Development of a sequence automaton for recognition of deviations indicators in diagnosis of natural systems

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Abstract. Much attention is now being paid to the development of automated devices for rapid disease diagnosis in veterinary medicine and medicine in general. One of the directions in medical instrumentation designing is the development of methods for automated disease diagnosis. This article is devoted to the automatization of pathology detection in histological analysis. The topology of pathologies of morphostructural changes in cells may have a tree-like structure, which makes the development of methods, software and hardware implementation of tools relevant for determination of the disease pathology. The three-level pathology system of structural changes in cell tissues obtained by histological analysis has been studied. It was suggested to use sequential logic, based on the Mealy machine, for the development of automated system for pathology indicators detection. Hartley binary measure for this topology of structural changes in tissues has been calculated and the indicator encoding has been given. The method of automated diagnosis based on the analysis of pathology indicators has been developed. An example of building an automatic recognition machine of pathology indicators on hard logics considered. It is relevant when using programmable logic device. The logical equations implemented in the combination scheme of the device are obtained. Simulation modeling to identify pathology indicators is performed. It is suggested to use the developed method of determining the disease indicators when designing the automated histological analyzer.

1. Introduction
The development of rapid diagnosis of diseases in veterinary medicine and medicine in general is an urgent task. At this juncture, histological analysis of structural changes in animal tissues is carried out manually. Therefore the time to clarify the diagnosis of disease and its treatment is delayed. Approaches based on wavelet image analysis [1,2], macro and micro diagnostics [3], neural networks [4,5,6] and other methods are used for automated recognition of disease pathologies. In this research paper the use of the finite automata theory for recognition of pathology indicators in histological analysis is proposed.
2. Equipment and devices used in studies

Theoretical approaches were based on the application of Finite Automata theory, such as the Mealy machine, Minimal disjunctive normal form, Karnaugh maps. The practical solution was implemented by means of Electronics Workbench software. Laboratory research on histological analysis was carried out using a system of histological wiring (histological processor “Leica”), a rotary microtome (Thermo Scientific HM 325) and other equipment.

3. The results of the study and their discussion

Let us consider the tree-like structure of the cell pathology given in [7,8]. For example, branch $Y_1$ describes the main pathology of the cell: $Y_1 = f(y_{11}, y_{12}, y_{13})$, where $y_{11}$ – karyopycnosis, $y_{12}$ – carirexis, $y_{13}$ – karyolysis, which in turn can be broken down into subpathologies (figure 1).

![Figure 1. Tree-like cell pathology structure.](image)

To build an automatic pathology indicator recognizer it is used the Mealy machine: $M = f(X, S, Y, \delta, \lambda, S_0)$, where $X = (x_1, x_2, ..., x_n)$ is a set of input signals;
$S = (s_1, s_2, ..., s_n)$ – set of states, $S_0$ – initial state;
$Y = (y_1, y_2, ..., y_n)$ – set of pathology indicators (output signals);
$\delta: X \times S \rightarrow S(t+1)$, $\lambda: X \times S \rightarrow Y$ – transition functions.

When constructing a sequence automaton for the considered structure, the length of vector $X$ can be calculated by the Hartley binary measure: $I = \log_2 3 = 1.58$.

Let us round out, 1.58 to 2, i.e. vector $X = (x_1, x_2)$ take the length of 2 bits. The generalized structure of the recognition machine is shown in figure 2.

![Figure 2. Generalized structure of the pathology indicator machine.](image)
Let us consider the indicator recognition task: Core pathology / karyolysis / mode_2, that corresponds to the encoding of the branch - \( Y_1/y_{13}/y_{132} \). The first branch can be encoded in the following way (table 1).

Table 1. Coding of the first branch level indicators.

| Number | \( x_2x_1 \) | Indicator name | Indicator |
|--------|---------------|----------------|-----------|
| 0      | 0 0           | Core pathology | \( Y_1 \) |
| 1      | 0 1           | Cell wall pathology | \( Y_2 \) |
| 2      | 1 0           | Mitochondria pathology | \( Y_3 \) |
| 3      | 1 1           | Backup         |

The second branch of the first \( Y_1 \) can be encoded in the same way (table 2).

