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INVESTIGATING ELEMENTARY DESIGN METHODS

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ABSTRACT

The aim of investigating elementary methods is to increase the acceptance of methodical working in practice by developing a systematic approach for the deduction, description and improvement of design methods. The purpose of this paper is to give an overview about the goals and modularization methods of design methods with the Genome Approach.

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1 INTRODUCTION

Many design methods intend to make the design process more effective and efficient. The definition of design methods used here is based on the fact that periodically occurring sub-processes can be accounted for and standardized for the purpose of rationalization. Each designer uses an individual mix of methods, selecting the most suitable design methods based on factors, such as user skills, infrastructure and working aids (Zier et al., 2011).

Examples of this are found in well-known references, such as Pahl and Beitz (2007), Lindemann (2007) and Ulrich / Eppinger (2009), who assign design methods to certain design phases or rate them to special access items. A large number of new methods are introduced in various publications and at important conferences.

It seems reasonable to assume that they aren’t all new methods but are derivatives of known methods. However, their descriptions often vary in type (structure and content) and volume. The same circumstances or facts are described in varying terms and in different sequences (Birkhofer et al., 2002). Additionally, method descriptions are quite often insufficient for the application of methods in design projects.

To clarify this, three descriptions of methods can be compared. Comparing, for instance, the descriptions of methods in Birkhofer and Kloberdanz (2010), Pahl and Beitz (2007) and Lindemann (2007) using a relatively distinct method like the Morphological Box, the descriptions differ from each other. Birkhofer and Kloberdanz (2010) focuses on the description of the presentation of the classification scheme as well as on the vivid and comprehensible depiction of partial solutions as diagrams. Pahl and Beitz (2007) also emphasizes the consideration of compatibility between the individual partial solutions and includes selection and assessment steps within the description. They describe the mathematical combination and give suitable mathematical formulas. Both authors refer the method directly to the respective point in the development process (concretization of functions). Lindemann (2007) on the other hand keeps his method description general in nature. Instead of sub functions he uses the term “sub problems”. 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 is not clear to them which method description is best suited to the current design stage and how they generally differ. In addition, all three descriptions provide hardly any indication of how the method can be adapted to the actual problem at hand.

