

# The interdisciplinary engineering knowledge genome

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**Abstract** Parallel to the concept of the human genome and its impact on biology and other disciplines, we revealed a similar concept in engineering sciences, termed the “*Interdisciplinary Engineering Knowledge Genome*”, which is an organized collection of system and method “genes” that encode instructions for generating new systems and methods in diverse engineering disciplines. Resting on the firm mathematical foundation of combinatorial representations, the Interdisciplinary Engineering Knowledge Genome unifies many engineering disciplines, providing a basis for transforming knowledge between them, supporting new educational practices, promoting inventions, aiding design, and bootstrapping new discoveries in engineering and science. Given the formal underlying combinatorial representations, these merits could be automated. This paper elucidates this new concept and demonstrates its value and power in engineering design.

**Keywords** Human genome · Biomimicry · Knowledge management · Knowledge representation

## 1 Introduction

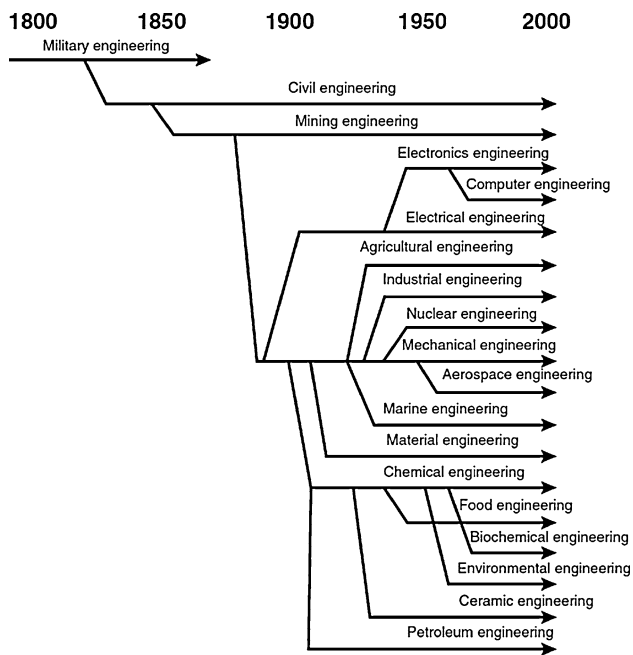
The human kind quest for understanding the nature of knowledge is ancient. Knowledge has been studied and

debated on in science, philosophy, engineering, and art. Meanwhile, the practice of science and engineering has never lost time or opportunity to progress. The early history of engineering saw the master builders and the Renaissance engineers as integrators of practical knowledge who mastered all necessary knowledge to start and complete projects. Since the industrial revolution, engineering disciplines emerged and diverged. In France, civil engineering oriented by mathematics was developed and begun to be taught formally, and in England, mechanical engineering emerged as a more empirical discipline. The second industrial revolution saw the emergence of chemical and electrical engineering. The progress in the natural sciences led to turning “engineering” into “engineering sciences” whose education moved away from practice to being science-based and subsequently led to further specialization and subdivision. After World War II, new disciplines appeared such as engineering management, nuclear engineering, materials engineering, environmental engineering, computer engineering, software engineering, biomedical engineering, and systems engineering. A graphic view of this subdivision is shown in Fig. 1.

From an engineering perspective, with this proliferation, whether justified on the basis of knowledge explosion or not, engineers working collaboratively on projects face major language or terminological difficulties as well as differing world perspectives (Bucciarelli 2002; Kayworth and Leidner 2001; Smith and Blanck 2002; Sargent et al. 1992). Such differences can easily give rise to difficulties in different research projects (Bryman 2004; Katzenbach and Smith 1993) and could lead to team performance deficiencies (Cramton 2001). As these disciplines grow and flourish, the information they generate continues to accumulate at an unprecedented pace and the hope for convergence becomes slim.

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**Fig. 1** The proliferation of engineering disciplines over the years. *Source:* Tadmor (2006). Redefining Engineering Disciplines for the Twenty-First Century. *The Bridge* 36(2):33–37. Reprinted with permission of the National Academy of Engineering

From a scientific perspective, integrative or interdisciplinary<sup>1</sup> studies have become popular as a way to address complex societal problems that require the input of many disciplines (Rafols and Meyer 2007; Szostak 2009). A recent move has been made to refer to such inquiry practices as transdisciplinarity (Max-Neef 2005). In her presidential address to the American Association for the Advancement of Science, Jackson (2005) stated that major scientific and engineering development and progress could occur only if multidisciplinary is practiced. A popular example for such interdisciplinary research is in the field of nanotechnology. However, a study showed that the amount of interdisciplinary research has grown by only a mere 5% over the 30-year period between 1975 and 2005 (Porter and Rafols 2009). Another study contended that the amount of interdisciplinary work in the highly supported nanoscience is small (Schummer 2004).<sup>2</sup>

<sup>1</sup> We use the term *interdisciplinary* to denote a concept that provides an integrative framework for knowledge from different disciplines. The term *multidisciplinary* is closely related but is often meant to describe the parallel working of multiple disciplines without integrating their body of knowledge. Another term, *transdisciplinary*, might have been more appropriate, but it has recently come to refer to solving societal problems that transcend single disciplines and require different design and inquiry practices. While our long-term goal is similar, we have no example of such use of the concept we propose that supports referring to it as being transdisciplinary.

<sup>2</sup> This has led researchers to look at new ways to measure the amount of interdisciplinary work in a scientific discipline (Porter and Youtie 2009; Rafols and Meyer 2007).

One proposal to address information explosion is through the development of information systems or knowledge management tools for the subsequent creation of shared memory (Konda et al. 1992). These tools could record information in the form generated by these disciplines, be used to efficiently search for information, and provide support for the empirical consolidation of concepts and models through social construction (e.g., *n*-dim, Subrahmanian et al. 1993, 1997; Reich et al. 1999). However, these ideas have not yet led to the integration of different disciplines, implying that new ideas are still needed for realizing the goal of shared memory or interdisciplinary integration.

