Combination of Topology and Nonmonotonic Logics for Typicality in a Scientific Field: Paleoanthropology

Christophe Jouis[1, 2], Claude Jouis[3], Franck Guy[4],

Bassel Habib[2], Jean-Gabriel Ganascia[2]

[1]Université Sorbonne Nouvelle, 17, rue de la Sorbonne, 75005-PARIS (France)

[2]LIP6 (Laboratoire d'Informatique de Paris 6), Université Pierre et Marie Curie and CNRS (UMR7606), ACASA Team, 4, place Jussieu, 75252-PARIS Cedex 05 (France)

{christophe.jouis, bassel.habib, jean-gabriel.ganascia}@lip6.fr

[3]Ecole Polytechnique, route de Saclay, 91128-PALAISEAU Cedex (France)

jouis.claude@gmail.com

[4]Université de Poitiers -Faculté de sciences – CNRS UMR6046– IPHEP (Institut de Paléoprimatologie et de Paléontologie Humaine, Evolution et Paléoenvironnements) 40, avenue du Recteur Pineau, 86022 - POITIERS Cedex (France)

franck.guy@univ-poitiers.fr

Abstract

In computer science, ontology is a model of a domain in the form of classes and of relationships between these classes. Classes are organized in a graph the arrows of which are semantic relations. Ontology is static because the class hierarchy is fixed. In paleontology, systematic (i.e., the class hierarchies and the class relationships) is complicated by the time variable. Morphological changes over time yield, by natural selection, the emergence of new forms (taxa) differing from the ancestral morph and contemporaneous taxa of the same class hierarchy. Discovering new taxa implies, therefore, the rearrangement of the class hierarchy or the definition of new classes, based on the degree of atypicality of the new morph. Note that this phenomenon occurs in many domains such as physics, biology, linguistics, for example.

1. Introduction

We propose here a computer treatment of atypical entities in a scientific domain, the paleoanthropology, with the particular case of the emergence of the genus Homo, based on topological axioms and non-monotonic logics.

The evolutionary history of our family (hominin) is mainly documented by fossil remains, yet rare and fragmentary. Our history is exclusively African from 7 to 2

My, when some representatives of the genus Homo migrate to Eurasia. For the last 7 million years, the early hominin populations evolve to produce original species that are a group of individuals sharing a set of morphological novelties relative to an ancestral form. Hence, the human lineage is represented by numerous and diverse species through time and space. Evolutionary hypotheses for the human lineage are naturally improved (or invalidated) with new fossil discoveries. Moreover, new discoveries may entail a rearrangement of the (zoological) class hierarchy describing our family (taxonomy), and the relationships between species within our family (phylogeny). For instance, a new specimen exhibiting atypical morphology relative to the established classes may require the invention of a new class. Hence, the hierarchical system in paleontology used both static (normal morphological variation within species) and dynamic (variation through time) data.

On the contrary, in computer science, an ontology is a model for a domain of classes and of relationships between these classes. An ontology is static since the class hierarchy is fixed; considering classes, the ontology describes a state of a domain that is a condition where the beginning and the end are not considered; rearrangements or modifications of the classes through time (events, processes) are not considered either. The transitions from one state to another concern only the class individual

entities which may emerge, become extinct or for which properties may change.

In this article, we postulate that dynamic data can be represented in the ontologies using interior, border, and exterior concepts derived from the general topology and the non-monotonic logics, with an inclusion/exclusion relation system-based.

First, we propose a model derived from the general topology and the non-monotonic logics. Then, we'll briefly describe some basic paleontological concepts, with particular regard to the emergence of the genus Homo. Third, an application of our model to the concept of atypical entities in paleoanthropology is presented.