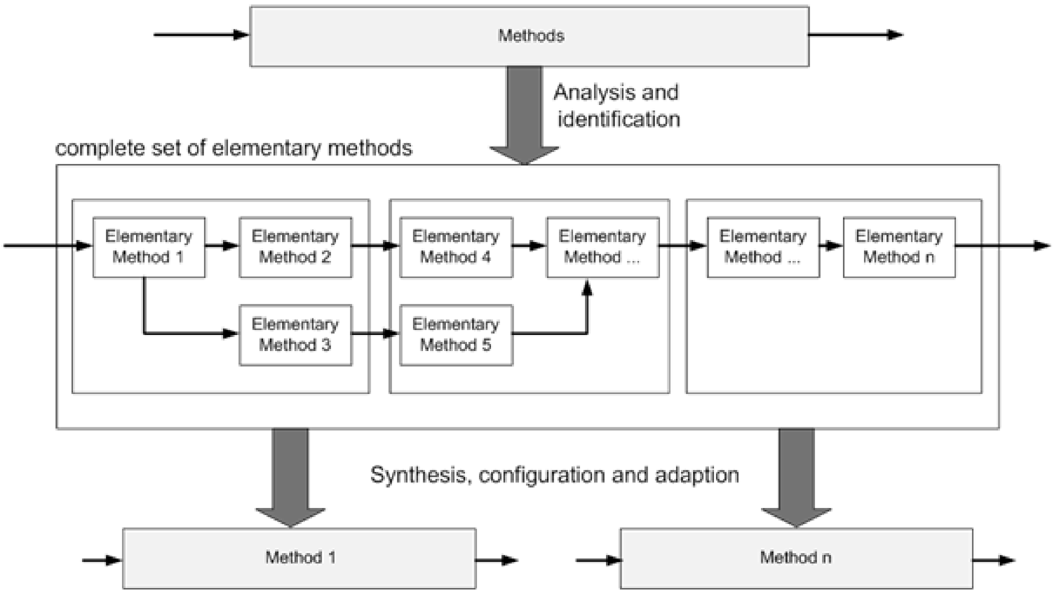


Figure 1: Objective of Elementary Methods

To identify the core of methodological working in this paper, the Genome Approach (Birkhofer, 2007) is explained as an analyzing approach. It is used to model more than one hundred descriptions of design methods as ‘genomes’. Genomes are directed graphs that depict method sequences as a series of 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 design methods can be described as formally or objectively as possible to assess them in a neutral way. With this approach it is then possible to obtain clarity about basic processes in individual methods as well as show the actual substantial core of each method. These insights allow for a combination of elementary methods with applicable design methods and to create specific sequences of elementary methods according to a specific task and design situation (Figure 1).

The approach aims to distil the world of design methods, which is a demanding, almost utopian, goal when compared to previous attempts by various authors.

2 BACKGROUND

A wide range of research work intends to capture the basic nature of design methods or improve application by giving advice. Some approaches structure design methods according to specific characteristics like generalized steps of problem solving (Lindemann, 2007) or specific objectives (Jones, 1970). Some approaches like the “Process-oriented Method Model” (PoMM) (Birkhofer et al., 2002) or the “Basic Structure of Design Methods” (Dobberkau, 2002) focus on how to describe the variety of methods more generally to see similarities and differences.

Other approaches link methods to design phases (VDI Guideline, 1993), (Pahl and Beitz, 2007), or typical applications (Wach, 1993). Several attempts, for example, Zanker (2000) and Walter (2003), define elementary design methods as basic prescriptive procedures. In doing so, the researchers wished to reduce the large number of published design methods to a limited set of basic (elementary) methods that represent the “Petri dish” of design methodology.

Nevertheless, there is no consensus within the community about a prefered specific approach. There seems to be a gap between the demands on the individual researcher creating their own structure of design methodology and the perceptible benefits of these approaches to the research community. Beyond it, the use of such approaches for improved transfer into design practice and for long-term application seems to be quite doubtful.

The PoMM is a tool to describe methods completely and in a well-structured manner. Eight modules are used to give an overview of all required information for each method. Input, sequence and output are the modules concerning the process character of design methods. Hints, the user, general conditions and working aids are defined. See figure 2.

In order to investigate elementary design methods, this contribution focuses on the method sequences.

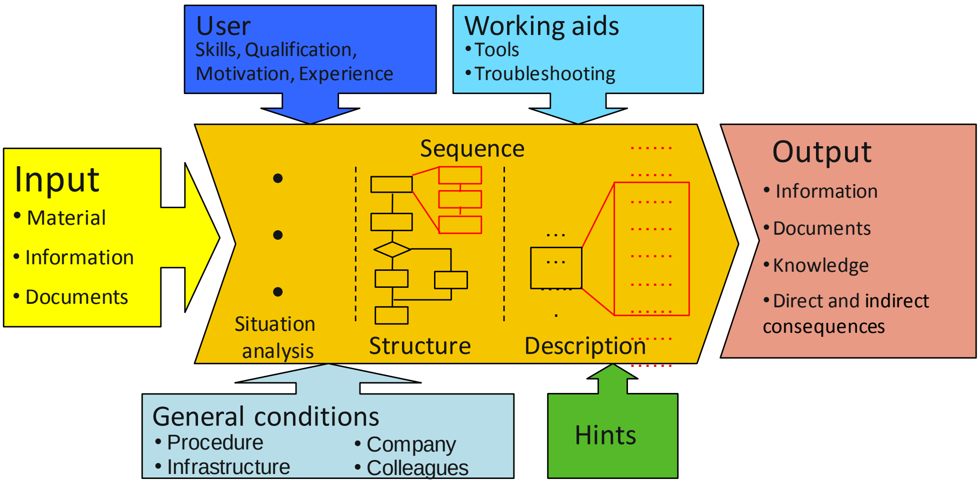


Figure 2: The Process-oriented Method Model (PoMM)

3 ANALYZING APPROACH

Walter (2003) presents the list-approach. He states that with just five operations (listing, assigning, connecting, merging and dividing) and seven different types of list content, all method descriptions in the area of design can be modeled as transformations of lists, tables and matrices.