One place to look for new ideas is nature. Engineering has benefited significantly from embracing concepts from nature, merely consider the proliferation of various algorithms based on natural phenomena (such as genetic programming (Goldberg 2002), ant colony algorithms (Dorigo et al. 1996), artificial immune systems (Dasgupta 1999), etc.) and the various products developed following nature principles [such as Velcro™ as an analogy to the mechanism allowing burrs to attach to furs, or the Gateshead Millennium Bridge as an analogy to an eyelid form (Root-Bernstein and Root-Bernstein 2001)]. Studying nature to get ideas to solve sustainability problems has recently received new attention under the new name of biomimicry (Benyus 1997).

In biology, the primary source of these nature analogies, the discovery that the DNA is the carrier of genetic information (Avery et al. 1944) and the identification of its double helix structure (Watson and Crick 1953) was a revolutionary moment (Berg and Singer 1992). This discovery created new concepts and a single basis for envisioning and orchestrating future discoveries, in particular, through the human genome (HG) project. From a broad perspective, engineering disciplines are in a pre-DNA discovery era. Does engineering have a concept similar to the human genome that could act as a unifying force?

## 2 Methodology and state of art

One could approach this question through the positivist scientific method by studying different disciplines trying to form a grand theory of underlying principles. However, in contrast to nature where genomic material exists in all organisms and could, therefore, be observed and studied, in engineering, a genome would be an artificial conceptual entity and consequently must be constructed through design.

If design is the methodology, it is clear that there might be multiple solutions. It is also clear that different

approaches set themselves to achieve different objectives and the choice of one proposal over another would be subjective. Consequently, it is instrumental for a study on the subject to review related approaches, their objectives, successes, and difficulties, and to propose a new design that demonstratively improves the state of the art.

Over the years, there have been many proposals to organize and systematize engineering knowledge. Many arose out of artificial intelligence including the following: rule bases or knowledge-based systems (Coyne et al. 1990) and their limitations (Cowan 2001); constraints (Fu and de Pennington 1993; Bowen and Bahler 1992); and qualitative reasoning (Bozzo and Fenves 1994; De Jong 2004). While these approaches were developed to be general, their successful implementations have been in niche well-structured areas and they could not be used to bridge disciplinary knowledge across disciplines.

There have also been attempts to provide representations and reasoning schemes more specific to design such as design grammar (Mullins and Rinderle 1991; Schmidt and Cagan 1997), bond graphs (Borutzky 2009) with an infrastructure (Bradley et al. 1992), functional reasoning (Chandrasekaran et al. 1993; Bracewell and Sharpe 1996; Chakrabarti and Bligh 1994; Erden et al. 2008), prototypes and Function-Behavior-Structure (Gero 1990) and their criticism (Dorst and Vermaas 2005), networks of parameters (Duffy et al. 1996; McMahon and Xianyi 1996), metamodels (Tomiya et al. 1989), and others. While some of the above approaches received attention and studied, and their limitations were articulated or their basis was criticized, most other proposals remained as research attempts of small groups of researchers.

Few of these representations matured enough to be used in design practice and even these, mostly in the analysis phase. One such exception is the bond graph approach for modeling engineering systems from different disciplines. Bond graphs, while seemingly similar to the combinatorial representations of the IEKG we introduce shortly, are different. They do not have similar concepts as those proposed here, and furthermore, they could be captured by specific combinatorial representations of the IEKG, but demonstrating this is beyond the scope of this paper.

One clear hurdle preventing the success across applications, even in the same discipline, of the aforementioned efforts, has been the problem of using idiosyncratic language in each application. Ontology building has been proposed as a mechanism for unifying the language across applications; however, its potential is only utilized in specific problem domains as manifested by the CYC project that has been underway since 1984 (Lenat et al. 1986). In design, different ontologies have been developed for different things such as design activities (Sim and Duffy

2003) and most notably functions (Hirtz et al. 2002; Kitamura and Mizoguchi 2004). The status of these ontologies and their difficulty to converge is manifested by the existence of different function ontology proposals and the necessary and partially successful effort to bridge them (van Eck 2010).

Unification of knowledge means that knowledge taken from one domain could be reused elsewhere. There have been studies explicitly addressing this objective, for example, analogical reasoning (Goel 1997). TRIZ (Altshuller 1984) could also be considered as a method for reusing knowledge of phenomena to solve new problems. Knowledge reuse continues to be an active research area (Baxter et al. 2007; Zdrahal et al. 2007). Nevertheless, these previous proposals do not have the reuse properties afforded by the IEKG. No existing method allows for similar transfer of knowledge and supports discovering new concepts, solutions, and methods. No existing approach guarantees that the mapping between disciplines leads to the desired results.

We propose a concept similar to the genome in biology with potentially similar consequences for engineering sciences: the “*Interdisciplinary Engineering Knowledge Genome*” (IEKG). The IEKG encompasses many concepts similar to the HG concept. Among the key concepts are engineering knowledge genes that are the basic building blocks of the IEKG. We describe two types of genes: system genes and methods genes. Subsequently, we illustrate work to date that demonstrates the value of the concept.

The IEKG is related to infused design (ID; Shai and Reich 2004a, b). ID started as a method that rests on a solid mathematical foundation of combinatorial representations of systems that allows transferring solutions and methods between disciplines. In this context, combinatorial representations are graphs and matroids from discrete mathematics (Recski 1989; Shai 2001a, b). Their choice as a foundation of ID and consequently of IEKG is borne out of numerous studies showing how they can be used to translate knowledge between different domains as summarized in (Shai and Reich 2004a).

As the study of ID continued, it became clear that the body of knowledge it uses has special properties that deserve focused attention. The IEKG arose out of this observation. The IEKG is the body of knowledge about the combinatorial representation of systems and their intricate relations. The development of the IEKG would improve significantly the capabilities of ID as well as provide insight about disciplinary knowledge not necessarily related to ID. The IEKG could be viewed as static view of knowledge (i.e., ontology) while ID as the way to utilize this knowledge (i.e., praxis).

Section 3 describes the concept of engineering knowledge genes. Section 4 builds on these concepts and introduces the concept of the IEKG. Section 5 discusses the role of the IEKG in promoting design creativity and knowledge transfer, and Sect. 6 puts the IEKG in the broader context of research on engineering knowledge representation and management. Section 7 provides some future directions, and Sect. 8 concludes the paper.

