

Expanding GO annotations with text classification

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Linking literature to GO

- GO literature annotations reference articles that illustrate the underlying concept of a GO Term
 - Not meant to be a comprehensive list of relevant literature
- Researchers could use a resource that expands amount of GO-related literature
 - Quick understanding of functions for unfamiliar genes and proteins

ReelTwo Linking Medline to GO

Reel Two's Gene Ontology Knowledge Discovery System already classifies Medline according GO



Not validated

www.go-kds.com



The Next Step

- Researchers found GO KDS useful in some areas
- Reel Two expected category bias in training
- Reel Two wanted validation and user feedback
- Goal: a more accurate, user friendly research tool
- Next step: Collaboration with EBI and Flybase

Validation

- Reel Two developed an interactive version of GO KDS
- Curators from EBI and Flybase performed validation using the GO Slim taxonomy
- Validation took place over 10 days in November 2003



Results

Positive

- System performance generally quite accurate
- Top 100-200 articles were ~90-98% correct
- Poor performing categories typically improved with user input

Negative

- Certain biases found in categories with few training examples
- Accuracy often fell off by midway through predictions
- Sometimes required confirming or correcting several dozen predictions



Examples

- cellular component > extracellular matrix (GO:0005578)
 - Generally accurate Some bias toward collagen.
- molecular function > nucleotide binding (GO:0000166)
 - High confidences correct, by ~50% many false positives. Bias to ABC transporters and ATP binding.
- biological process > behavior (GO:0007610)
 High confidences incorrect due to strong bias toward HPRT.
- biological process > cell homeostasis (GO: 0019725)
 - No training data. Example of system learning.

Observations

- Confidence above 70-80%
- Confidence at ~40%
- Category bias
- Quick improvement
- Obsolete or changed GO terms
- Some GO terms probably too broad
- Possible bias in electronic annotation

Improving Training Data

- Training data used all go/gene_association files, including electronic GO annotations
 - May have led to bias
- Possible revised approach:
 - Filter out electronic annotations
 - Check for redundant Pubmed ID/GO term pairs
- Goal: more representative training set



Getting Results to Researchers

- Expand system to cover all of GO
- Interface for user feedback
- Interface for users' own curations
- System learns and improves updates on weekly basis
- Could be deployed to research community via GO site by mid-2004, given funding







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