2. Combined use of a non-monotonic logic and general topology to represent a scientific or technical text

2.1. Non-monotonic logics

One of the main problems the logic-based artificial intelligence has to deal with is to conciliate the specificity of singular cases with general rules. This problem has been recognized as crucial for many years now and many logicians spent a lot of time to solve it. Depending on the domain of application, it has got different names: "frame problem", "common sense reasoning", etc. For the sake of clarity, let us give a classical example illustrating the problem. Usually birds fly. One would like to take advantage of such a general knowledge by having a rule that can be easily translated in first order logic *"∀X if bird(X) then fly(X)"*. But, if a particular bird, named Tweety for instance, is an ostrich, it cannot fly, which could contradict the general rule stating that birds fly. It would then be suitable to modify the initial rule and to write: *"∀X if bird(X) & not ostrich(X) then fly(X)"* Nevertheless, this rule should also be rewritten for penguins and other non-flying birds. As a result, we have both a lengthy rule (translating a very common knowledge) and an inefficient rule, since, to be triggered, the computer has to check that the bird under investigation is neither an ostrich, nor a penguin, etc.

One of possible solutions that is envisaged to solve this problem, is to have rules saying, for instance, that *"∀X if bird(X) & not inconsistent fly(X) then fly(X)"*. The formalisms that can support such rules cannot be reduced to first order predicate logic, since predicate "inconsistent" is clearly a second-order predicate, i.e. a predicate of which arguments are predicates. Classical mechanical proof procedures used in artificial intelligence, for instance Robinson resolution rule are not appropriate to deal with such rules. Moreover, usual properties of formal systems are not conserved. For instance, they are not monotonic. In the past, many Artificial Intelligence researchers tried to simulate non-monotonic reasoning, i.e. reasoning based on general rules and accepting exceptions. Several formalisms have been developed, for instance, default logic (Reiter 1980). However, mechanical solvers based on those formalisms were quite inefficient.

2.2. Answer Set Programming

Recently, a new general formalism called Answer Set Programming (ASP) (Baral 2003) has been developed to simulate non-monotonic reasoning. It has been designed to unify previous non-monotonic reasoning formalisms. ASP formalism is also fully operational. More precisely, ASP proposes both a clear formalization with a well define semantics and efficient operational solvers, which renders automate demonstrations possible.

Within this formalization, it is possible to specify logical properties of objects with programs Π that are sets of expressions ρ of the following form:

$$\rho : L_0 \ or \ L_1 \ or \ ... \ L_k \leftarrow L_{k+1}, L_{k+2}, ... L_m, not \ L_{m+1}, ..., not \ L_n$$

where L_i are literals, i.e. atoms or atom negations, and "not" is a logical connective called "negation as failure". The intuitive meaning of such a rule is that, for all Herbrand interpretations that render true all literals in $\{L_{k+1}, L_{k+2}, ... , L_m\}$ while not satisfying any literals in $\{L_{m+1}, ..., L_n\}$, one can derive at least one literal in $\{L_0, L_1, ... L_k\}$. Let us first remark that ASP formalism contains two negations that need to be distinguished: a classical negation noted "¬" and a negation by failure noted "not", which means that a literal cannot be proved in the absence of sufficient informations. As we shall see, the non-monotonic properties are mainly due to this "negation as failure" connector.

The second remark concerns the strict declarative character of this formalism: the order in which are given the different rules and the order in which are written the literals in rules do not influence the results. In this respect, it has to be distinguished from classical logic programming techniques, results of which largely depend on the order in which clauses are written. Moreover, there is neither "cut" as in PROLOG, nor any procedural predicate in programs.

Being given a program Π, an Answer Set (or a stable model) is a minimal subset of the Herbrand base of Π, which satisfies all rules of Π. Each subset describes a possible world that renders true the rules of Π. Let us note that this intuitive meaning of the programs may be easily formalized, which provides a formal semantics of ASP.