### 3 Engineering knowledge genes

The fundamental driver of the analogy between HG and IEKG is the concept of a gene: a collection of building blocks whose structure determines the composition of another object in a designated medium. In biology, we describe the composition of genes as a sequence of 4 amino acids whose ordering determines the creation of proteins. However, we should remember that the choice of building blocks is subjective and is based on parsimony or conciseness principles (i.e., Occam's razor). One could have used atoms to describe genes without changing their function. Such difference in representations would cause their description to be more difficult for us. Knowledge genes are subdivided into two distinct groups: *system genes* and *method genes*.

**Definition** System genes are models of objects that are represented with formal abstract mathematical representations called combinatorial representations and are concise, useful, and efficient.

Genes could be models of simple physical objects such as mass, spring, damper, resistor, coil, capacitor, beam, and actuator, or models of complex objects such as mechanical or electrical amplifiers, unidirectional gear trains, or electronic rectifiers. Genes could also be models of simple conceptual objects such as information channel.

The last part of the definition admits many models to become genes. We, therefore, clarify it through three preferences:

Preference 1: We prefer to call a gene, a model whose function could be described in a “concise” way, that is, one that could be clearly described and is not too complex. For example, “an amplifier of a high-frequency signal” would be modeled into a gene, while “a car” would not.

Preference 2: We prefer to call a gene, a model that is “useful,” for example, a model of a system that is useful today or one that we foresee to be reused in the future.

Preference 3: We prefer to call genes, models of systems that are “efficient” in some manner. For example, if two

systems had the same functionality, we might prefer the most efficient or simpler and use its model as the gene.

Such preferences are clearly design choices meant to make genes useful for designers. Nevertheless, in a multi-objective world, there are examples where these preferences are not worthwhile to exercise, for example, inefficiency is not categorically bad as it could provide robustness or other benefits. Therefore, there needs to be a future study on the value of these preferences in particular contexts.

The combinatorial representations (*graphs or matroids*) (Recski 1989; Shai 2001a, b) are the languages for describing genes similar to the four bases used to describe human genes. For example, consider a common simple system in electronics: the full-wave rectifier, Fig. 2a. The system model in a particular combinatorial representation called Potential Graph Representation (PGR) (Fig. 2b) is a system gene. In addition, the model of each of the system's atomic components (i.e., diodes and a resistor) is also a gene. This hierarchical nature of the IEKG is revisited later. Once created, genes could be used to create systems in diverse disciplines. For example, the gene in Fig. 2b could drive the creation of diverse systems such as a mechanical rectifier (Fig. 2c). Due to the formal procedures underlying such derivations, the new systems are guaranteed to have the same rectifying functionality. The route from Fig. 2a–c is depicted in Fig. 3a, which is a partial graphic representation of the IEKG.

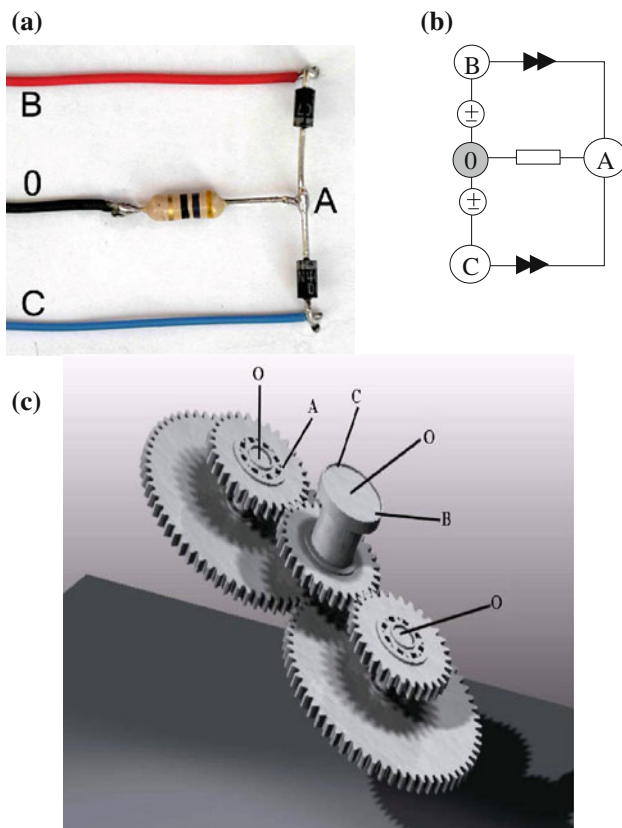
There is no limit to the size of systems that could be represented by combinatorial representations; therefore, genes could be formed with varying size and complexity.<sup>3</sup> This raises a practical issue of managing the content of the IEKG and the operation of ID. One way to commence addressing this complexity is through organizing the content of the IEKG, see Sect. 4.1.

**Definition** Method genes are useful methods operating on combinatorial representations.

Method genes are created in the same way as system genes, by transforming disciplinary methods into methods operating on combinatorial representations. Once a method has been developed in one engineering discipline, it can be transformed into other disciplines through the method genes.

Similar to the system genes definition, we need to clarify this definition with a preference:

<sup>3</sup> We see similar trend in the biology literature, gradually moving from studying genes, to single protein pathways, and analyzing the complete network of protein interaction (Barabási and Oltvai 2004), as well as the identification of hierarchical structures in protein pathways (Dobrin et al. 2004; Kashtan et al. 2004). Through this, the concept of the genome evolves continuously.



**Fig. 2** The full-wave rectifier in **a** takes two alternating potential sources ( $CO$ ) and ( $OB$ ) and outputs a rectified potential over ( $OA$ ). Its gene in PGR representation is depicted in **b**. The implementation of the same gene in planetary gear systems is shown in **c**. The gear system operates by alternating rotation of link  $COB$  that is transformed to a rectified rotation of  $OA$

Preference: We prefer to call method gene, a method that is used in at least one discipline for addressing real-design problems.

