Innovative Databases in Ecomonitoring Information Systems: Images of Genetic Codes as Keys

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ABSTRACT

Introduction: Images of biological objects are used very often now for the creation of novel information systems for biology and medicine. But the sphere of their use, tasks which are possible to solve with them, can be successfully expanded. Problem statement: Contemporary biomedical relational databases (DBs) very often include images. But additionally, images themselves can play important functional roles in DBs.

Purpose: To use images of fishes' genetic codes fragments as keys for the construction of relational DB; this has to ensure the reliability of biomedical information storage better than in prototypes, and to provide better data integrity.

Methods: DB Design, object-oriented system analysis for DBs design in an optimal way, ER diagrams design.

Results: An algorithm for the construction of relational DBs with images, other biomedical information, analytical approaches and recommendations for doing this in an optimal way were presented. The main attention was paid to the creation and application of the most functionally high-quality codes for keys in DB (including primary keys). To perform this function, usages of codes based on images of fishes' genetic codes fragments were proposed. The example for such a task solution, described in this article, was the creation of DBs with information about fishes (or other aquatic organisms) and chemical inorganic environmental pollutants which affected them.

Conclusions: The results of the use of images of genetic codes fragments as keys for the construction of DBs with ecological data in an information system for environmental monitoring were presented. Through the high level of individualization of the data in a system with such keys the maintenance of species-specific information is substantiated. The work has theoretical and practical values. It may also be applied in an academician process for teaching students.

KEYWORDS

Information and computer technology, information system, image, database, coding

1. Introduction – Biomedical information systems with databases of images and algorithms of ecological monitoring

The first versions of information systems with databases were constructed for the purposes of technique. The idea of developing databases (DBs) and information systems (ISs) for biology and medicine was formulated comprehensively in its complicity and was formalized, probably for the first time, at the International Conference on Very Large Data Bases (VLDB) in 2000. [1] Biomedical objects specifics stimulate new inventions, the development of new methods and approaches in the design of such DBs and ISs. [1–4] In the present article we will demonstrate the results of our work in this direction.

Reliable information on the various schemes of distribution of biological species is necessary for the work in medicine, ecology, biogeography, for preserving these species, etc. Numerous projects have been initiated and realized to unite great volumes of data on the taxonomy of organisms and their distribution. [2–30] Novel mathematical methods were invented and perfected in the process of these works. [31–32] Electronic atlases, data from museums and DBs should provide relevant information to the developers of electronic maps which could predict changes in the future number of species (also under the influence of chemical substances – environmental pollutants). [25–28] Some of such DBs can be used as determinants in the future, provided they meet the required high quality standards. [1,21,23] The construction of future electronic DBs with information on living organisms which may be accessed via the Internet is an extremely important task; it will simplify the problem of identifying organisms for thousands of users and facilitate a wide range of applications, such as the use of expert systems in medicine, agriculture, etc. At the time of its construction, each of such biomedical systems was a perfect functional structure. Today they contain huge amounts of data and continue to be updated on a daily basis; they are utilized by thousands of users around the world. However, today there are new requirements that these ISs can no longer meet. For example, the question of the possibility of using such ISs as determinants is open. This requires the significant improving of the quality of the material in these DBs, including the quality of images. Thus, the quality of images of organisms should be improved by using specially designed digital photography, the definition of species/subspecies should be improved through the use of cluster analysis methods and so on. [3,4] Such projects have already been implemented in natural history museums in the USA, Great Britain, Germany and other countries. [1,2,13,16,17,21,24] Such contemporary requirements should be taken into account in the process of creating domestic analogues. There were also attempts to solve the linked problems of species conservation, environmental protection, etc. by using electronic academic DBs and by means of modeling based on these data.

Interdisciplinary approaches like the creation of electronic DBs with a spatial distribution of information on the Internet and modern mathematical modeling based on the data from such DBs allow exploring the following problems at a contemporary level: how regular and daily factors (geographical, environmental and ecological), as well as the same factors which have been influences throughout history, have affected the spread of organisms and biodiversity. [3,4,17,21,23,26] In addition, such approaches allow us to determine better how to preserve biodiversity in the face of a rapid increase of anthropogenic impact.

