Phenote: Curation Software for Evolutionary Phenotypes

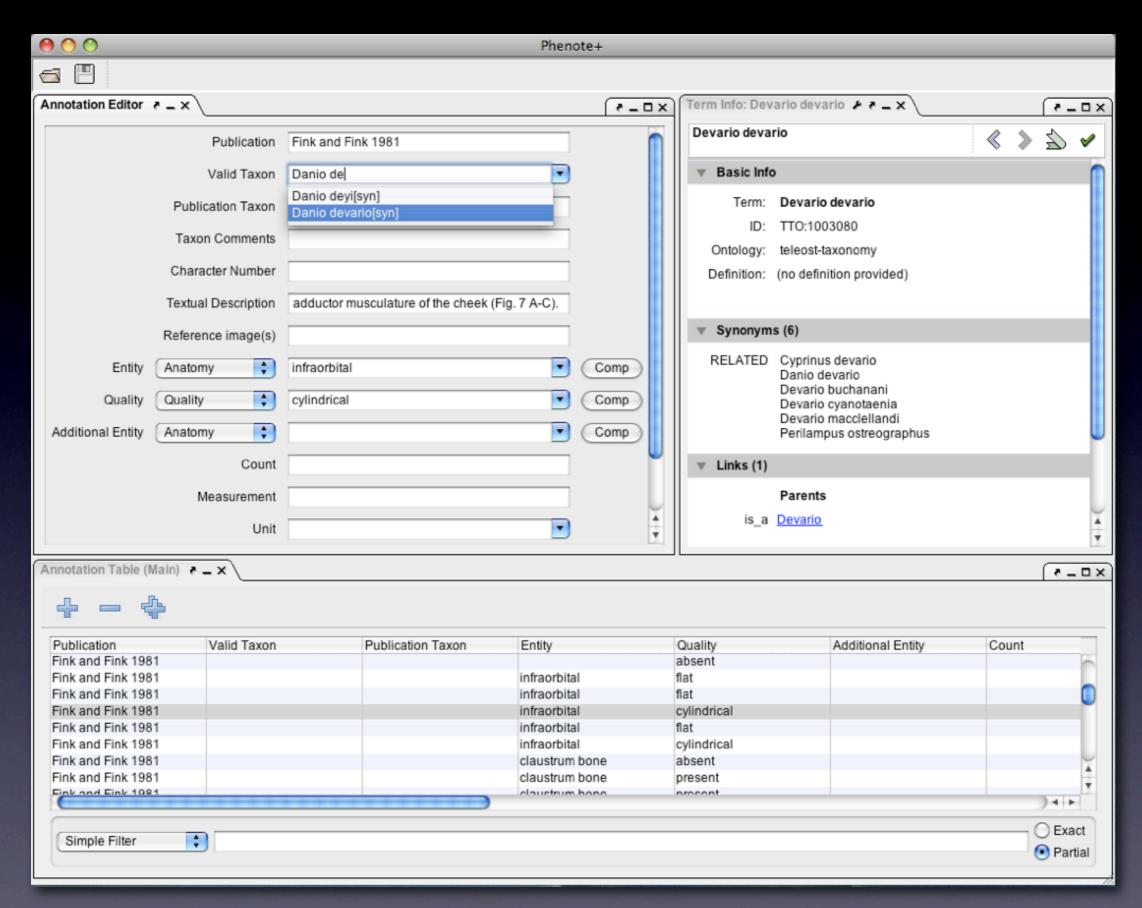
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Phenote

- Developed for annotating genetic mutant phenotypes using ontologies
- NCBO & BBOP (lead developer, Mark Gibson)
- Used by curators at ZFIN, Flybase,
 Dictybase, Wormbase, others

