BIOLOGICAL DATABASES
USING OBJECT-ORIENTED SYSTEM ANALYSIS

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The aim of the work was to develop electronic database of biological organisms (fishes, viruses) on the base of the methods that have been used before in mathematics, engineering, physics. The methods of object-oriented system analysis, construction of models of subject spaces (problem space, solution space), *ER*-diagrams, of constructing databases and others were applied. The examples of prototypes of modern databases with information about fishes developed over the past years in Western European and American countries were presented. An overview of applied methods, concepts and terminology from the areas of object-oriented system analysis, database designing was disclosed. In conclusions the description of constructed database and practical recommendations for the development of databases with the information about domestic biological organisms for electronic information systems are given.

Key words: object-oriented system analysis, biological objects, electronic information systems, fishes, viruses.

Electronic information systems with databases for biotechnology, environmental protection of bioobjects and other biological sciences. Electronic information technology (IT) penetrated deeply into our life — industry, technology, science; they have become a feature that characterizes our reality and level of development of the countries. Being an integrative part of the Europe and modern industrial world, Ukraine is also incorporated into the world scientific and technological progress and has all opportunities to develop progressively new technologies in its own territories. Over the last 30 years, computer technique and related new technologies — network, Internet technologies, and others — have become widespread even in the everyday life of the people. Consequently, the information and computer revolution in classical biology and medicine has happened too. To the solution of these problems the people came about 30 years ago. One of the most actual contemporary tasks is the creation of information systems (ISs) in medicine and biology, and the majority of these ISs operate with the data that have been ordered in electronic databases (DBs). In the last 20–25 years in medicine and in the last 15–20 years in biology, the number of new electronic ISs has been increased rapidly; they had their own peculiarities and specifics in comparison with similar systems in engineering, physics and other similar industries. The number of such ISs in biology and medicine is growing from day to day. Nowadays, at the beginning of the XXI century, the scientists in the field of information and computer technologies (ICTs) discussing further development of new software and computer technology specifically

for medicine and biology. In contemporary world there is an important idea to use such novel ICTs with DB for ordering of information about living organisms — for example fishes [1]; their accounting, descriptions and even for determination of such organisms on the base of these new technologies [2–20]. Sure, in base of electronic information systems (ISs) elaboration the real biological data have to be placed [1, 21–36]. Such primary versions of ISs in Ukraine have been done; technologies of their elaboration partially are described [37–49], and the data about different objects of fauna [21–36, 45, 46] and flora [50–52] may be ordered in them. For the success of such works it is necessary to use positive experience of prototypes development; either of practical or theoretical ways of these tasks solutions [2–20, 53–172]. Some of such prototypes were developed for monitoring of biodiversity changes in fauna or ecological changes also under anthropogenic pressure using ICTs [2–7, 9, 14–18, 46–48, 56, 59, 81, 148, 149, 153, 165, 169–172, 174–176, 178, 183, 186–188]. Some works of this article authors were defended by patents [32, 173–189]. Contemporary knowledge of ICTs technologies, electronic DBs construction were used for present work fulfillment [190–192].

A number of important reasons determine the necessity of the work on the creation of IS with the databases (DBs) in biology. Actually, the previous author's works [45, 46] are the continuation of the works done in present article, because relative databases developments [45] have to be based on the resuts of object-oriented system analysis from present publication. Primarily, the ICTs with databases were developed, first of all, for the needs of technology and such fields as mathematics, physics, statistics and economy (first of all, for energetic). These technologies began to be developed in biological sciences later because of the set of reasons: objects with which the biology deals with are much more complicated, main attention in contemporary societies is paid on high industry development, and so on. In general, ICT with databases comes in two ways to medicine and biology: through the acceptance of ISs that were developed earlier for other industries with further their transformation depending on the specifics of medicine and biology, and by creating of original types of these systems. Today, the samples of ISs with databases in biology are not numerical in comparison with technique, they do not satisfy all practical needs, and therefore almost all new works in these industries

are valuable and find their application. In addition, the material in these items that was given our publications has the practical value because it can be the basis for the creation of new types of systems.

