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About Integration Opportunities between TRIZ and Biomimetics for Inventive Design

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Abstract

This paper presents the first results of a Ph.D. program aimed at investigating the domain interface between TRIZ and Biomimetics within the scope of inventive design. Indeed, a few authors have already proposed as a relevant direction of research the identification of integration opportunities between TRIZ and Biomimetics towards a more effective and efficient inventive design methodology. The paper presents a comparison between the tools based on functional modeling used during the process of problem solving within TRIZ and Biomimetics. This comparison intends to elicit overlaps, complementarities and incongruences of these techniques. The indications about how to improve the process of describing natural solutions in an engineering way and how to describe technical problems in order to use natural information as source of inspiration are given by analyzing few examples. The results are discussed in terms of necessary modifications in the engineering problem description in order to use a database of biological functions (i.e. the Biomimicry Taxonomy) as a source of natural knowledge in the process of inventive design.

Keywords: Inventive Design, Bio-Inspired Design, Biological Functional Database, Biomimicry Taxonomy;

1. Introduction

Life evolution is estimated in 3.8 billion of years and it is commonly agreed that Nature has evolved objects with high performance with commonly found materials using clever and elegant solutions [1]. The use of these solutions for technical purposes is old, at least, as the human life and humans have respectfully looked at Nature until the industrial revolution. The lack of resources has led some scientists to rethink the way we look at Nature in order to learn from it, instead of overworking it [2]. Using Nature as a source of inspiration allows developing breakthrough innovation, but it is necessary to consider that, the process of Bio-Inspired Design is broad and highly interdisciplinary. This fact is clearly expressed in [3], where the author interprets the concept of "Biologically Inspired Design" as the understanding of design competence from biological evidence.

Nowadays, the new challenge is related to the attempt of creating a solid bridge between Biomimetics Research and Industrial Applications. In 2011, we are witnessing at the consolidation of this bridge by the creation of a new series of conferences called International Bionic Engineering Conference, a new Journal (Journal of Bionic Engineering) and a new series of books by CRC press called Biomimetic: Nature Based Innovation.

There are several contributors in this field of research and many are the attempts to create an up-to-date state of the art of this discipline known as Bionics [4], Biomimetics [5], Biomimicry [6], Bio-Inspired [7] Design etc. For example, [8] is an interesting description of the Biomimetic process and a good review of the research can be found in [9]. A different attempt to collect and classify the knowledge and the applications related to the process of Nature Based Innovation has been done by Yoseph Bar Cohen in [10].

Different schools of thought have proposed extremely different approaches in order to systematize the process of Bio-Inspired Design. The first attempt was made by [11], which opened the way to the development of several more detailed algorithms as [12-16].

Still in the Bio-Inspired Design process, major limitations remain in the identification of the most appropriate biological resources suitable for addressing an engineering problem, due to the huge dimension of the information fund and to the lack of a proper guidance for engineers about how to orientate themselves in biological literature. Not surprisingly, the most acknowledged consulting services operating with biomimetics as a reference technique are run by biologists, or at least by experts with a solid background in biology. This characteristic certainly constitutes a crucial bottleneck to the extensive adoption of biomimetics in industrial R&D activities.

The ultimate goal of the research presented in this paper is to contribute to the successful and efficient adoption of Bio-Inspired Design practices by designers and problem solvers with a typical engineering background.

The second section of this paper positions its contents with respect to the field literature. Then, in the third and fourth chapters, an original comparison between the Biomimicry Taxonomy and two functional modeling approaches typical for the engineering design domain, as well as the resulting outcomes are respectively detailed. The last section brings the concluding remarks and an anticipation of the further developments the authors are working on.

2. State of the art

Three main approaches emerge in literature among the possible strategies to allow designers and technicians to access and use Natural solutions, and more in general, the knowledge about Nature contained in the models of natural systems described in the biological literature: the Database approach, the Text-Mining approach and the TRIZ approach.

2.1. Database Approach

The Database Approach aims at creating a collection of biological effects/phenomena classified by a specific functional taxonomy. Some examples are AskNature (http://www.asknature.org/) and Bionics2Space (http://atlas.estec.esa.int/bionics2space/). This approach is widely used in practice since it appears as a typical task for a designer to formulate a knowledge need in terms of functions to be delivered. Besides, biological literature is not necessarily aimed at the description of living organisms in terms of functions. Moreover, as discussed in [15], at least four classes of knowledge transfer from biology to engineering can be identified: parts and materials; organs (physical effects, phenomena and state changes); attributes; actions and functions. Therefore, just the last category is properly addressed by currently existing databases. Moreover, they provide too many responses to a typical designer's query; this is an extremely risky fact from an efficiency perspective since the process of solution search can grow without control.