To illustrate method genes, consider the Willis method from gear systems used to transform complex analysis of planetary gears (Fig. 4a) into analysis of equivalent simple gear systems (Fig. 4b). The method has been transformed to a combinatorial representation of Potential Line Graph Representation (PLGR) (Shai and Mohr 2004), Fig. 3b. At that level, abstracted from any particular discipline, it is considered a method gene. This gene works by exchanging the reference vertex to make the corresponding system simpler to analyze (Fig. 4c, d). This gene was then implemented as a method for analyzing complex linkages by transforming them into simple linkages, thus maintaining the spirit of a “simplifying reformulation” (Fig. 5). Furthermore, from PLGR, the Willis method could be transformed into a Potential Graph Representation (PGR) and to a Flow Graph Representation (FGR) to form two new method genes, Willis II and Willis III, respectively.

The latter gene has been implemented in trusses as another analysis method. There again, the new method works by simplifying a complex truss into a simpler one for analysis purposes through changing the reference vertex. The ability to perform such transformation is a direct consequence of the *topology* of the IEKG.

Method genes are not represented by combinatorial representations. They are algorithms operating on such representations. Therefore, their description and management is more complicated, and recognizing their relationships requires careful analysis of their effect on combinatorial representations.

#### 4 The interdisciplinary engineering knowledge genome

A biological genome is the complete genetic material stored in the set of chromosome of an organism and the knowledge associated with it, which is growing and being refined continuously. While each species has its own genome, there are overlaps in the genetic information and similar genes could be found in many organisms, responsible for the same processes across species. Similarly, the *Interdisciplinary Engineering Knowledge Genome* is defined as follows:

*Definition* The *Interdisciplinary Engineering Knowledge Genome* is the known set of system and method genes and the knowledge associated with these genes.

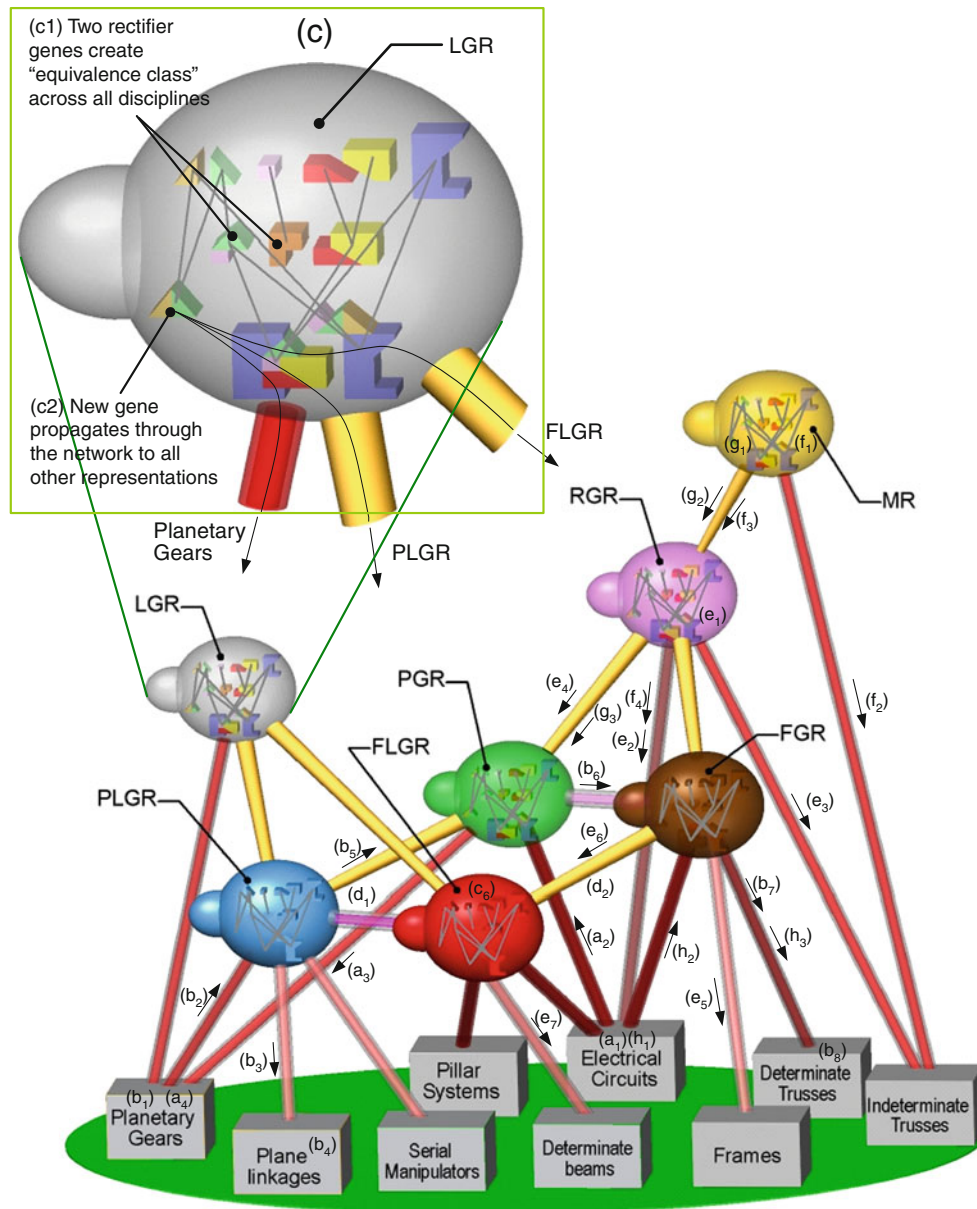
In contrast to biological genome that is finite for each organism (but could change or grow slowly through evolution), there is no limit to the number of system or method genes in principle. However, it is encouraging to see that there is an internal structure to the IEKG. Over the system and method genes, there exist several relations with interesting properties (Fig. 3c).

##### 4.1 Structure of the system genes

Preliminary results suggest that there are a finite number of system genes corresponding to a given function.<sup>4</sup> These system genes are termed the “domain of concepts” of that function.

