BIO Web of Conferences **93**, 01010 (2024) https://doi.org/10.1051/bioconf/20249301010
Forestry Forum 2023

Algorithms for plant disease diagnostics by leaf image

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Abstract. This article discusses the task of detecting diseases of cultivated plants. When determining the phytosanitary status of cultivated plants, images of their leaves are considered as initial data. To solve the problem under consideration, a model of diagnostic algorithms based on two-dimensional threshold functions is proposed. The main idea of the proposed algorithms is to form a set of preferred diagnostic features and make decisions aimed at making a diagnosis based on a comparison of these features. The classification stages of the diagnostic algorithm model are presented. An assessment of the applicability of the proposed model is demonstrated using the example of solving the problem of diagnosing wheat diseases by leaf images. Keywords: diagnostic algorithms, basic image slices, diagnostic features, preferred features, calculation of the overall score.

1 Introduction

In recent years, the tasks of creating and using information systems and technologies in agricultural production have become one of the main factors in the advancing of innovative and research and technical developments in this area. One of the main tasks of using modern information technologies is related to the creation of computer systems designed to diagnose crop diseases and predict their development. In recent years, a number of research papers devoted to the diagnosis of plant diseases, in particular [1-6], have appeared. The problem of creating a computer system based on processing of images of cultivated plant leaves, which is intended for diagnosing diseases of their fruits, is considered. The introduction of automated diagnostic systems makes it possible to use unbiased information on the diagnosis of cultivated plants, to diagnose plant diseases in a timely and sufficiently accurate manner. This creates conditions for making decisions on plant protection measures [5, 6]. Image recognition methods and algorithms play a key role in the creation of computer systems designed to diagnose plant diseases.

An analysis of scientific sources on pattern recognition, in particular [7–20,32], shows that by now a number of recognition models have been created and rather well studied.

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Among them, the following most common recognition models can be distinguished: models based on the use of the separation principle; models based on methods of mathematical statistics; models built on the basis of potential functions; models based on calculation of estimates, etc. These models are mainly aimed at solving recognition problems with a small number of features that characterize objects in the image. But, in practice, tasks related to recognizing objects in a large-volume feature space (for example, assessing the state of development of economic entities, facial recognition, etc.) are more common. When solving the problem of diagnosing plant diseases by leaf images, the processed data are expressed in the form of a numerical matrix [5, 6, 21, 33]. In this case, there is too much information in the leaf image to make a diagnosis. Many local features calculated for each fragment of a given image are interrelated. The development of a diagnostic algorithm in such conditions entails difficulties associated with performing compute-intensive calculations. In this regard, the problems of developing, changing and improving existing algorithms for diagnosing plant diseases by images of their leaves are topical.

This work proposes a unique approach to the issue of determining the phytosanitary status of cultivated plants based on images of their leaves. The main feature of the proposed approach is the formation of a set of preferred features characterizing plant leaf images, and the development of algorithms for diagnosing plant diseases based on their analysis. It should be noted that this article is a revised and expanded version of work [5], devoted to the problem of extracting features from plant leaf images for diagnostics.

The purpose of this article is to develop a model of algorithms for diagnosing plant diseases based on the analysis of images of their leaves. The model of the proposed algorithms is based on the construction of two-dimensional threshold functions [22, 23].

2 Statement of the problem

Initial information about the plants being studied is presented in the form of matrix T of size $\hbar \times w$ (of leaf images). Let us assume that $\mathbb{L}$ is a set of images of all leaves accepted for study. The elements of this set, according to a certain rule, are divided into k sets of disjoint subsets (that is, diagnoses):

$$D_1, D_2, \ldots, D_k \left(\bigcup_{j=1}^{k} D_j = \mathbb{L},\ D_i \cap D_j = \varnothing, i \neq j, i, j \in \{1, \ldots, k\}\right) \quad (10)$$

