

Evaluation of a Germ Stability of a Differentiable Mapping Defined by a Mathematical Model

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Abstract

The paper presents a set of algorithms to assess: the set of singular points of a differentiable mapping defined by some mathematical model; the stability of the germ of this mapping in its singular point, and (in the case of its stability) the form of such a germ in cases of corank 1 and all the possible relations of dimensions of the domain and mapping image. The stability of these germs in all singular points of the mapping under study is a necessary condition for the stability of the mapping in its domain. The implementation of the developed algorithms can be used to verify the model under study by investigating mappings defined by it.

Keywords Germ of smooth mapping; Germ stability; Singular point; Algorithm; Mathematical model.

1 Introduction

As is known, in natural science and economics to study properties of the objects under investigation are widely used mathematical models related to different classes. Important stage of accepting a model to use it in practice is verification and validation - V&V[1, 2]. Successful testing of the model using V&V methods gives reason to carry on the practice the conclusions drawn on the basis of calculations of the model.

Note that the currently used V&V methods contain no estimates of conditions for preserving qualitative properties of the considered models under arbitrarily small changes in these models. That is, these methods permit transfer of initial model (under its arbitrarily small changes) to the model with totally different properties[3]. Necessary conditions for preserving qualitative properties of model under its small changes can be conditions of the weak structural stability of the model, being dynamical system and stability conditions of mappings, defined by the model under study[4–6].

The study of authors Ashimov et al on the basis of the Robinson theorem on sufficient conditions for the weak structural stability and an algorithm for constructing a symbolic set provide convenient for practice numerical algorithms for the evaluation of weak structural stability of dynamical systems[4, 7–9]. Such system stability is required for small sensitivity of its phase portrait to small disturbances in model. These papers also provide the application examples of these algorithms to macroeconomic models.

In literature [8] authors propose V&V method, based on stability estimation of the defined by the model differentiable mappings in the sense of definition used in the theory of singularities of differentiable mappings[5, 6]. Literature [5] provide sufficient theoretical conditions for the stability of differentiable mapping when the mapping is an immersion, submersion or submersion with a fold. Proposed in [8] on the basis of these theoretical propositions the numerical algorithms permit to evaluate the set of singular points of the studied mapping, and also its stability (and instability) when the mapping belongs to the specified class of mappings. If using these algorithms the defined by model mappings are evaluated as stable, the appropriate model can be considered as more adequate to describe corresponding phenomena of reality.

However, the proposed in [8] algorithms are insufficient to assess the stability of these differentiable mappings in general case (if they do not belong to classes of immersions, submersions or submersions with a fold). Based on the fact that a required condition for the stability of a differentiable mapping is the stability of its germs in all the singular points of the mapping, the present work provides (based on theoretical propositions of Arnold et al[6]) an algorithm to estimate the stability of such germs. Also this paper proposes three algorithms to evaluate the form of stable germ with corank 1 for the cases of all possible ratios of dimensions of the domain and the image of the studied mapping. The use of the developed algorithms in the framework of V&V mathematical model would enable to evaluate the conditions of the low sensitivity of qualitative properties of the models to its small perturbations.

2 Algorithms to Evaluate a Set of Singular Points of Differentiable Mapping and Germ Stability of The Mapping in Its Singular Point

As noted above, the evaluation of stability of the given by model mapping F can be replaced by the evaluation of stability of germs of F in all singular points of this mapping. Ashimov et al[8] proposed an algorithm to estimate the set of singular points of the differentiable mapping in the parallelepiped D

$$F : D^0 \rightarrow E \quad (1)$$

(where $\dim(D) = m$, D^0 - the set of internal points D) using the set of parallelepipeds \tilde{D} with arbitrarily small size, covering the estimated set. For the convenience of the reader, this algorithm (as well as an illustration of its application), we present below.

Designate the vector of arguments of the mapping (1) through $p = (p^1, \dots, p^m) \in D$, and respective image of the point p - vector of the model solutions designate through $y = y(p) = (y^1, \dots, y^n) \in E$, ($D \subset R^m$ and $E \subset R^n$ - some domains). In this case the Jacobian matrix with dimension $v * n$ for the mapping (1) in the

point p would be written as follows:

$$J(p) = \left(\frac{\partial y^i}{\partial p^j}(p) \right)_{i=1, \dots, n; j=1, \dots, m} \quad (2)$$

Evaluation of the Jacobian matrix (2) in some point $p \in D$, derived using the numerical differentiation, we also designate through $J(p)$. Designate total quantity of maximal order minors in $J(p)$ through l . Estimate of determinant value of such a minor of order $\min(v, n)$ in $J(p)$ for $p \in D$ designate through $|M_i(p)|$, $i = 1, \dots, l$.

Algorithm 1 to estimate a set of singular points of mapping (1).

