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Ecology of Fish Community: Niche Modeling Based on Fish Morphological Parameters

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Introduction

This book is a monograph deconstructing morphological models of river fish communities. It provides a new method for studies of fish community niches and addresses morphological modeling, software analysis, and applications.

Over long-term evolution, fish interactions with their environment have led to the formation of new species, the exploitation of various ecological niches, and the development of species communities. Although organisms can be dated from fossils, the niche composition of fish communities 200 years ago remains unknown. The lack of data on the evolution of ecosystem structure and function affects studies of ecology. The purpose of this book is to establish a systematic method for determining niches based on species morphology and the morphological characters of fish communities, as well as to discuss the niche composition of community species through historical records of “qualitative” species. This book attempts to provide a method to clarify community species structure in a given ecosystem and to establish a standard for evaluating ecosystem changes based on community species structure. This book may provide a community structure reference system for river ecosystem assessment and restoration based on natural attributes. Using fish morphological data, we establish a model for fish community studies based on morphological characters. This book also examines the relationships between fish species in communities from the perspective of ecological niches, and it attempts to establish a fish community research tool for the ecological restoration of rivers.

This integrative, cross-disciplinary book, which is both deeply theoretical and has strong practical value, is a rich source of basic information and research content. This book should be useful to researchers, teachers, and students of higher education as a reference for ecological river management, environmental protection, and fishery resource management.

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Foreword

Rivers, an important part of the earth's ecological system, can be described as the basis of life and biological growth. Rivers, which predate human beings, support life on earth, and human survival and development depend on rivers. For example, the Chinese civilization originated in the Yellow River valley, the ancient Egyptian civilization originated in the Nile Valley, the Indian civilization originated in the Ganges valley, and the ancient Babylonian civilization originated in the Tigris and Euphrates valleys.

River water supports life. Water content differs among biological species but is generally 60%–97%. Water is the basis of life activities. The water content of the human body is about 65%. Fresh water is the basic material that drives the activity of the human body. Although water covers 71% of the earth, with a total water volume of 1.386 billion km^3, freshwater accounts for only 2.53% of the total water resources, and 87% of the freshwater is in the form of polar ice caps, Alpine glaciers, and permafrost. River water, lake water, and shallow groundwater are the main freshwater resources that can be utilized by human beings, and this only accounts for 0.26% of the earth's total water. Globally, about 9000 km^3 of freshwater resources can be used effectively per year.

There are more than 1500 rivers in China, with a basin area of more than 1000 km^2. China's water resources are about 2680 km^3/yr, which is equivalent to 5.8% of the total global runoff, ranking fourth in the world. In total river runoff, China ranks sixth in the world. China's per capita runoff is 2530 km^3, about a quarter of the world's total per capita runoff. It is clear that China is a water-poor country, while China's water resources maintain the survival and reproduction of 1.4 billion people.

Ecology is the state which defined the existence and development of living things in a certain natural environment. When we close our eyes and think about it, the ecological environment that unfolds in our minds is a picturesque landscape of clear water and green mountains. However, as a result of human economic and social

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activities, rivers have been divided by numerous dams, natural waters have been occupied, and freshwaters have been polluted. Yet, we live in this environment as if unaware of the destruction of aquatic ecology. Human activities are also unwittingly exacerbating the destruction of nature.

Fish are some of the most advanced organisms in the aquatic ecosystem, interacting with other aquatic organisms and the aquatic environment to maintain the dynamic equilibrium of the ecosystem. However, as society and the economy have developed, anthropogenic influences on river ecosystems have become increasingly severe, and fish communities have suffered serious environmental stress. Species extinction, loss of diversity, and declining resources are common problems facing the river environment worldwide. Fish already suffer, and humans would also be affected by the stress that fish are suffering. Fortunately, our society and government pay attention to ecological problems and have put forward new requirements for an ecological civilization. Rivers are expected to return to their natural states, our living environments will gradually improve, and man and nature will return to harmonious coexistence. However, we have to work together to make this happen.

Under the background of ecological protection, we wonder about the nature of river ecology. What kind of relationship exists between organisms and the environment in an aquatic ecosystem? What can we do to protect aquatic ecosystems? It is necessary to report to society our ideas and findings, which are based on the results of multi-year research, in order to clarify the direction of our work with respect to aquatic ecological protection and to better support ecological protection activities. To those thinking, we have decided to publish the “River Ecology Series.”

The “River Ecology Series” relies on several platforms, such as the Pearl River Fishery Resources Observation and Experimental Station of the Ministry of Agriculture and Rural Areas; the Pearl River Basin Fishery Ecology Environmental Monitoring Center of the Ministry of Agriculture and Rural Areas; the Key Laboratory of Fishery Resources and Environment Diversity Protection and Utilization of the Chinese Academy of Aquatic Sciences; the Pearl River Fishery Resources Survey and Evaluation Innovation Team; and the Pearl River Fisheries Research Institute of the China Academy of Aquatic Sciences. During the development of this discipline, a team was established to study hydrochemistry, toxicology, plankton, benthos, fish, and biodiversity conservation. The work of this team revealed the characteristics of river water quality, the composition of biological communities, and the evolution of food chains under environmental stress. A quantitative sampling method called the “River Section Control” method, was used to monitor floating fish eggs and larvae and to improve the quantitative assessment of fish resources in rivers. An observation system for locating and monitoring early floating fish resources was established, which provided data for studies of fish population dynamics. The relationships between environmental factors and larval species, river structure, and river volume with respect to drifting larvae were interpreted over various time scales. The regularity of occurrence and annual variations in early fish resources were determined. The research platform “Ecological information database of floating fish eggs and larvae in the Pearl River” was established. Our long-term data on early fish resources can be used to expand basic research in various fields, including hydrology and meteorology, for transdisciplinary studies. With respect to the research of alga, a monitoring and analysis system for long-term and high-intensity sampling has been established, which expands the research scope for elucidating the current state and succession of river ecology. Some frameworks for the protection of river fish biodiversity, the restoration of fish resources, and ecological restoration engineering have also been developed. These efforts have gradually exhibited our team's work in the understanding, research, and service of river ecosystems. The "River Ecology Series" will focus on fishery resources and ecological domains, constructing a framework for the series from the perspective of the relationship between fish and the environment in an aquatic ecosystem.

With respect to the river ecosystem itself, this series will publish the team's exploratory research, including discussions of the characters of the water environment, changes in the water environment, the structure of the food chain, the relationship between the food chain and the environment, and certain problems and solutions for the river ecosystem. The "River Ecology Series" began with two books about studies of fish, including "The Pearl River system fish primary color atlas (Guangdong section)" and the "Hainan freshwater and estuarine fish primary color atlas," and the five books in the observations of the changes and succession of fish resources, including "Floating fish eggs and larvae monitoring diary (2006) in the Zhaoqing section of the Pearl River," "Floating fish eggs and larvae monitoring diary (2007) in the Zhaoqing section of the Pearl River," "Floating fish eggs and larvae monitoring diary (2008) in the Zhaoqing section of the Pearl River," "Floating fish eggs and larvae monitoring diary (2009) in the Zhaoqing section of the Pearl River," and "Floating fish eggs and larvae monitoring diary (2010) in the Zhaoqing section of the Pearl River." We also exhibit our understanding of fish distributions in the book of "The distribution of the main fishery resources in the Pearl River", and the changes in river ecosystem structure and function in the water areas in the book "A study of the aquatic ecological characteristics of the river network in the Pearl River Delta", the mechanisms of fish resources in key river ecological units and an evaluation system for river ecosystems based on the number of early fish resources in the book of "Early river fish resources", and the theory and method of functional management of spawning grounds for the functional evaluation system for spawning grounds in the book of "Studies on spawning grounds of river fishes". This series aims to improve the management of river fishery resources and river ecosystem management through the ecosystem and fish community construction theory.

Through the publication of the "River Ecology Series," we express our understanding of river ecology to the reader. We hope that our ideas in this book series can inspire thinkings in river ecology and are useful to the reader.

More than 14 950 species of freshwater fish worldwide (Tedesco *et al.*, 2017) belong to 47 orders, 209 families, and 2298 genera (Richard van der Laan, 2017). Fish in a given ecosystem form communities based on the functional characteristics of the food web and the ecological niche, in this way, completing the river ecosystem energy cycle in different environments. The fish community evolves with changes in the environment.

Due to the impact of human activities on the environment, the changes in fish communities are exacerbated and lead to changes in the aquatic ecosystem. Fish are the key organismal group in the food chain of the river ecosystem, determining the state of energy output. River systems influenced by human disturbance are generally in a state of eutrophication. Fish play an important role in the water purification process, performing energy and nutrient output functions in the water. When water quality becomes a strategic demand for a human being, it is necessary to study the relationships within the fish community in order to maintain the optimal energy output of the river fish community.

Over long-term evolution, fish interactions with their environment can lead to the occurrence of new species, the exploitation of different ecological niches, and the development of species communities. Although organisms can be dated from fossils, the niche composition of fish communities 200 years ago remains unknown. The lack of data on the evolution of ecosystem structure and function obstructs the studies of ecology. The purpose of this book is to establish a systematic method for determining niches based on species morphology and the morphological characters of fish communities and to discuss the niche composition of species communities using historical records of "qualitative" species. This monograph attempts to provide a method to clarify community species structure in a given ecosystem and to establish a standard for evaluating ecosystem changes based on community species structure. This work may provide a community structure reference system for river ecosystem assessment and restoration based on natural attributes. Using fish morphological data, we established a model for fish community studies based on morphological characters. This paper also examines the relationships among fish species and fish communities from the perspective of the ecological niche and attempts to establish a fish community research tool for the ecological restoration of rivers. This book is part of the "River Ecology Series."

The book is supported by the Fishery Administration Bureau of the Ministry of Agriculture and Rural Areas, the Yangtze River Basin Fisheries Administration Bureau of the Ministry of Agriculture and Rural Areas, the Science and Technology Agency, and the Department of Agriculture and Rural Areas of Guangdong Province. I would like to express our heartfelt thanks to the experts who have encouraged and supported the authors in the preparation of this book.

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In October 2022, Ecology of Fish Community: Niche Modeling Based on Fish Morphological Parameters was published in Chinese by Science Press (Li X.-H., *et al.*, 2022). Readers can scan the QR code in the book to download Chinese version of Niche Modeling software (http://fmodel.prfri.ac.cn). The authors would like to express their gratitude to Science Press and EDP Sciences for publishing the English edition of Ecology of Fish Community: Niche Modeling Based on Fish

Morphological Parameters. This book is mostly base on the published Chinese edition except for removing the chapter to introduce the Chinese version of Niche Modeling software.

This integrative, cross-disciplinary book, which is both deeply theoretical and strongly practical significance, is a rich source of basic information and research content. The book can be used by scientific workers, teachers, and students at colleges and universities as a reference for ecological river management, environmental protection, and fishery resource management. Due to the limitations of time and scope, there are inevitable omissions in this book. We hope that readers will make valuable suggestions for future improvements.

Prof. Xinhui LI

May 31, 2020

Chapter 1

Fish Communities and River Ecosystems

A biological community refers to the distribution of organisms in a certain time and space, usually including animals, plants, microorganisms, and other species populations. Biological communities are the living parts of an ecosystem. Biological communities depend on the environment; usually, each environment has a corresponding specific biological community. Therefore, the ecological environment includes the biological community and the biological habitat. More complex environmental conditions imply that the biological community has a more complex structure and higher species richness, with a greater number of ecological niches and a lower intensity of competition among organisms within the community. Therefore, complex environments generally have relatively stable community structures, while less complex environments generally have more unstable communities.

The word “niche” first appeared in 1910 in the ecology treatise of the American scholar R. H. Johnson. The early concept of “niche” applied to the species distributions of flora. In 1924, Grinnell applied “niche” to the concept of “space.” In 1927, Elton defined an animal’s niche as its place in the environment, including the relationship between food and predators. In this way, “niche” includes a conception of “function.” In 1957, Hutchinson described “niche” as a multidimensional space in which all non-biological and biological species elements existed, using the phrase “basic niche.” Under this concept, a species niche may become a “niche” without boundaries or a natural niche. A “natural niche” contains all of the elements of the survival of species or communities and is as well a system, a concept of the whole, and an ideal ecological space. However, due to competition among species in nature, each species can only occupy a part of the basic niche, which is known as the actual niche. Niche represents the minimum threshold of habitat that is necessary for each organism to survive in an ecosystem. Therefore, what is usually studied is the relative niche. By means of artificial segmentation, the main conditions for the survival of interacting species are separated from the natural niche and become a bounded niche space; the relative niche is a part of the natural niche. In fact, the niche varies with the environment. For example, when the main food source is scarce, an animal will increase its prey species and tend to expand its feeding habits, broadening the

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niche; when the food sources are rich, the number of prey species will probably decrease and feeding habits will tend to become more specialized, narrowing the niche. Consequently, the same food source faces different predators, which is considered niche overlap.

The basic characteristics of a biological community include species diversity, community growth form and structure, dominant species, relative abundance, and nutrition structure. In response to the specific ecological conditions, the community spatial structure includes different horizontal and vertical structures. In the community, there are dominant species, and the species in the community often change over time. These species are constantly interacting with each other, so the niche is in a dynamic state. Any organism in a given community has both competitive and mutually beneficial aspects, and the balance between these aspects should be one of the main characteristics of an ecosystem. Currently, community studies focus on competition, predation, mutualism, and abiotic stress relationships among species (Bruno *et al.*, 2003). As human development is increasingly dependent on ecosystem services, future community research will focus on the functional needs of ecosystems, and functional communities of organisms will become the tools that help the ecosystem to achieve its functional goals. The mechanisms of functional community construction not only provide a theoretical system for restoring ecosystem function but also lay a foundation for the shaping of functional communities.

Ecological environmental elements constitute the spatial dimension of the community. Different species occupy special positions in the community. Species diversity corresponds to the multi-spatial dimension of the community ecosystem, which is the basis of the niche concept. A niche refers to the space occupied by species in the system and reflects the functions of species in the system, the relationships among species in the community, and the functional state of the ecosystem. The morphological characters of individuals can reflect the niche status of a species. In the ecosystem, the sizes of individuals within a species can reflect differences in living space and energy utilization, while variations in the sharpness of animal teeth can reflect differences in food lineages and feeding niches. Differences in leaf morphology indicate differences in energy absorption, which correspond to differences in energy niches.

Taxonomy adds a temporal dimension to species in a community, reflecting the response of "niches" to environmental evolution. The community is in a multi-dimensional system, which shapes the morphological and biological characteristics of different species. All aspects of life phenomena can provide features for classification, including physiology, biochemistry, proteins, genes, and mating behaviors. The evolution of organisms into different species is usually described based on species characteristics or attributes, but the most intuitive classification method is morphological classification, especially based on external morphology. People recognize species based on morphological characteristics, and morphology refers to the appearance of things, or, under certain conditions, a reflection of gene expression. Morphology is the basis for species classification. Through the analysis of the characteristics of species diversity, all of the species in a community sample can be distinguished based on the average "distance" among species. This is the simplest character measure, and its association with phylogenetic and functional diversity forms the analytical framework for systematic classification (Clarke and Warwick, 1999). Abellán *et al.* (2006) argued that environmental changes or human activities cannot change the taxonomic properties of species. Organisms have many characteristics. In morphological classification, characters are divided into morphological characters and quantitative characters. The morphological characters are extracted into taxonomic characters to identify species. By using a large number of numerical classification features to form a data matrix, a biodiversity index of classification features (Leonard *et al.*, 2006) can be established on a computer operating system and used to study community structure and species relationships. By constructing a digital dataset of morphological characters comparable among species, a multi-dimensional system can be formed to characterize species and environments. This system can be used to study the interactions among species, as well as the stability and evolutionary trends of the community.

Species classification and taxonomic data can correspond to sequential changes in interspecies order and reflect the evolution of species communities. Therefore, the morphological data for a given organism include information about adaptation, niche, and system evolution. Community characteristics are the result of the adaptation of a species to environmental change, including changes in the niches of various species. Because the number of factors involved in the theoretical niche has no boundary, it is difficult to establish a standard niche to evaluate community status. In model analysis, many environmental factors have uncertain aspects, including variable boundary, data quantity, analysis statistics, model, and theory. It is difficult to establish a standard for assessing the status of communities and niches.

Freshwater fish are fish inhabiting rivers, lakes, reservoirs, and other freshwater water bodies. There are about 32 500 species of fish worldwide, of which more than 15 000 live in freshwater. Less than 10% of all migratory fish species migrate between freshwater and marine habitats. Fish community characteristics include regional specificity, systematic correlation, relative stability, and interspecific relationships such as mutualism, competition, parasitism, and predation. The number of species comprising a community can vary greatly depending on the abundance of nutrients. Over the past half-century, freshwater fish in China have become steadily more threatened. Compared with the 1980s, the fish resources in the Yangtze River and the Pearl River have decreased by more than 60%, and more than one-third of the fish species in these communities have experienced substantial succession. The decline of fish resources affects the food chain in the river ecosystem, resulting in insufficient energy and material circulation in the water body. Guaranteed water quality has become an important problem to be solved in social development. Water quality assurance, the restoration of fish resources, and the rebuilding of fish communities have become integral issues in the restoration of river ecosystems. Fish community status is closely related to the environment, and fish communities differ with respect to species diversity, biomass, and function.

The communities discussed in this book are fish in river ecosystems. Fish are aquatic vertebrates that breathe through their gills, swim by wiggling their tails and trunks in coordination with their fins, and feed by opening and closing their jaws. Fish make up about 53% of all vertebrate species, and about a third of all fish live in freshwater. Fish are active consumers. Fish may be carnivorous, herbivorous, or omnivorous. In studying fish, we assumed that the boundary was an ecological unit in a section of a river, in which a community is composed of many species of fish. The "biomass" of each species and the "biomass" of the total community were regarded as the niche of the corresponding species. That is, "biomass" was used to represent the spatial niche occupied by fish in the water body. The quality of fish in a river ecosystem is affected by the environment, and the degree of interannual quality change can reflect the degree of environmental change. In the analysis model of species morphological characteristics, the influence of environmental factors on species can be determined by taking the biomass abundance of species as the adaptive variable to the environment. The results of the morphological character analysis model included the comprehensive effects of the community species' response to environmental change. The results of this niche analysis indirectly introduced environmental factors. Before the introduction of the model, this chapter reviews the basic characteristics of fish and their role in river ecosystems.

1.1 Species

A species is a group of closely related organisms in which males and females mate and produce fertile offspring. Species are the basic units of biological reproduction, and each species maintains a series of ancestral characteristics. There are obvious differences between species, and hybrids that cannot mate or copulate cannot reproduce. Species are the basic unit of biological classification. Each species has unique characteristics. No two species are identical. Each species has a taxonomic status; the boundary, phylum, class, order, family, and genus can reflect the evolutionary history of the species.

Natural fossil records of prokaryotic bacteria and cyanobacteria date back more than 3 billion years, while eukaryotes, such as gold algae and green algae, have been found in strata dated between 1.4 billion and 1.5 billion years ago. The diversity of life on Earth is so great that there are thought to be at least 6–14 million species on the planet, including animals, plants, and microbes. Others think that there are around 30 million species. About 1.75 million species have been identified. As the planet evolves, the species in biological communities are constantly changing: some species go extinct, and some new species emerge.

1.1.1 Species Classification

Classification dissects the parts of an individual of a given species to establish identification indexes from the features of various parts, such as body shape and organ structure (including anatomy, histology, and organology), the cell, the tissues, the organ process, and other parts of the organism. Based on the similarities and differences among systematic characteristics, biological groups are classified using a category-based system (*i.e.*, boundary, phylum, class, order, family, genus, and species).