It is preliminarily assumed that the rule for partitioning the set $\mathbb{L}$ into subsets (i.e. the algorithm that implements partition (1) is unknown, but some initial information, namely $D_1, D_2, \ldots, D_k$, about possible plant conditions is given. This information is designated as E_0:

$$E_0 = \{\mathfrak{L}_1, \ldots, \mathfrak{L}_i, \ldots, \mathfrak{L}_m;\ \tilde{\alpha}(\mathfrak{L}_1), \ldots, \tilde{\alpha}(\mathfrak{L}_i), \ldots, \tilde{\alpha}(\mathfrak{L}_m)\}, \tilde{\alpha}(\mathfrak{L}_i) = \left(\alpha_{i1}, \ldots, \alpha_{ij}, \ldots, \alpha_{ik}\right), \quad (2)$$

where α_{ij} is $P_j(\mathfrak{L}_i)$ $\left(P_j(\mathfrak{L}_i) = "\mathfrak{L}_i \in D_j", \mathfrak{L}_i \in \mathbb{L}\right)$, the value of the predicate, $\tilde{\alpha}(\mathfrak{L}_i)$ is $\mathfrak{L}_i$, the information vector of the image, and $|\alpha_{i1}|_{mxk}$ matrix is the information matrix of the sample $\tilde{\mathfrak{L}}^m \left(\tilde{\mathfrak{L}}^m = \{\mathfrak{L}_1, \ldots, \mathfrak{L}_i, \ldots, \mathfrak{L}_m\}\right)$.

It should be noted that each $\mathfrak{L}_i$ leaf image corresponds to a set of pixels specified in the form of the numerical matrix T [21, 24, 25]:

$$\mathrm{T} = \begin{bmatrix} \mathrm{t}_{11} & \cdots & \mathrm{t}_{1j} & \cdots & \mathrm{t}_{1w} \\ \cdots & \cdots & \cdots & \cdots & \cdots \\ \mathrm{t}_{i1} & \cdots & \mathrm{t}_{ij} & \cdots & \mathrm{t}_{iw} \\ \cdots & \cdots & \cdots & \cdots & \cdots \\ \mathrm{t}_{\hbar 1} & \cdots & \mathrm{t}_{\hbar j} & \cdots & \mathrm{t}_{\hbar w} \end{bmatrix} \quad (3)$$

The main task is to develop the recognition algorithm A that determines the value of the predicate $P_j(\mathfrak{L}_i)$ according to initial data (2):

$$A(E_0, \mathfrak{L}_i) = \tilde{\beta}(\mathfrak{L}_i),$$
$$\tilde{\beta}(\mathfrak{L}_i) = \left(\beta_{i1}, \dots, \beta_{ij}, \dots, \beta_{ik}\right),$$
$$\beta_{ij} = P_j(\mathfrak{L}_i), \beta_{ij} \in \{0,1,2\}.$$

Here, β_{ij} is described in the same way as in [7]. If $\beta_{ij} \in \{0,1\}$, β_{ij} the value of the predicate $P_j(\mathfrak{L}_i)$, then it calculated using algorithm A based on the characteristic features of the image $\mathfrak{L}_i$. Otherwise, the algorithm A is considered to have failed to calculate the values of the predicate $P_j(\mathfrak{L}_i)$.

3 Proposed solution method

To solve the problem formulated above, a model of diagnostic algorithms based on threshold functions is proposed. The main idea of the proposed model is, based on the analysis of leaf images, to determine a set of preferred features that characterize the diagnosis, and based on these features, recognize the phytosanitary status of the plant. In this case, the spatial (two-dimensional) structure of leaf images is expressed as a vector (one-dimensional) feature space of large dimension. Each feature describes only a certain part (fragment) of the considered image. It is believed that the same fragment of the same image can be described by several features (digital characters).

Building a model of diagnostic algorithms based on threshold functions includes the following main steps.

