Evaluation of semantic similarity measures

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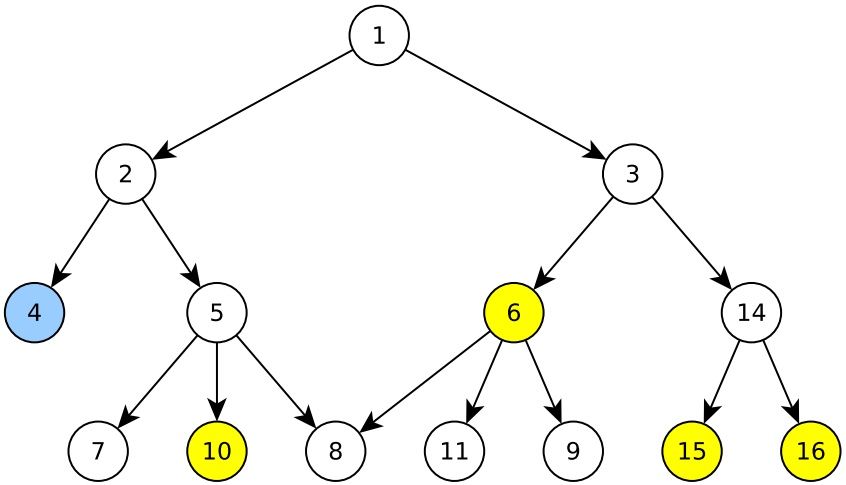
Semantic Similarity Measures

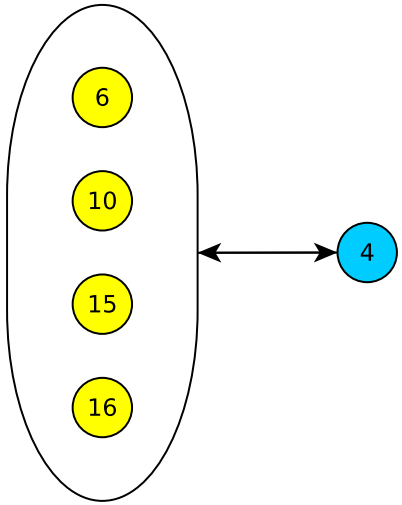
- Semantic similarity measures capture the strength of interaction between concepts based on their meaning.
- Widely used in bioinformatics
  - Protein-protein interaction identification
  - Gene-Disease associations
  - Patient diagnoses

Semantic Similarity Measures

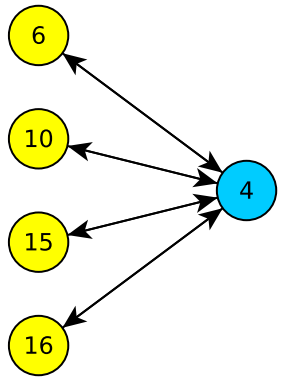


Protein 1

Protein 2



Groupwise Similarity Measures



Pairwise Similarity Measures with combination strategy

Motivation and Aim

- Large number of semantic similarity measures has been developed:
  - 21 groupwise
  - 38 pairwise with 7 different combination strategies
  - Available in Semantic Measures Library
    `http://www.semantic-measures-library.org/`
- Classify semantic similarity measures by their sensitivity to the:
  - number of annotated classes
  - difference of the number of annotated classes

Materials

- Gene Ontology (GO)
- 6,108 gene annotations from Yeast Genome Database. Annotation sizes vary from 1 to 55
- 5,500 randomly generated annotations
  - 55 groups with 100 genes in each:
    - 1st group annotated with 1 GO class
    - 2nd group annotated with 2 GO classes
    - 3rd group annotated with 3 GO classes
    - and so on

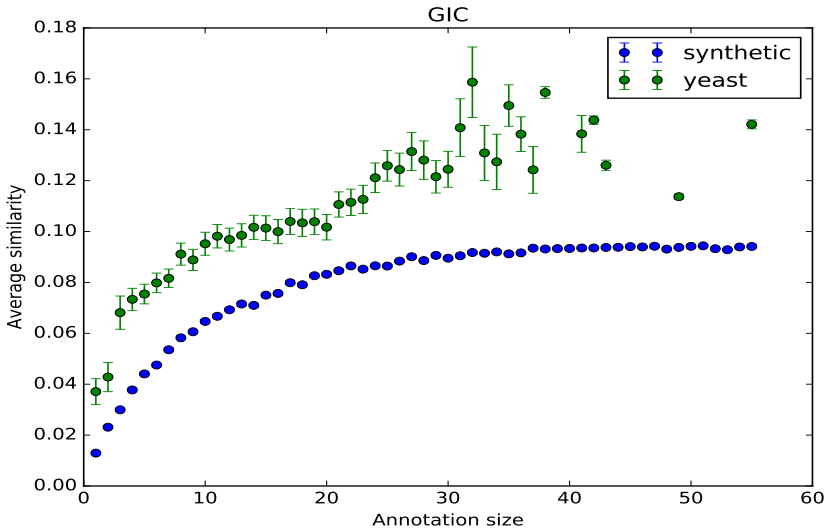
Methods

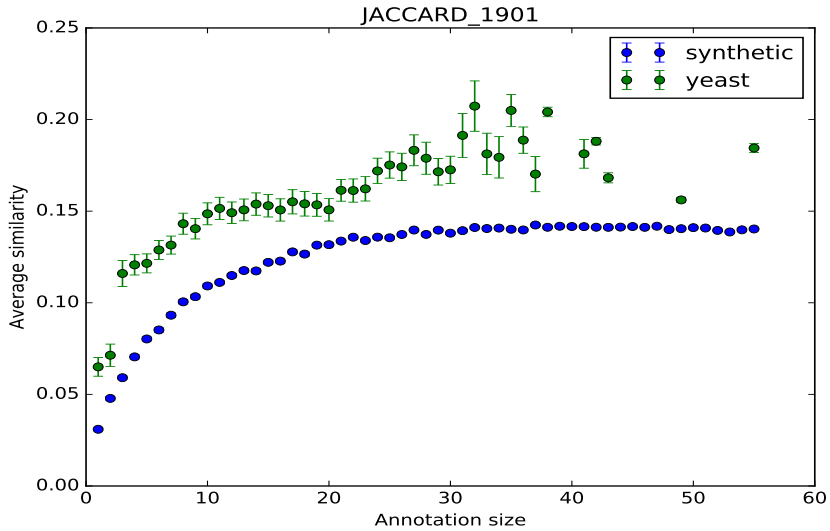
- Compute similarity between each pair of genes
  - 18,656,886 similarity values for yeast annotations ((6108 + 1) / 2 * 6108)
  - 15,127,750 similarity values for random annotations
- Group similarities by annotations size
- Group similarities by annotations size difference
- Take average similarities for all groups

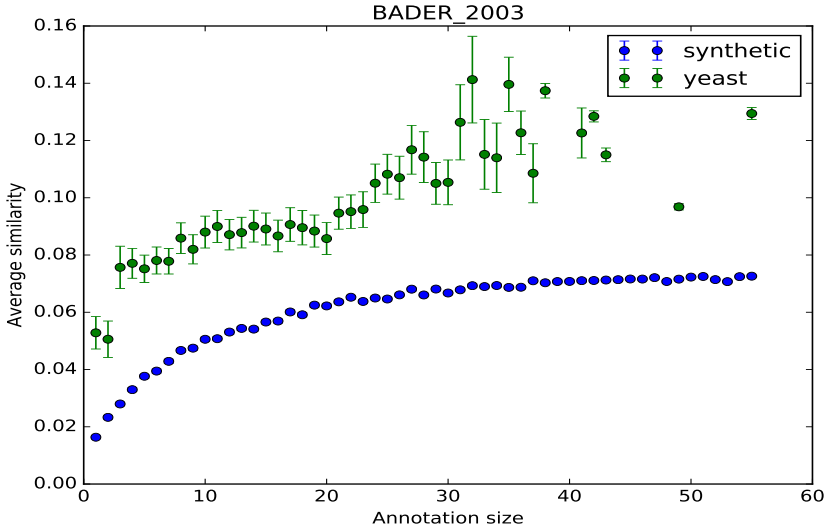
Results

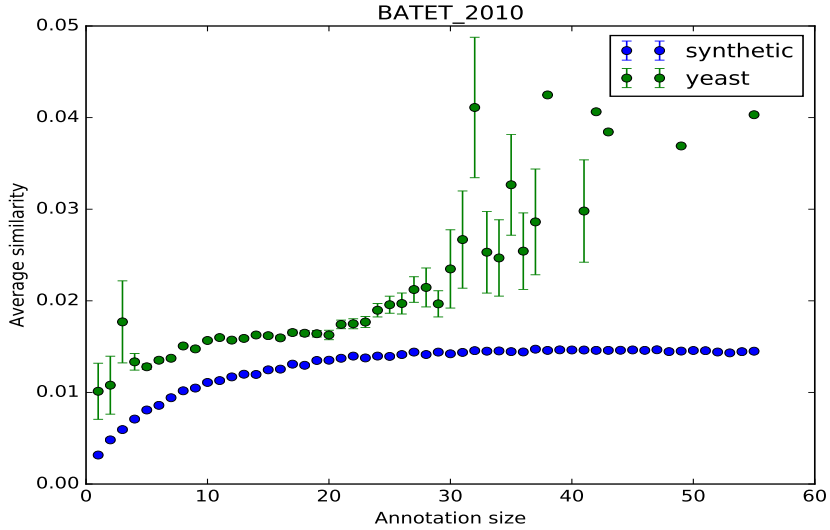
- Sensitive
  - Similarity value increases when annotation size (difference) increases
  - Similarity value decreases when annotations size (difference) increases
- Not sensitive