1) Parallelepiped D is divided into sufficiently great number of (elementary) parallelepipeds D^k with the same size, and a grid P composed of N points is determined, which are vertices of chosen parallelepipeds: $P = \{p_j : j = 1, \dots, N\}$.

2) Values of all $J(p_j)$ matrix elements are computed for $j = 1, \dots, N$.

3) For $i = 1, \dots, l$; are computed determinants $|M_i(p_j)|$.

4) For every $i = 1, \dots, j = 1, \dots, l$ the set $D(i)$ is determined in the following way. $D(i)$ is a union of all (closed) parallelepipeds D^k with the property: not all values of $|M_i(p_j)|$ in vertices D^k have the same sign.

5) The set $\tilde{D} = \bigcap_{i=1}^l D(i)$ is found.

6) If set \tilde{D} is empty, then stop.

7) If not, the steps 1 - 5 of this algorithm are performed with replacement of domain D by \tilde{D} and decrease of parallelepipeds size, participating in subdividing \tilde{D} until the diameter D^k is not less than some given forward number .

The abovementioned algorithms (as well as provided in [8] algorithms for evaluating points of a fold) were tested based on the Whitney mapping, defined by relations $y_1 = x_1^3 + x_1x_2$, $y_2 = x_2$, where $(x_1, x_2) \in R^2$. It is known that singular points of this mapping form parabola $3x_1^2 + x_2 = 0$ and all points of this parabola, except the origin of coordinates, are fold points; origin of coordinates - the point of cusp[6]. Fig.1 presents the derived by the mentioned algorithms points estimates of the Whitney mappings fold as the set of vertices of parallelepipeds \tilde{P} covering the fold. Note that the distance from every point in the set \tilde{P} to the fold does not exceed the diameter of elementary square from the set , namely, the number $0.05\sqrt{2}$.

Here are further required to construct an algorithm to evaluate the stability of the germ of a differentiable mapping notations and the theoretical propositions from [6]: definitions of a stable and infinitesimally V - stable germ, as well as theorems, enabling to obtain sufficient conditions for the stability of the germ by conditions of its infinitesimally V - stability. Then the conditions from the definition of infinitesimally V - stable germ we have rewritten equivalently as Condition 6. The proposed further Algorithm 2 permits to evaluate Condition

6, that is, the infinitesimal V - stability, and therefore the stability of the germ under study.

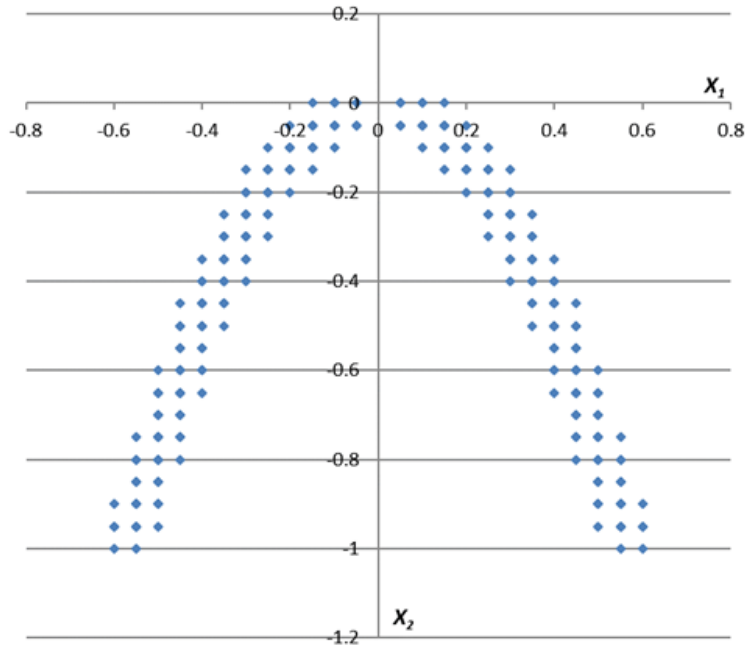


Fig. 1 Estimate of the Whitney mappings fold.

Here are further required to construct an algorithm to evaluate the stability of the germ of a differentiable mapping notations and the theoretical propositions from [6]: definitions of a stable and infinitesimally V -stable germ, as well as theorems, enabling to obtain sufficient conditions for the stability of the germ by conditions of its infinitesimally V -stability. Then the conditions from the definition of infinitesimally V -stable germ we have rewritten equivalently as Condition 6. The proposed further Algorithm 2 permits to evaluate Condition 6, that is, the infinitesimal V -stability, and therefore the stability of the germ under study.

Consider a germ of a differentiable mapping $F : R^m \rightarrow R^n$ in some of its singular point $x_0 \in R^m$. We denote also the mapping $F : D \rightarrow R^n$, specifying the germ, determined in a certain parallelepiped $D \subset R^m$ centered at point x_0 . Such a germ is called stable if for any other arbitrarily close (in the corresponding topology) to it mapping \bar{F} there exist diffeomorphisms in some neighborhoods of points of the domain x_0 and image $F(x_0)$, during application of which the mapping \bar{F} converted into F . The formal definition of the (*left - right, differentiable*)

stability of germ F is provided in the monograph[4].