Nevertheless, it is worth to notice that the potentialities of this approach are well recognized and indeed the European Space Agency (ESA) uses it within the Advanced Concept Team (ACT) to develop innovative solution for space missions.

2.2. Text-Mining Approach

The Text-Mining Approach "rather than creating an enormous database of biological knowledge to specifically support engineering design" has the objective to exploit "the large amount of biological knowledge" available in books, journals, etc. [17]. Difficulties here derive from the difference between the language adopted by biologists and engineers, such that the latter often miss to formulate the proper query. In order to face with this limitation, researchers of the University of Toronto have proposed an algorithm capable to "generate a non-obvious keyword provided by a domain expert as one of many other non-obvious but relevant keywords", starting from the analysis of one single source: "Life. The science of biology". Despite the promising perspectives of computational linguistics, this approach still seems not scalable for its extensive application to any biological source.

The same approach has been followed by Stroble et al [18] that generated a thesaurus which contains biologically connotative terms related to engineering function and flow terms. The thesaurus has the structure and classification of the reconciled Functional Basis [19] in order to make available the biological knowledge for engineers and designers.

2.3. TRIZ Approach

The third approach here mentioned is based on TRIZ. Altshuller himself in [20] pointed to biological systems as possible sources of inspiration although "yet only a tiny fraction of Nature's inventions are used". He also was aware that the enormous amount of natural prototypes is arranged in unknown way. It is like to use a patent library with unknown classification. The proposed solution was "to search for prototypes among pre-historical animals" (considered simpler) or to examine general tendencies in order to compare them with technical evolution. The Altshuller's guidelines have been followed by Vincent et al. who identified TRIZ as the best methodology in order to transfer "knowledge between different scientific and engineering disciplines" [11], [21]. They used TRIZ as a set of procedures and tools to generate technical systems imitated from Nature and developed the Bio-TRIZ Matrix derived from the TRIZ Matrix of Contradictions. Similarly, Hill has adopted the TRIZ concept of contradiction to develop the Bionic-Oriented Construction Process, where goal setting is carried out trough contradiction analysis [22].

In both cases, the identification of natural models as inspiration sources for inventive design is done through a contradiction search. In the first approach the search is based on contradictions related to the use of resources by both natural and technical systems, classified in terms of information, energy, time, space, structure and substance. Besides, Hill proposes to index contradictions through a functional basis. In this case, the search allows finding contradictions between not only resources, but also related to specific natural solutions and strategies.

2.4. Detailed objectives

With regards to the above mentioned approaches, the present paper aims at improving the usability of biomimetics databases organized according to a functional classification, by re-indexing natural functions into an engineering-oriented perspective.

The Biomimicry Taxonomy is an initiative of the Biomimicry Institute, which is developing a collection of natural effects classified through an original taxonomy. As it will be detailed in the following section, its structure has several incongruences from an engineering design point of view, thus limiting its extensive applicability.

Besides, it is typical for engineers to describe systems in terms of functions, despite the reference models can be different. Two main functional modeling approaches can be recognized, those based on energy-material-signal flows transformations [19] and those characterized by a triad carrier-action-object. The OTSM TRIZ Function model will represent the latter in this paper.

Thus, more in detail, the specific objective of the present paper is to analyse the taxonomy proposed by the Biomimicry Institute and to map it with respect to the NIST Functional Basis and the OTSM Functional Model. The comparison of these alternative modeling techniques allows to analyze the degree of correlation

between the models of natural systems and the functional models of technical systems, in order to integrate bio-effects as sources of inspiration in the process of inventive design.

According to this objective, the paper describes all the main outcomes of the comparative analyses performed so far by the authors:

− As detailed below, three complementary comparisons have been accomplished, two among the Biomimicry Taxonomy and the NIST Functional Basis and one between the Biomimicry Taxonomy and the OTSM Functional Model respectively; these analyses systematically applied to all the sub-categories of the Biomimicry Taxonomy allow to determine the degree of overlap between the two methodological approaches of this study.
− Then, the paper proposes a novel sub-classification of the Biomimicry Taxonomy, with the aim of highlighting its lack of homogeneity that hinders its embedment into a systematic problem solving approach.