Annotation size - Groupwise Similarity Measures

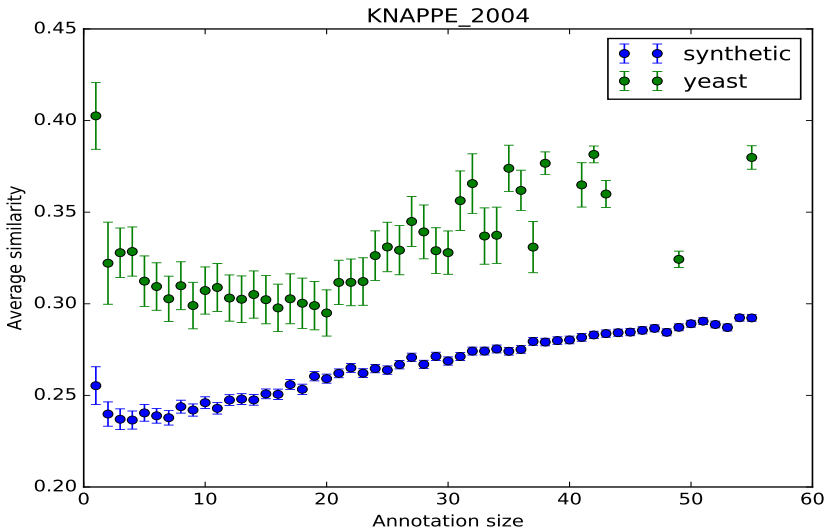


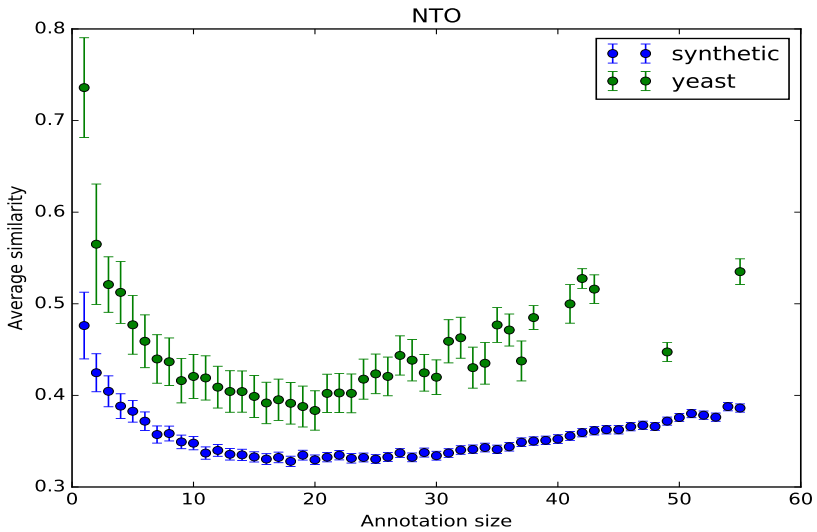


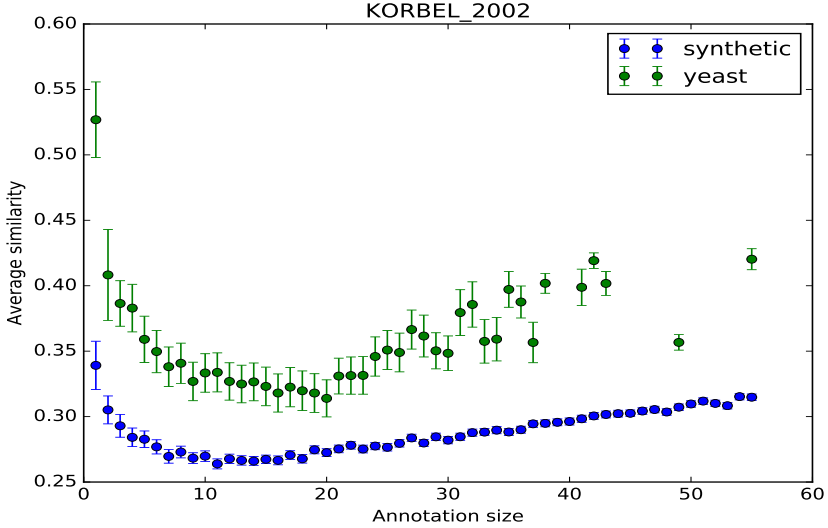


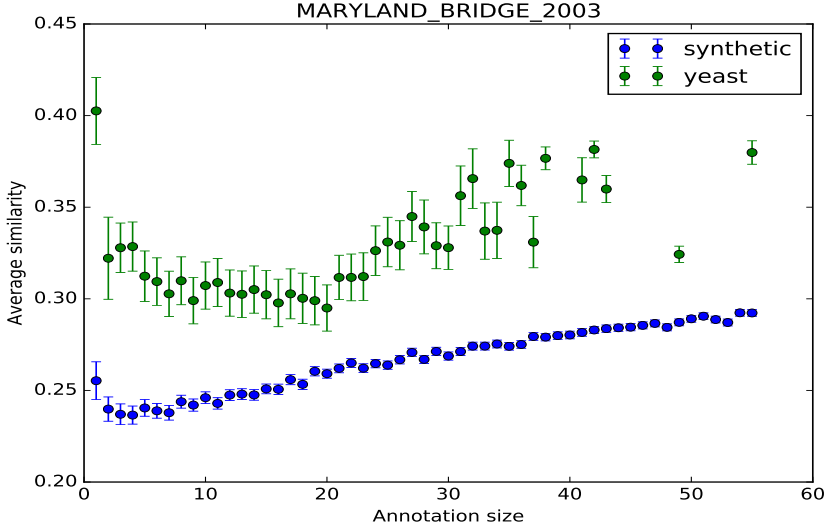


Annotation size - Groupwise Similarity Measures

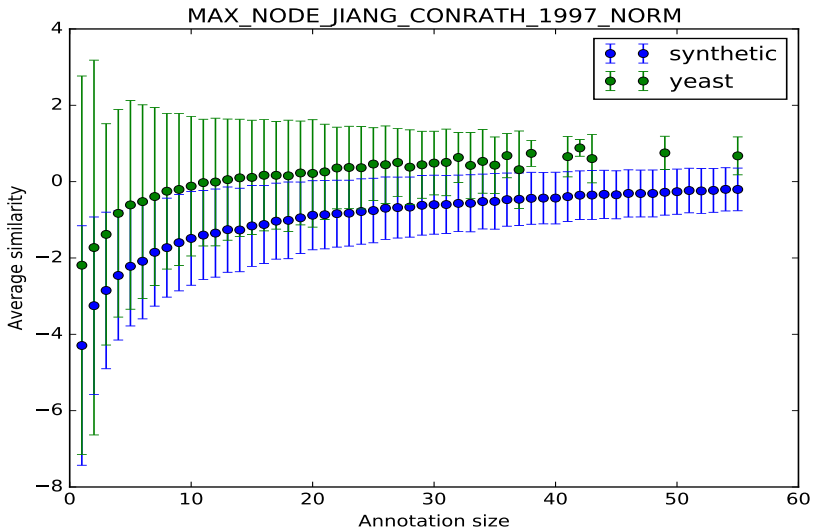


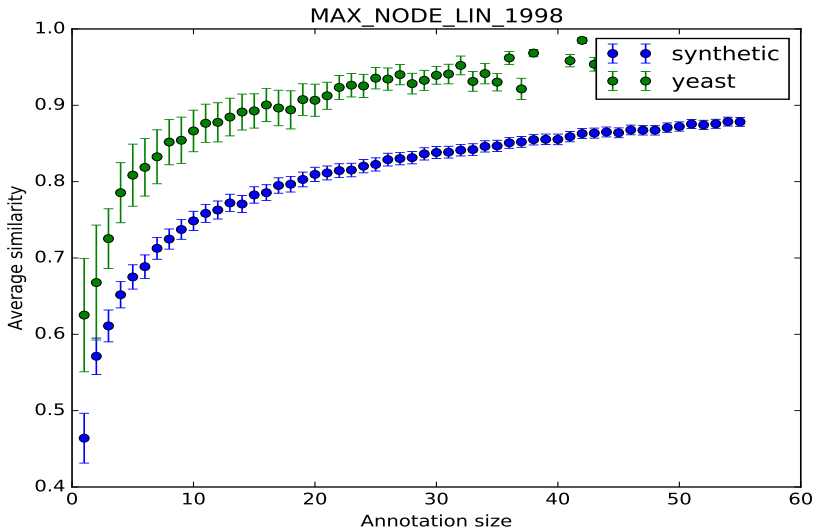


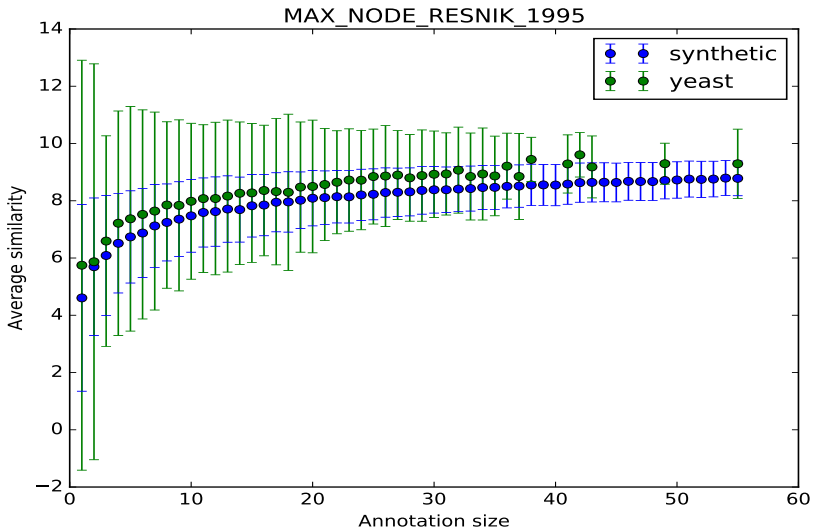


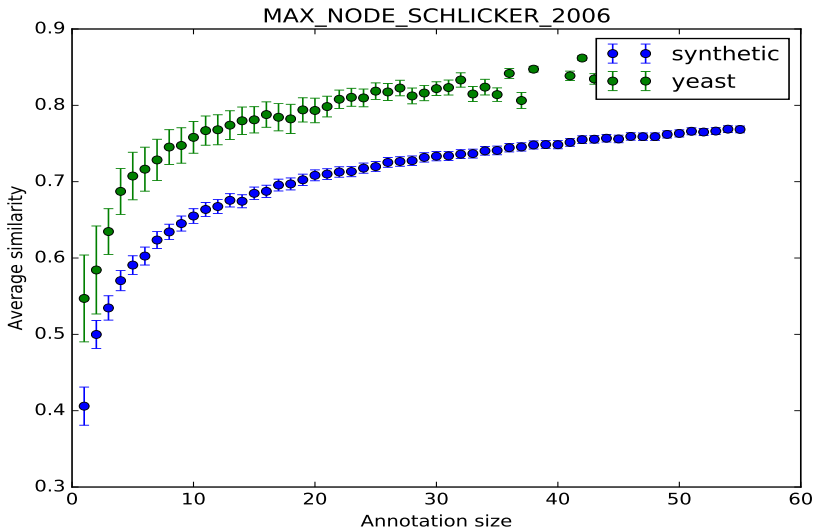


Annotation size - Pairwise Similarity Measures









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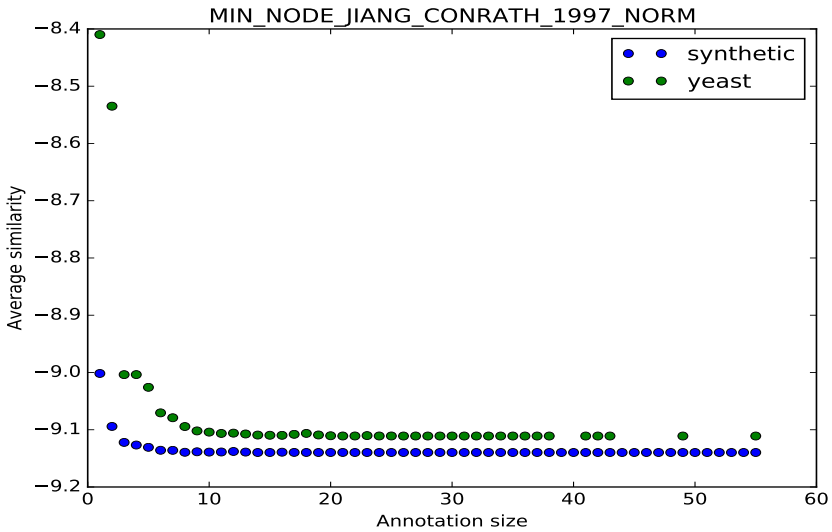

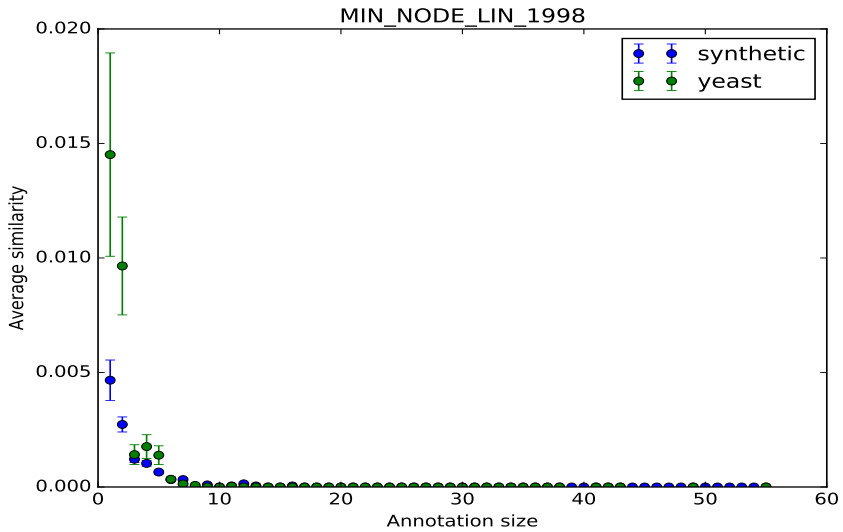

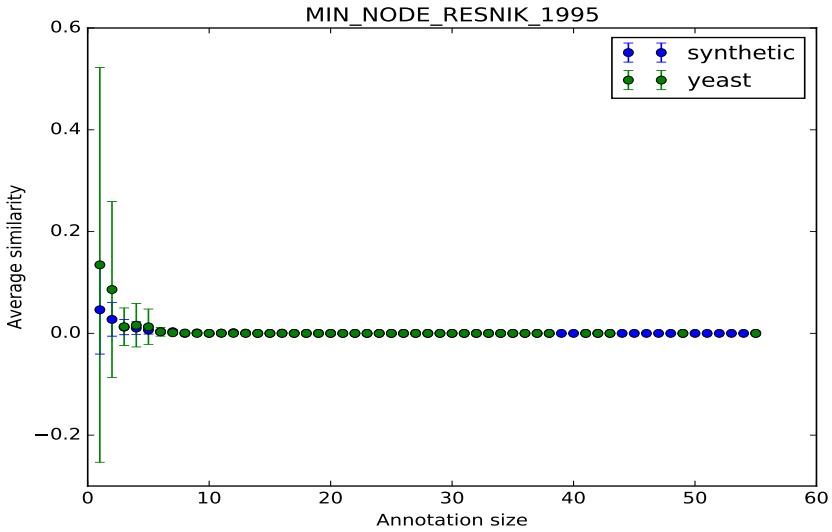

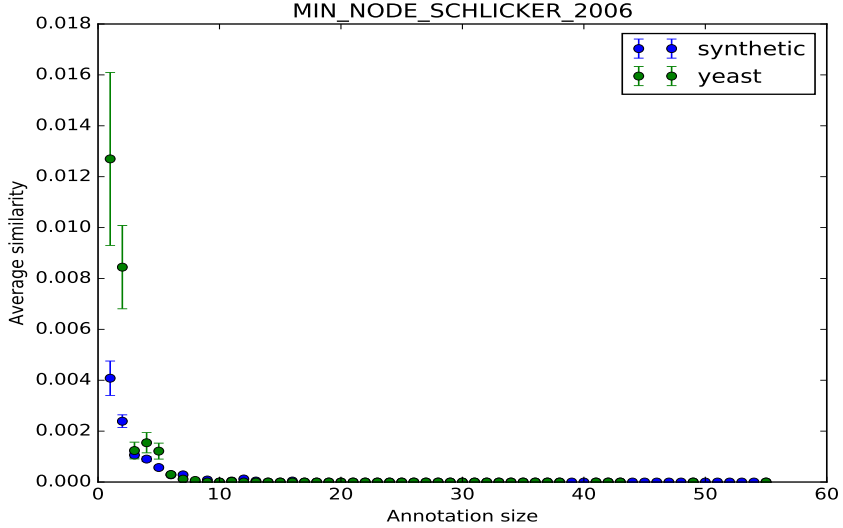

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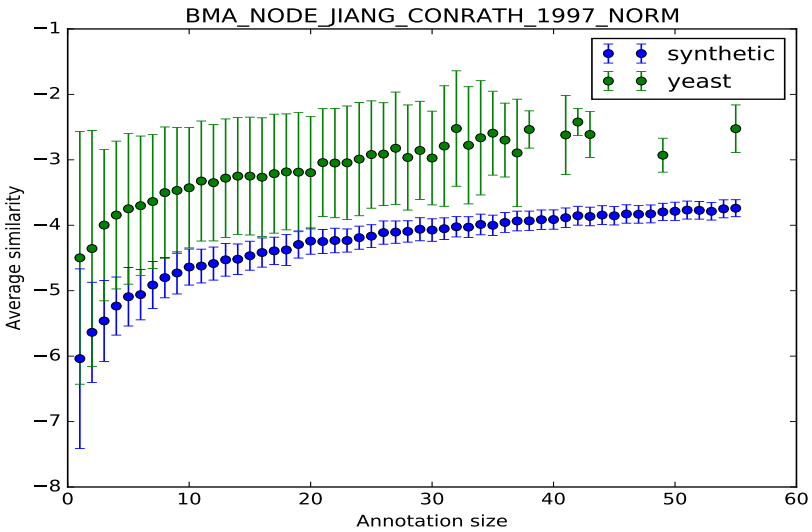