Table 2. Coding of the second sublevel indicators of branch \( Y_1 \).

| Number | \( x_2x_1 \) | Indicator name | Indicator |
|--------|---------------|----------------|-----------|
| 0      | 0 0           | Karyopycnosis  | \( y_{11} \) |
| 1      | 0 1           | Carirexis      | \( y_{12} \) |
| 2      | 1 0           | Karyolysis     | \( y_{13} \) |

Coding of indicators of the third sublevel of Core pathology / Karyolysis branch is shown in table 3.

Table 3. Coding the indicators of the third branch sublevel Core pathology / Karyolysis.

| Number | \( x_2x_1 \) | Indicator name | Indicator |
|--------|---------------|----------------|-----------|
| 0      | 0 0           | mode_1         | \( y_{131} \) |
| 1      | 0 1           | mode_2         | \( y_{132} \) |
| 2      | 1 0           | mode_3         | \( y_{133} \) |

The rest of the pathology tree branches (figure 1) can be encoded using the same method. Then the branch: \( Y_1/y_{13}/y_{132} \) will represent a sequential set: 021.

Let us build the primary table of transitions, to construct the logical function of the automatic recognition machine. At the first stage of building the table, let us mark the correct (stable) code with red color incoming signals are ordered by the Gray code (table 4). The automaton's inputs may also receive codes corresponding to other pathologies, which are also included in table 4.

Table 4. Initial transition table.

| Tact number | \( x_2x_1 \) | Correct code, \( y^F \) | Incorrect code, \( y^F \) |
|-------------|---------------|----------------|----------------|
| 1           | 0 0 1 1 1 0  | 2 0 0         | 0 0 0         |
| 2           | 5 3 4 2     | 0 0 0         | 0 0 0         |
| 3           | 3 1 0 1     | 0 0 0         | 0 0 0         |
| 4           | 4 0 1 0     | 0 0 0         | 0 0 0         |
| 5           | 5 0 0 1     | 0 0 0         | 0 0 0         |

In order to simplify the automaton's design, a minimized table of transitions was built (table 5).

Table 5. Minimized transition table.

| merging rows | \( x_2x_1 \) | Correct code, \( y^F \) | Incorrect code, \( y^F \) |
|--------------|---------------|----------------|----------------|
| 1,3          | 0 1 3 2      | 0 0 0         | 0 0 0         |
| 2,4,5        | 5 0 4 2      | 0 0 0         | 0 0 0         |
Let us build a transition-exit table (table 6).

**Table 6. Sequential automaton transitions/outputs table.**

| s(t) | 00 | 01 | 11 | 10 |
|------|----|----|----|----|
| 0    | 0  | 1  | 1  |    |
| 1    |    |    |    | s(t+1) |

Using the transitions/exits table we can synthesize logical equations to find pathology indicators and construct the characteristic trigger equation \( s(t+1) \). Using table 6, like Karnaugh maps, we can find the trigger control function (figure 3). By filling in the empty cells and conducting the Minimal disjunctive normal form (MDNF), we have obtained the following equation for the trigger element: \( s(t+1) = s(t) \lor x_2 \lor x_1 \).

**Figure 3.** Drawing and analyzing the Karnaugh maps for the Trigger.

Having performed similar actions for the indicator of pathology \( y^T \), we will get a logical equation: \( y = s(t) x_1 \).

Let us build a combination circuit using a D-trigger. The results of the experiment are shown in figure 4. When the sequential code 021 is received, the indicator (figure 4c), which corresponds to the indicator of pathology \( y_{132} \), is activated.
4. Conclusions
The article performs an example of using a sequential automatic indicator recognition machine that has a nested tree-structure. It allows doing histological analysis of the pathology of morphological changes at the cellular level. The technique of building a recognition automaton on a mandatory dependency (hard logic) is shown. Its advantages are speed and reliability.

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