1. *Formation of basic parts of leaf images*. The first step of building a model is to form a set of basic parts (fragments) of the image depending on the parameter $\eta(\eta = \eta_{\hbar} \times \eta_{w})$ [25, 26]. This parameter specifies the number of fragments (subsets) created when segmenting the considered image. By assigning different integer and positive values to this parameter, it is possible to obtain feature sets of different sizes. There is no doubt that the value of the parameter κ depends on the actual size of the given leaf image. However, in some cases it can be determined on the basis of a priori information about leaf images. At that, both cases require that the number of elements (pixels) in each image fragment be the same.

After completing this step, we will obtain divided into equal rectangular parts η of each $\eta_{\hbar}$ and η_{w} sides of a given image, respectively. If the size of this image is equal to $\hbar \times w$, then the size of the individual parts (fragments) of the image is equal to κ_η:

$$\kappa_\eta = \hbar_\eta \times w_\eta, \eth_{\hbar} = \left[\hbar/\hbar_\eta\right] + \eth_{\hbar}, w_\eta = \left[w/\eta_{w}\right] + \eth_{w}, \tag{4}$$

$$\eth_{\hbar} = \begin{cases} 0, & \text{if } \hbar \div \eta_{\hbar} = 0 \\ 1, & \text{otherwise} \end{cases} \qquad \eth_{w} = \begin{cases} 0, & \text{if } w \div \eta_{w} = 0 \\ 1, & \text{otherwise} \end{cases} \tag{5}$$

Here, $\hbar, w$ are the number of rows and columns of matrix (3), respectively. In the expressions (4) and (5), the notations $[m/n]$ and $\div$ denote the result of dividing numbers m and n (i.e., natural number) and the reminder, respectively.

Thus, if, in division, there are reminders, then one pixel can be added to all parts of the image, and to fill the missing pixels, the border of the remaining parts (fragments) is shifted to the left or up by one pixel, and, as a result, all pieces (fragments) will have the same size.

2. *Identification of a set of diagnostic features by leaf images.* At this stage, a complex of diagnostic features is formed. They are defined as some digital characteristics of the considered part (fragment) of the image; for example, texture marks can be obtained based on the first-order statistical characteristics of the part of the image. They are invariant with

respect to pixel shifts [21, 24]. As diagnostic features of an image, in addition to features that characterize the texture, entropy, autocorrelation, moments, etc. can be used. [25, 26]. Having calculated the features $n\ (n = \eta \times \eta')$ for each part (fragment), we have obtained the diagnostic features η'.

It should be noted that each of the features calculated for all parts of the image is considered as a formed space of features. For example, the entropy calculated for all slices in an image forms one space of features, and the first-order moments form another space of features.

3. *Identification of subsets of strongly connected diagnostic features.* At this stage, a system of "unrelated" subsets of diagnostic features is determined (separately for each space of features), and it should be noted that their composition depends on the parameter n' [20, 27]. At that, each space of features is considered separately (for example, entropy or first-order moments) or all features are considered together.

Subsets of strongly connected features are determined based on the calculation of proximity estimates between subsets of diagnostic features. Let us assume that $\mathfrak{G}_{\mathrm{j}}(\mathrm{j} = \overline{1, n'})$ is a subset of diagnostic features consisting of interrelated features. Then the measure of proximity $\mathfrak{N}(\mathfrak{G}_{\mathrm{i}}, \mathfrak{G}_{\mathrm{j}})$ between the subsets $\mathfrak{G}_{\mathrm{i}}$ and $\mathfrak{G}_{\mathrm{j}}$ can be determined in different ways, for example, by the average distance between the elements of these subsets [28].

The procedure for determining subsets of strongly connected features is considered in scientific articles [27, 29] in more details. As a result of this step, a set of "mutually unrelated" subsets of strongly connected diagnostic features is determined and denoted as $\mathfrak{Z}_A(\mathfrak{Z}_A = \{\mathfrak{G}_1, \mathfrak{G}_2, \dots, \mathfrak{G}_n\})$.

