Exploratory Research on Semantic Knowledge Extraction for Biodiversity

Authors: Liu Jianhua, Liu Jianhua

Date: 2016-06-12T00:00:00+00:00

Abstract

[Objective] To expand the species-centered biodiversity knowledge extraction framework and explore methods for implementing semantic knowledge extraction.

[Methods] By integrating current mainstream research in biodiversity extraction and focusing on species, we designed a knowledge extraction framework encompassing multiple entities and inter-entity relationships. Utilizing numerous existing professional databases, we designed and implemented corresponding recognition methods.

[Results] We designed a species-centered knowledge extraction framework, explored and implemented semantic knowledge extraction methods for multiple entities and inter-entity relationships, thereby expanding the content and approaches for extraction in the biodiversity domain.

[Limitations] The completeness and accuracy of entity recognition in this study are significantly influenced by the underlying knowledge base, and the types of inter-entity relationships are limited to co-occurrence, hierarchical, and grammatical relations, requiring further investigation.

[Conclusion] This work expands the content and approaches for extraction in the biodiversity domain and can effectively support subsequent semantic retrieval and scientific computing.

Full Text

Study on Semantic Knowledge Extraction in Biodiversity

Jianhua Liu[1],[2], Ying Wang[1], Zhixiong Zhang[1], Chuanxi Li[1]
[1] National Science Library, Chinese Academy of Sciences, Beijing 100190, China
[2] University of Chinese Academy of Sciences, Beijing 100190, China

Abstract

[**Objective**] This study aims to expand the biodiversity knowledge extraction framework centered on species and explore semantic knowledge extraction methods. [**Methods**] By synthesizing current mainstream research in biodiversity extraction and adopting a species-centric approach, we designed a knowledge extraction framework encompassing multiple entity types and inter-entity relationships, and implemented corresponding recognition methods by leveraging numerous existing specialized databases. [**Results**] We developed a species-centered knowledge extraction framework and explored semantic knowledge extraction methods for various entities and their relationships, thereby expanding the scope and approaches of biodiversity domain extraction. [**Limitations**] The completeness and accuracy of entity recognition in this study are significantly influenced by the underlying knowledge bases, and the types of inter-entity relationships are limited to co-occurrence, hierarchical, and syntactic relationships, requiring further investigation. [**Conclusions**] This work expands the content and methodology of knowledge extraction in biodiversity, effectively supporting subsequent semantic retrieval and scientific computing.

Keywords: biodiversity; species; knowledge extraction; relation extraction

Classification Number: G250

This research is supported by the National Twelfth Five-Year Science and Technology Support Plan Project "Construction and Application Demonstration of Knowledge Organization System for Foreign Scientific and Technical Literature Information (STKOS)" sub-project "Automatic Processing of Information Resources, Intelligent Retrieval and STKOS Application Service Integration" (Project No.: 2011BAH10B05).

With global warming and frequent natural disasters, species extinction is accelerating, making biodiversity conservation and sustainable utilization an increasingly critical focus of research. This has led to a surge in relevant scientific publications. A key challenge in biodiversity informatics is helping researchers rapidly discover needed information from documents rich in species names (scientific names, synonyms, common names, variety names, etc.), genes, experimental equipment, and other entities. In response, researchers are actively leveraging existing biodiversity databases—such as species catalogs, specimen collections, image libraries, and gene banks—to extract knowledge objects from biodiversity descriptive texts or literature. Through semantic content annotation techniques, they aim to achieve automatic deep indexing of knowledge objects and enable semantic integration and linking among digital resources, thereby supporting advanced semantic retrieval, data mining, and scientific computing.

Building upon an analysis of current research in biodiversity information extraction and addressing the practical requirements of the "Biodiversity Domain Ontology Construction and Semantic Organization Application Demonstration

Platform" project at the National Science Library, Chinese Academy of Sciences, this paper designs a biodiversity semantic knowledge extraction framework, explores and implements corresponding semantic knowledge extraction methods, and develops a biodiversity demonstration platform.

