INVESTIGATING ELEMENTARY DESIGN METHODS – USING AND EXTENDING THE GENOME-APPROACH

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ABSTRACT

Nowadays most of the design methods introduced in literature are not new but rather modifications or further developments of existing methods. Therefore the system of methods and method descriptions has an evolutionary grown character. Hence the aim of investigating elementary methods is to develop a systematic approach for the deduction, description and improvement of design methods.

This paper shows a systematic approach for investigating elementary design methods.

Thus, in this paper the so called Genome Approach [1] is used to model and analyze a certain number of methods from different areas. The application of this approach is revealed in examples. Both, strengths and limitations of this approach become visible.

To benefit from the strengths of this approach, first some extensions are discussed, to deal with the limitations, for the moment. Furthermore, long term possibilities to improve this approach are described.

Keywords: Elementary Design Methods, Methods, Design Methods

1 INTRODUCTION

In the field of product development many methods exist intended to carry out the product development process more effective and more efficient. The definition of design methods used here is based on the fact, that periodically occurring sub-processes can be marked-off and standardized for the purpose of rationalization. Each designer uses an individual mix of methods. S/he selects the most suitable design methods depending on several factors, e.g. user skills, infrastructure and working aids [2].

Examples are presented in well known references such as Pahl/Beitz [3], Lindemann [4] or Ulrich/ Eppinger [5] who assign design methods to certain design phases of product development, or rate them to special access items. In addition a large number of new methods are introduced in various publications and at significant conferences.

It seems reasonable to assume, that these aren't all new methods but rather derivatives of methods already known. However, the descriptions often vary concerning the kind and volume, and quite often they are insufficient for the application of methods in design projects. The kind of description differs in structure and content. The same circumstances or facts are described in various terms and in different sequences [6].

In order to clarify this, three different descriptions of methods can be compared. Comparing for instance the descriptions of methods of Birkhofer [7], Pahl/ Beitz [3] and Lindemann [4], using a relatively distinct method like the Morphological Box, it can be seen that the descriptions differ from each other. Birkhofer focuses in the description on the presentation of the classification scheme as well as on the vivid and comprehensible depiction of partial solutions as diagrams. Pahl/ Beitz also emphasizes to consider compatibility between the individual partial solutions and already includes selection and assessment steps within the description of methods. Furthermore he describes the mathematical combination and gives suitable mathematical formulas. Both authors refer the method directly to the respective point in the development process (concretization of functions). Lindemann on the other hand keeps his method description general in nature. Instead of sub functions he speaks of sub problems. Moreover he describes the arrangement of the lists (sub problems and sub solutions) at great length and gives suggestions of, in his opinion, smart further actions.

If these method descriptions are given to a user or student it does not become clear to him which method description is best for the current stage of development and wherein they differ in general. In addition all three descriptions barely give indication of how the method can be adapted to the actual problem at hand.

In this Paper the Genome Approach [1] is used to model a certain number of methods as so called genomes. Genomes are directed graphs, depicting method sequences as a series of so called elementary methods. This idea is driven by the vision that the above mentioned myriad of method descriptions is referable to a limited number of elementary methods. Thus development and construction methods can be described as formally/ objectively as possible to assess them in a neutral way. With this approach it is now possible to obtain clarity about basic processes in single methods as well as to show the actual substantial core of each method. These insights allow for a combination of elementary methods to applicable product development methods and to create specific sequences of elementary methods according to a specific task and design situation. See figure 1.

Furthermore the approach serves as a tool to summarize method descriptions objectively. That way complete method descriptions can emerge (e.g. from the Morphological Box) which are allowed to make a claim to universal validity.

In total, the approach aims to "tidy up" the world of design methods, which seemed to be a most demanding, even utopian goal regarding previous attempts of various authors. [6]