There are millions of species living on Earth. Species classification means to classify, rank, and name living things according to certain rules. Humans have long identified and named species. Erya, a book written in the Early Han Dynasty of China, describes animals in four categories: insects, fish, birds, and beasts. J. Ray used genera and species to distinguish plants in 1682. In 1753, Carl Linnaeus divided nature into plants, animals, and microorganisms. He then organized animals and plants into a hierarchal system using boundaries, classes, orders, genera, and species. Each species occupies a place in the taxonomic system, forming a ranking system for species identification. In 1859, with the publication of Darwin's On the Origin of Species, the taxonomic system was established. Taxonomy is the elucidation of the historical origins of species, such that the classification system reflects evolutionary history. Taxonomy sets boundaries between species, analogous to the "bits" that define a species.

1.1.2 Fish

Fish are aquatic vertebrates that breathe using gills. Fish have a head, trunk, and tail with fins on the back, thorax, and abdomen. Fish swim in the water by moving the tail and trunk in coordination with the fins. The mouth is at the front or lower end of the head, and the fish feeds by closing the upper and lower jaws. Fish belong to the subphylum Vertebrata in the phylum Chordata. About 32 000 species of fish are found worldwide, distributed in the oceans and freshwater. Two-thirds of all fish live in the oceans, and the remainder inhabits freshwater.

1.1.3 Morphological Characters for Classification

Form refers to the appearance of things, or, under certain conditions, the form of expression. The body part of a species is a state that can be grasped, perceived, or understood. Morphological characteristics can also include the appearances and structures of organs, cells, and tissues, as well as the characteristics of organogenesis. Species morphology is the result of interactions within species communities during niche competition, which is determined by the relationships among species and between species and the environment. The morphological characters of species reflect competition, mutual benefit, and balance among species, as well as the regional habitat or environment. The morphological characteristics of species represent the characteristics reflected by the best niche in which the species is located.

1.1.3.1 Fish Morphology

1.1.3.1.1 Fusiform

Fusiform fish have spindle-shaped bodies that are slightly flattened. The head–tail axis is the longest, followed by the dorsal–ventral axis and the left–right axis. Fusiform fish swim well because their whole body is streamlined or slightly flattened to reduce drag as they move through the water. The basic fish body is spindle-shaped; this body type is shared among a number of different fish taxa, including carp, crucian carp, and sharks.

1.1.3.1.2 Oblate Sides

In fish with oblate sides, the left–right axis is the shortest, with the head–tail axis about the same length as the dorsal–ventral axis, forming a symmetrical flat shape from left to right. These fish live in the middle and lower layers of the water and are less able to swim than spindle-shaped fish. Fish with oblate sides include butterfish, bitterlings, and species in the genus *Acheilognathus*.

1.1.3.1.3 Club Type

Club-type fish have particularly long head–tail axes, with very short left–right and dorsal–ventral axes of nearly equivalent length. Thus, the body of the fish resembles a club or rod. Club-type fish, such as eels, are stronger swimmers than flat-sided or flat fish and often inhabit subaqueous holes in soil or sandstone.

1.1.3.1.4 Flat Type

Flat-type fish are sluggish because they have a particularly long left–right axis and a particularly short dorsal–ventral axis. Flat fish are benthic and include rays and flounder.

1.1.3.2 Body Composition

The body of a fish consists of a head, a trunk, and a tail. One of the differences between fish and land vertebrates is that the head and trunk of the fish are joined and thus cannot rotate with respect to one another. The dividing line between the head and the trunk is the posterior edge of the operculum in teleost fish or the hindmost pair of gill lobes in the Chondrichthyes. The trunk and tail are generally demarcated by the posterior edge of the anus or the beginning of the anal fin.

1.1.3.2.1 Spine

The spine joins the head and tail to form the trunk that supports the body. The spine consists of the vertebral body, vertebral arch, medullary spine, transverse process of the vertebral body, anterior articular process, and posterior articular process. The number of vertebrae from head to tail is one of the characteristics used in morphological classification.

1.1.3.2.2 Fins

Fish fins consist of skin and spines. There are three types of fin spines: soft spines, hard spines, and soft-hard mixed spines. The positions of the fins vary and include dorsal fins, pectoral fins, ventral fins, anal fins, and caudal fins. Fins also may have a variety of shapes. There are two kinds of fins, odd fins, and even fins. Odd fins are unpaired and include the dorsal fins, caudal fins, and anal fins. Paired fins include the pectoral and pelvic fins and correspond to the fore and hind limbs of terrestrial vertebrates. Each fish has a maximum of one pair of each type of paired fin. The basic functions of the dorsal and anal fins are to maintain balance, prevent tilting and rocking, and assist swimming. The caudal fin acts as a rudder, controlling the direction and propelling the fish forward. Fins with hard spines can also be used in attack or defense. In general, fish have five types of fins: pectoral, ventral, dorsal, anal, and tail. However, there are a few exceptions to this rule. For example, Monopterus albus has no even fins and has degenerated odd fins, Anguilla japonica has no abdominal fins, and Electrophorus electricus has no dorsal fins. Fin shape and quantity differ among fish taxa.

1.1.3.2.3 Scales

Scales, a class of skin derivatives, are a biological feature of certain fish and reptiles, as well as a small number of mammals and birds. Scales are generally flaky and have a protective effect. According to their origin, scales can be divided into bony scales (dermal scales) and cuticular scales.

1.1.3.3 Measurable Characters

Measurable characters are traits that can be measured. Measurable characters include plant or animal height or length. Measurable characters are easily influenced by the environment. Individual differences within a population generally fall along a continuous normal distribution, and it is thus difficult to group these differences. There are no qualitative differences among continuously varying individuals in a population, only quantitative differences.

1.1.3.3.1 Full Length

The full length refers to the length measured from the rostral end to the tail fork.

1.1.3.3.2 Body Length

Body length refers to the length measured from the rostral end to the junction of the trunk and the caudal fin.

1.1.3.3.3 Body Height

Body height refers to the height measured from the abdomen to the highest point of the dorsal fin.

1.1.3.3.4 Body Width

Body width refers to the thickness of the fish's body when placed flat.

1.1.3.3.5 Lips Length

The lip length of the fish is the distance between the front tip of the mouth and the mouth slit.

1.1.3.3.6 Eye Distance

Eye distance refers to the minimum distance between the two eyes.

1.1.3.3.7 Eye Diameter

The eye diameter refers to the diameter of the orbit.

1.1.3.3.8 Scale Formula

Scale form describes the characteristics of the scales covering the fish's body. The lateral line scales are a series of regular concave scales from the operculum to the tail stalk. The upper scale number refers to the complete scale number between the beginning of the dorsal fin and the lateral line. The under-scale number refers to the complete scale number between the beginning of the anal fin and the lateral line. Most fish have obvious lateral line scales, but some fish lack lateral line scales entirely.

1.1.3.3.9 Fin Formulas

Fin patterns are described using certain patterns of letters, numbers, and symbols. In most cases, the first letter of the English name for each fin is used to represent the fin category. For example, "D" corresponds to the dorsal fin, "A" corresponds to the anal fin, "P" corresponded to the pectoral fin, and "C" corresponds to the caudal fin. To avoid confusion, "V" is used for pelvic fin. Roman numerals in capital letters represent the number of hard spines and Arabic numerals indicate the number of soft spines. The apostrophe (') indicates the range of quantitative variation in the spines or soft spines. Hard spines connected to soft spines are denoted using a dash (-); hard spines not connected to soft spines are denoted using a comma (,).

For example, the fins of *Cyprinus carpio* (Linnaeus, 1758) are described as follows: DIII-IV-17-22; PI-14-16; VII-8-9; AIII-5-6; C20-22. This pattern indicates that *C. carpio* has a dorsal fin with three to four hard spines and 17–22 soft spines; a pectoral fin with one hard spine and 14–16 soft spines; a ventral fin with two hard spines and eight to nine soft spines; an anal fin with three hard spines and five to six soft spines; and a caudal fin with 20–22 soft spines.

1.2 Community

The biological community refers to all of the living things in a specific environment, including animals, plants, microorganisms, and other species. Typically, a "community" refers to organisms existing in a certain range of time and space. Biological communities have certain basic characteristics and can be described based on features such as species diversity, a form of community growth (including species types and growth state), community structure (including spatial structure, time composition, and species structure), dominant species (species in the community that play a decisive role in the community due to physical size, abundance, or activity), relative abundance (the relative proportions of different species in the community), and nutrition structure.

1.2.1 Composition

Composition describes the species composition of a biological community. Species composition is an important feature of a community, and habitat status affects community composition. The abundance of nutrients is an important indicator of environmental status, which affects species composition and diversity in a given community.

1.2.2 Proportion

Proportion refers to the quantitative spatial relationships among all of the conspecific individuals in a given community. These characteristics include proportion density, age structure, sex ratio, immigration rate, emigration rate, birth rate, mortality rate, spatial features, and other quantitative characteristics. Of these, proportional density is the most fundamental quantitative proportional characteristic and refers to the number of individuals per unit area or volume.

1.2.3 Structure

Community structure has spatial properties. Community structure is influenced by ecological conditions such as light intensity, temperature, humidity, and interspecific relationships. Each population in the community lives at the structural level corresponding to the most suitable ecological conditions for that particular population. Therefore, the specific ecological conditions determine the biological populations comprising the community. More complex community structures imply that the organisms use the resources in the ecosystem more fully. For example, the utilization rate of light energy in the forest ecosystem is much higher than that in the farmland and grassland ecosystems. The more complex the community structure, the more complex the environmental conditions and the more stable the community.

Community structures can be divided into horizontal and vertical structures. For example, the vertical stratification of trees, shrubs, and ground herbs is closely related to light availability, as is the stratification of underground and aquatic organisms. With respect to horizontal structure, different organisms may congregate in certain areas on the horizontal plane due to similarities among environmental requirements or interdependence. Community characteristics are usually determined by a number of dominant species.

1.2.4 Community Habitat

Community habitat is the spatial extent of abiotic factors in an ecosystem. Over evolutionary time, organisms gradually develop requirements for certain physical conditions and chemical components in the environment, such as air, light, water, heat, and inorganic salts. The life-form composition of a given community can reflect environmental characteristics, and the community habitat is the synthesis of the interactions between species and the environment.

1.2.5 Environment

The environment describes the overall living conditions, including energy, atmosphere, water, and soil. Due to mutualism, competition, parasitism, and predation among species in the community, the environmental factors pertinent to some species also include the biological environment formed by other species. Each population in a community requires specific ecological conditions, such as light intensity, temperature, humidity, food, and interacting species.

1.2.6 Ecological Characters

Ecological characteristics usually refer to the conditions necessary for the survival of a species. All living things need materials and energy and adapt to different physical and chemical conditions. The longer a community evolves, and the more favorable and stable its environment is, the more species it will contain. Therefore, the ecological character of a biological community is a complex system character.

1.2.7 Spatial Pattern

Spatial pattern refers to the distribution of species in space. For survival, activity, and reproduction, living things need a certain amount of space, material, and energy. In quantitative analyses, three types of distribution are often used to express the positional relationships of an individual in space: the uniform distribution describes the spatial pattern produced by the uniform distribution of individuals over a certain distance; the random distribution states that the likelihood of the appearance of an individual at a certain point in the space is random, and the position of one individual does not affect the distribution of other individuals; and the cluster distribution corresponds to an uneven distribution of biological individuals in space, with individuals often appearing in dense groups, clusters, or patches.

1.2.8 Temporal Characteristics

Different species inhabit different environments. Therefore, environmental conditions determine community composition. The community was in a state of dynamic stability during the evolution of the earth's environment, which was accompanied by species formations, lineage differentiation, population formation, and species extinction. The species' numbers in a community often change with time. For example, some flowers bloom and animals are active following a circadian rhythm, while the overall temperate and polar communities have obvious seasonal rhythms. Therefore, descriptions of community status must be accompanied by specific time ranges.

1.3 Niche

In nature, to avoid competition, closely related species, or species with very similar needs and habits, are often found in different geographical areas or different habitats within the same area; some such species may also adopt alternative lifestyles to avoid competition. For example, species may utilize different food sources or may be active at different times of the day or season. Organisms form niches according to the following principles: the principle of adaptation, the principle of competition, the principle of development, and the principle of balance. The adaptation principle states that an organism seeks a suitable ecological niche due to instinctive need. This adaptation behavior describes the constant change in resources needed by the organism. The competition principle occurs during the competition between different organisms for the same resources or environment. The principle of colonization refers to constant colonization and occupation of all of the available spare niches by organisms. The principle of balance states that, in open ecosystems, niche potential (*i.e.*, the competition-driven gap between the ideal niche and the actual niche) tends to decrease over time, because a system with too much ecological potential is unstable.

Niche content includes the region scope and the function of the organism itself in the ecosystem. In the natural environment, there are different biological communities in different ecological environments. The better the ecological environment, the more species make up the community and *vice versa*. Community habitat is the living space of community organisms, which together constitute the ecosystem. There are different kinds of living things in each particular position, and the activities and interactions of a given organism depend on its particular structure, physiology, and behavior. Therefore, each organism has a unique niche. The relationships among species and between species and the environment develop through niche competition. The concept of niche not only refers to living space but also emphasizes the function and status of the organism itself within the community, especially the nutritional relationship of a given species with other species.

Organisms in a community are constantly interacting. For example, organisms acquire nutrients *via* complex food relationships; plants photosynthesize, animals feed, and microorganisms capture nutrients through their body surfaces. Species relationships can be competitive or symbiotic, depending on the mutual interests of each species (*i.e.*, parasitic, partial symbiosis, and mutually beneficial). If two species utilize the same resources (niche overlap), they must compete, and one species will be excluded. However, if the resource demands of one species change (niche differentiation), the two species may coexist.

1.3.1 Ideal Niche

Ideally, species occupy a given niche without competition or disturbance. A niche has systematic characteristics that are measured based on its position in space, which is a portion of the position occupied by a given species in the total community space. Species account for the total energy demand of a community. Due to the multi-channel nature of species energy (for example, the energy of predatory species can be obtained from other species), niche relationships among species are complicated by energy space. Similar to time, air, water, and energy, it is difficult to determine the boundaries of space.

1.3.2 Real Niche

The ecological niche occupied by the environmental resources needed by a given species in a natural state under competition pressure is usually represented by variations in the breadth of a given species' niche as the environment changes. Niche studies usually focus on a certain time and space background. The conditions of the survival needs of a given species within the ecosystem are defined in the minimum threshold analysis.

1.3.3 Conservation

The niche is conserved because the community includes phylogenic characters. Therefore, when fish from the same family or genus inhabit the same community, the niches of neighboring species often differ (Cavender-Bares *et al.*, 2006). This is consistent with speciation characteristics: for every new species formed, a new niche is created within the community.

1.3.4 Multidimensionality

Niche is a combination of the physical environment (*e.g.*, energy, water, and habitat) and the biological environment (*e.g.*, mutualism, competition, parasitism, and predation). Each environmental factor becomes a dimension, meaning that the conceptual niche space is an N-dimensional hypervolumic space.

1.3.5 Overlap

Niche overlap refers to the phenomenon when two or more species with similar niches share or compete for common resources when they inhabit the same space. Competition among niche-overlapping species always leads to reductions in the degree of overlap, which may be affected by inhabiting or foraging in different spatial positions.

1.3.6 Niche Breadth

Niche breadth corresponds to the sum total of the different resources utilized by species. In the absence of any competition or other enemies, the total resources utilized are called the "original" niche. Owing to interspecific competition, it is impossible for an organism to utilize all of the resources of the ideal niche, and thus organisms occupy only the actual niche. The niche breadth of a species varies with the environment. Niche breadth is usually defined within the axis of an ecological factor.

1.3.7 Ecological Equivalents

Two organisms with similar functional niches, but distributed in different geographical regions, can be considered in some senses ecological equivalents. However, a given species will have a different niche in different communities. The niche of a species is determined by its diet and habitat.

1.3.8 Coincident Species

Scale form describes the characteristics of the scales covering the fish's body. The lateral line scales are a series of regular concave scales from the operculum to the tail stalk. The upper scale number refers to the complete scale number between the beginning of the dorsal fin and the lateral line. The under-scale number refers to the complete scale number between the beginning of the anal fin and the lateral line. Most fish have obvious lateral line scales, but some fish lack lateral line scales entirely.

1.3.9 Species Evolution and Niche

Species consist of groups of organisms with the same genetic characteristics. Individuals mate with one another to form populations with small genetic differences, aiming to maximize energy utilization and each occupying certain niches within the community. Species have an inherent tendency toward continuous differentiation, which drives the continuous subdivision of the earth's ecological niches. Due to competition for energy, populations differentiate into new species that make use of the original share of energy but do not compete with each other, forming new, complementary niches with the original species and becoming new members of the community. However, because each niche has a fixed energy capacity, species differentiation is restricted by an energy threshold. That is, the niche space cannot accommodate unlimited new species. As a result, species differentiation, population formation and extinction, and species niches within a community form a "stable" but dynamic equilibrium.

1.4 River Ecosystem Elements

A natural ecosystem is the unified composition of organisms within a specific environment. In an ecosystem, organisms interact with their environment and with each other in a state of dynamic equilibrium. Ecosystems are open systems. To maintain stability, the ecosystem must continuously input energy, and many basic materials in the ecosystem are continuously recycled. The total volume of the earth's water is 1.386 billion km, of which 96.53% is in the sea. Fresh water accounts for only 2.53% of the total volume of water resources, and 87% of the freshwater is in polar ice caps, Alpine glaciers, and permafrost. Rivers, freshwater lakes, and shallow groundwaters account for only 0.26% of the earth's total water volume, about 9000 cubic kilometers per year.

"Aquatic ecosystem" is a general term for the various aquatic ecosystems on the surface of the earth. The organisms in an aquatic ecosystem consist of autotrophs (*e.g.*, algae and aquatic plants), heterotrophs (*e.g.*, various invertebrates and vertebrates), and decomposers (*e.g.*, various microorganisms). All types of biological communities interact with the aquatic environment to maintain a specific materials cycle and energy flow; together, these communities constitute a complete ecological unit. The river ecosystem describes the ecosystem of a river water body ecosystem, which is a type of flowing water ecosystem.

1.4.1 Water Chemistry

Water, which is composed of hydrogen and oxygen, is a colorless, odorless, transparent liquid under normal temperature and pressure. In rivers and lakes, the ions naturally dissolved in the water are primarily potassium, sodium, calcium, magnesium, chlorine, sulfate, hydrogen carbonate, and carbonate ions, as well as micronutrients such as bromine, iodine, and manganese. River-water composition depends on the types of rocks and soil in the area over which the water flows and on the source of recharge. The degree of river mineralization is generally lowest with rainwater recharge, slightly higher with snowmelt recharge, and highest with groundwater recharge. There are more dissolved substances in groundwater than in surface water, and dissolved substances in groundwater are only weakly mixed. In general, rivers worldwide are moderately mineralized, with the exception of inland areas that receive little rainfall. Groundwaters are mostly weakly acidic, neutral, or weakly alkaline, with typical pH values of 5–9. The chemical composition of groundwater changes from shallow to deep groundwater: salinity gradually increases and the hydrochemical makeup of the water shifts from bicarbonate to sulfate/chloride.

