

# 2016-02-03 Meeting notes

## Date

03 Feb 2016

## Attendees

- Clayton L Birkett
- Jean-Luc Jannink
- user-21bda
- Peter James Bradbury

## Goals

## Discussion items

Time	Item	Who	Notes
	T3 Barley report generator	Kevin Smith, Dave Matthews	<ul style="list-style-type: none"><li>• As we discussed, users would select lines, trials, and traits, then the datafarm would generate multi-trial means and an LSD/HSD for comparisons among lines for each trait. We are getting this years winter barley trials uploaded and could test it out with data already in T3 whenever you are ready.</li><li>• see <a href="https://t3sandbox.org/t3/wheatplus/analyze/table.php">https://t3sandbox.org/t3/wheatplus/analyze/table.php</a> Ready to deploy?</li></ul>
	T3 Barley share code base with wheat	Dave Matthews, Clay Birkett	real differences: the color, whatsnew, toronto.php. git-incompatibility: merge problems will arise in some files, e.g. admin_header.php, curator/input_line_names_check.php
	interactive pedigrees on T3 /Oat.	Clare Saied	
	schedule dates for OS upgrade	Clay Birkett, David Hane	install Ubuntu 14.04 on tcap machine
	updates on QTLNetMiner, QTL Harvesting, imputation	Clay Birkett et. al.	display pvalue on JBrowse, look into how to use pvalue in meta analysis, colaborate with QTLNETminer developers
	update on combining genotype experiments	Jean-Luc	discuss next week
	new TCAP hardware?		discuss next week
	PAG 2017 planing		does our workshop overlap with "Plant Phenotypes"? should our session become "Computer Demo"?
	T3 BRAPI		FlapJack
	streaming JSON objects		
	International collaborations on data		WheatIS(several nodes around the world host index and links to resources), BRAPI, GOBII

## Action items

