

Structural Theory of Elastoplastic Material Models

Petr A. Belov¹ and Natalia Ya. Golovina²

1. Institute of Applied Mechanics, Russian Academy of Sciences, Moscow 125040, Russia

2. Tyumen Industrial University (TIU), Surgut Branch, Surgut 628400, Tyumen Region, Russia

Abstract: This paper presents the second stage of a research program on the genetics of elastoplastic materials. The first article in the series introduced a genetic interpretation of the functional space spanned by the fundamental solutions of the constitutive differential equation governing a material model. In the present paper, the emphasis shifts from the terminology of genes, chromosomes, and phenotypes to a structural theory of elastoplastic material models. The central thesis is that the primary object of structural classification is not the observable deformation curve itself, but the ordinary differential equation governing the material model and the hereditary mathematical information encoded in that equation, from which the curve emerges as a phenotypic realization. The paper distinguishes between a phenotypic description, based on observable deformation curves, and a genotypic description, based on the smoothness class, characteristic spectrum, gene space, and governing ODE (Ordinary Differential Equation) of the material model. Accordingly, the direct and inverse problems of materials genetics are reformulated. The direct problem is interpreted as the transition from the governing ODE of the material model to the observable deformation curve. The inverse problem is shown to have a two-level structure: spectral identification reconstructs the gene basis from the observed phenotype, whereas genotypic identification recovers the governing ODE of the material model from the smoothness class and the identified spectral structure. This distinction establishes a theoretical bridge between the published foundations of materials genetics and subsequent studies of canonical representation, analogical DNA portraits of materials, operator identification, computational spectral modules, and libraries of material genomes.

Key words: Materials genetics, structural theory, elastoplastic material model, deformation curve, governing ODE of the material model, gene space, phenotype, genotype, inverse problem, spectral identification, genotypic identification.

1. Introduction

Classical constitutive descriptions in mechanics of materials are commonly organized around an observable deformation curve [1-3]. Within this framework, the stress-strain curve is treated as the principal object of approximation, comparison, and classification. This approach is natural from both experimental and engineering perspectives. Nevertheless, it leaves open a deeper structural question: is the curve itself the object of classification, or is it merely the phenotypic manifestation of a more fundamental generating structure?

The first article in this series introduced the mathematical language of materials genetics [4]. In that work, the space of fundamental solutions of the governing ODE (Ordinary Differential Equation) of the

material model was interpreted as the gene space of the model. Its generally non-orthonormal basis elements were denoted by $g_i(\varepsilon)$ and termed genes. An orthonormal basis of the same space was denoted by $h_i(\varepsilon)$ and termed the chromosome basis. The coefficients f_i and F_i in the corresponding stress expansions were interpreted as gene and chromosome phenotypic coefficients. The concepts of an allele, a canonical chromosome, and a DNA portrait of a material were also introduced. The terminology of materials genetics is introduced by analogy with biological genetics. In particular, the term *DNA portrait of a material* does not refer to deoxyribonucleic acid itself. Rather, it denotes an abstract information structure introduced by analogy with biological DNA, whose role is to encode, preserve, and transmit

Corresponding author: Petr A. Belov, D.Sc., Chief Research Scientist, Institute of Applied Mechanics, Russian Academy of Sciences, research fields: mechanics of materials, constitutive modeling, inverse problems, materials genetics.

structural information about a material. The present paper adopts these definitions as an established conceptual foundation and does not repeat their derivation.

For completeness, the principal terms are briefly recalled. The genome, or genotypic structure of a model, is associated not with an individual experimental curve, but with the governing ODE of the material model and the space of fundamental solutions generated by that equation. A gene g_i is a basis element of the solution space associated with the constitutive differential operator. The gene space is the functional space of fundamental solutions of the corresponding ODE, and its natural basis is generally non-orthonormal. A chromosome h_i is an element of an orthonormal basis of the same gene space, obtained after a scalar product has been specified and the original gene basis has been orthogonalized. The phenotypic coefficients f_i and F_i provide coordinate representations of a particular deformation curve in the gene and chromosome bases, respectively. Thus, the observed curve is a phenotypic realization within the space defined by the governing ODE of the material model. In the present paper, genetic terminology denotes mathematical objects of a variational-spectral model and is not intended to imply biological mechanisms.

