On the Relationship between a Computational Natural Logic and Natural Language

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- Abstract: This paper makes a case for adopting appropriate forms of natural logic as target language for computational reasoning with descriptive natural language. Natural logics are stylized fragments of natural language where reasoning can be conducted directly by natural reasoning rules reflecting intuitive reasoning in natural language. The approach taken in this paper is to extend natural logic stepwise with a view to covering successively larger parts of natural language. We envisage applications for computational querying and reasoning, in particular within the life-sciences.

For better or for worse, most of the reasoning that is done in the world is done in natural language.

G. Lakoff: Linguistics and Natural Logic, Synthese, 22, 1970.

1 INTRODUCTION

Traditionally, computational reasoning with information given in natural language is carried out by conducting a translation of sentences into first order predicate logic, see e.g. (Fuchs et al., 2008; Kuhn et al., 2006), or derivatives thereof such as a description logic dialect, as in (de Azevedo et al., 2014; Thorne et al., 2014). There are also natural logic approaches which extend syllogistic proof systems (Pratt-Hartmann and Moss, 2009) or which call on forms of logical type theory, thereby taking advantage of an assumed compositional semantics for natural language drawing on higher order denotations (Fyodorov et al., 2003).

The project described here relies on appropriate forms of natural logic decomposed into graphstructured knowledge bases. Natural logics are tiny, stylized fragments of natural language in which the deductive logical reasoning can be carried out directly by simple, intuitive rules, that is, without taking resort to predicate-logical reasoning systems such as resolution. Natural logic originates from the traditional Aristotelian categorial syllogistic logic (van Benthem, 1986; Klíma, 2010; Nilsson, 2015), which became further developed and refined in late medieval times. However, in the course of the late 19th century development, forms of logic coming close to natural language were largely deemed obsolete by Frege's introduction of the more general, mathematically inclined quantifier-based predicate logic. As is well-known, the latter subsequently prevailed throughout the 20th century.

This paper pursues the idea of choosing natural logic as a target language for dealing computationally with appropriately constrained and regimented, yet rich, forms of affirmative sentences in natural language. The purported methodological advantage of the present approach lies in the proximity of natural logic to natural language, very much in contrast to predicate logic. Indeed then, the translation of the considered natural language fragments becomes a partial recasting of the considered sentences into an even smaller language fragment, namely natural logic sentences. Obviously, the chosen natural logic then determines and confines the semantic range for partial coverage of the considered sentences. A related use of natural logic principles for partial computational understanding of natural language is found in (MacCartney and Manning, 2009). The language translational relationships are planned to be initially implemented using the well-known, rather unsophisticated definite

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clauses (clause grammars).

The paper is structured as follows: In section 2 we describe the semantic basis of the considered dialect of natural logic presented in section 3. In section 4 we discuss various mainly conservative extensions of the natural logic in order to accommodate expression forms common in natural language. Section 5 discusses various sentence cases and the problems involved in approaching free natural language formulations. Finally, in section 6 a summary concludes the paper.

2 SEMANTIC MOTIVATION

Our semantic framework comprises a selection of stated classes of entities together with binary relationships between the classes akin to the popular entityrelationship models. First of all, there is a fundamental isa subclass relationship known from formal ontologies. In addition, class-class relationships may be be introduced according to needs, as discussed in (Smith et al., 2005; Schulz and Hahn, 2004; Bittner and Donnelly, 2007; Yu, 2006).

It is a key feature of our approach that the given named classes may be used to form subclasses *ad libitum* by restriction with relationships to other classes in the natural logic. As an example, given the classes cell and hormone and the relation(transitive verb) produce, one may form the subclass

cell that produce hormone

This is a phrase in the applied natural logic forming a new class which is a subclass of cell.

Unlike what is the case in predicate logic, in our framework the entities belonging to the classes are not dealt with explicitly. Individual entities may, however, if necessary, be dealt with as stipulated singleton classes (having no subclasses in so far as the empty class is left out in our setup).