3.1 The substantiality of the list-approach

Zier (2011) enlarged and detailed the basic assumptions of Walter (2003) and the PoMM (Birkhofer et al. 2002) and proved them by analyzing a variety of design-related method description. More than one hundred different method descriptions in the fields of systematic design, quality management, creativity techniques and machine elements were analyzed to verify the vector-matrix approach. The detailed analysis results in depiction of all described sequences of related design methods in the vector-matrix approach.

The elaborated modelling procedure was validated with a comparative evaluation of the modelling results of different users. The result showed that these findings are not only a manifestation of a formal aspect of presentation, but indicate a basic content concept behind the approach and may provide the key for a better understanding of the nature of methodical work. Perhaps designers and engineers use vector and matrix-based presentations not only out of habit, but because they represent best cognitive processes in engineering thinking, especially for reducing the complexity of “real world problems”.

3.2 The genome approach

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, tables 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.

3.2.1 Elements and relations

In analyzing more than one hundred design method descriptions, two types of syntactic units, elements and relations became obvious.

Elements are items that are processed and/or regarded in design methods. The only elements that occur repeatedly in design methods are values and objects.

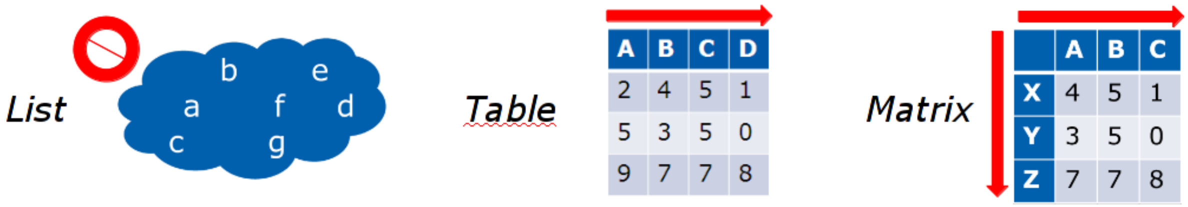
A *value* is a part of a total quantity which has to be defined precisely. From this, it follows that the length of a list of values is known exactly. Values can be numbers, alphabetic characters, RGB colors, and binary/discrete states. All elements which do not satisfy this condition are *objects*, e.g. ideas, possibilities and chances.

Relations are responsible for linking elements. They are represented by arrows that also show the main direction of the models.

3.2.2 Constructs

There are three ways to arrange elements: Lists, tables and matrices.

Lists represent an amount of elements without any order or orientation. A list must contain either values or objects; it is not possible to mix elements. In *tables*, elements are ordered in one direction. They can be seen as lists with an order. The arrangement is defined by a top row or column. In most cases, tables contain a header row and are arranged column by column, though the transposed orientation is also possible. *Matrices* are arranged in both directions, so they contain a top column and a top row.



A	B	C	D
2	4	5	1
5	3	5	0
9	7	7	8

	A	B	C
X	4	5	1
Y	3	5	0
Z	7	7	8

Figure 3: Constructs

3.2.3 Operations

Semantic units are created when two lists of elements are linked together by relations. Examples of semantic units are “a cam drive has certain efficiency” and “the efficiency has a value of 92 %”. Applying a relation to a construct of elements is called an operation. The operations list, assign and connect are possible.