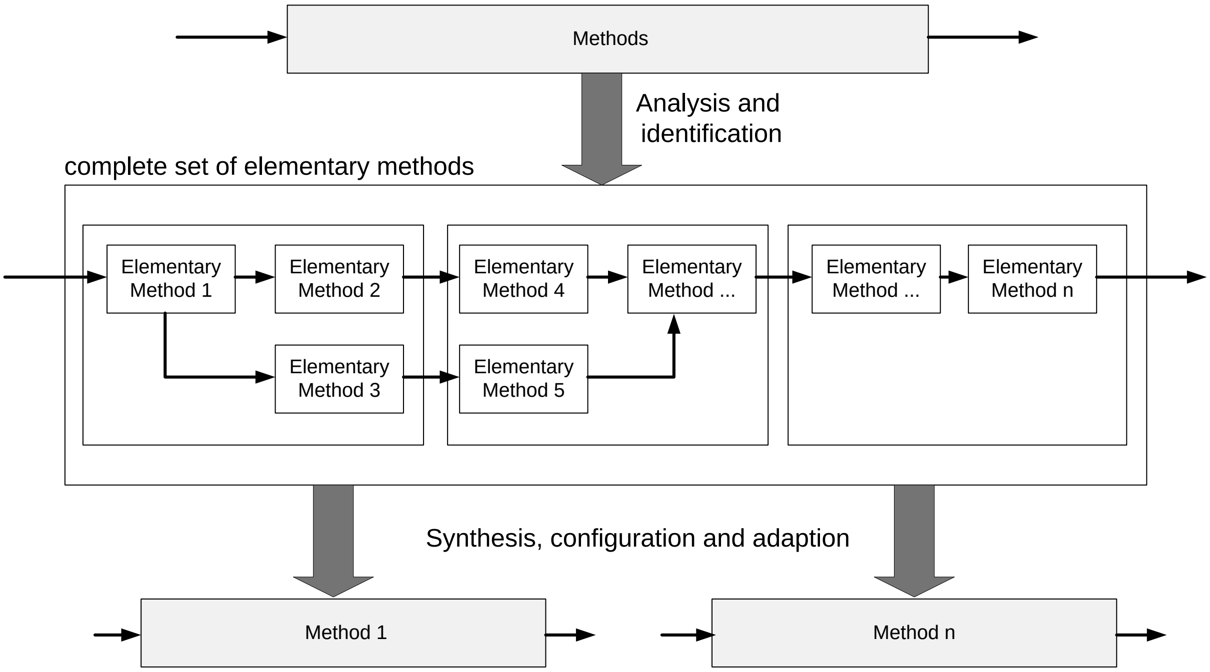

Figure 1: Objective of Elementary Methods

2 ANALYZING METHOD

The mentioned contribution of Birkhofer [1] presents the so called Genome Approach to define elementary design methods. This approach differs substantially from a wide range of other research work that intended to capture the basic nature of design methods or to improve application by giving advices.

The Genome Approach uses the often occurring list (vectors) and matrix structure of design methods (e.g. QFD, Paired Comparison, FMEA, etc.) to model methods as networks of operations that transfer lists and matrices. Thereby, method descriptions are diagramed. The emerging diagrams remind the beholder on pictures of biological chromosome sets (genomes), which give this approach the name Genome Approach.

Basically the Genome Approach uses seven different kinds of elements (Process, Function, (Physical) Effects, (Working) Principles, (Real) Objects, Properties and Values) and five different operations (List, Assign, Divide, Merge, Connect) to model methods. See table 1. The linking of two specific elements with operations resulting in a scalar, vector or matrix is called elementary method.

Table 1: Codes for Elementary Design Methods [8]

Operations / Elements	List	Assign	Connect	Divide	Merge
Processes	1.1	1-1.2	1-1.3	1.4	1.5
Functions	2.1	2-2.2	2-2.3	2.4	2.5
(Physical) Effects	3.1	3-3.2	3-3.3	3.4	3.5
(Working) Principles	4.1	4-4.2	4-4.3	4.4	4.5
(Real) Objects	5.1	5-5.2	5-5.3	5.4	5.5
Properties	6.1	6-6.2	6-6.3	6.4	6.5
Values	7.1	7-7.2	7-7.3	7.4	7.5

Thereby close attention has to be paid to the operations “assign” and “connect”.
Table 1 does not show that with the help of these operations also various elements (e.g. Functions and (Physical) Effects) can be assigned to or connected with each other.
In table 2 the allocations in the operation “assign” are displayed. The same is true for the operation “connect”.