Definition 1. A germ F is called *stable*, if for arbitrarily small neighborhood U of point x_0 exists such a neighborhood E of the mapping F , that for any mapping \bar{F} from E is found the point $\bar{x} \in U$ such that the germ \bar{F} in \bar{x} (left-right, differentiable) equivalent to the germ F in x_0 .

Topology in the set of all differentiable germs in point x_0 is given by the set of neighborhoods of the form[6]:

$$E = \{F : \sup_{|\alpha| \leq K, x \in U, i=1, \dots, n} \left| \frac{\partial^{|\alpha|}}{\partial \alpha x} F^i(x) - \frac{\partial^{|\alpha|}}{\partial \alpha x} F_0^i(x) \right|\} \quad (3)$$

Here F^i - coordinate function of the germ $F = (F^1, \dots, F^n)$, ($i = 1, \dots, n$); F_0 - fixed germ - the center of neighborhood E ; U - some neighborhood of point x_0 ; $x = (x^1, \dots, x^n)$, $\alpha = (\alpha_1, \dots, \alpha_m)$; α_j - integral non-negative number; $|\alpha| = |\alpha_1 + \dots + \alpha_m|$; K - arbitrarily large number; $\frac{\partial^{|\alpha|}}{\partial \alpha x} = \frac{\partial^{|\alpha|}}{\partial \alpha_1 x^1 \dots \partial \alpha_m x^m}$.

Further we introduce the following notations. Let $\partial F / \partial x^j$ - a germ of the mapping, defined by partial derivatives of coordinate functions of the mapping $F : \partial F / \partial x^j = (\partial F^1 / \partial x^j, \dots, \partial F^n / \partial x^j)$; $j = 1, \dots, m$. Basis germs of mappings $R^m \rightarrow R^n$ we call constant germs e_r , ($r = 1, \dots, n$) which have r -th coordinate function identically equal to 1, and the rest coordinate functions zero: $e_1 = (1, 0, \dots, 0), \dots, e_n = (0, 0, \dots, 1)$. Let A_{x_0} - algebra of all germs of differentiable functions $R^m \rightarrow R$ in point x_0 , $(A_{x_0})^n - A_{x_0}$ - module of all germs of differentiable mappings $R^m \rightarrow R^n$ in point x_0 . Designate trough - submodule in $(A_{x_0})^n$ generated by the following $m + n^2$ germs of mappings: $\partial F / \partial x^j$, where $j = 1, \dots, m$ and $F^i e_r$, where $i, r = 1, \dots, n$.

Definition 2. [5] A germ of the mapping F in point x_0 is called *infinitesimally V -stable*, if factor module $(A_{x_0})^n / B$ is generated above R images of basis germs e_1, e_2, \dots, e_n .

Note that from infinitesimal V -stability of a germ follows its stability. This fact follows from the following Theorems 3 and 4, provided in Arnold et al[6].

Theorem 3. Infinitesimal V -stability of a germ is equivalent to its infinitesimal stability.

Theorem 4. (Mather theorem (local version)) Infinitesimally stable germ is stable.

Using facts:

- submodule B is a set of all linear combinations of germs of mappings $\partial F / \partial x^j$ and $F^i e_r$ with coefficients from A_{x_0} and

- fulfillment of condition of Definition 2 is equal to the fact that any element of the factor module $(A_{x_0})^n / B$ of the form $G + B$ where G - some germ from $(A_{x_0})^n$ can be written as the sum of some linear combination of germs e_1, e_2, \dots, e_n with numerical coefficients and submodule B reformulate the condition of infinitesimal

V -stability of the germ F from Definition 2 by the following equivalent way.

Condition 5. Any germ G from $(A_{x_0})^n$ can be presented as the sum of some linear combination with numerical coefficients of constant germs e_1, e_2, \dots, e_n and linear combination with coefficients from A_{x_0} of the mentioned germs $\partial F / \partial x^j, F^i e_r$.

Since for the case $x_0 = 0$ any germ G from $(A_{x_0})^n$ can be written as the sum of constant germ (resulting from linear combination with numerical coefficients of germs e_1, e_2, \dots, e_n) and the germ taking zero value in point x_0 , and the last germ is written as the sum of linear combinations of functions of the form $x^j e_r$ (x^j - j -th coordinate of vector x) with coefficients from A_{x_0} , then in Condition 5, the term “any germ G ”, can be replaced by “any germ of the form $x^j e_r$ where $j = 1, \dots, m; r = 1, \dots, n$ ”. Moreover, for sufficiently small neighborhood $x_0=0$ coefficients of germs, generating submodule can be considered in the rough (with precision till infinitely small of high-order infinitesimality) polynomial germs $Q_K(x)$ from A_{x_0} , of order not exceeding K , where K - sufficiently large fixed number:

$$Q_K(x) = \sum_{\alpha: |\alpha| \leq K} c_\alpha x^\alpha \quad (4)$$

Here $x^\alpha = (x^1)^{\alpha_1} \dots (x^m)^{\alpha_m}$, c_α - coefficient of the polynomial. Therefore, for the case $x_0=0$ Condition 5 infinitesimally V -stable germ F can equivalently be rewritten in the following way.