1.4.2 Water Quality

Water quality is an index system that describes the quality of water containing dissolved substances. Considering the ecological function of the water, the contents of dissolved substances in the water are divided into different grades to indicate water quality, forming a water quality index. The quality of water is expressed by physical, chemical, and biological indices. Physical indicators of water quality include smell, temperature, turbidity, transparency, and color. There are four types of chemical indexes: (a) the non-specific indexes, including conductivity, pH value, hardness, alkalinity, and inorganic acidity; (b) the inorganic indexes, including toxic metals, toxic quasi-metals, nitrate, nitrite, and phosphate; (c) the non-specific organic indicators, including total oxygen consumption, chemical oxygen consumption, biochemical oxygen consumption, total organic carbon, the potassium permanganate index, and the phenolic index; and (d) the biological indicators, including the total number of bacteria, the number of coliform bacteria, and the number of algae. Radioactivity indicators include α-rays, β-rays, uranium, radium, and thorium. Some single indicators correspond to a physical parameter or the concentration of an expressed substance, such as temperature, pH, or dissolved oxygen. Other indicators reflect the shared characteristics of groups of substances that are indicators of water quality. Such indicators are known as composite indicators. For example, biochemical oxygen demand is an indicator of the level of biodegradable organic compounds in the water, while total hardness indicates the water content of inorganic salts, such as calcium and magnesium.

1.4.3 Aquatic Life

"Aquatic organisms" is a general term for organisms that inhabit various types of water bodies. Aquatic organisms are diverse, ranging from microorganisms and algae to aquatic vascular plants, invertebrates, and vertebrates. Aquatic organisms also have various lifestyles and may float, swim, be sessile, or dwell in caves.

1.4.3.1 Aquatic Bacteria

Aquatic bacteria are microorganisms that grow in water bodies. There are several types of aquatic bacteria, including cocci, bacilli, vibrios, and spirochetes. Bacteria have a simple structure, including a cell wall, plasma membrane, cytoplasm, and nucleus. Bacteria reproduce rapidly and divide once every 20–30 min. Bacteria have a wide distribution. The abundance of aquatic bacteria in a given water body is closely related to the fertility and quality of the water. Aquatic bacteria are part of the aquatic food chain and provide inorganic salts (*e.g.*, phosphates and nitrates), carbon dioxide, and water to plants by breaking down organic matter, including dead organisms. Autotrophic bacteria are primary producers, consuming nutrients for growth.

1.4.3.2 Phytoplankton

The term "phytoplankton," which refers to tiny aquatic, planktonic plants living in the water, is usually used for planktonic algae, such as the Cyanophyta, Chlorophyta, diatoms, Chrysomyta, Xanthophyta, dinoflagellates, cryptoalgae, and Gymnophyta. Changes in phytoplanktonic species composition, community structure, and abundance directly affect water quality, energy flow, material flow, and biological resources. Phytoplankton is also globally important for carbon and nitrogen fixation. The total amount of carbon and nitrogen fixed by phytoplankton in the oceans and freshwaters is seven times that of terrestrial plants. Phytoplankton fixes about 170 million tons of nitrogen each year. The world produces about 100 billion tons of carbon dioxide annually, about 50% of which is taken up by phytoplankton. Phytoplankton is not only the most important primary producers in aquatic ecosystems, but these organisms are also the main providers of aquatic dissolved oxygen. Phytoplankton plays a vital role in energy flow, material circulation, and information transmission in aquatic ecosystems.

1.4.3.3 Zooplankton

Zooplankton is heterotrophic invertebrates and notochordates found in the water column. Zooplankton includes a wide variety of species, including protozoans, coelenterates, ctenophores, rotifers, crustaceans, gastropods, uropods, benthos, fish larvae, and fish juveniles. Zooplankton is important components of aquatic ecosystems that not only feed on phytoplankton, bacteria, and organic detritus but also are preyed on by fish and aquatic animals.

1.4.3.4 Aquatic Plants

Aquatic plants are plants that grow in water. Aquatic plants absorb aquatic nutrients and water through their roots and fix nitrogen through photosynthesis in their leaves. These plants are an important part of the global energy cycle, as well as a major source of food for terrestrial and aquatic organisms. Generally, aquatic plants can be grouped into emergent plants, floating plants, submerged plants, and hydrophytes.

1.4.3.5 Benthos

The benthic fauna is aquatic animals that spend most or all of their life at the bottom of a water body. The organisms of the benthos are typically invertebrates, including mollusks, arthropods, crustaceans, and flatworms. Protozoans, such as common worms, benthic crustaceans, and bivalve mollusks, can use dissolved oxygen directly from the water. The secondary benthos mainly includes various aquatic insects and mollusks. Zoobenthos feed mainly on plankton and sediment.

1.4.4 Organic Detritus

Organic detritus includes the materials into which organisms decompose after death, the organic detritus formed by aquatic organisms, and the organic detritus imported from land, as well as large volumes of dissolved organic matter and its aggregates. Organic detritus is derived from intermediate products during the decomposition of dead organisms by bacteria (the final stage is inorganic), from food residues that are not fully ingested and digested, from the low-molecular-weight extracellular organic matter produced by phytoplankton during photosynthesis, and from the particulate organic matter imported from terrestrial ecosystems. Organic detritus can be used directly as food by certain organisms.

1.4.5 Productivity of Water Bodies

Productivity indicates the number of organisms produced by the water body per unit of time. It can be expressed as the rate at which solar energy is fixed by chloroplasts or the rate at which organic matter is produced by photosynthesis. Productivity units vary and include the weight of organic carbon/unit surface (body) product/unit time, and heat/unit face (body) product/unit of time. Primary productivity is the rate at which the total energy or total organic matter is produced by chloroplasts per unit surface product per unit time. Primary consumers transform primary productivity into their own material and energy, which is called secondary productivity. And so on for the third level of productivity, etc. The final production link in the food chain is referred to as ultimate productivity. The process of productivity is essentially a process of energy transformation and organic matter cycling for all of the levels of nutrients in an ecosystem.

1.4.6 Trophic Level

A trophic level refers to the level of an organism in the food chain of an ecosystem. The food energy flow in an ecosystem is graded according to an organism's position in the food chain. In an ecosystem, chloroplasts and other autotrophs are classified as the first trophic level and the starting point of the food chain; animals feeding on chloroplasts and autotrophs are classified as second trophic level (herbivores); carnivores that feed on herbivores are classified as the third trophic level; and carnivores that feed on carnivores are classified into higher trophic levels, such as the fourth and fifth trophic levels.

The nutritional relationship between the senior consumer and the underlying producers is called the food chain, which is both a material chain and an energy chain. Organisms located on the same link in the food chain are classified into the same trophic level, which simplifies the structure of the food web. Organism interactions are a form of food restriction, with chloroplast energy and nutrients derived from photosynthesis transferred up the food chain. However, only about 10% of photosynthesis-derived energy and nutrients are transferred to upper trophic levels; about 90% of the energy is returned to the environment as heat dissipation, which is known as Lindemann's 10th law.

1.4.7 Natural Balance

The natural balance refers to a state in which the relationship between the living and nonliving elements of a system is highly adaptive, coordinated, and unified. Within an ecosystem, producers, consumers, decomposers, and the abiotic environment maintain a relatively stable state of dynamic input and output of energy and matter within a certain period of time. External interference cannot disrupt the equilibrium among the proportional components of the system.

1.4.8 Water Pollution

Water pollution refers to poor sensory characteristics (*e.g.*, pungent smell and changes in watercolor), inorganic pollutants, organic pollutants, microorganisms, radioactivity, and five other categories of abnormality indicators. Pollutants can poison or affect aquatic organisms, leading to the reduction or extinction of organisms and resulting in ecological imbalance.

1.4.9 Algal Blooms

Algal blooms are a type of water pollution caused by excessive amounts of nitrogen and phosphorus in water bodies including rivers, lakes, and reservoirs. Nutrients in the water cause the rapid multiplication of algae and other plankton. This rapid increase in algal/plankton abundance cannot be supported by the food chain, leading to reductions in the dissolved oxygen content of the water. Thus, algal blooms can cause the die-off or extinction of algae, plankton, plants, fish, and other aquatic life, leading to the deposition of many dead aquatic organisms on the water bottom. During the decomposition of these organisms by microorganisms, large amounts of dissolved oxygen are consumed, further deteriorating water quality and accelerating the eutrophication of the water body in a vicious cycle.

1.5 Freshwater Fish

Freshwater fish are those that inhabit freshwater bodies such as rivers, lakes, and reservoirs. Freshwater fish also include migratory fish that migrate back and forth between freshwater and marine habitats. The migration of fish from the ocean to fresh water for reproduction is called anadromous migration (for example, *Acipenser sinensis*), and the migration from fresh water to the ocean for reproduction is called catadromous migration (for example, that of *Anguilla marmorata*). There are about 32 500 known fish species worldwide, of which about 15 000 are freshwater and about 10% are migratory.

1.5.1 Global Freshwater Fish Communities

There are a great variety of fish species worldwide, with Tedesco *et al.* (2017) reporting 14 953 species of freshwater fish belonging to 47 orders, 209 families, and 2298 genera (Richard van der Laan, 2017). Community composition ranges from simple to complex and is related to the watershed area (see table 1.1). Islands usually form in one of three ways: separation from the mainland, underwater volcanic eruptions, or marine corals that grow into reefs. Studies of freshwater fish species on small islands show that the fish community composition progresses from simple to complex; invasive alien species also impact the evolution process. For example, there are seven species of fish in the Azores, of which only one is indigenous and the remaining six are alien (see table 1.1). The composition of the fish community is simple (https://www.fishbase.de/2021,0810). It is also possible for native fish to differentiate into new species, such as the two species of Goby (*Awaous stamineus* and *Lentipes concolor*; Fishbase) found in Hawaii. In addition, there are 1603 freshwater fish species in China's interior, which are distributed in the Yangtze River, the Pearl River, and other water systems. Fish community composition differs strongly among river systems, reflecting differences in the ecological environment of each river basin. In nature, fish must form their own niche according to the function of the food web, thus developing a distinctive fish community and completing the same energy cycle functions in different river ecosystems.

The indigenous species in the community constantly adapt to changes in the environment and differentiate into new species. Simultaneously, the invasion of alien species also impacts the structure of the original community. Fish communities are constantly changing to adapt to changes in the environment, reflecting the characteristics of community structure constrained by space and time.

Tab. 1.1 – Fish community composition in some inland waters (Fishbase).

	Native species	Endemic species	Total species	Alien species
Azores	1Order 1Family 1Species	0Order 0Family 0Species	5Order 6Family 7Species	6
Hawaii (US)	3Order 4Family 7Species	2Order 2Family 4Species	14Order 24Family 60Species	53
New Zealand	8Order 12Family 42Species	6Order 6Family 21Species	12Order 16Family 62Species	21
Australia	27Order 56Family 349Species	6Order 16Family 136Species	32Order 67Family 379Species	30
South Africa	20Order 36Family 152Species	2Order 4Family 32Species	23Order 43Family 180Species	28
Angola	14Order 27Family 353Species	5Order 7Family 68Species	14Order 27Family 355Species	2
Zimbabwe	15Order 23Family 127Species	0Order 0Family 0Species	19Order 29Family 144Species	17
France	18Order 23Family 73Species	2Order 2Family 3Species	20Order 30Family 99Species	26
USA (North America)	27Order 43Family 896Species	2Order 8Family 370Species	34Order 60Family 963Species	67
Philippines	22Order 49Family 286Species	3Order 6Family 87Species	28Order 69Family 337Species	51
Malaysia	22Order 75Family 605Species	4Order 13Family 50Species	24Order 79Family 625Species	20
Vietnam	26Order 70Family 709Species	0Order 0Family 0Species	29Order 75Family 729Species	20
Thailand	27Order 75Family 806Species	3Order 9Family 19Species	29Order 82Family 828Species	22
Cambodia	25Order 72Family 462Species	1Order 1Family 1Species	26Order 75Family 475Species	13
China	24Order 74Family 1576Species	6Order 18Family 124Species	27Order 82Family 1603Species	27

1.5.2 Community Characteristics of Freshwater Fish in China

China is among the countries with the greatest number of rivers worldwide. Fishbase indicates that 1603 species of freshwater fish are found in China's inland waters. Zhang and Zhao (2016) studied the functional diversity of 1384 species of fish, while Xing *et al.* (2016) and Nelson *et al.* (2016) described more than 1000 species of freshwater fish endemic to China. The composition of the fish community in each river system reflects the adaptation of each species to the environment (see table 1.2).

The composition of the fish community varies from river to river. However, there are some fish taxa in larger rivers that are widely distributed, including *Mylopharyngodon piceus* (Richardson, 1846), *Ctenopharyngodon idella* (Valenciennes, 1844), *Elopichthys bambusa* (Richardson, 1845), *Squaliobarbus curriculus* (Richardson, 1846), *Hemiculter leucisculus* (Basilewsky, 1855), *Parabramis pekinensis* (Basilewsky, 1855), *Xenocypris argentea* (Günther, 1868), *Hypophthalmichthys molitrix* (Valenciennes, 1844), *Hypophthalmichthys nobilis* (Richardson, 1845), *Cyprinus carpio* (Linnaeus, 1758), *Carassius auratus* (Linnaeus, 1758), *Pelteobagrus fulvidraco* (Richardson, 1846), and *Siniperca chuatsi* (Basilewsky, 1855). Some fish species are widespread due to crust movements, which distributed homologous species to different areas. Others were introduced by human activities, and the number of these fish is increasing in the major rivers of the country. These species became important factors influencing local river ecosystems.

1.5.2.1 Cold Temperate Zone

The main families of fish in Heilongjiang waters are hardy species, such as three species of lampreys in the class Cyclostomata, 10 species of Salmonidae, two species of Aniseiidae, one species of Camelidae, and one species of Cyprinidae in the order Osmeriformes, *Lota lota* (Linnaeus, 1758), *Acipenser schrenckii* (Brandt, 1869), *Huso dauricus* (Georgi, 1775), and *Gasterosteus aculeatus* (Linnaeus, 1957). The cold temperate zone is characterized by a variety of fish, such as *Coregonus chadary* (Dybowski, 1869), *Esox reicherti* (Dybowski, 1869), *Phoxinus phoxinus phoxinus* (Linnaeus, 1758), *Rhynchocypris percnurus* (Pallas, 1814), *Gobio cynocephalus* (Dybowski, 1869), *Cyprinus carpio* (Linnaeus, 1758), *Carassius auratus auratus* (Linnaeus, 1758), *Silurus asotus* (Linnaeus, 1758), *Culter alburnus* (Basilewsky, 1855), *Hemibarbus labeo* (Pallas, 1776), and *Chanodichthys mongolicus mongolicus* (Basilewsky, 1855) (Zhang Chunguang *et al.*, 2020; Dong Chongzhi, 1996a, 1996b).

1.5.2.2 Mesothermal Zone

In China, much cold-water fish inhabit northeastern Mongolia and northern Xinjiang. Some of the fish here are characteristic of European waters, for example *Acipenser baeri* (Brandt, 1869), *Lucioperca lucioperca* (Linnaeus, 1758), *Thymallus arcticus arcticus* (Pallas, 1776), *Leuciscus idus* (Linnaeus, 1758), *Esox lucius* (Linnaeus, 1758), and *Perca fluviatilis* (Linnaeus, 1758), In addition, local species

Tab. 1.2 – Distribution of endemic fish species in the main rivers of China.

	Fish species	Endemic fish species	References	Author
The Yangtze	426	175	Freshwater fishes of China: species richness, endemism, threatened species and conservation [J]. Diversity and Distribution	Xing *et al.*, 2016
The Yellow	127	30		
The Pearl	682	243		
The Heilongjiang	124	9		
The Lancang River	890	202		
The Yili	21	2	Xinjiang ICHTHYOLOGY	Institute of Zoology, Chinese Academy of Sciences, etc., People's Publishing House, 1979
The Tarim	12	4		
The Irtysh River	16	4		
Nandu River	85	10	Freshwater and Estuarine ichthyography of Hainan Island Olor map of freshwater and estuarine fishes of Hainan Island	Pearl River Fisheries Research Institute, Chinese Academy of Aquatic Sciences, 1986; Xinhui Li *et al.*, 2020f

include *Coregonus ussuriensis* (Berg, 1906), *Osmerus mordax* (Mitchill, 1814), *Hypomesus* spp. (Gill, 1862), *Abramisbrama orientalis* (Berg, 1949), *Gobio acutipnnatus* (Men'shikov, 1939), *Brachymystax lenok lenok* (Pallas, 1773), *Hucho taimen* (Pallas, 1773), *Lota lota* (Linnaeus, 1758), *Pseudogobio vaillanti* (Sauvage, 1878), *Oncorhynchus keta* (Walbaum, 1792), *Cyprinus carpio* (Linnaeus, 1758), *Carassius auratus auratus* (Linnaeus, 1758), *Culter alburnus* (Basilewsky, 1855), *Hemibarbus labeo* (Pallas, 1776), and *Chanodichthys mongolicus mongolicus* (Basilewsky, 1855) (Cai Lingang *et al.*, 2017; Li Guogang *et al.*, 2017; Ren *et al.*, 2002; Li Shuguo *et al.*, 2000; Mu-Lian *et al.*, 1998; Dong Chongzhi, 1996a, 1996b).

1.5.2.3 Warm Temperate Zone

The warm temperate zone includes the Tarim River system, the Yellow River, the Yangtze River, the Hai River, and the Huai River. There is much warm temperate fish, including *Lampetra reissneri* (Dybowski, 1869), *Coregonus chadary* (Dybowski, 1869), *Rhynchocypris lagowskii* (Dybowski, 1869), *Cyprinus carpio* (Linnaeus, 1758), *Gymnocypris przewalskii* (Kessler, 1876), *Silurus lanzhouensis* (Chen, 1977), *Carassius auratus auratus* (Linnaeus, 1758), *Squaliobarbus curriculus* (Richardson, 1846), *Parabramis pekinensis* (Basilewsky, 1855), *Hypophthalmichthys molitrix* (Valenciennes, 1844), and *Hypophthalmichthys nobilis* (Richardson, 1845) (Li Sizhong, 2015; Cai Wenxian, 2013).

1.5.2.4 Subtropical Zone

The subtropical region, which includes the Yangtze River system and the Pearl River system, has the most abundant fish species. Many fish are characteristic of subtropical regions, such as *Acipenser sinensis* (Gray, 1834), *Acipenser dabryanus* (Dumeril, 1868), *Anguilla japonica* (Temminck and Schlegel, 1846), *Abbottina obtusirostris* (H. W. Wu and Ki. Fu. Wang, 1931), *Abbottina rivularis* (Basilewsky, 1855), *Acheilognathus* sp. (Bleeker, 1860), *Acrossocheilus fasciatus* (Steindachner, 1892), and species in the Culterinae. In the Yangtze River system, both the abundance and the richness of species in the Cyprinidae are very high, and this system can be regarded as the germplasm resource center for Cyprinidae in Asia. The main taxa characteristic of the Pearl River water system includes the Cyprinidae, Danioninae, Labeoninae, Barbinae, and the Siluriformes (*e.g.*, the families Akysidae, Cranoglanididae, Siluridae, Clariidae, Pangasiidae, Schilbeidae, and Amblycipitidae). The fish in the Lancang River system include species of Labeoninae, the loach genus in the loach family, the flat fin family, the Bagrid family, the catfish family, the finless eels in the Lamibranchia, and *Channa argus.* These fish are also found elsewhere in Asia, while the species of Schizostominae and loach are also found in the Northwest Plateau Region. Fish species from the Lancang River system are mixed with those from Asia and the Northwest Plateau Region. The fish taxa found in Lancang River and elsewhere in Asia include the Labeoninae, the Botiidae in Cobitidae, the Balitoridae, the Bagridae, *Silurus* (Linnaeus, 1758) in Siluridae, *Monopterus albus* (Zuiew, 1793), and *Channa argus* (Cantor, 1842). Similar to the

Northwest Plateau Region, there are also some species in the Schizostominae and Noemacheilinae.

