

Application of a Genetic Approach to the Formation of Object Characteristics in Project Products

Sergiy Rudenko^{1,†}, Tetiana Kovtun^{1,*†}, Tetiana Smokova^{1,*†}, Iryna Finohenova^{1,†} and Dmytro Kovtun^{1,†}

¹ Odesa National Maritime University, Mechnikova str. 34, Odesa, 65000, Ukraine

Abstract

The modern development of the theory and practice in management, including project management, is characterized by a tendency to converge various methodologies and approaches. Approaches typical of the natural sciences, in particular genetics, have recently been actively used in project management. The genetic approach, combined with the systemic and process approaches, considers a project as an open, dynamically developing system at the supra-biological level of an organization. The genetic approach is based on the use of genetics principles and methods in project management and allows you to build a genetic model of the project. The genetic model of project products, which is created during the project initialization process, contains information about the characteristics of project products. The genetic model project products consist of object, technological, and financial chromosomes of project products. The article discusses the process of forming the object chromosomes of project products. There are connections between the object chromosomes of products that reflect the peculiarities of the formation product parameters. Taking these features into account during the initialization process allows you to increase project efficiency, which is measured by the discounted payback period as an element of the phenotype, which is also reflected in the genetic model of the project.

Keywords

genetic approach, genetic model, project products, project object chromosomes

1. Introduction

The genetic approach to project management is actively used by researchers within the paradigm of convergence of approaches, which has been determining the direction of development in project management methodology in recent years.

Genetic algorithms are most often used as a heuristic mechanism for finding an optimal solution, similar to the selection processes in nature. Genetic algorithms are used to study various aspects of project activities. It is proposed to use genetic algorithms in the process

Woodstock'22: Symposium on the irreproducible science, June 07–11, 2022, Woodstock, NY

* You should use this document as the template for preparing your publication. We recommend using the latest version of the CEURART style.

* Corresponding author.

† These authors contributed equally.

✉ rudsv@i.ua (S. Rudenko); teta.kovtun@gmail.com (T. Kovtun); smokova.tm@gmail.com (T. Smokova); irina.finogenova@ukr.net (I. Finohenova); mail.dmitrij.kovtun@gmail.com (D. Kovtun)

📄 0000-0002-1671-605X (S. Rudenko); 0000-0002-5410-4783 (T. Kovtun); 0000-0002-0688-5677

(T. Smokova); 📄 0000-0001-9409-6135 (I. Finohenova); 0000-0003-3443-2 (D. Kovtun)



© 2023 Copyright for this paper by its authors. Use permitted under Creative Commons License Attribution 4.0 International (CC BY 4.0).

of evaluating project performance in [1]. The problem of finding a compromise between the cost and time in project completion under uncertain conditions is solved using genetic algorithms in [2]. Project risks are investigated using genetic algorithms in [3]. The issue of project task planning and resource allocation in projects using genetic algorithms is addressed in [4]. Genetic algorithms are also used in optimization problems of transport enterprise's operational activity [5,6]. All of the above works are distinguished by the use of the mathematical apparatus of genetic algorithms to model and solve the project's management topical issues.

The use of genetic approach tools is also considered by researchers at the conceptual level. An important area in the genetic approach is the application of biological analogies to projects, which allows us to view broader project management. The basic concepts of genetics are transformed into project management methodology in work [7]. The genetic code of the project is formed as a tool for navigating its life path [8]. A benchmarking model based on genetic mechanisms in project management was created in [9]. Paper [10] proposes a genome methodologies model for managing projects, programs, and portfolios of organizational projects. Thus, the application of the genetic approach to project management has a different focus and can significantly enrich the project management methodology with new models and methods.

2. Structure of the genetic model created in the process of project initialization

At the initial stage of project development, in the process of its initialization, a project prototype is created, which displays the future project's main characteristics.

The genetic approach considers initialization as a process that results in the synthesis of the project product's genetic model [11]. As a result, multiple parameters of project products are formed, the information about which is localized in the gene's form in product chromosomes, which are characterized by the following features.

Object chromosomes consist of genes characterizing specific features in products as consumptive objects.