2 Related Research Overview

Through the efforts of numerous researchers, many information extraction tools for the biodiversity domain have emerged. These tools employ either single methods such as natural language processing, dictionary matching, machine learning, rule templates, shallow or deep syntactic parsing, and probabilistic classification, or hybrid approaches combining several of these techniques. The majority of these tools focus on recognizing various species names (scientific names, synonyms, common names, variety names, etc.), while some also address species trait identification. Anne E. Thessen et al. [1] reviewed current research on species name recognition using natural language processing and machine learning algorithms in biodiversity science, while Nona Naderi et al. [2] introduced various biomedical domain tools available within the GATE framework. These publications provide comprehensive reviews of conventional biodiversity information extraction workflows, mainstream extraction methods (dictionary-based, rule-based, shallow parsing, deep syntactic parsing, etc.), and major extraction tools at each stage. Rather than repeating these discussions, this paper focuses on examining the extraction content in the biodiversity domain by analyzing current important extraction tools, providing a foundation for our proposed knowledge extraction framework.

Current biodiversity extraction research can be summarized into the following main categories:

2.1 Species Name Recognition and Normalization

Due to variations in language and regional terminology, the same species name appears in diverse forms in scientific literature. Some follow the standard binomial (or trinomial) nomenclature in Latin, consisting of genus and species names (with an additional subspecies name for subspecies), where the genus name precedes the species name, the genus is capitalized, the species name is lowercase, both are fully spelled out, and the author' s surname typically follows [3]. Others use abbreviations with only the genus initial and full species name. Some employ common names (in English or other languages, which may vary across countries or regions) [4]. These variations significantly increase the difficulty of species name recognition. Consequently, many researchers have focused specifically on species name recognition, normalization, and organization, which represents the mainstream of current biodiversity extraction research. Notable achievements include dictionaries for species name recognition and normalization such as NCBI taxonomy [5], BioNames [6] (an online database linking animal names with source descriptions, classifications, and phylogenetic trees), and the Species 2000 global species catalog [7], as well as mature recognition tools like NetiNeti [8], Linnaeus [4], OrganismTagger [9], and TaxonGrab [10].

2.2 Species Trait Recognition

For taxonomic researchers, species trait descriptions—such as the color and length of roots, stems, and leaves—are crucial references for species classification. Therefore, some bioinformatics researchers have explored automatic recognition methods for various species traits. Taylor [11] manually established rules and dictionaries based on textual syntactic features to identify species parts, characteristics, and states. Tang et al. [12] built upon this work by using predefined templates for supervised learning of rules to recognize leaf shape, size, color, arrangement, and fruit shape characteristics. Hong Cui et al. [13] developed CharaParser, which employs heuristic methods and syntactic features to generate rules and effectively recognizes multiple species traits. Duan Yufeng et al. [14] continue to explore information extraction from Chinese plant species diversity descriptive texts.

2.3 Biological Network Recognition [15]

Various biological entities (species, molecules, genes, proteins, etc.) have multiple relationships that can be expressed as network graphs, enabling biological system analysis through graph analysis [16]. Proteins and genes are major focuses in biomedicine, and research on their recognition extends beyond biodiversity. In current biodiversity literature, researchers can identify species phylogenetic relationships through gene sequencing or study related issues by using protein or gene technologies to influence biological internal and external environments or characteristics. Therefore, recognizing proteins and genes involves not just identifying the named entities themselves but also extracting biological network relationships formed by various biological entities through verbs (or verb phrases), prepositions (or prepositional phrases), possessive forms, and other connectors. This enables subsequent resource reorganization, semantic retrieval, and computational analysis.

3 Semantic Knowledge Framework Design

Based on the analysis of current extraction content and related tools in biodiversity, and addressing the practical requirements of the "Biodiversity Domain Ontology Construction and Semantic Organization Application Demonstration Platform" project at the National Science Library, Chinese Academy of Sciences, we manually annotated 100 scientific documents in the biodiversity domain. Centering on species, we comprehensively analyzed potential knowledge unit types related to species research and their interrelationships, designing the biodiversity semantic knowledge framework shown in [Figure 1: see original paper]. This framework serves as the foundation for our knowledge extraction and organization efforts.

The framework comprises two aspects of semantic knowledge: semantic knowledge units and semantic relationships between these units.

3.1 Knowledge Units in the Semantic Framework

Knowledge units refer to the semantic types listed in each text box in [Figure 1: see original paper]. In scientific literature, these units typically appear as named entities or phrases. Annotating mentioned named entities or phrases in literature according to the semantic types defined in [Figure 1: see original paper] enables recognition of these semantic units. All knowledge unit semantic types in [Figure 1: see original paper] center on the species in the middle, covering various aspects including names, distribution, characteristics, developmental stages, and influencing factors. Some major facets have further subdivisions, and some facets share semantic units.