1.5.2.5 Tropical Zone

The tropical regions of China are located in southern Yunnan, Leizhou Peninsula, southern Taiwan Province, and Hainan Province. Some of these fish, including species in the Labeoninae and Botiinae, are also found in India, Burma, Vietnam, and Thailand. Some fish in the Schizothoracinae are also found in the Northwest Plateau. The composition of the fish fauna is similar to that of Vietnam, Thailand, Myanmar, and India, with taxa including the Cyprinidae, Danioninae, Labeoninae, Barbinae, and various families in the Siluriformes (*e.g.*, Akysidae, Cranoglanididae, Siluridae, Clariidae, Pangasiidae, Schilbeidae, and Amblycipitidae).

1.5.2.6 Plateau Zone

The southern and southeastern parts of the Qinghai-Tibet plateau have dense river networks and are the source of many famous rivers in Asia, such as the Yangtze River, Yellow River, Salween River, Lancang River, Yarlung Tsangpo River, Ganges River, and Indus River. The well-known fish characteristic of the plateau includes the Schizothoracinae, Sisoridae, and *Triplophysa* (Rendahl, 1933) (China Digital Science and Technology Museum https://www.cdstm.cn; Qinghai-Tibet Plateau Fish Database, Institute of Northwest Plateau Biology, Chinese Academy of Sciences; http://ptsc.nwipb.cas.cn/lxwm/).

Chapter 2

Fish Morphological Models and Mechanisms

The natural environment is constantly changing as organisms adapt to and change with the environment. The species composition of the ecosystem community is restricted by time and space. Speciation changes with the environment, and when the change goes beyond the dimension of the species, new species, and new communities are formed.

Changes in species distribution and abundance are the key processes of niche evolution, but most previous studies do not address these areas (Gaston, 1996, 2009). Niche is affected by biotic and abiotic factors, so it is difficult to establish the system boundary. The species niche is affected by the size of the geographical range and the environmental changes over time (Gaston, K. J.; Fuller, R. A.). Species diffusion and habitat heterogeneity are the determinants of species distributions, and the need to reduce environmental uncertainties are well recognized (Wright *et al.*, 2006). Genetic isolation, genetic differentiation, individual or population variation, biological invasion, climate, and other scale factors have been proposed as the boundaries of species distributions (Sexton *et al.*, 2009), but reducing the influence of environmental uncertainties is still a challenge for community studies. Therefore, the applicability of the species distribution model (SDMS) to interspecific relationships still needs to be improved (Elith and Leathwick, 2009). Clarke and Warwick (1999) defined the length of the path as the distance between two species and the sum of the relationships between species and their environment. In this way, expressing the relationship between species is also essentially the embodiment of the community relationship. According to Hirzel *et al.* (2002), the niche theory of Hutchinson SA is indispensable for the establishment of models that objectively reflect the niche relationships of communities. Václavík and Meentemeyer (2009) stated that models of species distribution must solve the problems of questionable systematic data, uncertain systematic boundaries, and doubtful system representativeness. Many factors seem to be considered in studies of niche, but the "environmental factor" has no boundary, and artificial values tend to be subjective.

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The ecological niche of a species in a community is influenced by the complexity of the environment. However, within the same geographical region, the environmental conditions of each community species are the same, so the environmental factors are similar. Under such a conceptual background, the establishment of a model purely of interspecific relationships can avoid the problem of "environmental factors" without boundaries and can be used for community niche research. The morphological characters of a species are formed due to the interactions between species and the environment as well as among species. These traits also contain evolutionary information, reflecting the phylogeny of species (that is, information about environmental factors). Due to the differences among classification characters, species size, and food habits, the food chain has complementary ecological niches that are formed by energy utilization, and these differences reflect the ecological functions of the community. Morphological characters can also reflect the migration ability of a species, as well as the spatial characters or range of its habitat, such as air, land, water, and different water layers. We believe that characters with species-specific attributes are the key to deciphering the niche.

The river is a zonal ecosystem. Only fragmentary data can be collected at small scales, and the heterogeneity of the large-scale environment is so great that it is difficult to establish a research model that can systematically reflect the spatial niche relationships among fish. To solve the problem of environmental factors, we aim to characterize the niche relationships among species in the fish community based on morphological characteristics. In this study of fish communities, it is assumed that the morphological characters of species are a direct reflection of the interactions between species and the environment. Because "characters" are the result of interactions between species and environment, the term "integrated morphological character" is used to record "niche" information. In this book, the morphological characters of each species recorded in rivers are digitized, and a data information matrix for all of the species in the community is established. After character digitization, the recorded information includes the time and space boundaries of the system as well as the spatiotemporal dimension of the community, which solves the problem of determining community boundaries. In this type of community model, the defined species determine the boundary of the research system. Changes in the species community indicate that the studied system has changed. For example, species extinctions or speciation events are spatiotemporal changes in the system.

Over evolutionary time, a certain "trait" is determined by the "initiation" of a new niche formed by another species as part of its adaptation to the environment. It can be said that the characters of all of the species in the community include the "initial" characteristics when the niche is formed. Therefore, the "initial" characteristics present when communities were formed can be obtained. These results also give rise to the concept of the "initial" niche in interspecific relationships among communities. This concept should be compared with the "initial" reference frame in the context of drastic changes in the present environment. The results of this comparison might serve as the "initial niche" frame of reference.

Characteristic features are the basis of taxonomy, and community research reveals systems. The quantitative characteristics of the systematic morphology of a species reflect the evolution of that species in the community. By means of the quantitative transformation of traits into data that can be analyzed with a computer, trait data are transformed into image data, combining the theoretical niche hypothesis with real niche analysis and the image-information space transformation method to determine the species composition of the theoretical niche in the studied community and to provide an analytical method for evaluating community evolution and community species construction. Through the application of computer technology, data for n fish species are used to form a community data matrix describing "species + taxonomic characters." This matrix is transformed using multivariate statistics, reducing the dimensions of Galway's information to a "projection" in the Cartesian coordinate system. After model implementation, the n species in the community are distributed in the two-dimensional plane in the form of a niche (scattered points). The n sites in the plane reflect the fixed relationships among species in the community. In a community composed of n species of fish, the niche summation value of each species of fish is equal to "1." It is difficult to disassemble the niche quantitation value of n species of fish from "1." It is difficult to disassemble the niche quantitation value of n species of fish from "1."

It is assumed that the positions in the Cartesian coordinate system reflect the ecological spatial relationships among the species in the community and that these species have quantitative attributes that are key to the quantification of relative community species abundance. Thus, when deriving the niche value, if the niche value assigned to n species of fish is Xi ($i = 1, 2, 3, \ldots, n$), then $\sum Xi = 1$. In the digital matrix describing the morphological traits of n species, the number sequence of the numerical group Xi (which is a random number sequence that is a variable factor in the matrix) is newly introduced as the assumed niche value of each species (a random number or the measured abundance ratio of each species in the community) to construct a new matrix including "species (assumed n species) + taxonomic traits + assumed niche value." At this point, in the two-dimensional graph of the model analysis, in addition to the original n species of fish, a site "A" is identified, where "A" corresponds to the sequence of variable numbers that varies with the number of species in the studied community in the data matrix. In the following 19 fish examples, "A" is the number "20" in the two-dimensional graph studied, and the distance between "A" and the origin of the coordinates is defined as the niche deviation. The farther "A" is from the origin of the coordinates, the more unbalanced the niche of n species in the community. In contrast, when the deviation value is "0," the ecological niche of each species in the community is in the most reasonable relationship equilibrium among species. Therefore, the deviation value can be used as a measure of the adaptation of a community of species to environmental changes.

The matrix analysis model of morphological parameters, which integrates the essential taxonomic features, expands the application of character difference analysis in the quantitative community niche. A high-dimensional analysis model of morphological parameters was established to study community composition from the perspective of spatial niche. The random sample analysis method avoided the concept of species boundaries in reality and was especially suitable for the analysis of community standards and for community reconstruction. In this study, only the characteristics of species were used to study community structure, which eliminated the disruptive effects of uncertainty with respect to environmental factors and revealed the community-species relationships more clearly.

In this model, the two-dimensional coordinates "species + taxonomic characters" were used as the reference frame. By "correcting" the "A" value (usually deviating from the origin of the coordinates) in the "Species + taxonomic traits + assumed niche" value ("A") to "0," the niche value "A" of each species in the community (total value "1") was obtained. The result of this iteration corresponding to "A" was regarded as the proportional abundance of the fish in the community and the niche value of the fish in the community. Under this analysis model, the value of the "vector" (actually the scalar) of each fish in the two-dimensional graph was iterated, and the value of the niche of each fish was adjusted, such that the "A" point approached the origin of the coordinates, generating the "A" result. The "A" results reflect the proportion of species in the study community, that is, the estimated value of the natural niche.

Taking the species in a fish community as a unit, the method for examining interspecific relationships was established with taxonomic parameters as variables. The boundary of this research system is determined by the species, and the most suitable niche relationships among species in the community are defined by the positional relationships among species in the model and are equivalent to the ideal niche relationship. Under the ideal niche state, the proportion of each species in the community (*e.g.*, space, abundance, and biomass) is in the most reasonable state. That is, at the state of maximum utilization of energy in the ecosystem, the comprehensive value of the antagonistic rate among species was "0." Due to abrupt changes in the environment, niche imbalance is reflected in variations in species niches, which are in turn reflected in variations in abundance and biomass. Niche imbalance leads to an imbalance among species proportions in the community, and the absolute value of the comprehensive antagonism rate among species will be greater than "0." Therefore, niche deviations between "0" and an absolute value greater than "0" identified by the model can be used to establish a control system to evaluate community status (or to reconstruct community species) and thus to solve the difficult problem of evaluating community change. In this chapter, we introduce the method used to establish a quantitative model to evaluate the niche of a species within a community.

2.1 Multivariate Statistics

Multivariate statistical analysis (MSA) can be used to analyze the characteristic rules of multiple interrelated objects and indexes. If each individual has multiple observations that can be represented as a p-dimensional Euclidean space, the data are called multivariate data, and the statistical method for analyzing multivariate data is called multivariate statistical analysis.

Multivariate statistical analyses can be divided into narrow-sense and broad-sense methods. The narrow-sense multivariate statistical analysis assumes that the data distribution is a multivariate normal distribution; otherwise, the data are referred to as generalized. Narrow-sense multivariate analyses are widely used. There are several important classifications of multivariate methods that are based on the nature of the practical problems handled.

2.1.1 Regression Analysis

Regression analysis is a statistical analysis method that quantifies the interdependence between two or more variables. Based on the number of dependent variables involved, regression analyses are divided into univariate regression analyses and multiple regression analyses. If the relationship between an independent variable and a dependent variable can be expressed in an approximately straight line, the regression analysis is called a univariate regression analysis. A regression analysis is said to be a multiple regression analysis if it includes two or more dependent variables in a linear relationship. The relationships between independent and dependent variables can be divided into univariate regression analysis and multiple regression analysis.

2.1.2 Linear Discriminant Analysis

Certain classification conditions of various eigenvalues can be used to determine the type of research object. The basic principle is to establish one or more discriminant functions according to certain discriminant criteria, to use a large amount of data about the object to discriminate the undetermined coefficients in the functions, and to calculate the discriminant indexes. Thus, it is possible to determine the classification of the sample. Sample classification methods can be divided into parametric and non-parametric methods, as well as qualitative and quantitative data discriminant analyses. Based on the number of discriminant data sets, discriminant analyses can be divided into two-group and multi-group discriminant analyses; based on the mathematical model used in the discriminant analysis, discriminant analyses can be divided into linear and non-linear discriminant analyses; and based on the method used to process variables, discriminant analyses can be divided into step-by-step and sequential discrimination analyses.

2.1.3 Cluster Analysis

Cluster analysis, which is also called group analysis, groups sets of physical or abstract objects into classes composed of similar objects and classifies the data sources into different clusters by measuring the similarity among different data sources. Cluster analysis is an exploratory analysis for classification; because it is not necessary to give the classification criteria in advance, it is possible to perform automatic classification starting from the sample data. Using different cluster analysis methods will often generate different clusters. Thus, researchers must determine whether the analysis results are applicable.

2.1.4 Principal Component Analysis (PCA)

PCA is a multivariate statistical analysis method, in which several variables are transformed into a few representative variables by a linear transformation. The process aims to recombine the original variables into a new set of independent composite variables. Based on the research object, as few comprehensive variables as possible can be used to reflect the original variable. PCA is also a method used in mathematics to reduce the dimensions used.

2.1.5 Correspondence Analysis

Correspondence analysis is also called association analysis and R-Q factor transformation analysis. The associations between variables were revealed by analyzing the interaction summary table of samples and variable composition. If the subject is a sample, then Q-type factor analysis is used; namely, the factor analysis for finding the common factor for the sample. If the subject is a variable, then R-type factor analysis is used; namely the factor analysis for finding the common factor for the variable. Correspondence analysis can reveal the differences among different categories of the same variable and the corresponding relationships among different categories of different variables. Correspondence analysis can also reduce the dimensions of many samples and many variables simultaneously on the same graph according to the internal relationships of the factor R- and Q-type data. In this analysis, the categories and attributes of the samples are directly and clearly shown on the graph. Correspondence analysis not only classifies samples directly, but it can also indicate the main parameters (main factors) and reveal the basis for classification. Correspondence analysis can omit complicated mathematical operations as well as intermediate processes such as factor selection and factor axis rotation.

2.1.6 Factor Analysis

Factor analysis refers to the extraction of common factors from the group of variables to find hidden representative factors. Grouping variables of the same nature into a single factor reduces the number of variables and tests hypotheses of relationships among variables.

2.1.7 Canonical Correlation Analysis

Canonical correlation analysis is the study of the correlation between two groups of random variables. In the two groups of variables, the representative comprehensive variables U_1 and V_1 (the linear combination of the variables in the two groups of variables) are extracted, and the correlation between the two comprehensive variables is used to reflect the overall correlation between the two groups of indicators.

2.2 Morphological Data Model

It is difficult to include complete community species data in the model or actual evaluation, which results in an incomplete model analysis. Species with small distributions are difficult to monitor due to their small niche and small population, and it is difficult to integrate such species into the model system. The species data for historical communities can be used to accumulate recorded species distribution data based on systematic data. These data can reflect the relationships within the species community, as well as the structure and function of the ecosystem. The origin and development of species interactions in contemporary ecosystems can also be revealed through the comparative analysis of phylogenetic community structure. Studies of the phylogenetic structures of communities, including different species and trophic levels across various spatial and phylogenetic scales, also contribute to our understanding of trait evolution (Vamosi *et al.*, 2009).

In nature, speciation, competition among species, mutual benefit, and relationships with the environment are essential elements of the community. Relationships among species affect community status, and community composition is related to geographical range (Anderson and Raza, 2010). This indicates that determining how to select the "community" and the "species distribution area" is critical for modeling studies, and the "boundary" of a community is difficult to determine in reality. Macroscopically, all of the species in a community inhabit the same environment, and the results are "fair" to all of the species in the model when the same factors are removed for examinations of the community niche. The results of such studies of interspecific relationships among communities may be purer. Moreover, in community studies, the corresponding species, with the exception of the target species, can be considered part of the environmental conditions, and the taxonomic characters of each species are the result of the interactions between the species and the environment as well as among species. Therefore, pure biological traits actually contain "environmental" information and objectively do not exclude "environmental factors."

Fish characters can reflect the ecological function of the fish, and the trophic level of the fish corresponds to its special functional morphology. For example, *Siniperca kneri* (Garman, 1912) has a large, high head, a forward dorsal fin, and large, upturned eyes, while *Ancherythroculter lini* (Luo, 1994) and *Ochetobius elongatus* (Kner, 1867) have fusiform bodies, rearward dorsal, and caudal fins, deeply forked tails, long, narrow caudal handles, and small heads, all of which are favorable for hunting with speed. The intestine of herbivorous fish is longer than that of carnivorous fish, which is related to the energy acquisition process and the energy niche of the species. The size, eye position, eye diameter, mouth position, and mouth beard are related to predation and niche. The functional process of the fish in the ecosystem is embodied by the food chain, in which each species is a basic functional unit. Because species are related to characters, species characters are in turn related to species' function in the ecosystem. Different fish have different characters, which represent species characters. The model of community characters can be used to analyze the species relationships in a community. This book uses taxonomic morphological characters to study community characteristics. The same environmental factors are not considered in the model. The model adopts the correspondence analysis method of multivariate statistics.

2.2.1 Data Source

Based on the morphological characters used in fish taxonomy (Guangxi Zhuang Autonomous Region Institute of Aquaculture, 2006; Zhu Jiang Institute of Aquaculture, Chinese Academy of Aquatic Sciences, 1986, 1991; Chu *et al.*, 1989, 1990; Wu *et al.*, 1963, 1964, 1989; Zheng, 1989; Hunan Provincial Institute of Aquatic Sciences, 1977; Zhang, 1960), a total of 59 traits used to identify fish species were extracted as candidate modeling factors. Morphological traits were digitized into distinguishable values. Qualitative traits, such as "mouth position," are usually described as "mouth superior," "mouth inferior," and "mouth end" in fish taxonomy, and these three types can be digitized as "1," "2," and "3," respectively. Similar features, such as "caudal fin obtuse," "caudal fin pointed," "caudal fin circular," and "caudal fin forked" were distinguished using the numerical values "1," "2," "3," and "4," respectively. The numerical values of quantitative traits can be presented directly in a matrix table. The values of the 59 taxonomic characters are shown in table 2.1.

2.2.2 Data Matrix

To model the inter-species relationships in the fish community, it is necessary to record fish community sample data and construct a matrix of quantitative taxonomic characters. The n lines (from 1 to n in formula 2.1 represent the species in the studied fish community (that is, the sample for the statistical analysis of the model). P is a data column (from 1 to p) used to identify the taxonomic traits (*i.e.*, the variables for the statistical analysis of the model) of each species in the community; column p contains both qualitative and quantitative data.

A data matrix with n samples, p factors, and a target (column p + 1), where each sample corresponded to the factor data Xij and target data Yi (where the software runs and the model does not need a target factor, but still adds a dummy value), was constructed as follows:

$$\begin{pmatrix} \mathrm{X}_{11}, \mathrm{X}_{12}, \ldots\ldots \mathrm{X}_{1\mathrm{p}}, \mathrm{Y}_1 \\ \mathrm{X}_{21}, \mathrm{X}_{22}, \ldots\ldots \mathrm{X}_{2\mathrm{p}}, \mathrm{Y}_2 \\ \ldots\ldots \\ \mathrm{X}_{\mathrm{n}1}, \mathrm{X}_{12}, \ldots\ldots \mathrm{X}_{\mathrm{np}}, \mathrm{Y}_{\mathrm{n}} \end{pmatrix}_{\mathrm{n}(\mathrm{p}+1)} \tag{2.1}$$

Formula 2.1 Model data matrix.

Tab. 2.1 – Morphological classification parameters and differences among several fish*.

