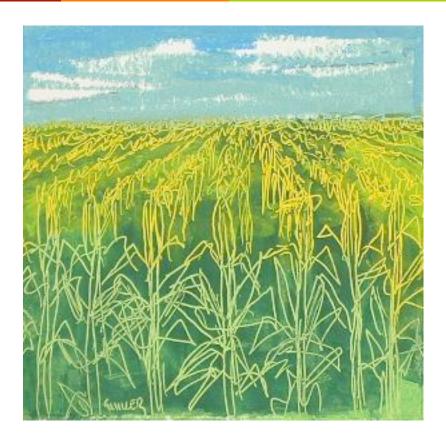
Enabling Cross-Species Computation 7 on Phenotype in Plants

Carolyn J. Lawrence, Iowa State University



Preview

Phenotype as a datatype

Ontologies

What's possible (examples)

What we can do to predict plant biology

Three slides

Current trends

Opportunities

Bottlenecks

Phenotype

- A phenotype (from Greek phainein, 'to show' + typos, 'type') is the composite of an organism's observable characteristics or traits, such as its morphology, development, biochemical or physiological properties, phenology, behavior, and products of behavior. A phenotype results from the expression of an organism's genes as well as the influence of environmental factors and the interactions between the two. -wikipedia
- Phenotype is EVERYTHING

Phenotype

- Extremely diverse data type (can range from expression profile to behavior)
- Associated to individuals, populations, or species
- Different levels (summary, measurement data)
- Can be comparative (mutant vs. wild type) or absolute (days to flowering of a cultivar)
- Data integration needs extensive connections to other types of data (e.g., seed stocks, genes, experimental methods, publications)
- Database schema and interface design
- Data representation how to represent the data in a consistent way across experiments, research communities, and species
- Data accessibility how do we get data out of literature and into the database?

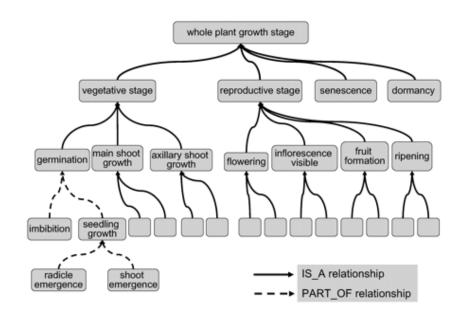
Ontologies



scholarsresource.com

Metaphysics:

The study of being or existence



Pujar et al., 2006 Plant Phys.

Biological applications: A structured vocabulary that includes definitions of terms in a domain and relationships among them

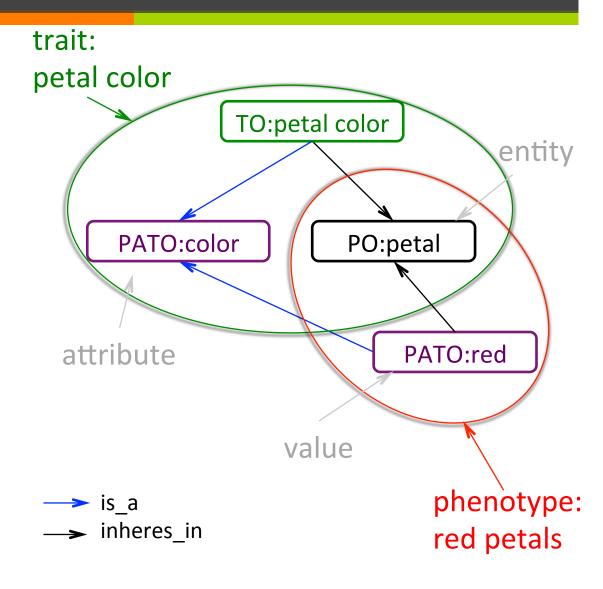
Traits versus phenotypes

A trait is a combination of an entity and an attribute.

Example: petal color

A **phenotype** is a combination of a **entity** and a **value**.

Example: red petals



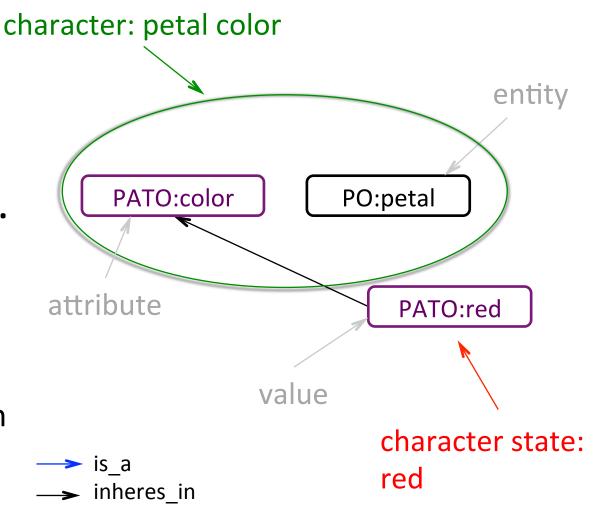
Characters and character states

A character is a combination of an entity and an attribute.