The proposed terminology is unrelated to genetic algorithms or biological evolution. It is introduced exclusively as a mathematical language for describing operator-generated functional structures.

The proposed terminology should not be regarded merely as a linguistic metaphor. Rather, it establishes a structure-preserving correspondence (a structural isomorphism) between two systems of relationships. In the present theory, genes correspond to the fundamental solutions of the governing ODE of the material model, chromosomes correspond to an orthonormal basis of the same functional space, the genotype corresponds to the operator-generated hereditary mathematical structure, and the phenotype corresponds to its observable realization. The

biological vocabulary is introduced because it faithfully reflects this mathematical correspondence and provides a compact language for describing the hierarchy of structural objects.

The present paper extends the theoretical framework established in the first article of the series. Rather than revisiting the genetic terminology, it uses that terminology as a established foundation. Its main purpose is to show that structural classification should be transferred from observable deformation curves to the governing ODEs of material models and the hereditary mathematical structures generated by those equations.

2. Phenotypic Paradigm of Material Description

2.1 Existing Empirical Models

The phenotypic description has historically been the earliest and remains the most widely used representation of material response. Within this paradigm, the experimentally observed deformation curve is treated as the principal object of approximation. The constitutive model is then required to reproduce, with the required engineering accuracy, the function

$$\sigma = \sigma(\varepsilon), \quad (1)$$

or one of its local branches.

A broad class of empirical and semi-empirical models follows this approach. Some describe the elastic region, the transition to yielding, hardening, or the limiting stage by separate analytical expressions. Others employ multistage descriptions in which different strain intervals are fitted by different formulae. Spline and piecewise-polynomial representations develop the same idea in a more flexible mathematical form: the curve is divided into segments, each of which is represented by a local approximation satisfying prescribed continuity conditions [5-7].

Such descriptions are effective when accurate reproduction of the curve is the primary objective. They make it possible to approximate experimental data, interpolate between measured points, compare the

responses of different materials, and construct engineering diagrams for subsequent calculations. From this viewpoint, the phenotypic paradigm is indispensable: the deformation curve is the directly observable object, and any structural theory must ultimately return to it.

Accurate reproduction of a curve, however, should not be confused with identification of the structure that generates it. A curve may be approximated with high accuracy without revealing the governing ODE of the material model, its smoothness class, its characteristic spectrum, or the functional space of fundamental solutions that defines the admissible family of responses. Phenotypic models therefore describe what is observed, but they do not necessarily reveal why a particular family of curves is admissible for the selected material model.

2.2 Limitations of the Phenotypic Description

The first limitation of the phenotypic paradigm is the nonuniqueness of representation. The same experimental deformation curve can often be reproduced by different analytical models. A power law, an exponential expression, a rational approximation, a spline representation, or a multistage empirical formula may all provide acceptable numerical accuracy over the same strain interval. At the level of the observable curve, these models may therefore appear equivalent even though their internal mathematical structures differ.

The second limitation is the converse aspect of the same difficulty. The same empirical model can be applied to physically different materials. Its parameters vary from one material to another, whereas its analytical form often remains unchanged. Thus, a model may be useful as an approximation tool without necessarily defining a structural classification of materials. Materials governed by different internal mechanisms may be assigned to the same phenotypic family merely because their observable curves are well approximated by similar functions.

A third limitation concerns the status of model parameters. In a purely phenotypic description, parameters are often introduced as fitting constants. They improve agreement between an analytical curve and experimental data but do not necessarily correspond to invariant structural objects. In particular, such parameters may depend on the selected approximation class, fitting interval, segmentation procedure, or data normalization. Consequently, they cannot always be interpreted as stable characteristics of a material.

A fourth limitation is the absence of a canonical internal space. A deformation curve is a visible trajectory in the (ε, σ) plane. By itself, it does not specify the functional space in which it should be represented. It does not determine whether the admissible functions arise from a second-, fourth-, sixth-, or higher-order ODE. Nor does it determine whether the corresponding basis is natural, orthonormal, real, generated by complex roots, degenerate, or mixed. The observed curve therefore contains phenotypic information, whereas the genotypic architecture that generates this information remains hidden.