Technological chromosomes contain genes reflecting the peculiarities of product technologies.

Financial chromosomes include genes containing information about the project's financing specifics at various stages of the life cycle [12].

To create a product's genetic model, we need information not only about the expected genotype of the project but also about its corresponding phenotype. It is proposed to use such criteria of project efficiency as discounted payback period, capital gain, and project financing costs as phenes [10].

Based on the above, the formation of a genetic model products in the initialization process includes three stages, which synthesize chromosomes containing information about certain aspects of products (Fig. 1).

As a result, the product parameters genes are selected, which are internal input data for making management decisions at the next stage of the initialization process, and also serve as a basis for carrying out the process of planning the project products resource supply.

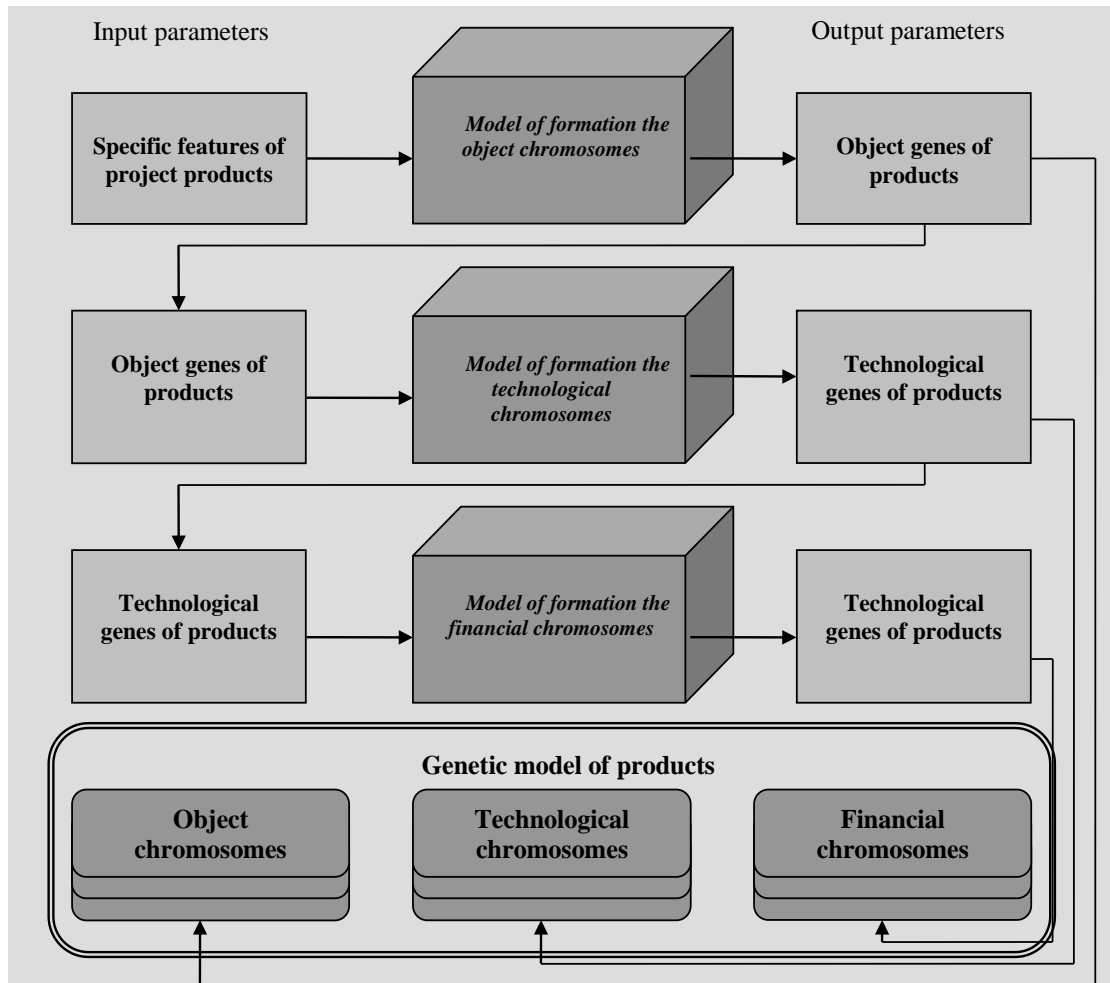


Figure 1: Model system for initialization of product's project parameters.