4. *Identification of representative diagnostic features*. As a result of this step, only one feature is selected from each subset of strongly connected features, and after considering all subsets, a set of representative features is determined. The main idea of selecting representative features is to extract, from each subset, a representative feature that characterizes the subset. In the process of forming a representative set of features, each selected feature must be a typical representative of its strongly connected set of features. The result of this step is a reduced space of diagnostic features, the size of which is significantly smaller than the size of the specified space of features, i.e., $n(n' < n)$. Then the obtained space of features is denoted as T': $\mathrm{T}' = (\mathrm{t}'_1, \mathrm{t}'_2, \dots, \mathrm{t}'_{n'})$.

The procedure for identifying a set of representative features is considered in scientific works [29, 30].

5. *Determination of preferred diagnostic features*. As a result of this step, the preferred features of the plant leaf image are formed. Let us consider the process of identifying preferred features from a set of representative diagnostic features. Let us assume that there is a set $\{\mathrm{t}'_1, \dots, \mathrm{t}'_i, \dots,\ \mathrm{t}'_{n'}\}$ of the representative features defined in the previous step. It is known that for each object $\mathfrak{L}\ (\mathfrak{L} \in \mathbb{L})$ in the space of representative features T', there is n'-dimensional vector $\overline{a}\ (\overline{a} = (a_1, \dots, a_i, \dots, a_{n'}))$. Preferred features are selected from the set T' on the basis of assessing the superiority of the feature in question when dividing the leaf images included in the set $\widetilde{\mathfrak{L}}^m$ into two subsets, i.e., $\widetilde{D}_j$ and $C\widetilde{D}_j$.

$$\Pi_{ij} = \left(\mathbb{m}_2 \sum_{j=1}^{2} \sum_{S \in \widetilde{D}_j} \sum_{S_u \in \widetilde{D}_j} (a_i - a_{iu})^2\right) / \left(\mathbb{m}_1 \sum_{S \in \widetilde{D}_j} \sum_{S_u \in C\widetilde{D}_j} (a_i - a_{iu})^2\right), \qquad (6)$$

here $\mathbb{m}_1 = \left(m_1(m_1 - 1) + m_2(m_2 - 1)\right)/2\,, \mathbb{m}_2 = m_1 \times m_2, m_1 = \left|\widetilde{D}_j\right|, m_2 = \left|C\widetilde{D}_j\right|$.

It should be noted that when calculating the value Π_{ij}, $\mathfrak{L}$ and $\mathfrak{L}_u$ are considered different images (i.e., $\mathfrak{L} \neq \mathfrak{L}_u$). The main idea of determining preferred diagnostic features is based on the following rule: the smaller the value Π_{ij}, the greater the preference the corresponding feature has in distinguishing images of leaves belonging to the class $\widetilde{D}_j$. If two or more features have the same preference, either one will be selected.

As a result of this step, based on the analysis of the considered diagnostic representative features belonging to the class $\widetilde{D}_j$, the preferred features are determined. Let us denote the set of preferred features by $\widetilde{\mathfrak{X}}_j$. Here, the index j shows that the set of features are preferred when recognizing leaf images belonging to the class D_j. Thus, at this stage many preferred diagnostic features $\widetilde{\mathfrak{X}}_j\left(j=\overline{1,k}\right)$ are formed:

$$\widetilde{\mathfrak{X}}_j = \{\mathfrak{x}_1^j, \mathfrak{x}_2^j, \dots, \mathfrak{x}_{k_j}^j\},$$

where k_j is the power of the set of preferred features ($k_j = |\widetilde{\mathfrak{X}}_j|$).

Further, only preferred features will be considered.

6. *Determination of the difference function* $d(\mathfrak{L}_u, \mathfrak{L}_v)$ *between two leaf images* $\mathfrak{L}_u$ and $\mathfrak{L}_v$. At this stage, in the space of preferred diagnostic features $\left(\widetilde{\mathfrak{X}}_j\right)$, the difference function that describes the difference between the two, that is $\mathfrak{L}_u$ and $\mathfrak{L}_v$ leaf images, is determined, where $\tilde{\chi}_j$ is the set of preferred features determined by formula (6). When constructing the function $d(\mathfrak{L}_u\mathfrak{L}_v)$, the following principle is used: "the greater the value of the function $d(\mathfrak{L}, \mathfrak{L}_v)$, the greater the difference between these images."