2. Methodology

Design of DB, object-oriented system analysis for design of DBs in an optimal way, ER diagrams design, ecological monitoring with ordering results in DBs.
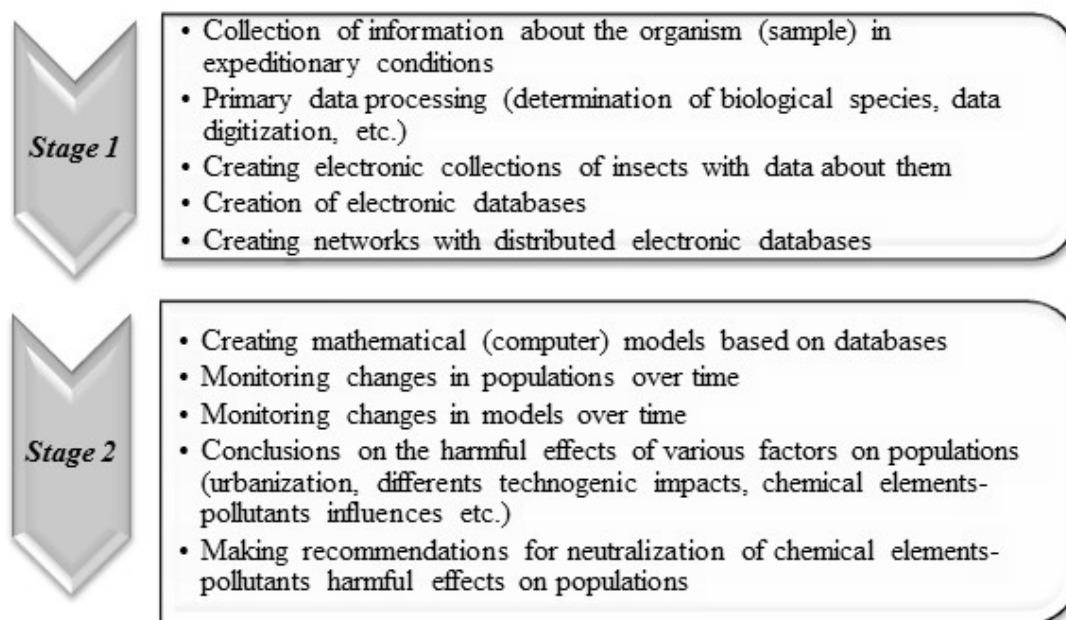
3. Purpose

The purpose of our work was to use images of fishes' genetic codes fragments as keys for the construction of relational DBs; this has to ensure the reliability of biomedical information storage better than in prototypes, and to provide better data integrity.

4. Results

Processing of environmental monitoring data based on the use of information systems with databases. Necessity to create databases with specific keys.

Nowadays, the ecological monitoring of biological organisms in order to prevent the reduction of their numbers due to various factors of damage – urbanization, anthropogenic influences, etc. is an important task. The sequence of steps for solving such problems, which could be regarded as standard today, can be described in two stages by the algorithm in Figure 1. [3,4]

Stage 1
- Collection of information about the organism (sample) in expeditionary conditions
- Primary data processing (determination of biological species, data digitization, etc.)
- Creating electronic collections of insects with data about them
- Creation of electronic databases
- Creating networks with distributed electronic databases

Stage 2
- Creating mathematical (computer) models based on databases
- Monitoring changes in populations over time
- Monitoring changes in models over time
- Conclusions on the harmful effects of various factors on populations (urbanization, differents technogenic impacts, chemical elements-pollutants influences etc.)
- Making recommendations for neutralization of chemical elements-pollutants harmful effects on populations

Figure 1: Two stages of processing environmental monitoring data based on the use of information systems with databases:

1. **Stage 1** – Creation of a collection of biological organisms and electronic databases.
2. **Stage 2** – Monitoring of populations and areas of species inhabitance using DB-based models (see details in text).[3,4]

Biomedical data constitute a substantial portion of input information for contemporary information systems (ISs) with databases (DBs). As a consequence, numerous ISs with DBs have been globally constructed to record, store, and process such data. Numerous publications have describes this extensive experience in detail.[1–29] Our research endeavors over the past sixteen years were also dedicated to this domain. [2–4,27,28] Previous works by our team were documented in the context of constructing biomedical ISs and DBs, specifically focusing on information related to fishes 3 and insects *(Noctuidae, Lepidoptera)* [4,27,28]. The construction of DBs in information systems necessitates high-quality input data. Our sources for biomedical data include our own research findings [2,3,27,28,33,34] and contributions from our colleagues. [30–32] Standard algorithms were employed for the development of relative DBs. [35, 36] Taxonomic data for biological organisms' DBs were extracted from previous works [37–40] and based on our research. We secured patents for some of our ISs with DBs dedicated to ecological monitoring. [27, 28]

The abundance of publications worldwide on DBs with information about fishes attests to the evolving nature of this knowledge domain. [3,21–26,29,37–40] Our team actively contributes to advancing this field. In this article, we introduce an original method utilizing images as keys in relational DBs, representing a potential avenue for innovation. As an illustrative example, we elaborate on the construction of a database containing information about fishes and the inorganic chemical pollutants affecting them.

The methodologies employed encompass DBs design, object-oriented system analysis for optimal DB design, and ER diagram design. [3,4]

The method presented in this article is distinctive, introducing innovative approaches that hold relevance. The heightened information protection characteristics sought in DBs, such as individualization of data for each biological species (or individual person), data integrity, and overall data protection necessitate the development of novel methodologies. Addressing these challenges, Dr. Klyuchko proposes a potent innovative method for key coding in DBs with biomedical information based on codes derived from fragments of genetic sequences represented as images. Previous publications from our team delved into and described the simplest case, where a single genetic sequence fragment code corresponded to one fish species. [41–43] In this article, we explore scenarios where several different fragments of the genetic code of a species may correspond to one fish species, presented in the form of images (as detailed below). To accommodate this, we introduce an additional object, namely, the "image of a genetic code fragment" (Figures 2 and 3).

The article follows a logical sequence, encompassing a description of object selection for relational DB construction through logical analysis, the subsequent design of an ER diagram tailored to the defined task, an elucidation of the analysis and procedure for key formation in relation to the database using "traditional" keys, and a proposal of a newly invented method for key formation using images of genetic code fragments from organisms, demonstrated by using fishes as an example. Object-oriented analysis initiates the database construction algorithm.

