Idea Inspire 3.0—A Tool for Analogical Design

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Abstract There is a continuous demand for novel and innovative products in the market. In order to develop novel ideas, natural systems are considered to be superior source of inspiration. In order to assist designers in ideation, an analogical design tool called Idea Inspire 3.0 is developed; it is a revised version of Idea-Inspire developed in 2005. The latest version is web-based, and supports retrieval, visualizationand addition of systems. It uses a novel, dynamic representation with amulti-system, multi-instance SAPPhIRE model as basis, and a multi-modal explanation for enhanced understanding that shouldlead to better ideation. In this paper, these latest features of Idea-Inspire along with their potential benefits are discussed.

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1 Introduction

There is intense competition among products in the market. Since existence of a product is temporally limited, there is a need for designers continue to innovate products [1]. Analogical reasoning is vital in developing ideas for new products [2]. Most often, these ideas are inspired from the artificial domain since their designers are familiar only with this domain [3]. However, research indicates that ideas inspired from more distant domains such as nature are likely to be more novel [4].

A variety of products has been developed using ideas from nature, e.g. Velcro was inspired from burrs [5]; the shape of 'Shinkansen' train was inspired from the beak of a Kingfisher [6]. Inspiration from biological systems offer several advantages [7]. Firstly, biological systems utilize minimal amounts of energy and resources [8]. Secondly, biological systems are adaptable to variable external conditions [9]. Thirdly, they are environmentally sustainable [10]. Further, they are self-regulating intelligent systems [9]. In addition, they are capable of self-assembly using processes like synthesis, reproduction and succession [11]. Hence, nature is a potential source for inspiration for developing novel products [12]. In order to provide inspiration with which to trigger ideation, a tool needs to be developed for retrieval and visualisation of systems (as inspiration) from the biological domain. Further, the tool should support users share their knowledge of biological systems by adding these into the database, so that the database can progressively expand to support better ideation.

In order to utilise information about biological systems for new product ideation, the user needs to understand these systems [13]. Due to knowledge gap, comprehending biological information is usually a challenge for engineers [14]. A comprehensive approach involves understanding all sub-systems that constitutes a system [15]; the sub-systems themselves can aid ideation. A representation needs to be developed, for both systems and sub-systems, that could help designers retrieve and understand systems [16]. Usually, systems are explained using text. However, other modes of representation, e.g. images and videos have proven to assist in novel idea generation [17]. Hence, a multi-modal representation for systems/sub-systems is necessary.

The tool that we intend to develop needs to support the following: (i) *retrieval* of systems from the biological domain; (ii) *understanding* of these systems for ideation; and (iii) *addition* of further systems into its database by its users. For these, developing an appropriate, multi-modal representation for systems/sub-systems is necessary.

1.1 Background

Analogical design has been a major source of support for enhancing creativity in design [18]. Many tools have been proposed to aid in this process, but with a

variety of limitations. Firstly, some of these tools provide a vast number of results as inspiration, many of the results are not relevant. Secondly, the language used in such tools is often highly domain-specific, which makes it difficult for a non-biologist to understand [19]. A few of the major tools are reviewed below.

TRIZ (Theory of Inventive Problem Solving) is a suite of approaches towards problem solving (system development), conceptualized over reduction of engineering contradictions, which happen when increase of one parameter in a system causes decrease in another. From Altshuller [20] and Domb [21] a definitive set of 39 contradiction features were juxtaposed against one another in a contradiction matrix, from which conflict pairs could be obtained. Each of the conflict pairs are matched with the ones in existing, solved problems in order to retrieve an analogy, which in turn would act as a hint in to solve the current problem. This idea was utilized in by Vincent et al. [22, 23], which led to development of BioTRIZ matrix. Instead of 39 contradiction features, BioTRIZ matrix holds six fields: substance, structure, space, time, energy, and information. This work makes use of a System Operator, which is a 3×3 matrix for the object (component or system) under consideration. Vertically, the operator represents a hierarchy of 'Super-system', 'System', and 'Sub-System'. Horizontally, at each level of the hierarchy, time is represented using 'Before', 'Now' and 'After'. The Term-Patent Matrix, similar to contradiction matrix, was developed for PAnDA (Product Aspects in Design by Analogy), for patent retrieval to support analogical design [24].