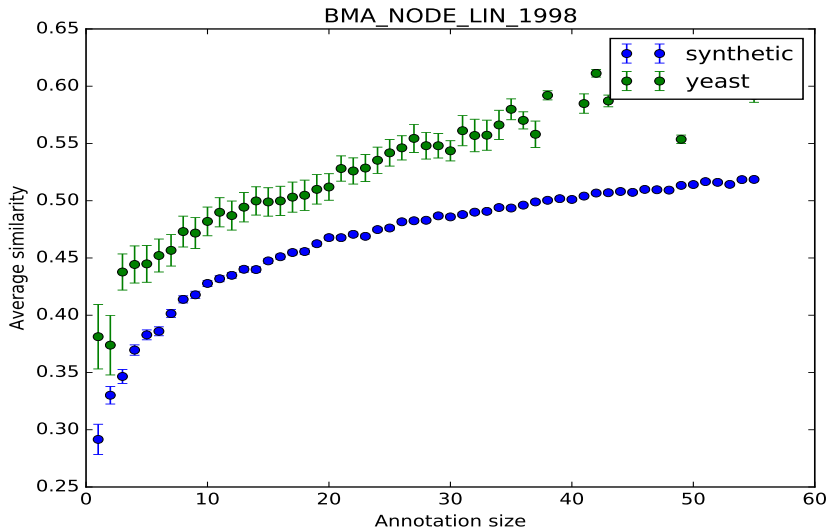

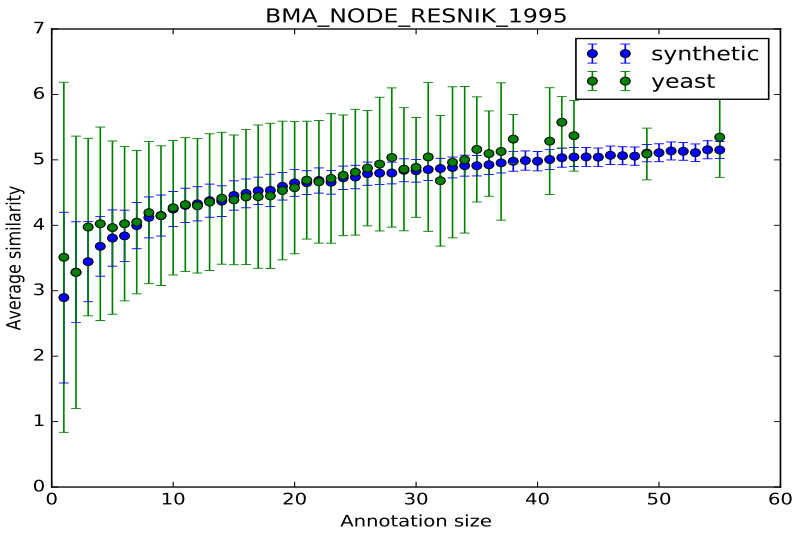

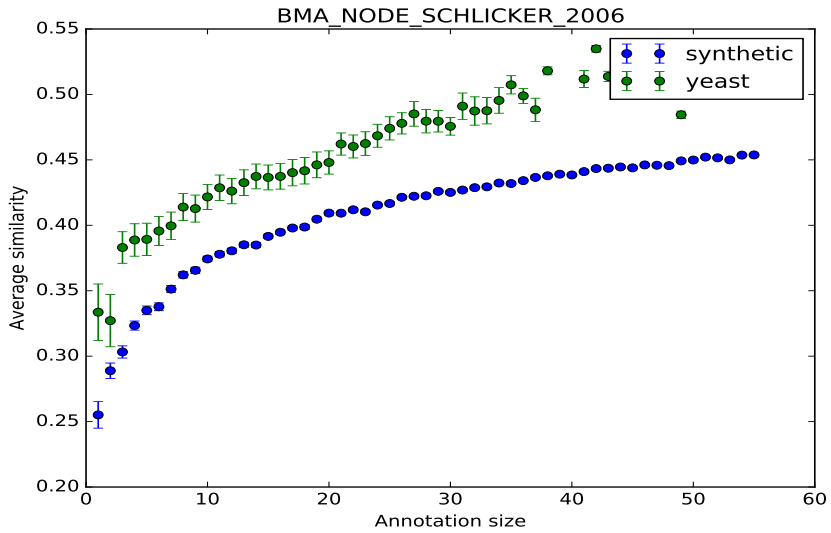

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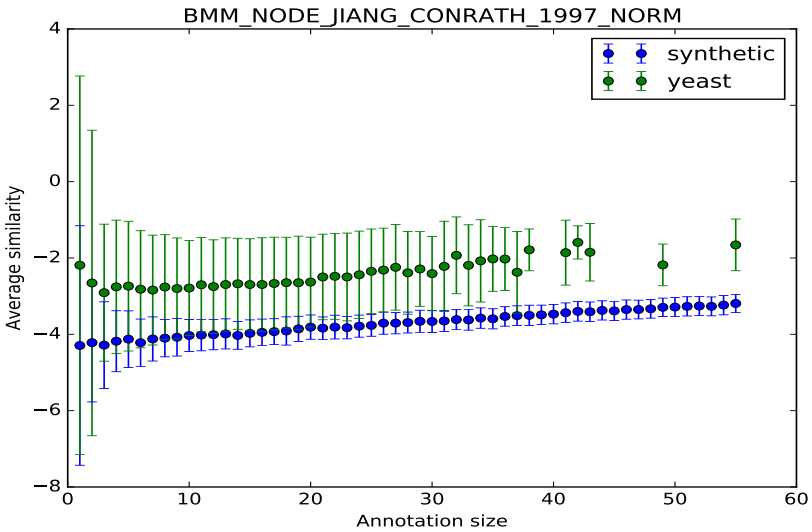

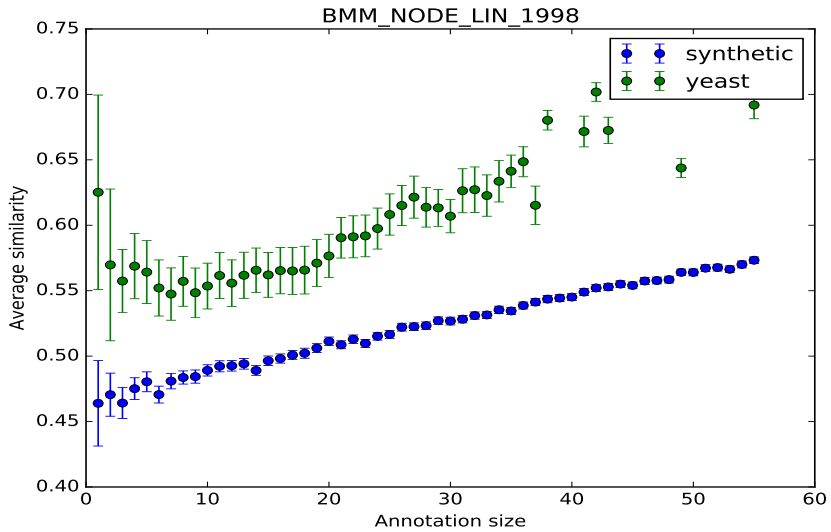

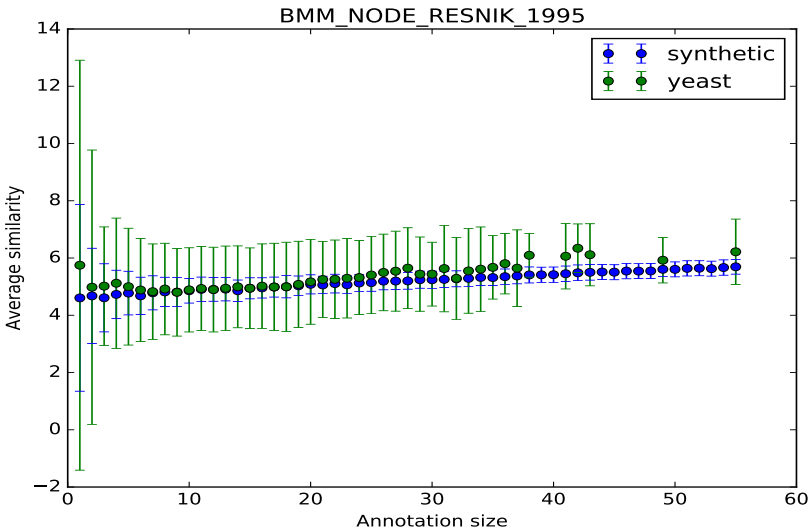

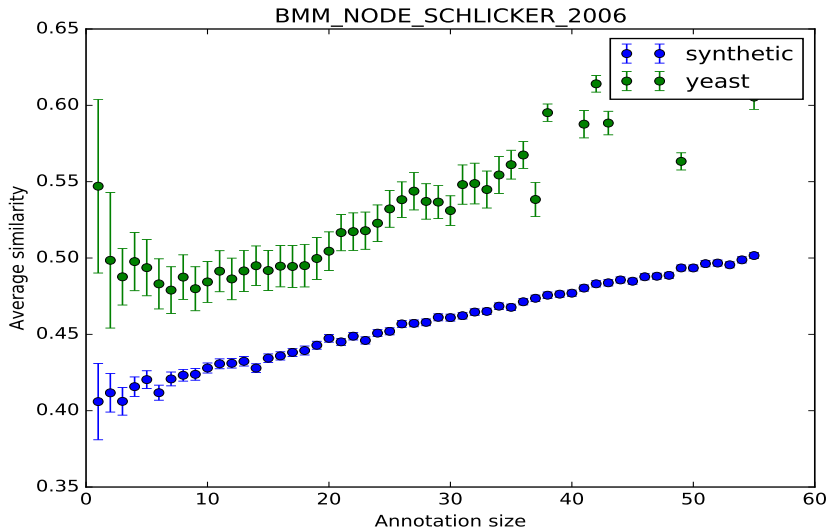

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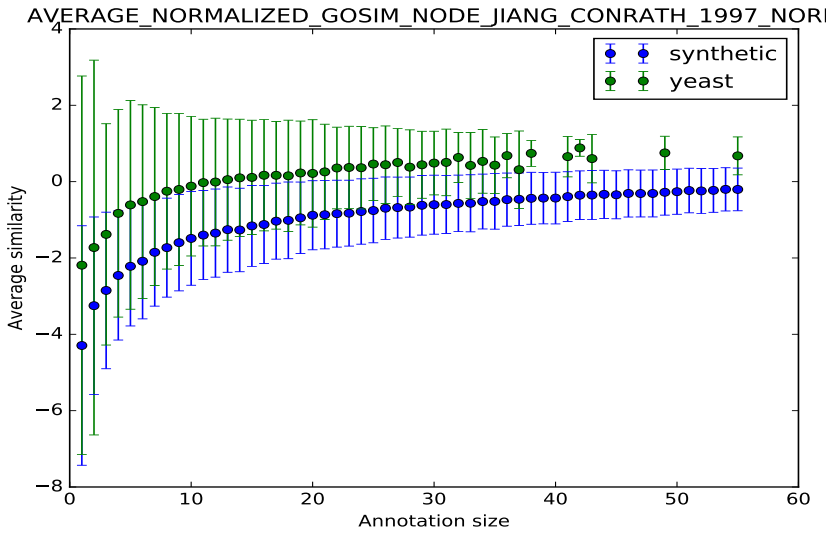

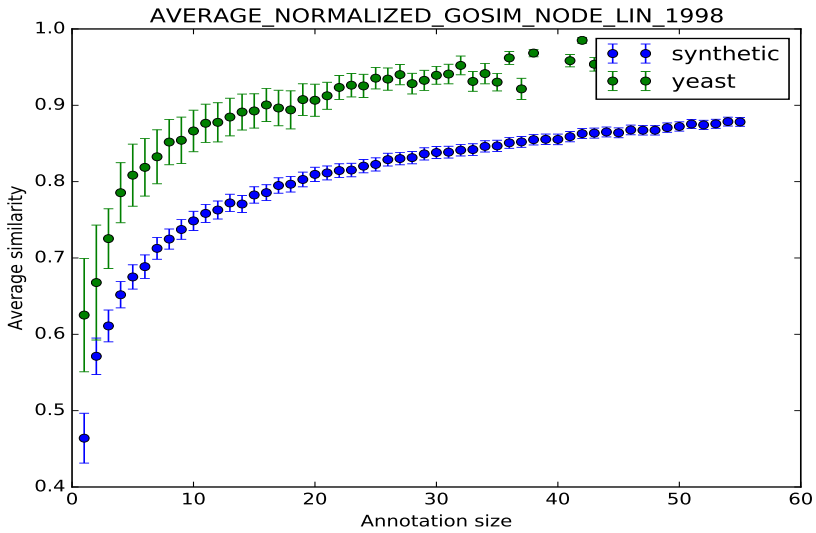

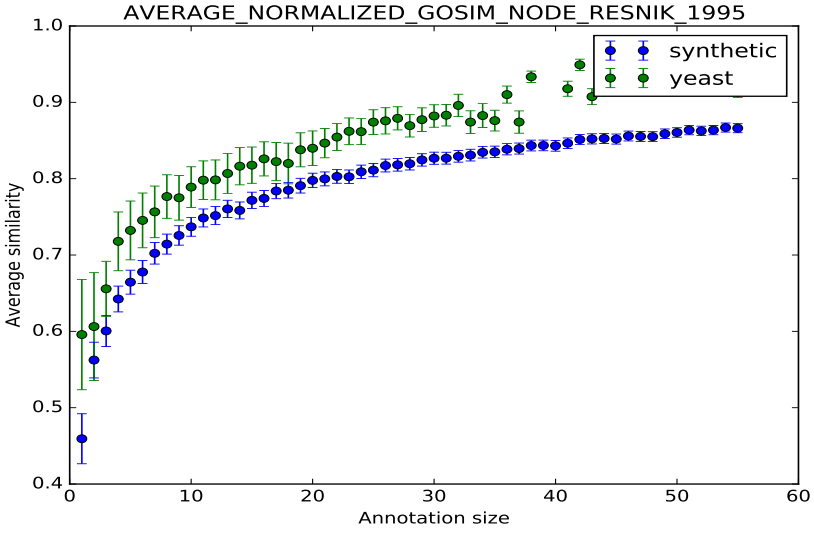

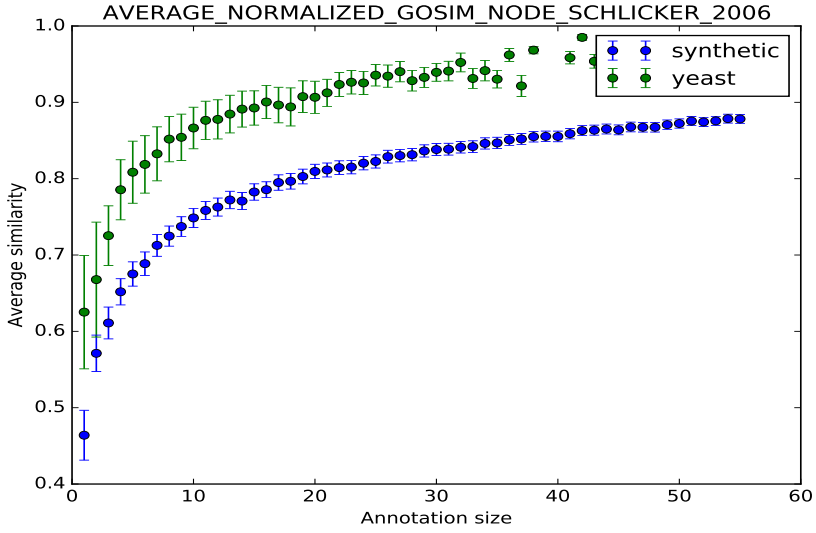

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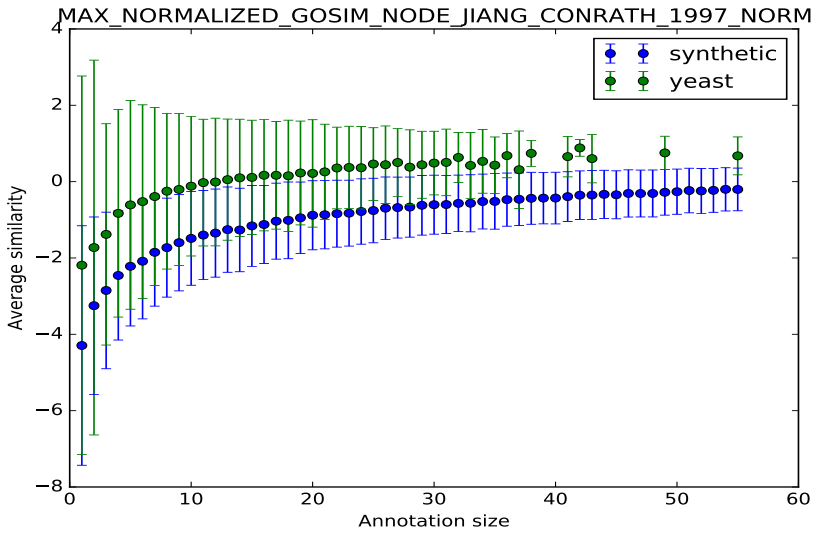