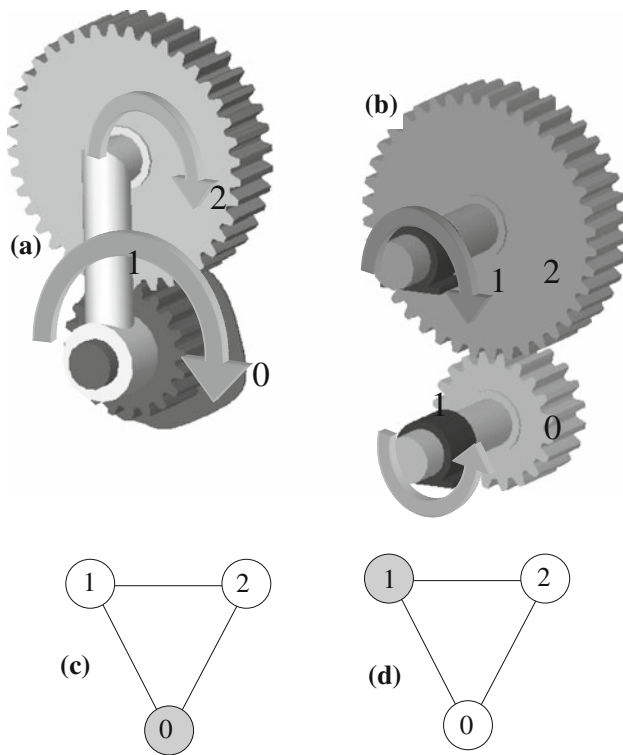
For example, consider rectifying an input signal, which is a common function in electronics. One rectifier is depicted in Fig. 2a, its gene in Fig. 2b, and its implementation in mechanical gears in Fig. 2c. The implementations in electronics and mechanics are equivalent since they are traced to the same system gene.

<sup>4</sup> Presently, this property is related to simple single functions. It remains to be demonstrated for complex functions.

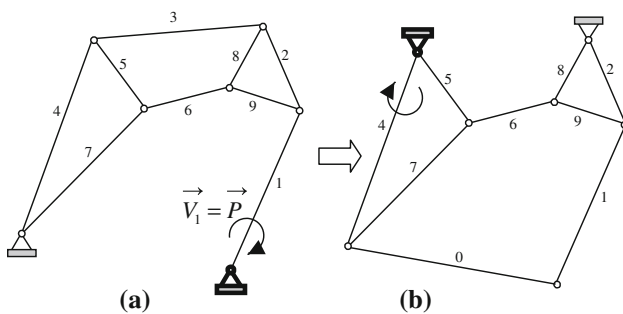


**Fig. 3** The “big picture” showing the network of combinatorial relations and their relations to particular disciplines. The “peanuts” are different combinatorial representations. A peanut is composed of two connected balls: the system genes part (*large*) and the method genes part (*small*). The peanuts are connected with relations. The large ellipse below is the level of the different engineering disciplines. Each discipline is depicted as a *box* and connected to its appropriate representation(s). (a) The route ( $a_1$ ) to ( $a_4$ ) yielding the mechanical rectifier in Fig. 2c from the electrical rectifier Fig. 2a. (b) The route ( $b_1$  to  $b_8$ ) generating the “Willis gene” from planetary gears ( $b_1$ ) and transforming it to linkages ( $b_4$ ) and then to trusses ( $b_8$ ). (There is also a direct route between planetary gears to trusses without visiting the linkages discipline.) (c) The internal hierarchical organization of genes within a particular representation.  $c_1$  shows the relation between the two similar rectifier genes.  $c_2$  shows the combination of two genes into a new one. Once created, this gene can be implemented or transferred through all the relations of this representation. (d) There

are two types of links: links between combinatorial representations and links connecting representations and disciplines. The “channels” between the representations denote the existence of a formal relation between these representations:  $d_1$  is a duality relation, and  $d_2$  is a generalization. Duality means that the two representations have the same representation power, whereas generalization means that the more general representation is more powerful for modeling physical phenomena. (e) Path showing the duality established in the RGR representation ( $e_1$ ), between the node method in electrical circuits ( $e_2$ ) and the displacement method in structural mechanics [e.g., trusses ( $e_3$ ), frames ( $e_5$ ), and beams ( $e_7$ )]. (f) Path showing the implementation of circuit mesh gene found in MR ( $f_1$ ) as force method in indeterminate trusses ( $f_2$ ) and mesh method in electrical circuits ( $f_4$ ). (g) Path showing the duality of force and displacement methods found in RGR ( $g_3$ ) by their derivation from the circuit and cutset genes that are dual in MR ( $g_1$ ). (h) The route generating the force “rectifier” ( $h_3$ ) in Fig. 6c from the diode bridge ( $h_1$ ) in Fig. 6a



**Fig. 4** The effect of Willis gene in gear systems. In **a**, gear 0 is fixed and gear 2 performs a compound movement, rotating both around its axis and around the axis of gear 1. In **b**, 1 is fixed and both gears 0 and 2 rotate around their axis. The PLGR representations of the system reflect the effect of the Willis gene: the reference vertex (gray vertex) moves from 0 (c) to 1 (d)



**Fig. 5** The effect of Willis gene in linkages: transforming a linkage from **a** to **b** by exchanging the reference support allows solving it with a sequence of steps where at each step, solving a simple contour containing exactly two unknown variables, while the rest of the variables are known from previous iterations. For example, such a sequence can be: (4, 7, 5) → (5, 6, 8) → (8, 9, 2) → (7, 0, 1, 9, 6), where the *bold font* designates known quantity. On the other hand, one can see that all the contours in the original linkage have three or more unknown variables

Interestingly, there is another design of a full-wave rectifier in electronics: the diode bridge depicted in Fig. 6a whose gene appears in Fig. 6b. The two genes in Figs. 2b and 6b are different; similarly, their implementations in all

disciplines are different but have similar relation as the relation between the genes.