Idea-Inspire was the first searchable, computational repository of biological systems for supporting bio-mimetic and biologically inspired design. Developed in 2005 by Chakrabarti et al. [25], the tool aids in synthesis of novel designs by drawing inspiration from over 1200 natural and artificial systems stored in a database. Each system is described using two representations, along with images and videos: one based on FBS [26] model, and the other using SAPPhIRE model. SAPPhIRE model evolved as an integration of, and therefore has been argued to be richer than, various other models in literature such as those in FBS [26], SBF [27], Domain Theory [28], Theory of Technical Systems [29] and Metamodel [30]. The constructs are decomposed into Verb, Noun, and Adjective according to SAPPhIRE model and used as search criteria for retrieval of systems. Idea-Inspire was the first tool that supported addition of new systems into the database. However, the tool was standalone; the design solutions added by one user could not be reused by other users. Further, each system is represented using only a single SAPPhIRE model instance, irrespective of the complexity of how it functioned.

AskNature, a web-based tool introduced in 2008 [31], has a repository of over 1600 biological strategy pages. It is a web-based platform where engineers and biologists can collaborate and form a knowledge network. The database is categorized according to taxonomy with the following constructs: Group, Subgroup, Function, and Strategy. In a systematic search, the user selects one group of strategies, converges to a sub-group and obtains a list of functions [32]. However, the level of detail provided on each system is not extensive. Further, users often practise traditional, keyword-based search instead of using the taxonomy provided.

AskNature does not provide any facility for users to add new systems into the database.

Introduced in 2012, DANE [19] is another tool for providing biological stimuli in design problems; it is based, among others, on a study conducted on biologically inspired design [33]. The tool works with a database that houses nested SBF [27] (Structure—Behaviour—Function) models of natural and engineered systems. A nested model is represented using nodes (systems) connected across systemic levels and edges that indicate hierarchical relationships. DANE, similar to Idea-Inspire, supports addition of new design solutions by its users [19]; however, studies conducted on DANE shows that it is difficult to add data using this feature; it is also stated that the SBF models were incomplete in most of the systems added in the database. The systems are hierarchically linked with one another to represent systems that are more complex. However, the connectivity between such systems is lost. The reasons behind incomplete SBF models and inadequate hierarchical representations are as follows: Firstly, the database for the tool is populated using a set of students who have less or no experience with biological systems or SBF representations to carry out efficient system decomposition and construct knowledge-rich models. Secondly, a hierarchical model is not sufficient to represent a highly convoluted biological system, in which events occur sequentially and simultaneously across several systemic levels to achieve an intended functionality. Since it is a standalone tool, sharing of design solutions from elsewhere is not possible, and hence the enormous opportunity for crowd-sourcing and knowledge multiplication is lost. Later, Baldussu [34] used a combination of SAPPhIRE model and DANE representations for synergic benefit.

In summary, the limitations of previous work have been the following: results are not specific to the design problem and hence, compromise *relevance*; the representations lack the desired level of systemic *detail*; except for in Idea-Inspire, *digital-support* like audio, images and videos are largely absent; standalone tools do not support *sharing* of systems across the WWW. To overcome these limitations, a thoroughly revised version of Idea-Inspire [25]—Idea-Inspire 3.0—has been developed.

2 Methodology

2.1 Multiple Instance, System-Subsystem Model

The systems included in the database of Idea-Inspire 3.0 are structured according to the SAPPhIRE model [25] of causality. Modelling is carried out by experts from the biological domain who possess richer knowledge to provide adequate system detail. As discussed earlier, the model provides a richer description of the functionality of natural and engineered systems. Many systems can be represented using a single instance of a SAPPhIRE model. However, complex systems that demand greater

levels of description require more than one SAPPhIRE model for representation. Such systems are represented as a combination of simpler structures and functionality. Hence two additional representational aspects are introduced: a system-subsystem hierarchy [35], and combination of multiple-instances of SAPPhIRE model.