Because the specifics of biology ever were the works with complex objects, living systems, multifactorial influences on them, and etc. thus, an analysis of such specificity and its discussion is really relevant. It is also important that because of peculiarity and specifics of medical and biological objects, accumulation in these areas of great numbers of the results of experiments, observations, etc. — the use of modern information and computer technologies with databases will contribute to the next progress in these areas, since it will allow ones to analyze and to process a huge (and constantly growing!) amount of the data. With the use of previous technologies this was impossible indeed, and this led to the loss with time a significant part of obtained results (including the results of expensive high-precision experiments).

Importance of object-oriented system analysis in process of electronic databases construction. The construction and development of electronic databases (DB) of biological organisms (local DB (separated) or as a part of ISs) is an important task still. Such databases should, as far as possible, contain a collection of information about individual biological organisms, their communities and other related information. The scope of such databases usage is broad: solution of problems in biotechnology, molecular biology and genetics; in preserving of species diversity, protecting the environment from harmful influences; database as the electronic determinants of living organisms and many other applications [37–49]. In our previous works we have provided already the information on developing a database of biological organisms, for example, *Noctuidae* (*Lepidoptera*) and some other *Arthropodae* [37, 45, 46]. However, the methods of DB constructing which have been demonstrated in our publications [37–49, 173–176, 178, 183, 186–188], are standard for use when creating a database of all biological organisms, not just *Arthropodae* [2–20]. Therefore, in this publication we woud like to demonstrate the possibility of their use for other groups of living organisms: fishes and viruses — pathogens of fishes' diseases, in order to involve our fauna representatives as fully as possible in our works. In addition, due to the limited volume of our previous publications,

we were not able to pay necessary attention to the important set of works preceding the process of database development — to object-oriented system analysis of virtual space containing the objects that have to be included into the developed electronic database.

Object-oriented system analysis of the investigated space is extremely important for the reasons of the most rational design of the databases. Our Nature includes a huge number of different groups of organisms. Each of these organisms has its own characteristics, which must be included into the database— there are billions of records. In case of insufficiently qualified determining of such characteristics, establishment of wrong links between organisms, etc., the DBs become irrationally constructed, overloaded with unnecessary details and lack of important information. This leads to slowdown the information search, and even to impossibility of data mining in an imperfect database. Accordingly, the time of data mining in such imperfect databases increases. The situation is even more complicated in case of different databases combining, for example, if they were constructed at different universities. Consequently in present publication, basing on the authors' experience, some practical recommendations were given for the development of modern, perfect biological, Internet-based databases (primarily relational) taking into account the specifics of medical and biological objects, which confirms the relevance of the work performed.

Some examples of modern databases and information systems with information about the fishes. In this section, let's observe some examples of modern databases with information about fishes.

A. Global Information System On Fishes. A global biodiversity information system on fishes is called "FishBase" [16]. Its initial goal is to provide key facts on population dynamics for 200 major commercial fish species. Now DB of this IS grown to having a wide range of information on all fish species currently known in the world: taxonomy, biology, trophic ecology, life history, and uses, as well as historical data reaching back to 250 years.

At present, FishBase covers more than 33,000 fish species compiled from more than 52,000 references in partnership with more than 2,000 collaborators (>300,000 common names and >55,000 pictures). The breadth and depth of information in the database, combined with the analytical and graphical tools available in the web can satisfy different

needs of diverse groups of users (scientists, researchers, policy makers, fisheries managers, donors, conservationists, teachers and students). Its various applications are aimed for sustainable fisheries management, biodiversity conservation and environmental protection. FishBase is result of the work of non-profit, non-governmental organization engaged in the development and management of global databases on aquatic organisms, including their distribution and ecology. FishBase provides the database and web interface for free for 25 years.