The project's product parameter formation sets are carried out by implementing a system of initialization process models. Each model is characterized by the corresponding phenotype element – phen (target function), the genome constituent elements – genes (control parameters) and contains constraints that reflect the possibility of entering into the project gene pool for this or that allele gene. The gene pool forms the area of project products' external parameters, which includes genes that have the potential to take part in selection.

3. Object parameters formation of project products

The first step in the initialization process is the formation of the project product parameters, reflecting their specific features as objects of consumption. Each product has certain characteristics, the identification of which is a prerequisite for further initialization stages. All project products are interrelated and interdependent. Looking at the goal-setting process, the sequence formation genes of product parameters have a direction opposite to the temporal aspect for their obtaining, since the product parameters of the previous phase are determined by the product requirements formed at the subsequent phase. In other

words, the technical and operational features of the product of the investment phase - a vehicle purchased during the investment phase - depend on what set of characteristics the product of the operational phase has - the transport service that the enterprise intends to provide to consumers. Similarly, the basic parameters of the pre-investment phase product - a documented project - are formed depending on the characteristics of the vehicle. Thus, the initialization of the genome fragment containing genes localized in the object chromosomes in project products is carried out in the sequence shown in Fig. 2.

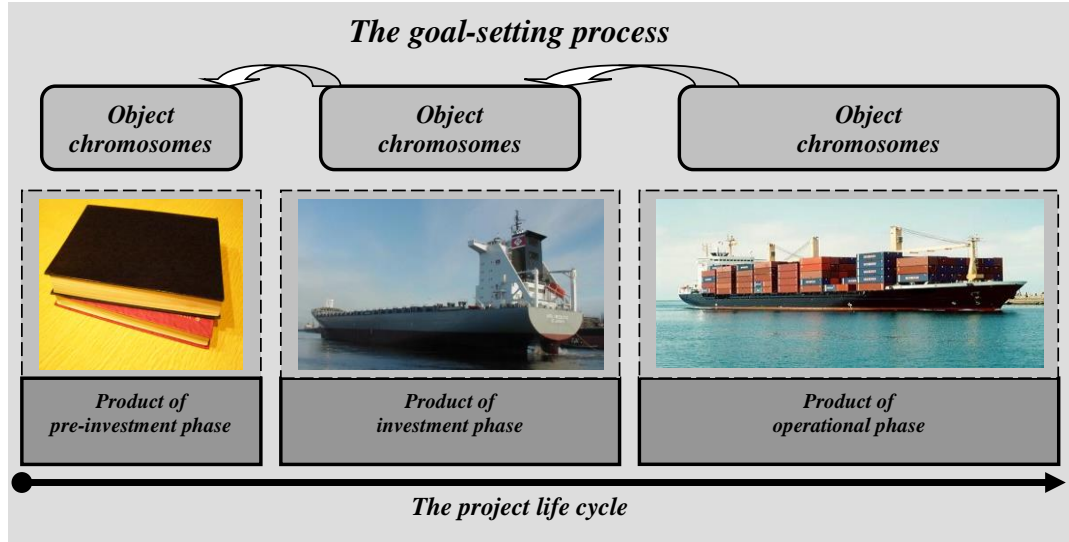


Figure 2: Initializing object parameters of project products.

The next stage in the project product parameters formation is specification, which consists of determining the indicators for assessing the product's attractiveness and creating their multilevel neural network structure, which allows to identify clusters from the set of each product chromosome clusters, that satisfy the project objectives to the greatest extent.

4. A model for the formation of object chromosomes

In object chromosomes of products, the genes characterizing the product essence are localized.