Simplification of Systems

In this work, systems are classified as biological or artificial; they differ in the nature of their complexity. Artificial systems are built using components that are assembled to form the whole structure; the components exist at different systemic levels and carry out one or more functions. On the other hand, natural systems are more complex: in general, the number of components present in these systems is greater and their associated functionalities are more elaborate. Functionalities are intertwined with a large number sub-functions occurring sequentially as well as simultaneously [36]. Hence, in order to get a sufficiently rich explanation, it is important to simplify a biological system based both on its structure and functionality. Structural complexity is captured using the System-subsystem hierarchy, and functional complexity using a combination of multiple SAPPhIRE instances. Below, two examples are used to illustrate the representation proposed: single-phase induction motor from the artificial domain, and the soaring of albatross from the biological domain.

A single-phase induction motor, (Fig. 1, left), has a stator, a rotor and a centrifugal switch. Initially, within the stator, a lead in voltage is established to produce a magnetic flux, resulting in a fluctuating magnetic field. In the rotor, induced electromotive force produces a net torque that in turn generates mechanical power. The centrifugal switch disconnects the auxiliary winding. Soaring of an albatross (Fig. 1, right) is governed by three, major, simultaneously acting phenomena: *dynamic soaring* enhances the wind gradient; the tubular nose of the Albatross *senses*
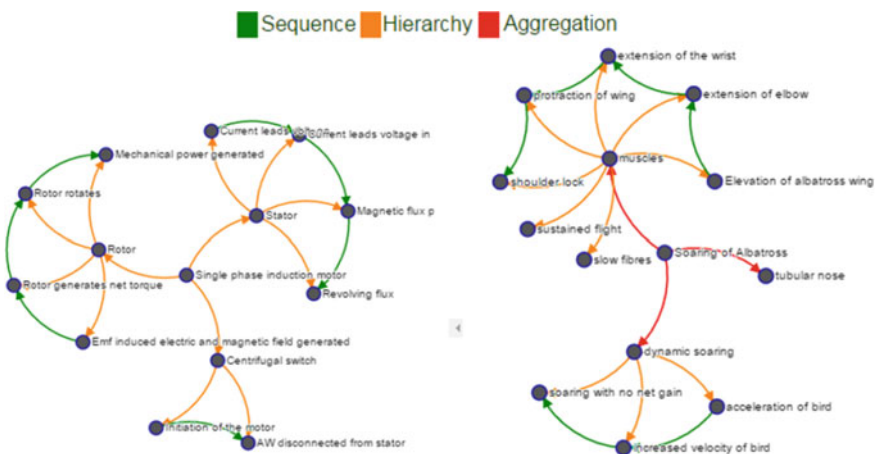

Fig. 1 Model of induction motor and soaring of albatross

pressure difference; the varied muscle composition of the bird engages *shoulder lock* for controlled flight. Each phenomenon is further decomposed into sub-actions.

Multiple-Instance, Multiple-System SAPPhIRE Model

A multiple-instance, multiple-system SAPPhIRE model combines several SAPPhIRE instances; the instances sit at the same or different systemic levels (Fig. 1). The types of links present in a multi-instance SAPPhIRE model are as follows:

Sequential link: As in [37, 38]—*sequential links* combine two events occurring sequentially. Using this link, two SAPPhIRE instances are linked in a sequence in which the *action* of one becomes the *input* for the other.

Aggregation link: Multiple events occurring at the same time are called parallel links [37]. In our work, some SAPPhIRE instances act simultaneously to provide the output for a higher-level system, and are connected using an *aggregation link*.

Hierarchical link: Brown and Chandrasekaran [39] propose that task/function/ system is a hierarchical collection of sub-systems starting with the overview of the entire system and later narrowing down to specific parts or components. Following the same ideology, a system and its sub-systems are connected using *hierarchical links*.