B. A database of fish biotransformation rates for organic chemicals. A method published by other authors [17] for estimating whole-body in vivo metabolic biotransformation rate constants (kM) is applied to a database of measured laboratory bioconcentration factors and total elimination rate constants for fish. The method uses a kinetic mass balance model to estimate rates of chemical uptake and elimination when measured values previously were not reported. More than 5 400 measurements for more than 1 000 organic chemicals were critically reviewed to compile a database of 1 535 kM estimates for 702 organic chemicals. Biotransformation rates range over six orders of magnitude across a diverse domain of chemical classes and structures. Screening-level uncertainty analyses provide guidance for the selection and interpretation of kM values. In general, variation in kM estimates from different routes of exposure (water vs diet) and between fish species is approximately equal to the calculation uncertainty in kM values. Examples are presented of structure-biotransformation relationships. Biotransformation rate estimates in the database are compared with estimates of biodegradation rates from existing quantitative structure-activity relationship models. Modest correlations were found, suggesting some consistency in biotransformation capabilities between fish and microorganisms. Additional analyses to further explore possible quantitative structure-biotransformation relationships for estimating kM from chemical structure were encouraged, and recommendations for improving the database were provided.

C. A global database on freshwater fish species occurrence in drainage basins. In their actual publication the authors stated that nowadays the growing interest is devoted to global-scale approaches in ecology and evolution that examine patterns and determinants of species diversity and the

threats resulting from global change [18]. These analyses obviously require global datasets of species distribution. Freshwater systems house a disproportionately high fraction of the global fish diversity considering the small proportion of the earth's surface that they occupy, and are one of the most threatened habitats on Earth. The authors provided complete species lists for 3119 drainage basins covering more than 80% of the Earth surface using 14 953 fish species inhabiting permanently or occasionally freshwater systems. The database results from an extensive survey of native and non-native freshwater fish species distribution based on 1 436 published papers, books, grey literature and web-based sources. Alone or in combination with further datasets on species biological and ecological characteristics and their evolutionary history, this database represents a highly valuable source of information for further studies on freshwater macro ecology, macroevolution, biogeography and conservation.

D. Databases of freshwater fish species distributions. Another report about the databases of freshwater fish species distributions was suggested in [18]. The authors discussed the paradox of fishes species that approximately 40% of all described fish species inhabiting freshwaters, while the remaining 60% are marine habitants. Describing global scale freshwater fish diversity patterns, understanding the environmental drivers and evolutionary processes shaping such diversity and revealing the major human-related threats were the major goals that motivated the compilation of presented database. They conducted an extensive survey of freshwater fish species distribution based on 1 436 published papers, books, grey literature, databases and web-based sources, resulting in species lists for 3 119 drainage basins covering more than 80% of the Earth surface. To date, these databases have been used in several studies that have increased our understanding of freshwater fish species distributions. These studies allowed to accurately map global patterns of native, endemic and non-native freshwater fish species richness and to reveal their environmental and human-related determinants. The databases were also used to evaluate non-native species influence on native communities' structure, to forecast climate change effects on species extinction processes and to analyse effects of current and future scenarios of species introductions

on fish faunas homogenization processes. Recent studies also focused on analyzing the influence of past river connections on the present distribution of native fish species, on analyzing geographical and other differences in diversification rates and origin of actinopterygian fish families, and on evaluating human-related extinction drivers.

Methods of object analysis, constructing of models of subject spaces when creating a biological database about fishes and viruses that they infect. This section deals with the consideration and the characteristics of the methods of analysis of subject space and model construction [191–192]. To solve such problems, the object analysis methods [190] have been developed, which is described below.

The main purpose of objective analysis is to represent a subject space (SbS) as a set of objects with their properties and characteristics that are sufficient for their defining and identification, as well as for determining the behavior of objects within the framework of the chosen system of concepts and abstractions.

For example, in present work we would like to make the database about fishes and viruses that they infect; respectively, for our object analysis in framework of this task solution we have to select primary such main objects as "Fish" and "Virus". Sure, with time in process of task solution, other objects may be added to these first two.

All SbS concepts are essences. Each object is a unique element; it has at least one property or characteristic and a unique identifier in a set of objects.

Analysis of SbS is carried out using object-oriented methods and corresponding standards. The ultimate objective of the object-oriented analysis of SbS is the definition of the object model (OM) with the help of selected objects, the relations between them and their properties and characteristics.