Condition 6. Any germ of the mapping of the form $x^j e_r$ where $j = 1, \dots, m; r = 1, \dots, n$ (with precision till infinitely small of high-order infinitesimality) can be written as linear combination of germs $\partial F / \partial x^j, F^i e_r$, with polynomial coefficients as (4).

From Theorem 4 results that Condition 6 is sufficient for the stability of germ F in its singular point - the origin of coordinates. Here are based on an assessment of Condition 6 enlarged algorithm to evaluate the stability of the germ in a singular point x_0 of the mapping F (defined in D_ε parallelepiped centered at x_0 , where ε is a diameter of the parallelepiped) defined by some model. Estimate of singular point x_0 can be obtained by Algorithm 1 and selecting one point from the obtained set \tilde{P} .

Algorithm 2 to estimate the stability of germ of the differentiable mapping

1) Appropriate parallel shift and normalizing coordinate system in R^m yields that singular point x_0 corresponds with the origin of coordinates, and parallelepiped D_ε is close to cube. Here ε - sufficiently small given number.

2) Dividing every edge D_ε into sufficiently large even integer N of equal segments, yields a grid P_ε composed of N^m points.

3) Determine grid functions $F^i, i = 1, \dots, n$, corresponding to coordinate functions of the mapping F and determined in grid junctions $p \in P_\varepsilon$.

4) Using numerical differentiation (with step less than step of the grid P_ε) mine grid functions F_j^i , $i = 1, \dots, n, j = 1, \dots, m$, determined in grid functions P_ε and being estimates of partial derivatives $\partial F / \partial x^j$ in points $p \in P_\varepsilon$.

5) Setting grid mapping - linear combination of germs by its coordinate grid functions determined in P_ε (here $i = 1, \dots, n$):

$$y^i = R^i(x, \{\alpha_j : j = 1, \dots, m; |\alpha_j| \leq K\}, \{\alpha_{i,r} : r = 1, \dots, n; |\alpha_{i,r}| \leq K\}) \\ = \sum_{j=1}^m Q_j(x) F_j^i + \sum_{r=1}^n Q_{i,r}(x) F^r \quad (5)$$

Here Q_j and $Q_{i,r}$ some polynomials of degrees, not exceeding K with arbitrary coefficients α_j and $\alpha_{i,r}$ respectively. K - sufficiently large fixed number.

6) Using numerical differentiation (with step less than step of the grid P_ε) determine grid functions F_β^i , $i = 1, \dots, n$, $\beta = (\beta_1, \dots, \beta_m)$, $|\beta| \leq K$, determined in grid junctions P_ε and being estimates of partial derivatives $\frac{\partial^{|\beta|}}{\partial \beta x} F^i$. (For the cases $|\beta|=0$ and $|\beta|=1$ these functions were determined above, correspondingly, in steps 3 and 4 of the algorithm).

7) Setting grid functions R_β^i , $i = 1, \dots, n$, $\beta = (\beta_1, \dots, \beta_m)$, $|\beta| \leq K$, determined in grid functions P_ε and being estimates of partial derivatives $\frac{\partial^{|\beta|}}{\partial \beta x} R^i$ using the derived F_β^i values and values of partial derivatives of polynomials: $\frac{\partial^{|\beta|}}{\partial \beta x} Q_j$, $\frac{\partial^{|\beta|}}{\partial \beta x} Q_{i,r}$ in the mentioned grid functions.

8) For every $\bar{r} = 1, \dots, n$ and $\bar{j} = 1, \dots, m$ the steps 9, 10, 11 are performed.

9) For $i = 1, \dots, n$ determine functions

$$M_{\bar{r}, \bar{j}}^i(\{\alpha_j : j = 1, \dots, m; |\alpha_j| \leq K\}, \{\alpha_{i,r} : r = 1, \dots, n; |\alpha_{i,r}| \leq K\}) \\ = \sup_{x \in P_\varepsilon; \beta: |\beta| \leq K} \left| R_\beta^i(x) - \frac{\partial^{|\beta|}}{\partial \beta x} \left(x^{\bar{j}} e_{\bar{r}}^i \right) \right| \quad (6)$$

Here for $\beta = 0$, $\frac{\partial^{|\beta|}}{\partial \beta x} \left(x^{\bar{j}} e_{\bar{r}}^i \right) = x^{\bar{j}}$, if $i = \bar{r}$ and $j = \bar{j}$, if not, $\frac{\partial^{|\beta|}}{\partial \beta x} \left(x^{\bar{j}} e_{\bar{r}}^i \right) = 0$. For cases $|\beta| > 1$ $\frac{\partial^{|\beta|}}{\partial \beta x} \left(x^{\bar{j}} e_{\bar{r}}^i \right) \equiv 0$.