This basis, while being application-neutral at the outset, appears to be particularly useful for applications within the bio-sciences as discussed in (Smith et al., 2005; Schulz and Hahn, 2004) as well as in our (Andreasen et al., 2014a; Andreasen et al., 2014b; Andreasen and Nilsson, 2014; Nilsson, 2015; Andreasen et al., 2015). General, natural language descriptions in natural sciences abound with classes, let us just mention the Linnean and chemical and medical taxonomies. The class-relationship framework might also find more innovative use for ontology-structured knowledge base concept organization and specification in semi-exact sciences, e.g. in linguistics.

3 CORE NATURAL LOGIC

Having introduced the semantic motivation, we turn next to the logical sentences serving the mentioned class-relationship setup. We consider a natural logic which has the general form of expression shown in (1):

$$Q_1 Cterm' R Q_2 Cterm'' \tag{1}$$

where

- Q_i are quantifiers (determiners) every/all, some/a,
- the grammatical subject term *Cterm*['] and the grammatical object term *Cterm*^{''} are class expressions, and
- *R* is a relation name.

In linguistic parlance, the *Cterms* are noun phrases, and R is a transitive verb. In simpler cases *Cterms* are just class names (nouns) C. Among the quantifier options here, we focus on the quantifier structure

every
$$Cterm' R$$
 some $Cterm''$ (2)

This form is pivotal in our treatment because it represents the default interpretation of sentences like *betacells produce insulin* in ordinary descriptive language. Further, it conforms with the functioning of the class restrictions as to be described. Example: every betacell produce some insulin. An explication of this form in predicate logic with quantifier structure $\forall x \exists y$ is straightforward, cf. our references above, and therefore not repeated here. The inherent linguistic structural ambiguity corresponding to the scope choice $\forall x \exists y$ versus $\exists y \forall x$ is overcome by stipulating the $\forall x \exists y$ reading, which is the useful one in practice. See also (2) Accordingly, we have

$$\forall x(betacell(x) \to \exists y(produce(x, y) \land insulin(y))$$

Observe that we are not going to translate the sentences into their predicate logical form with individual variables. Rather, it is a crucial feature of our approach that we decompose the sentences into simpler constituents forming a graph without variables as explained in section 3.4.

Our natural logic notations rely on the convention that if no quantifiers are mentioned explicitly, the interpretation follows the scope pattern $\forall x \exists y$. Thus, the sentence betacell produce insulin is semantically equivalent to our sample sentence above, every betacell produce some insulin. Note further that we persistently use uninflected forms of nouns and verbs rather than morphologically correct forms in our natural logic expressions.

3.1 Subclass Through Copula Sentence

Within the above natural logic affirmative sentence template in (1), there is an extremely important subclass, namely the copula sentence form shown in (3)

$$Cterm' \text{ isa } Cterm'' \tag{3}$$

known from categorial syllogistic logic. cf. (Nilsson, 2013). Using the symbol *C* in class names as in C' isa C'' we say that the class C' specializes the class C'', and, conversely, that C'' generalizes the class C'. As explained in (Nilsson, 2013) the copula form (3) may actually be understood as a special case of the above general form (2) with the relation being equality. For example, the sentence betacell isa cell is predicate logically construed as

$$\forall x(betacell(x) \to \exists y(x = y \land cell(y))$$

giving in turn

 $\forall x(betacell(x) \rightarrow cell(x))$

Note once again that we are not using these predicate logical forms in our reasoning with natural logic.

The categorial syllogistic no C' isa C'' is not made available, since class disjointness is assumed initially for pairs of classes by default in our setup, cf. (Nilsson, 2015), which also discusses the relation to the well-known square of opposition in traditional logic. The upshot of our convention is that two classes are disjoint unless one is stipulated as a subclass of the other, or that they have a common subclass introduced by the copula form. This default convention conforms with use of classes in scientific practice as reflected in formal ontologies. However, one may observe that the convention deviates from the description logic principle, which follows predicate logic with the open world assumption.