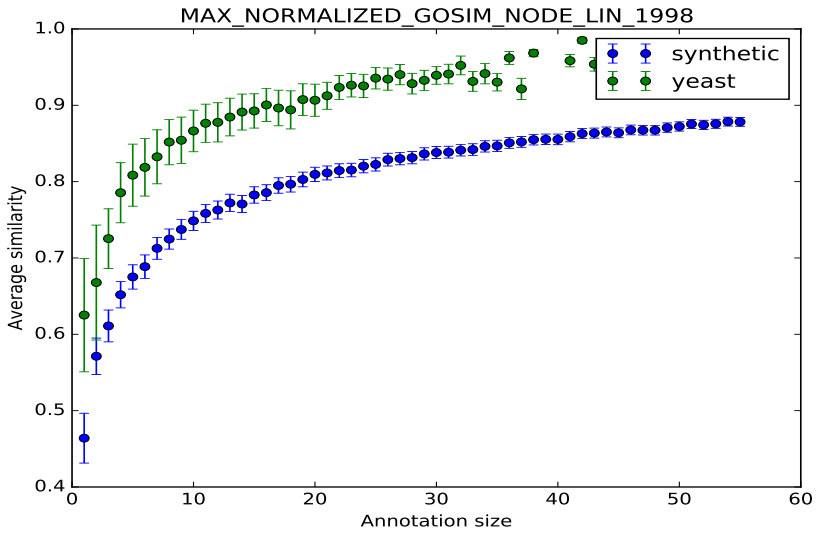

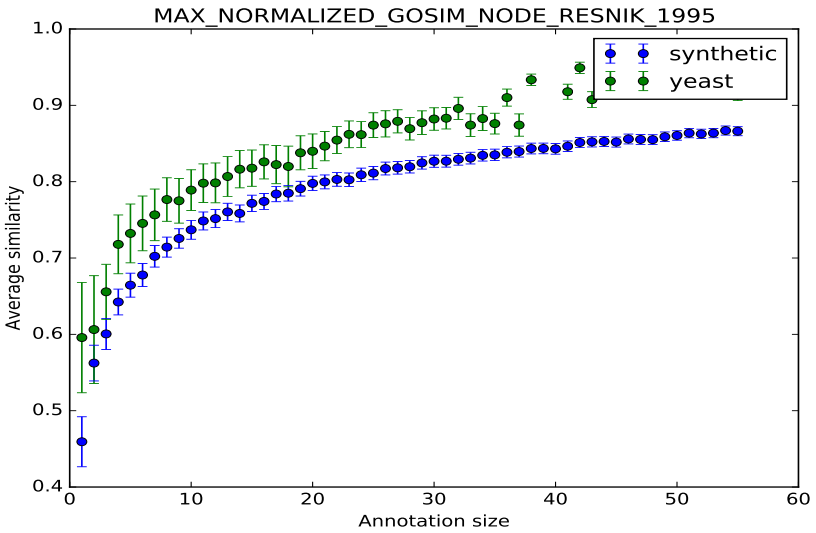

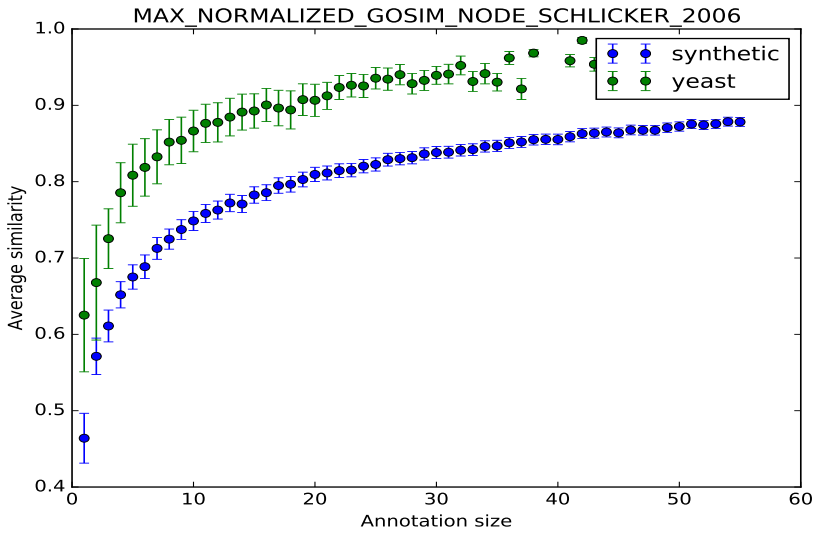

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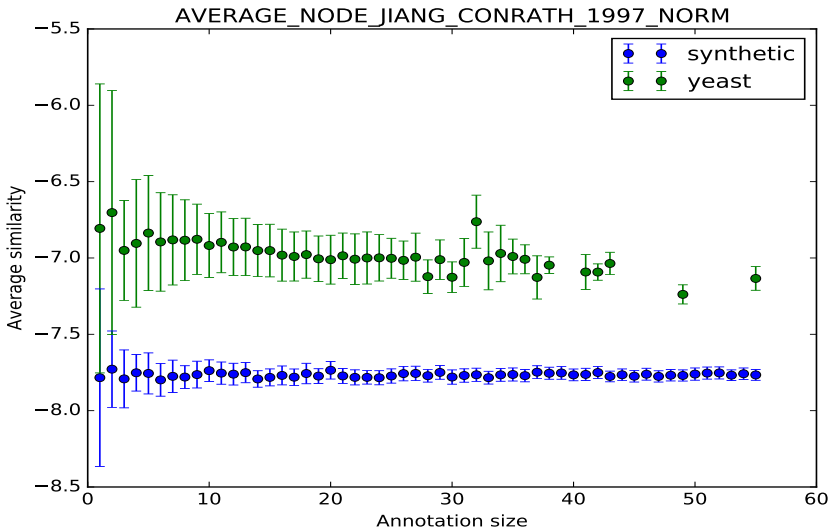
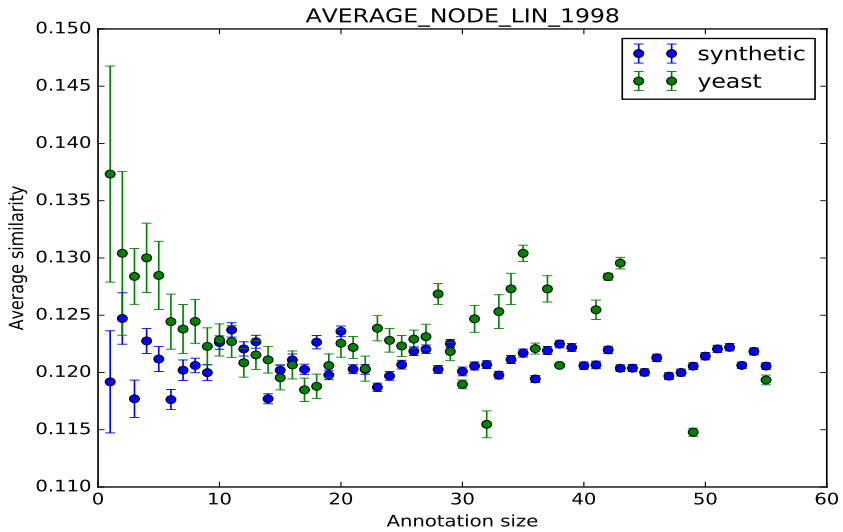
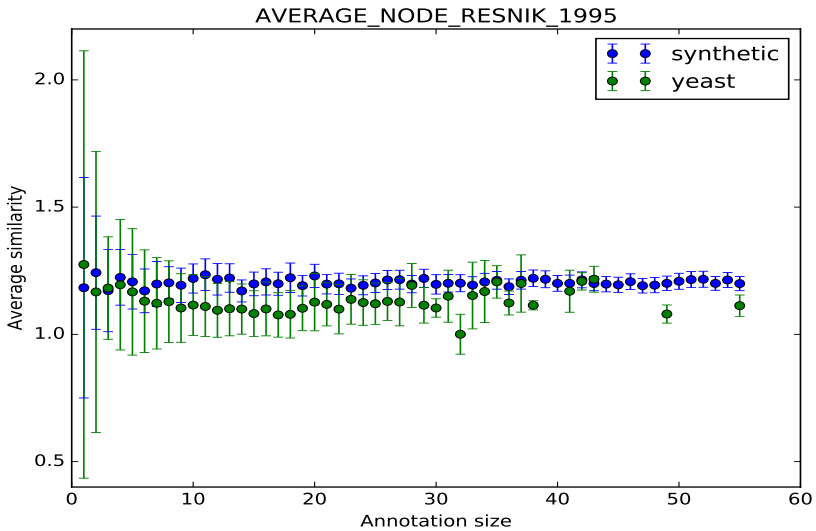
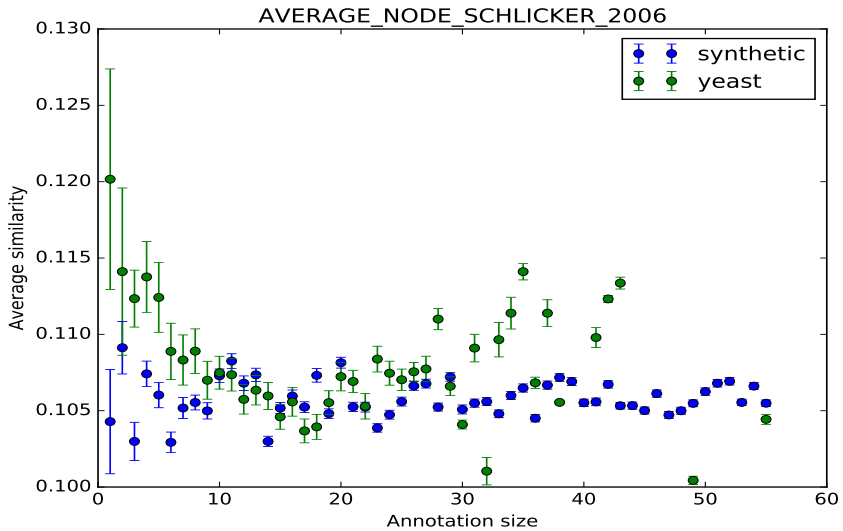
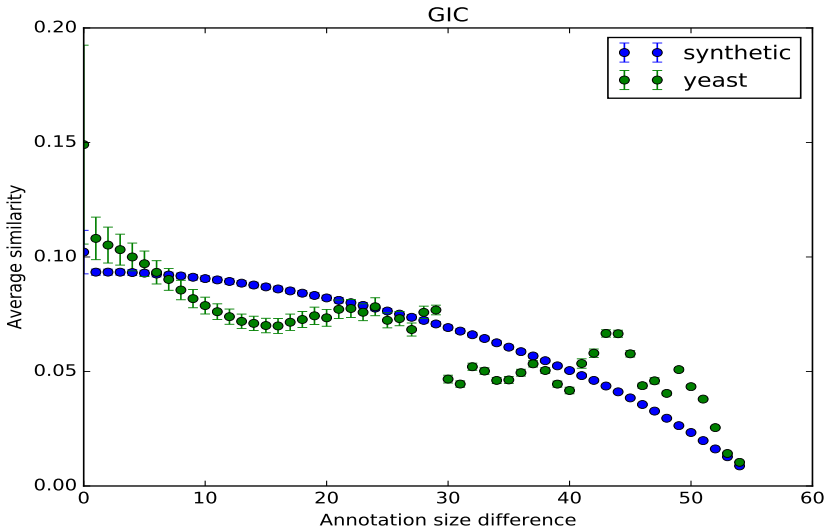