Genes formation set - a set of parameter values $X_j^i = \{x_1^i; x_2^i; \dots; x_j^i; \dots; x_J^i\}$,

where $(i = \overline{1, I})$ - project products, $(j = \overline{1, J})$ - parameters of products, is a heuristic operation. For each product, it is necessary to form a set of parameter genes reflecting its specificity. Object features of products determine their economic parameters and can be both quantitative values and qualitative characteristics. Depending on the belonging of the parameter to the corresponding group, the scaling rule and the method of determining the parameter similarity are selected. If at the initial stage of initialization it is possible to express the characteristic value in quantitative values, the scale of absolute values is used as an evaluation scale. Otherwise, a qualitative scale of relative values is used.

Allele genes allocation in the product's objective parameters allows grouping them into chromosomal clusters characterized by a set of certain traits close values. At the same time, the descriptive model should contain information both about whether or not each cluster is characterized by certain qualitative traits and about possible ranges of trait values that have a quantitative expression for each chromosome cluster.

The clustering problem solution consists of partitioning the space of gene values product parameters $D_k^i \left(k = \overline{1, K^i} \right)$, corresponding to specific chromosomal clusters. The specified separation should be performed in such a way as to ensure the minimum value of errors in attributing products to "unfamiliar" clusters. The result of such an operation is the belonging identification of the product having object genes set parameters $X_j^i \left(j = \overline{1, J^i} \right)$, that correspond to allelic genes $X_{jm}^i \left(m = \overline{1, M^j} \right)$, to the chromosome cluster D_k^i .

Thus, the use of evaluation scales allows chromosome selection containing close-in values and alternative variants of object parameter genes in future project products. The product represented by a chromosome containing n parameter genes should be considered as a point in n -dimensional space.

The decomposition of the product characteristic space is performed using separating hyperplanes. A set of hyperplanes divides the space into several sets, that contain vector chromosomes with a similar gene characteristics set. Thus, chromosomal clustering of project products is performed.

The next initialization stage of project products is genome codification, which includes the creation of object gene structural models. Codification includes the following operations:

1. selection of ways to determine the similarity between allele genes;
2. code structure creation of chromosomal clusters matrix.

The project product's structural models contain encoded information reflecting the features of the product's chromosome clusters defined by descriptive models at the previous stage. The choice of the scale of evaluation in product object parameters justifies the rule of determining the similarity measure, reflecting the degree of correspondence of the parameter of the alternative product variant to the values of this parameter characteristic of the representatives in certain clusters. For the features expressed quantitatively, the similarity measure can be not the value of the parameter value, but the fact of falling into a certain interval containing the parameter values of the cluster representatives. If the product characteristic is expressed only qualitatively using a scale of relative values, the similarity measure is determined by the presence or absence of this parameter value in the alternative product variant.

Formalizing a similarity measure ω_{jmk}^i of a product having allelic values of the target genes $X_{jm}^i \left(j = \overline{1, J^i} \right)$, $\left(m = \overline{1, M^j} \right)$, chromosome cluster $D_k^i \left(k = \overline{1, K^i} \right)$, is possible through the use of Boolean relations between allele genes contained in the object

chromosome of the alternative product variant and allele genes in the product chromosome cluster. The operation result is a matrix of genes chromosome clusters in the project product (Table 1).

Table 1

The gen matrix of chromosome clusters in project product

Chromosomal clusters	Object chromosome																					
	x_1^i			...			x_j^i			...			$x_{j^i}^i$									
	Allelic genes			Allelic genes			Allelic genes			Allelic genes												
	x_{11}^i	x_{1m}^i	$x_{1M^1}^i$	x_{j1}^i	x_{jm}^i	$x_{jM^j}^i$	$x_{j^i 1}^i$	$x_{j^i m}^i$	$x_{j^i M^j}^i$	$x_{j^i 1}^i$	$x_{j^i m}^i$	$x_{j^i M^j}^i$										
D_1^i	1	...	0	...	0	0	...	1	...	0	0	...	0	...	1	
...
D_k^i	0	...	1	...	0	0	...	1	...	0	1	...	0	...	0	
...
$D_{K^i}^i$	0	...	0	...	1	1	...	0	...	0	0	...	1	...	0	