To illustrate the proposed problem-solving approach, we selected four objects for analysis: 1) "Fishes' species" as the biological object (in the DB construction process, various fish species were chosen); 2) "images of fragments of genetic codes", material sourced from contemporary genetics laboratories where such fragments have been examined with results accessible on the Internet—this object was selected to realize our idea of using images of genetic code fragments for key coding in relation to DBs; 3) "inorganic chemical elements" found in wastewaters, either dissolved or present as pollutants in industrial regions of Ukraine, negatively impacting fish fauna; [44] and 4) "taxonomic category," a suggested fourth object for the ER diagram. The designed ER diagram is depicted in Figure 2.

The initial steps in the algorithm for constructing such DBs are briefly described to facilitate an understanding of the invented coding technique. In the center of Figure 2, the primary selected object, "fishes' species," is represented as a rectangular symbol. This object is characterized by attributes denoted as ellipsoid symbols, which signify the main blocks of information intended for insertion into the database related to the "fishes' species" object. Attributes include, among others, the fish's name in Ukrainian and Latin, its area of inhabitance, and the "code of genetic sequence," a specific attribute elaborated upon later.

Figure 2 illustrates that the selected and designed object, "fishes' species", possesses identified characteristics represented as attributes within the DB context. The same principle applies to the other objects: "images of fragments of genetic codes", "chemical element", and "taxonomic category". In the context of this task, we selected and listed specific characteristics (attributes) for these objects, as presented in Figure 3. The second and third objects, namely "images of fragments of genetic codes" and "chemical element" (inorganic elements were exclusively selected for this model), adhere to the same attribute principles. Further details regarding selected characteristics (attributes) for all three objects are outlined in Figure 3.

The ER diagram employs main geometric symbols, as described previously. [3,4] The designation "ellipsis" with alternating dots signifies that additional characteristics, not explicitly detailed in the figures, can be chosen for such schemes. The "rhombus" symbol denotes the type of relations between objects, characterized by verbs explaining the sense of relations (e.g., "fish species are influenced by specific chemical elements"). For these relations, our newly invented codes for the keys—images of genetic fragments—will be employed.

In summary, the objects represent nouns, denoting main entities for which all data and characteristics must be included in the DB (in rectangles): fishes' species, chemical elements, and images. Attributes represent object characteristics essential for object description (in ovals), while relations (rhombus) signify logical links uniting objects where logical connections exist (e.g., "fishes' species" is affected by "chemical elements"). The same principles apply to the fourth object, "taxonomic category." The geometric symbols used in the ER diagram have been extensively elucidated in numerous manuals and articles. [3,4,35,36] Symbols such as "many dots" are employed in subsequent figures within this article.

The characteristics (attributes) outlined in Figures 2 and 3 were derived from determinants of fishes species. [37–39] The selection of inorganic elements (environmental pollutants) was based on information derived from monographs detailing inorganic substances and their derivatives, recognized as pollutants in wastewaters in industrial regions of Ukraine. [44] Information about images of genetic code fragments was sourced from. [42,43,45,46]
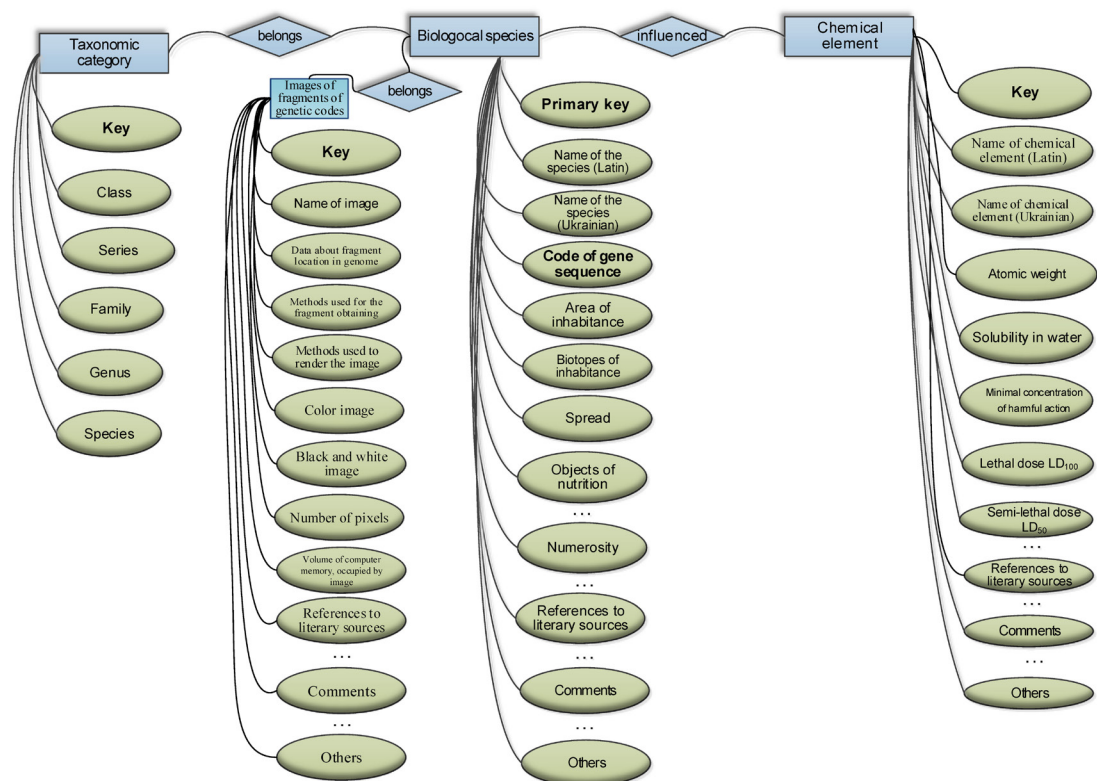

Figure 2. Fragment of ER diagram "fishes' species and inorganic chemical elements influencing them» for various fishes' species. The diagram was designed for 4 objects: "fishes' species", "images of fragments of genetic codes", "chemical elements", and "taxonomic category" (see explanations in text).

