

Task list 9/1/2016

T3 website to-do list

New features

1. (1) Setup database synchronization between production machine in Albany and mirror machine at Cornell
2. (4) Add analysis tools from Calvin (weather info/google maps, CoreHunter2)
3. (5) Fix errors in BEAGLE imputation and validate
4. (6) Add outlier filtering to curation tools
5. (7) Add p value from metap on QTL page
6. Marker filter by heterozygosity
7. Run BLAST on new genome assembly for wheat (can not release to public)
8. Add analysis of single genotype experiments to analysis tools that only work for consensus data
 - a. Tool1
 - b. Tool2
 - c. Add shiny server (with ZBrowse) to web server
10. Add QTLNetMiner to website
11. Add variant effect predictor analysis to website
12. Add SolR index to website so that it is searchable by WheatIS
13. Add PopVar analysis to website (Genomic Breeding Tools)
11. Improve import scripts (allow .xlsx files) using new version of Excel Reader
12. Provide access to T3 via Galaxy
13. Spatial analysis / adjustment tools
14. Should we add [BiPlot](#) analysis to T3? There are several R scripts for this.
15. Should we add more HeatMap tools on T3? This could include plot level data.
16. Which annotation fields would you like to query on (any of fields in experiment)?
17. Improvements for "Select Lines by Genotype Experiment". Add more description of genotyping labs
18. Add graphs to experiment design page
19. On download page do we need instruction on how to select filter settings? Using the defaults you sometimes get empty sets.
20. Organize breeding programs and data programs in a rigorous way.

Bugs

1. ~~Remove old accounts (pre website hack) from production machine - done~~
2. ~~(2) Fix outliers caused by loading errors of excel files, identified by Calvin's outlier detection - problem were only in test database not production~~
3. ~~(3) Fix content status page to report genotype data stored as single genotype experiments~~

Website refactoring

1. (8) remove phpids, use only prepared statements
2. database abstractions – could use BRAPI as access to database
3. allow command line access to analysis tools
4. save data results in user history
5. remove prototype.js framework, jquery is better

BRAPI

1. update and add new calls

USER GROUP

1. Consolidate Data Farms with the TCAP databases
2. JMP format for downloads (is it a published format?)