Phenote features

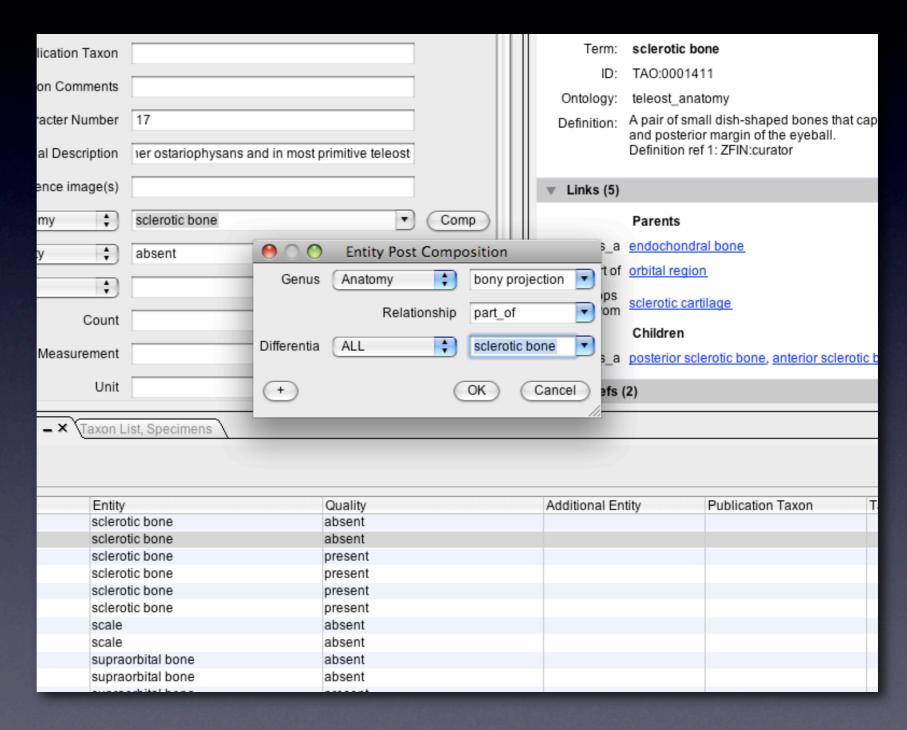
- Simple table interface
- Loads any OBO format ontology checks for updates
- Configure input fields for specific ontology
- Type-ahead term search in input fields
- Ontology navigation panel and term info panel
- Cross-platform Java desktop application



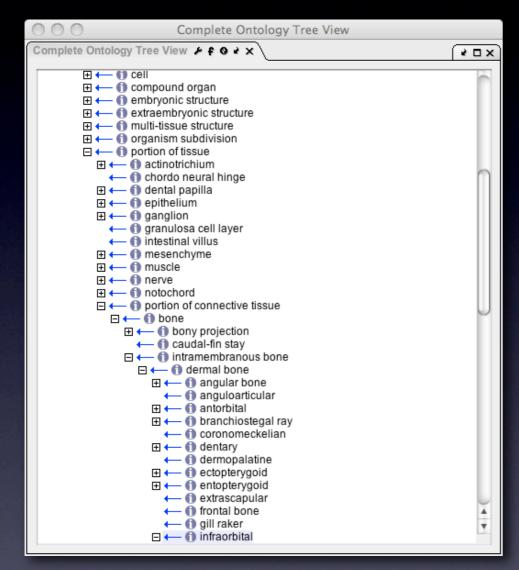
Type-ahead can match name, synonyms, definition