10) Finding estimate of deviation of the germ $x^{\bar{j}} e_{\bar{r}}$ from approximating it linear combination.

$$m = \frac{1}{\varepsilon} \inf_{\{\alpha_j: j=1, \dots, m; |\alpha_j| \leq K\}, \{\alpha_{i,r}: r=1, \dots, n; |\alpha_{i,r}| \leq K\}} \left(\sup_{i \in \{1, \dots, n\}} M_{\bar{r}, \bar{j}}^i \right) \quad (7)$$

11) If $m > \delta$, where δ - sufficiently small given forward number, then go to step 13.

- 12) The germ F is assessed as stable. Stop.
- 13) Two-fold decrease of ε and all of the edges of parallelepiped D_ε .
- 14) If $\varepsilon > \varepsilon_0$, where ε_0 - sufficiently small given forward number, then go to step 2.
- 15) Question about F germ stability left unanswered. Stop.

3 Algorithms to Estimate The Form of Stable Germ of Corank 1 of The Differentiable Mapping

After evaluation by the Algorithm 2 of the studied germ F in its singular point x_0 as a stable, there is a question on the evaluation of its form in accordance with [6] classification of genotypes of stable germs. In [6] there are three Morin theorems determining the form of stable germ in the case where the germ has corank 1; the question on classification of stable germs with greater corank is still open. Here corank of germ F its singular point x_0 is determined as the difference between the number $\min(m, n)$ and the rank of the Jacobian matrix of germ F in x_0 . This section presents these Morin theorems and developed algorithms enabling for respective estimation of the form of the germ F , and to evaluate some of the other characteristics of the germ under study.

Let there be a differentiable mapping $\bar{F} : R^m \rightarrow R^n$ defined in some neighborhood of its singular point $0 \in R^m$, $\bar{F}(0) = 0 \in R^n$. Next, consider the options of relations of dimensions values m and n .

2.1. Let the dimension of the image and the full domain of the germ \bar{F} match: $n = m$. The Morin theorem[6], which describes these stable germs is as follows.

Theorem 7. A stable germ $\bar{F} : (R^n, 0) \rightarrow (R^n, 0)$, of corank 1 left-right equivalent to the germ (i.e., driven by a diffeomorphic changes of coordinates in the spaces of domain and the image to the form)

$$\begin{cases} \tilde{y}^1 = (\tilde{x}^1)^k + \tilde{x}^2(\tilde{x}^1)^{k-2} + \dots + \tilde{x}^{k-1}\tilde{x}^1, \\ \tilde{y}^2 = \tilde{x}^2, \\ \dots \\ \tilde{y}^n = \tilde{x}^n, \end{cases} \quad (8)$$

Here $\tilde{y} = (\tilde{y}^1, \tilde{y}^2, \dots, \tilde{y}^n)$ and $\tilde{x} = (\tilde{x}^1, \tilde{x}^2, \dots, \tilde{x}^n)$ - new coordinates correspondingly in spaces of image and domain of the germ F . k - integer (indicator of germ), $2 \leq k \leq n + 1$.

We present an enlarged algorithm for assessing the axis $O\tilde{y}$ for mapping (8), and the k - order value of genotype specified in this theorem of the mapping F . It is based on the obvious remark that in the space of images R^n there is the only direction (defined by the axis $O\tilde{y}$), satisfying the following property: the derivative of the mapping coordinate F corresponding to \tilde{y}^1 at the origin of coordinates

O in any direction in domain of F is zero. For any other axis in space of images the corresponding derivative at point O in some direction is different from zero.

Algorithm 3

1) Finding by Algorithm 1 estimate P of the set of singular points of the mapping $F : D \rightarrow R^n, D \subset R^n$.

2) If P is empty, then stop. There are no singular points of the mapping F .

3) Choosing the singular point $x_0 \in P$ and estimating the stability of the germ F in x_0 by Algorithm 2.

4) If the germ F is not assessed as stable, then stop.

5) Computing the Jacobian estimate of the mapping F in point x_0 and its rank $r = \text{rank}(J(x_0))$.

6) If $r \neq n - 1$ then stop. Corank F in singular point x_0 is greater than one.

7) Setting the shifted mapping $y = F(x - x_0) + F(x_0) = \bar{F}(x)$, for which $x = 0$ is the investigated singular point and $\bar{F}(0) = 0$.

8) Finding the estimate of axis $O\tilde{y}^1$.

8.1) For arbitrary unit vector \tilde{y} ($|\tilde{y}| = 1$) setting coordinate function of n variables $a = \bar{F}_{\tilde{y}}(x) = pr_{\tilde{y}}\bar{F}(x)$ - projection of vector $\bar{F}(x)$ to vector \tilde{y} .