A. Brief overview of object-oriented methods for analyzing and constructing of models. For today, more than 50 object-oriented methods of SbS analysis are known, which have been practically tested. In present work we used only 3 of them:

1. Object-Oriented System Analysis (OOAS). This is a method, which allows identifying the entities and objects of SbS, defining their properties and relationships, as well as building on their basis an information model, a model of objects state and processes of presentation of data flows (dataflow) [190].

2. Object Oriented Analysis (OOA). This is a method, which provides simulation of OM and formation of requirements for SbS by means of a notion "entity-relationship ER", specification of data streams and related processes [190-192]. The scheme — ER-diagram for abstract objects "Fish" and "Virus" is given on Fig. 1.

3. Object Oriented Analysis and Design (OOAD). This is methodology, which is based on ER-modeling of entities and relationships in SbS object model. OOAD provides a system definition and organization of the data using structured diagrams, diagrams "entity-reations" and the matrix of information management [190].

The study of object-oriented methods varieties shows that they have many common features (for example, *ER-modeling*, Dataflow), as well as their specific features. Each developer of the method of object-oriented analysis invented his own new necessary concepts, which semantically coincide often with similar concepts in other methods. Therefore, the terminology the very conceptual apparatus used in this sphere does not always coincide in different methods.

B. Basic concepts of the methods of object analysis of SbS. To the basic concepts of the methods of SbS object analysis would belong the following:

SbS object is an abstract image with behavior that depends on its characteristics and relationships with other SbS objects.

Entity is a semantically important object or type of object, that exists in SbS in reality or it is an abstract concept, whose information must be known and / or recorded.

Concept is the value of some abstract entity of SbS, it is denoted by a unique name or identifier. A group of such concepts is a parent concept, which is obviously determined by some set of common attributes. The concept, along with its attributes is presented graphically in OM or in text form.

Attribute is an abstraction that has all abstracted essence of concepts. Each attribute is denoted by a name unique within the concept description. The set of grouped attributes denotes the identifier of this group. A group of attributes can be combined into a class and to have a class identifier.

Relationship is an abstraction of a set of relations that take place between different kinds of SbS objects which are abstracted as concepts. Each relationship has its unique identifier. Relationships can be textual or graphical. To formalize relationships between concepts, the auxiliary attributes and links to identifiers of these relationships are added. Some relationships are formed as consequence of other relationships existence.

Class is a set of objects with the same properties, operations, relationships, and semantics. Any object belongs to a class. A class is represented by various methods (for example, by lists of objects, operations,
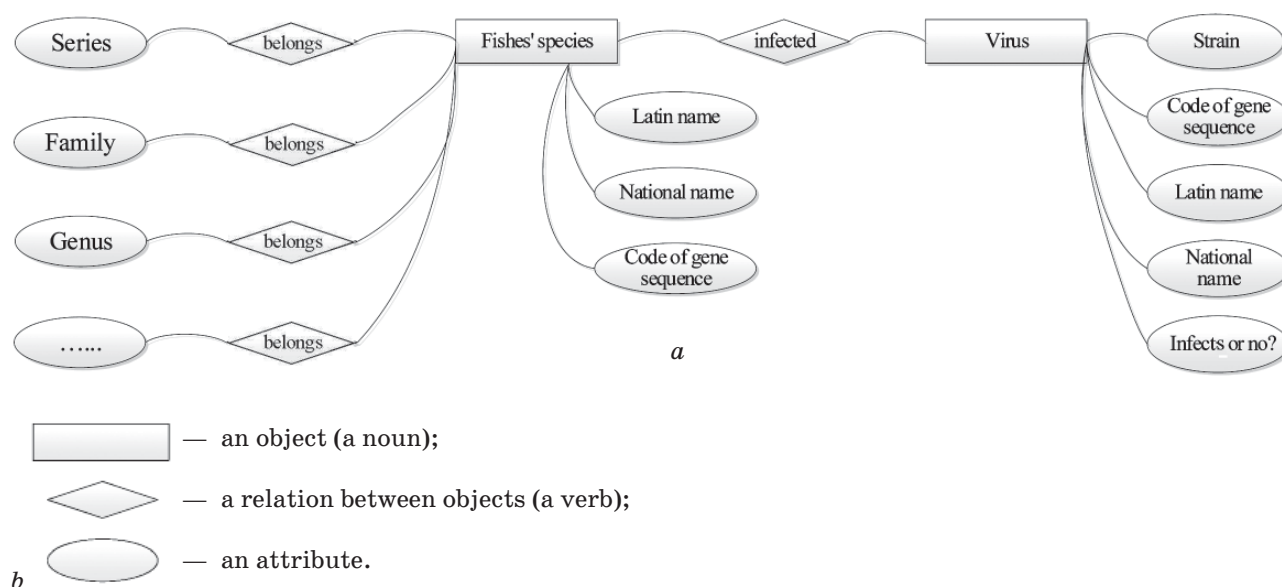