These limitations show that the phenotypic paradigm classifies visible realizations rather than generating mechanisms. It compares curves, fitting parameters, stages, and local approximations, but it does not necessarily identify the governing ODE of the material model that determines the admissible family of fundamental solutions. A transition to structural theory is therefore required.

2.3 Motivation for the Structural Transition

The structural transition does not reject phenotypic data. On the contrary, the phenotype remains the only directly observable object and therefore provides the starting point for identification. It is no longer regarded, however, as the final object of classification. Instead, the observed curve becomes the input to a deeper chain:

$$\sigma(\varepsilon) \rightarrow \{f_i, F_i\} \rightarrow \mathcal{G} \rightarrow \{g_i\} \rightarrow \mathcal{L}. \quad (2)$$

This chain captures the central methodological shift

of the present paper. The deformation curve is interpreted as a phenotypic realization of a genotypic architecture. The task of structural theory is therefore to move beyond phenotypic fitting and identify the architecture that generates the phenotype. The mathematical objects in this chain are defined in Eqs. (3)-(7).

In the adopted terminology, stress on a segment can be represented in the gene basis:

$$\sigma(\varepsilon) = \sum_{i=1}^n f_i g_i(\varepsilon), \quad (3)$$

where $g_i(\varepsilon)$ are genes, that is, basis elements of the functional space of fundamental solutions of the corresponding ODE, and f_i are gene phenotypic coefficients. The gene space is defined as

$$\mathcal{G} = \text{span}\{g_1(\varepsilon), \dots, g_n(\varepsilon)\}. \quad (4)$$

The natural gene basis is generally non-orthonormal. To obtain an orthonormal representation, a scalar product is introduced in $\mathcal{G}$. On a segment $[\varepsilon_a, \varepsilon_b]$, it may be written, for example, as

$$\langle u, v \rangle_{\mathcal{G}} = \int_{\varepsilon_a}^{\varepsilon_b} u(\varepsilon)v(\varepsilon)w(\varepsilon) d\varepsilon, \quad w(\varepsilon) > 0, \quad (5)$$

where $w(\varepsilon)$ is a positive weight function. Once the scalar product has been specified, the Gram-Schmidt procedure transforms the initial gene basis into an orthonormal basis of the same space. Its elements are termed chromosomes:

$$\langle h_i, h_j \rangle_{\mathcal{G}} = \delta_{ij}, \quad h_i \in \mathcal{G}. \quad (6)$$

In the chromosome basis, the same stress field is written as

$$\sigma(\varepsilon) = \sum_{i=1}^n F_i h_i(\varepsilon), \quad (7)$$

where F_i are chromosome phenotypic coefficients. These two expansions describe the same observable stress field but provide different coordinate representations of the same gene space $\mathcal{G}$.

This distinction is fundamental. The visible curve is not the primary structural object; it is a realization

obtained through coefficients in a functional space. At a deeper level lies the space $\mathcal{G}$, and deeper still lies the governing ODE of the material model that generates it. Structural classification must therefore be transferred from the curve itself to the operator-generated architecture underlying that curve.

2.4 From Classification of Curves to Genotypic Classification

The phenotypic paradigm may be characterized as classification by curves. It asks whether the deformation curves, hardening stages, yield plateaus, changes in curvature, or fitting parameters of two materials are similar. This approach is useful but incomplete, because similarity of phenotypes does not imply identity of genotypes.

The genotypic paradigm asks a different question. It asks whether two models are generated by structurally equivalent ODEs, whether those ODEs possess the same smoothness class, whether their characteristic spectra have the same organization, and whether their gene spaces admit equivalent basis architectures. Within this formulation, two materials may have different visible curves and nevertheless belong to the same genotypic class if their generating structures are equivalent. Conversely, two materials may have visually similar curves but belong to different genotypic classes if the ODEs and gene spaces generating those curves are structurally different.