List is the only operation that is able to create the list construct. Every model and every input inside the model starts with this operation that collects all relevant information from the environment, e.g. catalogues, experience, textbooks, etc. Lists can also be used for merging other lists and for extracting elements into a list. Lists are mandatory for each method. The exact way of listing is disregarded. In real life, listing is commonly the most cumbersome step, so among other things it is accountable for the lack of acceptance of methods. It is possible to see whole methods as “Creating a list”, e.g. Brainstorming. In fact, most methods require inputs that are based on brainstorming.

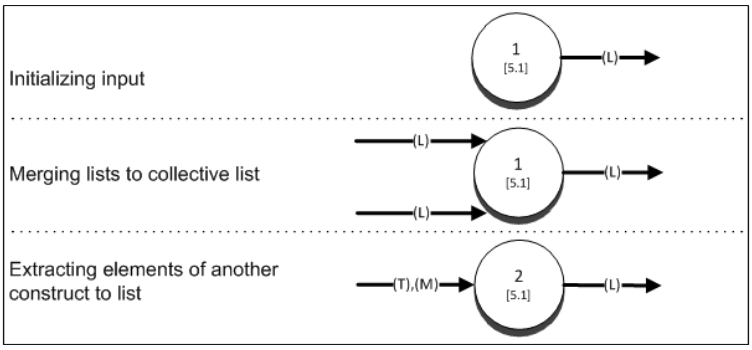


Figure 4: Elementary Methods "List"

Assign is the main operation in building the model. It is responsible for the method of adding further information to the model and is used in nearly every method (the most important exception is algorithms, in case they can be seen as method). The input must contain one or two constructs. Assign sums up the operations ‘extract to table/matrix’, ‘add’, ‘add selectively’, ‘replace’ and ‘span’. The output is a table or matrix, depending on the operation performed.