Fig. 1. **ER-diagram for the database "Fishes And Their Virus Diseases":**
analysis for two main objects "Fish" and "Virus":
a — fragment of ER-diagram (explanations see in text);
b — symboic denotation of objects, relations and attributes at the scheme

states). Class is measured by the number of the samples, operations, etc.

Subject space (SbS) is what is analyzed in order to isolate a specific set of concepts (entities, objects) and relations between them. On the set of these concepts, the tasks are defined for the purpose of their automated solution. The *subject space* can be divided into the *problems' space* and the *solutions' space*. The *problems' space* includes the entities, the concepts of SbS, and the *solutions' space* is the set of software implementations of the tasks, including functional components that provide the solution of the tasks and functions of SbS represented in this space.

Allocation of SbS entities is carried out taking into account the differences determined by the relevant conceptual structures. SbS model is a set of precise definitions of concepts, objects and their characteristics, as well as a set of synonyms and classified logical relationships between these concepts.

Relations or links are established for model objects. There are static (permanent) relations that do not change or change rarely, and dynamic relations that have certain states and change during the operation of the system. The state of connections between objects can evolve over time.

The links between the objects can be following (Fig. 2):

• *one-to-one relationship* (1: 1) exists when one sample of an object of a certain class is associated with a single sample of another class, i.e. single instances of the classes are involved in communications;

• *one-to-many relationship* (1: N) exists when one samples of an object of a certain class is associated simultaneously with one or more samples of another class or of the same class;

• *many to many relationship* (M: N) exists when several samples of objects of two classes take part in relationships, i.e. one or more samples of another class is associated with one or more samples of the first class.

Hierarchical model of biological objects' organization and classification from the point of view of DB construction.

Hierarchical model is extremely important model of objects' organization either in living Nature or in object-oriented methods of programming; in our models we have to refect obviously this hierarchical type of objects' organization. In our previous publications [37] we have written already that hierarchical models in informatics are enough similar to hierarchy of living organisms in nature. As example of DB construction let's study now the pair of organisms: the fish (carp) and virus that cause its disease. It is known that for hierarchical classification of organisms in living nature, Carl Linnaeus proposed his scheme on 1 761 [70, 37]. Let's represent according to his scheme such well-known fish as ordinary carp (*Cyprinus carpio* L.) that belongs to animals from *Eukaryota* Domain (Fig. 3).

Further in our investigation we would like to unite in linked databases the information about fishes (for example, the carp *Cyprinus carpio* L.) and viruses that are the reasons of fishes' diseases. For example, for *C. carpio* it is known that they have such virus diseases: (spring viremia of carp, infectious necrosis of hematopoietic tissue, infectious necrosis of pancreas, viral necrosis of erythrocytes, herpesvirus infections, iridovirus infections, and etc.), which are characterized by acute flow with high mortality of fishes that causes significant economic losses to world aquaculture.

At the next step we have to describe at one scheme these 2 objects (carp-virus) with all their important characteristics and relations between objects. Such scheme one could see on Fig. 4, that is "*ER*-diagram" modified for the fish "Carp" (compare with Fig. 1)

Functional role of ER-diagram is to represent in whole all *objects* from the database with all their *relations* and with all characteristics of the objects that are called "*attributes*". Sure, characteristics those are important from the point of view of the database representation! For example, such characteristic as "Maria likes to fry carps"

Fig. 2. **Power of reactions between the objects during the database elaboration:**
"M: N" — "many-to-many". In this example, this means:
"M species of fishes have been infected by N strains of viruses"

Domain	*Eukaryota*
Kingdom	*Metazoa*
Type	*Chordata*
Subtype	*Craniata*
Class	*Actinopterygii*
Infraclass	*Teleostei*
Series	*Cypriniformes*
Family	*Cyprinidae*
Genus	*Cyprinus*
Specie	*Cyprinus carpio* L.

