Metaphorical Conceptualization in Cell Biology

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Abstract

Metaphorical conceptualization (MC), in the sense used by Lakoff, is prevalent in scientific knowledge, particularly in medicine and associated domains such as cell biology, molecular biology or genetics. Indeed, these fields are now central to new approaches in medicine, and their terminology is a challenge for both terminologists and translators. Our working hypothesis is that metaphorical conceptualizations are closely linked to terminology and phraseology, and our aim is to describe their structure and characteristics in cell biology, specifically in cell transport and communication. This article presents a typical example of how the structures of entities in cell biology are metaphorically conceptualized. The presence of two metaphorical conceptualizations, as revealed by the linguistic expressions found in a highly specialized scientific corpus, is reminiscent of the metaphorical duality observed by Lakoff. It suggests that the combinatory rules governing term co-occurrences in specialized languages are closely linked to metaphorical conceptualizations specific to various fields of knowledge.

1 Introduction

Given the importance of cellular mechanisms in the new approaches used in medicine, our objective is to describe the structure of the principal metaphorical concepts used in cell biology. At one time, cell biology, together with molecular biology and genetics, were at the periphery of clinical medicine. Now, they have become prominent in all new therapeutic approaches. Consequently, the terminology used in these fields has become central to medical knowledge. Moreover, since most concepts are first formulated in English, creating terms and using an appropriate phraseology in other languages presents a challenge for translators, as well as for researchers and scientific writers. It is important, therefore, to understand the cognitive mechanisms underlying how scientific knowledge and discourse are constructed: this process is essential for the definition and use of the cognitive tools needed to face this challenge. One of the main characteristics of gathering scientific knowledge and elaborating theories is related to the role of metaphorical conceptualization (MC). Previous work has shown that it is particularly prevalent in the Internet terminology [Meyer 1997; 1998], but also in medicine and science [Raad 1989; Liebert 1995; Van Rijn-vanTongeren 1997]. Our working hypothesis is that MC is involved in the choice of terms and phraseology. Consequently, understanding metaphorical structures is an important element in building a cognitive tool for making decisions in the translation process, and for helping understand concepts and terminology networks.

2 Metaphorical conceptualization

In this article, we refer to *metaphorical conceptualization* using the definition of a *metaphor*, or a *conceptual metaphor*, given by Lakoff [1993] i.e., "a cross-domain mapping in the conceptual system" as well as his definition of a *metaphorical expression* as one that "refers to a linguistic expression that is the surface realization of such a cross-domain mapping", which is the meaning traditionally given to the term *metaphor*. It is important to understand that the surface realization of a metaphorical concept may take place at various levels of linguistic expressions i.e., "a word, a phrase or a sentence". According to Lakoff, *cross-domain mapping* refers to the use of the conceptual structure and the terms of a source-domain to describe a target-domain: this phenomenon occurs primarily in the same language. Consequently, mapping conceptual metaphors involves tracking metaphorical expressions that reveal the correspondences established between a source domain and a target domain. This set of correspondences participates in the structure of the *frame* (e.g. Fillmore & Atkins 1994) in which a particular term is used.

An important observation is that the principles of cell biology (as is the case in other scientific fields) are conceptualized at the international level. The mainstream of Western scientific thought stems from agreement on a number of concepts (for example, the structure of cells, their components, the molecular structure of viruses, etc.). As a result, the surface realization of scientific concepts is usually made in English first, because of the imperatives of international scientific communication. Non-English speaking scientists indulge in inadvertent translations that are, to a certain extent, transcultural, and their linguistic realization is strongly influenced by the English language. Therefore, the surface realization of a *linguistic frame* in a particular language is likely to be an interaction of this language with a *cognitive scene* [Fillmore 1985] that pertains specifically to Western scientific thought, rather than an adaptation primarily involving the linguistic particularities of the source and target languages.