3. Structured comparison between engineering functional modeling and the Biomimicry Taxonomy

The comparison presented in this paper has been developed following a series of steps in order to understand which of the functional models, actually used to describe technical systems in engineering design, is the most appropriate to create an overlap with the Biomimicry Taxonomy used to classify natural systems. The comparison has been carried out at different levels of detail as described in the following paragraphs.

In order to clarify the comparison processes it is important to introduce the specific features of the Biomimicry Taxonomy (BT), the NIST Functional Basis and the OTSM Functional Model.

The BT is a collection of information classified according how organisms meet different "challenges". The taxonomy provides an index of "Strategies" considered as potential solutions to those challenges [23]. The information is hierarchically structured in three levels of detail:

- Groups;
- Sub-Groups;
- Functions;

An example of record contained in the BT is reported in Table 1.

Table 1. Structure and exemplary record of the Biomimicry Taxonomy

Biomimicry Taxonomy	Examples
Group	Maintain physical integrity
Sub-Group	Protect form biotic factors
Function	Protect from animals
Strategy	Nonoscale protrusion

The NIST Functional Basis [19] is a taxonomy of functions expressed by a number of functional verbs applied to EMS (Energy, Material, Signal) flows. The formers are hierarchically subdivided into:

- 8 classes
- 21 secondary
- 24 tertiary actions on flows the latter are classified in three levels including:
- 6 secondary and 11 tertiary material flows
- 12 secondary and 4 tertiary energy flows
- 2 secondary and 7 tertiary signal flows

This Functional Basis aims at describing technical systems in an unambiguous way. The basis enables to describe different systems that perform the same function with one model and try to avoid the use of the same

model to describe systems that perform different functions. This is a key point in the process of knowledge transfer from Nature to technology and allows to reduce the misapplications of natural solution in the process of inventive design [24].

As mentioned above, functions can be also described as carrier-action-object triads. The peculiarity of the OTSM Functional Model is to describe the action performed by the function carrier through a standard verb and an Object-Parameter. The reference verbs in this case are just four: Change, Increase, Decrease, Stabilize. Besides, Object-Parameters can be freely chosen among the features of the object receiving the function.

3.1. Comparison Features

The comparison has been carried out at three levels of detail:

a. BT (Sub-Groups) versus NIST (Actions)
b. The first analysis aims at identifying the correspondences between the Sub-Groups and the actions listed in the NIST classification function classes. BT Sub-Groups are thus compared with the explanatory descriptions of NIST Functional Basis Actions.
c. BT (Sub-Groups, Function) versus NIST Functional Basis.
d. After mapping BT Sub-Groups with NIST actions, it is possible to search for matches between the BT functions and the NIST Functional Basis in terms of specific pairs Action/Flows of the NIST taxonomy. Even in this case, the descriptions of the NIST functional basis (both action and flows) constitute the reference for identification of matches.
e. BT (Sub-Groups, Function) versus OTSM Functional Model.
f. The last analysis presented in this paper concerns the OTSM-TRIZ Functional Model in order to understand the opportunities to integrate the tools of TRIZ and the natural functions classified by the Biomimicry Taxonomy. The comparison has been accomplished by reading each model of the BT (Sub-Group, Function) and identifying the most suitable feature of the object receiving the function impacted by the action. The most appropriate verb among the above-mentioned standard of the OTSM Functional Model is then recorded.

3.2. Biomimicry Taxonomy Functions Subdivision

Some of the items belonging to the leafs of the BT, i.e. the classes at the highest detail level, cannot be considered as proper "functions" since they do not involve any active role by the biological system with respect to an external object receiving the function.

Therefore, it is worth to propose a new sub-classification of the BT functions, based on the type of features they describe, rather than on the nature of the function itself. In detail, we propose a subdivision of the BT functions into five classes by analyzing the pairs action/flows of the NIST matches described in section 3.1. BT functions appear as specifications of the Sub-Groups with details related to the object flow, its parameters, its context (space and time) etc. This sub-classification is detailed in Table 2.