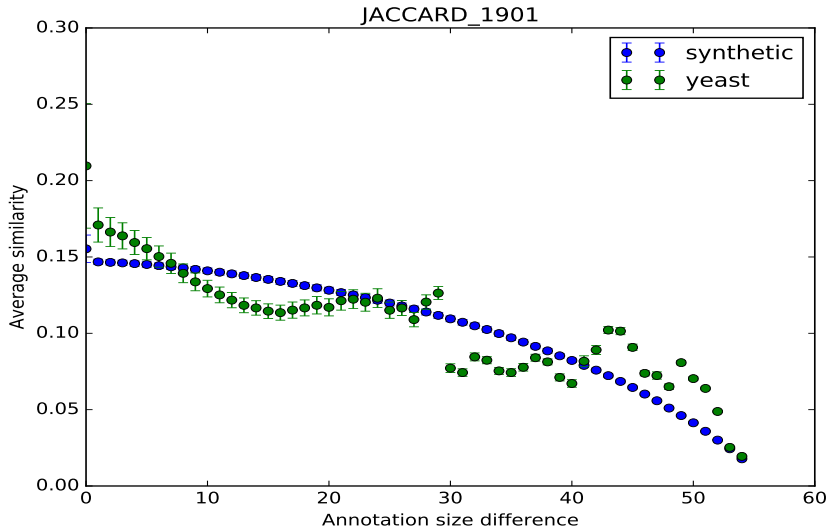


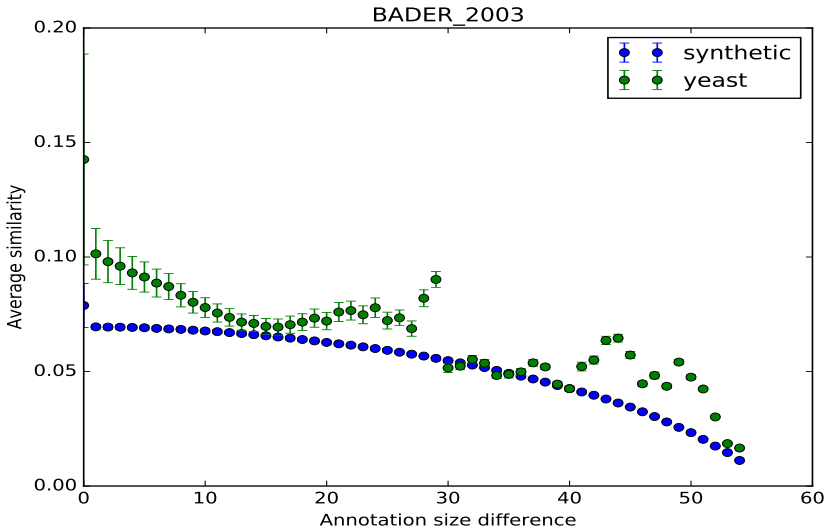


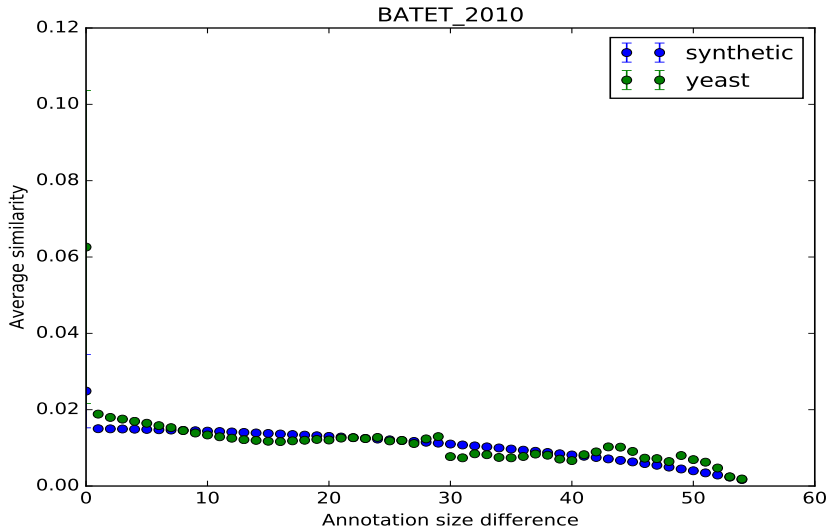


Annotation size difference - Groupwise Similarity Measures









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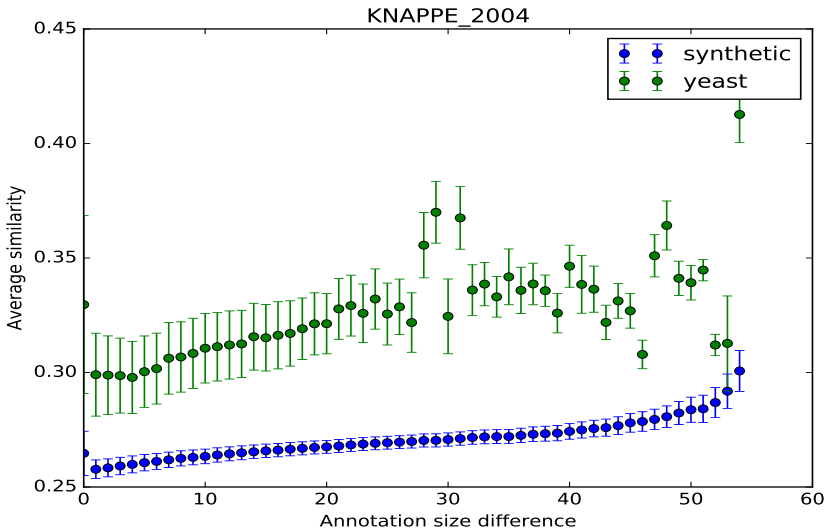
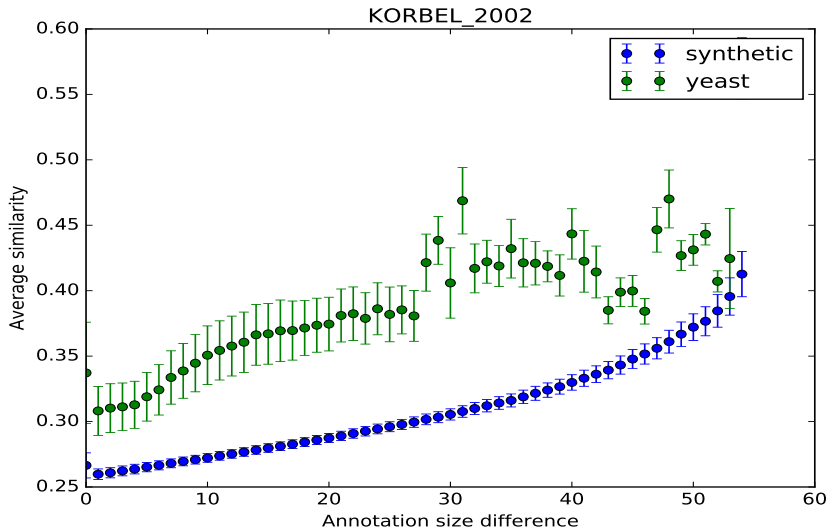
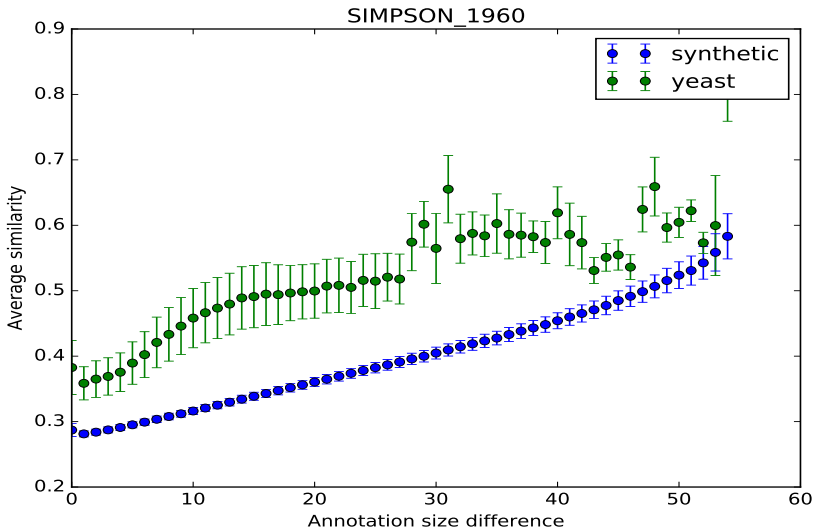
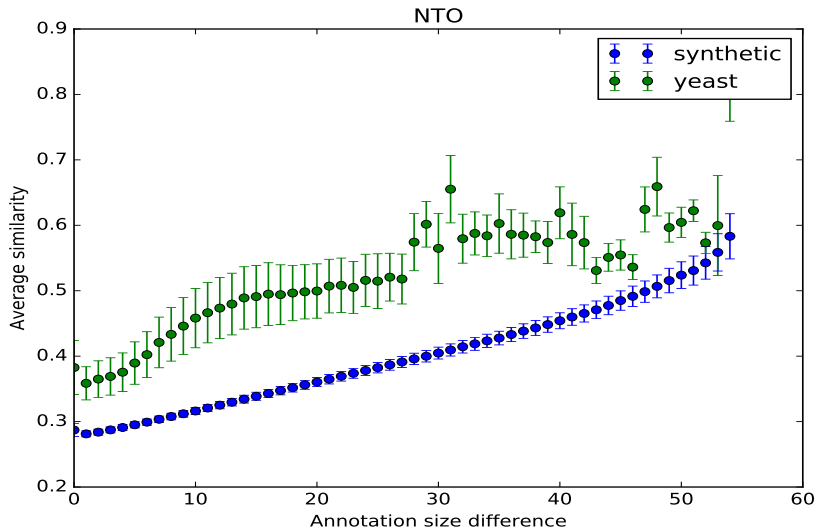
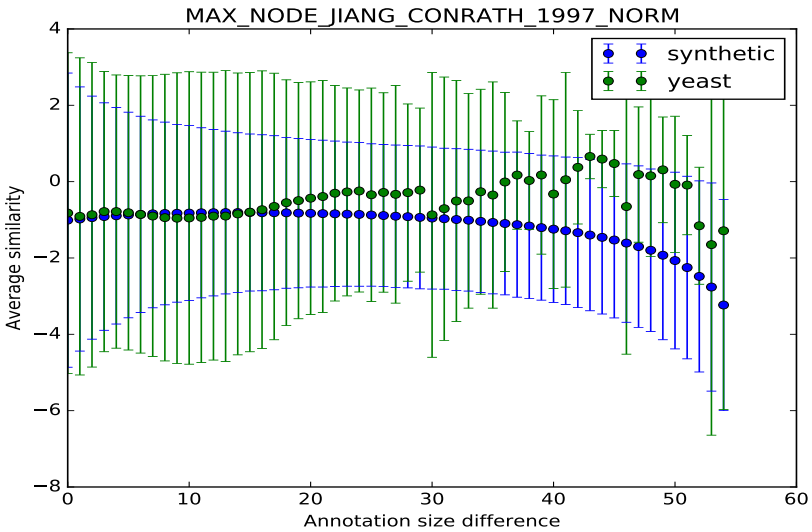