Let two images $\mathfrak{L}_u$ *and* $\mathfrak{L}_v$ be given in the space $P(n_0 = |P|)$:

$$\mathfrak{L}_u = \left(a_{u1}, \dots a_{un_0}\right) и \mathfrak{L}_v = \left(a_{v1}, \dots a_{vn_0}\right).$$

The difference between these images is as follows:

$$\mathcal{R}(\mathfrak{L}_u, \mathfrak{L}_v) = \sum_{i=1}^{n_0} \mathscr{v}_i \, (a_{ui} - a_{vi})^2,$$

here $\mathscr{v}_i$ is the weighting factor.

7. Formation of strongly connected subsets of images. At this stage, a system of "mutually unrelated" subsets of images is formed. Let us assume that $\mathfrak{S}_A$ is the system of all disjoint subsets of the considered $\{\mathfrak{L}_1, \dots, \mathfrak{L}_i, \dots, \mathfrak{L}_m\}$ images. Let us denote the system of all such subsets as $\mathfrak{Q}$. At this stage, we define the system $\mathfrak{S}_A(\mathfrak{S}_A \subset \mathfrak{Q})$ of subsets of strongly connected images in m' quantity:

$$\mathfrak{S}_A = \{\mathcal{G}_1, \dots, \mathcal{G}_u, \dots, \mathcal{G}_{m'}\}.$$

Here, the elements of the subset $\mathfrak{S}_A$ meet the conditions:

$$\bigcap_{u=1}^{m'} \mathcal{G}_u = \emptyset; \bigcup_{u=1}^{m'} \mathcal{G}_u = \mathfrak{S}_A;\ m' = |\mathfrak{S}_A|.$$

By introducing various measures of proximity between subsets of strongly connected images ($\mathcal{G}_u$ and $\mathcal{G}_v$) and a function describing the quality of their partition into subsets, it is possible to obtain various procedures designed to form subsets of strongly connected images.

The elements of the subset $\mathcal{G}_u$ $(u = \overline{1, m'})$ obtained at this stage depend not only on the parameter m', but also from its initial data. Therefore, in general they are different for each $\mathcal{C}_j$ class. It should be noted that at this stage only features that describe images of the class $\mathcal{C}_j$

under consideration are determined. Thus, at this stage the parameter m' is set and its value is determined when solving specific problems.

8. Determination of representative images in each strongly connected subset. At this stage, many representative images are formed. Each representative image in this $\mathfrak{L}'_u$ ($\mathfrak{L}'_u \in \mathcal{G}_u$) set is a typical representative of the subset $\mathcal{G}_u$ of strongly connected images. The method for selecting representative images from subsets of strongly connected images depends on their power. Therefore, strong subsets with one, two or more elements are considered one at a time separately [29]:

$$\mathcal{Q}_1 = \{\mathcal{G}_u | \, |\mathcal{G}_u| = 1\}, \mathcal{Q}_2 = \{\mathcal{G}_u | \, |\mathcal{G}_u| = 2\}, \mathcal{Q}_3 = \{\mathcal{G}_u | \, |\mathcal{G}_u| \geq 3\}.$$

In this case, all elements of the set $\mathcal{Q}_1$ are selected as representative images because the set $\mathcal{Q}_1$ consists of subsets of isolated images that differ sharply from others. Selection of representative images from the subsets $\mathcal{G}_u$ ($\mathcal{G}_u \in \mathcal{Q}_3$) of the set $\mathcal{Q}_3$ is carried out as follows. The element of the subset $\mathcal{G}_u$ that is closest to the other elements is determined and selected as a representative image. The representative image $\mathcal{G}_u$ is selected from the subset $\mathcal{G}_u$ ($\mathcal{G}_u \in \mathcal{Q}_3$) based on identifying the subset element that is significantly different from other selected representative images.

