

Vlad: A Visual Annotation Display Tool

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Directed (Acyclic) Graphs

- Becoming commonplace
 - ontologies
 - gene families
 - strain histories
 - metabolic pathways
 - ...
- Need frameworks for dealing with them

DAGs in MGI

- MGI has general framework supporting:
 - DAGs with any kind of node
 - Vocabularies, which may have DAG structures
 - Annotations, associating vocabulary terms with objects such as genes
 - software infrastructure to support loading, querying, updating, etc.
- Used for growing number of applications in MGI:
 - GO, mouse adult anatomy, phenotype ontology, etc.

Vlad 0.1

- Visualization is an increasingly important theme
- Vlad began as an experiment:
 - visualize MGI annotations against the GO
 - emphasis on data display, intended for users and curators of MGI
 - Vlad stands for VisuaL Annotation Display
 - implement in Python, use GraphViz
 - rough out an architecture for visualizing DAGs
- Short talk presented at GO Meeting in Bar Harbor

Visual Techniques

- All intended to help focus attention on “hot” spots
- All based on scores
- Coloring (HSV)
 - nodes in a DAG have same color hue
 - intensity varies by score
- Collapsing
 - draw more important nodes at full size, including labels and scores;
 - draw less important nodes as small circles
- Pruning/abridging
 - remove uninteresting nodes
 - reattach unpruned descendents -> abridged edges

Vlad 1.0

- Differences:
 - reimplemented in Java
 - not specific to MGI
 - annotations read from flat file - user chooses
 - GO structures read from MGI
 - added P-value scoring

proto.informatics.jax.org

- A new MGI web site
- For deploying prototype tools, early access to upcoming releases, getting user feedback
- Currently:
 - mockups of MGI 3.0 release
 - GO tools installed/developed by Mary Dolan
 - Vlad

Demo

Software Architecture

- Directed graphs
- Graph traversals and transformations
- GraphViz interface
- Support for DOT language constructs
- Statistics
- Specific “stylists”
- Java/CGI

Other Tools

- GO::Term Finder
- GO Miner
- GenNav
- Gene Ontology Tree Machine

Similarities to GO::Term Finder

- Computes P-values for annotations
- Displays results as image and as table
- Useful in contexts such as interpreting microarray results
- Tools intended both as apps and as libraries

Differences from GO::Term Finder

- Supports raw counts
- Doesn't implement correction
- More emphasis on the image
- Not yet available for download
- Web installation supports multispecies
- Java vs. Perl
- Architecture

Vlad To Do (partial)

- Finish adapting for stand-alone config
- Make available for download
 - source code
 - shrink-wrapped app
- Explore precomputing/caching to improve performance
- Making results downloadable
- Lots o' tweaks

Further Work

- Adapt for doing cross-species comparisons
- Apply infrastructure to build other analysis and visualization tools for MGI
 - e.g., expression data against anatomy

Credits

- MGI, especially:
 - Judy Blake
 - Carol Bult
 - David Hill
 - Harold Drabkin
 - Mary Dolan
- Gary Churchill