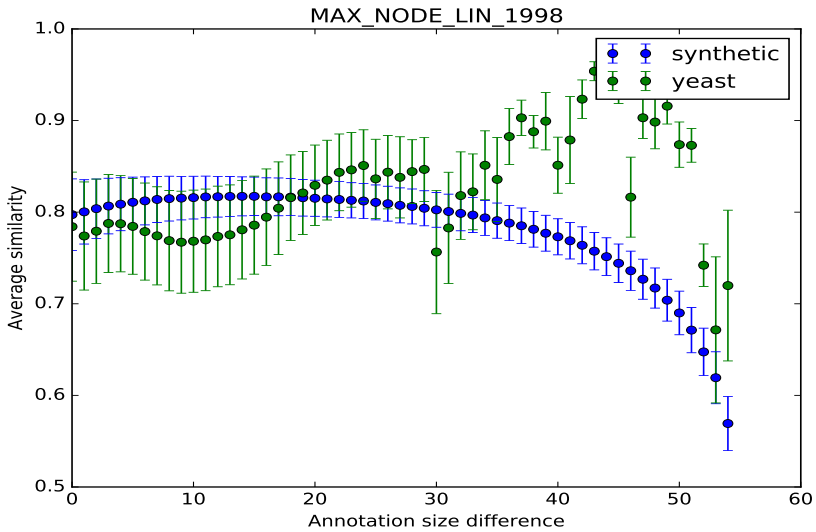


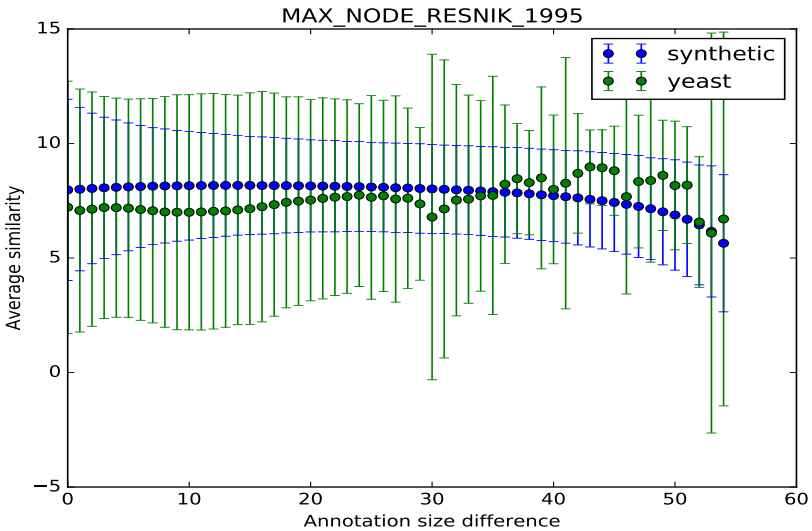


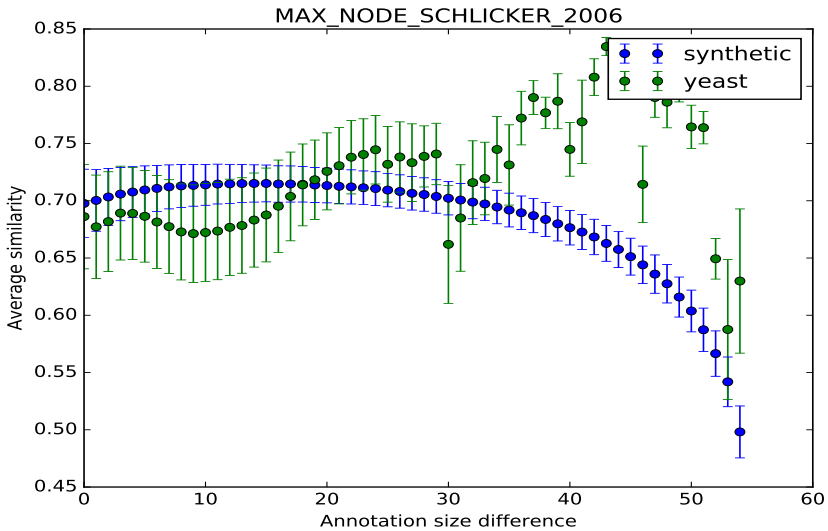


Annotation size difference - Pairwise Similarity Measures

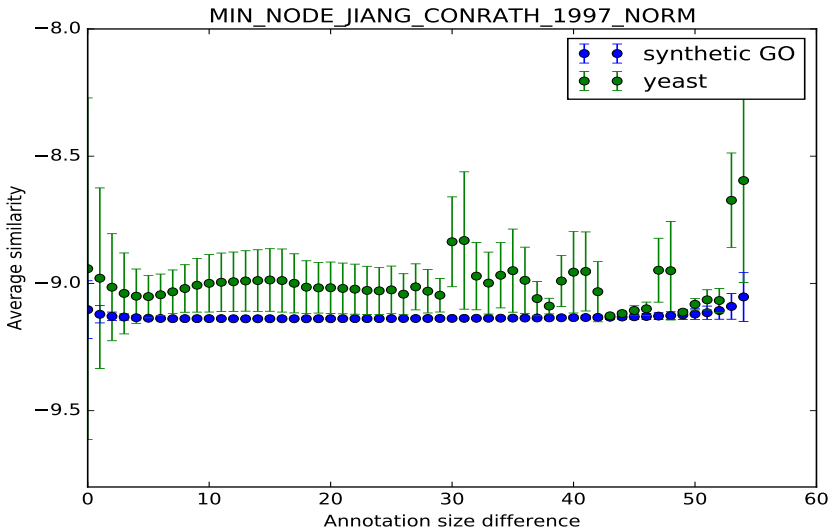


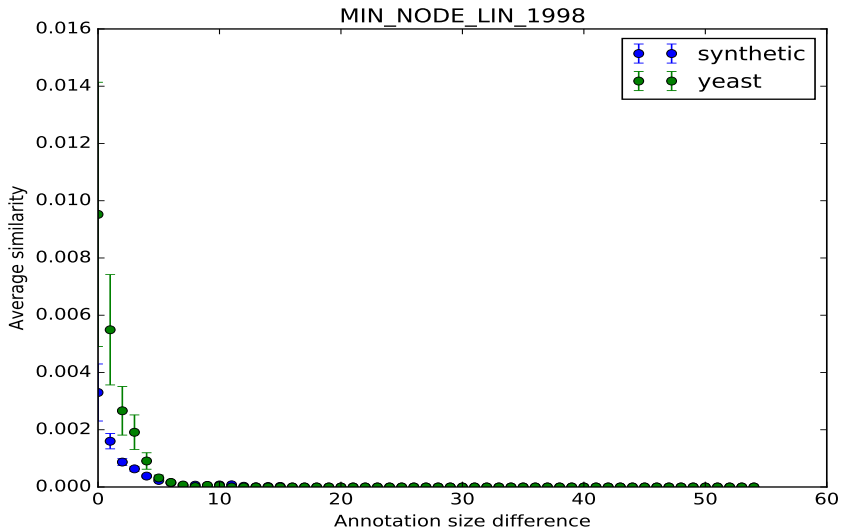


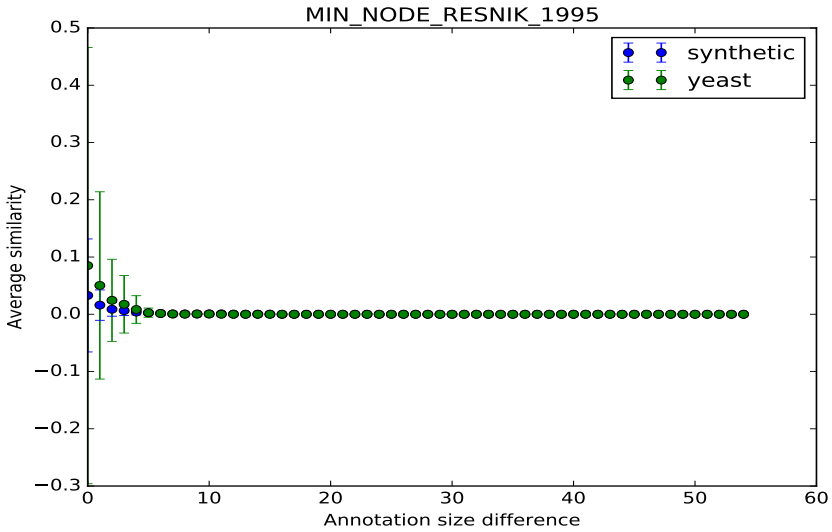


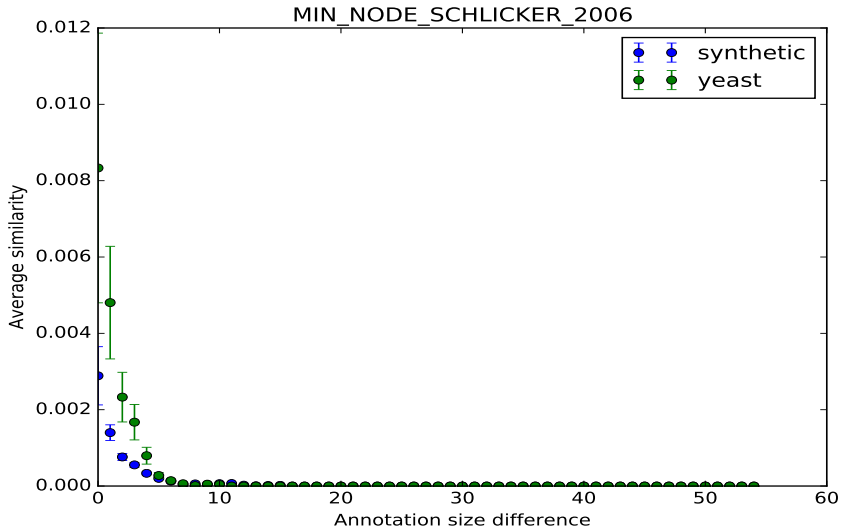


Annotation size difference - Pairwise Similarity Measures

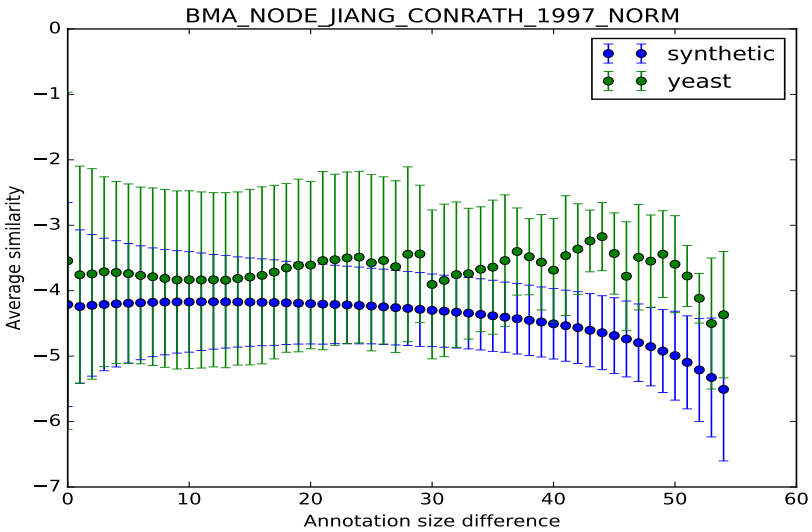


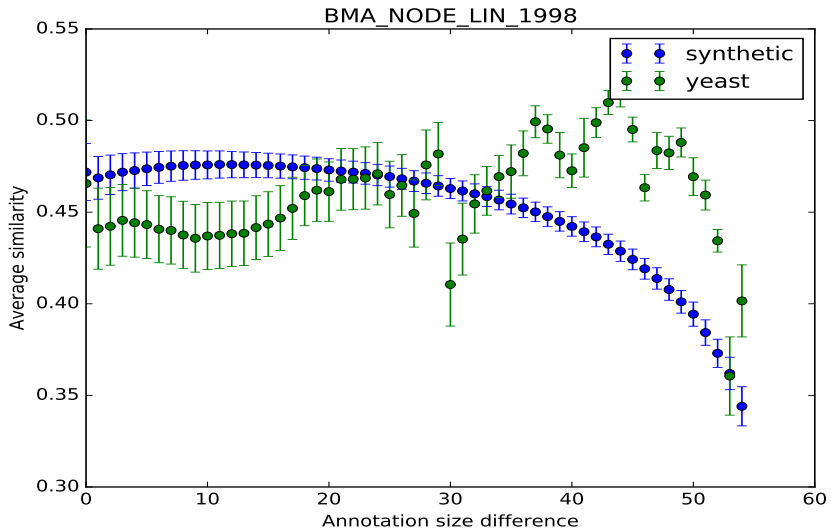


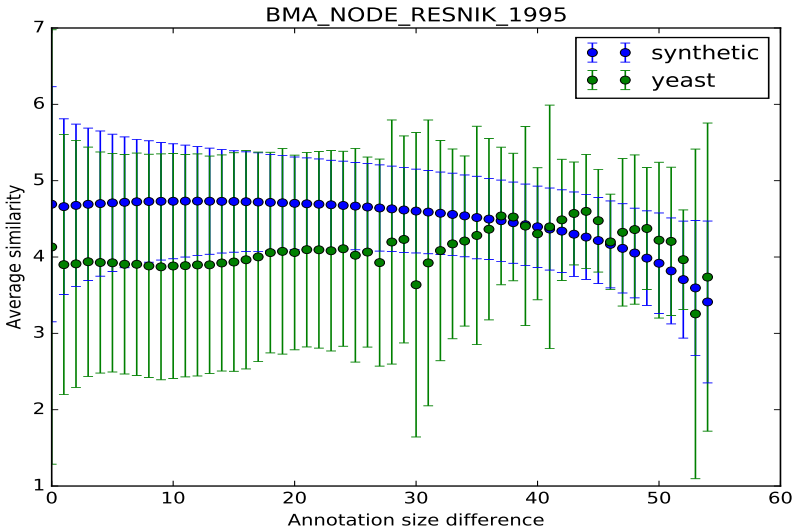


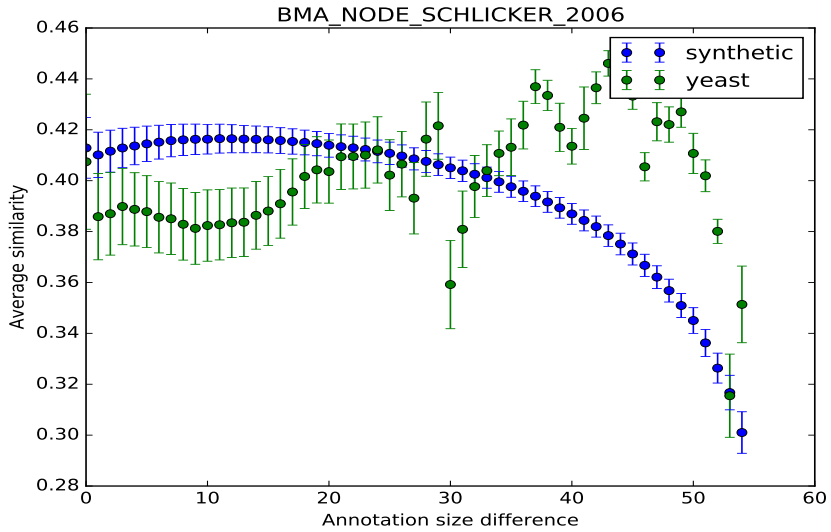


Annotation size difference - Pairwise Similarity Measures

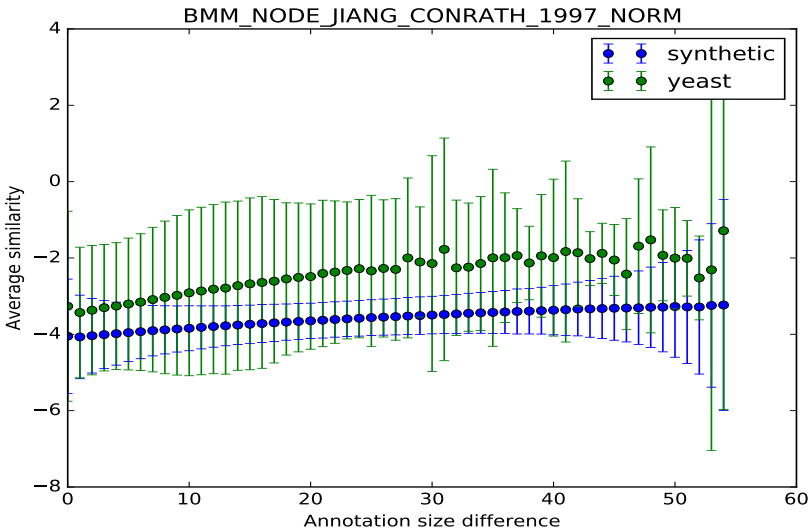


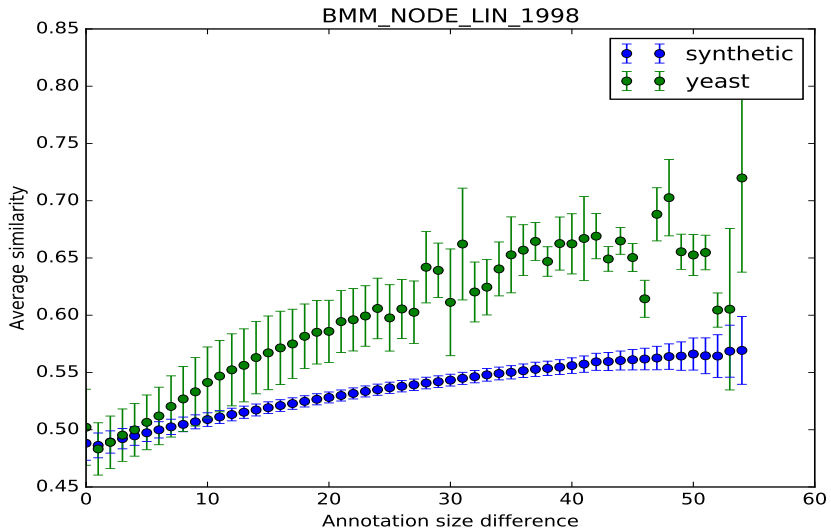


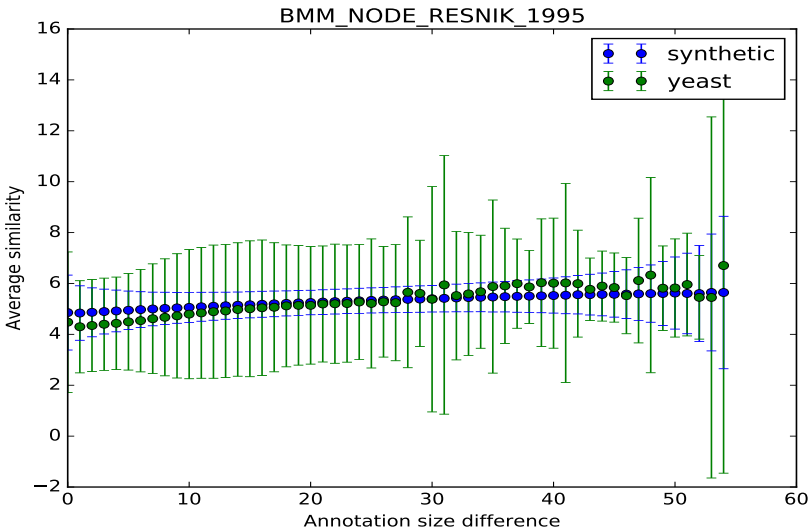