8.2) Setting function of n variables $s = G(\tilde{y}) = \sum_{i=1}^n \left(\frac{\partial \bar{F}_{\tilde{y}}(x)}{\partial x^i} \right)_{x=0}^2$, where $\frac{\partial \bar{F}_{\tilde{y}}(x)}{\partial x^i}$ - appropriate difference derivative.

8.3) Finding the estimate of constrained minimum s_0 of function $s = G(\tilde{y})$ under constraint $|\tilde{y}| = 1$.

8.4) If $s_0 \approx 0$ then the detected \tilde{y} is an estimate of axis unit vector \tilde{y}^1 , if not, then stop. In this case recalculation of steps 1-8 of the algorithm is possible with decreased values of grid steps and increments.

9) Finding the estimate of value of indicator k of the germ F .

9.1) For arbitrary unit vector x ($|x| = 1$) setting the constraint of coordinate function $\bar{F}_{\tilde{y}^1}(x)$ on axis, determined by this vector: $c = f_x(t) = \bar{F}_{\tilde{y}^1}(tx)$.

9.2) Assignment $k = 2$.

9.3) Finding the estimate of maximum value of module of k -th derivative of function $c = f_x(t)$ at zero: $m = \max_{x, |x|=1} |f_x^{(k)}(t)|_{t=0}|$, where the estimate in the form of corresponding difference derivative is used as a derivative.

9.4) If $m > \varepsilon$, where ε - sufficiently small number, then output of k value and stop.

9.5) Increasing k value by one: $k := k + 1$.

9.6) If $k \leq n + 1$, then go to step 9.3.

9.7) Indicator k of point x_0 is not defined. Stop.

2.2 Consider now the case, when the germ image dimension \bar{F} is strongly greater than the domain dimension: $n > m$. Take the Morin theorem[5], describ-

ing the mentioned stable germs for this case.

Theorem 8. In the case $n > m$ stable germ $\bar{F} : (R^m, 0) \rightarrow (R^n, 0)$, of corank 1 is right-left equivalent the germ (that is, reduced by diffeomorphic substitution of coordinates in spaces of domain and image to the form)

$$\left\{ \begin{array}{l} \tilde{y}^1 = (\tilde{x}^1)^k + \tilde{x}^2(\tilde{x}^1)^{k-2} + \dots + \tilde{x}^{k-1}\tilde{x}^1, \\ \tilde{y}^2 = \tilde{x}^k(\tilde{x}^1)^{k-1} + \tilde{x}^{k+1}(\tilde{x}^1)^{k-2} + \dots + \tilde{x}^{2k-2}\tilde{x}^1, \\ \dots \\ \tilde{y}^t = \tilde{x}^{(t-1)k-t}(\tilde{x}^1)^{k-1} + \tilde{x}^{k+1}(\tilde{x}^1)^{k-2} + \dots + \tilde{x}^{tk-t}\tilde{x}^1, \\ \tilde{y}^{t+1} = \tilde{x}^2, \\ \dots \\ \tilde{y}^n = \tilde{x}^m. \end{array} \right. \quad (9)$$

Here $k \geq 2$ – integer; $t = n - m + 1$; $t(k - 1) \leq m$; $\tilde{y} = (\tilde{y}^1, \tilde{y}^2, \dots, \tilde{y}^n)$ and $\tilde{x} = (\tilde{x}^1, \tilde{x}^2, \dots, \tilde{x}^n)$ – new coordinates correspondingly in spaces of image and domain of the germ F .

We present an enlarged algorithm for assessing the plane Π spanned by the axes $\tilde{y}^1, \tilde{y}^2, \dots, \tilde{y}^t$ for mapping (9), as well as the value of k genotype order of the mapping F specified in this theorem. In the construction of this algorithm is used the following remark. For any axis of the plane Π the coordinate derivative of the mapping F corresponding to the axis at the origin O in any direction in space of the inverse images is zero. For any axis that is not in from the space of images the derivative at point O in some direction is different from zero.

Algorithm 4.

1) Finding by Algorithm 1 estimate P of the set of singular points of the mapping $F : D \rightarrow R^n, D \subset R^m$.

2) If P is empty, then stop. There are no singular points of the mapping F .

3) Choosing the singular point $x_0 \in P$ and estimating the stability of the germ F in x_0 by Algorithm 2.

4) If the germ F is not assessed as stable, then stop.

5) Computing the Jacobian estimate of the mapping F in point x_0 and its rank $r = \text{rank}(J(x_0))$.

6) If $r \neq m - 1$ then stop. Corank F in inverse image in singular point x_0 is greater than one.

7) Setting the shifted mapping $y = F(x - x_0) + F(x_0) = \bar{F}(x)$, for which $x = 0$ is the investigated singular point and $\bar{F}(0) = 0$.