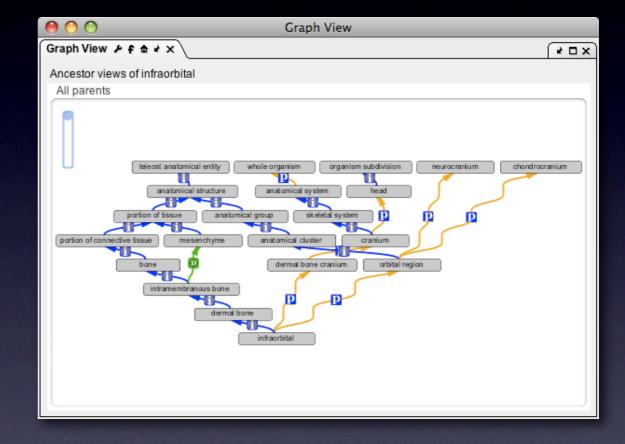
Post-composition

Create more specific terms as cross-products of existing terms



Panels from OBO-Edit



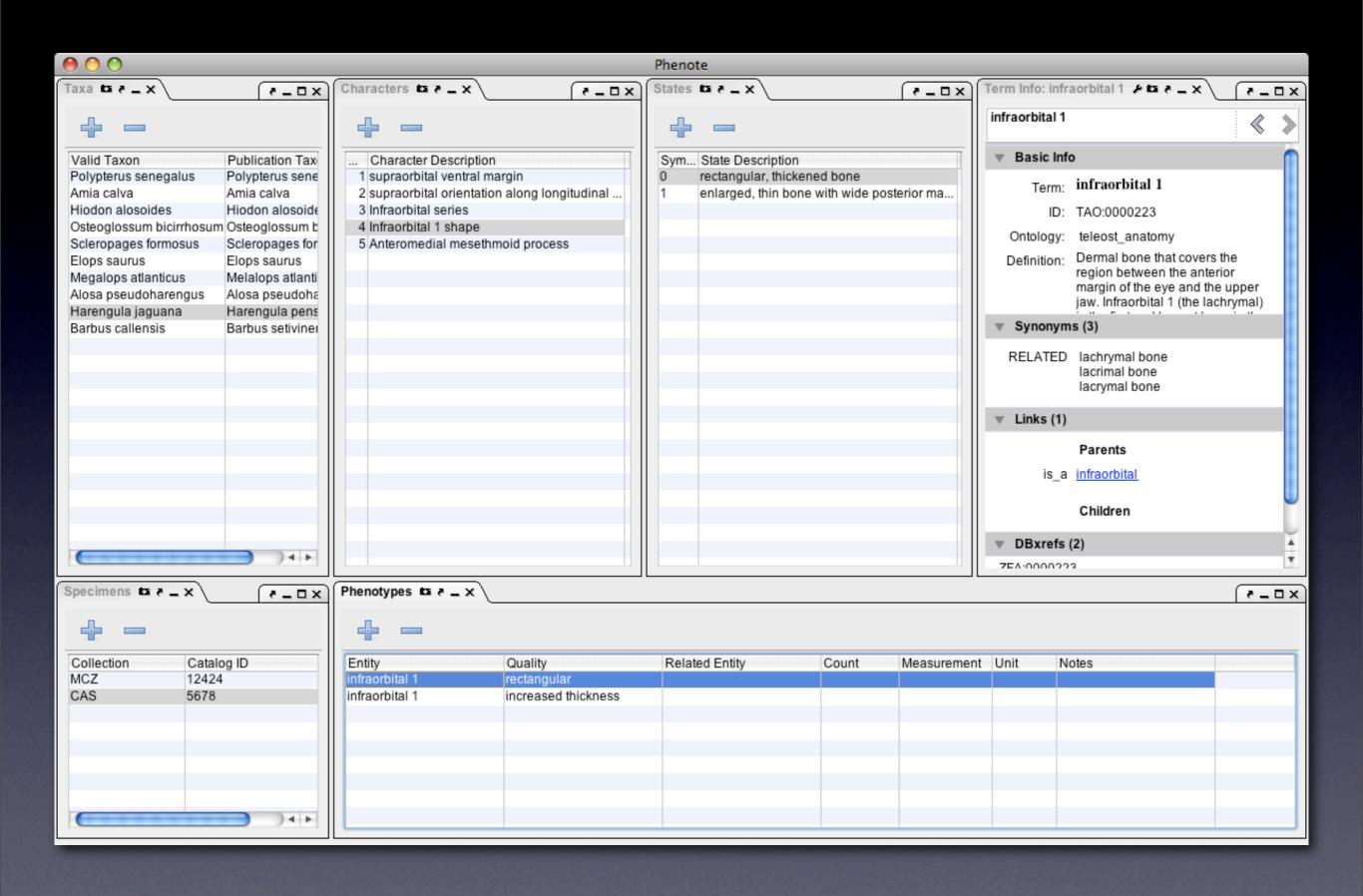


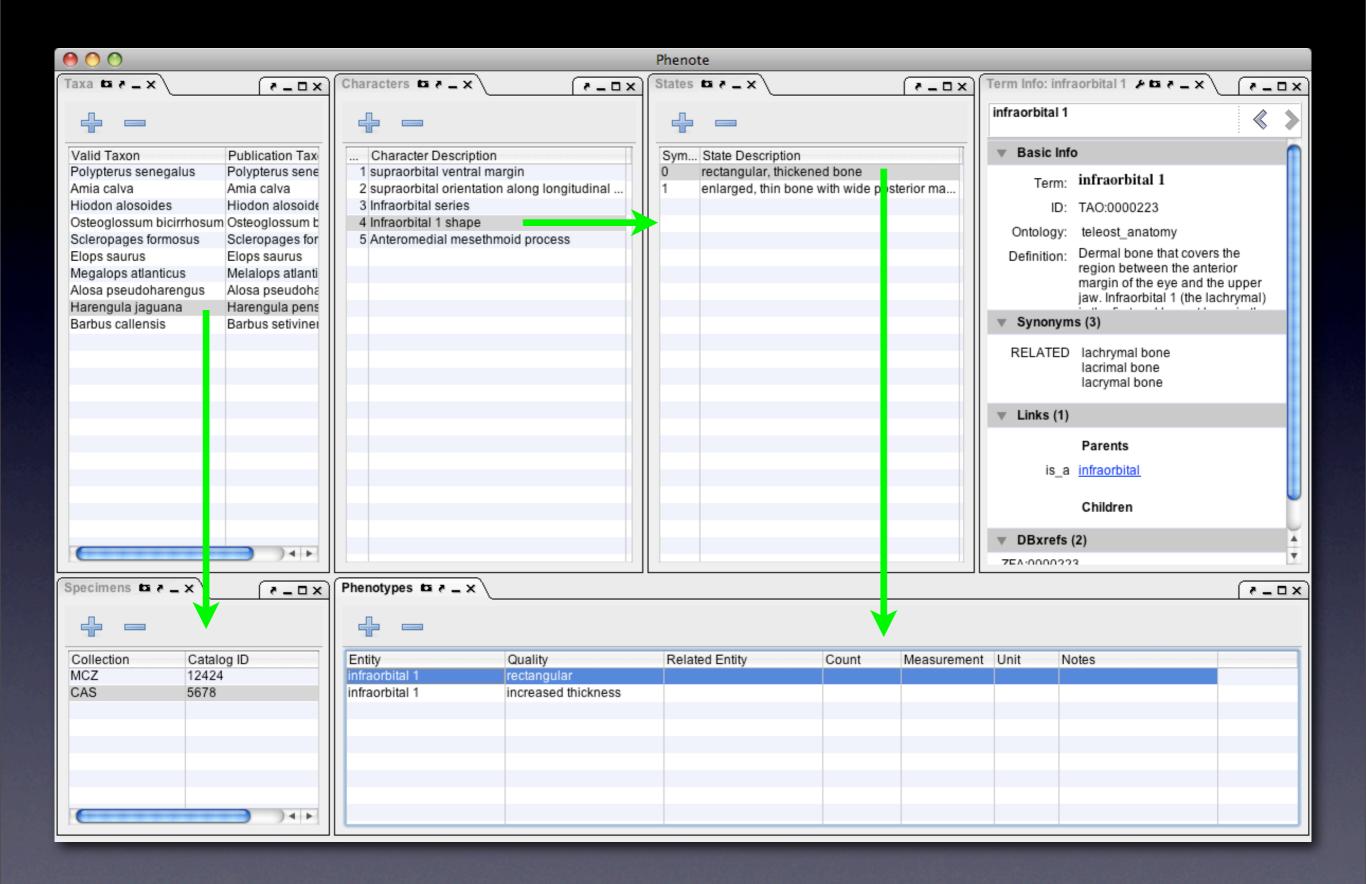
Browse entire ontology (can drag and drop onto input fields)

Quickly see inheritance neighborhood of selected term

Phenoscape interface

- Modeled on components of character matrix file (instead of flat table interface)
- Panels for Taxa & Specimens, Characters,
 Character states
- Attach EQ phenotype annotations to character states
- Attach taxonomy ontology IDs to taxa





Phenote + NeXML

- NeXML next generation XML form of NEXUS (led by Rutger Vos)
- EQ annotations can be embedded in State elements as PhenoXML
- Attach taxonomy ontology identifiers to Taxon elements
- Free-text data and character matrix can be edited in Mesquite - without destroying attached ontology info
- In progress for both Phenote & Mesquite

Acknowledgments

- Phenote/BBOP: Mark Gibson, Nicole Washington, Chris Mungall
- NeXML: Rutger Vos
- Phenoscape: Wasila Dahdul and everyone else
- NESCent & NSF