2019-01-23 Meeting notes

Date

23 Jan 2019

Attendees

- Clayton L Birkett

Goals

Discussion items

Time	Item	Who	Notes
	JBrowse		• waiting for GrainGenes switch to new JBrowse (v15.4) • where will T3 logo appear in GrainGenes JBrowse • separate track for each platform or map
	T3 survey		more tutorials identifying markers across platforms
	Data Loading	David	
	KnetMiner		is it useful best way to access GWAS updates for new release of Knetminer
	Ensembl Plant v42		gene annotations inter-Homeologous Variants (3.6 million Inter-Homoeologous Variants (IHVs) called by alignments of the A,B and D component genomes), Polymarker uses this information already
	GWAS		use genome assembly position for markers
	collaboration		working with Thomas Walk, NDSU Oat - Dr. Jessica Schlueter
	big projects		triticumbase • trait ontology • loading phenotype data • loading genotype data practical haplotype graph

Action items

- [ ] Clayton L Birkett - create map for HapMap platform, add to JBrowse, then create tutorial on how to select markers from all platforms on Browse
- [ ] Clayton L Birkett - indicate platform in GWAS
- [x] Clayton L Birkett - ask Keywan how many T3 genes link to other resources (need protein, description, ontology....)
- [ ] Clayton L Birkett - add description/pictures for VEP terms