I: Fish, II Morphological classification parameters, III Character numbers	III II I	*Mylopharyngodon piceus* (Richardson, 1846)	*Misgurnus anguillicaudatus* (Cantor, 1842)	*Rhinogobius giurinus* (Rutter, 1897)
1	Mouth position	3	3	3
2	Caudal fin character	3	2	1
3	Number of air bladders	2	2	0
4	Upper jaw/lower jaw	1.5	1.5	0.1
5	Gill raker I	0	0	0
6	Gill raker II	18	36	9
7	Lingual tooth	0	0	0
8	Hypopharyngeal teeth I1	4	0	0
9	Hypopharyngeal teeth I2	0	0	0
10	Hypopharyngeal teeth I3	0	0	0
11	Hypopharyngeal teeth II1	5	0	0
12	Hypopharyngeal teeth II2	0	0	0
13	Hypopharyngeal teeth II3	0	0	0
14	Dorsal fin spine I	3	3	6
15	Dorsal fin spine II	0	0	1
16	Dorsal fin branched rays	7	8.5	8.5
17	Hard spine of anal fin	3	2	1
18	Anal fin branched rays	8	5	7.5
19	Hard spine of pectoral fin	1	1	0
20	Pectoral fin branched rays	16	12.5	18.5
21	Hard spine of ventral fin	1	1	1
22	Ventral fin branched rays	8	7	5
23	Body length/body height I	3.7	3.6	4.2
24	Body length/body height II	3.8	4.05	4.6
25	Body length/body height III	3.9	4.5	5

Tab. 2.1 – (Continued).

I: Fish, II Morphological classification parameters, III Character numbers	III II I	*Mylopharyngodon piceus* (Richardson, 1846)	*Misgurnus anguillicaudatus* (Cantor, 1842)	*Rhinogobius giurinus* (Rutter, 1897)
26	Body length/head length I	3.5	3.5	2.9
27	Body length/head length II	3.65	3.55	3
28	Body length/head length III	3.8	3.6	3.1
29	Head length/length of lips I	4	2	2.8
30	Head length/length of lips II	4.3	2.25	2.95
31	Head length/length of lips III	4.6	2.5	3.1
32	Head length/eye diameter I	5.2	4.5	4.9
33	Head length/eye diameter II	5.4	5.2	5
34	Head length/eye diameter III	5.6	5.9	5.1
35	Head length/interorbital width I	2.3	3.6	6.5
36	Head length/interorbital width II	2.35	4.2	7
37	Head length/interorbital width III	2.4	4.8	7.5
38	Tail stalk length/tail stalk height	1.38	1.08	2.25
39	Lateral line I	42	0	0
40	Scale above lateral I	6	0	0
41	Scale above lateral II	6	0	0
42	Scale above lateral III	6	0	0
43	Scale below lateral I	4	0	0
44	Scale below lateral II	4	0	0
45	Scale below lateral III	4	0	0
46	Lateral line II	43	0	0
47	Anterior dorsal fin scale I	15	0	20
48	Anterior dorsal fin scale II	16	0	45
49	Anterior dorsal fin scale III	17	0	70
50	Coccygeal scale I	16	0	12

Tab. 2.1 – (continued).

51	Coccygeal scale II	16.5	0	19
52	Coccygeal scale III	17	0	26
53	Mouth length/eye diameter	1.4	2.5	1.8
54	Maxillary barbel	0	1	0
55	Mouth barbel (a pair)	0	2	0
56	Dorsal fin position I	2	2	1
57	Dorsal fin position II	2	3	4
58	Shape of dorsal fin	1	1	2
59	Number of ventral fins	5	5	3

[*] “0” indicates no such trait was present.

2.2.3 Principles of the Correspondence Analysis Model

Correspondence analysis is a combination of R-type factor analysis and Q-type factor analysis. By transforming the matrix data, the relationship between each row and column in the data table is represented by a low-dimensional graph that reveals the differences among different categories of the same variable and the corresponding relationships among different categories of different variables. This analysis is also known as correlation analysis or R-Q factor transformation analysis (Yu and Ren, 1999; Luo *et al.*, 1986). This analysis mainly reflects the internal relationships between the factors and the different sides of the sample as a whole. To reflect the factor information, as well as the samples and the relationships between factors and samples, on a two-dimensional surface, the model combined R-factor analysis and Q-factor analysis statistically. The results of the Q-type factor analysis were obtained directly from the R-type factor analysis. Between these steps, we used transition matrix Z to find covariance matrix A of the variable and covariance matrix B of the sample. Then, we determined the eigenvalues of A and the eigenvectors of B. Finally, the load matrix of the R factor and the Q factor was obtained, such that factor and sample information was available in the same two-dimensional plane.

To determine the covariance matrix of variable A, we first find the covariance matrix of the i and j variables as well as W_{pn} (where p is the factor number and n is the sample number). For example,

$$Z_{pn} = W_{pn}. \tag{2.2}$$

The covariance matrix of the variable is

$$A = Z', \text{where } Z' \text{ is the transposed matrix of } Z\ldots \tag{2.3}$$

In variable R factor analysis, the factor axis F_α is the product of the eigenvector of matrix A and the square root of its corresponding eigenvalues, namely,

$$\begin{gathered} F_\alpha = (u_{1\alpha}, u_{2\alpha}, \ldots, u_{p\alpha})' \sqrt{\lambda_\alpha} \\ (\alpha = 1, 2, \ldots, m, m < p), \end{gathered} \tag{2.4}$$

where λ_α is the eigenvalue of matrix A (and the contribution of the α factor to the total variance) and $(u_{1\alpha}, u_{2\alpha}, \ldots, u_{p\alpha})'$ is the eigenvector corresponding to λ_α.

Using the same method, we can find the covariance matrix B of the sample, which is

$$B = Z'Z. \tag{2.5}$$

The number of principal factors and the load matrix of the R-type factor are calculated as follows: According to the theorems of linear algebra, both the A and B matrices have the same characteristic non-zero root. Thus, the result of the Q-type can be obtained directly from the R-type factor analysis. We then use $A = ZZ'$ to find the result of $\lambda_1 \geq \lambda_2 \geq \cdots \lambda_p$. When the cumulative variance contribution rate to $(\lambda_1 + \lambda_2 + \cdots + \lambda_m)/(\lambda_1 + \lambda_2 + \cdots + \lambda_p) \geq 70\%–85\%$ (the lower limit is 70% when $m \geq 10$, and 85% when m is less than 10%), m is the number of main factors.

After choosing the m of $\lambda_1 + \lambda_2 + \cdots + \lambda_m$ and the corresponding unit of U_1, U_2, …, U_m, we can obtain the R-type factor load matrix as follows:

$$F = (u_{i\alpha}\lambda_\alpha)_{pm} \tag{2.6}$$

The load matrix of the Q-factor is determined as follows: Because $B = Z'Z$, the preceding eigenvalues are $\lambda_1 \geq \lambda_2 \geq \cdots \lambda_m$, and the corresponding unit eigenvectors are $V_1 = Z'U_1$, $V_2 = Z'U_2$, …, $V_m = Z'U_m$. Therefore, the load matrix of the Q factor is

$$G = (V_{j\alpha}\lambda_\alpha)_{nm}. \tag{2.7}$$

Using the load of the R-factor and Q-factor, the reduced-dimensional diagram of the variable (factor) and the sample point can be positioned on the plane of the two-factor axis.

2.2.4 Contribution to Variance

In multivariate statistical analysis, it is necessary to transform the m original variables linearly and to construct m new variables (called principal factors or principal components). Each new variable contains m information about the original variables, but the new and original variables are independent of one another. When calculating the eigenvalues λ_i and the eigenvectors of each principal component, the first principal component has the largest variance, the second principal component has the second largest variance, and the last principal component has the smallest variance. The ratio of the variance each principal component to the total variance (referring to each of principal axis in the reduced dimension graph) is the variance contribution ratio, which also reflects the relative total information contained in each principal axis in the reduced-dimensional graph. The variance contribution rate can be understood as the proportion of information: higher contribution rates indicate more important principal components. The contribution to the variance of the first principal component is

$$\lambda_i/(\lambda_1 + \lambda_2 + \lambda_3 + \cdots + \lambda_m). \tag{2.8}$$

In multivariate statistical analysis, it is necessary to know the variance contribution rate of each principal axis. The higher the variance contribution rate of the principal axis, the higher the information occupancy rate and the stronger the objectivity and reliability of the analysis. When the high-dimensional data information in the matrix is reduced to a two-dimensional graph, the cumulative variance contribution rates of the first and second principal axes represent the credibility measures of the graph interpretation. If the variance contribution rate of the first and second axes is more than 75% (if the dimension is higher, this accumulated-value requirement can be reduced appropriately), the total information contained in the two-dimensional graph is more than 75%. The selection of model parameters should carefully consider the variance contribution rate and its cumulative value. The larger the variance contribution rate and its cumulative value, the higher the information credibility of the two-dimensional graph. In general, the variance contribution of the first principal axis is greater than that of the second principal axis, in which case the position of the sample (or variable) point on the horizontal axis is more important than the position of the second principal axis. Thus, the influence of the sample (or variable) point on the absolute value of the first principal axis is usually greater than that on the absolute value of the second principal axis.

In the two-dimensional graph of the fish community model, adjacent sample points were closely related and were regarded as generally similar sample points. These factors were also assumed to have a similar influence on the sample points and were classified into the same class. The closer the relationship between the sample and the factor, the greater the influence of the factor on the sample. However, in the study of point-to-point relationships, it is also necessary to pay attention to the difference in the variance contribution rate of the different axes (information ratio) and its impact on the results.

2.2.5 Graph Representation of the Interspecific Relationships Within Fish Communities

The results of the inter-species relationship model of fish communities were represented as a two-dimensional graph. In other words, the different coordinates (values) of the x- and y-axes on the plane map were used to study the relationship between different community types (samples) and various common characters (variables). According to the information provided by the matrix, the points were distributed in the two-dimensional plane in a way that could be distinguished during model operation. The numbers marked on the four corners of the plane map were the maximum and minimum values of the coordinate axis of the interspecific relationship within the community. The line between the origin of the two-dimensional graph and the locus of the sample or variable reflected the vector (length) of the sample or variable, and this vector was regarded as a measure of the spatial relationships within the community. Three kinds of two-dimensional distribution graphs were obtained *via* model analysis.

2.2.5.1 Relationships Between Species and Traits

The results of the correspondence analysis of the species-character matrix of the community were shown on a two-dimensional plane. The species and traits were represented by graph points, and the black circle represented the species; these were numbered according to the sequence in the matrix. The red circle represented the character, and the numbers corresponded to the “character sequence number + maximum number of species” from the matrix (*i.e.*, if the number of species was 1, 2, 3,..., 10, then the character number 1 was “1 + 10” in the graph or character number 11, and character number 2 was 12). The line connecting the circle (red or black) to the origin of the coordinates (red or black) indicated the positional relationship between the species or trait and the coordinate system, the value of which is determined by the value of the x- and y-axes indicated by the graph angle (see figure 2.1).

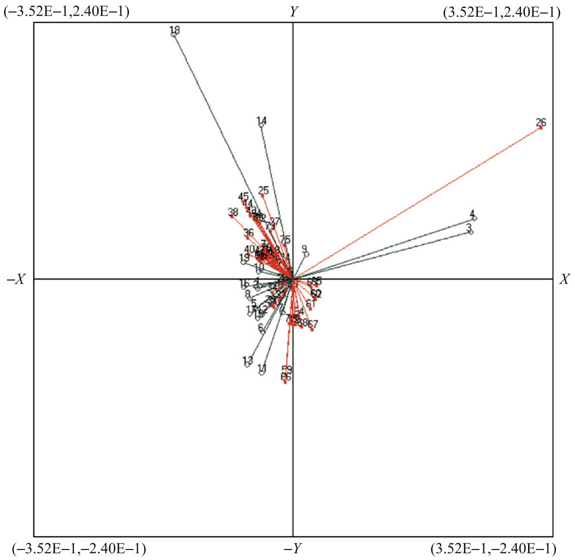


Fig. 2.1 – The two-dimensional graph of the 19 species × 59 trait matrix, showing the sample-character relationships.

Figure 2.1 shows the result of the model analysis of the 19 × 59 matrices composed of 19 fish species as communities and the 59 taxonomic characters listed in the table (see table 2.1). The numbers 1–19 represented 19 different species of fish, as follows: “1,” *Mylopharyngodon piceus* (Richardson, 1846); “2,” *Ctenopharyngodon idella* (Valenciennes, 1844); “3,” *Hypophthalmichthys molitrix* (Valenciennes, 1844); “4,” *Hypophthalmichthys nobilis* (Richardson, 1845); “5,” *Megalobrama terminalis* (Richardson, 1846); “6,” *Parabramis pekinensis* (Basilewsky, 1855); “7,” *Xenocypris argentea* (Günther, 1868); “8,” *Squaliobarbus curriculus* (Richardson, 1846); “9,” *Cirrhinus molitorella* (Valenciennes, 1844); “10,” *Cyprinus carpio* (Linnaeus, 1758); “11,” *Elopichthys bambusa* (Richardson, 1845); “12,” *Ochetobius elongatus* (Kner, 1867); “13,” *Siniperca kneri* (Garman, 1912); “14,” *Sinibotia pulchra* (Wu, 1939); “15,” *Hemiculter leucisculus* (Basilewsky, 1855); “16,” *Squalidus argentatus* (Sauvage and Dabry de Thiersant, 1874); “17,” *Pseudolaubuca sinensis* (Bleeker, 1865); “18,” *Lcucosoma chinensis* (Osbeck, 1765); and “19,” *Rhinogobius giurinus* (Rutter, 1897). The numbers 20–78 represented different variables (*i.e.*, taxonomic parameters) in the order shown in table 2.1.

2.2.5.2 Interspecific Relationships

The results of the species-character matrix of the community were graphed on a two-dimensional plane. The species were represented by numbered circles, and the numbers were derived from the serial numbers of the species in the matrix. The line connecting each circle to the origin of the coordinate system indicated the positional relationship between the two coordinate systems. The value of the line was determined by the value of the x- and y-axes indicated by the graph angle. Figure 2.2 only shows the results of 19 species.

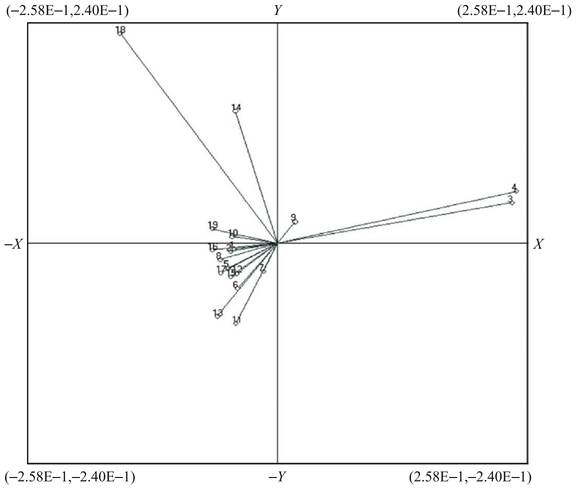


FIG. 2.2 – The two-dimensional graph of the 19 species × 59 traits matrix, showing the interspecific relationships.

2.2.5.3 Character Relationships

The results of the species-character matrix of the community were shown on a two-dimensional plane, with the red circles representing different characters. The characters were numbered following the "maximum number of species + character sequence number" in the matrix. Figure 2.3 shows the results of the variable such as the 59 different characters (numbers 20–78) in figure 2.1.

2.2.5.4 Coordinates

After reducing the dimensions of the inter-species relationships, each species corresponded to coordinates in the two-dimensional result map. In the same data matrix, changes in the position of a row (character factor) or column (fish sample) did not affect the two-dimensional coordinate value of each species in the community. That is, each coordinate was unique. Of course, different species and numbers, as well as different character factors and numbers, constitute different data matrices, showing that the coordinates of different fish differ. Table 2.2 shows the coordinate values for 19 species of fish based on the data in figure 2.1.

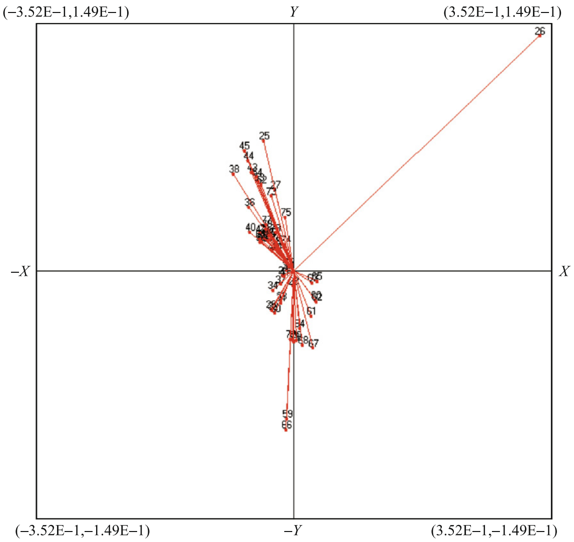


Fig. 2.3 – Two-dimensional graph of the 19 species × 59 character matrix, showing character relationships.

Tab. 2.2 – Coordinates of the 19 species shown in figure 2.2.

Number	Fish species	x-axis coordinates	y-axis coordinates
1	*Mylopharyngodon piceus*	−0.044874	−0.005854
2	*Ctenopharyngodon idella*	−0.048582	−0.008689
3	*Hypophthalmichthys molitrix*	0.240778	0.044257
4	*Hypophthalmichthys nobilis*	0.245318	0.057038
5	*Megalobrama terminalis*	−0.051155	−0.026847
6	*Parabramis pekinensis*	−0.041304	−0.048978
7	*Xenocypris argentea*	−0.014737	−0.0306
8	*Squaliobarbus curriculus*	−0.059231	−0.01754
9	*Cirrhinus molitorella*	0.017656	0.023696
10	*Cyprinus carpio*	−0.046981	0.007503
11	*Elopichthys bambusa*	−0.042912	−0.086624
12	*Ochetobius elongatus*	−0.042176	−0.032617
13	*Siniperca kneri*	−0.062285	−0.079371
14	*Sinibotia pulchra*	−0.043638	0.143961
15	*Hemiculter leucisculus*	−0.0485	−0.036018
16	*Squalidus argentatus*	−0.067134	−0.007238
17	*Pseudolaubuca sinensis*	−0.0586	−0.032028
18	*Lcucosoma chinensis*	−0.162126	0.228608
19	*Rhinogobius giurinus*	−0.067629	0.016062

2.2.5.5 Contribution to Variance

The variance contribution rate is the proportion of information of every dimension in the model analysis result. In a two-dimensional graph, only x and y are marked, but in system analysis, the background can reflect the proportional information associated with each dimension.

The dimension-reduction analysis of the 19 fish × 59-factor data matrix is shown in figure 2.1, while the information for each dimension is shown in figure 2.4. The sum of the variance contributions of all axes was "1." The variance contribution of the first axis was 0.44, the variance contribution of the second axis was 0.24, and the variance contribution of the third axis was 0.1. After the 14th axis, the variance contribution of each axis was too small to show. The variance contribution rate of the first and second axes was 68%, which indicated that the information rate of the two-dimensional graph derived from the model was 68%.

FIG. 2.4 – The variance contribution rates of each principal axis for the 19 species × 59 character matrix.

The variance test thus showed that the results of the model analysis were suitable for our analysis, and the species relationships in the two-dimensional graph met the analysis requirements.