3.2 Simple and Compound Class Terms

Compound terms *Cterm* in the natural logic take the form of a class name *C* adorned with various forms of restrictions giving rise to a virtually unlimited number subclasses of *C*. Linguistically, this "generativity" is provided by constructions like restrictive relative clauses and adnominal prepositional phrases (PPs).

Accordingly, in the present context we consider *Cterm* in the form of a class name (noun) *C* optionally followed by

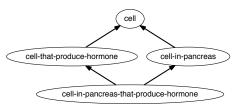
- a stylized relative clause: that *R Cterm* or optionally by
- a PP in the logical form *R*_{prep} Cterm, in turn optionally followed by a relative clause.

The relation R_{prep} is to be provided by the entry for the pertinent preposition in the applied vocabulary.

Sample class terms illustrating these patterns:

cell cell that produce hormone cell in pancreas cell in pancreas that produce hormone

Ontologically, these four classes form a (transhierarchical) diamond by the isa subclass relation:



The sample class term cell in pancreas that produce hormone is aligned as in cell (in pancreas) (that produce hormone).

For the moment we disregard the more tricky restrictions provided by adjectives (even when assumed to behave restrictively), noun-noun compounds¹, and genitives. This is because these constructs, unlike the case of relative clauses and PPs, do not explicitly yield a specific relation R, cf. the discussions in (Jensen and Nilsson, 2006; Vikner and Jensen, 2002).

The natural logic sub-language where *Cterm* is simply a class name we call *atomic natural logic*.

As described below, in due course we shall also admit conjoined constructions with the conjunction and in class terms, and, further, compound relation terms, *Rterm* for *R*, linguistically comprising selected adverbs and adverbial PPs modifying verbs and verb phrases. See also (Andreasen et al., 2014b) for various extensions of the natural logic.

3.3 Reasoning with Natural Logic

The key inference rules for the considered natural logic are the so-called monotonicity rules (van Benthem, 1986). They very intuitively admit specialization of the grammatical subject class and generalization of the grammatical object class. Accordingly, given A isa B and [every] B R [some] C, one may derive [every] A R [some] C,

 $\frac{A \text{ isa } B \quad [\text{every}] B R [\text{some}] C}{[\text{every}] A R [\text{some}] C}$

and given [every] B R [some] C and C isa D, one may

¹Some class names (given terms) in an application may consist of more than one word,but are still to be considered as simple, fixed terms.

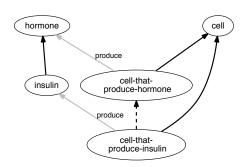


Figure 1: Inferred inclusion by subsumption.

derive [every] B R [some] D,

$$\frac{[\text{every}] B R [\text{some}] C \quad C \text{ isa } D}{[\text{every}] B R [\text{some}] D}$$

In particular, these rules provide transitivity of the isa subclass relationship with *R* being isa.

In addition, we provide a subsumption inference rule which makes the properties assigned to classes act restrictively as detailed with an algorithm in (Andreasen et al., 2015). By way of example, the subsumption rule ensures that

cell that produce insulin

is recognized as a specialization of cell that produce hormone,

given that insulin isa hormone, cf. figure 1.

3.4 Atomic Natural Logic as Graph

In our framework and prototype system, the core natural logic introduced above is decomposed into atomic natural logic devoid of compound class names, that is, *Cterm* is simply a class name *C*. This is accomplished by introduction of fresh, internal class names such as cell-that-produce-hormone, which is formally conceived of as a class name. In turn, this is defined by two atomic natural logic sentences

cell-that-produce-hormone isa cell

cell-that-produce-hormone produce hormone.

The knowledge base of the decomposed sentences may be viewed as one single labeled graph whose nodes are uniquely labeled with classes. Except for those relationships that follow from transitivity, we make sure that all valid isa relationships between nodes are materialized in the graph by the subsumption rule, so that for instance

cell-that-produce-insulin isa

cell-that-produce-hormone

is recorded. As such, the graph appears as an extended formal ontology with the isa relationship forming the skeleton, as it were.