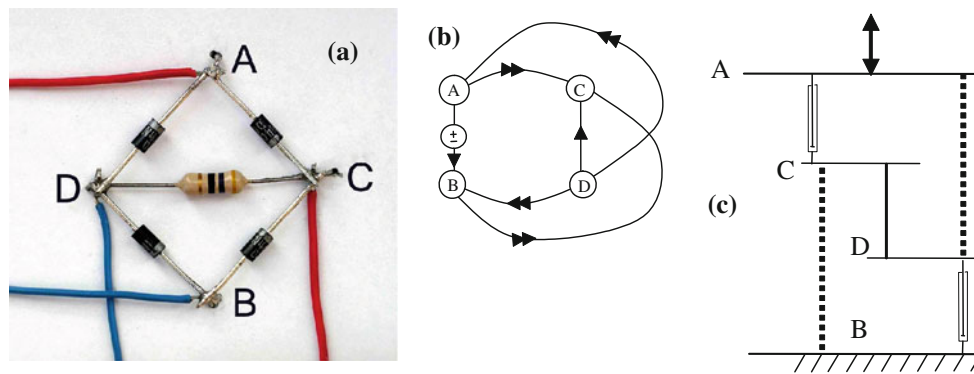
For the function “full-wave rectifying,” the domain of concepts has two genes as any rectifying device could be modeled by one of the two aforementioned genes. While both genes could rectify, they differ in other characteristics; therefore, the choice of one gene over another, or implementing one gene over another, depends on the context. Clearly, the availability of multiple genes allows for greater flexibility in implementing functions. We envision that in complex situations, such as when multiple functions are simultaneously sought, there would still be a small number of concise genes that could be used to implement them efficiently.

Since different genes could have similar functionality and since genes could be realized in multiple ways, it becomes imperative to begin understanding the nature of “good” genes. Which of the genes lead to more robust, economical, or flexible systems? Such studies would add further structure to the knowledge genome topology. For example, the rectifier in Fig. 6 could rectify flow and potential (current and voltage), while the one in Fig. 2 could only rectify potential (voltage), rendering the first one more flexible.

Each function creates an equivalence class across all disciplines as it has a distinct set of genes associated with it, and this set is mapped to a corresponding distinct set in each discipline. Further, genes could be combined to yield larger genes such as a rectifying amplifier. The relations between the combined gene and the original genes create a specialization-generalization relation between them. In this manner, the function of complex engineering systems could be realized by combining different existing system genes, each providing a single or a subset of these functions, with the potential need to apply condensation operations on the result (Roman 2005). The resulting hierarchical structure of system genes makes it easier to manage the complexity of the IEKG.

In addition, system genes are combinatorial representations of systems, and since combinatorial representations are connected through a *network of relations* such as duality or generality (Shai and Reich 2004a, b)<sup>5</sup> (see also Fig. 3d), genes (implemented) in different representations are related through the same network of relations. Consequently, the genes associated with one representation have the same underlying structure as in all other representations. Nevertheless, devices in different disciplines are definitely not the same as they deal with different technologies, energy forms, and physical embodiment.

<sup>5</sup> This network of relations is growing steadily with further analysis of new representations and new engineering disciplines.



**Fig. 6** The diode bridge rectifier (a) and its gene in RGR representation (b). The transformation of this gene to a mechanical implementation (c) produces a mechanical system that satisfies that

the force in rod CD is always in compression mode independent of the direction of the externally applied force between AB

#### 4.2 Structure of the method genes

Topological properties exist also in relation to method genes. For example, it has been shown that starting from a fundamental method gene, the cutset method on FGR and Resistance Graph Representation (RGR), one can derive the well-known displacement method in structural mechanics (e.g., trusses, frames, and beams) (Fenves and Branin 1963; Shai 2001a, b) and the node method in electrical circuits (Balabanian and Bickart 1969). Consequently, these methods are equivalent and are elements of the same method genes “equivalence class” (Fig. 3e).

It is more difficult to show equivalence between method genes than between system genes since the former requires the latter and the representation of methods is algorithmic in contrast to the graph representation of system genes. Sometimes such relations are hard to derive because the derivation involves complex representations. For example, the mesh method in electricity and the force method in indeterminate trusses are implementations of the circuit method gene. Nevertheless, this gene could be revealed only at the Matroid Representation (MR) (Fig. 3f).

In addition, since force and displacement methods are the derivations of the circuit and cutset methods, respectively, and the latter two are proved to be dual in MR (Shai 2001a, b), it is revealed that the displacement method and force methods of structures are dual methods (Fig. 3g), an observation that is unfamiliar to most engineers. This duality combines the previously thought-to-be distinct cutset and circuit equivalence classes into one class.

This new surprising observation inspires a boundless search for new properties of known combinatorial representations or even new combinatorial representations that might reveal presently unknown relations between seemingly disparate method genes as well as inventing new method genes. For example, knowledge transferred from kinematics led to the formation of a new class of rigid

structures, termed Assur Trusses (Shai 2009), with special properties in the rigidity theory community (Servatius et al. 2010), which in turn led to the development of a new method for finding rigid tensegrity structures in statics (Reich et al. 2008; Shai et al. 2009b, 2012). Such results related to method genes further support our conjecture about the existence of a structure underlying engineering knowledge that is waiting to be discovered.

#### 4.3 Additional properties of the IEKG

While biological genes are composed of only four amino acids, their functioning is determined not only by their composition but also from the structure of the DNA helix, the 3-dimensional interconnections between the genes, and many other factors determined by the gene context and system relationships. Consequently, we assume that similarly, the structure of systems including the connection between genes will appear as an important element in the IEKG.

And indeed, it turns out that the structure of systems has interesting properties that influence systems design, analysis, and behavior: all well-constrained system topologies could be composed uniquely from basic components that we call structural system genes—s-genes (Shai and Reich 2011):

*Definition:* A system  $G$  represented by a combinatorial representation is an s-gene if it is a well-constrained graph and removing any set of vertices does not result in an s-gene.

It turns out that the set of s-genes is ordered in a way that they all could be derived from one basic s-gene by performing two operators (Shai 2009). Through this discovery, we can now take models of systems from diverse disciplines and decompose them uniquely into primitive s-genes building blocks (Shai and Reich 2011). Clearly, in our terminology, the decomposition method is a method gene.



## 5 Design and creativity through knowledge transfer and generation

For engineers, the most challenging task is the synthesis of systems for given specifications. System and method genes provide excellent basis for supporting this activity while bringing to bear the wealth of experience available in all disciplines that participate in the IEKG: The design space afforded by the IEKG is truly tantalizing. The IEKG structure makes it extremely helpful for design. If we find an unfamiliar system gene or a useful system whose function is distinct from others, we effectively extend the known structure of the IEKG and should expect to find a completely new “equivalence class” across all disciplines (see Fig. 3c).