The result of this step will be a set of images with much fewer images than the current m ($m' < m$). Let us denote the set of generated images by $\tilde{\mathfrak{L}}^{m'}$ $\left(\tilde{\mathfrak{L}}^{m'} = \left(\mathfrak{L}'_1, \dots, \mathfrak{L}'_u, \dots, \mathfrak{L}'_{m'}\right)\right)$.

9. Determination of the difference between the images $\mathfrak{L}'_u$ and $\mathfrak{L}$ in the two-dimensional subspace of preferred features. At this stage, in the two-dimensional subspace of preferred features $\mathcal{D}_i$ $\left(\mathcal{D}_i = \left(\mathrm{t}_{i_1}, \mathrm{t}_{i_2}\right)\right)$, a function that describes the similarity of objects $\mathfrak{L}'_u$ and $\mathfrak{L}$ is introduced. The distances between these($\mathfrak{L}'_u$ и $\mathfrak{L}$, $\mathfrak{L}'_u, \mathfrak{L} \in \mathcal{L}'$) images in the subspace of preferred features, that is, in the $\mathcal{D}_i$ space, are determined as follows:

$$d_i(\mathfrak{L}'_u, \mathfrak{L}) = \sum_{v=1}^{2} \xi_v (a_{u,i_v} - a_{i_v})^2 \tag{7}$$

Then, using expression (7), we can determine the following threshold function specified in $\mathcal{D}_i$ — the two-dimensional subspace of preferred features:

$$t_i(\mathfrak{L}'_u, \mathfrak{L}) = \begin{cases} 1, \text{if } d_i(\mathfrak{L}'_u, \mathfrak{L}) \leq \varepsilon_i; \\ 0, \text{if } d_i(\mathfrak{L}'_u, \mathfrak{L}) > \varepsilon_i, \end{cases} \tag{8}$$

where ε_i is the proximity function parameter.

10. Calculation of the proximity estimate of arbitrary image $\mathfrak{L}$ by class D_j in the subspace $\mathcal{D}_i$. At this stage, the overall estimate of the image $\mathfrak{L}$ in the subspace $\mathcal{D}_i$ is calculated relative to the leaf images belonging to the class D_j. Let us assume that representative leaf images $\mathfrak{L}'_{k_{j-1}+1}, \mathfrak{L}'_{k_{j-1}+2}, \dots, \mathfrak{L}'_{k_j}$ belong to the class D_j $\left(\{\mathfrak{L}'_{k_{j-1}+1}, \mathfrak{L}'_{k_{j-1}+2}, \dots, \mathfrak{L}'_{k_j}\} \in \mathcal{L}' \cap D_j\right)$. Then, we consider the overall estimate of the image $\mathfrak{L}$ in the subspace $\mathcal{D}_i$ in relation to representative images of the class D_j. The values of two-dimensional threshold functions$t_i\left(\mathfrak{L}_{m_{j-1}+1}, \mathfrak{L}\right), t_i\left(\mathfrak{L}_{m_{j-1}+2}, \mathfrak{L}\right), \dots, t_i\left(\mathfrak{L}_{m_j}, \mathfrak{L}\right)$ should be calculated by formula (8). The overall estimate for the class is calculated as follows:

$$\phi_i(D_j, \mathfrak{L}) = \sum_{\mathfrak{L}_u \in \tilde{D}_j} g_u t_i(\mathfrak{L}_u, \mathfrak{L}), \; \tilde{D}_j = \mathcal{L}' \cap D_j$$

where $\mathcal{g}_u$ is the algorithm parameter.

11. Estimating the proximity of an image to a class over all subspaces. At this stage, the proximity of the image $\mathfrak{L}$ to the class $D_j(j = \overline{1,l})$ is estimated. According to the 10th stage of this model, for each subspace $\mathcal{D}_i$ of representative features, an estimate of proximity of the image $\mathfrak{L}$ to the class $D_j(j = \overline{1,l})$ was calculated. In this case, the final estimate of proximity of the image $\mathfrak{L}$ to the class $D_j(j = \overline{1,l})$ is determined as the sum of the total estimates obtained for all subspaces:

$$B(D_j,\mathfrak{L}) = \sum_{i=1}^{\mathrm{n}'} \gamma_i \,\phi_i(D_j,\mathfrak{L}),$$

here γ_u is the algorithm parameter ($i = 1, \dots, \mathrm{n}'$).