2.3 The Model

In community-building, one theory states that species are in competitive relationships (Green, 1971), and that community composition is dominated by species groups; another theory states that species groups in a community are governed by chance (Hubbell, 2001) and that their total abundance corresponds to the total biomass of the community (de Mazancourt, 2001). Competition theory holds that species with similar ecological niches cannot coexist, while stochastic theory holds that species with similar ecological requirements can coexist. Ulrich *et al.* (2010) reported evidence of the co-occurrence of niche differentiation and speciation, reflecting the complexity of the biological composition of the ecosystem and the need for diversity to maintain the system. Therefore, species competition and niche-like species co-exist in the community. This is related to the need for system functions to meet the needs of adaptation to high environmental variability, which reflects the diversity or high buffer function of ecosystems. Niche is a basic concept in biology that states that species occupy a specific ecological space in the ecosystem (Vandermeer J H, 1972). Species distributions are governed by multidimensional space. Drake *et al.* (2006) constructed a model of nine environmental factors related to 106 plant species and their growth and characterized the niche of Hutchinson analyzed the relationship between phylogenetic distance and ecological similarity, explaining the mechanism of community structure based on the relationship between phylogenetic similarity and niche. The intensity of niche conservativeness (habitat filtration) and species interaction (competition or mutual benefit) affect community structure through phylogeny.

The study of biodiversity and ecosystems requires functional, community, and biogeographic studies, in conjunction with the development of an ecological and taxonomic approach to quantitative analysis (Naeem and Wright, 2003). A quantitative analysis method for extended population and community studies (Jacobson B and Peres-Neto P R, 2010) is also necessary, and quantitative research is needed for the development of ecology (Devictor *et al.*, 2010). The spatial variability within ecological communities is extremely complex, and the accuracy of the species distribution model is influenced by the sample size (Stockwell and Peterson, 2002). Quantitative spatial and environmental factors are one of the main objectives of community studies (Henriques-Silva *et al.*, 2013). The species niche is the core of many ecological applications. An understanding of the niche can help to analyze the evolutionary relationships among coexisting species from the perspective of species phylogenies, and the number of taxon nodes isolated from phylogeny can be used as an index of the phylogenetic correlations among species. From this, the phylogenetic structure of a species community can be understood, and the basis of the niche structure of a community and the evolutionary relationships among characters can be explored (Webb *et al.*, 2002).

The current biodiversity crisis is prompting ecologists and conservation biologists to develop models to predict the impact of human-induced natural resource transformation on species distributions and to try to understand the drivers of biodiversity patterns. Species niche distributions are related to the environment (Randin *et al.*, 2006). Environmental variables can explain the mechanisms of fish population construction, indicate the existence or function of a specific mechanism, and support hypotheses about this mechanism (Miller, 2007). Statistical models for predicting species distributions include the generalized linear model and generalized additive models (GAM), quantitative regression (QR), structural equation modeling (SEM), and geographically weighted regression (GWR) (Austin, 2007). The model needs to be explanatory, predictive, and provide a good balance of features that reduce overfitting of the model (Rangel and Loyola, 2012). Despite previous research efforts, it has gradually become recognized that the objects, models, and theories studied are local, limited, and difficult to encompass. The study of biological communities, like other fields of natural science, needs to take the best of each family, and to focus, as far as possible, on multi-angle observations and studies to develop a more comprehensive understanding of biological communities.

The niche concept of Hutchinson SA applies to the role of interspecific competition in the formation of species distribution patterns. Pulliam (2000) expressed the effects of niche breadth, habitat availability, dispersion, and interspecific competition by quantifying the temporal and spatial relationships between niche dimensions and specific populations. In this way, the relationship between species distributions and the availability of suitable habitats was observed. Jackson and Overpeck (2000) retraced environmental conditions and the forms of biological responses in a historical period using a model of community reorganization. If late quaternary climate changes continue to occur on a large time scale, then the magnitude of changes in biological communities will fluctuate over time. The responses of land, animal, and plant populations to habitat change may be migration or extinction, and these results also reflect the degree and speed of environmental change. Biomes are affected by spatial processes, and species in communities have their own spatial structural characteristics.

Interspecific relationships can be explored using quantitative trait analysis or genetic analysis. Clarke and Warwick (1999) hypothesized that species distance embodies the inter-species relationships in a community, as well as the summation of the relationships within species, among species, and between species and the environment. Elith *et al.* (2006) devised an analytical method to study species distribution and interspecific relationships using museum specimen data. Robert *et al.* (2010) argued that niche studies can yield objective results if they are framed in the right context and that the concept of "relative niche" allows further community analysis. All of that can be obtained by assessing taxonomic differences within ecosystems, such as the taxonomic characteristics of biodiversity (Leonard *et al.*, 2006), the relationships between biodiversity indicators and community structure, the relationships between traditional diversity and new concepts of diversity and richness, and the spatial niche of community composition (Shen *et al.*, 2015). Most commonly, communities are defined by interspecific relationships, also known as niche relationships, and it is important to develop methods to quantify community niches. The patterns of interspecific relationships and community species diversity are influenced by selection, drift, species formation, and diffusion, in which differences in species fitness reflect interspecific relationships, changes in abundance reflect drift, speciation events reflect the creation of new traits, and the movement of organisms across space reflects diffusion. The theory of community dynamics states that species are formed and added to a community, and the relative abundance of these species drives community dynamics through drift, selection, and sustained diffusion. The key to revealing the interspecific relationships within communities is a clear understanding of the spatial distributions of organisms or the spatial occupancy of species (Velend, 2010).

Speciation is the result of interactions between organisms and the environment. Although organisms are constantly adapting to the changing environment, the characteristics of the "species" (*i.e.*, the taxonomic characters) do not change. The "environment" here corresponds to the summation of other species and their conditions, as well as predation and the competition for food. Therefore, the morphological characteristics of a "species" record the information affected by the environment (*i.e.*, niche information). Taxonomic parameters quantify species characteristics and the differences among species in communities. Such data address the difficulty of quantifying the relationships among species in communities (*i.e.*, the problem of identifying a data source for the analysis of "niche"). The relationships between species and the environment are also generally considered a niche relationship, and the niche of a species can be represented by its spatial position. The "amount of space" for a "niche" can be expressed as a percentage of space occupancy (%). In the systematics concept category, the total niche occupied by each species in the community is "1."

2.3.1 Species Relationship Model

The relationships between ecosystem boundaries and species are a major concern of community studies because species respond differently to their environment at different geographic scales (Gotelli and Engstrom, 2003). The community function is ultimately reflected in changes in species composition, species richness, and taxonomic diversity (Heino *et al.*, 2005). Community formation across space, including uncertain dynamic processes, biological interactions, and community effects, is ultimately reflected in differences in species distributions and functional traits (Guisan and Thuiller, 2005).

There is a positive linear correlation between the size of the geographical boundaries and the individual sizes of the species in the community. However, in small-scale environments, the largest and smallest species occur less frequently and medium-sized species occur more frequently (Inostroza-Michael *et al.*, 2018). The geographical distributions of biological species vary by orders of magnitude from broad to narrow. For example, microbial species rarely occupy large ecological spaces but are characterized by local richness. Differences in microbial distribution range can be predicted by taxonomic characteristics, phenotypic traits, genomic attributes, and habitat preference (Choudoir *et al.*, 2018), which suggests that the community niche can be revealed by biological characteristics. Each community's environment is different, which reflects the different functional states of each ecosystem. The environment determines the species composition of the community. In studies of community niches, geological information about time dimensions and biological information about evolution can be used for analyses of community niche change (Marc Kéry *et al.*, 2010). Database data mining is important for the study of species relationship models (Dudei and Stigall, 2010).

Zintzen *et al.* (2011) studied fish communities along marine bathymetric gradients; the results demonstrated that the number of species in each bathymetric community was stable and did not change significantly with depth. However, taxonomic similarities in species composition among communities in different habitats along the environmental gradient decreased with depth, and there were no obvious patterns relating depth to the average taxonomic difference. Interestingly, taxon trees constructed for species from deeper samples had more variable path lengths than shallow samples. There were taxonomic differences associated with depth, and functionally similar species were found at similar depths, indicating that functional niches are formed in relatively stable extreme environments (*e.g.*, similar levels of darkness and water pressure). These results also showed that certain fish species occupy the community niche and fulfill ecosystem function, which is the basis of community functional ecology. Over large spatiotemporal scales, the species in an ecosystem are characterized by "traits." The disappearance of "traits" will lead to the disappearance of species, and the appearance of new "traits" will lead to the emergence of new species. In model studies, the "character" value of a given species is "fixed," and changes in the community are reflected by changes in species abundance. In communities with identical species compositions, species adjust their interspecific relationships *via* changes in abundance, realizing the niche balance.

In the mathematical analysis system, the relationships among species niches in a community are not an exclusive mechanism, and the rational distribution of energy in the system means that objects occupy the space on a "first come, first served" basis (Aarssen *et al.*, 2006). That is, later species always "squeeze" the space occupied by the original object to obtain corresponding positions. As a result, the space occupied by the early objects is large, but the space is then gradually squeezed by latecomers, and the space occupied by the position is gradually reduced.

A matrix analysis model of morphological parameters, which integrates the essence of taxonomic features and expands the analysis functions of character differences, is proposed by establishing a multidimensional model with characters as variables, community species as samples, and taxonomic characters as variables. Thus, the spatial relationships among species in a community can be studied using multi-dimensional mathematics. The spatial niche of a species in a community was defined by two-dimensional coordinates and vector double-positioning. Interspecific mutual benefit and competition are the key factors that determine niche and community formation. In the model, only the taxonomic characters of species were selected, and the concepts of species and environmental boundaries were avoided. This model is suitable for the analysis of pure species relationships within the community and can provide a reference for niche succession in a community in response to environmental change. The model is also suitable for community reconstruction, as it provides an analytical means for predicting niche relationships among species.

Species abundance is one of the key indicators of community species niche. In this study, "species + traits" were used to establish a "fish morphological model" for studying community species relationships. The positional relationships within the model community in space were solidified by coordinate demarcation, and these positions were identified as the ideal niche of each species in the community. Then, "species abundance" was introduced as a synthetic variable (which can be introduced randomly such that the sum of the values of "species abundance" equal "1"), and the variations in synthetic variables were compared with the "spatial positional relationships among solidified community species" in order to quantitatively study the niche based on proportional relationships among species abundance (comprehensive variable).

Based on multivariate statistical theory, the model "solidifies" the relationships between "species + traits" into spatial relationships among species in the community, obtains various two-dimensional coordinates and "vectors" for the community, and constructs a spatial ecological conformation to reveal the standard "ideal niche" pattern. The proportional "species abundance" (referred to as the "niche value" at the beginning of this chapter) was introduced as an indicator of niche value. It is assumed that the niche value of the ideal community should satisfy the "ideal niche pattern of the community," as calculated by the "species + traits" model. Using computer iterative positioning technology, the proportional "species abundance" in the community was adjusted, and the spatial positions of the species in the community tended toward the "ideal ecological position" (*i.e.*, the position determined by the two-dimensional coordinates and "vector" double positioning). The result of this iteration is the "ideal niche" species abundance ratio in the community, which is equivalent to the quantitative niche.

In the model, "species abundance" in the community was introduced as a comprehensive variable, and its vector (deviation degree) affected the species abundance ratio of the community. At the lowest vector values, the species abundance ratio of the community was the most reasonable. At larger vector values, the species abundance ratio was more unreasonable. Therefore, changes in the vector reflect changes in community species abundance, and the species model can be named the "fish community niche research model." This model can be used as a tool to transform interspecific relationships into quantitative niche relationships.

Little attention has been paid to the role of fish morphology in the functional mechanisms of fish communities and ecosystems (Zhang, 2005). Morphology provides a very promising indicator of biodiversity because morphological characters are multifunctional and do not just indicate taxonomy and phylogeny (Xiong *et al.*, 2015). One of the main theoretical hypotheses of ecomorphology is that the ecology of an organism is related to its morphology. Morphology can be used to understand the relationship between ecological factors (both physical and biological) and functional traits. The fish community niche model is not influenced by environmental factors, as it only considers fish and fish characters. Usually, all of the species in a community are in the same environment. Therefore, models ruled out that the same environmental conditions are "fair" to all species in the model, and the results are purer. Moreover, in community research, species besides the target species can be considered environmental conditions. The taxonomic characters of each species are the result of the interaction between species and the environment as well as among species. Therefore, pure biological traits actually contain "environmental" information and objectively do not exclude "environmental factors."

The theoretical underpinnings of this model are as follows:

I. Biodiversity (species richness) measurements are influenced by habitat type and complexity, and it is difficult to compare data from different habitats or habitat types. Taxonomic traits do not have this problem. There is no difference in sampling effort or rigor among workers, and the differences in taxonomic characters among species have been tested by history. Classification difference analysis has theoretical and mechanical advantages compared to the evaluation of many uncertain data measures (Warwick and Clarke, 1998).
II. Blackburn *et al.* (1997) studied species distributions and suggested that there is a fixed structural relationship among species within a community. Peterson *et al.* (1999) performed reciprocal geographic predictions of niche models for sister taxa of birds, mammals, and butterflies in southern Mexico and showed that niche conservativeness exceeds millions of years of independent evolution; this

conservation is reflected at the species level. Communities with similar structures live in similar habitats, and community structure has little relationship to species richness (Bellwood *et al.*, 2002). This conclusion also demonstrates that the "ideal niche" can be obtained from species community data.

III. Enquist *et al.* (2002) used biodata from different biogeographic regions, continents, and geological epochs to study the taxonomic and ecological characteristics of communities, as well as to reveal the mechanisms of species interactions. The results showed that the community species data reflected the environmental attributes.

IV. Multiple regression analysis and its generalized form (GLM) are very popular methods for species distribution modeling. Techniques such as neural networks, ranking and classification methods, Bayesian cognitive science, and local weighting methods (GAM), which are probabilistic in nature, can be used to support analyses of community characteristics and niches (Guisan and Zimmermann, 2000).

V. Hirzel *et al.* (2002) studied biological communities, and the first factor from the multidimensional space of ecological variables was extracted as the maximum range of activity of the target species. This factor was then defined as the optimal ecological distance between the species in the study area and the average habitat, and the feature vector was used to demarcate the suitable range map of the species' habitat. The feature vector can be used as a scalar to measure or distinguish species characteristics, thus determining the "niche scope" for species in the community.

Interspecific interactions are important for the maintenance of community status. In this book, we introduce the vector concept of the interspecific interaction force in our analysis of species' spatial effects. That is, we hypothesize that there is an interaction force among species in a natural biological community. When the community is in a state of natural stability, the resultant force of interaction among species is "zero." Otherwise, the community niche is not stable, or the community structure is in a state of environmental disturbance. The absolute value of the composite vector of a stable community is "0," and values between "1" and "0" reflect not only the state of the community but also the possible degree of environmental disturbance. Due to the changing environment of the species community, the absolute value of community resultant force cannot be "0" in reality.

In general, in the same ecological unit under study, the effects of environmental conditions on each species in the community can be regarded as equal, but different species respond differently to the environment. This difference results in the development of different taxonomic characters, which in turn leads to the formation of new species, which become members of a diverse community in an ecological unit. The variables in the fish community morphological model were quantified based on the morphological characters of each species, and the results of the morphological character analysis can be regarded as the theoretical niche.

As shown in figure 2.1, a simulated variable (A) representing the abundance of the 19 species was added to the hypothetical community matrix of 19 species × 59 traits. A new matrix, defined as "19 species × 59 characters + A" was formed,

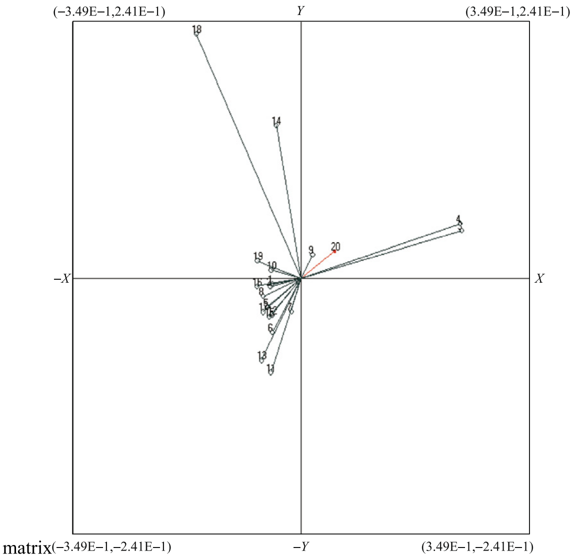


FIG. 2.5 – The position of "20" ("A") deviates from the origin of the coordinates, indicating that the community is disturbed.

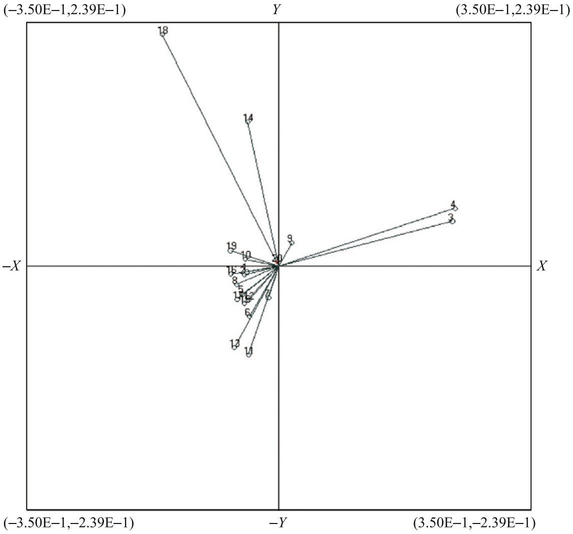


FIG. 2.6 – The position of "20" ("A") at the origin of the coordinates indicates that the community is a natural niche.

where A was numbered "20" and deviated from the central point (see figure 2.5). This indicated that the interspecific relationships in the community corresponded to a non-natural niche relationship. That is, our results indicated that the simulated community was disturbed. We then explored how the niche of 19 fish species in a simulated community might look in an undisturbed community. These results were obtained by adjusting the abundance ratios of each species. The result $A = 0$ was obtained by adjusting abundance relationships among the 19 fish species. Figure 2.6 shows the status of the "undisturbed community," which also could be considered the "ideal niche," after adjustment for the model parameter (A).

With the help of computer technology, the species abundance ratio was introduced into the morphological species model as the niche evaluation value, which can be applied to the study of the niche relationships of fish communities that include any combination of species. This model provides an analytical method for the study of fish community structure. Mutual benefit and competition are common phenomena. Understanding the relationships among different species in the community is the basis of community reconstruction. The interactions among adjacent species can reflect the response of these species to environmental change.

2.3.2 Character Fitness

Communities are constantly adapting to changes in their environment. This historical process is reflected in species' evolutionary trees. The adaptation of organisms to the environment is manifested not only in the change of niche but also in the change of characters. For example, the number of lateral scales varies across the range of a single fish species, as does the number of teeth across humans. These changes are the result of intraspecific differences and the adaptation of the population to environmental changes. Many of the changes in a species are also the basis for the emergence of new species. These changes can be applied to the niche model by systematically quantifying the characters of the species in the community using unified community variables and identifying characters that can be refined. For example, if tooth (T) is a characteristic trait that can be refined, and a species has 28–32 teeth, three characteristic variables can be refined: the minimum number of teeth (T_1), the average number of teeth (T_2), and the maximum number of teeth (T_3). In this way, the volume of data in the community species matrix can be increased, and the niche relationships obtained by the model will be more objective.

2.3.3 Applicability of New Species

According to Burns and Strauss (2011), we can understand the mechanisms of community construction by exploring the potential relationships between phylogenetic similarity and niche, with special consideration of the relationship between phylogenetic distance and ecological similarity. It is believed that niche conservation (habitat filtration) and species interactions (competition or promotion) are the basis of community formation and maintenance. The adaptation of biological communities to environmental change eventually leads to the formation of new species communities (*e.g.*, *via* species extinction, new species formation, and alien species invasion). In such cases, species change in the community, as well as species abundance (*i.e.*, quantity), is in a stable transition period. The model can be used to estimate the "rationality" of the niche community structure after new species formation and to predict the direction of changes in community abundance.