Thus, the transition from a phenotypic to a genotypic description is not merely a change in terminology; it changes the object of classification itself. The deformation curve remains the observable phenotype, whereas the genotypic chain becomes the structural object to be identified:

governing ODE of the material model $\rightarrow P(\mu)$

$$\begin{aligned} &\rightarrow \{\mu_i\} \rightarrow \{g_i\} \rightarrow \{h_i\} \\ &\rightarrow \{f_i, F_i\} \rightarrow \sigma(\varepsilon). \end{aligned} \quad (8)$$

Here, $P(\mu)$ is the characteristic polynomial, μ_i are the characteristic roots, g_i are the genes, h_i are the chromosomes, and f_i, F_i are the phenotypic

coefficients in the corresponding bases.

The conclusion of this section is clear: a theory confined to $\sigma(\varepsilon)$ is a theory of phenotypic realizations. A structural theory of material models must identify the ODE-generated architecture underlying those realizations. This observation prepares the formulation of structural equivalence and the transition to a genotypic description.

3. Structural Theory of Elastoplastic Material Models

3.1 Structural Object of Classification

The transition from phenomenological description to structural theory begins with a change in the object of classification. The observed function $\sigma(\varepsilon)$ is no longer treated as the primary structural object. Instead, it is interpreted as a realization belonging to the functional space generated by the governing ODE of the material model.

The preceding analysis shows that the observable deformation curve cannot serve as the sole object of classification. It is the experimentally accessible phenotype of the material response, but by itself it does not determine the mathematical structure that generates that response. A structural object must therefore be identified to replace the curve as the primary object of classification.

Let the material response on a segment be described by a spline of a prescribed smoothness class. In the simplest hierarchy, three levels are naturally distinguished:

$$C^0, \quad C^1, \quad C^2. \quad (9)$$

The class C^0 corresponds to a piecewise-linear spline, C^1 to a cubic spline, and C^2 to a quintic variational spline. Each of these descriptions may reproduce the same experimental curve with high accuracy, including localized features such as a yield tooth. However, the mathematical structures underlying these approximations are different.

The essential point is that each smoothness class is associated with a distinct admissible functional architecture. The smoothness class determines the

order of the corresponding local model, the number of admissible boundary or contact conditions, and the dimension of the space of fundamental solutions. Therefore, transition from C^0 to C^1 or from C^1 to C^2 is not merely an improvement in the visual quality of approximation. It changes the structural type of the model.

For a fixed segment, stress is not identified with a single basis function. It is represented by a linear combination of elements of the gene basis:

$$\sigma(\varepsilon) = \sum_{i=1}^n f_i g_i(\varepsilon), \quad (10)$$

where $g_i(\varepsilon)$ are genes, i.e., elements of a generally non-orthonormal basis of the space of fundamental solutions, and f_i are the corresponding gene phenotypic coefficients. After orthonormalization of the same functional space, the same stress can be written in the chromosome basis:

$$\sigma(\varepsilon) = \sum_{i=1}^n F_i h_i(\varepsilon), \quad (11)$$

where $h_i(\varepsilon)$ are chromosomes and F_i are chromosome phenotypic coefficients.

Hence, a spline curve observed in an experiment is determined not only by the choice of functional space but also by the expansion coefficients on each segment. These coefficients specify the phenotype of the local response. When the coefficients f_i or F_i vary from one segment to another, the shape of the curve changes while the underlying gene space may remain the same. This is why segmentation has a structural meaning: a spline is not a collection of unrelated curves but a sequence of phenotypic realizations belonging to an admissible functional architecture.

This distinction is particularly clear in the description of a yield tooth. A pronounced yield tooth can be approximated by a piecewise-linear C^0 spline with a sufficiently large number of short segments. The same feature can be described by a cubic C^1 spline with fewer segments or by a quintic variational C^2 spline with still fewer segments. In all three cases, the

experimental curve may be reproduced with comparable accuracy. Nevertheless, these approximations correspond to different smoothness classes, different admissible spaces of fundamental solutions, and therefore different structural architectures.

This leads to a fundamental conclusion:

High approximation accuracy is not a criterion of structural equivalence of elastoplastic material models.