Fig. 3. **Scheme of ordinary carp (*Cyprinus carpio* L.) hierarchic classification**

probably, is not so important for academic databases. But for such DB are too important the data (attributes) as gene sequences, specie, family, genus and other similar. For the representation of these 3 main notions of *ER*-diagram the special symbols are used (Figs. 1, 4): rectangle (object), rhombus (relation), oval (attribute). A rectangle (object) usually includes a noun — for example, the "fish". A rhombus (relation) is ever a verb — for example, "to infect". And an oval (attribute) ever includes characteristics: species (or other classification unit), color, dimensions, etc. Such diagram helps to analyze better all entities that we would like to include into the database and to represent them in their entirety. Without such analysis the construction of DB of a high quality would not be possible.

Since each species of fish may be infected by several viruses (N), and each virus can infect different species of fish (M), then the links between the objects have to be marked as "M:N", which actually means: "M species of fishes can be infected by N strains of viruses" (Fig. 2). As noted above, other variants are possible, like "M:1" — means "M species of fishes can be infected by the virus of one strain". Also "1:1" — means "one specie of fish can be infected by the single virus strain". Such abstraction allows us to design a high-quality database and to verify its accuracy in the visual diagram — "ER-diagram" in future.

Development of the database with information about fishes' on the base of "ER-diagram". The scheme "ER-diagram" we need for further development of the database with information about fishes on its basis. Let's study the representation of such database in the form of a set of tables, which are given on Fig. 5. It is easy to see that:

1. Objects of "ER-diagram" were turned into separate tables.

2. Attributes were turned into the fields of these tables (in our case — in the columns).

3. The relations between the objects were turned into relations between separate tables.

At the same time, the power of reations reflects the number of tables that need to be linked with the object; and the developer deside what number have to be. If the power of reation is 1, then the link is formed with one table, if "M" — with "M" numbers of tables.

Objects in our model can be characterized by the number of attributes. The lists of some attributes is given below. On Fig. 5 one can see the tables with the less number of attributes because of limited space of the page.
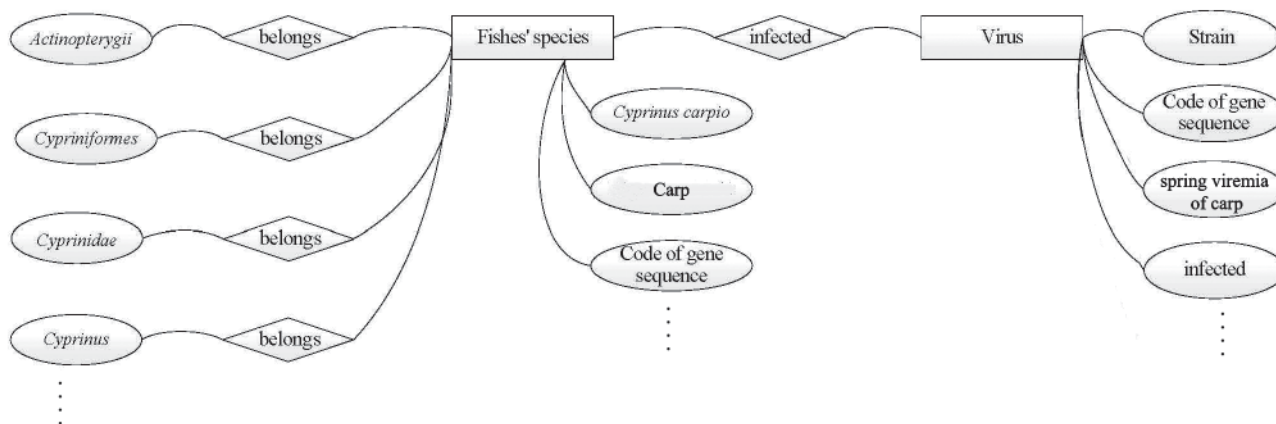