Table 2. Proposed sub-classification of BT Functions

Description	
Time of Action	function specifies the time in which the action takes place
Environment of Action	The function specifies the environment in which the action takes place
Object-Flow	The function specifies the flow of energy, material, signal which is the function object
Object-Parameter	The function specifies a parameter of the object which is modified by the function
Others	The BT item is not a function or does not fit in any of the previous classifications

3.3. Comparison metric

All the above-mentioned comparisons have been formalized through a reference metric, as summarized in table 3. Since mismatches might hinder practical implementations of Biology-to- Engineering information transfers, it is worth analyzing in further details the reasons of partial matching, in order to allow the exploitation of the maximum portion of the BT, as proposed in table 4. More in details, the most frequent types of mismatch found between BT Functions and the closest items of the NIST Functional Basis are summarized in table 4, with some illustrative examples.

Table 3. Reference metric for taxonomy mapping

	Correspondence	Automatic retrieval and information transfer
Match Partial No Match	ExactSomeNo	Yes
		Necessary indexing of the mismatch No

Table 4. Main causes of partial correspondence between BT functions and NIST action-flow representation.

BT Function examples	NIST Functional Model partial correspondences			Mismatch set
	Action	*Flow*		
Distribute Energy	Branch, Distribute		Energy	Too generic: *Just primary level flow*
Protect form abiotic factors (Fungi)	Control Magnitude, Stop, Inhibit		Material, Solid	Too detailed: *Absence of Biological class*
Modify physical state	Control Magnitude, Change, Increment/Decrement/Shape/Condition		-	Depending on the Specific Situation: *More than one correspondence*

4. Results and Discussion

In order to appropriately consider the relevance of BT functions, the authors have assumed the number of records of the AskNature database as a suitable reference. In detail, the relevance score of a given BT function is calculated as the ratio between the number of database records in that class and the total number of records registered in the database. It is evident that AskNature updates will imply a possible variation of such relevance score; nevertheless, the database has already reached a certain maturity, therefore the expected changes are negligible for the scopes of the present research. For the sake of clarity, the analysis here presented is based on the status of the database as it was available online from 7 to 14 April 2011. At that moment, the database contained 2785 records, classified in:

- 8 Groups
- 30 Sub-Groups
- 162 Function classes

The following paragraphs will detail the global results of the analysis with a brief description of the best matches between the BT classes and the specific functional models.

4.1. BT (Sub-Groups) versus NIST (Actions)

Looking at the overall picture of the BT with respect to the NIST actions, it emerges that they present a good match in any BT Group, even if it is possible to find some lacks in each of them. The only BT Sub- Group, which has a relative match of 100%, is the group "Make".

- Match: 57.7%
- Partial: 38.8%
- No Match: 3.5%

The high value of the partial matches is an important fact to take into account for the above-mentioned reasons. The sub-groups of the BT are often too general to have a unique description with the NIST actions. For instance: BT (Modify, Modify Physical state, Size/Shape/Mass/Volume) can be associated to several NIST Actions: Increment, Decrement, Shape, Condition, all belonging to the secondary level Control magnitude, Change.

Besides, other sub-groups just partially match with the NIST Actions for the opposite reason: the latter miss to fully represent the BT sub-groups meaning, because these contain complementary information about the action. For example, BT (Move or Stay Put, Move, In/On Liquid) can be associated to NIST Action (Channel, Transfer, Transport) where both the reflexive meaning of the action and the environment where it occurs is missing. In other cases, BT sub-groups are related to a specific biological situation such as (Process Information, Sense Signals/Environment Cue, Body Awareness) which has just a partial correspondence with the NIST Action (Signal, Sense, Detect/Measure).

In this comparison, the percentage of No-Match is low; these sub-groups are mostly related to BT items which are considered functions from a biological perspective, but that cannot be described as such by a formal engineering functional model: e.g. BT (Maintain Community, Coordinate, Activities).

4.2. BT (Sub-Groups, Function) versus NIST Functional Basis

By improving the level of detail of the matching analysis, i.e. by comparing BT functions with NIST action-flow pairs, the degree of overlap dramatically changes. Perfectly matching entries are less than half of the previous comparison (from 58% to 25%) and in this case, there are no correspondences in the Sub- Groups "Move" and "Modify". However, only in the "Break Down" Sub-Group, there is a complete relative match between the two taxonomies and there is a good correspondence also in the Sub-Group "Get, Store or Distribute Resources".

- Match: 24.9%
- Partial: 42.8%
- No Match: 32.3%

The level of at least partial mismatch has increased mostly because BT functions are sometimes vaguely defined: e.g. BT (Get/Store or Distribute Resources, Capture/Absorb or Filter, Chemical Entities) can be linked to 2 different NIST Actions: (Branch/Separate/Extract or Provision/Store/Collect) and the related flow is too generic: Material, Solid.