- **Species Names**: Including various species names, variety names, cultivar names, form names, and common names.
- **Species Characteristics**: Including various organs, cells, genes, etc.
- **Species Distribution**: This includes both geographical distribution and distribution across different ecological environments. Therefore, knowledge units in this facet encompass geographic names such as continents, countries, regions, cities, and counties, as well as biological communities, landforms, and physical environments (altitude, temperature, humidity).
- **Species Developmental Stages**: Including developmental stages of species and their organs.
- **Factors Influencing Species**: These include abiotic factors (temperature, humidity, altitude, soil, etc.) and biotic factors (various cells, chromosomes, proteins, DNA, gene fragments, chemical elements, compounds, etc.).
- **Classification Standards and Niche Model Tools**: Various standards and ecological niche modeling tools for species classification.
- **Experimental Methods and Equipment**: Various analytical methods and instruments used in species experiments.
- **Other Basic Information**: Including people, institutions, and noun phrases with currently undefined semantics.

These knowledge units essentially cover the main knowledge units in current biodiversity research, particularly species diversity research, forming the primary knowledge points of related studies.

3.2 Semantic Relationships in the Framework

The knowledge units analyzed above do not exist independently in scientific literature; they often have various semantic relationships. Combining these relationships maximizes the utilization of knowledge units for deep text mining. Based on practical applications and realistic identification capabilities, we defined several limited types of semantic relationships that can serve as factual triples to support further text analysis. Examples include:

- under
- acts on
- acts on
- acts on
- presents
- has
- distributed in
- has <Landform, vegetation, soil characteristics>

3.3 Other Considerations

Beyond the two aspects explicitly shown in the knowledge framework diagram, we noted that scientific literature contains many other semantically valuable annotations. Based on manually annotated documents, we found that considerable knowledge cannot be simply represented as individual knowledge units or inter-unit relationships, such as complete experimental conditions (e.g., combined concentration and temperature control of chemical elements) or entire experimental processes. These may contain multiple knowledge units and relationships. For such content, we can employ knowledge sentence groups—organizing closely related phrases or short sentences together to ensure knowledge integrity. Based on their content, these can be categorized into methods, processes, and results. Together with the two types of semantic knowledge described above, they constitute the biodiversity semantic knowledge framework. Identification methods for this portion of knowledge will be elaborated in future research; the following sections focus on recognition of the first two knowledge types.

4 Implementation of Semantic Knowledge Extraction

Based on the defined biodiversity semantic knowledge framework, we employed integrated methods including dictionaries, rules, and syntactic analysis to identify knowledge units and their relationships from abstracts of biodiversity-related scientific literature.

4.1 Experimental Data and Corpus Selection

To explore knowledge extraction in the biodiversity domain, we obtained approximately 23,000 journal abstracts from *Plant Physiology* and *The Plant Cell* in the PubMed database, and 27,049 abstracts from the Web of Science based on a list of 20 core journals provided by the Institute of Botany, Chinese Academy of Sciences. This study designed methods to identify semantic knowledge mentioned in these abstracts. To improve recognition efficiency, we collected and organized relevant corpora through expert consultation and reference to related research from the Institute of Botany [17], including: the G2000 plant ontology database provided by botanical institutions, NCBI species database, relevant domain terms and vocabulary from UMLS, geographic name gazetteers, and small compound names from Chemical Entities of Biological Interest. These domain resources serve as important support for entity name recognition.

4.2 Design of the Knowledge Extraction Framework

To better implement recognition of knowledge units and their relationships, we designed the extraction framework shown in [Figure 2: see original paper]. The specific steps are as follows:

[Figure 2: see original paper] Semantic Knowledge Extraction Framework

1. **Input Data Sources**: 主要包括待抽取的科技文献及相关领域资源（植物多样性本体、NCBI 物种库等）。
2. **Extraction Tools and Methods**: By employing various natural language processing tools (including Stanford Parser, Berkeley Parser, etc.), we achieve part-of-speech tagging, syntactic dependency analysis, and grammatical-semantic analysis of texts. Combined with different extraction rules and distance metric algorithms, we identify entities and relationships within sentences.
3. **Entity Extraction and Relationship Extraction**: These processes are implemented iteratively and cross-reinforcing. Entity extraction itself is iterative, with newly recognized named entities added to user dictionaries for subsequent recognition rounds. Relationship extraction results can also be used to discover new entities, which then feed into the next round of relationship discovery.
4. **Storage of Extraction Results**: Based on the type of extraction results, we employ both RDF storage and database storage for entities and relationships.