8) Finding the estimate of plane Π , spanned by the axes $\tilde{y}^1, \tilde{y}^2, \dots, \tilde{y}^t$ (where $t = n - m + 1$) for the mapping (9).

8.1) For arbitrary unit vector \tilde{y} ($|\tilde{y}| = 1$) setting coordinate function n of variables $a = \bar{F}_{\tilde{y}}(x) = pr_{\tilde{y}}\bar{F}(x)$ - projection of vector $\bar{F}(x)$ to vector \tilde{y} .

8.2) Setting function of n variables $s = G(\tilde{y}) = \sum_{i=1}^n \left(\frac{\partial \bar{F}_{\tilde{y}}(x)}{\partial x^i} \right)_{x=0}^2$, where $\frac{\partial \bar{F}_{\tilde{y}}(x)}{\partial x^i}$

- appropriate difference derivative.

8.3) Assignment $k = 1$, where k - enumerator of coordinate axes of the required plane Π .

8.4) Finding the estimate of constrained minimum s_0 of function $s = G(\tilde{y})$ under constraints: $|\tilde{y}| = 1$, $\tilde{y} \cdot \tilde{y}^i = 0$, where $i = 1, \dots, k - 1$ - numbers of the derived at the previous steps coordinate axes of the plane Π , \cdot - sign of scalar product (when $k = 1$ this constraint is not used).

8.5) If $s_0 \approx 0$ then the detected value \tilde{y} is an estimate of axis unit vector \tilde{y}^k , if not, then stop. In this case recalculation of steps 1-8 of the algorithm is possible with decreased values of grid steps and increments.

8.6) Increasing k by one: $k := k + 1$.

8.7) If $k \leq t$, then go to step 8.4.

9) Finding the estimate of value of indicator k of the germ F .

9.1) For arbitrary unit vector $\tilde{x} \in R^m$ ($|\tilde{x}| = 1$) and arbitrary unit vector $\tilde{y} \in R^n$ ($|\tilde{y}| = 1$) setting the constraint of coordinate function $\tilde{F}_{\tilde{y}}(x)$ on axis, determined by this vector: $c = f_{x,y}(t) = \tilde{F}_{\tilde{y}}(tx)$.

9.2) Assignment $k = 2$.

9.3) Finding the estimate of maximum value of module of k -th derivative of function $c = f_{x,y}(t)$ at zero: $m = \max_{y \in \Pi, |y|=1, x, |x|=1} \left| f_{x,y}^{(k)}(t) \Big|_{t=0} \right|$, where the estimate in the form of corresponding difference derivative is used as a derivative.

9.4) If $m > \varepsilon$, where ε - sufficiently small number, then output of k value and stop.

9.5) Increasing k value by one: $k := k + 1$.

9.6) If $t(k - 1) \leq m$, then go to step 9.3.

9.7) Indicator k of point x_0 is not defined. Stop.

2.3 Now consider the rest case, when the dimension of \bar{F} germ image is less than the dimension of domain: $n < m$. We present the Morin theorem[6] for this case, describing the mentioned stable germs of corank 1.

Theorem 9. In the case $n < m$ the stable germ $\bar{F} : (R^m, 0) \rightarrow (R^n, 0)$ of corank 1, the corank of the second differential the genotype of which at zero does not exceed 1, right-left is equivalent to the germ (i.e., by diffeomorphic substitutions of coordinates in spaces of domain and image reduced to the form).

$$\begin{cases} \tilde{y}^1 = (\tilde{x}^1)^k + \tilde{x}^2(\tilde{x}^1)^{k-2} + \dots + \tilde{x}^{k-1}\tilde{x}^1 \pm (\tilde{x}^{n+1})^2 \pm (\tilde{x}^{n+2})^2 \pm \dots \pm (\tilde{x}^m)^2, \\ \tilde{y}^2 = \tilde{x}^2, \\ \dots \\ \tilde{y}^n = \tilde{x}^n. \end{cases} \quad (10)$$

Here $\tilde{y} = (\tilde{y}^1, \tilde{y}^2, \dots, \tilde{y}^n)$ and $\tilde{x} = (\tilde{x}^1, \tilde{x}^2, \dots, \tilde{x}^n)$ - new coordinates correspondingly in spaces of image and domain of the germ F . k - integer (genotype order), $2 \leq k \leq n + 1$.

Below is presented an enlarged algorithm for assessing the axis $O\tilde{y}^1$ for the mapping (10), and k order value of the genotype of the specified in this theorem mapping F . The first part of the algorithm (steps 1-8) is similar to the corresponding steps of Algorithm 3.

Algorithm 5.

1) Finding the estimate P of the set of singular points of the mapping $F : D \rightarrow R^m, D \subset R^n$ using Algorithm 1.

2) If P is empty, then stop. There are no singular points of the mapping F .

3) Choosing the singular point $x_0 \in P$ and estimating the stability of the germ F in x_0 by Algorithm 2.