For instance, let us consider the following rules:

$$fly(x) \leftarrow bird(x), not \ \neg fly(x)$$
$$\neg fly(x) \leftarrow ostrich(x), not \ ab\_ostrich(x)$$
$$bird(rocky) \leftarrow$$
$$bird(tweety) \leftarrow$$
$$ostrich(tweety) \leftarrow$$

There is a unique answer set for this program. $S = \{fly(rocky),\ \neg fly(tweety),\ bird(rocky),\ bird(tweety),\ ostrich(tweety)\}$

Let us now suppose that *Tweety* is in a plane; we can add the three following facts that translate that *Tweety* is in a plane, that one flies whene is abnormal situation for an ostrich to be in a plane:

$in\_plane(tweety) \leftarrow$

$fly(x) \leftarrow in\_plane(x)$

$ab\_ostrich(x) \leftarrow in\_plane(x)$

Then, the only answer set is: $S = \{fly(rocky),\ fly(tweety),\ bird(rocky),\ bird(tweety),\ ostrich(tweety),\ in\_plane(tweety),\ ab\_ostrich(tweety),\ \}$

Without going into technical details, efficient solvers able to compute all the stable models for a given program act in two steps. At the first step, the program variables are grounded, i.e. they are instantiated by all Herbrand universe terms; through the second step, a "sat" solver generates all the interpretations that satisfy the instantiated rules.

The principal advantage of such formalism is that it renders possible the expression of default rules by the use of the "negation as failure".

Moreover, ASP formalism has a clear semantics, i.e. a well defined mathematical meaning, and there exist solvers that automate the computation of Answer Sets[1]. It is then possible to get specific formalizations and efficient simulations that fully validate the formalizations, because they generate correct mathematical proofs.

2.3. Why using general topology?

Literally, topology means the study of the area and defines the nature of an area (also called a space E) and its properties. We postulate that networks of concepts and semantic relations between concepts can be represented on a plan. Instances are points of the plan, while classes are demarcated areas of the plan, which consist of: (a) an **interior** (the typical elements belonging to the class), (b) an **exterior** (the elements that are not in the class), (c) a **border** (atypical elements that do not check all the properties of the class, i.e. atypical elements that are neither within nor outside the class).

2.4. Integration of non-monotonic logic

Non-monotonic logics can be seen as an illustration of the general topology described above, and can be used to represent exceptions in ontologies. Given an element X and an ASP expression C (or class, that is to say a part of E), we have the following assertions:

- If C(X) is true, unless otherwise indicated, then this corresponds in topology to say that X is at the **interior** of C. From the perspective of ontology, it is also to say that X is a typical element of C.
- If C(X) is false, unless otherwise indicated, then this corresponds in topology to say that X is at the **exterior** of C. From the perspective of ontology, it is also to say that X is an unrelated C.
- Finally, if the C (X) is "partially" true, that is to say, it does not check all the properties of C, then this corresponds in topology to say that X is on the **border** C. From the perspective of ontology, it is also to say that X is an atypical C.

We have the same three equivalence with classes and typical or atypical subclasses[2].

3. Paleoanthropology: A brief introduction to human evolution

The human family (i.e., the hominin), including modern humans and their fossil relatives, emerges from a group of African apes. The dichotomy, from a common ancestor, of two lineages: one leading to the modern chimpanzee (panin) and one leading to our species (Homo sapiens) occurs, at least, 7 million years ago (Late Miocene); this age corresponding to the oldest evidence of an african hominin representative.

The first steps of the evolutionary history of our family take place in Africa and remain limited to the african continent from 7 to about 1.8 My. Numerous hominin (contemporaneous and successive) species are known from this period, humanity was diverse. The genus Homo emerges a short time before 2 My (at about the same period, emerges also a group of "robust" australopithecines) and exhibits a series of major morphological novelties along with new practices and strategies (e.g., tool manufacture). Unfortunately, the late Miocene African sites are still uncommon and irregularly distributed. Besides, the fossil remains that support the paleoanthropological studies, belongs to various individuals, from spatially (east, central and south Africa) and chronologically (several million years) distant sites, which complicates the interpretation of the evolutionary processes and pathways within our family.

