

WAGER Version 2.0.1 Release Notes

Release Date: 20th March, 2009

The following enhancements were incorporated in this release:

WAGER Portal

- 1) The screens for WAGER Portal have been modified so that they expand to fit the width of the current browser window. This has allowed some buttons and fields to be relocated on the screens and some screens to be reduced in scrolling length so as to provide an improved user experience.
- 2) The "Support" button on WAGER Portal that links to the User Guide has been changed to a "Help" button and the information within "Help" pertaining to WAGER functionality has been expanded.

Study Manager Enhancements

- 1) A Pedigree Management function has been added to Study Manager. This allows WAGER users to upload pedigree files for the subjects in their study. Prior to this users had to send their pedigree files to the WAGER Informatics Team for upload. Users may also edit individual Pedigree records.
- 2) A SubjectID/LabNo module has been added to Study Manager. This allows WAGER users to upload files containing SubjectID/LabNo mappings. Prior to this users had to send the mappings to the WAGER Informatics Team for upload.
- 3) In version 2.0.0 the data upload screens would occasionally time out during a large data load, even though the data load was actually successful. The data loading routines have been changed to run as a background job if it is estimated to take longer than 1 minute. Users can check the status of loads on the job upload screen.
- 4) Uploading NULL "" data into a genotype position. Previously, a bug existed where a genotypic file upload would have "" (ie NULL) values converted to "NN". This has been amended to not convert the "" values, and store the NULL entries "as is". On extract, the user now has the option to convert all invalid genotype data (ie "NN", "--", "**", "??", etc) to "" (ie NULL), giving only 3 possible genotypes, and one NULL data in the data export (eg "AA", "AB", "BB" and "")
- 5) Uploading file error/report – information. During genotypic file upload, the "download report" button was not working correctly. This has been fixed.
- 6) The automatic consent function has been updated to correct the issue where consent information was being overwritten when subjects were re-uploaded.

Data Analysis Enhancements

- 1) Users may now choose to encrypt the subjects ids in files extracted for analysis so that the recipients of the data files cannot tie the subject ids in the analysis files back to the actual study subjects. The encryption passphrase/key is chosen by the person doing the extraction and is stored in the File Output parameters.
- 2) Users now have the ability to search for a specific marker in the genotype selection screen during extraction; this makes it much easier to find a small number of markers when there are a large number of markers within the study.
- 3) Users now have the ability to define a marker position range when searching for markers to extract for subsequent analysis. This search will now bring

back the markers in the range with and without genes that haven't had the gene details updated consistently.

- 4) Previously, WAGER 2.0.0 would fail to create a dataset if “cross-sectional” was selected when longitudinal data existed. In V2.0.2 if longitudinal data is present, the cross-sectional option will be unavailable to the user, and “date collected and age” automatically checked. In a subsequent release users will have the option of generating a cross-sectional file from longitudinal data based on certain parameters (ie choosing the datapoints where the date collected is closest to the subjects study consent date)
- 5) When users now enter the screen for choosing phenotypes to extract, no sub-studies or collections will be chosen by default. This forces the users to choose one or more sub-studies and collections before any phenotypes will be displayed for selection. In version 2.0.0 some pre-selection of sub—studies and collections was done by the system which caused some confusion.
- 6) Users may now choose to add a password to the zip file that contains all of the files extracted for analysis.
- 7) In version 2.0.0 all subjects were included in the output analysis files, regardless of whether they had pheno or geno data in the chosen output fields. In Version 2.0.1 only subjects that have at least one non NULL pheno and/or geno field will be included in the analysis files. Selected subjects with no pheno or geno data in the fields chosen for extraction will not be included in the analysis files.
- 8) Previously when adding a gene the description was lost on adding a chromosome. This has been resolved.

LIMS Enhancements

- 1) The field currently labelled as “box” in location details under the biospecimen details screen has been renamed to "rack" and the field labelled "tray" has been renamed to "box". This has been done to ensure consistency with the Inventory tab.