12. Decision rule. The decision is made for each element [7], i.e.

$$\beta_{ij} = C\left(B(D_j,\mathfrak{L})\right) = \begin{cases} 0, \text{if } B(D_j,\mathfrak{L}) < c_1, \\ 1, \text{if } B(D_j,\mathfrak{L}) > c_2\,, \\ \Delta, \text{if } c_1 \leq B(D_j,\mathfrak{L}) \leq c_2, \end{cases}$$

here c_1, c_2 is the algorithm parameter.

Thus, a model of diagnostic algorithms based on the construction of two-dimensional threshold functions is considered. Any algorithm *A in this model* is completely determined by a set of parameters π. The set of all diagnostic algorithms in the proposed model is denoted as $A(\pi, \mathfrak{L})$. The construction of the best diagnostic algorithm for the given problem is carried out in the space of parameters π by searching for its extreme values [27].

4 Experimental study

In order to test the capabilities of the diagnostic algorithms built by the developer, the task of diagnosing wheat leaf rust using leaf images is considered. It is known that rust of grain crops, especially wheat, is one of the most harmful and dangerous diseases in many regions of the world. The amount of damage and loss in the yield of wheat caused by this disease depends on a number of factors, for example, on the period of primary damage (that is, the stage of wheat development, the time of onset of the disease) and the intensity of the disease. Correct determination of the development stage is of great importance not only when studying harmful rust diseases, but also when conducting research to predict the development of diseases and organize protective measures for wheat in crop fields.

Wheat fields were photographed and baseline data was collected to diagnose wheat rust. A set of 300 images of wheat leaves was selected as the initial data. The number of possible diagnoses (that is, the phytosanitary status of wheat) is 2: 1) images of wheat leaves with yellow rust (D_1); 2) images of wheat leaves without yellow rust (D_2).

In the first part of the set (D_1), there are 150 images. In the second part of the set (D_2), there are also 150 images. The division of these images into training and control samples is shown in Table 1. To eliminate successful (or unsuccessful) division into equal parts, *t×q-fold cross*-validation method was used [31].

Table 1. Dividing the source data into training and control samples

Diagnosis	Training sample size	Control sample size
D_1	100	50
D_2	100	50
Total	200	100

Using this method, the data was divided into training and control samples as follows: the source images, or rather the vectors of features corresponding to them, were randomly divided into 30 equal parts (blocks). The number of images and the proportions of classes in each block are approximately equal. To eliminate successful (or unsuccessful) partitioning, 20 blocks will be included in the training sample and the remaining 10 ones will be included in the control sample. The diagnostic algorithm is trained on this sample, and the algorithm of the trained method is tested on the control sample (the remaining blocks). Based on the results of each test, an assessment of the quality of diagnostic algorithms based on the control sample is determined and collected. When performing each subsequent step, one block from the control and training samples is selected and exchanged. In this case, the attached blocks from the control sample are correspondingly separated so that they do not participate in the selection of candidates for inclusion in the training sample. This process is repeated until the access of all the blocks to the training and control samples has ceased, i.e., 30 times. The assessment of the quality of diagnostic algorithms is determined after the procedures of all iterations. The assessment of the quality of diagnostic algorithms is determined by the average values of all experiments and is simplified in descending order. This made it possible to express the results presented in tables 2 and 3 in natural numbers.

