Welcome to OntoGene

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1. Description

OntoGene is a research project based at the <u>Institute of Computational Linguistics</u> (<u>Department of Computer Science</u>) of the <u>University of Zurich</u>. Please check our <u>list of publications</u>.

Our work focuses on the extraction of semantic relations (e.g. *bind*, *activate*, *block*) between specific biological entities (such as **Genes** and **Proteins**) from the scientifical literature (e.g. <u>PubMed</u>).

Our approach is based upon high-precision robust syntactic parsing of the target documents.

2. Genia Dependencies

You are welcome to test our <u>dependency interface</u> which allows visualization and download of Dependency Annotations for the GENIA corpus

The full **DepGENIA v2.0** corpus is also <u>available for download</u>.

March 2006: DepGENIA v2.0 has been generated with a new version of the parser. DepGENIA v1.0 is still accessible from the same page.

3. ATCR Corpus

Please have a look at our work over the <u>ATCR corpus</u> (Arabidopsis Thaliana Circadian Rhythms), including syntactic and semantic querying.

4. OntoGene Web Query (v0.1)

A preliminary version of our interface for querying relations over GENIA and ATCR can be found here

5. BMC Bioinformatics publication

whatsnew

One of our papers has been recently published in BMC Bioinformatics, please see here

6. Password protection

Currently access to most of this site is restricted. Only the sections "Home" and "Resources" are publicly available. Different areas might have specific login/passwords, which we have

personally notified to those authorized to access them. Larger areas of the web site might become available in the near future.

Note:

The Pro3Gres parser has been already licensed to a number of academic institutions, among them: <u>MITRE</u>, the University of Sussex, the University of Geneva, the Tsinghua University (Beijing, China) and the Communication University of China (Beijing).