Object "Fishes' species"
Attributes:
Primary key (based on the image of the fragment of genetic sequence) Name of the fish (Latin) Name of the fish (Ukrainian) **Code of gene sequence** (if it is known) Area of inhabitance. Biotopes of inhabitance Spread Location Numerosity Reasons of numerosity changes Features of biology Objects of nutrition Reproduction in captivity Protection measures …………. References to literary sources. …………. Comments. Others

a)

Object "Images of fragments of genetic codes"
Attributes:
Key Name of image Data about fragment location in genome Methods used for the fragment obtaining Methods used to render the image Color image Black and white image Number of pixels Volume of computer memory, occupied by image …………. References to literary sources …………. Comments Others

b)

Object " Chemical elements" (for inorganic elements"
Attributes:
Key Name of chemical element (Latin) Name of chemical element (Ukrainian) Atomic weight Chemical structure (for inorganic compounds) Solubility in water Minimal concentration of harmful action Lethal dose LD_{100} Semi-lethal dose LD_{50} …………. References to literary sources …………. Comments Others

c)

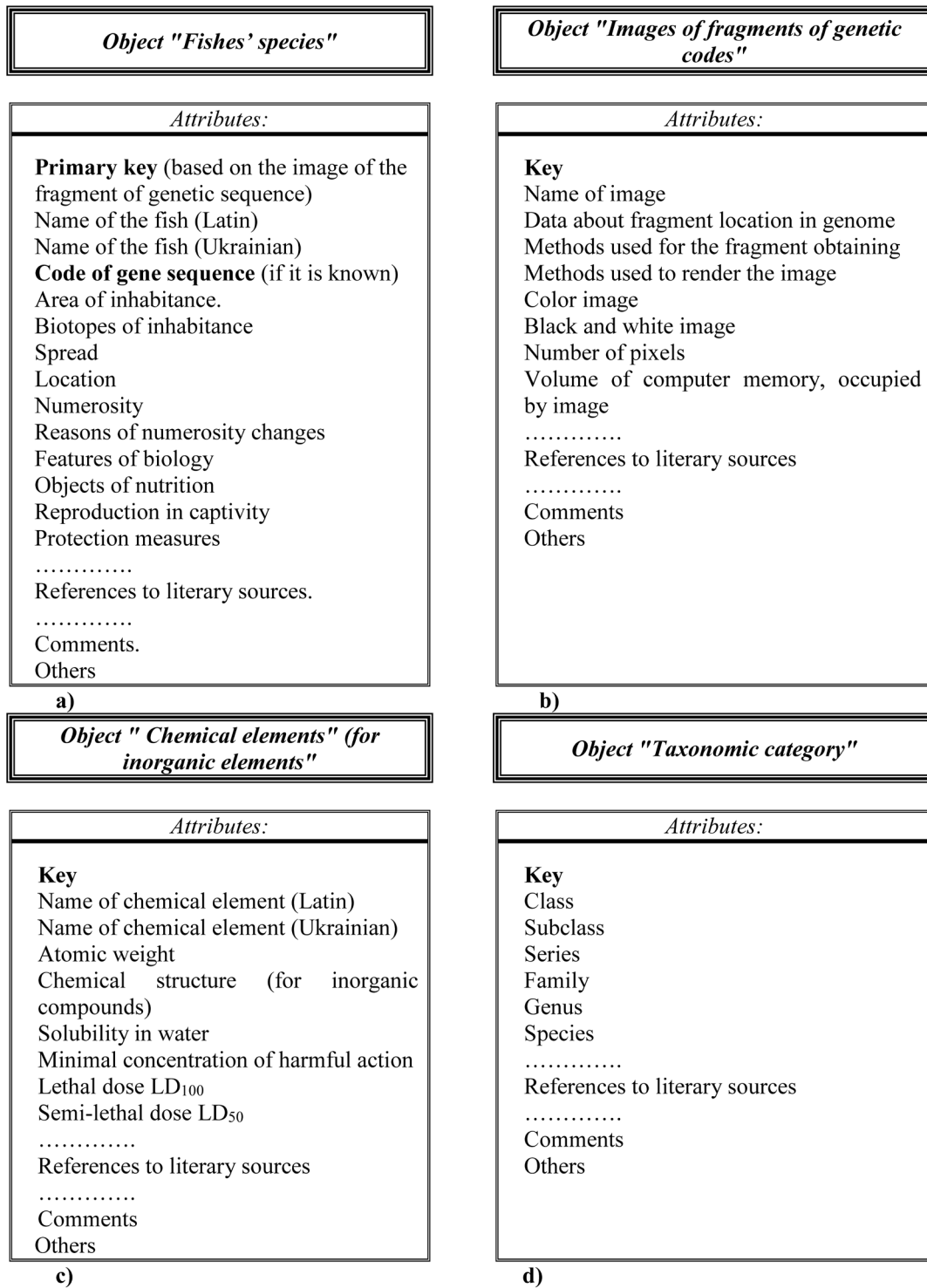| **Object "Taxonomic category"** |
|---|
| *Attributes:* |
| **Key**
Class
Subclass
Series
Family
Genus
Species
………….
References to literary sources
………….
Comments
Others |

d)

Figure 3: Attributes of objects "fishes' species", "images of fragments of genetic codes", "chemical elements"(environmental pollutants), and "taxonomic category".