Fig. 4. **Fragment of ER-diagram "Fishes And Their Virus Diseases" on example of *Cyprinus carpio* L.**

Object "Fish"
Attributes:
Primary key
The name of the fish (in Latin, Ukrainian and Russian).
   Class
   Subclass
   Series
   Family
   Genus
   Species
   Area of inhabitance.
   Biotopes of inhabitance.
   Objects of nutrition.
   Data of fishing.
   References to literary sources.
   ………….
   Comments.
   Other.

Object "Virus"
Attributes:
Primary key
The name of the virus (in Latin, Ukrainian and Russian).
   Dimentions
   Code of gene sequence (if it known)
   Name of disease
   Symptoms of disease
   References to literary sources.
   …………………..
   Comments.
   Other.

Relations between the tables using "keys." In order not to lose the information that is filled in the database of biological objects, the technique of "keys" is used.

"Keys" are necessary "tools" for relations establishing between the objects; they guarantee that the information from the database is accessable and it always may be obtained from there. Indeed, there is no sense to write thousands of data records into a structure if these data can not be used, if they are not accessible! Consequently, the "keys" are the elements of each table; they are related to each other through programmed links. By obtaining the information from one table, it is possible to obtaine the information from another table associated with it through a link that unites their keys. Usually, as a "key" serves a certain code (numbers or other symbols), and the links between such codes from individual tables in many modern software environments, even a young developer can make by themselves (Fig. 5).

At our tables (Fig. 5) there are 2 codes (or keys) have to be linked:

1) 1* (*Cyprinus carpio* L.) and
2) kB (Rhabdovirus carpio — Spring Viraemia of Carp Virus (SVCV)).

This means that when user in Internet will "click" on "*Cyprinus carpio* L." he will see consequently the information about (Rhabdovirus carpio (Spring Viraemia of Carp Virus (SVCV)) — virus that infects carp.

In addition, it is easy to follow in the diagram whether all entities are linked together. In this case it makes possible to access all records, so, the information from the database becomes fully available for everybody (the condition of the "integrity" of the data is fulfilled). Alternatively, if this condition is violated, the user will not be able to obtain the information from those parts of the database that are not connected by such links. However, using the methods described above, the programmer can easily recover connections based on the ER-diagram and linking the objects using keys. In the application of the abovedescribed methods, there are no differences between biological and technical databases and anybody for such purpose can study this technique using appropriate manual. The previous works of Klyuchko O.M. [45, 46] are the continuation of the works done in present article, because relative databases developments [45] have to be based on the resuts of object-oriented system analysis from present article.

Thus, according to the purpose of the work there were demonstrated that the methods for relation electronic databases construction, that were developed earlier for physics, engineering, etc. can be applied in other branches which traditionally do not refer to technical disciplines. Usually these were done by their acceptance in the new spheres of application, for example, in biology and medicine. In present publication, the following set of methods was used to develop databases with biological content: object-oriented system analysis (OOAS), object-oriented analysis (OOA) and OOAD (object-oriented analysis and design) — the latter methodology is based on ER-modeling of entities and relationships in the object model (ER-diagram).

Actually, the previous author's works [45, 46] are the continuation of the works done in present article, because relative databases developments [45] have to be based on the resuts of object-oriented system analysis from present publication. At the beginning of present article, a number of examples of electronic databases of biological objects that were developed in different countries of the

Table "Fish"

Primary key	Name of species (Latin)	Name of species (national)	Photo	Class	Sub-class	Series	Family	Genus	..
1*	*Cyprinus carpio* L.	Короп звичайний	Foto 1: http://www2.dnr.cornell.edu/cek7/nyfish/Cyprinidae/common_carp.jpg	*Actinopterygii*	*Neopterygii*	*Cypriniformes*	*Cyprinidae*	*Cyprinus*	
2*	*Salmo labrax* Pallas	Лосось чорноморський (сьомга)	Foto 2: https://redbook-ua.org/media/images/main/a-327.png	*Actinopterygii*	*Neopterygii*	*Salmoniformes*	*Salmonidae*	*Salmo*	
3*	*Salmo trutta* L.	Лосось струмковий (форель струмкова)	Foto 3: https://ih1.redbubble.net/image.65006165.3846/flat,800x800,070,f.u2.jpg	*Actinopterygii*	*Neopterygii*	*Salmoniformes*	*Salmonidae*	*Salmo*	
...									