In our system, besides deductive querying the graph is used for pathfinding between classes (Andreasen et al., 2015). Actually, in our system the

atomic natural logic graph is embedded in functionfree logical clauses (e.g. DATALOG). This embedding approach means that natural logic sentences become encoded as variable-free logical terms. The logical variables in the clauses then range over class and relationship terms enabling formulation of the inference rules and hence reasoning and deductive querying. The clausal embedding also facilitates formulation of domain specific inference rules such as transitivity of causation (Andreasen et al., 2014b).

4 EXTENDING CORE NATURAL LOGIC

We now turn to a partial treatment of natural language sentences using natural logic as a vantage point. In a conventional approach, one may proceed by devising a (partial) translation from the considered natural language text sentence by sentence into natural logic. Here, we choose to proceed by introducing a series of conservative extensions to core natural logic. Thus, these extensions do not increase the semantic range of the core natural logic as stipulated above. However, the extensions provide paraphrases commonly encountered in natural language. These extensions, when taking jointly, form an extended natural logic coming closer to free natural language formulations, remaining, however, within the confines of the semantics of core natural logic. The extensions may be used in turn in developing a partial translator from natural language into core natural logic.

4.1 Extension with Conjunctions

Let us first consider conjunctions of *Cterms* including the linguistic conjunction *and* assuming distributive (in contrast to collective) readings. Conjunctions in the grammatical object

Cterm' R Cterm["]₁ and Cterm["]₂

as in

pancreas contain betacell and alphacell straightforwardly give rise to the decomposition:

Cterm' R Cterm''₁ Cterm' R Cterm''₂ Conjunctions in the grammatical subject

Cterm'₁ and Cterm'₂ R Cterm"

as in

betacell and alphacell is-contained-in pancreas are conventionally interpreted as disjunction rather than overlap of the two classes and therefore decomposed into

Cterm'₁ R Cterm'' Cterm'₂ R Cterm'' These conventions are justified by the underlying predicate logical explication of core natural logic.

The linguistic disjunction or in the linguistic subject seems irrelevant from the point of view of the considered domains. It may be considered a case where predicate logic covers more than needed.

More interesting are disjunctions in the grammatical object, viz.

Cterm' R Cterm'' or Cterm''

which cannot simply be decomposed into two core natural logic sentences. One approach is to appeal to a common general term $Cterm_{sup}^{\prime\prime}$ for $Cterm_{1}^{\prime\prime}$ and *Cterm*["]₂ if one is available in the KB. More precisely, one seeks a Cterm_{sup}, such that

Cterm^{''}₁ isa Cterm_{sup} Cterm^{''}₂ isa Cterm_{sup}

and such that for all different $Cterm_x$ having these properties $Cterm_{sup}$ is $Cterm_x$. This supremum requirement seems reasonable in cases where the considered disjunction is pragmatically relevant at all.

Notice that all of the above reductions of conjunctions endorse the desired commutativity and associativity properties.

It goes without saying that the presence of conjunctions together with relative clauses and prepositions gives rise to structural ambiguities. Introduction of appropriate default readings and/or addition of auxiliary parentheses are the simplest ways to eliminate these.

Collective, i.e. non-distributive, readings such as co-presence of A and B cause C call for separate treatment, which goes beyond the scope of the present approach.

Extension with Appositions and 4.2 **Parenthetical Relative Clauses**

Let us consider natural logic sentences Cterm' R Cterm"

extended with appositions bounded by commas Cterm', [a|an] Ctermappo, R Cterm"

This is paraphrased into the pair

Cterm' R Cterm"

Cterm' isa Ctermappo

Analogously for the grammatical object, *Cterm*["], as in

betacell produce insulin, a peptide hormone

In this extended natural logic, the pronoun 'that' is formally set off for restrictive relative clauses as accounted for above.

By contrast, consider the case of parenthetical relative clauses for which in the formal natural logic we use 'which' together with commas

Cterm', which R_{par} $Cterm_{par}$, R Cterm''

as in

insulin, which is a peptide hormone, ...

Retaining logical equivalence, this can be paraphrased into the joint pair

Cterm' R Cterm"

Cterm' R_{par} Cterm_{par} and similarly and recursively for Cterm" and Cterm_{par}.