4.3 Knowledge Extraction Process

(1) Knowledge Unit Annotation and Extraction Named entity recognition methods primarily include dictionary-based and rule-based approaches, as well as statistical methods. Our approach is dictionary-based, supplemented by rules and statistics.

1. **Domain Dictionary-Based Entity Annotation**: We analyze and extract domain resources to create domain dictionaries for named entity extraction, enabling annotation of entities mentioned in scientific literature. During implementation, we strictly follow the dictionaries to annotate and obtain entity information in sentences, as shown in [Figure 3: see original paper] where colored portions represent annotation results.

2. **New Entity Recognition Based on Dictionary Similarity**: Dictionary-based recognition cannot handle unknown words. By identifying potential named entities in text and calculating their distance to entities in the dictionary, we can recognize some out-of-vocabulary terms. For example, "Solanum section Petota" appears as a single entity

representing a taxonomic section, but dictionary-based methods might only recognize "Solanum." Through similarity expansion, we can achieve proper recognition of the entity "sect. Petota."

3. **New Entity Recognition Based on Grammatical Relationships**: Some entities remain unidentifiable through the above methods, such as ser. Longipedicellata, ser. Tuberosa, ser. Yungasensia, and S. matehualae. These can be recognized by analyzing syntactic dependency and grammatical relationships (parallel sentence components) combined with statistical analysis algorithms.
4. **Term Identification in Literature**: Beyond named entities, domain terms play a crucial role in indicating document content, and their identification helps users gain direct and concise understanding. Through lexical analysis methods (noun phrases, etc.), we annotate important terms in literature, such as "Species boundaries," "phenetic analyses," "morphological data," and "tetraploid species."
5. **Geographic Location Recognition**: For this exhaustively enumerable information, we use geographic dictionaries to identify cities, countries, etc., such as "Mexican," "South American," and "United States."
6. **Numeric Information Recognition**: This primarily identifies numerical information in text, such as years, dates, experimental data, and related descriptive values, mainly through morphological rules and special numeric dictionaries. For example, from the text we can identify "six tetraploid species" and "three species." For the sentence "The inhibition constant values were 0.46 (using acetolactate as substrate) and 0.19 [mu]M (acetohydroxybutyrate), respectively," we can extract the contained numerical values.
7. **Entity Attribute Annotation**: Beyond annotating named entities, annotating descriptive information for recognized entities provides more comprehensive information. By analyzing contextual information around named entities (specific grammatical rules, syntactic dependency rules, etc.), we can annotate entity attributes. For instance, in the phrase "wild potatoes," entity recognition identifies "potatoes," and through NP chunk syntactic dependency, we can annotate "wild" as an attribute of this entity, providing more precise information.

(2) Relationship Extraction

1. **Multi-level Co-occurrence Relationships**: Co-occurrence relationships at different locations can be used to calculate associations between entities. This study focuses on co-occurrence at the title, abstract, and sentence levels. By analyzing the positions of annotated named entities, we can obtain co-occurrence relationships.
   - **Sentence-level co-occurrence**: <S. fendleri, S. hjertingii>,

  <S. hjertingii, S. matehualae>, <S. verrucosum, S. demissum>, <Solanum avilesii, S. stoloniferum>, <S. fendleri, S. papita>···
  - **Abstract-level co-occurrence**: <potatoes, S. berthaultii>, <S. stoloniferum, S. fendleri>, <S. fendleri, S. verrucosum>, <S. gourlayi, S. avilesii>, <S. demissum, S. fendleri>···

2. **Appositive Grammatical Relationship Extraction**: For the above examples, we obtain appositive relationships such as: <S. verrucosum, S. avilesii>, <S. gourlayi, S. avilesii>, <S. fendleri, S. matehualae>, <Solanum section Petota, wild potatoes>, etc.