This has tremendous potential for enriching engineering knowledge; now, the collective inventive power of engineers is mobilized to solve difficult problems by utilizing inventions in other disciplines. More specifically, if a problem in a particular discipline is too complex to solve, a designer could try to use ID to bring forth known solutions from other disciplines. Failing to do so triggers a search in other disciplines to find a discipline in which it would be feasible and efficient to develop a new solution that could then be transferred by ID to the original discipline.

The choice of discipline to focus the effort in order to find that solution depends on domain expert judgment regarding the relative difficulty to find a solution there, compared to finding it in other disciplines. Sometimes more than one transfer is required and each transfer back and forth adds something to our knowledge that ultimately results in a solution in a bootstrapping effect (Reich et al. 2008; Shai et al. 2009b, 2012). The transformations between domains are part of ID, while working on extracting the genes from solutions is part of the IEKG. We now elaborate more on the above.

### 5.1 Working with known system genes

Infused design (Shai and Reich 2004a, b) is a systematic way to exploit the new design space created by the IEKG. The following example demonstrates the ability of the IEKG to support design creativity, which is obtained through transforming genes, implementations from one engineering field to another. Suppose an engineer has to design a static system (e.g., one-dimensional truss) that one of its rods should always be under compressive loading, while the external force applied upon the system is intermittent (for instance has a sinusoidal shape). Utilizing knowledge from the IEKG to solve this problem, it becomes a process of searching for a device in one of the engineering fields, where the input flow is rectified in one of the elements. The diode bridge and full-wave rectifiers

discussed before rectify potential. But, since one of the devices (diode bridge) has a gene with structure with a special property—self-duality—this gene could be applied also for rectifying flow. This property also makes the diode bridge gene better than or at least more general than the full-wave rectifier. Implementing this gene in this design case will yield a device where the force in one rod is only compressed (see Figs. 3h, 6c for the transformation process).

In general, given a problem and a presently available IEKG, ID works by roughly executing the following steps:

1. Model the problem into desired functions (e.g., force amplification, ability to provide support in arbitrary point, and orientation in space) and objectives (e.g., cost and ease of use).
2. Map the functions to available genes (including several functions into a single gene). The IEKG can support this step in several ways including function decomposition, and hierarchical indexing of system genes in a computer-based system that will allow engineers to locate the mappings that best fit their needs. Creating such an index is an important future research issue.
3. If several solutions have been identified to address the functions, potentially in multiple disciplines, combine them into a single model to obtain the overall functionality (including merging several genes into one) (e.g., Roman 2005). Multiple candidates could be formed to allow for proper evaluation and selection of the better solution.
4. Implement the gene structure in potentially multiple interacting disciplines (e.g., MEMS; Shai and Rubin 2003).

This process was found to be applicable even for devices based on novel engineering concepts. For example, a new active torque amplifier was invented by transforming an electronic transistor concept into mechanics. The device takes the needed energy from an external power supply without the need of any electronic system control and is composed of only three mechanical elements. We successfully built and tested this device at a Tel Aviv University laboratory (Shai et al. 2009a).

In summary, this process supports synthesis, including highly creative generation of system concepts. Simply consider that any invention in one discipline can be transferred to new designs in all other disciplines or to multidisciplinary devices.

### 5.2 Discovering new system genes

But there are cases where step 2 or 4 fails. Failure of step 2 indicates that the IEKG is missing genes. Failure of step 4 indicates that the discipline where the solution is sought is

lacking the required technology. For example, consider the full-wave rectifier case; suppose we started from the mechanical model before the invention of the diode and we wanted to implement the gene in electronics, the implementation would have been difficult trying to create an equivalent diode behavior from other components. Failure to do so effectively would trigger focused search and may lead to new genes or technology.

But the topology of the IEKG provides further insight for creative design or even creative research even without such opportunities. By studying the IEKG, independent to solving any particular design problem, one might find holes in the structure and attempt to fill them. This was the case when we attempted to transform knowledge between mechanisms and determinate trusses and found two concepts in mechanisms—joint linear velocity and instant center—missing from the determinate truss domain (Shai et al. 2009b, 2012). In IEKG terminology, such omission means that the language for describing genes in one discipline is incomplete. This omission directed an activity to complete the language with new concepts and associated methods. In the process, a system gene and a method gene involved in this transformation became clearly identified.

This specific process was subsequently modeled with C–K theory (Hatchuel and Weil 2003, 2009), showing how ID provides a new bridge between the C and K spaces and within the K space (Shai et al. 2009b, 2012). For C–K, the IEKG could serve as another knowledge structure that could be used by all its operators that work on the K space to support creative design.

The complete process of using the IEKG for inventing a product and the disciplinary concepts and synthesis methods required for this design have been exemplified through the design of an adjustable deployable tensegrity robot (Reich et al. 2008; Shai et al. 2009c). One method gene that was invented in this process is based on the knowledge gained in mechanisms for finding the singular (dead center) positions of mechanisms (Shai and Polansky 2006; Yan and Wu 1989; Yang et al. 2001). This method was transferred through the IEKG into a method for finding the singular positions of a tensegrity structure, which in turn was used in the design of the adjustable deployable tensegrity robot invented and built in our laboratory; the robot works all the time in a singular position.

## 6 Discussion and future directions

### 6.1 The IEKG and the human genome

The interaction of the IEKG and biology is expected to be both particular and conceptual. In relation to particular problems, the IEKG might be used to solve problems in

biology. For example, in calculating protein flexibility (Jacobs et al. 2001), it is assumed that whether the lines of all bonds of an atom intersect at the same point are immaterial to the kinematic degree of freedom (DOF) of the molecule. This assumption is referred to in the literature as the “molecular conjecture” (Whiteley 1999); it was very difficult to prove (Katoh and Tanigawa 2011). Employing knowledge afforded by the IEKG will provide a new perspective to understanding this topic from a physics viewpoint since it supplies an interdisciplinary view on different domains such as kinematics, statics, and rigidity theory. In this case, the concept from kinematics of decomposing any linkage into atomic components, termed Assur groups (Assur 1952), has been reformulated in terms of rigidity theory and was termed Assur graphs (Servatius et al. 2010). It has been subsequently extended into three dimensions (Shai 2009). Based on the latter results, it is expected that the problems in counting the degrees of freedom of 3D structures will be resolved through the decomposition of the 3D structures into Assur graphs, providing a physics-based solution to the molecule conjecture.