Approximation accuracy characterizes the quality with which the observable phenotype is reproduced. Structural equivalence must refer to the generating architecture: the smoothness class, governing ODE of the material model, characteristic spectrum, gene space, and admissible basis structure. Two models may therefore be almost indistinguishable at the level of $\sigma(\varepsilon)$ while belonging to different structural classes.

There is also an important relation between smoothness class and the number of segments required to achieve a prescribed accuracy. For the same experimental curve and the same admissible approximation error, a lower smoothness class usually requires a greater number of segments. A higher smoothness class, by contrast, possesses a richer local functional space and can therefore reproduce the same deformation feature with fewer segments. As a structural principle, this relation can be written as

$$N_{C^0} > N_{C^1} > N_{C^2}, \quad (12)$$

where N_{C^k} denotes the minimum number of segments required to reproduce the given curve with a prescribed accuracy in class C^k .

This relation should not be interpreted as a universal numerical law independent of the data. It expresses a structural principle: lowering the smoothness class transfers complexity from the local functional space to curve segmentation, whereas increasing the smoothness class enriches the local model and reduces the number of segments required to reproduce the same phenotype. The same phenotypic accuracy may therefore be achieved through different distributions of structural complexity.

3.2 Principle of Structural Equivalence

High-fidelity reproduction of an experimental curve does not, by itself, imply that the mathematical structure governing material behavior has been identified. A simple example illustrates this point.

Consider an experimental deformation curve with a pronounced yield tooth. At first glance, such a distinctive feature might appear to imply a unique mathematical model. It does not.

Suppose first that the curve is approximated by a piecewise-linear spline of smoothness class C^0 . Since each segment is a straight-line interval, satisfactory accuracy is attained only with a sufficiently large number of segments. Nevertheless, even a complex feature such as a yield tooth can be reproduced with practically any prescribed accuracy.

Now consider a cubic spline of class C^1 . Owing to the greater flexibility of each segment, the same experimental curve is described by substantially fewer intervals while retaining essentially the same approximation accuracy.

Finally, consider a quintic variational spline of class C^2 . Each segment of this model has still greater approximation capability, and an even smaller number of segments is usually required to reproduce the same curve.

Thus, the same experimental curve may be described almost equally well by models of different smoothness classes. If comparison is restricted to experimental and calculated curves, all three models appear equivalent at the phenomenological level.

A natural question then arises: should these three cases be regarded as instances of the same material model? The answer is no. Despite nearly identical quality in reproducing the experimental curve, the models belong to different smoothness classes and are described by different governing ODEs of the material models. Changing the ODE inevitably changes the characteristic polynomial, the characteristic spectrum, and the space of fundamental solutions. Hence, only the observable result—the deformation curve—coincides, whereas the mathematical mechanism generating it is

different.

This example reveals a fundamental limitation of the phenomenological approach. If only the experimental curve is treated as the object of study, all three models appear equivalent at the phenomenological level. If the mathematical structure of the model becomes the object of study, their differences become fundamental.

The example leads to a conclusion that marks the boundary between phenomenological and structural theories of materials.

Corollary 3.1 (on the impossibility of phenotypic structural classification). Neither the approximation error, nor the analytical form of the deformation curve, nor the numerical values of model parameters can serve as criteria for structural classification of materials.

All these characteristics belong exclusively to the phenotypic level of description. They permit assessment of how accurately the observable curve is reproduced but contain no information about the mathematical structure that generated it.

Consequently, two models may possess practically the same approximation accuracy, similar analytical dependences, and even comparable numerical parameter values, while remaining representatives of different structural classes. Conversely, models belonging to the same structural class may produce different phenotypic manifestations depending on experimental conditions, the strain range, or the parameter-identification procedure.

The transition from phenomenological to structural theory therefore requires a change in the criterion by which models are compared. The comparison must concern not the calculated results but the governing ODEs of the material models, because these determine the smoothness class, characteristic spectrum, space of fundamental solutions, and ultimately the entire mathematical architecture of the model.

For this reason, the object of structural classification is not the experimental deformation curve but the governing ODE of the material model that determines its hereditary architecture.