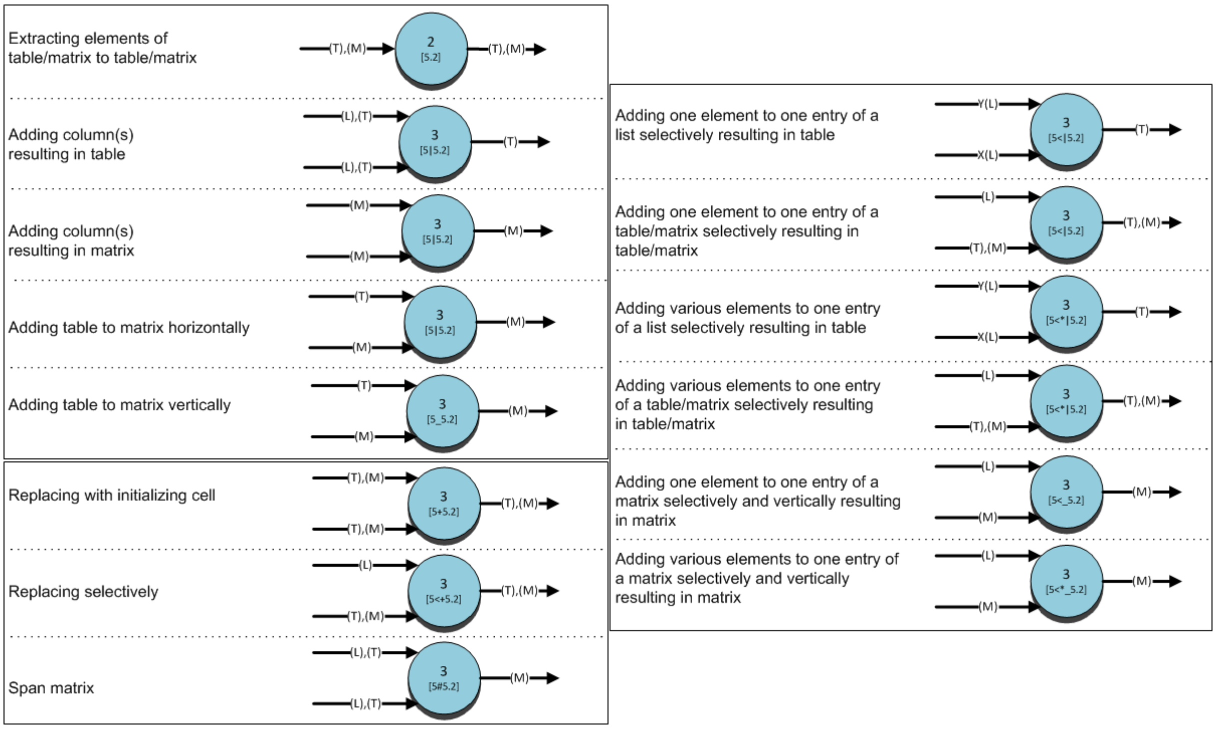


Figure 5: Elementary Methods "Assign"

Connect is the operation that can be used to handle calculations inside the model. As a result, all mathematical and logical operations are Connect operations. With Connect it is theoretically possible to convert matrices into tables and tables into matrices.

4 RESULTS AND FINDINGS

The neutral description of method sequences as genomes, allows a new quality of comparing different method descriptions with each other. Some differences are obvious, others need a detailed analysis. To identify differences and similarities of method descriptions, an automated pattern recognition procedure was elaborated.

Result of the analysis of the modelled method descriptions is, that they all are based on only five modules.

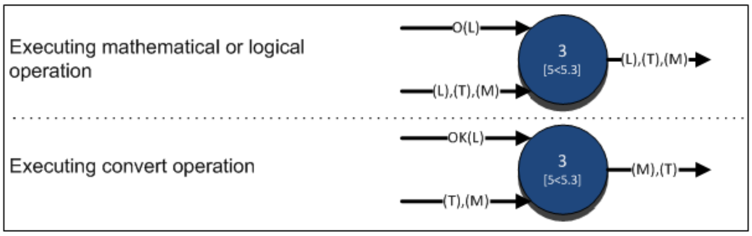


Figure 6: Elementary Method "Connect"

4. 1 Automated pattern recognition

To identify reoccurring method modules, an automatic algorithm for pattern recognition was developed. The term “module” refers to a completed functional unit of a method. Modules consist of a sequence of at least two elementary methods and may occur in different methods. Modularization is used to improve the understanding and synthesis of methods. Automated pattern recognition can be carried out in two ways: search for known modules and search for unknown modules of unknown structure.

4.1.1 Search for known modules

During classification, the amount of data is searched for predefined patterns. For this reason, the approach is focused on finding a perfect match of features. Based on expert knowledge and manual analysis, modules are identified. The genome then gets automatically sought after these modules. Thus it can be checked whether a module is present in the genome.

When a sequence is found in several different methods descriptions it may be a potential module.

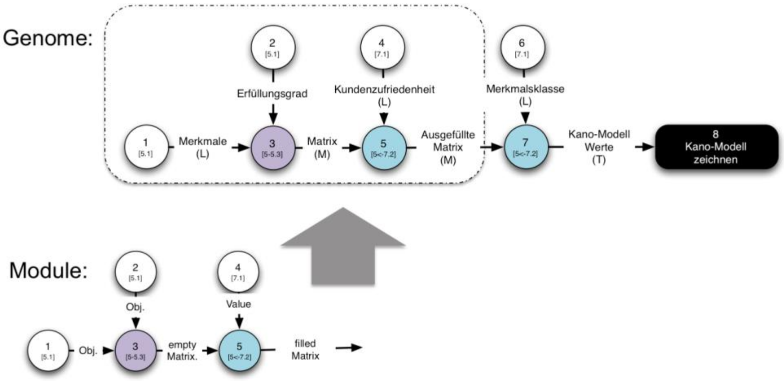


Figure 7: Search for known modules

4.1.2 Search for unknown modules of unknown structure

The second analysis method deals with the search for modules of which neither the precise nature nor the structure is known. Since there is no knowledge of the modules to be scanned and their structure, a heuristic method is needed that allows the gradual approximation to potential modules.