The multiple-instance, multiple-system SAPPhIRE model is an evolution of the previous version [25] that supported only single instances. The size of the hierarchy of a complex system is not limited, unlike in [22], [32]. In contrast to DANE [19], the model uses any number of sequential and aggregation links at any level of the hierarchy to provide a richer description of a system without losing information on its connectivity. A multiple-instance, multiple-system model could be simplified to generate several instances, each residing at some systemic level. Hence, a system could not only be decomposed into elemental units, but also used as a building block for more complex systems. The tool supports both features.

3   Development of the Tool

Idea-Inspire 3.0 is a web-based tool that allows users access and ideation using the tool from anywhere. Our aim is to support a knowledge sharing network, where users can *browse* the tool for systems in biological and artificial domains to *understand* these, *develop* novel ideas, and *add* new systems to the database that could help in subsequent ideation, by the same as well different users.

The tool has been coded in PHP and JavaScript. Hence, the tool would run in any internet-accessible computer, without the need for plug-in. Systems are retrieved from a MySQL database. Retrieval is fast and secure unlike in other platforms that use SQLite. In the following sections, the features of the tool such as retrieval, representation and addition of systems are explained. The tool also supports other features like blog, verification and authentication (but not discussed in this paper).

3.1 Retrieval of Systems

Systems with potential for stimulating ideation for solving a given problem are retrieved from the database using a parameter based search, based on the design requirements provided by users based on the problem. As shown in Fig. 2, the parameters provided by the users are: Action (verb), Action (noun), Action (adjective), State change, input (noun), Input (adjective), Physical laws governing the system, Components (noun) and Components (adjective). These parameters constitute the various aspects of the functioning of a system, and are in alignment with SAPPhIRE constructs. In view of ARIZ methodology, this retrieval feature allows the designer to decompose the problem and obtain the specific requirements (parameters), which in turn act as search criteria.

The search algorithm is similar to that in the previous version [25]. However, search parameters in the current version are linked to WordNet [40] database, a feature similar to that in [24]. The requirements entered by the user are compared with the descriptions of systems in the database. For capturing their synonyms, the

Fig. 2 The retrieval feature in Idea Inspire version 3.0

entries are further searched in WordNet; the synonyms captured are also compared against the descriptions of systems in the database.

   An example: A problem as a set of requirements as provided by the user, would be as shown in Fig. 2: Action (verb)—move, Input (noun)—force and Component (noun)—motor. Together, these describe the requirement to retrieve systems that contain motor-like components, and in which a force input leads to a movement as an output action. The results shown on the right-hand side include biological systems, e.g. muscles, protraction of wings, etc., and artificial systems e.g. stator, rotation of rotor, etc. The order of display of results is according to exact match (highest priority), partial match, exact synonym match, or partial synonym match (lowest priority).

3.2   *Representation of a System*

The systems retrieved are represented in the tool as shown in Fig. 3. The elements of the multi-modal representation used include: a multiple-instance, multiple-system model (top left), individual SAPPhIRE models (top right), audio (middle left), text (middle right), image (bottom left) and video (bottom right). The left and right arrows traverse through the different systems that constitute the multi-instance model; the content represented change according to the current sub-system being shown.

   Dependency graph (top left): The multiple-instance, multiple-system model is a dependency graph displayed using JavaScript. It uses a recursive function that takes a system ID as argument and displays all the systems for which the current argument is parent. The systems are then connected using edges, so the the multi-instance, multi-system model can be visualized. The dependency graph is a dynamically changing script that is updated with updates in the database. Systems newly added or linked with existing ones are immediately reflected in the visualization. This feature is not present in any earlier tool. Further, as noted earlier, it supports any level of hierarchy.