4.3 Beyond Core Natural Logic

From the point of view of application functionalities, verbs should be allowed extensions with adverbial PPs yielding restricted relations, *Rterm*, for plain *R*, say, as in

A produce in pancreas B

with variants A produce B in pancreas and in pancreas A produce B, with obvious additional structural ambiguity problems.

On our agenda for non-conservative extensions of core natural logic, let us mention passive voice verb forms, nominalisation, and plural formation. As far as negation is concerned we rely throughout on the closed world assumption in the query answering.

Of course there are numerous genuine (that is, non-conservative) language extensions which go beyond the semantic range of core natural logic, even within the given scope of monadic and dyadic relations in affirmative sentences. Thus admission of anaphora as in the infamous donkey sentences breaks the boundaries as mentioned in (Klíma, 2010). An example of this is seen in every cell that has a nucleus is-controlled-by it. The point is that in the applied natural logic, the subject noun term and the object noun term are independent, connected solely by the relator verb and unconnected by anaphora.

5 **COMPUTING NATURAL** LOGIC FROM SENTENCES

Methodologically, rather than the usual forward or bottom-up translation following the phrase structure, we devise a top down processing governed by the natural logic. In this process we try to cover as much as possible of the considered sentence in a (partial) "best fit" process.

A prototype is under development and is currently functioning in a preliminary version. In the present approach natural language input is processed sentence by sentence. Thus sentential context is not exploited. Each input sentence is preprocessed for markup, and the result is further processed by a parser that also

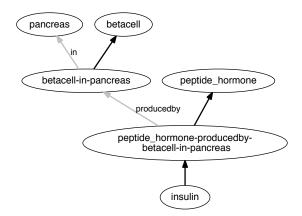


Figure 2: Graph representation of the sentence insulin is a peptide hormone produced by betacells in the pancreas.

functions as a natural logic generator. During the preprocessing the sentence is tokenised into a list of lists, where each word from the sentence is represented by a list of possible lexemes specifying base form of word and word category (part of speech) for each word. A lexeme is included as possible if it matches the lemma of the input form of the word. Finally, the preprocessing applies a domain specific vocabulary to identify multiword expressions in the input sentence. To ensure that multiwords are treated as inseparable units they are replaced by unique symbols. A preprocessing of the sentence: Insulin is a peptide hormone produced by betacells in the pancreas returns the following tagged and lemmatised word list, where the word sequences 'is a', 'peptide hormone' and 'produced by' are replaced by symbols:

{{insulin/NN}, {isa/VB}, {peptide_hormone/NN}, {produced_by/VB}, {betacell/NN}, {in/JJ, in/NN, in/RB, in/IN}, {pancreas/NN}}

Each possible lexeme for a word (and multiword) W_i is included as an element L_{ij}/C_{ij} if W_i has lemma L_{ij} for category C_{ij} . The categories are denoted using Penn Treebank POS-tags. VB, NN, RB, JJ and IN correspond to verb, noun, adverb, adjective and preposition, respectively.

Our approach to recognizing and deriving natural logic expressions from natural language texts can be considered a knowledge extraction task where the goal is to extract expressions that cover as much as possible of the meaning content from the source text. The search is guided by a natural logic grammar, and the aim is to create propositions that comprise well-formed natural logic expressions. The "best fit" approach is basically a guiding principle aiming for largest possible coverage of the input text. Thus, if an expression, that covers the full input sentence can be derived, it would be considered the "best", and if not, the aim is a partial coverage where larger means

"better".

In the prototype, we apply a simple approach to deriving a partial coverage. A "best fit" is provided by iterating through a series of "sub-sentences" of the input sentence of repeatedly smaller size until one is found from which a proposition can be derived. A sub-sentence arises from removing zero, one or more words from the input sentence. This approach has obvious drawbacks, most importantly, it's quite inefficient – especially due to load from forcing the parser to repeat identical subtasks over and over again. However, it has one important advantage as a prototype approach – it allows a clear separation of parsing and selection of partial expressions.