As a starting point for the analysis, the elementary method that occurs most frequently within one or more methods can be used. Based on the most common elementary method, all two elementary sequences that proceed from this basic method are listed.

When different methods are analyzed the most common sequences are potential modules.

The listed genome sequences are just a collection of potential modules and not complete modules. It is assumed that sequences that occur frequently are likely to act as modules. These potential modules are then checked with the first method.

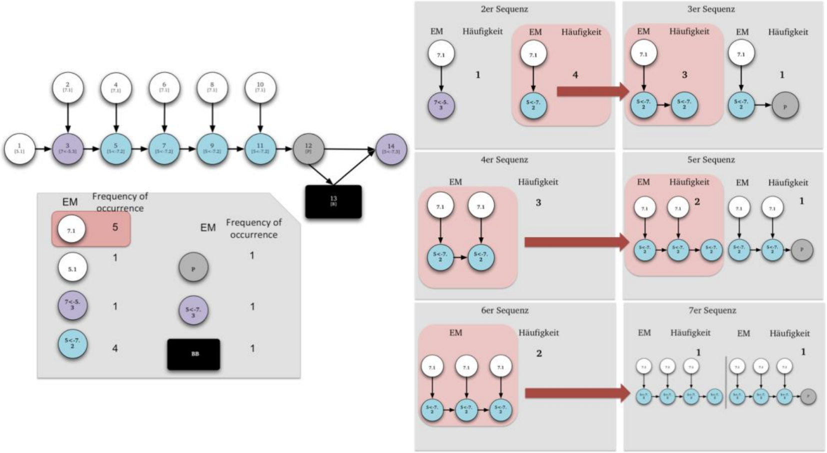


Figure 8: Search for unknown modules of unknown structure

4.2 Identified Modules

The results of the pattern recognition analysis support the basic assumption. It was possible to identify five constantly reoccurring method modules (Figure 10). With the five modules it is possible to model almost each and every design method description as a genome.

It is surprisingly easy to name the models after the design activity they support. The names used here are:

- Detailing / Creating a table
- Sorting
- Filtering
- Creating and completing a matrix
- Calculating

With this finding, deep insight into the principles of methodical working is possible. As an example, the module “Detailing” is described in the following section. Due to lack of space the other modules are not described here.

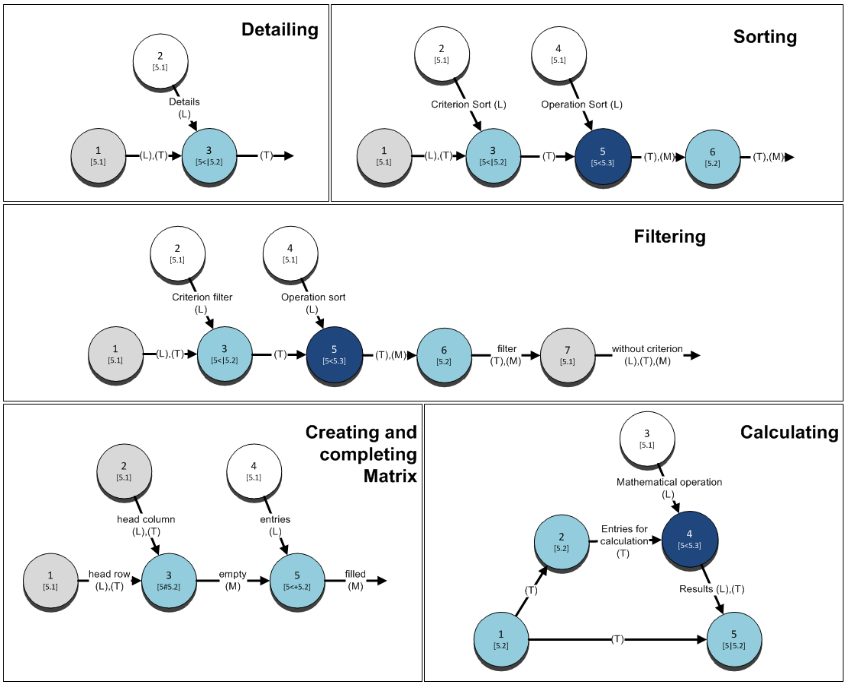


Figure 9: Identified method modules

Detailing

- An existing list or table is detailed by assigning another list with further information. A table is created from two lists.