2.4 Examples of Model Application

Species change over evolutionary time, but the environment has changed dramatically in recent decades, and many species have gone extinct due to their inability to adapt to these sudden environmental changes. The loss of ecological species niches due to environmental change has become a common worldwide phenomenon that has disordered river ecosystem function and led to declines in an ecosystem service function. It has become gradually clear that water quality depends on fish, but more research is needed to explore the interspecific relationships and niche functions of fish communities in river ecosystems. The fields involved in ecologies, such as taxonomy, phylogeny, and biodiversity, are developing toward quantification (Devictor V *et al.*, 2010). Based on the concept that the ideal niche is related to the spatial composition of the species community, the proportional abundance of the species in the community was characterized. The fish community morphological model may thus provide a new method for niche research. Quantification of the ideal niche will provide a reference system for community succession analysis, which may help clarify fish morphological niches, leading to improvements in the restoration and guarantee of river ecosystem function, as well as the restoration and reconstruction of fish communities.

The distribution patterns of quantitative analyses help to clarify the processes that shape species distributions. In ecosystems, the range over which species are distributed is constrained by environmental conditions, and the niche patterns of species are regular. The ranges of genera, families, orders, and species of plants and animals usually vary by several orders of magnitude; these differences are related to changes in individual size, population density, dispersion patterns, latitude, altitude, and depth (in ocean systems). To analyze and evaluate changes in species communities, it is necessary to establish standards by which to judge change. The method of quantitative analysis of the "ideal niche" established in this study can quantify the "standard" model of the ideal niche for each species in fish communities composed of "any species," providing both a reference for the study of fish communities and an analysis platform for the exploration of the mechanisms of community species formation. In this section, the model of the Pearl River fish community is analyzed in order to specify the technical details of the model.

2.4.1 Characterization of Community Species Relationships

Taxonomic traits are the result of interactions between organisms and their environment over evolutionary time. These interactions lead to the development of "fixed" traits that distinguish individuals and species. Although organisms are constantly changing in the environment, the usual changes are not sufficient to change the characteristics of the species (that is, if the characteristics of the species are changed, it is generally believed that a new species has formed). Therefore, species characteristics can be regarded as "unchanged." In an investigation of fish resources in the middle and lower reaches of the Pearl River, we found that 19 species of fish accounted for more than 70% of the fishing resources (Li *et al.*, 2008, 2010, 2020a, 2020b, 2020c, 2020d, 2020e, 2021a, 2021b; Xu *et al.*, 2018; Tan *et al.*, 2010). This study of 19 species of fish, representing the target fish community, reflects certain information about species relationships in the studied section of the Pearl River. The parameters were selected from the 59 candidate morphological characters in table 2.2; in total, 24 morphological characters were selected for analysis. Fish abundance data were extracted every two days from the daily data collected by our laboratory in the Zhaoqing section of the Pearl River and corrected using cross-sectional runoff data. The total amount of early recruitment for each species was calculated and converted to the percentage of early recruitment for the 19 species. This value was used as a proxy for abundance data (niche space occupancy) for this group (see table 2.3).

TAB. 2.3 – Proportion of early floating fish resources in the Zhaoqing section of the Pearl River in 2012.

Number	Species	2012
1	*Mylopharyngodon piceus*	0.10
2	*Ctenopharyngodon idella*	1.13
3	*Hypophthalmichthys molitrix*	2.76
4	*Hypophthalmichthys nobilis*	1.15
5	*Megalobrama terminalis*	22.30
6	*Parabramis pekinensis*	0.56
7	*Xenocypris argentea*	9.32
8	*Squaliobarbus curriculus*	50.48
9	*Cirrhinus molitorella*	4.59
10	*Cyprinus carpio*	0.00
11	*Elopichthys bambusa*	0.68
12	*Ochetobius elongatus*	0.31
13	*Siniperca kneri*	0.15
14	*Sinibotia pulchra*	1.39
15	*Hemiculter leucisculus*	3.44
16	*Squalidus argentatus*	0.92
17	*Pseudolaubuca sinensis*	0.40
18	*Lcucosoma chinensis*	0.13
19	*Rhinogobius giurinus*	0.19
20	Accumulates	100.0

The sample serial numbers shown in table 2.3 were included in the matrix. The numbers 1–19 correspond to the fish (*e.g.*, 1 corresponds to *Mylopharyngodon piceus* and 2 corresponds to grass carp). Number 20 is a comprehensive variable representing measured species richness. Numbers 21–44 correspond to the dependent variables (traits): 21 corresponds to gill raker I; 22 corresponds to hypopharyngeal teeth I1; 23 corresponds to hypopharyngeal teeth I2; 24 corresponds to hypopharyngeal teeth II1; 25 corresponds to hypopharyngeal teeth II2; 26 corresponds to dorsal fin spine I; 27 corresponds to soft spine of dorsal fin; 28 corresponds to soft spine of anal fin; 29 corresponds to hard spine of anal fin; 30 corresponds to soft spine of pectoral fin; 31 corresponds to soft spine of ventral fin; 32 corresponds to body length/body height III; 33 corresponds to body length/head length III; 34 corresponds to head length/length of lips III; 35 corresponds to head length/eye diameter III; 36 corresponds to head length/interocular septum III; 37 corresponds to tail stalk length/tail stalk height; 38 corresponds to lateral line I; 39 corresponds to lateral scale III; 40 corresponds to lateral sale III; 41 corresponds to inferior lateral line; 42 corresponds to anterior dorsal fin scale III; 43 corresponds to coccygeal scale I; and 44 corresponds to maximum body length.

The model is a morphological analysis model of the fish community. The positional relationships among the 19 species of fish were determined using multi-dimensional relationship analysis and reduced to a two-dimensional graph. As shown in figure 2.7, 19 species of fish were distributed in the plane (black circles), and the spatial niche relationships of the 19 fish species (based on larvae measured in 2012) in the Pearl River reach were studied. As shown in table 2.4, each species corresponded to coordinates in the two-dimensional plane, reflected in the position of the x- and y-axes. The line between the origin of the coordinates and the fish distribution points is the vectors of the points.

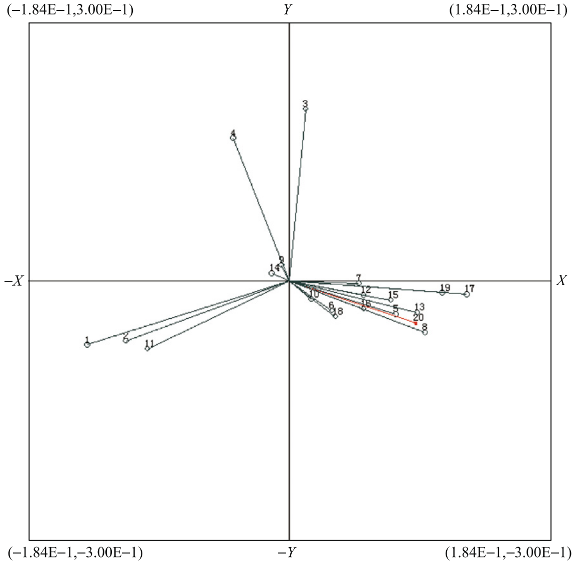


FIG. 2.7 – Community ecological map of 19 species of fish (fish abundance data based on larval measurements in 2012).

TAB. 2.4 – Coordinates of variables (19 species of fish) and independent variables (24 taxonomic traits) in the model analysis results.

Number	Fish	Characterization of the 24 taxonomic character parameters		Representing the measured larval abundance in 2012	
		x coordinate	y coordinate	x coordinate	y coordinate
1	*Mylopharyngodon piceus*	−0.151054	−0.046193	−0.142393	−0.073112
2	*Ctenopharyngodon idella*	−0.123994	−0.046818	−0.115161	−0.068696
3	*Hypophthalmichthys molitrix*	0.051495	0.193775	0.011141	0.200559
4	*Hypophthalmichthys nobilis*	−0.004695	0.169715	−0.039908	0.166425
5	*Megalobrama terminalis*	0.050262	−0.038226	0.074369	−0.037824
6	*Parabramis pekinensis*	0.027657	−0.043075	0.029563	−0.033252
7	*Squaliobarbus curriculus** (Representing the *Squaliobarbus*)	0.043327	−0.008284	0.048483	−0.002338
8	*Xenocypris argentea*	0.038162	−0.038585	0.095056	−0.058907
9	*Cirrhinus molitorella*	−0.00305	0.020642	−0.00588	0.01886
10	*Cyprinus carpio*	0.014746	−0.026327	0.015125	−0.020295
11	*Elopichthys bambusa*	−0.108723	0.060384	−0.099959	−0.077613
12	*Ochetobius elongatus*	0.052637	−0.029706	0.051985	−0.015654
13	*Siniperca kneri*	0.087724	−0.058959	0.089384	−0.035725
14	*Sinibotia pulchra*	−0.01003	0.011197	−0.012657	0.009464
15	*Pseudolaubuca sinensis*	0.067393	−0.036665	0.070946	−0.021377
16	*Hemiculter leucisculus** (Representing the *Hemiculter*)	0.047671	−0.043766	0.051766	−0.031513
17	*Squalidus argentatus* (Representing the *Squalidus*)	0.125002	−0.044006	0.124345	−0.014619

Tab. 2.4 – (continued).

18	*Lcucosoma chinensis*	0.028382	−0.050426	0.031993	−0.040283
19	*Rhinogobius giurinus** (Representing the GOBIES)	0.112105	−0.04279	0.107082	−0.012745
20	Abundance			0.08891	−0.047711

*Represented by dominant species.

The niche consists of species, geographical distribution, and abundance. According to the above hypothesis, if the variation reflecting the niche (abundance) deviates from the origin (the red circle in figure 2.7), then the community is disturbed by the environment. Table 2.4 shows that the community abundance variables representing the 19 species of fish were found at the x- and y-coordinates 0.08891 and −0.047711, respectively. It is thus obvious that this community niche is disturbed by the environment. The length of the red line is the deviation of the niche.

It is necessary to clarify the "ideal niche" of a simulated community of 19 species of fish. According to the assumptions described in the previous section, the ideal niche is the composite variable (a) representing species abundance that appears at the origin of the two-dimensional graph. The optimum species composition is used to adjust the comprehensive variable of species abundance to the origin of the coordinates, which can be achieved by adjusting the biological abundance of each of the 19 species of fish. In this way, the niche proportion of the specific attributes can also be obtained.

2.4.2 Determining the Ideal Niche

In the previous section of this book, we introduced the principle of the model: to analyze species relationships within a community based on the morphological classification parameters of fish. We also determined the niche of the community using the biomass abundance ratio. In other words, the synthetic vector of species abundance was taken as the hypothesized degree of disturbance in the niche. The proportion of community species abundance was adjusted using computer technology, and the "0" of the synthetic vector (*i.e.*, the synthetic variable at the coordinate origin of the two-dimensional graph) was realized in the course of iterative calculation. The proportion of species abundance should be consistent with the calculation of "1," allowing the "ideal niche" value of each species in the community to be obtained.

From 2006 to 2013, we conducted a long-term observation of the floating larvae in the Zhaoqing section of the Pearl River; in this study, the relative proportions of the annual early resources of the 19 species of fish were determined (Li Xinhui *et al.*, 2020a, 2020b, 2020c, 2020d, 2020e). The abundance ratios of the 19 fish species in the community differed across years, which indicated that the spatial niche of the 19 fish species changed dynamically and demonstrated that the environment of the fish habitat was changing. Table 2.5 shows the average proportion of the larval biomass of different species for each year, with the last column showing the multi-year average proportion of each species.

According to the records of the Pearl River fish resources over the last century (Guangxi Fisheries Research Institute, Report on the investigation of the natural resources of the Guangxi Zhuang Autonomous Region inland waters fishery, published by Guangxi Fisheries Research Institute, 1985; Pearl River Fishery Resources Survey Editorial Committee, Investigation report on fishery resources of Pearl River System, Pearl River Fishery Research, China Academy of Fishery Sciences, 1985),

Tab. 2.5 – Proportion of different species of early drifting fish in the Zhaoqing section of the Pearl River*.

Species	2006	2007	2008	2009	2010	2011	2012	2013	Average
Mylopharyngodon piceus	0.07	0.59	0.21	0.54	0.42	0.11	0.10	0.17	0.28
Ctenopharyngodon idella	2.15	0.29	1.14	1.28	1.19	2.10	1.13	0.94	1.28
Hypophthalmichthys molitrix	2.86	1.08	4.51	2.97	2.21	2.73	2.76	2.51	2.70
Hypophthalmichthys nobilis	1.14	0.12	0.51	0.78	0.57	0.96	1.15	0.82	0.76
Megalobrama terminalis	29.59	29.95	12.13	15.10	11.91	29.68	22.30	4.73	19.42
Parabramis pekinensis	1.21	1.39	1.57	0.57	0.74	1.14	0.56	0.37	0.94
Xenocypris argentea	22.02	19.32	10.44	8.91	26.53	21.89	9.32	6.45	15.61
Squaliobarbus curriculus	26.11	24.84	45.23	46.21	32.51	26.20	50.48	52.31	37.99
Cirrhinus molitorella	4.58	14.06	8.79	11.55	10.43	4.47	4.59	7.32	8.22
Cyprinus carpio	0.15	0.02	0.10	0.02	0.01	0.14	0.00	0.01	0.06
Elopichthys bambusa	0.32	0.25	0.62	0.40	0.42	0.50	0.68	0.27	0.43
Ochetobius elongatus	0.05	0.05	0.07	0.32	0.32	0.50	0.31	0.09	0.21
Siniperca kneri	0.34	0.09	0.37	0.23	0.20	0.34	0.15	0.09	0.23
Sinibotia pulchra	0.23	0.40	4.45	3.77	2.25	0.13	1.39	1.92	1.82
Hemiculter leucisculus	4.61	5.16	4.00	2.90	4.03	4.57	3.44	1.33	3.75
Squalidus argentatus	1.11	0.36	2.72	2.41	5.43	1.29	0.92	20.21	4.31
Pseudolaubuca sinensis	1.64	1.01	1.98	0.95	0.47	1.59	0.40	0.25	1.04
Lcucosoma chinensis	1.20	0.59	0.66	0.14	0.09	1.02	0.13	0.09	0.49
Rhinogobius giurinus	0.63	0.42	0.51	0.95	0.27	0.65	0.19	0.13	0.47
Total	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0

*Note: The relative proportions of the identified species.

the catch of the four major fish in the Pearl River section (*Mylopharyngodon piceus*, *Ctenopharyngodon idella*, *Hypophthalmichthys molitrix*, and *Hypophthalmichthys nobilis*) accounted for more than 40% of the total catch. Investigation of the early resources indicated that these four major fish were the dominant species; *Squaliobarbus curriculus* was less abundant, and the abundance of *Megalobrama terminalis* was less than 5%. In 2016–2018, our team conducted a sampling survey of inland fish catches in the Pearl River system. A total of 40 fishing boats were surveyed from five counties in the river waters of Guangdong Province for an average of 12.6 days from January to December, and 101.5 kg of samples were obtained daily. The catch of four major fish accounted for 10.5% of the total catch (see table 2.6).

TAB. 2.6 – Catch of the main species in the Pearl Rivers, Guangdong Province.

Number	Fish	Average share of each category from 2016 to 2018 (%)
1	Other Fishes	58.9
2	*Megalobrama terminalis* Richardson, 1846	10.7
3	*Ctenopharyngodon idella* Valenciennes, 1844	5.7
4	*Cirrhinus molitorella* Valenciennes, 1844	6.5
5	*Cyprinus carpio* Linnaeus, 1758	4.6
6	*Squaliobarbus curriculus* Richardson, 1846	2.7
7	*Pelteobagrus fulvidraco* Richardson, 1846	2.2
8	*Hypophthalmichthys molitrix* Valenciennes, 1844	2.4
9	*Hypophthalmichthys nobilis* Richardson, 1845	2.1
10	*Hemiculter leucisculus* Basilewsky, 1855	0.5
11	*Cichlidae*	1.1
12	*Parabramis pekinensis* Basilewsky, 1855	1.2
13	*Silurus asotus* Linnaeus, 1758	0.5
14	*Mylopharyngodon piceus* Richardson, 1846	0.2
15	*Siniperca kneri* Garman, 1912	0.2
16	*Hemibagrus guttatus* Lacepede, 1803	0.0
17	*Cranoglasis bouderius* Richardson, 1846	0.1
18	*Carassius auratus auratus*	0.1
19	*Ictalurus punctatus* Rafinesque, 1818	0.0
20	*Mastacembelus armatus* Lacepede, 1800	0.0
21	*Siniperca scherzeri* Steindachner, 1892	0.0
22	*Leiocassis longirostris* Gunther, 1864	0.0
23	*Elopichthys bambusa* Richardson, 1845	0.0
24	*Culter alburnus* Basilewsky, 1855	0.0
25	*Ptychidio jordani* Myers, 1930	0.0
26	*Culter recurviceps* Richardson, 1846	0.0
27	Total	100.0

Compared with the total biomass of the four major fish species, both tables 2.5 and 2.6 indicate that performance data are changing, but there is a lack of a uniform reference to measure the extent of changes in various species. It is necessary to establish a standard reference frame, especially a quantitative niche reference frame at the community structure level. This difficulty can be avoided by using the "ideal niche." Through comparison, the ratio of ideal niche to measured biomass as a comparison of ecological niche can understand the niche changes of various species in the community, which is of great significance for understanding the formation mechanism of fish communities. This is significant for an improved understanding of the mechanisms of fish community formation, predicting niche changes for fish reconstruction, and river ecological management. Figure 2.8 (see figures 2.8a–2.8c) shows the changes in the distributions of 19 fish species and the stage-by-stage presentation of the "niche" synthetic vector in the model. Table 2.7 shows that the vector representing the niche of 19 fish species approaches "0" and that the total relative abundance of the four major fish species with respect to the 19 fish species reached 57.46%. This was consistent with the data from the Pearl River Fish Resources Survey over the last century.

Historically, the Pearl River basin includes four major spawning grounds for fish: the Xijiang river system (Hongshui River and Xunjiang River), the Yujiang River system (Zuojiang River and Youjiang River), the Liujiang River system, and the Dongjiang River. After decades of cascading development, only the Xunjiang River in the Xi River system and the middle and lower reaches of the Liu River still retain spawning grounds. The few remaining spawning grounds are also threatened by habitat change. After this change in the river environment, the biomass of the fish community changed. About 170 000 tons of fish products were recorded in the Pearl River system in the 1980s, compared with 60 000 tons recorded by our team in

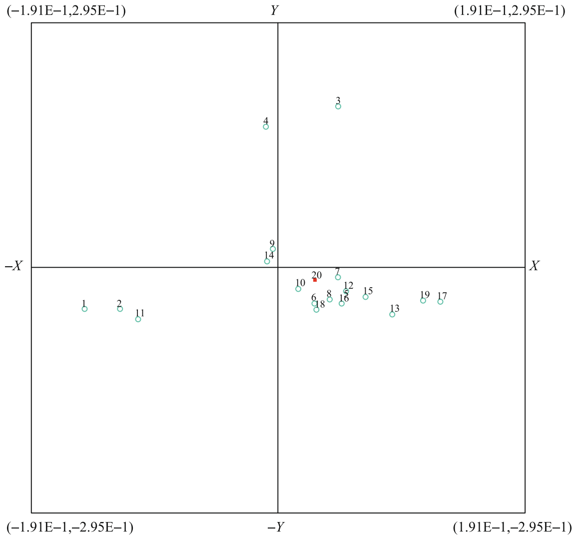


FIG. 2.8a – The "niche" vector (red number 20) deviates from the origin of the coordinates.