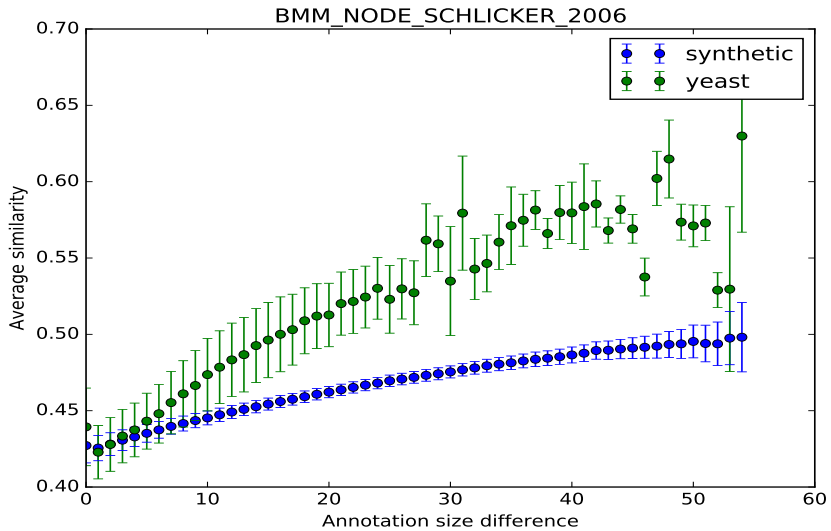


Annotation size difference - Pairwise Similarity Measures

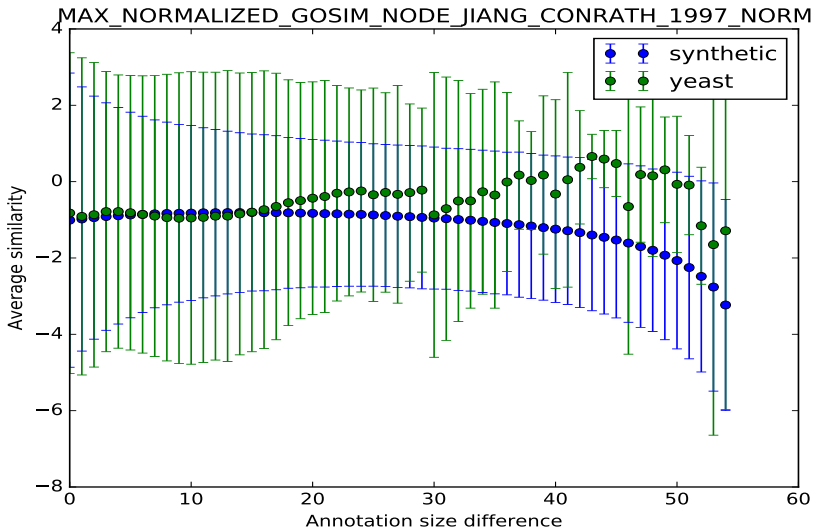


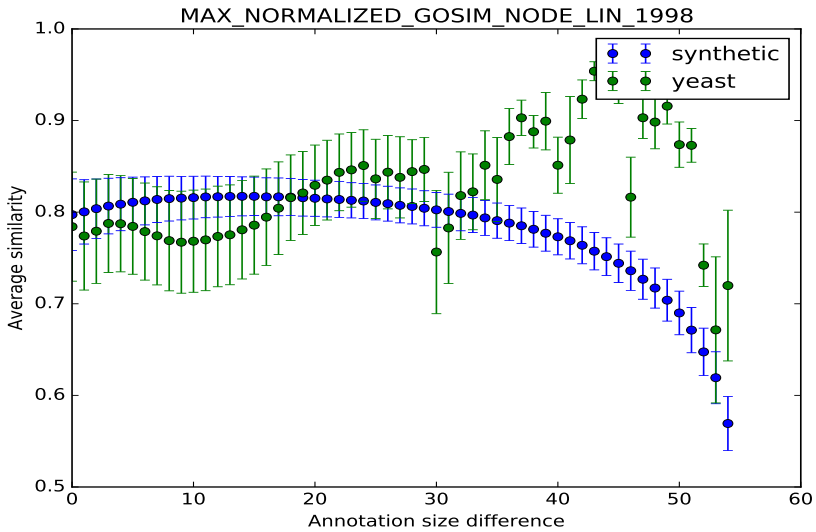


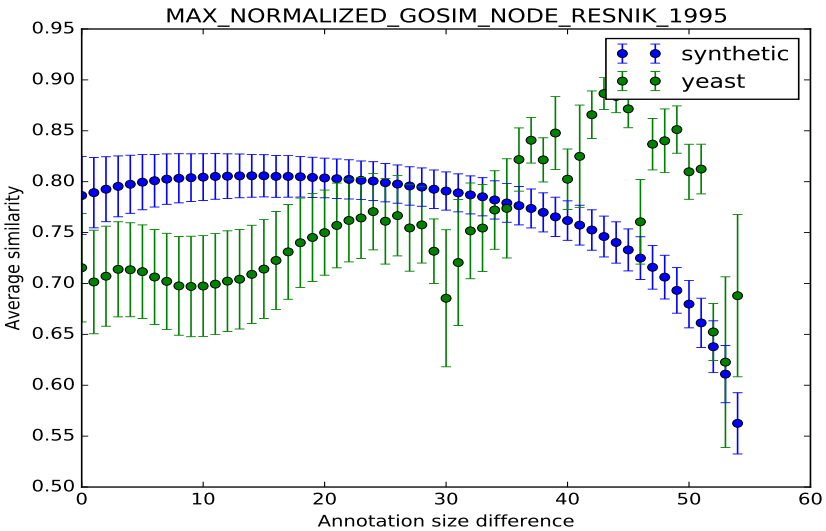


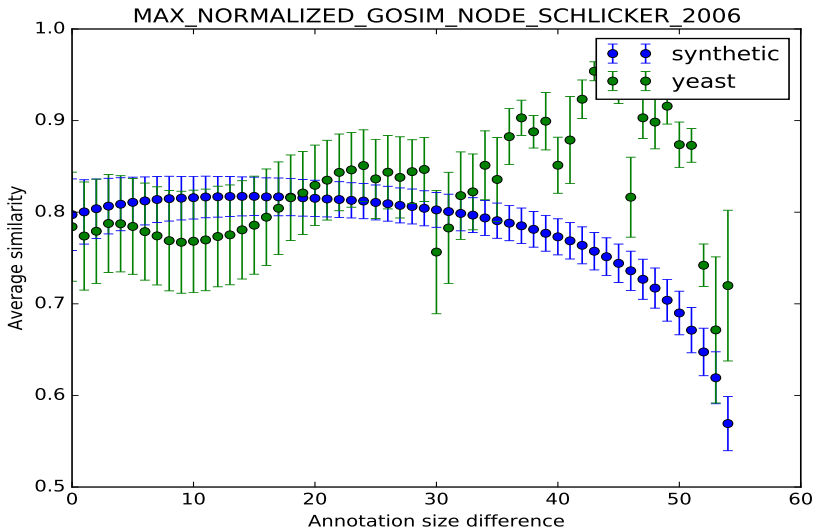


Annotation size difference - Pairwise Similarity Measures

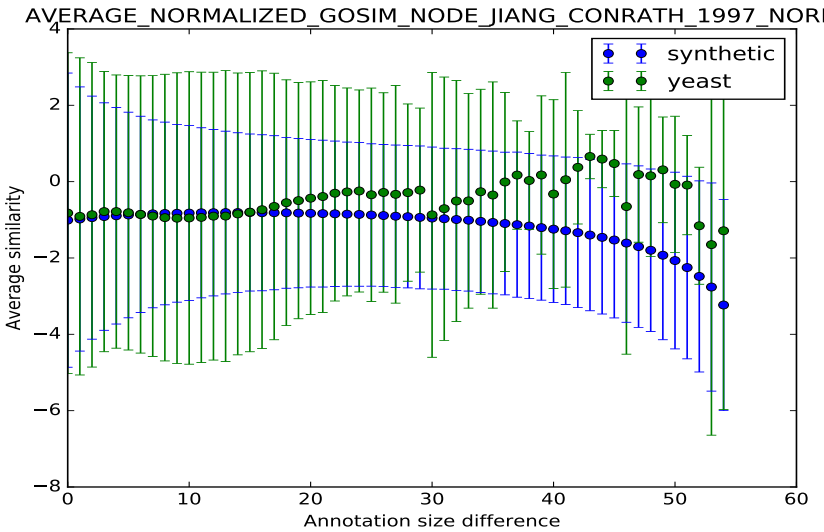


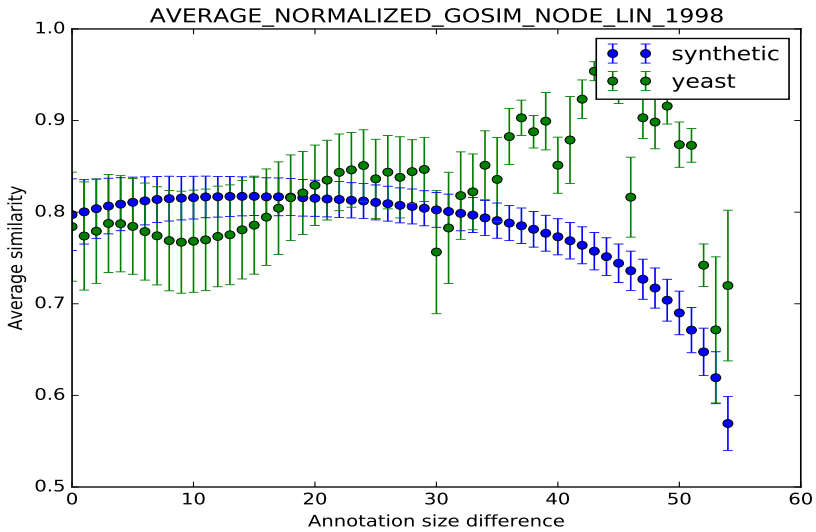


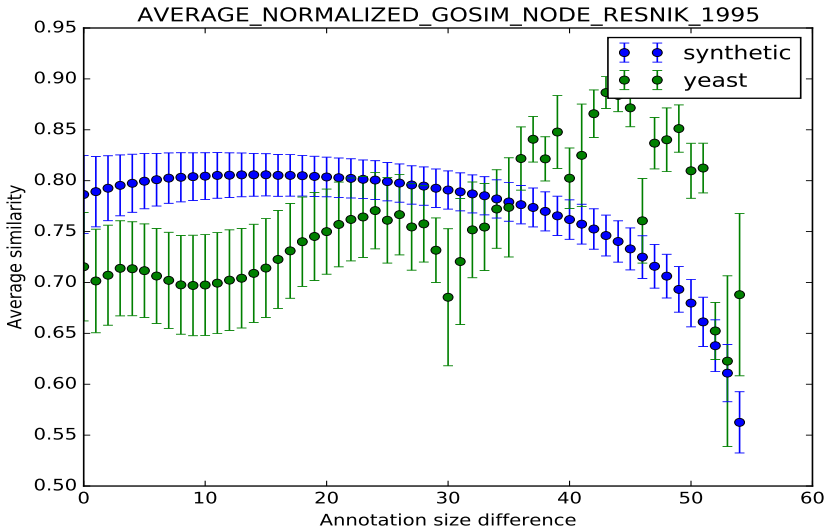


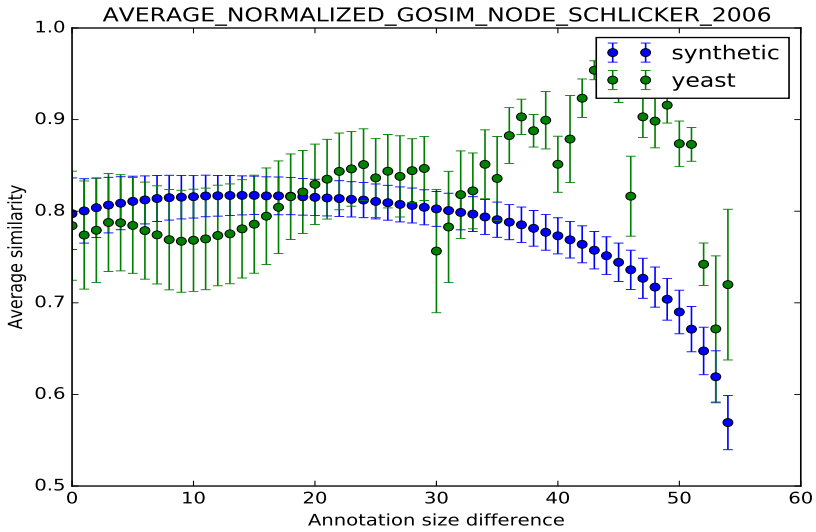


Annotation size difference - Pairwise Similarity Measures

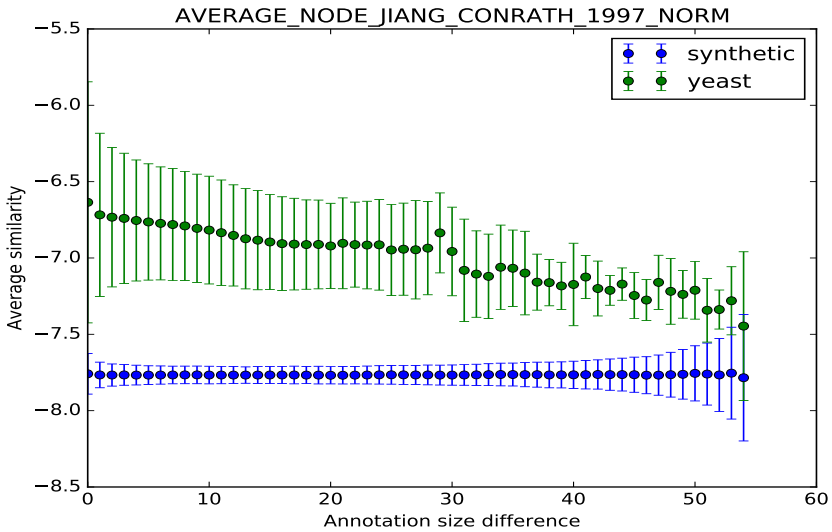


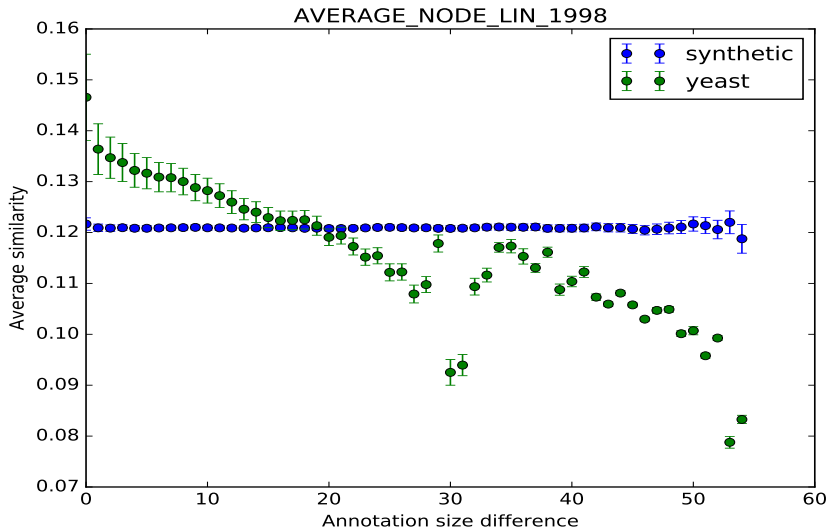


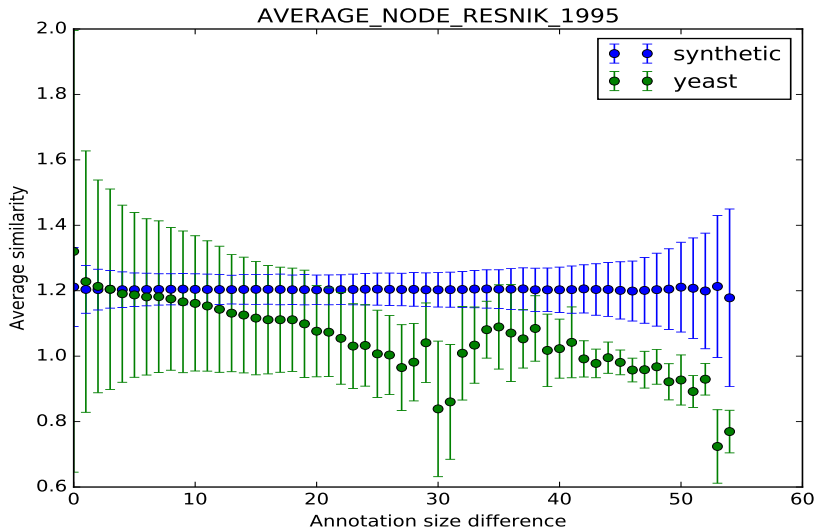


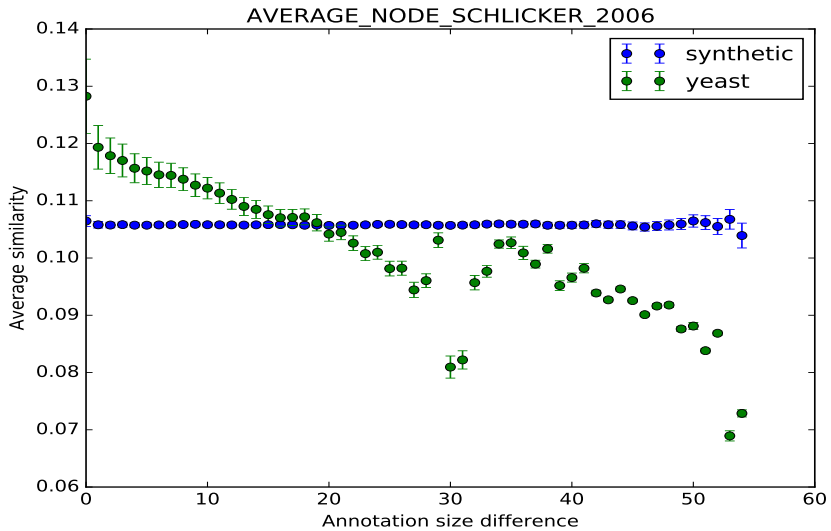


Annotation size difference - Pairwise Similarity Measures