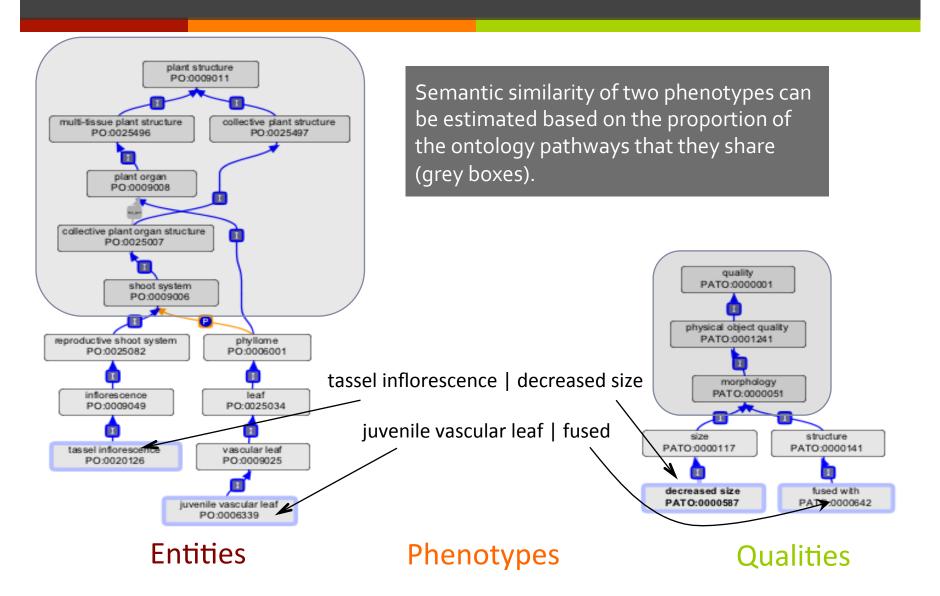
Example: petal color

A character state is a value. Meaningless without the entity from the character

Example: red



What does this look like?



What does this look like?

Conversion to ontology statements:

Description of Mutant Phenotype*	Atomized Phenotype statements	Entity	Quality
	Narrow leaves	PO: Vascular leaf	PATO: Narrow
Narrow leaves; Narrow, slightly elongated floral organs; Twisted siliques	Narrow floral organs	PO: Floral organ	PATO: Narrow
	Elongated floral organs	PO: Floral organ	PATO: Elongated
	Twisted Siliques	PO: Fruit	PATO: Twisted
Delayed flowering; Reduction in total chlorophyll	Delayed flowering	GO: Flowering	PATO: Delayed
	Reduction in total chlorophyll	CHEBI: Chlorophyll	PATO: Decreased concentration

*From Lloyd and Meinke, Plant Physiol. 2012 Mar;158(3):1115-29

Does it matter what we call these entity/ quality associations?

It doesn't really matter (to a computer) which word you use (trait, phenotype, or character), as long as you logically define your terms and specify the data structure

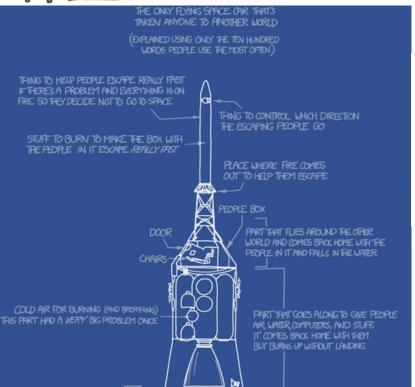


Aren't we losing something by using general terms?



THE UP-GOER FIVE TEXT EDITOR

CAN YOU EXPLAIN A HARD IDEA USING ONLY THE <u>TEN HUNDRED</u> MOST USED WORDS? IT'S NOT VERY EASY. TYPE IN THE BOX TO TRY IT OUT.





Carolyn J Lawrence shared a link. September 27, 2013 near Ames, IA

http://xkcd.com/1133/ Can you explain your science with the ten-hundred most used words in the English language? Try it here:

http://splasho.com/upgoer5/. I came up with this: "I help people to find out what others have learned about the most important green thing grown in the world."



