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Collaborative RO1 with NCBO Semantics and Services Enabled Problem Solving Environment For Trypanosoma Cruzi

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Collaborative RO1 with NCBO
Semantics and Services Enabled Problem Solving Environment For Trypanosoma Cruzi
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**Driving Biological Problem**

*Trypanosoma Cruzi (T. cruzi):*

T. cruzi is a protozoan parasite and a key causative agent of Chagas disease. Chagas affects 18 million people in Latin America leading to heart disease and sudden death.

**Specific Objectives of Project**

- **Development and Use of a Suite of Ontologies Using a Phased Approach**
  - Ontologies enable a semantic approach to information management and analysis. Phased approach promotes reuse of existing ontologies for developing new ones.
- **Semantic Annotation of Experimental Data Using Multiple Ontologies**
  - Promotes integration of disparate data sources at multiple levels. Diverse ontologies will be aligned.
- **Efficient Query Processing, Visualization and Extensibility**
  - Expressive querying on semantically annotated data using query builders and tools for intuitive visualization of results.
- **Semantic-driven PSE for T. cruzi hosted in BioPortal at NCBO**
  - Generic framework that can be specialized for other pathogens. T. cruzi data available from the University of Georgia.

**Preliminary Work**

- **T. cruzi Research:**
  - Large amounts of experimental genomic and proteomic data on T. cruzi has been produced. For example, proteomic data includes:
  - Whole proteome analysis of 4 life cycle stages (600 files).
  - Proteomics of glycosyltransferases from 3 life cycle stages (27 files).
  - Quantitative proteome analysis of plasma membrane proteins from 3 life cycle stages (48 files).
  - Proteomics of RNA editing proteins from 2 life cycle stages (24 files).

These data are from over 700 individual experiments in eight separate proteome projects. These analyses resulted in the accumulation of greater than 1 million tandem mass spectra and 12,000 individual peptide identifications.

- **Semantic Bioinformatics for Glycoproteomics:**
  - Ontology Development and Alignment
  - In previous projects we have developed 3 deep domain ontologies - GlyCO, PropreO, and EnzyO. Participated in designing and developing tools for ontology engineering and alignment such as Protégé, PROMPT, and OPTIMA.
  - Scientific Data Annotation

**Proposed Research**

- **Problem Solving Environment for T. cruzi**
  - Intuitive querying of multiple sets of heterogeneous databases.
  - Formulate scientific workflows to test hypotheses.
  - Compliance of usability issues to promote ease of use among biologists.

**Semantic Bioinformatics for Glycoproteomics**

- **Ontology Development and Alignment**
  - Identifying genes for knockout in T. cruzi.
  - Diagnostic techniques for identification of best antigens.
  - Identify genes for knockout in T. cruzi.

Questions related to these factors involve tedious sifting of vast amounts of information of different types (genomic, proteomic, publications). This problem is prevalent for other organisms as well.

**Scientific Workflows for High Throughput Proteomics**

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**Scientific Data Annotation**

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  - Scientific Data Annotation

**Evaluation**

- **Validation**
  - Several example queries will be selected for validation.
  - Correctness of the answers provided by the PSE to the queries will be rigorously tested.
  - Usability and computation time will be qualitatively measured and compared with previous manually intensive approaches.

**Exploration**

- **New metabolic pathways will be investigated and auxiliary questions will be answered**
  - PSE will facilitate the discovery of new potential therapeutic and immunological targets within the T. cruzi biology.

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