3.1. Paleontology

The paleontology describes, analyzes and interprets fossil remains (bone material, environmental indicators, stone tools) on which are based the evolutionary hypothesis. One

[2] For a complete description of the six topological relations and their properties (inclusion at the interior of a class, inclusion at the border of a class, etc.), see Jouis et al. (2008). In this paper, we use only the inclusion border relation because, in paleontology, the zoological classes are organized in a hierarchy based on the displayed morphological features within each class and their evolutionary significance (see § 3.1).

of the objectives is to reveal common characteristics (e.g., illustrating common ancestry) among diverse and disparate fossil material, i.e. representative of individuals that exhibit different ages, sexes, geographical and temporal origins. Basically, individuals that show common morphological features are gathered within a same class defined from a reference morph called holotype. The holotype represents a morphological type of a zoological class (usually species). To be integrated in a class, the individuals must exhibit most of the features of the class-holotype. Atypical individuals that do not correspond to any given type can become themselves a reference for a new class. The zoological classes are then organized in a hierarchy based on the displayed morphological features within each class and their evolutionary significance[3].

3.2. Features used for classification

We present here the morphological features (Maclatchy et al., 2010) – a group of innovations or characters inherited from the ancestor – as literals (in the sense of predicate logics):
I10 Body size
I11 Body weight
I12 Endocranial volume relative to body mass
I13 Bipedality
I14 Teeth morphology and relative teeth size
I15 Occlusal morphology, enamel thickness and molar wear patterns
I16 Skeletal morphology linked to bipedal locomotion;
    …
I20 Arboreal locomotion
I21 Diet
I22 Cranial vault thickness
I23 Post-orbital morphology
I24 Cranial vault profile
I25 Prognathism

The literals listed above document characters or group of characters which are classically used in paleoanthropology. Of course, they provide only a partial illustration of the complete set of criteria used for defining and classifying zoological classes. Most of them admit a normal variation within and between classes and they are presented only as an example.

For instance, this set of morphological characters is coded below for the fossil hominin *Australopithecus afarensis*:

I10 Average size, close to a chimpanzee
I11 Average body mass, close to a chimpanzee
I12 Endocranial volume increased, relative size reduced
I13 Bipedal at least occasional
I14 Reduced anterior dentition. Honing complex lost
I15 Thicker enamel
I16 Hind limbs adapted to bipedality
I20 Forelimbs retain arboreal features
I21 Canine reduced. Hard food is consumed.
I22 Mosaic pattern, primitive characters retained
I25 Variable, usually prognathism expressed

3.3 Evolutionary hypothesis

New discoveries periodically call into question evolutionary hypothesis formulated in hominin evolution. In fact, morphological novelties (in its evolutionary sense) generate atypical individuals; when discovered, these individuals imply the reinterpretation of the species relationships within our family and might require the invention of original classes within the hierarchy defining our group. In zoology, the class hierarchy is based on homogenous systems: the taxa. These biological classes gather individuals which present a comparable set of characters inherited from a common ancestor (taxonomy). To understand the evolutionary relationships (phylogeny) between taxa (and then establish a coherent hierarchy), paleontologists sort the morphological features following two categories: (1) the primitive elements are present in the ancestor morphology and remain unchanged in the descendant(s); (2) the derived elements correspond to morphological novelties in the descendant morphology relative to the ancestor state. The combination of topology and non-monotonic logics allows assessing both taxonomic and phylogenetic processes in order to facilitate the interpretation of atypical individuals in an objective manner.