As far as parsing is concerned, and as already mentioned, our approach is a top down processing governed by the natural logic. The word list given as input is ambiguous due to the multiple categories assigned to each word. Thus, the parser should be able to recognize an input proposition if such exists for at least one combination of possible lexemes of the input words. Therefore, in addition to processing the grammar (given below), the parser must ensure that all combinations are tried before failing the recognition of a proposition.

Core natural logic, as described in section 3, without the extensions sketched in section 4, can be specified by the following grammar.

 $\begin{array}{l} Prop ::= Cterm \ R \ Cterm \\ Cterm ::= \ NN \ [RelClauseterm \mid Prepterm] \\ RelClauseterm ::= \ [that|which|who] \ R \ Cterm \\ R \ ::= \ VB \\ R_{Prep} \ ::= \ IN \\ Prepterm \ ::= \ R_{Prep} \ Cterm \end{array}$

Notice that terminals are specified as either specific words or word categories using Penn Treebank-tags.

Example 1: The preprocessing result of the example sentence *insulin is a peptide_hormone produced*

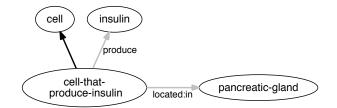


Figure 3: Graph representation of the sentence cells that produce insulin are located in the pancreatic gland

by betacells in pancreas is shown above. In this case, the full sentence can be recognized as a proposition with the given grammar and the following arcs can be derived from the parse tree:

insulin isa

peptide_hormone-producedby-betacell-in-pancreas peptide_hormone-producedby-betacell-in-pancreas

producedby betacell-in-pancreas peptide_hormone-producedby-betacell-in-pancreas isa peptide_hormone

betacell-in-pancreas in pancreas

betacell-in-pancreas isa betacell

The corresponding graph is shown in graph form in figure 2.

Example 2: Preprocessing the sentence *cells that produce insulin are located in the pancreatic gland* leads to:

{{cell/NN}, {that/WDT}, {produce/VB, produce/NN}, {insulin/NN}, {locatedin/VB}, {pancreatic_gland/NN}}

where 'is located in' and 'pancreatic gland' are replaced by symbols. As it appears, again the full sentence can be recognized as a proposition. From the corresponding parse tree the following 3 arcs can be derived:

cell-produce-insulin locatedin pancreatic_gland cell-produce-insulin produce insulin cell-produce-insulin isa cell

The result is shown in graph form in figure 3.

Example 3:The grammar above does not cover conjunctions. Thus *pancreas contains betacells and alphacells* will not be recognized as a proposition. However, the best-fit principle will iterate through partial-cover sub-sentences (where one or more words are left out). Among these are pancreas contain betacell and pancreas contain alphacell, which will both be recognized. Thus, in this case continued best-match iteration will lead to a result that complies with the conjunction.

6 SUMMARY AND CONCLUSION

We have described how to use dedicated forms of natural logic for partial computational comprehension of natural language with a particular view to descriptive scientific corpora within the life sciences. The applied natural logic, called core natural logic, has a welldefined semantic foundation in predicate logic, and we have devised an appropriate inference engine for query answering functionalities. Core natural logic is extended in the paper with common paraphrase schemes.

Our approach features – as explained and illustrated with the figures – a shared graph representation of all sentences. In this representation concepts are (at least ideally) uniquely represented as nodes. The directed arcs represent atomic natural logic sentences, and appropriate labelling conventions ensure that the individual natural logic sentences can be reconstructed from their atomic components in the graph, modulo paraphrasing. The graph representation eases pathfinding between concepts and serves deductive querying.

Finally, we illustrate processing of sentences from the text using core natural logic. As a next step, we are going to try our prototype on selected life science corpora.

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REFERENCES

Andreasen, T., Bulskov, H., Fischer Nilsson, J., and Jensen, P. A. (2014a). Computing pathways in bio-models derived from bio-science text sources. In *Proceedings of* the IWBBIO International Work-Conference on Bioinformatics and Biomedical Engineering, Granada, April, pages 217–226.