Principle 3.1 (of structural equivalence). Two material models are structurally equivalent if and only if the spaces of fundamental solutions generated by the governing ODEs of the material models coincide up to a nonsingular change of basis. Coincidence of an individual deformation curve is not a sufficient condition for structural equivalence.

3.3 The Governing ODE as a Carrier of Hereditary Information

Transferring the criterion of structural classification to the level of the governing ODE of the material model requires identifying the mathematical object that must be compared when different models are studied. In phenomenological theory, the observable deformation curve is the object of comparison. In structural theory, the object becomes the mathematical architecture that generates the entire set of admissible solutions.

The central genetic idea can be stated concisely:

The governing ODE of the material model encodes all hereditary mathematical information required to construct the deformation curve.

Within the classical theory of linear ODEs, each governing equation first determines its characteristic polynomial [8-10]

$$P(\mu). \quad (13)$$

The characteristic polynomial defines the characteristic spectrum

$$\{\mu_i\}, \quad (14)$$

which in turn determines the system of fundamental solutions, i.e., the system of genes:

$$\{g_i(\varepsilon)\}. \quad (15)$$

Thus, a natural causal chain exists between the governing ODE of the material model and the observable deformation curve:

$$\begin{aligned} \text{governing ODE of the material model} &\rightarrow P(\mu) \\ &\rightarrow \{\mu_i\} \rightarrow \{g_i\} \rightarrow \sigma(\varepsilon). \end{aligned} \quad (16)$$

This causal chain is central to the theory: each element is fully determined by its predecessor and, in turn, determines the next. A change in the ODE changes the characteristic polynomial; a change in the

polynomial changes the spectrum; a change in the spectrum changes the system of genes g_i and, with it, the admissible construction of solutions to the corresponding boundary-value problem.

The smoothness class is equally important. At first glance, it may appear to be merely a technical requirement governing continuity of derivatives across segment interfaces. The preceding analysis shows, however, that its role is much deeper. The transition from C^0 to C^1 and then to C^2 changes not only the segment-conjugation conditions but also the order of the governing ODE of the material model, the number of fundamental solutions, the dimension of the solution space, and the mathematical structure of the model itself. The smoothness class therefore characterizes not an external way of joining segments but the internal organization of the model.

It follows that the smoothness class is a hereditary characteristic of the model and must be regarded as part of its structural organization. Models of different smoothness classes cannot belong to the same structural class even when they reproduce the same experimental curve with practically identical accuracy.

The theorem on structural classification can now be stated.

Theorem 3.1 (on structural classification of materials). Two material models belong to the same structural class if and only if the spaces of fundamental solutions generated by the governing ODEs of the material models coincide up to a nonsingular change of basis. Coincidence of an individual deformation curve is not sufficient for the models to belong to the same structural class.

Proof. Consider two material models described by governing ODEs that generate the spaces of fundamental solutions $\mathcal{G}_1$ and $\mathcal{G}_2$. Let the stress in the

first model be represented in the gene basis $\{g_i^{(1)}\}$:

$$\sigma(\varepsilon) = \sum_{i=1}^n f_i^{(1)} g_i^{(1)}(\varepsilon), \quad (17)$$

and in the second model in the basis $\{g_j^{(2)}\}$:

$$\sigma(\varepsilon) = \sum_{j=1}^m f_j^{(2)} g_j^{(2)}(\varepsilon). \quad (18)$$

If $\mathcal{G}_1 = \mathcal{G}_2$, both systems of functions are bases of the same space of fundamental solutions. The transition from one basis to the other is therefore realized by a nonsingular linear transformation. The expansion of any element of this space in a chosen basis is unique; hence, the difference between the coefficients $f_i^{(1)}$ and $f_j^{(2)}$ reflects only a different coordinate representation and not a different structural class.

If $\mathcal{G}_1 \neq \mathcal{G}_2$, uniqueness of expansion applies in different spaces. Coincidence of a particular curve $\sigma(\varepsilon)$ then means only that this curve belongs to the intersection

$$\sigma(\varepsilon) \in \mathcal{G}_1 \cap \mathcal{G}_2. \quad (19)$$

Such coincidence may be particular or degenerate, but it does not imply equality of the spaces of fundamental solutions and does not make the hereditary mechanisms generating the curve identical. Structural equivalence is therefore possible only when the spaces of fundamental solutions coincide up to a nonsingular change of basis.