4) If the germ F is not assessed as stable, then stop.

5) Computing the Jacobian estimate of the mapping F in point x_0 and its rank $r = \text{rank}(J(x_0))$.

6) If $r \neq m - 1$ then stop. Corank F in singular point x_0 is greater than one.

7) Setting the shifted mapping $y = F(x - x_0) + F(x_0) = \bar{F}(x)$, for which $x = 0$ is the investigated singular point and $\bar{F}(0) = 0$.

8) Finding the estimate of axis $O\tilde{y}^1$.

8.1) For arbitrary unit vector $\tilde{y} \in R^m (|\tilde{y}| = 1)$ setting coordinate function n of variables $a = \bar{F}_{\tilde{y}}(x) = pr_{\tilde{y}}\bar{F}(x)$ – projection of vector $\bar{F}(x)$ to vector \tilde{y} .

8.2) Setting function of m variables $s = G(\tilde{y}) = \sum_{i=1}^n \left(\frac{\partial \bar{F}_{\tilde{y}}(x)}{\partial x^i} \right)_{x=0}^2$, where $\frac{\partial \bar{F}_{\tilde{y}}(x)}{\partial x^i}$ – appropriate difference derivative.

8.3) Finding the estimate of constrained minimum s_0 of function $s = G(\tilde{y})$ under constraint $|\tilde{y}| = 1$.

8.4) If $s_0 \approx 0$ then the derived value is an estimate of axis unit vector $O\tilde{y}^1$, if not, then stop. In this case recalculation of steps 1-8 of the algorithm is possible with decreased values of grid steps and increments.

9) Finding the estimate of value of indicator k of the germ F .

9.1) For arbitrary unit vector $x (|x| = 1)$ setting the constraint of coordinate function $\bar{F}_{\tilde{y}^1}(x)$ on axis, determined by this vector: $c = f_x(t) = \bar{F}_{\tilde{y}^1}(tx)$.

9.2) Assignment $i = 1$. i - enumerator of axes, corresponding to Morse singularity of function $\bar{F}_{\tilde{y}^1}(x)$.

9.3) Finding the estimate of maximum value of module of 2^{nd} derivative of function $c = f_x(t)$ at zero: $m = \max_{x, |x|=1; x\tilde{x}^j=0, j < i} \left| f_x^{(2)}(t)|_{t=0} \right|$ and corresponding vector \tilde{x}^i , where the estimate in the form of corresponding difference derivative is used as a derivative: $f_x^{(2)}(t)|_{t=0} = (f_x(h) + f_x(-h))/h^2$.

9.4) If $m < \varepsilon$ where ε - sufficiently small number, then stop. In this case the corank of the second differential of the studied germs genotype is estimated by the number greater than one.

9.5) Increasing the enumerator by one: $i := i + 1$.

9.6) If $i \leq m - n$, then go to step 9.3.

9.7) Assignment $k = 2$.

9.8) Finding the estimate of maximum value of module of k -th derivative of function $c = f_x(t)$ at zero: $m = \max_{x, |x|=1, x\tilde{x}^j=0, j < m-n} \left| f_x^{(k)}(t) \Big|_{t=0} \right|$, where the estimate in the form of corresponding difference derivative is used as a derivative.

9.9) If $m > \varepsilon$, where ε - sufficiently small number, then output of the required k value and stop.

9.10) Increasing k value by one: $k := k + 1$.

9.11) If $k \leq n + 1$, then go to step 9.8.

9.12) Characteristics k of point x_0 is not defined. Stop.

The use of Algorithms 2, 3 or 4 enables to evaluate the axis $O\tilde{y}^1$ (or the plane Π for the case $n > m$) in the space of the mapping image under study, with the following property. The coordinate derivative of the mapping F corresponding to this axis (or any axis of the mentioned plane for the case $n > m$) at the origin (corresponding to a singular point x_0) in any direction in space of the inverse images is zero.

Detection of the specified axis (or plane) may be important to study the behavior of the germ (in the singular point) of the mapping defined by the studied model. Coordinate function corresponding to this axis gives an example of the local invariant of model, in the sense that in some neighborhood of the singular point under study the derived function is constant (with accuracy up to infinitesimals of highest order) with respect to all exogenous parameters of the model involved in the construction of the initial mapping. If the studied point is estimated (using Algorithm 1) as a non-singular (regular) for this mapping, then space of images does not contain the axis with the above properties and the mapping has no local invariant in the neighborhood of this regular point.

4 Conclusion

This paper presents a set of algorithms that allow:

- To estimate the set of singular points of a differentiable mapping created by mathematical model.

- To estimate the stability of germ of this mapping in its singular point.

- In the case of such a stability of germ of corank 1 to estimate k indicator of its genotype and

- The corresponding axis in the domain of the germ, which determines the local invariant of the mapping under study.

The developed algorithms can be used to evaluate the possibility of transferring obtained on the basis of model results into practice.

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