Table 2: In Detail: Assign

Assign (X.2)	Processes	Functions	Effects	Principles	Objects	Properties	Values
Processes	1-1	1-2	1-3	1-4	1-5	1-6	1-7
Functions	2-1	2-2	2-3	2-4	2-5	2-6	2-7
Effects	3-1	3-2	3-3	3-4	3-5	3-6	3-7
Principles	4-1	4-2	4-3	4-4	4-5	4-6	4-7
Objects	5-1	5-2	5-3	5-4	5-5	5-6	5-7
Properties	6-1	6-2	6-3	6-4	6-5	6-6	6-7
Values	7-1	7-2	7-3	7-4	7-5	7-6	7-7

With the help of the Genome Approach, descriptions of methods are modeled based on elementary methods and shown as genomes. To do so, the following steps have to be processed:

<u>Modeling Methods as Genomes:</u>

1. Breaking down the original text of the method description to single steps
2. Assigning a serial number (step in the genome) to each step
3. Assigning the elementary code (see figure 1) to each step.
4. Defining in- and output for each step
5. Defining the system boundary

6. Drawing the genome

As an example an excerpt of the description of the method “Pairwise Comparison” according to Lindemann [4] is shown below.

Original Text (translation):

“At first the objects to be compared are juxtaposed in the matrix (object-matrix). Then every object is directly compared to each one of the others.”

Table 3: Analyzing Example

Original	Serial Number	Elementary Code	In-and Output
At first the objects to be compared are juxtaposed in the matrix (preference-matrix).	1	5.1	In: Objects Out: List of Objects
	2	5-5.1	In: List of Objects Out: Object-Matrix
Then every object is directly compared to each one of the others.	3	X.X	In: … Out: …
[…]	4	X.X	In: … Out: …

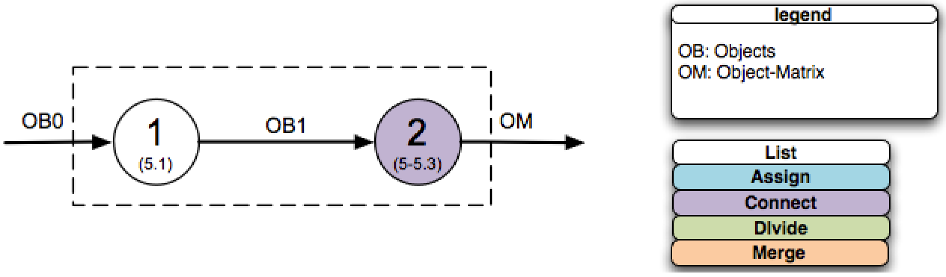

Figure 2: Example of a Genome

3 EXTENDING THE APPROACH

Birkhofer derived the explained Genome Approach (consisting of elements and operations) from the analysis of 90 Methods. To ensure suitability of this approach regarding range and diversity of development methods and, if necessary, to extend it, it was applied to 32 more method descriptions from different fields. In this way also limitations of the approach can be revealed. Table 4 shows an overview about the treated method descriptions.

Table 4: Analyzed Methods

Classical construction methods Lindemann [4]		**Design and dimensioning methods Birkhofer/ Nordmann [9]**
ABC-Analysis	Morphological Box	Verification of Strength of Shafts
List of Requirements	Utility Value Analysis	Life Cycle Calculation
Benchmarking	Pairwise Comparison	Welded Joints
Checklist	Portfolio	Bolt Calculation
Checklist by Osborn	QFD	**Methods of Product and Process Planning; Gausemeier [10]**
Effects Library	Sensitivity Analysis	Total Production Cost Calculation
Property List	Systematic Variation	Amortization Calculation
Influence Matrix	SWOT	ROI
FMEA	Comparison	Chance Risk Matrix
Questionnaire	Relation Matrix	Net Present Value Method
Quantification	Objective Preference Matrix	
Kano-Model		

Results of this investigation are possible extensions of the Genome Approach, which are presented in this paper.

Subsequently, these extensions are illustrated with examples. Here, each created genome is indicated for the respective method. The problems arising at modeling are explained and finally the extensions thereby necessary for the approach are shown.

Figure 3 shows the genome of the Morphological Box according to the description of Lindemann.