In the table, the similarity measure ω_{jmk}^i of the allele gene x_{jm}^i value of the alternative variant of the i -th product to the value of this gene x_{jk}^i inherent in the cluster D_k^i is expressed by Boolean variables, where

$$\omega_{jmk}^i = \begin{cases} 1, & x_{jm}^i \in \{x_{jk}^i\}, \\ 0, & x_{jm}^i \notin \{x_{jk}^i\}. \end{cases} \quad (1)$$

Thus, the process formalization to distribute the alternative product variants into clusters is characterized by the construction of structural models reflecting the object genes correspondence in product parameters to a certain chromosomal cluster, and allowing the clustering of products based on their structural genetic code. The next stage in the initialization process of the project product parameters is their specification, which includes:

1. formalization of evaluation indicators the products of the project phases and the project as a whole;
2. building a multilevel neural network structure of project products.

Each chromosomal product cluster has its distinctive features, which are reflected in the indicator assessing value and the compliance of this product with the project goal. Products in different phases of the project have certain specificity, which is why their evaluation indicators differ significantly. Since the project product formation parameters have an inverse direction compared to the process of obtaining these products, the formalization of evaluation indicators should take place as they are identified. For example, at the synthesis stage of transport service object chromosomes, the value of the cash flow income component in the operational phase of the project is forecasted - the cash inflow from the provision of transport service, which depends on the value of forecasted revenues. In the modeling process the object chromosomes of the vehicle, the cost characteristics of both the investment phase - the cost of the vehicle and the costs associated with its acquisition, and the operational phase - depreciation charges, operating costs are determined, since they directly depend on the technical and operational characteristics of the vehicle. The indicator for assessing the costs of project documentation development is the cash outflow, which includes management costs for the creation of a documented project.

The initialization model of product object parameters takes a discounted payback period as an indicator of the project performance as a whole as an integrated indicator that takes into account the effectiveness of the project management process at each phase of the life cycle.

Since the predicted values modeling of income and cash flow expense components is carried out at the initial stage of project development, it is practically impossible to determine their exact values. Therefore, their approximate values are used in the model, which makes it possible to consider the forecast values of future cash flows as conditionally constant values. This, in turn, allows us to calculate the discounted payback period of the project according to the formula:

$$DPP = \log_q \left[1 - \frac{I_0(1-q)}{CF_k \cdot q} \right], \quad (2)$$

Since the discounted payback period corresponds to the point in time when the *Net Present Value* (NPV) of the project becomes zero, it is easy to derive the value from the equation:

$$-I_0 + \sum_{i=1}^T CF_i \times q^i = 0,$$

where $q = \frac{1}{1+r}$ - discount factor,
 r - discount rate.

We'll get it $\sum_{i=1}^T CF_i \cdot q^i = I_0$.

It follows $CF_i = const$ from the assumption that $CF_k \cdot \sum_{i=1}^T q^i = I_0$.

$$\sum_{i=1}^T q^i = \frac{q(1-q^T)}{1-q}$$

Then according to the formula

$$\frac{q(1-q^T)}{1-q} = \frac{I_0}{CF_k}, \quad CF_k \cdot q(1-q^T) = I_0(1-q)$$

if

$$1-q^T = \frac{I_0(1-q)}{CF_k \cdot q}, \quad q^T = 1 - \frac{I_0(1-q)}{CF_k \cdot q}$$

Then $DPP = T = \log_q \left[1 - \frac{I_0(1-q)}{CF_k \cdot q} \right]$, under the conditions of $1 - \frac{I_0(1-q)}{CF_k \cdot q} > 0, q > 0$.

Thus, it is possible to evaluate the success of choosing an alternative project product variant not only with the help of a local evaluation criterion but also from the perspective of the product variant's contribution to the overall project performance expressed by the discounted payback period.

The set of operations performed is a preparatory stage for the creation of a multilevel project product neural network structure, the building process which is a sequence of the following actions:

1. formation of the alternative chromosome variants of clusters in project products by network levels;
2. identification of interrelationships between elements on different levels;
3. determining the threshold values of product evaluation indicators.

