that provided access.
- A function has been provided to allow users of Data Analysis to input a set of encrypted subjected ids, with the encryption key and then download a set of the decrypted subject ids.
- It is now possible to extract the phenotypic data through Data Analysis for withdrawn subjects.
- A dataset query generated and saved using the Data Analysis application can now be cloned and used as the basis for a new query.
- SNPs from the select list in Data Analysis are now hidden if no genotypic data is present.
- The option to select specific families for the extraction of pedigree data from Data Analysis has been added.
- It is now possible to rename data files that are downloaded from Data Analysis.
- The option to include Study Data fields (e.g. QID) in download files generated using Data Analysis has been provided.
- Record filtering functionality has been added to Data Analysis to allow users to refine their searches. For example, it would now be possible to only extract data for those subjects that have a BMI > 2.