For the continued development of the database, a more detailed specification is required regarding the selection of fishes' species and inorganic chemical elements-pollutants from industrial regions in Ukraine. For this illustrative example, we have chosen the following objects:

a) Fishes' species:

•   Oncorhynchus mykiss Walbaum (rainbow trout)
•   Cyprinus carpio L. (common carp)
•   Hypophthalmichthys molitrix (silver carp)

b) Inorganic elements-pollutants:

•   Lead (Pb)
•   Fluorine (F)
•   Aluminum (Al)
•   Copper (Cu)
•   Beryllium (Be)
•   Chrome (Cr)
•   Arsenic (As)
•   Cadmium (Cd)
•   Zinc (Zn)
•   Mercury (Hg)
•   And others

To further illustrate, Figure 4 demonstrates how the abstract forms described in Figures 2 and 3 can be populated with specific content, i. e. the names of fishes and the identification of specific chemical elements considered as pollutants. The alignment of these elements is visually presented in Figure 4.
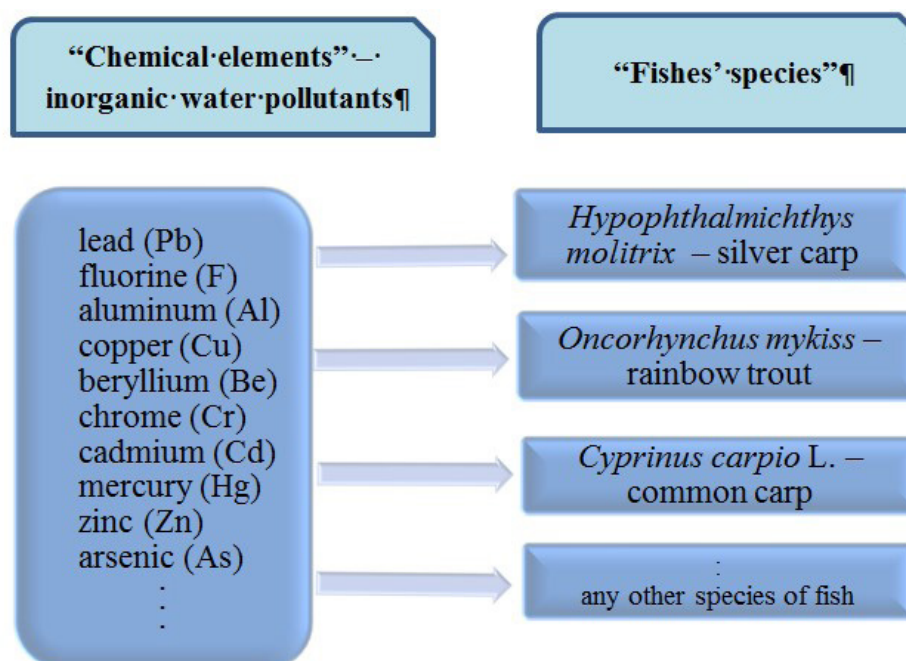
Figure 4: Construction of the database with data on fishes' species and inorganic chemical elements affecting them. Fragment of the ER diagram 'fishes' species and inorganic chemical elements that influence them,' illustrated with selected fishes' species from water basins in Ukraine. [44]