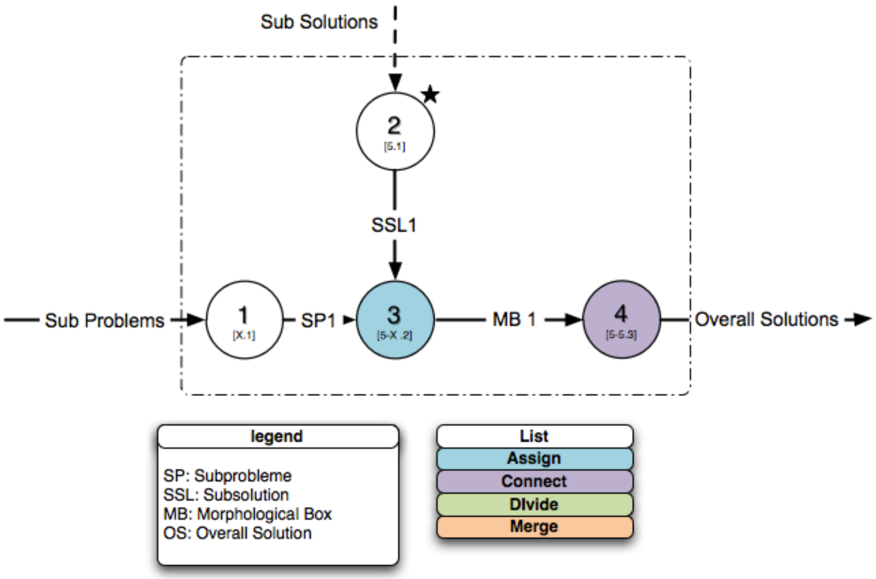

Figure 3: Genomes of the Morphological Box according to Lindemann without Gateway

While modeling this method description it is obvious at first sight that there is no element class for “Problems”. Looking at the possible elements in accordance to the Genome Approach, it is striking that these merely refer to product models. Beyond the work with product models concerning important other domains (requirements, creativity techniques, etc.) an extension of these possible elements is necessary.

Another point for the extension of the approach arises on the question about the origin of the lists used. While the source of the list “Sub-Problems” may turn out to be an output of previous methods, the origin of the list “Sub-Solutions” remains unexplained. A common source is the compilation from catalogues (e.g. Roth [11]). It is also conceivable though that the list of Sub-Solutions is compiled using creativity techniques. For analysis of the method sequence the question is of no great significance. However for the application of the method, knowledge about the source of each list would be essential action leading information. Hence as an extension to the approach it is proposed to label the lists with the help of creativity techniques using the *-symbol. Additional origins have to be described completely systematized. At the moment, the *-symbol is only a tool to label creative processes. However, there is evidence that using the Genome Approach, the development of the creative processes can be illustrated. That way elementary methods marked with * so far could be described in detail in the future, which could give a real insight into the core of creative thinking of designers.

Besides it is striking that the creation of the Morphological Matrix turns out to be assigning a “Sub-Solution” list to each entry in the “Sub-Problem” list. This is not obvious from the genome right away. For analysis of the basic principle of the method the genome illustrated in figure 3 is helpful and sufficient. However, to get closer to the mentioned main objective - namely creating applicable method descriptions - further action leading information for the user is necessary at this point. Therefore, to complement the approach, so called “Gateways” are introduced.

With the help of a XOR-Gateway known from the Business Process Modeling Notation (short: BPMN) [12] a loop can be modeled only terminating when to each “Sub-Problem” a list of “Sub-Solutions” is assigned.

In the modeling of other method descriptions more problems were found (such as: need for case distinction, random order of single steps, optional predecessors of elementary methods, etc.). These can be solved with the XOR and AND gateways, also introduced.

- AND – Gateways: Here the gateway enables at an input that all (two or more) outputs are further “tracked“. This allows the modeling of elementary methods running parallel.
- OR – Gateways: Here the gateway enables at an input that one or more outputs are further „tracked“. This allows modeling of optional elementary methods or elementary methods only iterated at a fulfilled condition.
- XOR – Gateways: Here the gateway enables at an input that one single output is further “tracked“. This allows the modeling of case distinctions.

Gateways can also be used as an operator for gathering different information. Analogue to the branching three kinds of gatherings can be logically distinguished.

For a better understanding Gateways and their outputs can be labeled. For example the condition “Morphological Box complete?“ can be written above the rhombus to the branching of a XOR-Gateway and both the outputs can be labeled “Yes “ and “No“. Another possible application arises with a variable number of steps at methods. This can be modeled as a loop with a XOR gateway including a return. In such a case numbering of the elementary methods remains problematic.

By application of the specified extensions only a single action leading method description by the Morphological Box is generated as a genome. See figure 4.

