2016-01-27 Meeting notes

Date

27 Jan 2016

Attendees

- Clayton L Birkett
- Jean-Luc Jannink
- user-21bda
- Clare SaiedCalvin Lietzow

Goals

Discussion items

Time	Item	Who	Notes
10min	issue and project manag ement	Clay, Jean- Luc	review JIRA, Confluence, Support Ticket, BaseCamp, Trello, Zoho, DropBox no one product will provide all the features we need so integration is important Clay likes JIRA/Confluence because it is managed by Cornell, free, many features
10min	ideas on using QTLNe tMiner	Clay and others	investigate how QTLNetMiner can be used by T3 and GrainGenes.
10min	combin e genoty pe experi ments	Clay, Jean- Luc	we should archive the _Panel experiment and try to find a way to enable combining the HWWAMP, HWWAMP_R, CSRV, and YQV lines, as determined by the user, for analysis with the T3 tools. Clay will make a stab at it and report back to us on what will be involved.
10min	additin al key in genoty ping experi ments	Jean- Luc	We usually think that people will not try to genotype the same line in the same genotyping experiment, so having those two indices will keep everything that needs to be separate separate. But in the oat genotyping project, we have come across the problem that sometimes the same line (maybe variety name versus experimental line name) was in the same genotyping trial twice. In cassava, the result of a genotyping experiment is associated with two keys "LineName:LibraryPrep". I think the LibraryPrep is unique within the Genomic Diversity Facility. So I wonder if we should try to implement that in T3, to have a T3-wide unique "genotyping assay" as an index within genotyping experiments, so that people could submit the same line however many times they wanted within the same experiment.
10min	Haplot ag files	Jean- Luc	How to display passport data? Link to Nick's website if he thinks it will be stable. Otherwise, save the HTML passport files on T3

Action items

- Clayton L Birkett email Cornell IT and ask if we can create collaborator account (JIRA, Confluence) for people in Albany. If not then sign up for Altassian Cloud service.
- Clayton L Birkett investigate methods of achiving TCAP90K_HWW_Panel
- Sean-Luc Jannink contact Marie Guttier and ask if we need general tool for combining genotype experiments or just for the one case she is working on
- Clayton L Birkett investigate how traits are linked to QTL's in QTLNETMiner