

# BioCuration 2016 Meeting notes

## Date

11 Apr 2016

## Attendees

- [Clayton L Birkett](#)

## Goals

## Discussion items

Time	Item	Who	Notes
Monday	iPTMnet	Cecilia Arighi	<ul style="list-style-type: none"><li>• protein post-translational modifications (PTMs) in systems biology context</li><li>• <a href="http://research.bioinformatics.udel.edu/iptmnet/">http://research.bioinformatics.udel.edu/iptmnet/</a></li></ul>
	Protein Information Resource (PIR)	Andrew Nightingale	<ul style="list-style-type: none"><li>• Protein Ontology</li><li>• UniProtKB</li><li>• use cytoscape for visualization</li><li>• UniProt contains PIR-PSD, Swiss-Prot, and TrEMBL databaes</li></ul>
	TopAnat	Frederic Bastian	<ul style="list-style-type: none"><li>• GO-like enrichment mapped to genes by expression</li><li>• <a href="http://bgee.org">http://bgee.org</a></li></ul>
	Glycobiolog	Jean-Philippe Gourdine	<ul style="list-style-type: none"><li>• Undiagnosed Disease Network</li><li>• <a href="https://www.genome.gov/27550959">https://www.genome.gov/27550959</a></li></ul>
	Cellosaurus	Amos Bairoch	<ul style="list-style-type: none"><li>• Cell lines</li><li>• <a href="http://web.expasy.org/cellosaurus/">http://web.expasy.org/cellosaurus/</a></li></ul>
	OBO Foundry	Lynn Schriml	<ul style="list-style-type: none"><li>• develop a family of interoperable ontologies that are both logically well-formed and scientifically accurate</li><li>• phenocarta - tool for analysis of gene expression profiles <a href="http://www.chibi.ubc.ca/Gemma/phenotypes.html">http://www.chibi.ubc.ca/Gemma/phenotypes.html</a></li><li>• <a href="http://www.obofoundry.org/">http://www.obofoundry.org/</a></li></ul>
	ontology mapping	Marie-Angelique Laporte	<ul style="list-style-type: none"><li>• comparison of ontology mapping techniques to map traits</li><li>• map CO to TO</li></ul>
Tuesday	WikiData	Andra Waagmeester	showed example of disease ontology in 100's of languages
	protein2GO		
	rethinking databases	Ivan Erill	domain specific databases work as submission portals, then transfer to mainstream repository. specific databases will die when funding goes away. CollecTF
Thursd ay	PhenoPackets		hierarchiacal JSON <a href="http://www.phenopackets.org">www.phenopackets.org</a> , <a href="https://github.com/phenopackets">https://github.com/phenopackets</a> Global Alliance for Genomics & Health FAIR findable, accessible attributeable, interoperable
	subscription-based funding model	Tanya Berardini	Arabidopsis Information Resource (TAIR) lost funding, now subscription based

## Action items

- ✓ Clayton L Birkett - Marie-Angelique offered to help us convert from CO to TO
- ✓ Clayton L Birkett - should T3 be responsible for submitting data to NCBI/Ensembl, which data? This is normally the responsibility of the PI
- ✓

Clayton L Birkett - collaborate with Edward Marcotte, professor of biochemistry at The University of Texas at Austin, who is doing MassSpec on wheat. Our group studies the large-scale organization of proteins, essentially trying to reconstruct the 'wiring diagrams' of cells by learning how all of the proteins encoded by a genome are associated into functional pathways, systems, and networks. Such models let us better define the functions of genes, and to link genes to traits and diseases. See more on the Research page.

- ☑ Clayton L Birkett - what is the resolution/size of QTL's? - Poland's 2015 paper on the POPSEQ map is says that the average gap is less than 1 cM and the maximum gap is 30 cM