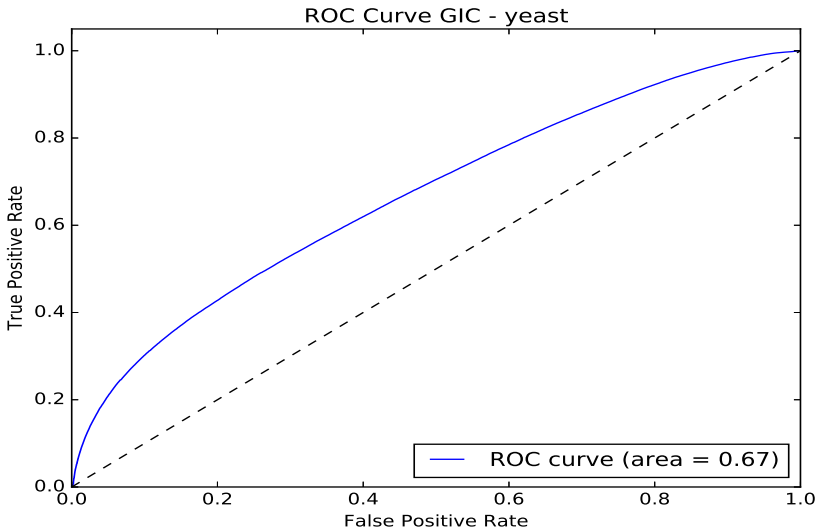


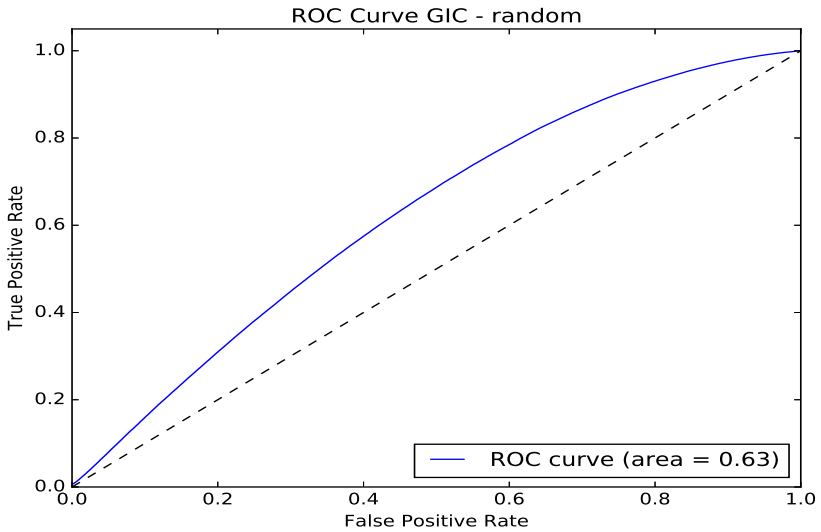


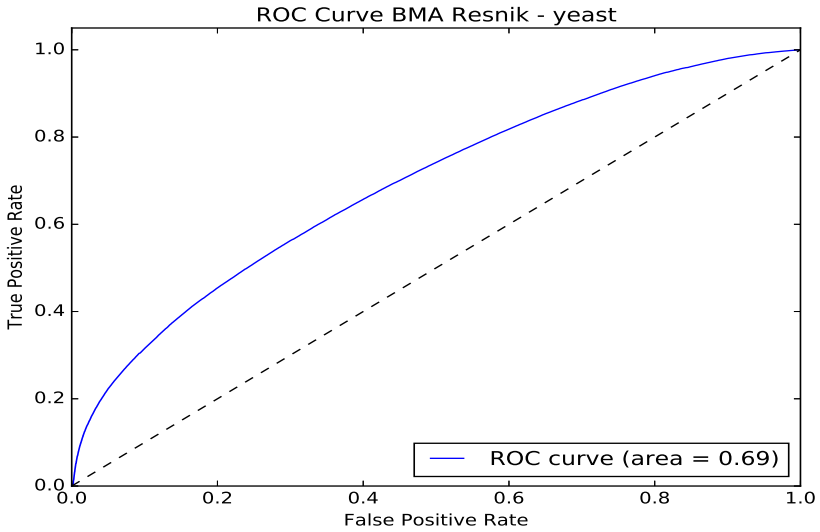
Summary

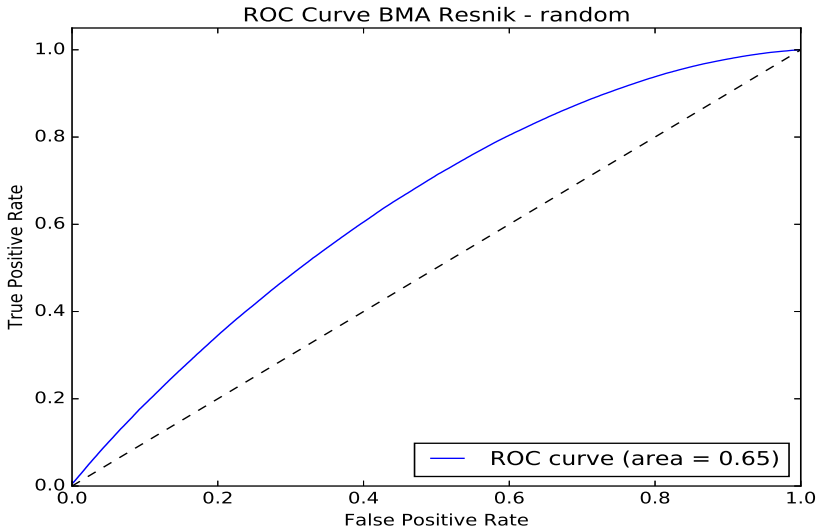
- Most of the similarity measures are sensitive to the annotation size
- Pairwise measures depend on combination
- Well annotated entities get higher similarities
- Studies which use similarity measures may be biased by annotation size

Protein-protein interaction predictions

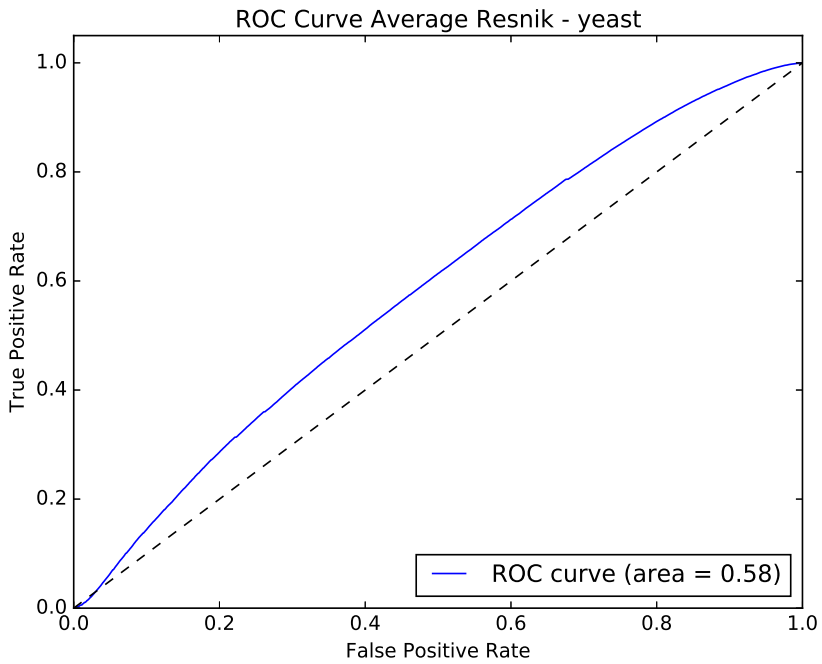


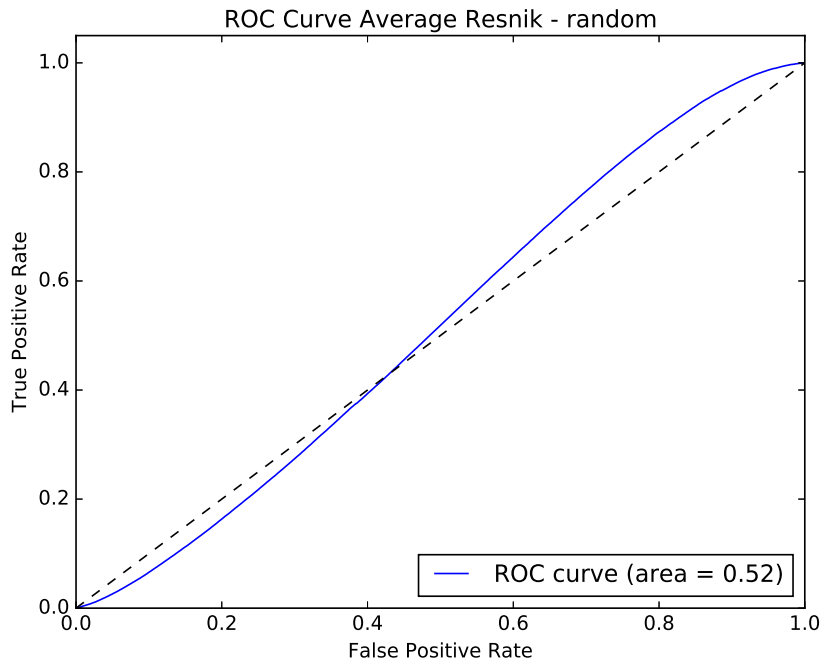






Protein-protein interaction predictions





Recommendations

- If annotations size variance is high, use pairwise similarity measures with average strategy

Thanks!

http://www.cbrc.kaust.edu.sa/onto/sim-eval/