3 Conceptualization of entities in cell biology

A previous work [Vandaele, 2000] has shown that a general metaphorical conceptualization of the *entities* (as defined by Sager [1990]) involved in physiological processes is reminiscent of figures participating in a scenario. However, conceptualization of the same entities in a pathological process evokes criminals (e.g. bacteria, virus, or even a gene) responsible for a crime (the disease): the patient is the victim, the researcher or the physician is a detective looking for the culprit. The cognitive scene involved results from mapping a source-domain (a scenario or a police investigation) to a target-domain (physiological processes or pathological processes, in the larger context of medical research). This can be used as a cognitive device that is useful, not only in understanding the general structure of a domain, but also, in helping to choose, or at least propose, appropriate terminology and phraseology.

However, these cognitive scenes are very general and do not suffice to reflect the details of both physiological and pathological processes. Other scenes in which entities are involved in cell biology must be described, and other cross-domain mapping must be deciphered. In particular, the scenes mirroring the various inter- and intracellular processes must take into account other characteristics of the entities themselves: these can be structures (how entities are built), functions (what they do), localization (where they are) and destiny (how they are produced and what they become). These characteristics pertain to molecules (proteins, lipids, etc.), but also to the structural components of the cell (membrane, nucleus, etc.). [1]

4 Conceptualization of protein structure

In this article we present some data related to the structure of proteins. This class of molecules is particularly interesting because of its high structural and functional diversity, as compared to that of nucleic acids and lipids. Furthermore, the variety of the terminology involved allows a detailed examination of how various modes of conceptualization and metaphorization are combined.

We will start with a few definitions for the couple of terms *protein/protéine* given in various English and French scientific papers published in journals with peer-review, or in textbooks written for students and researchers. In the corpus we are examining (more than 300,000 words in each language), vulgarized texts aimed at explaining science in a lay language have been excluded.

1. *Macromolecule made up of one or more chains of amino acids joined covalently through peptide bonds. Their functional architecture is conferred by disulfide bridges, hydrogen bonds and hydrophobic interactions.* [Delvin & Pham 1992]
2. *A linear polymer of amino acids joined by peptide bonds in a specific sequence.* [Lackie 1999]
3. *A polypeptide with a complex three-dimensional shape.* [Bolsover 1997]
4. *Constituant macromoléculaire majoritaire des cellules formé par un (ou plusieurs) enchaînement(s) d'acides aminés unis entre eux par des liaisons peptidiques.* [Muller 1995]
5. *Macromolécule constituée d'une chaîne d'acides aminés liés par liaisons peptidiques, dont le repliement tridimensionnel lui confère une architecture fonctionnelle. Celle-ci est maintenue par des ponts disulfures, des liaisons hydrogènes et des interactions hydrophobes.* [Delvin 1992]

6. *Molécule polypeptidique de Mr supérieure à 10 000. Les protéines sont caractérisées par :*
    1) *leur structure primaire, covalente (séquence des aminoacides), déterminée génétiquement;*
    2) *leur structure secondaire (zones en feuillets plissés ou en hélice alpha), correspondant à un aspect régulier, ordonné, grâce à la formation des liaisons hydrogène entre les -CO- et les -NH- des liaisons peptidiques;*
    3) *une structure tertiaire (globulaire ou fibrillaire) réalisée par formation de liaisons variées entre les groupes fonctionnels des chaînes aminoacides et qui conditionne le rôle biologique de la protéine. La structure tertiaire est profondément altérée par divers agents, physiques ou chimiques (dénaturation).* [Dictionnaire des sciences pharmaceutiques et biologiques, 1997]

These definitions describe proteins as being *linear*, as if they were a ribbon or a tape. At the same time, however, due to the way they fold up, proteins can also be visualized as *tri-dimensional objects*. Consequently, a number of terms used to describe their structure are consistent with the conceptualization of proteins as linear objects, while others are consistent with a conceptualization as tri-dimensional objects (Table 1). The French equivalents (indicated in brackets) are unambiguous and are not subjected to any synonymy, which makes the analysis easier.

Linear object (English/French)	
sequence	séquence
segment	segment
chain	chaîne
helix	hélice
ring	anneau
turn	coude
loop	boucle
sheet	feuillet
Tridimensional object (E/F)	
domain	domaine
region	région
site	site

Table 1: Lexical units reflecting the dual conceptualization of protein structure

It should be emphasized that the lexical units presented in Table 1 (or their French counterparts) are terms, in the sense that they refer to a specific notion in the field of cellular biology. They are not linguistic metaphors used idiosyncratically, picked up from general language to explain a scientific concept in a vulgarized manner. In other words, the use of such terms does not reflect an occasional semantic deviance. It is of primary importance to distinguish between terms used in the framework of a scientific model based on metaphorical conceptualization (in this instance, to depict protein structure) and those used in occasional metaphorical expressions.