3. **Coordinate Grammatical Relationship Extraction**: For the above examples, we obtain coordinate relationships such as: <S. matehualae, S. stoloniferum>, <S. polytrichon, S. hjertingii>, <S. fendleri, S. stoloniferum>, <S. hjertingii, S. papita>, <lesser extent S. demissum, S. verrucosum>, <S. hjertingii, S. stoloniferum>, etc.

4. **Factual Relationship Identification**: <S, P, O> (Subject, Predicate, Object) facts present in titles and abstracts provide important support for subsequent relationship inference. These include general facts and those defined in plant ontologies. Using syntactic dependency analysis and ontology mapping, we can extract from example text (1192769):

   - < “We” , “also analyzed morphologically” , “similar species” >
   - < “These data” , “explain the extensive taxonomic difficulty in” , “sect. Petota” >
   - < “South American representatives of other series” , “are difficult to distinguish from” , “Longipedicellata” >
   - < “These six tetraploid species” , “grow in” , “the southeastern United States (S. fendleri) and Mexico” >
   - < “We” , “also analyzed morphologically” , “more dissimilar species” >
   - < “Species boundaries” , “were assessed by” , “phenetic analyses of morphological data” >
   - < “a lesser extent S. demissum and S. verrucosum” , “are very similar to” , “members of ser. Longipedicellata” >
   - < “The results” , “support only” , “three species” >

5. **Semantic Hyponymy Relationship Discovery**: Using rule-based methods, we can discover semantic hyponymy relationships between terms. For example:

   - From “CSS grass margins could be improved as butterfly habitats if they are linked to existing habitats such as hedgerows···”, we can identify hedgerows as a hyponym of habitats: <hedgerows, hyponymy, habitats>.
   - From “We investigated all sections of genus Cochlearia recognised in the most common concepts, as well as some genera such as Ionopsidium, Bivonaea, Pastorea and Thlaspis···” , we can identify Ionop-

sidium, Bivonaea, Pastorea, and Thlaspis as hyponyms of genera: <Ionopsidium, hyponymy, genera>, <Bivonaea, hyponymy, genera>, <Pastorea, hyponymy, genera>, <Thlaspis, hyponymy, genera>.

6. **Species Trait Relationship Recognition**: For example, "wild potatoes" can be annotated to show that potatoes have the attribute wild: <potatoes, has property, wild>.

4.4 Application of Knowledge Extraction Results

Although knowledge extraction methods based on domain dictionaries and manually written rule libraries lack flexibility for rapid domain migration and recognition of new species or knowledge units, their accuracy can be effectively guaranteed, thereby supporting practical knowledge retrieval applications. Using the defined knowledge extraction framework and methods, we obtained 273,668 knowledge unit extraction results from titles and abstracts of over 60,000 related documents. The distribution by extraction type is as follows.

Based on these extraction results and combined with domain knowledge bases and other third-party resources, we further constructed a biodiversity domain semantic retrieval demonstration platform, providing users with applications such as domain knowledge revelation, semantic annotation, and ontology-based navigation.

Annotating literature titles and abstracts yielded 273,668 annotation results from 64,475 documents. The entity types and quantities are as follows:

[Figure 4: see original paper]-[Figure 7: see original paper] show relevant extraction results and their support for biodiversity domain semantic retrieval. [Figure 4: see original paper] shows examples of biodiversity domain entity extraction results. [Figure 5: see original paper] shows examples of biodiversity domain semantic relationship extraction results. From 30,665 documents, we obtained 133,922 grammatical relationship results, all of which are SPO grammatical relationships. From 15,259 documents, we obtained 35,903 semantic relationship results, all apposition_relation type.

[Figure 6: see original paper] demonstrates knowledge browsing, retrieval, and statistical analysis functions based on ontology concepts or entities. [Figure 7: see original paper] shows a knowledge graph of co-occurrence relationships for a single article based on semantic knowledge extraction.