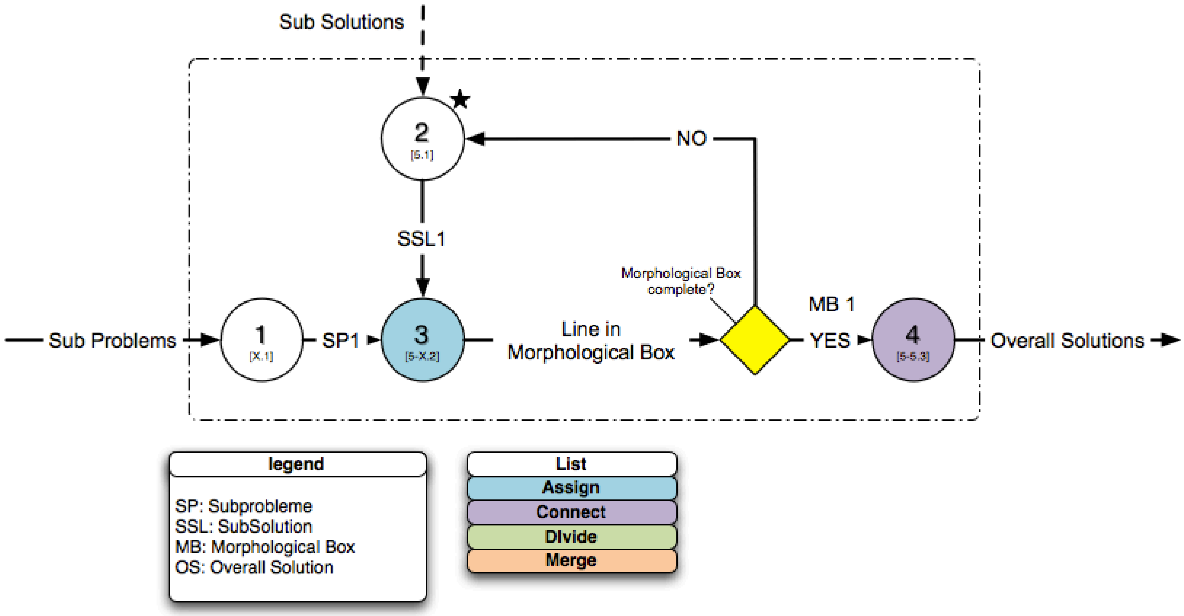

Figure 4: Genome of the method description Morphological Box according to Lindemann with Gateway

The Genome Approach is based on the idea that all elements used can be represented by lists. It involves the previously mentioned advantages. Nevertheless there are steps within methods that are difficult to be represented in a list. Figure 5 shows an excerpt from the life cycle calculation of bearings. Thereby a free body diagram is created from a list of forces and momentums as well as from a list of geometrical data. This in turn is used to again calculate a list of bearing forces. The free body diagram cannot be described using the known list items.

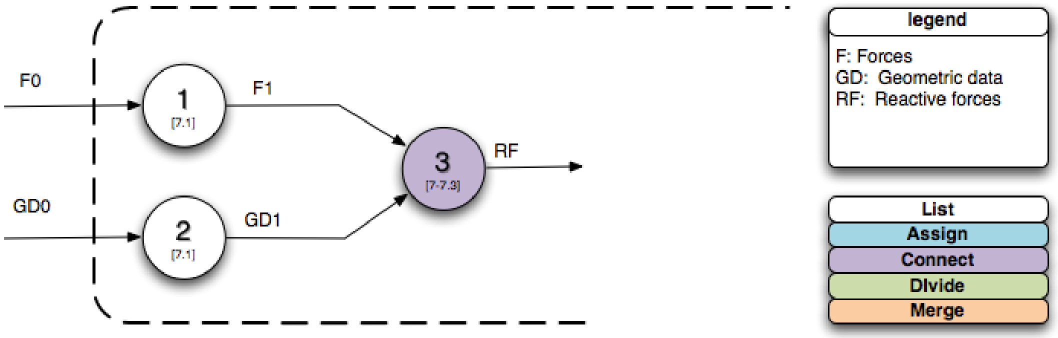

Figure 5: Excerpt of the genome of life cycle calculation of bearings without Black Box

To still be able to model method descriptions as complete genomes “Black Box” operations are introduced as tools to bridge these applications. Figure 6 shows this.