- It is the most identified module in all analyzed method descriptions.
- From a cognition research point of view, this module represents the stepwise proceeding nature of design methods, which supports the systematic solution of complex design problems. Jänsch (2007) states that means-end-analysis is one of the most powerful problem-solving procedures of a designer. Detailing can be interpreted as a means to solve an overall problem in a stepwise manner.

5 APPLICATION EXAMPLE

One of the methods modelled to validate the Genome approach is the House of Quality from the Quality Function Deployment (Figure 10). As described in Section 2, the Genome represents the core of the PoMM. Hints are shown as yellow boxes outside the core and contain parts of the method description that are not part of the sequence. The input for the HoQ is shown on the left. The sequence of the method is displayed as a genome. It consists of several elementary modules, which follow the instructions of the method description. The red circles identify steps 1-9 in the method description. In steps 6, 8 and 9, the outputs of the HoQ are created. Output is shown on the right hand side of the PoMM.
In the graphical representation of the second House of Quality (HoQ) of a Quality Function Deployment (QfD), its vector and matrix-based structure is obvious (Figure 11).

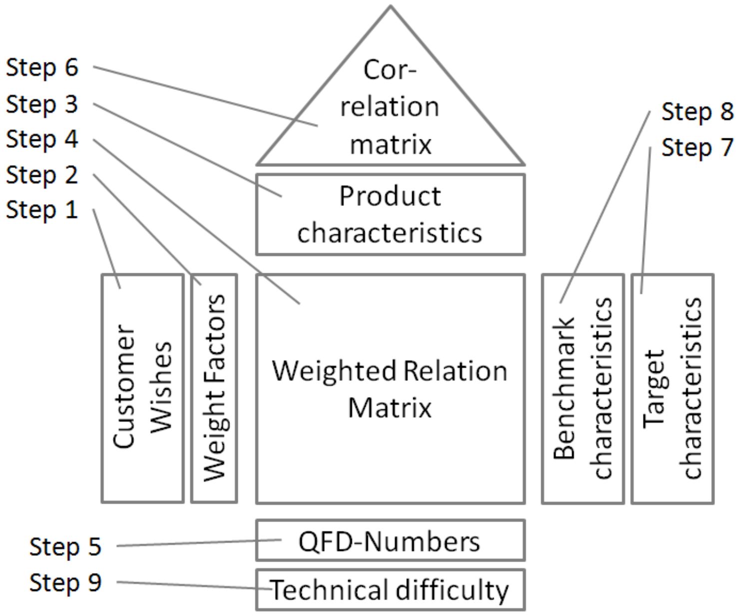


Figure 10: Second House of Quality (HoQ) of Quality Function Deployment (QFD)

As in other methods such as Morphological Box, Requirements List, Evaluation Charts and Design Structure Matrix, the HoQ links vectors or matrices either to themselves or to other vectors, resulting in new vectors or matrices. Beginning at the left side of the HoQ, a user has to follow the procedure:

1. List customer wishes in the first column (vector of customer wishes)
2. Assign a vector of weights (vector of weights)
3. List product characteristics
4. Span a matrix of customer wishes and product characteristics (central matrix)
5. Connect weight of customer wishes with product characteristics to a vector of QfD numbers
6. Connect product characteristics to themselves (correlation matrix or roof of HoQ)
7. Connect customer wishes to product properties
8. Connect product characteristics to target characteristics
9. Assign a vector of technical difficulty

The QfD may be reduced to a sequence of operations with vectors and matrices.