The terms that bring to mind a linear object, namely *sequence* and *chain*, refer to the model describing units (amino-acids) linked together to form the protein molecule. *Sequence of amino-acids* and *chain of amino-acids* (*séquence d'acides aminés* and *chaîne d'acides aminés*) can be used as synonyms. Other terms used to describe the shape of proteins that fold up like a ribbon refer to a linear conceptualization: *helix* (*hélice*), *ring* (*anneau*), *turn* (*coude*), *loop* (*boucle*), all refer to a particular conformation taken by the protein.

A number of other terms are used to describe the three-dimensional protein structure: *domain* (*domaine*), *region* (*région*), *site* (*site*). According to the chemical modelization that accounts for the space occupied by atoms, proteins are viewed as three-dimensional objects with an irregular surface: the linear aspect of the molecule is not directly referred to. A *region* is a part of a protein without any indication of function, while a *domain* denotes a region of a certain size that does have a function. A *site* refers to a small region with a function (it is usually able to bind with another molecule or is involved in an enzymatic reaction).

It is interesting to note that *region*, *domain* and *site* bring to mind spatial conceptualization, either in two or three dimensions, but not in one dimension. Indeed, a *domain* may refer to a part of the protein that is located at the surface of the molecule, or to a three-dimensional part of it.

However, a number of contexts in cellular biology concurrently summon up both a linear AND spatial conceptualization of proteins:

7. *La <u>séquence</u> du <u>domaine</u> extracellulaire a été déterminée.*

8. *This <u>domain</u> <u>sequence</u> is conserved among various proteins.*

Because the molecule folds up (this level of conceptualization is linear, as if the protein were a ribbon), a *region*, a *domain*, or a *site* (three-dimensional level) can extend over non-contiguous segments of the protein. For a non-specialist who is only acquainted with the general meaning of *sequence* or *domain*, the co-occurrence of these two lexical units is meaningless. The extended meaning that occurs in specialized language does not result from the metaphorical use, at a purely linguistic level, of *domain* or *sequence*, but from the metaphorical conceptualization of the proteins themselves.

The fact that the proteins may be simultaneously conceptualized as linear objects, as well as three-dimensional objects, is reminiscent of the phenomenon of *duality* descovered by Lakoff [1993]. Duality was first described when Lakoff observed that time is simultaneously conceptualized as a motion of an object and as a motion over a landscape.

Lastly, an interesting hypothesis needing further investigation, is that the particular use of terms (including nouns, but also, as L'Homme pointed out [1998], adjectives, verbs and adverbs) in specialized languages should reflect new combinatory rules closely linked to the metaphorical conceptualization of the field. This hypothesis concurs with the one emitted by Fontenelle who wrote, "It is then crucial to realize that metaphors can be used to account for some co-occurrence phenomena which should otherwise be considered as purely idiosyncratic" [Fontenelle 1994].

5 Conclusion

Metaphorical conceptualization in specialized languages must be taken into account when describing terms and their phraseological environment. This is not an easy task, since traces of metaphors are dispersed in scientific discourse and can be found in various grammatical categories. A number of methodological problems must therefore be resolved (constitution of the corpus, computer analysis, database structure). Formalizing metaphorical conceptualization is another difficult task, but a number of recent studies should shed some light on this [Fillmore 1994; Fontenelle 1994; Pustejovski 1995].

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Endnotes

[1] To help readers who may not be familiar with cell structure and function, let us briefly recapitulate by explaining that a cell can be viewed as a space delimited by a membrane, which is mainly formed by lipids and proteins. The internal cellular space, or cytoplasm, contains a number of structures such as the nucleus (in which the chromosomes are found) and other elements involved in the synthesis, distribution and degradation of molecules. These molecules may be proteinic or not, used inside the cells (e.g. proteins to regulate gene expression), or secreted outside the cells (e.g. hormones).

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