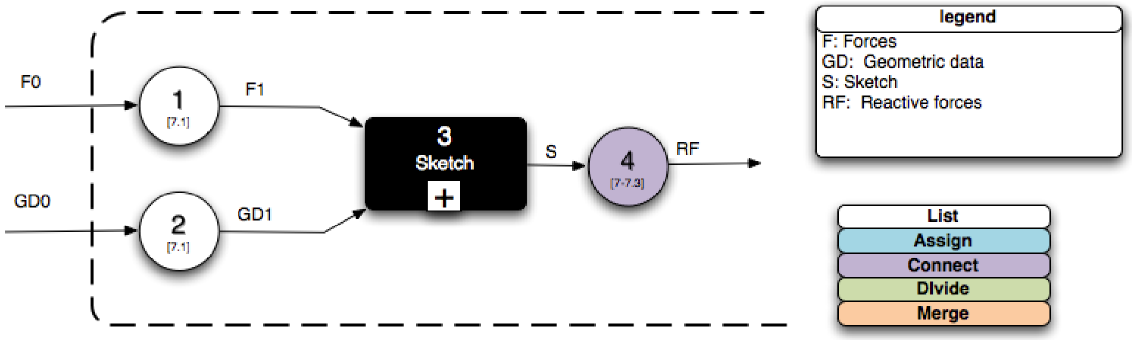

Figure 6: Excerpt of the genome of life cycle calculation of bearings with Black Box

According to the described problems the “Black Box” works well for both, processes which are not ascertainable in lists (abstract and not sufficiently specific described processes) and in case the representation of methods in a list is basically possible yet diverges from the actual procedure.

Thus the “Black Box” is a stopgap which is used when the actual proceeding cannot be represented in a list.

Also at this point it shall be emphasized that for analysis of the methods the use of a “Black Box” may not be necessary. Towards the intended method synthesis they are however helpful to provide action leading information for the user.

It is another long term objective not having to use this tool “Black Box” any more but to be able to process all existing elements in an analogue and systematic way. Especially the field of graphic representations will be of great importance for further research considering its significance for product development.

4 APPLICATION EXAMPLE

In this section the advantages of method modeling with the help of genomes shall be pointed out once again using a simple example.

For that, three different method descriptions of the method Morphological Box are modeled compliant to the proceeding described above. Thus the differences between the method descriptions can be neutrally compared with each other. Thereby it is striking that in the core of the method within the operation of assignment several lists of Sub-Solutions are associated with one list of Sub-Problems.

This core is depicted with minor differences in all three of the method descriptions compared here but always looks the same inside the genome (compare steps 1-3 in Figures 4, 7 and 8).

First differences become identifiable when looking at the description of the composition of Overall Solutions. It represents a separate kind of sub method and is therefore located outside the system boundaries.

More Differences can be found in the strategies for the reduction of the number of resulting Overall Solutions. While Lindemann and Pahl/Beitz point out the correct compilation of the two lists, the suggestions made by Birkhofer focus on the so called reduction strategies which are performed at the already created Morphological Box.

Furthermore the check on compatibility, which is a unique feature in the description of Pahl/ Beitz can be represented as a genome.

After modeling the complete method descriptions as one genome, it is possible to combine the methods into method modules. See figures 7 and 8.