4. Representation of Atypical Entities in our model: Implementation in AnsProlog*

4.1. Simplified representation of a taxon in AnsProlog*

For simplicity, AnsProlog * is a program that interprets expressions in the formalism of ASP. In AnsProlog *, one way among others to describe a taxon is to directly translate the taxon as a rule. For example, the taxon (or the class) *Australopithecus afarensis* is translated directly as a rule below. We have added a set of facts about an object named Joe, and verify all properties of the rule:

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[3] The concept of holotype is close to the notion of "typical object" defined in computational linguistics (Desclés J.-P., A. Pascu, 2005), (M. Freund, J.-P. Desclés, Pascu A ., J. Cardot, 2004). The "typical object" represents a completely unknown object, which does not really exist, but which has properties. The "typical object" is associated with a concept (or class). For example, if one takes the concept of "being-a-human", the typical object of this concept is an ordinary human being, with nothing else to say. Conversely, an individual entity named is determined: he has his own properties. For example, John is a man aged 30, height 1.80m, who lives in Paris, etc. If John is a typical human being, in addition to its own properties to itself, he inherits the properties of the typical object of class "being a human": bipedalism, etc.
So, for "abuse of language," we speak of "taxon" in computer science to refer not to a particular individual, but to a class.

```
"#domain object (O).
object (joe ; jean).
australopithecus_afarensis(O) :-
  average_body_size(O),
  average_body_weight(O),
  average_endocranial_volume(O),biped(O),
  reduced_anterior_dentition(O),
  thick_enamel(O),
  skeletal_adaptations_to_bipedality(O),
  not arboricolism(O),
  not canine_reduction(O),
  not derived_cranial_morphology(O),
  not primitive_characters_retained(O),
  not prognatism_variable(O)."
```

By adding the following facts, we get that "Joe" is a australopithecus_afarensis:

```
 "average_body_size(joe).
average_body_weight(joe).
average_endocranial_volume(joe).
biped(joe).
reduced_anterior_dentition(joe).
thick_enamel(joe).
skeletal_adaptations_to_bipedality(joe).

→ australopithecus_afarensis(joe)."
```

4.2. When topology, paleoanthropology and ASP meet defeasible logics

We note that the negative literals:
```
 "not arboricolism(O),
not canines_reduction(O),
not derived_cranial_morphology(O),
not primitive_characters_retained(O),
not prognatism_variable(O)"
```
have been validated as true by default (no information: negation as failure).

Now we can imagine that the paleontologist discovers, in a prehistoric site, Joe jaw. However, the paleontologist finds that Joe has the property "canine-reduction". In AnsProlog*, this corresponds to adding the new fact:
```
canine_reduction(joe).
```
But the literal:
```
not canine_reduction(joe)
```
becomes false. Hence the rule:
```
australopithecus_afarensis(O):-….
```
is no longer verified. Accordingly, AnsProlog* can no longer deduct the new fact:
```
australopithecus_afarensis (joe).
```
Thus, we have a revisable reasoning. The object "Joe" is no longer classified as class australopithecus_afarensis. The paleontologist must invent a new taxon to classify "Joe." Note the new taxon A_nov_taxon, which has the properties defined by the rule:
```
A_nov_taxon (O) :-
  average_body_size(O),
  average_body_weight(O),
  average_endocranial_volume(O),biped(O),
  reduced_anterior_dentition(O),
  thick_enamel(O),
```
```
  skeletal_adaptations_to_bipedality(O),
  canines_reduction(O),
  not arboricolism(O),
  not derived_cranial_morphology(O),
  not primitive_characters_retained(O),
  not prognatism_variable(O).
```