According to the artificial intelligence theory, the hierarchical levels in the neural network are sets of neurons, whose bodies in the case of fulfillment of the product specification in project phases, are alternative variants of product chromosomal clusters (Fig. 3).

There are connections between the levels of a neural network, which, by analogy with a biological neuron, are represented as dendrites (incoming information) and axons (outgoing information). Axons of one level are dendrites for another. Under deterministic conditions, connections are established only between those neurons (clusters) between which there is a correspondence of allele object genes.

To move to the next level of the neural network, it is not enough only to establish connections between neurons, it is also necessary to carry out a comparative value analysis of the estimated cluster parameter on a given level with some threshold value. Such comparison shows, by analogy with the signal strength in biological and artificial neural networks, the power level of the cluster potential expressed in the estimated value

parameter and allowing to judge the possibility of transition to the network's next level. The presence of threshold values allows to reduce the number of alternative product variants involved in further selection.

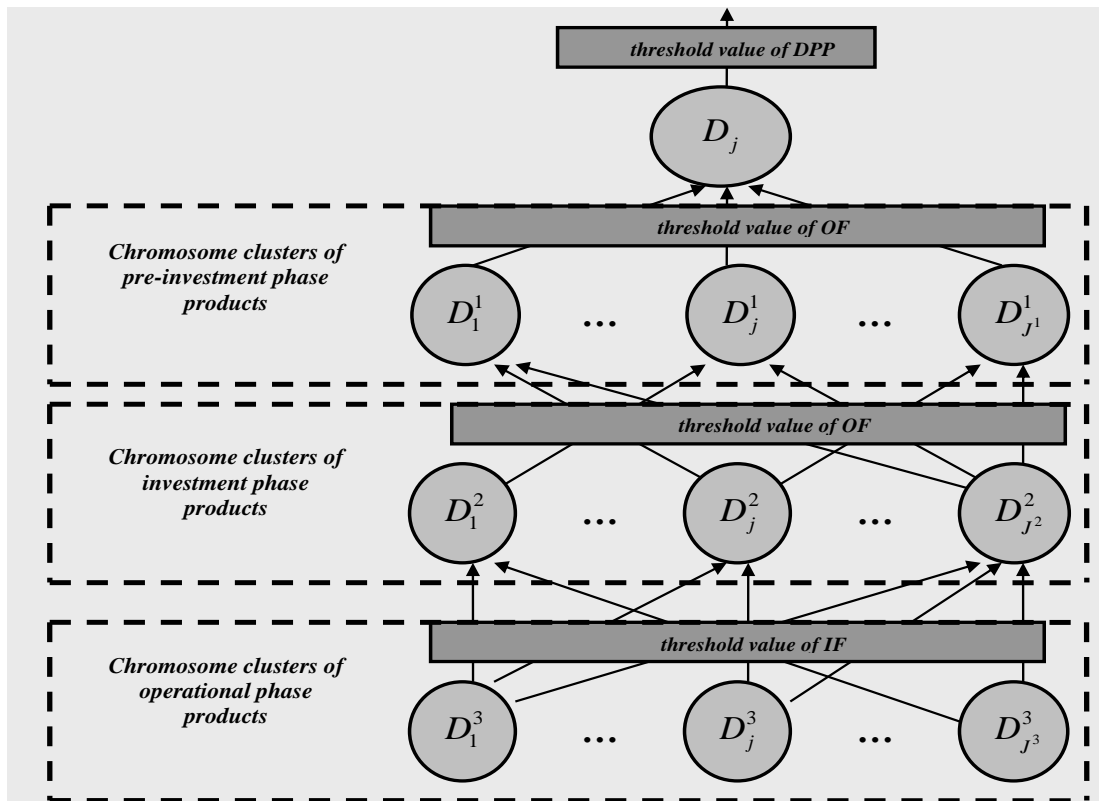


Figure 3: Model of multilevel neural network structure project products.

Thus, the preparatory stage to the real product alternatives selection in project phases, consisting of the formation of a multi-level neural network structure in project products, is represented as sequential procedure blocks (Fig. 4).