- Andreasen, T., Bulskov, H., Nilsson, J. F., and Jensen, P. A. (2014b). A system for computing conceptual pathways in bio-medical text models. In *Foundations of Intelligent Systems*, pages 264–273. Springer.
- Andreasen, T., Bulskov, H., Nilsson, J. F., and Jensen, P. A. (2015). A system for conceptual pathway finding and deductive querying. In *Flexible Query Answering Systems 2015*, pages 461–472. Springer.
- Andreasen, T. and Nilsson, J. F. (2014). A case for embedded natural logic for ontological knowledge bases. In 6th International Conference on Knowledge Engineering and Ontology Development.
- Bittner, T. and Donnelly, M. (2007). Logical properties of foundational relations in bio-ontologies. *Artificial Intelligence in Medicine*, 39(3):197–216.
- de Azevedo, R. R., Freitas, F., Rocha, R., de Menezes, J. A. A., and Pereira, L. F. A. (2014). Generating description logic ALC from text in natural language. In *Foundations of Intelligent Systems*, pages 305–314. Springer.
- Fuchs, N. E., Kaljurand, K., and Kuhn, T. (2008). Attempto controlled english for knowledge representation. In *Reasoning Web*, pages 104–124. Springer.
- Fyodorov, Y., Winter, Y., and Fyodorov, N. (2003). Orderbased inference in natural logic. Log. J. IGPL, 11(4):385–417. Inference in computational semantics: the Dagstuhl Workshop 2000.
- Jensen, P. A. and Nilsson, J. F. (2006). Ontology-based semantics for prepositions. In Saint-Dizier, P., editor, *Syntax and semantics of prepositions*, pages 217–233. Springer Science & Business Media.
- Klíma, G. (2010). Natural logic, medieval logic and formal semantics. *Logic, Language, Mathematics*, 2.
- Kuhn, T., Royer, L., Fuchs, N. E., and Schroeder, M. (2006). Improving text mining with controlled natural language: A case study for protein interactions. In *Data Integration in the Life Sciences*, pages 66–81. Springer.
- MacCartney, B. and Manning, C. D. (2009). An extended model of natural logic. In *Proceedings of the eighth international conference on computational semantics*, pages 140–156. Association for Computational Linguistics.
- Nilsson, J. F. (2013). Diagrammatic reasoning with classes and relationships. In *Visual Reasoning with Diagrams*, pages 83–100. Springer.
- Nilsson, J. F. (2015). In pursuit of natural logics for ontology-structured knowledge bases. In *The Seventh International Conference on Advanced Cognitive Technologies and Applications.*
- Pratt-Hartmann, I. and Moss, L. S. (2009). Logics for the relational syllogistic. *Review of Symbolic Logic*, 2(4):647–683.
- Schulz, S. and Hahn, U. (2004). Ontological foundations of biological continuants. In *Formal ontology in infor*mation systems. Proceedings of the 3rd international conference-FOIS, pages 4–6.

- Smith, B., Ceusters, W., Klagges, B., Köhler, J., Kumar, A., Lomax, J., Mungall, C., Neuhaus, F., Rector, A. L., and Rosse, C. (2005). Relations in biomedical ontologies. *Genome biology*, 6(5):R46.
- Thorne, C., Bernardi, R., and Calvanese, D. (2014). Designing efficient controlled languages for ontologies. In Bunt, H., Bos, J., and Pulman, S., editors, *Computing Meaning, Volume 4*, volume 47 of *Text, Speech* and Language Technology, pages 149–173. Springer.
- van Benthem, J. (1986). *Essays in Logical Semantics, Volume 29 of Studies in Linguistics and Philosophy.* D. Reidel, Dordrecht, Holland.
- Vikner, C. and Jensen, P. A. (2002). A semantic analysis of the english genitive. interaction of lexical and formal semantics. *Studia Linguistica*, 56(2):191–226.
- Yu, A. C. (2006). Methods in biomedical ontology. *Journal* of Biomedical Informatics, 39(3):252 – 266. Biomedical Ontologies.