AnsProlog can deduce a new fact:

```
→A_nov_taxon(joe).
```

These procedures parallelize methods used in paleoanthropology. The description of a fossil taxon is based, by nature, upon incomplete data such as cranial fragments, post-cranial elements, etc. Missing data might be inferred but usually remains unresolved until the discoveries of new material. The identification of a fossil specimen and its allocation to a preexisting or a new class constitute a first step of the paleontological work. This "taxonomic" work is the basis of the phylogenetic analyses which aim organizing taxa in natural groups, i.e. establishing ancestor / descendant relationships and defining kinship (sister groups). Hence, character analyses require considering the temporal variable: within an evolutionary lineage, one character may exhibit several states. Indeed, the morphology of a hypothetical ancestor is altered through time and presents various morphs in descendants. For instance, the figure 1 illustrate the modification of three characters within the Homininae (a group including the living chimpanzee, the modern human and their ascendants, these two taxa share a common ancestor). Each node (junction) indicates a common ancestor for the considered branches (clades); for instance, the gorilla shares a common ancestor with the group including the living chimpanzee and the Hominini (*Ar. ramidus*, *Au. anamensis*, *Au. afarensis* and modern humans – not shown). The states (morphs) of three morphological characters (A, B, C) are indicated for each clade. For instance, the character B illustrates the canine reduction. The canine is primitive for gorillas and chimpanzees (large canines) and derived for the Hominini (reduced canine). The character B shows three different states (derived stage 1 to 3) within Hominini which corresponds to three reduction stages of the canine, from moderate (*Ar. ramidus*) to important (*Au. afarensis*).
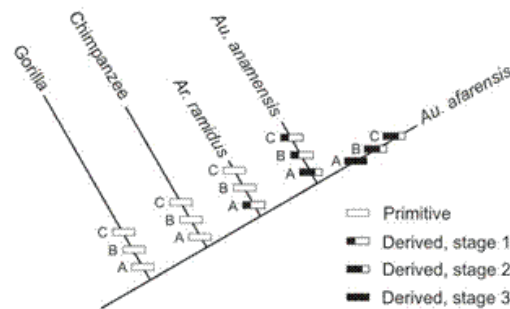

Figure 1: Simplified phylogeny of the Homininae and illustration of primitive/derived states for three morphological characters.

The characters are: A, more incisiform canine with lower crown and higher shoulder; B, Canine reduced relative to cheek teeth; C, thicker molar enamel. *Ar*. *ramidus*, *Au*. *anamensis* and *Au*. *afarensis* are three extinct species belonging to the modern human lineage.

Of course, phylogenetic analyses are based on more complex and on a larger number of characters than those presented in figure 1.

4.3. Representation of inferences in AnsProlog*

In this section, we illustrate how AnsProlog* allow making inferences with properties of type "derived" and properties of type "primitive", inherited by the taxa using the border inclusion links. In our second program, taxa are represented in the form of several facts (rules with only one literal in the left and no literal in the right part, that is to say literals always true). Information about a taxon are literals of the form:

```
taxon (name_of_taxon,
  {derived, primitive},
  characteristic).
```

Then, all the rules are written in the same manner, allowing inferring the primitive or derived characteristics. They take the following form:

```
inclusion_primitive
(T1, T3, characteristic_a):-
inclusion_border (T1, T2),
taxa (T1, primitive characteristic_a),
inclusion_border (T2, T3).
```

This rule is interpreted as follows. There is a primitive inclusion for the "A" characteristic between a taxon T1 and a taxon T3 if there is a border inclusion between the taxon T1 and an intermediate taxon T2, and if there is a primitive "A" characteristic for the taxon T1, and finally if there is a border inclusion between the taxon T2 and the taxon T3. We have the same rule format for the characteristic "B" and "C" and for derived inclusion. For example, on the facts:

```
inclusion_border (ar_ramidus, au_anamensis),
taxon (au_anamensis,
    derived, characteristic_a) and
inclusion_border(au_anamensis,
au_afarensis),
```

the rule we just stated allows to infer the new fact:

```
inclusion_derived (ar_ramidus, au_afarensis,
characteristic_a).
```

5. Conclusion

In this article, we aim to present a brief evaluation of an application of Topology and non-monotonics logics to practical issues in Paleontology. The implementation in AnsProlog of typicality/atypicality concepts based on zoological groups and morphological criteria leads to propose new solutions for resolving topologic trees in a systematics framework. This first step assessment of the method may be tested and extended in several ways including:

1. A formalization of the concept of typicality scale as a base for a "neo-topology" with boundary thicknesses.
2. A larger and a more detailed set of morphological characters, than introduced into our presentation, in order to better assess our method in a complex zoological framework.

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