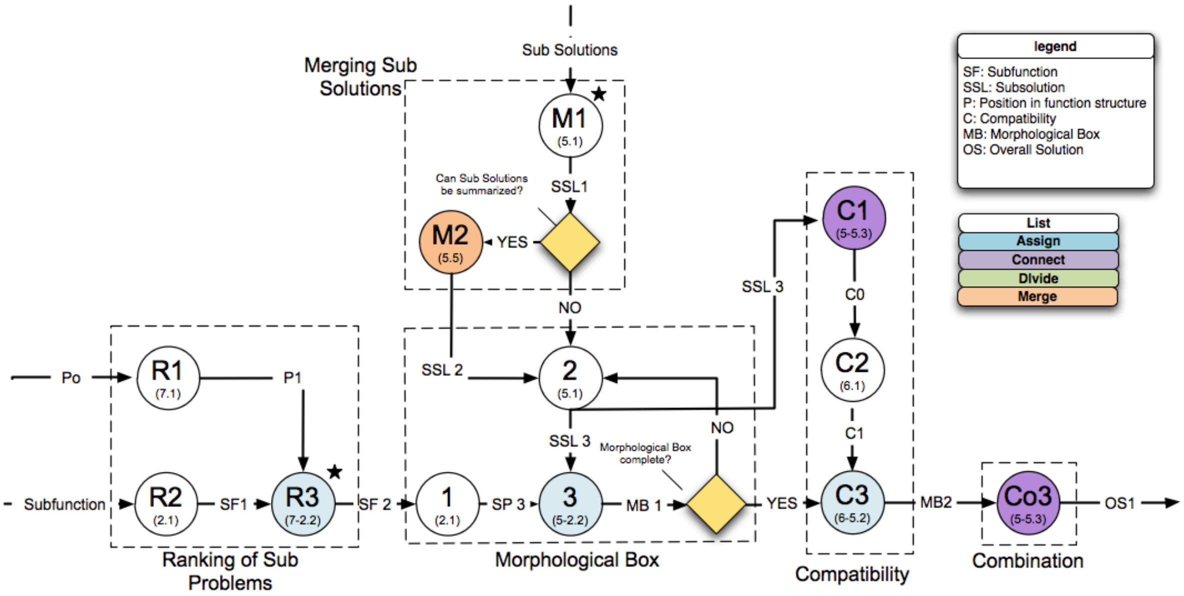

Figure 7: Genome of the method description Morphological Box according to Pahl/ Beitz subdivided into method modules

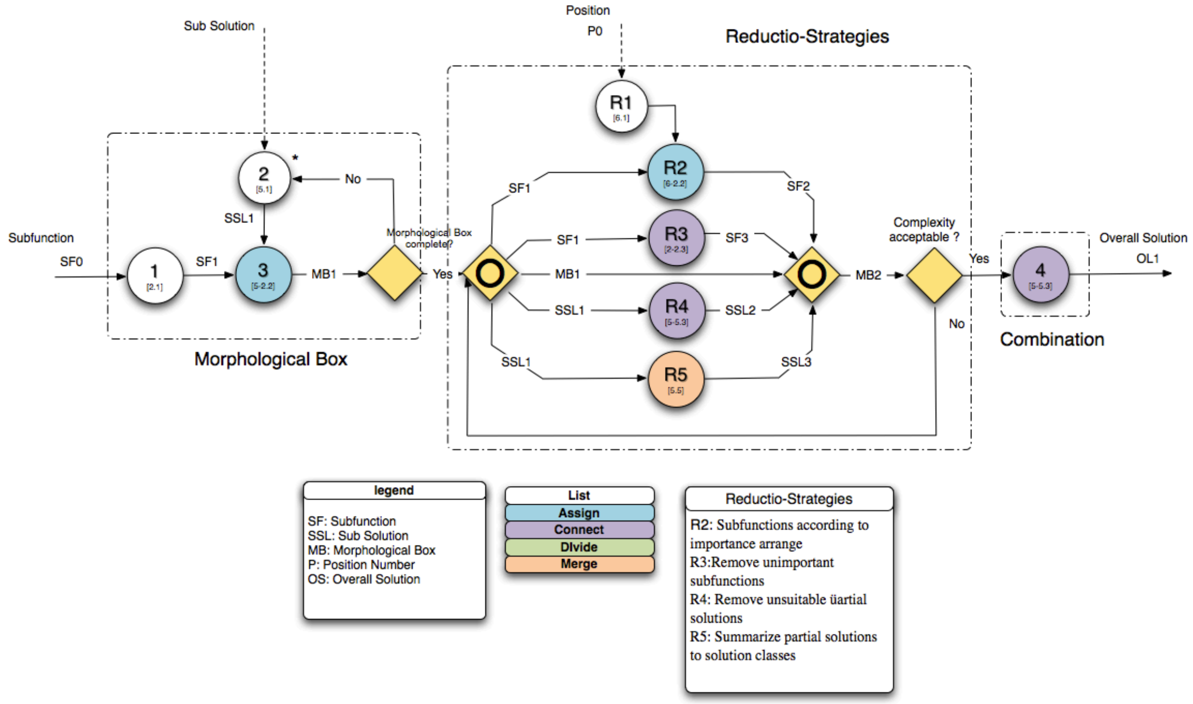

Figure 8: Genome of the method description Morphological Box according to Birkhofer subdivided into method modules

That way the application of methods can be adapted to the given situation, by omitting or adding single method modules.