This theorem clarifies the meaning of genotypic classification. The same curve may be described by different ODEs, but this does not imply structural equivalence of those equations. Structural equivalence refers not to a particular phenotypic realization but to the space of fundamental solutions and the hereditary mathematical information specified by the governing ODE of the material model.

4. Direct and Inverse Problems of Materials Genetics

The preceding result provides the basis for a new interpretation of the classical direct and inverse problems in mechanics of materials. Traditionally, these problems are formulated primarily in terms of calculating stresses, strains, or parameters of particular

models. Structural theory shows that such formulations reflect only the computational aspect of the problem and do not reveal the internal organization of the process by which the deformation curve is generated.

Once the governing ODE of the material model is recognized as the carrier of the model's hereditary mathematical information, the natural direction of causality becomes evident. The initial object is neither the experimental curve nor the fundamental solutions themselves, but the governing ODE of the material model. All other mathematical objects follow successively from its structure.

Each governing ODE of the material model uniquely determines a characteristic polynomial. The characteristic polynomial determines the characteristic spectrum (the set of characteristic roots). The spectrum determines the system of fundamental solutions, i.e., the genes of the material. After boundary and contact conditions are specified, the phenotypic coefficients are determined, and only then is the observable deformation curve formed.

The complete model-construction procedure therefore defines a single causal chain:

$$\begin{aligned} &\text{governing ODE of the material model} \rightarrow P(\mu) \\ &\quad \rightarrow \{\mu_i\} \rightarrow \{g_i\} \rightarrow \{f_i\} \\ &\quad \rightarrow \sigma(\varepsilon). \end{aligned} \quad (20)$$

Before boundary and contact conditions are imposed, all elements of this chain belong to the hereditary structure of the model. The governing ODE of the material model determines which fundamental solutions can exist at all. A particular curve appears only after the expansion coefficients associated with the boundary-value problem have been determined. The preceding elements of the causal chain are specified in Eqs. (13)-(15).

4.1 Direct Problem

The direct problem consists in constructing the deformation curve from a known governing ODE of the material model. The computational process follows the natural causal sequence from hereditary mathematical

information to its phenotypic realization:

$$\begin{aligned} &\text{governing ODE of the material model} \rightarrow P(\mu) \\ &\quad \rightarrow \{\mu_i\} \rightarrow \{g_i\} \rightarrow \{f_i\} \\ &\quad \rightarrow \sigma(\varepsilon). \end{aligned} \quad (21)$$

4.2 Spectral Inverse Problem

The inverse problem is fundamentally different. In the classical formulation, it is usually understood as determining model parameters from experimental data [11, 12]. The preceding analysis shows that this interpretation is incomplete. The observable curve does not directly contain the governing ODE of the material model. It contains information only about a particular phenotypic realization arising from the combined action of the hereditary structure and the conditions of a particular boundary-value problem.

Hereditary mathematical information therefore cannot be reconstructed in a single step. It naturally separates into two qualitatively different problems.

The first problem is to reconstruct, from the observed deformation curve, the genetic structure of the space of fundamental solutions. The result of this stage is the characteristic spectrum (whose elements are the characteristic roots) and the corresponding system of genes g_i . This problem is hereafter referred to as the spectral inverse problem:

$$\sigma(\varepsilon) \rightarrow \{f_i\} \rightarrow \{g_i\} \rightarrow \{\mu_i\}. \quad (22)$$

4.3 Genotypic Inverse Problem

Even after the spectrum has been reconstructed, the inverse problem is still incomplete. The governing ODE of the material model that generated this spectrum must still be determined together with the smoothness class and the entire hereditary structure of the model. This problem completes the reconstruction of genotypic information:

$$\begin{aligned} &(\mathcal{C}^k, \{\mu_i\}) \rightarrow P(\mu) \\ &\rightarrow \text{governing ODE of the material model}. \end{aligned} \quad (23)$$

Structural theory therefore divides the classical inverse problem naturally into two successive stages. The first reconstructs the spectral organization of the space of fundamental solutions. The second

reconstructs the governing ODE of the material model itself as the carrier of all hereditary mathematical information. A detailed mathematical theory, uniqueness and stability conditions, and numerical

procedures for these inverse problems lie beyond the scope of the present paper and will be addressed in subsequent works of the series.