Also in this case some "No Match" are due to too specific biological functions which miss an equivalent analogue in the NIST Functional Basis.

4.3. BT (Sub-Groups, Function) versus OTSM Functional Model

Thanks to the possibility to freely define the object parameter of an OTSM Functional Model triad, the comparison between BT functions and OTSM Function representation presents a higher correspondence than

the NIST Functional Basis. Besides, it must be observed that the OTSM approach brings to less repeatable results with respect to the NIST Functional Basis, since different persons might opt for different descriptions of the object parameter impacted by the function action, while NIST standardizes both actions and flows with pre-defined reference terms lists.

In this case, the relative match reaches the 100% of correspondences for the Sub-Groups "Move" and "Maintain Physical Integrity" and it reaches almost the complete correspondence for the Sub-Group "Modify":

- Match: 64.5%
- Partial: 27.4%
- No Match: 8.0%

The problems connected to the fact that BT functions are often vaguely defined and too strongly related to some specific biological contexts are found also in this comparison and the level of partial match is quite high here too.

4.4. Biomimicry Taxonomy Function Subdivision

The complete mapping of the above-described correspondence analyses cannot be reported here due to evident space limitations. The authors plan to make those associations public in the next future as alternative means for entering the Ask Nature database. Besides, it is possible to present and analyze here the sub-classification of the BT functions according to the criteria proposed in section 3.2.

The subdivision of the BT function based upon the five classes has reached the following results:

- Time of Action: 4.4%
- Environment of Action: 8.4%
- Object-Flow: 41.3%
- Object-Parameter: 38.5%
- Others: 7.2%

The BT functions belonging to the "Time of Action" cluster are limited in particular to Sub-Groups such as "Move", "Make" and "Process Information".

The "environment of action" is correlated with a bigger number of functions and is mainly present in the Sub-Groups "Move", "Maintain Community" and "Process Information".

The "Object-Flow" cluster contains functions related to almost any class, but only in the Sub-Group "Get, Store or Distribute Resources" there is a complete relative match. Besides, this class of functions is almost absent in in the Sub-Groups "Modify" and "Move".

Eventually, BT functions assigned to the Object-Parameter cluster are spread almost in all the BT Sub-Groups, but they don't appear in the BT Sub-Groups "Move" and "Get, Store or Distribute Resources".

A small amount of BT functions have not been clustered with any of the above, but being an almost negligible number they are associated in a residual sub-class "Others".

4.5. Exemplary application of the proposed correspondences

Some examples are here reported in order to illustrate the potential benefits of the proposed mapping tables. It is here assumed to tackle a technical problem and to search for biological inspirations through the associations discussed above.

After the definition of an exemplary design problem formulated in the form of a functional search, the identification of the relevant records of the Ask Nature database for concept inspiration has followed these steps:

1. Formulate the functional need as a pair Action-Flow of the NIST Basis and according to the OTSM formalism;
2. Individuate through the correspondence tables proposed in this paper the best fitting BT Groups, Sub-Groups, Functions;
3. Find the biological examples, in the AskNature database, related to the BT Groups and Sub-Groups identified in the previous step;
4. Select the most appropriate function as a source of inspiration for the inventive design process.

It is important to note that if the natural function from the BT cannot be expressed through the NIST and/or the OTSM models (i.e. a No Match has been recorded in all the above comparisons), there is no possibility to access the natural examples related to this portion of the information fund.

For example, let's consider the following problem: during the process of designing a new machine that works with a toxic fluid, it is important to prevent any loss of this gas, in order to reduce the risk of ambient contamination.
From an engineering point of view, the problem can be described with a NIST Functional Basis model such as:

- NIST (Control Magnitude, Stop, Inhibit – Material, Gas)
  Following the above-mentioned procedure, it is possible to individuate the corresponding BT Sub- Groups:
- NIST (Control Magnitude, Stop, Inhibit – Material, Gas) **-+** BT(Protect form abiotic factors, Gas/ Loss of Gases)

It is important to note that it is possible to find more than one BT function as a correspondent for the NIST model of the design problem. After having individuated suitable BT Sub-Groups where to look for the natural functions, it is possible to browse the Ask Nature database in order to find the proposed natural examples. For the specific case study, the natural examples are reported in table 5.