In the subsequent phases of the database (DB) construction process, certain transformations are necessary. The objects 'fishes' species' and 'inorganic chemical elements' (Figure 2) are transformed into tables, as depicted in Figures 4 and 5. The columns in these tables represent the transformed attributes of these objects (refer to Figure 5).
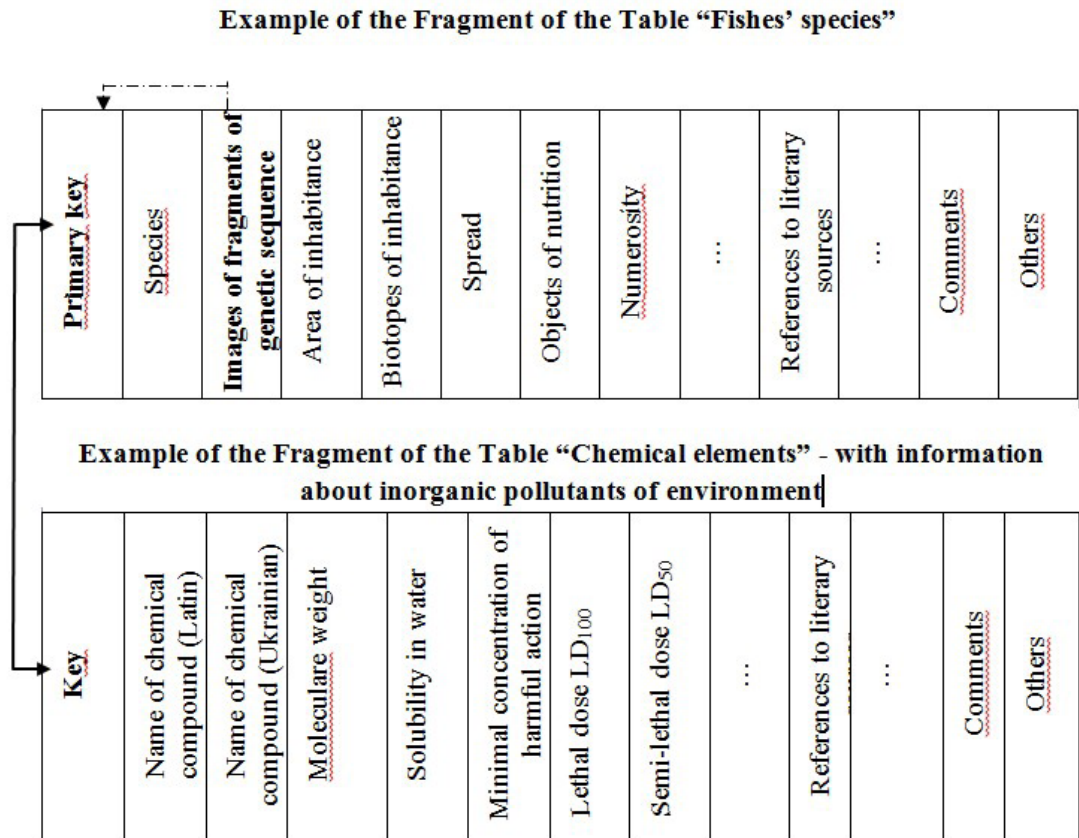
Example of the Fragment of the Table "Fishes' species"

Primary key	Species	Images of fragments of genetic sequence	Area of inhabitance	Biotopes of inhabitance	Spread	Objects of nutrition	Numerosity	...	References to literary sources	...	Comments	Others

Example of the Fragment of the Table "Chemical elements" - with information about inorganic pollutants of environment

Key	Name of chemical compound (Latin)	Name of chemical compound (Ukrainian)	Moleculare weight	Solubility in water	Minimal concentration of harmful action	Lethal dose LD_{100}	Semi-lethal dose LD_{50}	...	References to literary	...	Comments	Others

Figure 5: Two objects and their corresponding tables in a constructed relative database. Description of the invented method of the links formation through the images as "keys".

The transformations required during the DB construction process are as follows: [3, 4]

1. Objects ('entities') of the ER diagram must be transformed into linked tables.

2. Attributes must be transformed into the columns or 'fields' of these tables.

3. The relations ('rhombus') between the objects must be transformed into relations between the tables, facilitated through the mechanism of 'keys.'

The ER diagram provides a comprehensive overview, evaluation, and analysis of all entities (objects) that need to be integrated into the DB. It serves as an abstraction that facilitates a comprehensive demonstration of all DB objects, their relationships, and attributes as characteristics of these objects. This holistic representation and analysis are crucial for high-quality DB construction. For the biomedical DB under analysis, additional data, such as nucleotide sequences in gene fragments, taxonomic characteristics (family, genus, etc.), gain significance as attributes.

By accumulating monitoring data in databases, users can assess whether changes in ecosystems have

occurred under various influences, such as technogenic pressure and chemical pollution of the environment. This approach enables the identification of changes in fish organisms, entire ecosystems, and more. Consequently, it becomes possible to develop methods for nature protection against such adverse influences. These DBs facilitate operations such as sorting and filtering of biomedical data, searching for specific records, data output realization, data processing, and more. Such capabilities are valuable for both professionals and enthusiasts in their respective endeavors."

The mechanism of 'keys' serves as a critical tool for establishing connections ('relations') between objects in relational databases (DBs). These 'keys' ensure the accessibility of information in databases by establishing links between tables with diverse data. Leveraging 'keys' allows for the retrieval of data not only from one table but also from other tables linked to it. The connections between keys, represented as codes from the tables (derived from previously defined 'objects'), can be easily implemented using contemporary software. [3,4,35,36] The application of the 'keys' method enables accessibility to data in the DB and ensures data integrity, preventing data loss. Integrating genetic information into DBs enhances the level of information individualization within the database. Consequently, information about each species, and in some cases, individual-specific information, can be defined. [3,4,35,36, 41-43] Inaccessible data cannot be outputted, underscoring the crucial importance of keys.

The construction of keys commences with the design of the ER diagram and its subsequent analysis, ensuring that all entities (objects) are interconnected. A profound analysis of the ER diagram allows for a comprehensive understanding of the organization of keys; no element can be overlooked.

In our model, depicting the influences of inorganic chemical elements on different fishes' species (see Figure 2), we linked the objects 'fishes' species' and 'inorganic chemical elements' (pollutants) through keys in the DB. Subsequently, we can retrieve information on which inorganic substance influences any fishes' species and in what manner. For instance, one might seek to understand how the chemical element beryllium (Be) affects carps (or a carp population). Researchers are aware that beryllium in water indeed influences carps. Therefore, in the programme, the key 'ImageGenCodeCarp*' from the table 'fishes' species' must be linked with another key associated with 'beryllium' in the table 'chemical elements' (pollutants). Similar connections are established for other elements. Keys for chemical elements in Figures 4 and 5 can be coded in the traditional widely used way, employing a group of symbols (randomly generated numbers or letters) as exemplified by the key for 'beryllium.'