Initialization of the actual project products consists of selecting alternative product variants belonging to such a cluster, which is related to the previously defined product cluster of the previous level in a hierarchical neural network.

Acknowledgements

The proposed model of object parameters initialization in project products, which includes identification, codification, and specification stages resulting in descriptive, structural models and neural network structure, allows the identification of interrelationships between alternative product variants on different project phases belonging to certain chromosomal product clusters and reflects the prioritization of project phase results in the goal-setting process.

As a result of these procedures, selective project product genes are selected from the project gene pool, which is not only a component of the project genome localized in object product chromosomes but also participates as input parameters in the following models of the initialization process.

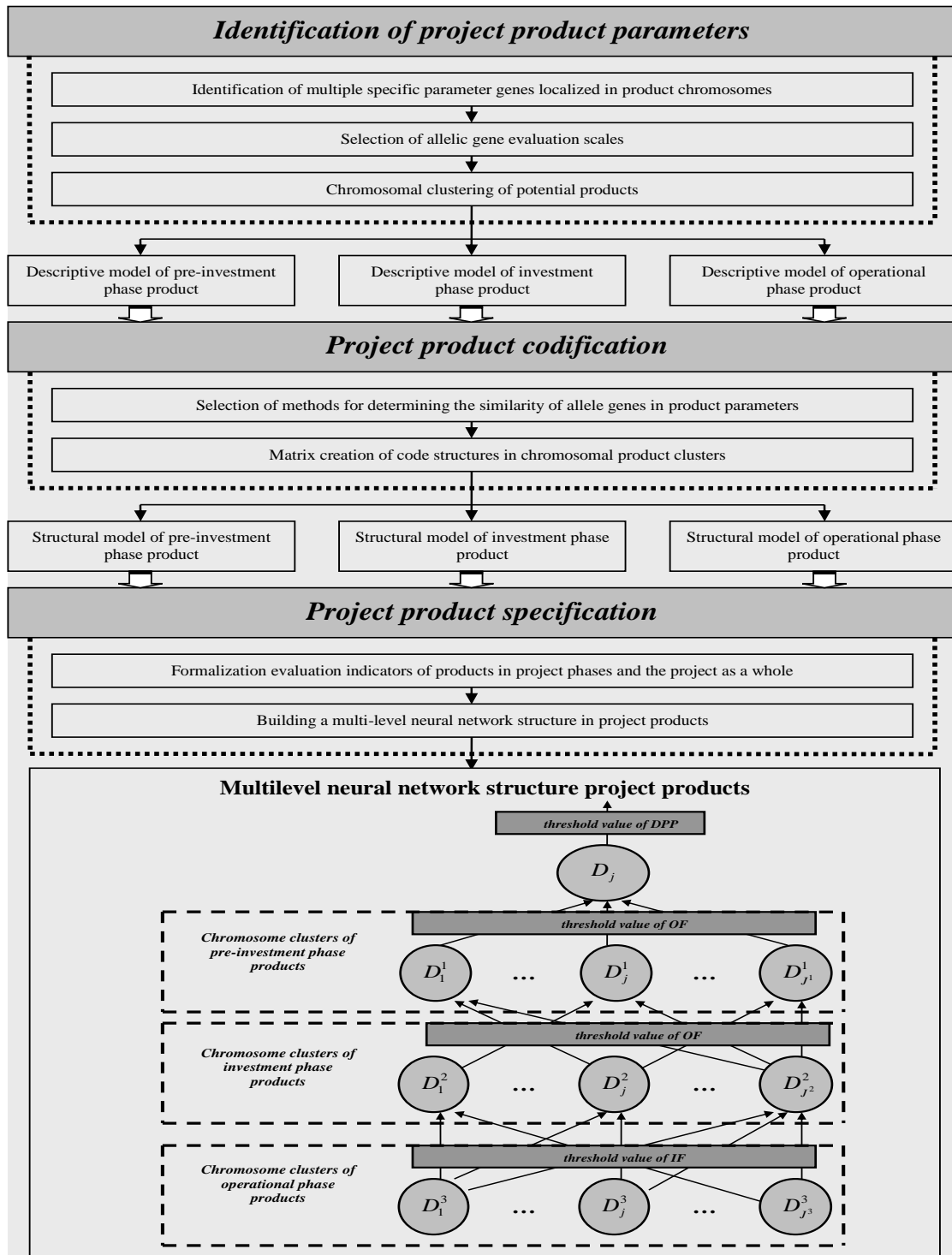


Figure 4: The sequence of creating a neural network of project products. Selective object-based parameter genes serve as inputs for selecting product technologies. The data obtained from modeling under deterministic conditions guide modeling under fuzzy conditions. At the final stage of initialization, the partial utility of the discounted payback period, which affects the utility of the entire project, is determined.

References

- [1] Min-Yuan Cheng, Yu-Wei Wu, Ching-Fang Wu, Project success prediction using an evolutionary support vector machine inference model, *Automation in Construction*, Volume 19, Issue 3, May 2010, pp. 302-307. doi.org/10.1016/j.autcon.2009.12.003.
- [2] H. Ke, A genetic algorithm-based optimizing approach for project time-cost trade-off with uncertain measure, *J. Uncertain. Anal. Appl.* 2, 8 (2014). doi.org/10.1186/2195-5468-2-8.
- [3] F. Reyes, N. Cerpa, A. CandiaVéjar, M. Bardeen, The optimization of success probability for software projects using genetic algorithms *Journal of Systems and Software* Volume 84, Issue 5, May (2011), 775-785.
- [4] C.K. Chang, M.J. Christensen, and T. Zhang, Genetic Algorithms for Project Management. *Annals of Software Engineering* 11, 107-139, 2001. doi.org/10.1023/A:1012543203763.