Table 5. Natural functions extracted from the AskNature database by means of the NIST Functional Basis correspondence

Strategy	Sub-Group	BT Function	Description
Maintain physical integrity	Protect from abiotic factors		
Gas			• Seed coat and enzymes protect seed: lotus
			• Ventilated nests remove heat and gas: termites
			• Vessels resist bubble formation: trees Loss of
		gases	• Respiration rate allows survival In low oxygen: blind shark
			• Embryos survive without oxygen: killifish
			• Augmenting soil ventilation: short- beaked echidna

The description of these records allows individuating the most appropriate source of natural inspiration and improving the process of inventive design.
Still with the aim of clarifying the usability of the proposed mappings, let's assume that the machine of the previous example needs to improve its capacity of gas storage. In this case, just for illustrative purposes, we will use a representation of the functional need by means of an OTSM Functional Model:

- OTSM (Stabilize – Volume of gas)
  Following the step 1 it is possible to individuate the correspondents BT Sub-Groups in which to look for:
- OTSM (Stabilize – Volume of gas) **-+** BT(Get, store or distribute resources – Store – Gases)

In this case, there is only a group of BT functions corresponding with the input model of problem. The AskNature database proposes a list of natural examples reported in table 6.

Table 6. Natural examples extracted from the AskNature database through the query: "Store-Gas"

Strategy	Sub-Group	BT Function	Description
Get, store or distribute resources	Store	Gases	Spider creates underwater air tank: water spider
			Air flow system, sacs provide efficient gas exchange: birds
			Leaves adjust to changing environment: common arrowhead
			Swim bladder retains gasses: ray-finned fish

4.6. Discussion

Analyzing the correlation tables between the BT and the NIST Functional Basis it is possible to note that the specificity of the BT functions is too high to use these two model tools as they are. Excluding the BT Break Down Sub-Group, which reaches a complete partial match, to use the NIST Functional Basis as a model tool to transfer knowledge and solutions some modifications are necessary. In particular, it is necessary a new set of biological functions with the specific objective of describing biological flows. The Break Down Sub-Group can be considered a "biological functional class" and this is the reason why the match between these two set of models has been complete. In this analysis, the partial matches have reached the highest percentage. This fact represents a big limitation for the above-mentioned hypothetical automatic transfer process.

In the case of using the OTSM Functional Model as a support to the process of information retrieval on AskNature the results change drastically and the correspondence is complete for three BT Sub-Groups: Move or Stay put, Maintaining physical integrity and Modify. In this case, the freedom in the choice of the Object-Parameter permits considering "biological functions" in order to fit more precisely with the BT biological functions. Besides, the proper formulation of the Object-Parameter requires a higher experience by the designer and in any case the lack of a reference list is a possible cause of limited repeatability.

5. Conclusions

The objective of this paper is to present the preliminary results of a Ph.D. program aimed at systematizing the process of Bio-Inspired Design. The study proposed in this paper has been focused on understanding the integration opportunities of available information resources in this domain and the necessary modifications to better develop the process of knowledge and solution transfer.

Two reference engineering functional modeling techniques have been considered, namely the NIST Functional Basis and the OTSM-TRIZ function model. Both have been compared with the Biomimicry Taxonomy with the aim of mapping BT groups and functions with the existing engineering matches. Both functional modeling systems allow to access the AskNature collection of biological functions as a source of inspiration in the process of inventive design, but the OTSM Functional Model revealed to cover a larger portion of the Biomimicry database. On the other hand, due to the lack of a reference terminology it potentially suffers for reduced repeatability of the functional triad carrier-action-object. In such cases, a potential negative consequence is a higher number of matches with the BT, with consequent divergence of the problem solving process.

Besides, the specificity of the NIST list of standard flows implies a smaller percentage of proper matches between the action-flow representation and the BT. The analysis of the specific causes of this partial lack of correspondence has revealed that some customization would be necessary. First, it is suggested to

include in the NIST Functional Basis some specific biological flows in order to reach a better match between these two models.

Due to the heterogeneity of its definition, some modifications are also necessary in the BT function classification, which is characterized by an ambiguous formalism as illustrated in the paper. The authors here propose to introduce a complementary clustering criterion of BT functions in order to clarify its classification principle.

The future developments of this work are related to the investigation of the opportunities of automating the identification of relevant AskNature resources starting from any problem modeling technique adopted in the engineering design domain, as well as to the extension of the same analysis to further Biomimetics databases.

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