Another aspect of the coding challenge involves determining which elements, groups of elements, or symbols should be selected as keys, meeting the aforementioned requirements. In relational DBs, codes, primarily sequences of numbers, letters, or other symbols, serve as 'keys.' In some of our previous publications addressing innovative key types for relational DBs, keys based on genetic codes were suggested—these involved fragments of genetic code sequences expressed as combinations of letters and numbers (alphanumeric codes). [41] Keys created in this manner were termed 'natural keys', wherein real natural objects (genetic code fragments, in our case) formed the basis for such codes, and these codes were organized in a single field within the completed DB.

In the following sections, we present one of our inventions where 'natural keys' take the form of IMAGES of fragments of genetic code sequences. These images are the foundation for this novel key type. Examples of such images of genetic code fragments for various fishes' species are illustrated in Figure 6. The object 'images...' depicted in Figure 1 is essential because an increasing number of deciphered fragments of the genetic codes of various fishes' species emerge daily, necessitating their organization within the constructed database. However, only selected images are proposed to serve as keys within the same database.

Such images of genetic code fragments in DBs containing information on living organisms have already been integrated as a separate field in some contemporary databases. This integration stems from advancements in genetics research, particularly in genome studies, where such information holds significant importance. However, prior to our work, these images played no functional role in the DB; they

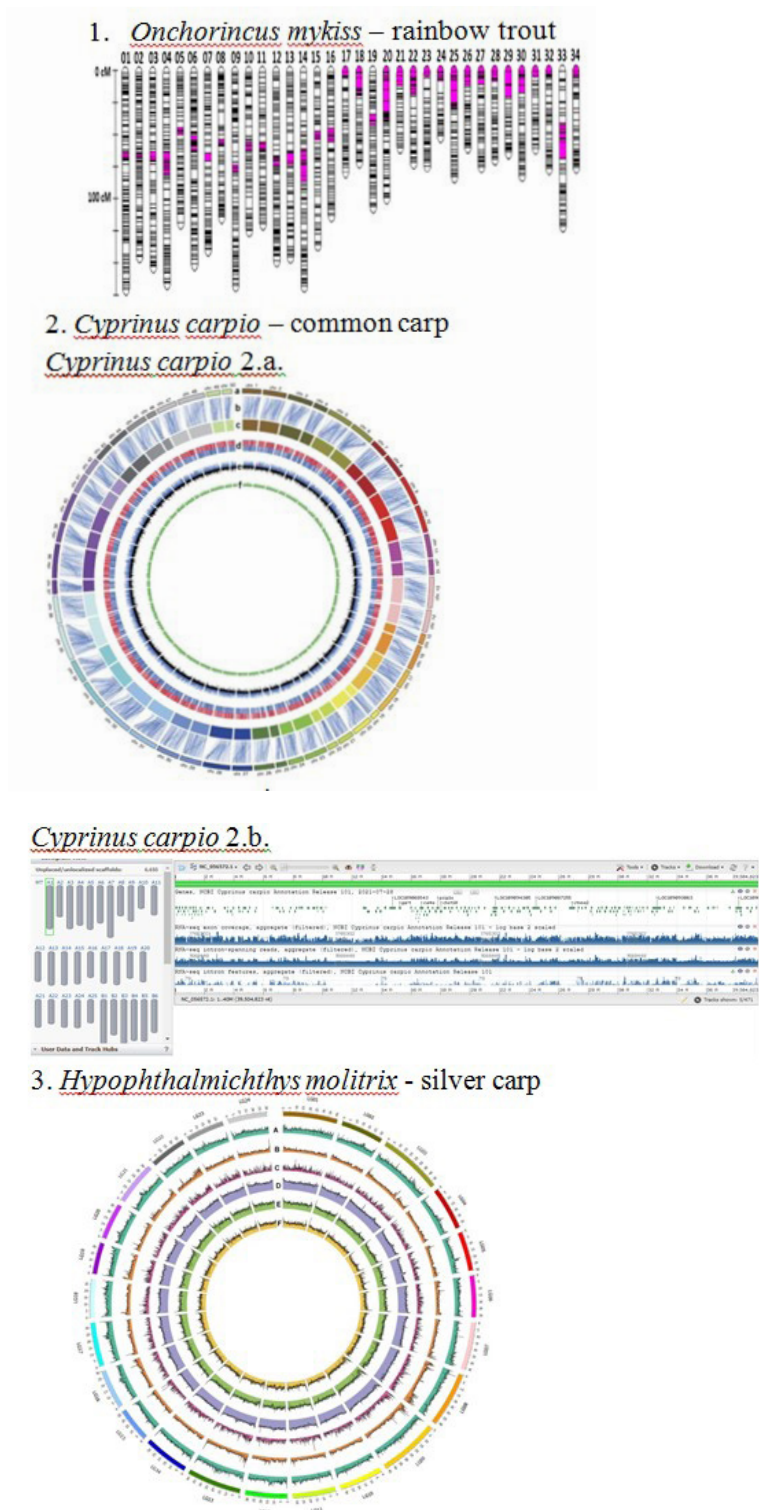merely constituted a volume of images organized in a separate field (never as keys).