Decision making on the problem under consideration was carried out according to the following formula (similar to the formula for the decision rule in the model of Yu.I. Zhuravlev) [7]:

$$\mathfrak{B}(\mathfrak{L}) = \begin{cases} 1, \text{if } \mathfrak{U}_1(\mathfrak{L}) = 1; \\ -1, \text{if } \mathfrak{U}_2(\mathfrak{L}) = 1; \\ 0, \text{if not}; \end{cases}$$
$$\mathfrak{U}_1(\mathfrak{L}) = \left(B\left(\widetilde{D}_j, \mathfrak{L}\right) > c_2\right) \wedge \left(B\left(C\widetilde{D}_j, \mathfrak{L}\right) < c_1\right);$$
$$\mathfrak{U}_2(\mathfrak{L}) = \left(B\left(C\widetilde{D}_j, \mathfrak{L}\right) > c_2\right) \wedge \left(B\left(\widetilde{D}_j, \mathfrak{L}\right) < c_1\right);$$

Here, $B\left(\widetilde{D}_j, \mathfrak{L}\right)$, $B\left(C\widetilde{D}_j, \mathfrak{L}\right)$ are estimates of belonging the image $\mathfrak{L}$ to the sets $\widetilde{D}_j$ and $C\widetilde{D}_j$, respectively. These estimates are calculated in the same way as those shown in the eleven stages of determining diagnostic algorithms.

If $R(\mathfrak{L}) = 1$, then the object belongs to the subset $\widetilde{D}_j$, if $R(\mathfrak{L}) = -1$, then object belongs to the subset $C\widetilde{D}_j$, if $R(\mathfrak{L}) = 0$, then it is impossible to determine the identity of the image $\mathfrak{L}$ to a subset.

This problem of determining the diagnosis is: 1) solved on the basis classical recognition algorithm based on the principle of potentials [13]; 2) using proposed algorithm. Table 2 shows the results of the experimental studies conducted to solve the problem under consideration using algorithms based on the principle of potentials.

Table 2. Results of solving a diagnostic problem using a classical algorithm based on the principle of potentials

Diagnosis	Number of correct diagnoses	Number of false diagnoses	Uncertain diagnosis	Diagnostic accuracy
D_1	34	12	4	68%
D_2	36	11	3	72%

Table 3 shows the results of the experimental studies conducted to solve the problem under consideration using the proposed algorithm.

Table 3. Results of solving the diagnostic problem using the proposed algorithm

Diagnosis	Number of correct diagnoses	Number of false diagnoses	Uncertain diagnosis	Diagnostic accuracy
D_1	45	4	1	90%
D_2	42	6	2	84%

According to the results of Table 2, when using the classical algorithm, the phytosanitary status was correctly recognized 70 times out of 100 studied wheat leaves, which is 70%. When using the proposed algorithm, 87 objects out of 100 (images of leaves) were correctly recognized, which is 87% (Table 3).

A comparison of the results obtained shows that the diagnostic accuracy of the proposed algorithm is higher than that of the other second algorithm. The high diagnostic accuracy of this algorithm is explained by the following:

1) the presented model of diagnostic algorithms takes into account the characteristic features of diagnostic features of wheat leaf images;

2) performing a number of additional procedures to improve diagnostic results.

It should also be noted that the diagnosis under consideration is carried out according to preferred diagnostic criteria.

5 Conclusion

One of the main problems of our time is crop management, based on diagnosing the phytosanitary state of crops and providing information for making decisions on their protection. However, the issues of developing and using automated systems for diagnosing diseases of cultivated plants have not been fully resolved.

A model of algorithms for diagnosing the phytosanitary status of cultivated plants based on leaf images has been developed. The main idea of the proposed model is to recognize the phytosanitary status of agricultural crops based on mutual comparison of diagnostic features. In this case, the formation of diagnostic features is based on the calculation of various statistical characteristics for each part (fragment) of a given image.

In the process of solving a practical problem, the following became clear: 1) the developed diagnostic model can be used in the development of various software packages aimed at solving problems of classifying objects presented in the form of images; 2) at the stage of forming subsets of “mutually unrelated” features (i.e., determining the number of subsets that need to be separated from the leaf image), the issues of constructing threshold functions in the space of representative diagnostic features turned out to be important. This means the need to continue research taking into account the identified areas.

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