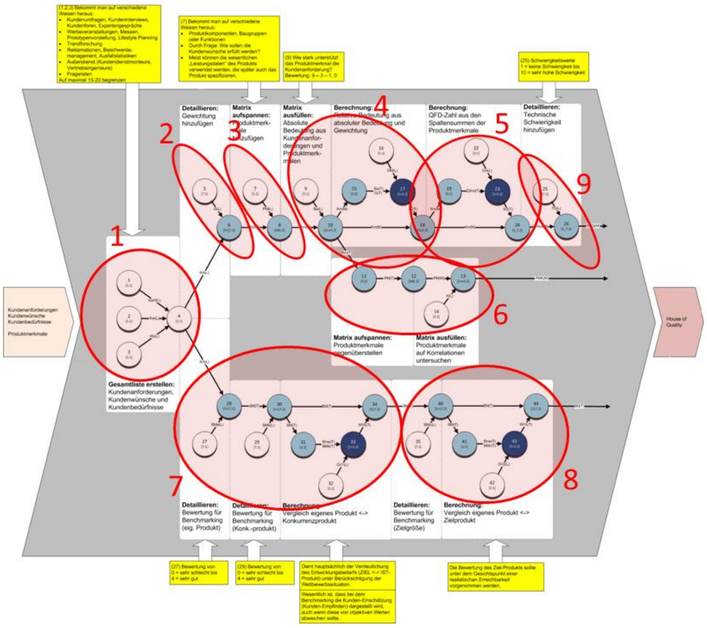


Figure 11: Complete PoMM (containing the Genome) of the House of Quality

6 SUMMARY AND OUTLOOK

The presented genome approach provides a neutral way to model sequences of design methods. Thus, method descriptions can be compared unbiased.

In this contribution the genome approach is used to model descriptions of design methods. Automated pattern recognition allows distilling them to only five reoccurring method modules. These modules represent the petridish of methodical problem solving procedures. That allows a flexible combination of the modules and therefore a flexible and adaptable problem solving.

Detailed knowledge about those five method modules and possible combinations can make a major impact on design teaching, design practice and design research. See Figure 12.

In the area of design research this knowledge will help authors to describe their methods more transparent and structured. By this means, methods become more flexible and adaptable to the current design problem, what will raise the acceptance of methodical working in design practise.

In the long term, these findings can also impact the way of design teaching. Instead of teaching rigid method descriptions, with a certain number of steps that have to be accomplished, these five modules can be taught in greater detail. Thus the students learn how to solve problems flexible but still methodically and not specific methods for specific problems.

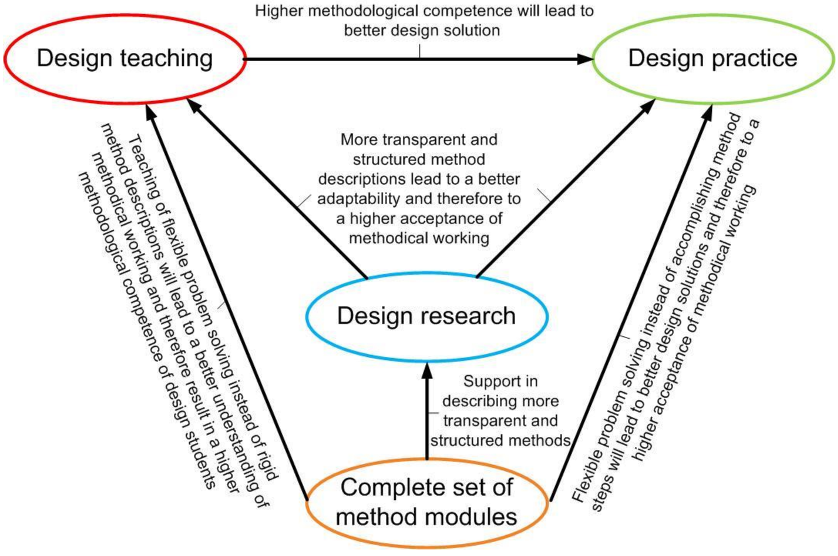


Figure 12: Impact of the identified results on design research, design teaching and design practice

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