Figure 6: Images of the fragments of genetic codes of some fishes that can be used as keys in the databases (as well as primary keys). [42,43,45,46]

Consider a scenario where the role of keys is assigned to specific images—referred to as 'natural keys' (Figure 6). In this case, the 'images of fragments of genetic codes' field in Figure 5 transforms into a field containing these image keys. Additionally, as depicted in Figure 2, the images on the ER diagram are represented by the 'Image…' object, characterized by its own attributes. Consequently, a situation of intriguing complexity arises. The subsequent analysis of this scenario and proposed solutions are elucidated in the following chapter.

An analysis of the inventive method of utilizing images of genetic code fragments as 'keys' for database construction unfolds new avenues for creative ideas in coding for DBs construction. Dr. Klyuchko has conducted research in this domain, yielding innovative methods, one of which is expounded here. In the context of the model task, biological organisms and species possess unique genetic codes. Previously, we published results regarding the use of genetic code fragments as keys, expressed in sequences of alphanumeric symbols. [41] These symbol sequences exhibit high individuality, specific to each species and, in some cases, each individual organism. Hence, leveraging such symbol groups as keys, including primary keys, is considered a promising idea.

Real nucleotide sequences correspond to these codes in symbolic form, and images of these sequences, obtained by geneticists, are illustrated in Figure 6. For example, the upper image of a genetic code fragment is characteristic of the fish rainbow trout (O. mykiss). This code serves as a key (including a primary key) in relational databases of fishes and other aquatic organisms. Each code entry is species-specific, and the images vary for different species. This naturally suggests the idea of using such images as keys in DBs with biological material. While a vast number of images may require significant computer memory, given contemporary technology, including 4G and 5G, this is not a hindrance.

Numerous examples of fragments of genetic sequences have been investigated to date. [45,46] Moreover, the number of decoded DNA and RNA fragments continues to grow daily, with new information being added to such DBs in subsequent years. From a contemporary standpoint, the necessity of using such detailed images of genetic codes as keys may be questioned. However, considering the capabilities of modern computers with substantial memory, the advantages of this method may outweigh the disadvantages. On the other hand, the challenge lies in determining what fragment of the genetic sequence to select as a suitable image for use as a key, which is contingent upon the specific task at hand.

Examining the modeling task at hand, which serves as a good example of utilizing a 'natural key' or 'primary key,' offers an opportunity to enhance data integrity in the DB. Other keys in Figures 3 were suggested for use as 'alternate keys', and in our case, such keys can also be formed as 'surrogate keys.'

The traditional method of key formation [35,36] has a drawback in that constructed DBs may not always operate reliably. The use of prototype methods may lead to data integrity violations, interruptions in information flows, and other adverse effects. In a biomedical information system, such integrity violations can hamper system performance, impacting the quality of monitoring the environmental effects of chemicals on living organisms in nature. To address these challenges, we propose using IMAGES of fragments of genetic codes AS KEYS in the process of DBs construction, especially as primary keys, based on primary unique information.

Considering the practical realization of this idea, two possible approaches are suggested:

1. The first approach involves using the image from the 'images of fragments of genetic sequence' field as the key itself. This application is depicted in Figure 5 with a dotted arrow, indicating that the image of the genetic code fragment is included in the 'key' field. In this case, there is no need for two separate fields—one for keys and one for images—since the images themselves serve as keys. This can result in saving computer memory, which is particularly crucial for large DBs with extensive biological material.

2. The second approach is for cases where keys for the DB were formed solely based on images of genetic code fragments, but not equivalent to them. In this scenario, a group of random characters (a mixture of numbers and letters) can be coupled with the image of the genetic code fragment to create 'intelligent keys'. Unlike the previous approach, in this case, two fields in the table are necessary, and there is no significant memory savings. However, this method also has its advantages, which will be discussed in future publications.

In conclusion, this article presents an algorithm for constructing novel relational DBs with images, other biomedical information, analytical approaches, and recommendations for optimal execution. Emphasis is placed on creating and applying the most functionally high-quality codes for keys in the database, including primary keys. The use of codes based on images of genetic code fragments of fishes, illustrated in the example of a DB on fishes and chemical inorganic environmental pollutants affecting aquatic organisms, is proposed and demonstrated. The examination and analysis of this task considered cases where one species of fish corresponds to multiple fragments of its genetic sequence, introducing the concept of an additional object, 'image of genetic code fragment'. The proposed method has theoretical and practical significance, expanding the capabilities of electronic systems. Several examples of the method's application were explored, each presenting its own set of advantages and disadvantages.

For instance, the described inventions can find application in constructing information systems for environmental monitoring and other biomedical information systems. [3,4,27,28] The method can also be applied to devices for reading information in barcodes. Barcodes, representing information in a format convenient for technical reading, such as linear-shaped readers or round-shaped fingerprint sensors, can benefit from these methods. Other practical prospects include applications in medicine, such as studying hereditary genetic diseases or DNA mutations under the influence of chemical pollutants (Figures 2–5), criminology, police and military databases, etc.

The method contributes significantly to the development of data protection methods, offering a balanced approach to ensuring the integrity and availability of data in DBs. By applying this method, information integrity is enhanced, leading to better continuity of information flows. The results described herein hold both theoretical and practical importance for improving methods of database construction and enhancing certain data protection methods. This material can be incorporated into courses for educating students.

3. Acknowledgments

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