Table 1 Phenotypic and genotypic paradigms of material description.

Phenotypic theory	Genotypic theory
Object: deformation curve	Object: governing ODE of the material model
Model parameters	Hereditary structure of the ODE
Description of behavior	Description of the generating mechanism
Classification of phenotypes	Structural classification of genotypes
Curve approximation	Identification of the space of fundamental solutions

5. Consequences for Structural Classification

The transition from phenotypic to structural description changes the object, criteria, and methodology of material classification. In the phenotypic paradigm, materials are compared by the shapes of their curves, approximation accuracy, fitting-parameter values, or the number of deformation stages. In the structural paradigm, comparison is transferred to the level of the governing ODEs of the material models and the spaces of fundamental solutions generated by them.

Several important consequences arise from this distinction. First, visual similarity of curves is no longer sufficient evidence of structural similarity between materials. Second, the same analytical form of $\sigma(\varepsilon)$ may be used for different materials without guaranteeing their structural proximity. Third, approximation parameters acquire structural meaning only as constituents of the corresponding governing ODE of the material model rather than as isolated constants. Fourth, the smoothness class becomes not a technical property of the spline but a part of the hereditary architecture of the model.

6. Discussion

The proposed structural paradigm does not supersede phenomenological descriptions. Experimental curves remain the initial empirical reality, and accurate approximation remains a necessary stage of analysis. Their scientific interpretation, however, shifts from empirical fitting to the structure generated by the

governing ODE of the material model.

From this perspective, phenotypic and genotypic theories address different questions. Phenotypic theory asks how accurately a model reproduces experimental data. Genotypic theory asks what hereditary mathematical structure makes the given family of curves admissible. The latter question defines the subject of structural classification of materials.

7. Conclusions

A structural theory of elastoplastic material models has been formulated by transferring the primary object of classification from the observable deformation curve to the governing ODE of the material model.

The conventional phenomenological approach compares models in terms of approximation accuracy, analytical form, and fitted parameter values. These characteristics belong to the phenotypic level and therefore cannot, by themselves, serve as criteria of structural classification. The governing ODE of the material model, by contrast, determines the smoothness class, characteristic polynomial, characteristic spectrum, system of fundamental solutions, and the full space of admissible phenotypic realizations.

Accordingly, the principle of structural equivalence has been established: two material models are structurally equivalent if and only if the spaces of fundamental solutions generated by the governing ODEs of the material models coincide up to a nonsingular change of basis. Coincidence of an

individual deformation curve is insufficient, because the same phenotype may belong to the intersection of different solution spaces.

The classical inverse problem has also been shown to have a two-level structure. The spectral inverse problem reconstructs the characteristic spectrum and the corresponding genes from an observed deformation curve. The genotypic inverse problem then reconstructs the governing ODE of the material model from the identified spectrum and smoothness class. This separation distinguishes reconstruction of the solution basis from reconstruction of the operator that generates that basis.

The present work therefore establishes both the object and the criterion of structural classification for elastoplastic material models. It also defines the direction of the subsequent research series. Subsequent studies will address the canonical representation of hereditary mathematical information, the uniqueness of structural identification from experimental data, the fundamental limits of structural identification, and the construction of libraries of material genomes and DNA portraits.

Thus, the governing ODE of an elastoplastic material model is identified as the carrier of hereditary mathematical information, whereas the operator-generated space of fundamental solutions becomes the principal object of structural classification. This provides a unified conceptual foundation for the further development of the genetic theory of elastoplastic materials.

The present paper establishes the object and

mathematical framework of structural classification. The computational algorithms, numerical solution of the inverse problems, DNA portraits, and practical identification procedures are intentionally reserved for the subsequent articles of the series, each addressing a distinct stage of the proposed theory.

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