This paper designs a biodiversity semantic knowledge extraction framework and explores corresponding semantic knowledge extraction methods based on an analysis of current biodiversity information extraction research and the practical requirements of the "Biodiversity Domain Ontology Construction and Semantic Organization Application Demonstration Platform" at the National Science Library, Chinese Academy of Sciences. Using the plant diversity ontology constructed under the Twelfth Five-Year Science and Technology Support Plan "Construction and Application Demonstration of Knowledge Organization

System for Foreign Scientific and Technical Literature Information (STKOS)" as the underlying dictionary, we implemented semantic knowledge extraction methods and developed a corresponding biodiversity demonstration platform. This study explores engineering-applicable knowledge organization frameworks and recognition methods from a practical application perspective. Consequently, dictionaries and manually written rules constitute important components of our knowledge extraction approach. However, the inherent limitations of dictionaries and manual rules also constrain recognition completeness and accuracy to some extent. In future research, refined recognition of various knowledge unit types will remain a key focus.

References

[1] Anne E T, Cui H, Mozzherin D. Applications of Natural Language Processing in Biodiversity Science[J]. Hindawi Publishing Corporation Advances in Bioinformatics, 2012, doi:10.1155/2012/391574

[2] Naderi N., Kappler T, Baker J.O C, et al. OrganismTagger: Detection, Normalization and Grounding of Organism Entities in Biomedical Documents[J]. Bioinformatics. 2011, 27(19):2721-9

[3] Species[EB/OL].[2016-04-12]. http://en.wikipedia.org/wiki/Species

[4] Gerner M, Nenadic G, Bergman C M. LINNAEUS: A Species Name Identification System for Biomedical Literature[J], BMC Bioinformatics, 2010(11):85

[5] The NCBI Taxonomy Homepage[EB/OL].[2016-04-12]. http://www.ncbi.nlm.nih.gov/Taxonomy/taxonomy

[6] Page RDM. (2013) BioNames: linking taxonomy, texts, and trees. PeerJ 1:e190 http://dx.doi.org/10.7717/peerj.190.

[7] Species 2000[EB/OL].[2016-04-12]. http://www.catalogueoflife.org/annual-checklist/2014/

[8] Akella L M, Norton C N, Miller H. NetiNeti: discovery of scientific names from text using machine learning methods[J]. BMC Bioinformatics. 2012(13):211

[9] The OrganismTagger System[EB/OL].[2016-04-12]. http://www.semanticsoftware.info/organism-tagger

[10] Koning D, Sarlar I N, Moritz T. Taxongrab: Extracting Taxonomic Names from Text[J]. Biodiversity Informatics, 2005(2):79-82

[11] Taylor A. Extracting Knowledge from Biological Descriptions [C]. In: Proceedings of the 2nd International Conference on Building and Sharing Very Large-Scale Knowledge Bases. 1995: 114-119

[12] Tang X, Heidorn P B. Using Automatically Extracted Information in Species Page Retrieval [OL]. [2016-03-29]. http://www.tdwg.org/proceedings/article/view/195/

[13] Cui H. CharaParser for Fine-grained Semantic Annotation of Organism Morphological Descriptions [J]. Journal of the American Society for Information Science and Technology, 2012, 63(4): 738-754

[14] Duan Y F, Huang S S. Information Extraction from Chinese Plant Species Diversity Description Text[J]. New Technology of Library and Information Service, 2016, 32(1): 87-96.

[15] Li C, Liakata M, Rebholz-Schuhmann D. Biological network extraction from scientific literature: state of the art and challenges[J]. Briefings in bioinformatics. 2013(2):6

[16] Skusa A, Rüegg A, Köhler J. Extraction of biological interaction networks from scientific literature[J]. Briefings in Bioinformatics 2005, 6(3): 263-276.

[17] Xu Z P, Cui J Z, Qin H N, Ma K P. On the architecture of biodiversity e-Science infrastructure in China[J]. Biodiversity Science, 2010, 18(5): 480-488.

Corresponding author: Jianhua Liu, ORCID: 0000-0002-4003-8834, E-mail: liujh@mail.las.ac.cn

Author Contributions:

Jianhua Liu: Proposed the overall framework, designed the semantic knowledge extraction framework, participated in the implementation and development of knowledge extraction, wrote the main content of the paper, and proofread and revised the final version.

Ying Wang: Participated in designing the semantic knowledge extraction framework and preparing corpora and storage structures for knowledge extraction development.

Zhixiong Zhang: Provided guidance throughout the research process and offered revision suggestions for the paper content.

Chuanxi Li: Primarily responsible for implementing knowledge extraction functions and providing development documentation.

Conflict of Interest Statement: All authors declare no conflict of interest.

Note: Figure translations are in progress. See original paper for figures.