Table "Virus"

Primary key	Name (Latin)	Name (national)	Genom	Family	Dimentions	Disease it cause	Symptoms of disease	Image	Other
kA	VHS virus	Virus of haemorrhagic septicaemia	RNA	Rhabdoviridae	180−240×60−75 nm	Viral haemorrhagic septicaemia, VHS	Darkening of the skin and fecundity of the fish. The sick fish slowly floats on the surface of the water, almost does not react to irritation. Gum is anemic, with striped hemorrhages. The hemorrhages are also found in the conjunctiva, darkening of the skin, anorexia, inhibition of fish. The disease runs in acute, chronic and nervous forms.	Image 1: https://en.wikipedia.org/wiki/Viral_hemorrhagic_septicemia#/media/File:VHS.png	
kB	Rhabdovirus carpio (Spring Viraemia of Carp Virus (SVCV))	Rhabdovirus carp	RNA	Rhabdoviridae	105−125×70−85 nm	Spring Viraemia of Carp Virus, SVCV	Darkening of the skin, anorexia, inhibition of fish. The disease runs in acute, chronic and nervous forms.	Image 2: https://nas.er.usgs.gov/XIMAGESERV ERX/2012/20120424150715.JPG	
...									

Fig. **5. Tables of developed database with information about fishes:** *a, b* — the attributes became the fields of the tables. "Primary keys" are the tools for the formation of the relationships between the tables. Cyrillic words are in tables for domestic use in Ukraine. The link between codes 1* and kB means that carp is infected by "Spring viremia virus" and this will be shown in future database

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world were given. Within the framework of the thesis on the correspondence of the hierarchical classification of living objects and the idea of hierarchical subordination of objects in some methods of computer sciences (including databases development), an example of the hierarchical classification of *Cyprinus carpio* L. carp was given. It was noted that similar type of subordination can be reflected in the attributes in process of relational biological database development, exactly this was done further by the authors.

This publication also provides a description of the concepts of objects, relationships, attributes, keys, and others.

In addition, on the example of biological objects, the types of relations 1:1, 1:N, M:N were shown. On the basis of such theoretical generalizations an ER-diagram for two types of objects was developed: for the carp *Cyprinus carpio* L. and viruses causing diseases of this fish. At the end of the pubication it was shown how relational tables of biological databases are formed, and how they are interconnected with the "keys". The authors hope that present work will be useful for training students of the corresponding specialties, as well as will contribute to the further elaboration of domestic biological databases in Ukraine.

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БІОЛОГІЧНІ БАЗИ ДАНИХ ІЗ ЗАСТОСУВАННЯМ ОБ'ЄКТНО-ОРІЄНТОВАНОГО СИСТЕМНОГО АНАЛІЗУ

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Метою роботи було розробити електронну базу даних біологічних організмів (риб, вірусів) на основі методів, які дотепер застосовували у математиці, техніці, фізиці. Під час виконання роботи використовували методи об'єктного системного аналізу, побудови моделей предметних областей (простір задач, простір рішень), *ER*-діаграми, методи конструювання баз даних та інші. У статті розглянуто приклади-прототипи сучасних баз даних з інформацією про риб, що їх розроблено протягом останніх років у країнах Західної Європи та Америки. Наведено огляд застосованих методів, концепцій та термінології з областей об'єктного системного аналізу, конструювання баз даних. У висновках подано опис сконструйованої бази даних та практичні рекомендації з розроблення баз даних з інформацією щодо вітчизняних біологічних організмів для електронних інформаційних систем.

Ключові слова: об'єктно-орієнтований системний аналіз, біологічні об'єкти, електронні інформаційні системи, риби, віруси.

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