Additionally it is then possible to form a common genome from the three genomes available. Thereby a complete description of the method would result, including all modeled method modules. Furthermore, subsequent method steps can be added, e.g. the valuation of Overall Solutions. See figure 9.

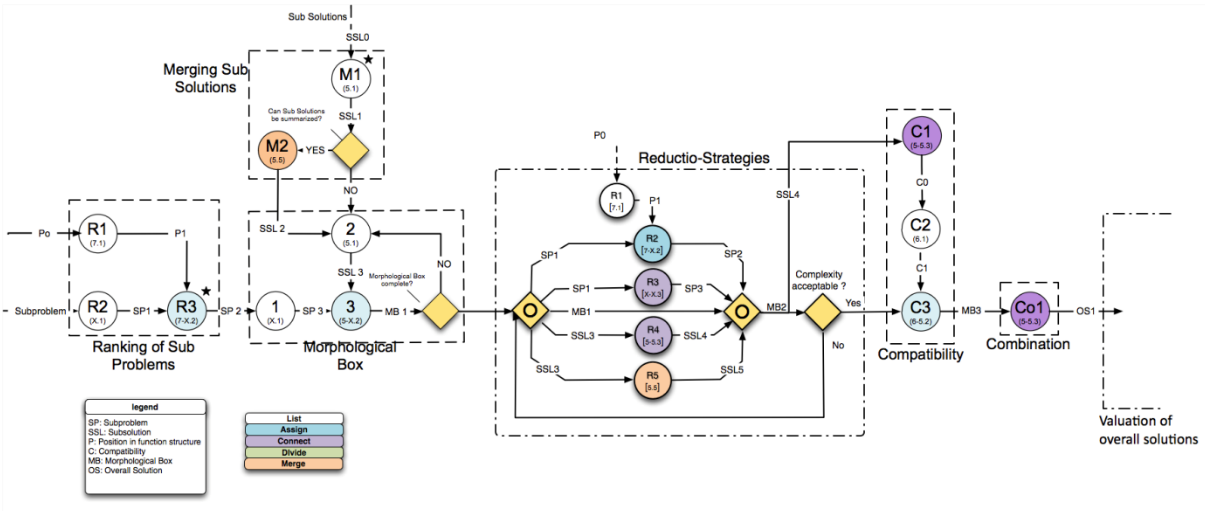

Figure 9: Overall description of Morphological Box according to Lindemann, Birkhofer and Pahl/ Beitz

5 CONCLUSIONS AND FURTHER WORK

It was shown that the Genome Approach by means of specific extensions is able to embody a neutral tool for the analysis of methods from different fields. The other objectives of this research project can be essentially divided into two main areas.

First a most complete modeling of existing methods is aspired. Therefore the elements and operations of the approach have to be systematically extended. The aim is to be able to model any new incoming method as a genome easily in a uniform and complete way. With the help of software (which interprets the genomes as directed graphs) all genomes can then be analyzed and frequently recurring patterns will be recognized. Therewith the actual cores of both, each method and a limited number of recurring method components can be identified. This would clear the diversity of existing method variants.

The second goal is the applicability of the identified method modules. So far this is accomplished by the action leading elements described in this paper (*-operations, Gateways, Black Boxes). In the future it is to be fully systematized for example by describing creative processes as a separate genome.

This bears advantages for the application of methods as well as for teaching. Furthermore, it will give a deeper insight in creative thinking of designers.

For method users, genomes are clear and complete guidelines. With some practice the experienced method user manages to compose methods appropriate to the situation from recurring method modules. In the application itself an easy and unambiguous overview about the necessary inputs and created outputs represents precious information.

By knowing that all existing methods rely on a limited number of recurrent patterns, learning methods becomes easier for both, students and practitioners.

Another aspect is the consideration of cognitive skills of designers. The elements (lists) of the Genome Approach are comparable with the operators of the human problem solving. Thus it could be proved that organization of development methods in elements (lists) and elementary methods generally correspond to a natural human problem solving method, and are so based on cognitive constraints. The goal is to support cognitive skills or qualities, which are prerequisite for successful developers, for example, decision making, generalization, association and deductive reasoning [13].

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