We can also explore the similarities and differences between the HG and the IEKG. We anticipate that these genomes could benefit from the further developments in each. For example, we anticipate that genes and other DNA material have meaningful substructures, and they or their substructures “cooperate” in similar ways to engineering sub-systems or modules to execute cell activities. We anticipate that this occurs in a much more profound manner than is presently known.

### 6.2 Other biology-related concepts and design

While the IEKG concept was borne out of intimate analogy between nature and engineering, there have also been other studies connecting biology to engineering design. Some studies called some of their concepts with names from biology. For example, product chromosome (Andreasen 1992) is the linked structure of the four models of a technical system (Hubka and Eder 1988). Through its interconnections, the chromosome describes the origin of the design and determines its functionality; it got its name due to this connotation. One of the models of technical systems, organ structure, models how system functions are carried out (Hubka and Eder 1988); this structure could be mapped to actual system components. The name organ comes from biology where organs are differentiated parts of the body that performs a particular function. Another recent concept is the nucleus (Horváth and van der Vegte 2003), whose name aims to convey its elementary status for building larger objects. A nucleus is composed of two physical objects represented by their geometry and their physical relationships in a particular situation.

One last use of a similar term is a synthetic DNA that holds information for a mechanical system and its function (Jin et al. 2009). Presently, it allows evolving simple mechanical systems to function in different environments. That study also refers to cells in a way that relates to the organ structure but also relates to the nucleus by calling a cell a mechanical, physical object with geometry, and interaction with the environment. All the above concepts use labels from biology to borrow some meaning, but none has the properties of, or the depth of interpretation, afforded by IEKG.

Another group of studies concentrated on using analogy to transfer knowledge from nature structures or phenomena to solve engineering problems (Chakrabarti et al. 2005; Mak and Shu 2008). Such analogies could be supported by careful study of organisms (Helfman Cohen et al. 2011). Bridging across the sources of analogies in biology texts and the target discipline, knowledge extraction from biological texts using natural language processing has also been attempted (Chiu and Shu 2007). Finally, the concept of genes was raised before in this context but in an intuitive manner. In an attempt to improve deficient products, reverse engineering of these products to extract “product genes”—referring merely to small product building blocks—and subsequently their improvement was advocated (Chen et al. 2005). However, these product genes are not conceptual genes that transfer across disciplines; they do not have the properties that the genes of the IEKG have. While these are interesting attempts, more benefit could arise for engineering if biological phenomena are connected to the IEKG.

## 7 Future directions

The IEKG main goal is the integration of engineering knowledge for its sharing and reuse in diverse disciplines. In order to best realize its benefits, we need to foster some “economy of scale.” Consequently, we need to make its benefits available to researchers and practitioners.

The first step involves building a tool that will facilitate and partially automate sharing knowledge represented in the IEKG. Such tool would allow representing Fig. 3 and the IEKG properties. It will support the representation of additional domains and of particular solutions to problems and the execution of ID using the IEKG. This will waive the “entrance fee” that one has to pay now to work with the IEKG. Such tool will also allow us to conduct various experiments about the utility of the IEKG in teaching engineering.

The second step is to benefit from the ability of the IEKG to direct attention to new conceptual or theoretical discoveries by building a tool that will crawl the IEKG to

locate omissions that could lead to future creative design or new knowledge generation as demonstrated in (Shai et al. 2009b, 2012) and discussed in Sect. 5.2.

A third step is the application of automated synthesis on top of the IEKG. An initial step on applying genetic algorithms on simple genes was successful in synthesizing linear systems for specific input–output relations (Pechter and Reich 2003). However, this effort needs to be extended to more complex genes and functionalities as well as to the synthesis of multidomain systems.

So far we established the value of the IEKG by our own work, but in order to get a community of researchers to continue develop it, we have to create the economy by which the specification of important problems made by researchers are acknowledged, and providing solutions to such problems by transferring them from remote disciplines is valued. Consequently, there would be value given to researchers who submit solutions to diverse problems, so that they could serve as a basis for solving future problems.

Last, we plan to continue train the methods to high school and university students, and to practicing engineers, to help them be more creative. We intend to study the level of creativity afforded by different uses of the IEKG.

## 8 Conclusion

We claimed that the IEKG could lead to numerous benefits. It is time to revisit them:

- The IEKG unifies many engineering disciplines: it does this and also adds new relations and value to mathematics. We expect that it would also provide value to biology.
- The IEKG provides a basis for transforming knowledge between disciplines: This has been demonstrated in numerous examples including real applications, for example, the method used to design the aforementioned adjustable deployable tensegrity robot (Reich et al. 2008; Shai et al. 2009c).
- Supporting new educational practices: A new teaching method was developed and applied in several high schools. In this approach, the students are first taught the combinatorial representations and only then do they learn the engineering material. Due to this innovative teaching, students have learned the engineering material from a new interdisciplinary perspective (Shai 2001a, b).
- Promoting inventions: For example, based on transforming the concept of electrical transistor, a new concept of torque amplifier was invented and built (Shai et al. 2009b, 2012); this design has promoted the

invention of other new devices, such as the “Personal Rescue Device”.<sup>6</sup>

- Aiding design: For example, the IEKG has been instrumental in developing analysis and synthesis tools for developing deployable tensegrity structures (Reich et al. 2008; Shai et al. 2009c). This design could hardly be done without the IEKG.
- Bootstrapping new discoveries in engineering and science: This has been demonstrated by the discovery of new concepts in mechanics (Shai et al. 2009b, 2012), methods in structures (Shai 2001a, b; Shai and Reich 2009), and by proving new theorems in mathematics (Reich et al. 2008; Servatius et al. 2010).

The IEKG and system and method genes are new concepts that underlie the nature of engineering knowledge in many disciplines and unify them. The IEKG concept has the potential to become a driving force for major advances in engineering and science as the human genome concept was for biology. Some of these advances could rely on present combinatorial representations, and others might require new representations. As such, the IEKG might present new challenges to computing.

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