James Schnable "I use computers to study how life turns light into power and how different types of life figured out how to do the same things." Not having 'plants' as a word is a major constraint.

Why on EARTH would we want to go to all this trouble?!?

High-quality discovery potential!

- Identification, through the similarity of recorded phenotypes, of other alleles of the same gene, other members of a signaling pathway, and orthologous genes and pathway members across species: Washington et al. 2009, PLoS Biol 7(11): e1000247. -> Novel, testable predictions!
- Prediction of Arabidopsis negative gravitropism as a model for human Waardberg disease (ear development) from phenolog associations (ancient vesicle trafficking system): McGary et al. 2010, PNAS 107(14): 6544–6549. -> Identification of new, tractable model systems!
- By expansion to cross-species inference, predicting novel players in genetic networks is possible (e.g., response to vernalization) Woods et al., BMC Bioinformatics 2013, 14:203. -> Functional prediction for uncharacterized genes!

What we can do to predict plant biology

In the absence of sequence-based homology, shared multidimensional attributes (complex biologically relevant associations) among characterized and uncharacterized genes enables discovery of novel genes that potentially cause a given phenotype.

Dwarf plants









Rolled leaves









Plant Phenotype Pilot Project

Done or in progress:

- Collect a broad set of phenotype descriptions for a representative set of plant species
- Identify ontologies to be used to describe phenotypes
- Develop standardized format and best practices to ensure consistency
- Translate phenotype descriptions into ontology statements

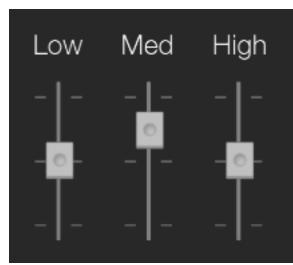
Next steps:

- Data analysis
 - Clustering of genes into pathways
 - Degree of correlation between sequence and phenotype
 - Computational prediction of gene candidates for uncloned mutant genes and QTL
- Apply lessons learned
 - Is the data set big enough?
 - Are the ontologies complete enough?
 - Is our annotation consistency good enough?
 - Better analysis methods?

Three slides:

- Current trends and state-of-the-art
- Opportunities





Current Trends and State of the Art



- High-throughput phenotyping within a species/crop
- Clear transition from thinking that genotype defines phenotype to recognizing phenotypic plasticity in varied environments and need to codify environment
- Interest and ability to compute on phenotype across domains of life and all described biological processes

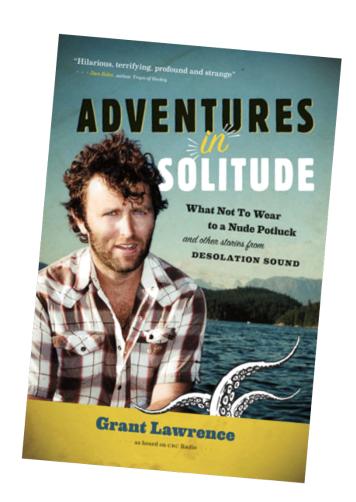
Opportunities



- Discover and complete biological pathways and interaction networks
- Predict potential phenotypes for uncharacterized genes (guilt by association)
- Develop non-obvious models for biological processes across taxonomic boundaries

Bottlenecks and Needs

- Creating the dataset(s) and integrating them takes curators (AKA well-trained humans)
- Making data logically accessible takes domain experts working with computer scientists (AKA well-trained superhumans)
- Embracing complexity! 'Big Data' is not limited in scope to enormous file size...



Phenotypes are Big Data (?)

Big Data is characterized as having extreme or variable values of one or more of the following characteristics:

▼ Volume¹ (size) Sequence, SNPs, expression data

Velocity¹ (acquisition <u>rate</u>) <u>Images, sequence</u>

Variety¹ (structure) Data formats, alternative standards

Complexity³ (in relationships) Mutation to genotype to phenotype...

Veracity (quality or provenance) Gold standard datasets

▼ Volatility (changes over time) Genome sequence assembly releases

¹ Doug Laney, "3-D Data Management: Controlling Data Volume, Velocity, and Variety," 2001.

² Brian Hopkins, "Blogging From the IBM Big Data Symposium - Big Is More Than Just Big," 2011.

³ Valentin T Sribar, et al., "'Big Data' Is Only the Beginning of Extreme Information Management," 2011.

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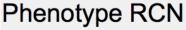
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Ramona Walls (iPlant)





Phenotype Ontology Research Coordination Network





sol genomics network











Questions?