   The **SAPPhIRE model (top right)** is structured according to the information fetched from the database. The **audio (middle left)** is generated using a text to speech translator that recites the textual information about the various systems and links in the multiple-instance, multiple-system model. However, the audio does not explain any system in detail. The **text (middle right)** that follows a template, gives a detailed explanation of the SAPPhIRE model and an overall explanation of the system currently viewed by the user. The **image (bottom left)** and **video (bottom right)** are open source materials fetched from the internet for providing additional information on the system. This, we argue, should provide a more integrated understanding of the system.
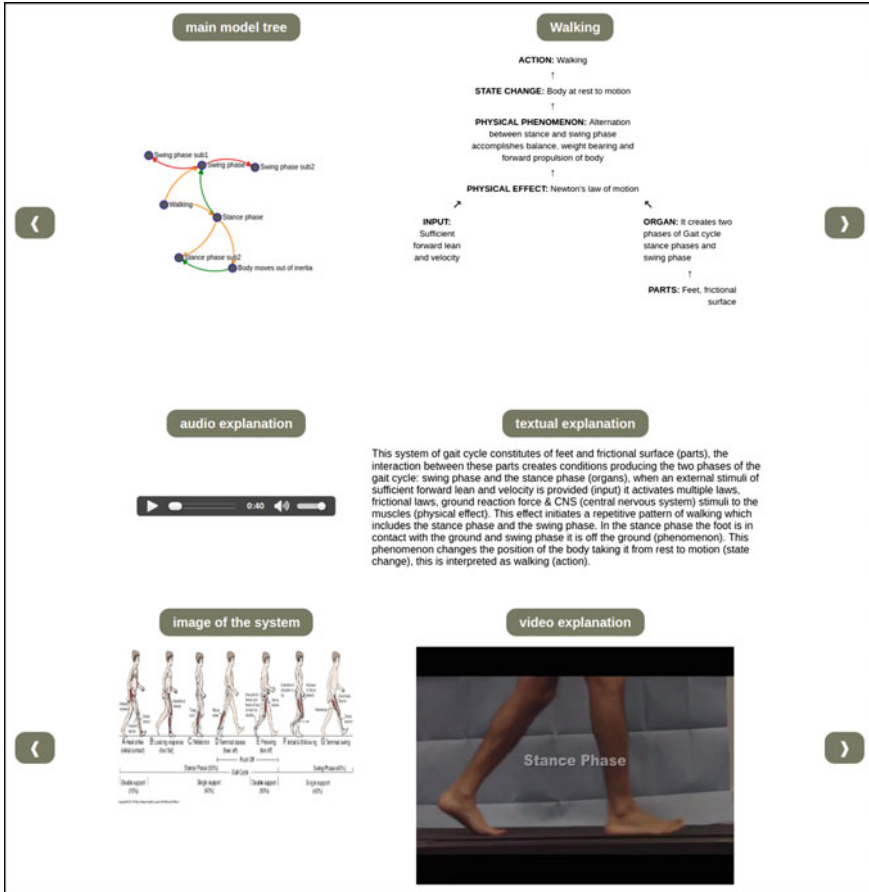
Fig. 3 A multi-modal representation of a system in Idea-Inspire 3.0

3.3 Adding/Linking a System

This feature supports the user to add new systems to, and to link existing systems in, the database; as explained before, this feature was not available in any earlier tools. The feature, however, is available only for authorized users. Using this feature, the user can add new systems, both as SAPPhIRE models and as textual explanations. Each SAPPhIRE instance is stored in the database as a new row for a system, which is retrieved for representing the system. The existing systems are linked through a different page for generating the dependency graph (Sect. 3.2), which shows a combination of existing systems represents a complex system.

4   Summary and Conclusions

The tool that we had intended to develop needed to carry the following features: given a design problem, one can retrieve descriptions of systems from natural and artificial domains that could act as stimuli for ideation to solve the problem; uniquely represent each system for adequate understanding; and support the user add new systems.

The system retrieved using the tool is displayed using a representation that utilizes multi-instance, multi-system model with individual SAPPhIRE instances, text and digital support. The newly introduced multi-instance, multi-system model is a dynamically changing script and supports any level of hierarchy. The representation, which is introduced in this web-based tool, is much advanced than its earlier version. Adding and linking of systems is a unique feature for the tool; the resulting changes could be visualized immediately. Idea Inspire 3.0 has novel features for supporting understanding, ideation, synthesis and expansion of its knowledge base. A preliminary testing of the tool suggested that there is need for user training before utilization of the tool. Further development and more extensive evaluation of the tool are part of the work in immediate future.

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