- [5] V.V. Romanuke, A.Y. Romanov, and M.O. Malaksiano, A Crossover Operators in a Genetic Algorithm for Maritime Cargo Delivery Optimization. *Journal of ETA Maritime Scienc.* 10(4) (2022) 223-236. doi.org/10.4274/jems.2022.80958.
- [6] V.V. Romanuke, A.Y. Romanov, and M.O. Malaksiano, Pseudorandom number generator influence on the genetic algorithm performance to minimize maritime cargo delivery route length. *Pomorstvo*, 36(2) (2022) 249-262. doi.org/10.31217/p.
- [7] I. A. Babaev, Innovatsiina tekhnologii v upravlinnia programmi rozvytku organizatsii na osnovnoi genetichnoi modeli proekt [Innovative technology in the management of programs for the development of organizations on the basis of the genetic model of the project]. Dis. for the acquisition of sciences. Doctor of Engineering. Sci.: Spec. 05.13.22 "Management. project. and progr", Kyiv, 2006, P. 41.
- [8] I.A. Babaev, S. D. Bushuev, and N. S. Bushueva, Formation of the genetic code of the project as a tool for navigation along its life path, *Project management and development of production*, 2 (2005), pp. 5-11.
- [9] S. D. Bushuev, D.A. Bushuev, N. S. Bushueva N.S., and Chernova L.S, Benchmarking model based on genetic mechanisms in project management *Management of development of complex systems*, 36 (2018), 12-20.
- [10] S. D. Bushuev, D.A. Bushuev, V.B. Rogozina, and O.V. Mikhieieva, Convergence of knowledge in project management. *Proceedings of the 2015 IEEE 8th International Conference on Intelligent Data Acquisition and Advanced Computing Systems: Technology and Applications, IDAACS 2015*, pp. 231-243.
- [11] S. Rudenko, T. Kovtun, T. Smokova, and F. Iryna, The genetic approach application and creation of the project genetic model. *International Scientific and Technical Conference on Computer Sciences and Information Technologies, 2022-November, 2022*, 434-437.
- [12] S. Rudenko, T. Kovtun, V. Smrkovska, T. Smokova, D. Kovtun, and I. Finohenova, Application of the genetic approach in the process of initiating a transportation services projInternational Scientific and Technical Conference on Computer Sciences and Information Technologies, 10-12 November 2022. doi: 10.1109/CSIT56902.2022.10000822.