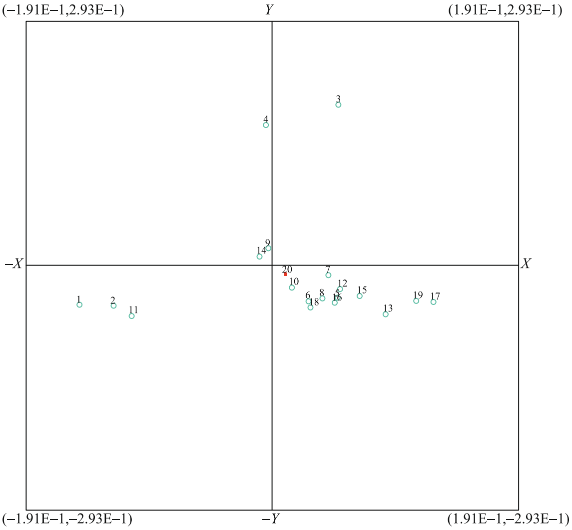


FIG. 2.8b – The “niche” vector (red number 20) was near the origin of the coordinates.

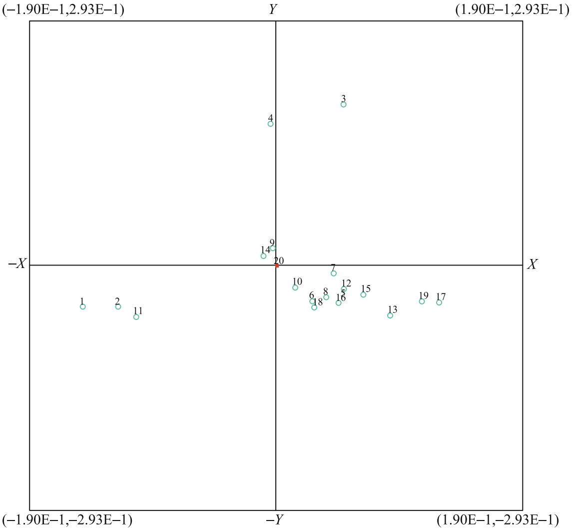


FIG. 2.8c – The “niche” vector (red number 20) coincides with the origin of the coordinates.

2016–18. This decrease in biomass suggested that the fish niche space decreased from 170 000 tons to 60 000 tons. The evaluation and restoration of the river ecosystem must be guided by the theory of the fish community niche.

Tab. 2.7 – Model-determined average relative biomass (*i.e.*, the total supplementary population) for each of the 19 fish communities and the corresponding coordinates in the Zhaoqing section of the Pearl River.

Number	Species	Annual quantity abundance from 2006 to 2013 (%)	Figure 2.8a			Figure 2.8b			Figure 2.8c		
			model-abundance (%)	x-coordinate	y-coordinate	model-abundance (%)	x-coordinate	y-coordinate	model-abundance (%)	x-coordinate	y-coordinate
1	*Mylopharyngodon piceus*	0.28	8	−0.149956	−0.049416	15.71	−0.150001	−0.046779	20.31	−0.150295	−0.045994
2	*Ctenopharyngodon idella*	1.28	7.7	−0.12276	−0.049483	11.78	−0.123255	−0.04719	10.31	−0.123619	−0.046702
3	*Hypophthalmichthys molitrix*	2.70	8.3	0.046492	0.194712	9.82	0.050867	0.193404	14.36	0.051264	0.193065
4	*Hypophthalmichthys nobilis*	0.76	7	−0.009414	0.169736	8.84	−0.005285	0.169548	12.48	−0.004722	0.169264
5	*Megalobrama terminalis*	19.42	10	0.052699	−0.037815	4.47	0.050272	−0.038067	3.90	0.05012	−0.0381
6	*Parabramis pekinensis*	0.94	5	0.028292	−0.042155	2.03	0.027418	−0.042614	3.80	0.027612	−0.042985
7	*Squaliobarbus curriculus*	15.61	15	0.046293	−0.008949	8.25	0.043555	−0.008631	0.06	0.043341	−0.0083
8	*Xenocypris argentea*	37.99	6.22	0.039798	−0.038001	6.11	0.038429	−0.038687	3.88	0.038036	−0.038445
9	*Cirrhinus molitorella*	8.22	3.6	−0.003775	0.02066	2.54	−0.003285	0.020812	0.07	−0.003055	0.020657
10	*Cyprinus carpio*	0.06	4	0.01551	−0.025996	1.33	0.01457	−0.026002	3.91	0.014695	−0.026216
11	*Elopichthys bambusa*	0.43	4.04	−0.108819	−0.061983	3.97	−0.109053	−0.060025	3.81	−0.108613	−0.060405
12	*Ochetobius elongatus*	0.21	2.9	0.052514	−0.02806	2.85	0.05244	−0.029344	3.90	0.052513	−0.029642
13	*Siniperca kneri*	0.23	4.55	0.088413	−0.05654	4.47	0.087591	−0.058565	3.91	0.087497	−0.058826
14	*Sinibotia pulchra*	1.82	4.8	−0.008631	0.010058	1.63	−0.010004	0.011166	0.03	−0.010065	0.011293
15	*Pseudolaubuca sinensis*	3.75	3.21	0.06769	−0.034819	3.15	0.067262	−0.036365	3.90	0.067165	−0.036542
16	*Hemiculter leucisculus*	4.31	4.67	0.049098	−0.042792	4.59	0.047819	−0.043723	3.89	0.04747	−0.04356
17	*Squalidus argentatus*	1.04	4.36	0.125567	−0.041018	4.28	0.124679	−0.043694	1.75	0.124769	−0.043919
18	*Lcucosoma chinensis*	0.49	2.39	0.02986	−0.049721	2.35	0.028573	−0.050238	3.89	0.028121	−0.049871
19	*Rhinogobius giurinus*	0.47	1.87	0.111975	−0.03964	1.84	0.111839	−0.042283	1.84	0.111706	−0.042578
20	Vector of "Niche"		Deviation from the center of coordinates	0.028583	−0.014448	Approaching the center of coordinates	0.009695	−0.009849	Coincidence	−0.000035	−0.000013

2.4.3 Iteration

In mathematics, iteration is the process of repeated computation with the goal of determining parameters. Each computation is called an "iteration," and the result of each iteration is used as the initial value of the next iteration. A computer has the characteristics of fast operation speed and is suitable for repetitive operations. It is possible to execute a set of instructions (or a certain step) repeatedly on the computer. After each instruction (or step) is completed, a new value of the variable is deduced from its original value, the final result is obtained by continuous calculation. This model studies the quantitative relationships among the niche values of species in a community, assuming that the abundance ratios representing the niche values of species in the community are not balanced. Thus, the abundance ratio values are used as variables. Because the vector of the comprehensive variables (referred to as "A") deviates from the origin, it is necessary to adjust the abundance ratio, and the "A" approach to the origin is the iterative goal under the two-dimensional species coordinate system. For example, in figure 2.9a serial number "20" ("A") approximates the center point through computer iteration, which involves the selection of various parameters and conditions in the software system.

2.4.3.1 Selection of the Iteration Target

Serial number "20," which is the abundance factor, can be located anywhere in the two-dimensional graph depending on the niche deviation of the species community (see figure 2.8a). The endpoint of the iteration is determined at any position by the values of the x- and y-coordinates according to the purposes of the study. If we want the "20" to approach the center point, we choose the x- and y-coordinates of the endpoint of the iteration as the origin (0, 0). If we need to study different niche relationships within the species community, we can also locate the endpoint of the iteration on any non-zero x- or y-coordinates. This process can also be used for community species restoration. Using the fish community shown in table 2.7 as an example, we can assume that the niche of *Mylopharyngodon piceus*, *Ctenopharyngodon idella*, *Hypophthalmichthys molitrix*, and *Hypophthalmichthys nobilis* had been disturbed and needs to be repaired to 50% of the theoretical value. In this case, the mean abundance of the damaged community from 2006 to 2013 (see table 2.7) can be used as the starting point. Using the theoretical 50% index of the four species, the theoretical niches of the other 15 fish species were obtained (see table 2.8). Thus,

TAB. 2.8 – Determination of the theoretical 50% niche of four fish species.

Number	Species	Current mean abundance	Model analysis abundance (%)	50% theoretical target (%)
1	*Mylopharyngodon piceus*	0.28	20.31	10.16
2	*Ctenopharyngodon idella*	1.28	10.31	5.16
3	*Hypophthalmichthys molitrix*	2.70	14.36	7.18
4	*Hypophthalmichthys nobilis*	0.76	12.48	6.24

following this principle, we can set the niche of any target in the community, obtain the theoretical niche quantity of other species by iteration, and provide the results of the morphological relationship model as a reference for community construction or restoration.

2.4.3.2 Coordinate Error of the Iteration End Point

Although we determine the end-point value of the iteration goal, it is not necessary for the computer to achieve 100% of the iteration location goal. With the premise that it is undesirable to affect the iteration result, it is acceptable that the end-point target (coordinate) of the iteration exhibits some error. In general, an absolute error of x or y in the range of 0.001–0.0001 satisfies the statistical requirements. If it is difficult to quickly iterate to the end result, the error precision can be increased to 0.005 or more, reducing the iteration time without affecting the result.

2.4.3.3 Determination of Iteration Step Size

When the computer iterates automatically, it must adjust the abundance ratio of each sample repeatedly. The value of each increment (or decrement) is called the "step length." The choice of step size is related to the accuracy of the result and the running time. Smaller step lengths correspond to higher precisions and longer running times, while larger step lengths correspond to lower precisions and shorter running times. Generally, we choose step lengths of 0.1–0.001.

2.4.3.4 Iterative Cycle Selection

The so-called small cycle iteration is applied to a sample in the data matrix: step size is increased or decreased repeatedly, such that the "abundance ratio factor" is set to the direction of the movement. The so-called large cycle iteration applied to each sample in the matrix was adjusted for the size of the abundance proportion values in the matrix until the abundance ratio was equivalent to the size of the adjustment of the iteration. Cycle iteration is essentially a statistical term that means to complete small and large loop iterations.

To move the "20" factor of figure 2.8a to the intended destination, the computer iterates by repeatedly adjusting the sample abundance ratios. The number of small loop iterations can be greater than or equal to 1. Greater numbers of small-cycle iterations will have a greater influence on iteration results on the sequence of sample iteration, and *vice versa*. We usually find that 1–5 times is most appropriate.

When the number of samples is large, the "20" factor in figure 2.8c is close to the requirements of the user. The proportional value of each sample is also basically determined. Therefore, the large-cycle number is set to five times in the system, which usually meets user requirements. When the destination has not been reached after five iterations, the computer will prompt the user to either continue the large cycle iteration or modify the iteration parameters. The user may make this decision according to the situation.

2.4.4 Sample Iteration Order

The order in which the samples are adjusted affects the results of abundance ratios when iterating over the sample. The model has three possible iteration types: in the first type, the samples are arranged in the order specified by the user, while in the other two types, the samples are arranged in either descending or ascending order according to the magnitude of the vector scalar value (*i.e.*, the content of the reference vector iteration method) associated with the samples in the two-dimensional graph.

During adaptation, organisms form a pattern of coexistence between large and small species, and the niche relationships among the species in a community are not an exclusive mechanism; niche relationships seem to be related to the maximum energy utilization in an ecosystem. A central objective of evolutionary ecology is to identify the general characteristics that maintain the diversity of species assemblages. By analyzing the classification and ecological characteristics of community species and studying the process mechanism of the coexistence and diversity of species, we found that the higher-scoring taxa species (with high abundance) were stronger than lower-scoring taxa species (with less abundance), and that regional communities were characterized by higher-scoring taxa (Enquist B J *et al.*, 2002).

The ecological niche of large trees was dominant, but there were gaps between trees that provided space for the survival of small species, and these spaces enabled the coexistence of large and small species (Aarssen L W *et al.*, 2006). In animal communities, the energy cycle requires the food chain, which constitutes the relationship between predator and prey. If the predator has an exclusive behavior in a given niche, there is no basis for its existence. Therefore, the "link" of the niche is the rational distribution of energy in the system, which provides the basic conditions for the coexistence of large and small species.

Large species use a larger proportion of the resources in the local ecosystem. Even though small species tend to have higher population densities, these high-density populations use lower levels of energy more efficiently. These types of relationships are common among birds, mammals, fish, and plants (Brown J H *et al.*, 1996). It is generally believed that several ecologically advantageous species monopolize more resources, and the resulting selection pressure may be the reason for the evolution of species in the direction of individual generality. This demonstrates that the energy utilization rate of a given species is related to its niche in the ecosystem.

Natural objects possess space on a "first come, first served" basis, and later species always obtain corresponding positions by "squeezing" the space occupied by the original objects. As a result, the space occupied by the early objects is large, and this space is gradually squeezed by latecomers such that the space occupied by the position is gradually reduced. Based on this principle, our model analysis procedure assumes that big species occupy the niche first. In this morphological model analysis system, the niche analysis program gives priority to the dominant species. It is possible to select a "large vector" to a "small vector" order iteration.

Communities are made up of species of different sizes, and the distribution of species follows certain rules. However, small species cannot be ignored. Based on observations of maximum plant height, leaf size, and seed size in several plant types, that the distribution of species sizes is universal, even at the intraspecies level, and that species distributions are the result of species self-adaptation during evolution. Thus, species distributions have nothing to do with the competitive ability of the species (traditionally, superior competitive ability requires a relatively large size/biomass production), and small species cannot be neglected in community studies. In the model analysis, the order of niche occupation by species in the community can be determined by the user according to the research goal.

2.4.5 Sample Iteration Constraints

Because iteration is a computer operation, it is necessary to give boundary values (*i.e.*, upper and lower limits) for the niche value of the species in the community as part of the program design. In this manner, the computer can automatically select the optimal niche value of a species in a community. This type of boundary value varies with different iterative methods and can be determined by the user or by the computer according to certain principles; these boundary values may be the same or different. It should be noted that the boundary values (upper and lower limits) of the iteration values may vary, and thus the final iteration results may vary.

2.4.6 Sample Normalization

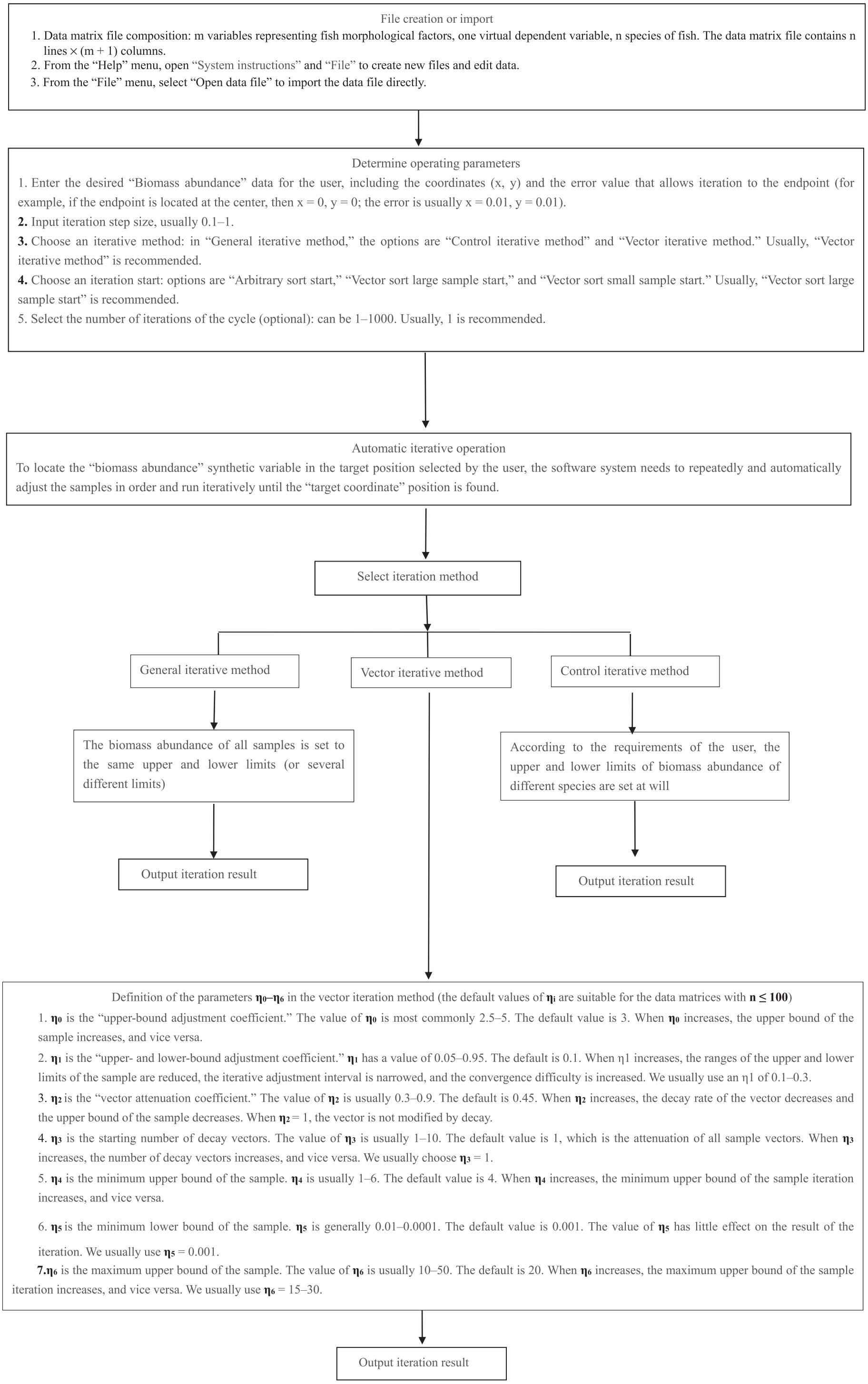
At the end of the automatic iteration, the sum of the relative niche values for all species in the community should be 100%. The normalized value is "1." Generally, only positive and negative errors less than 0.01 are allowed, with a range of 0.99–1.01. Otherwise, the normalization process should continue to operate until 100% is reached.

2.4.7 Model Checking

Any model study needs to be verified in practice. In model analysis, it is necessary to evaluate the analytical data (*e.g.*, the correlation coefficient and other parameters) to judge the accuracy and applicability of the model. This model uses the classification character parameter to identify the ecological space occupancy rate of the species community, as well as changes in this rate. Nonlinear multiple regressions were used to test the functional relationships between the measured biomass abundance data for the early fish resources and the coordinates of the corresponding species in the model. F-tests showed that the average confidence level was above 95%, while the average validation accuracy and average prediction accuracy of 19 species of fish biomass abundance were greater than 98% and 93%, respectively.

2.4.8 Model Workflow

System workflow diagram and explanations.



File creation or import

1. Data matrix file composition: m variables representing fish morphological factors, one virtual dependent variable, n species of fish. The data matrix file contains n lines × (m + 1) columns.
2. From the “Help” menu, open “System instructions” and “File” to create new files and edit data.
3. From the “File” menu, select “Open data file” to import the data file directly.

Determine operating parameters

1. Enter the desired “Biomass abundance” data for the user, including the coordinates (x, y) and the error value that allows iteration to the endpoint (for example, if the endpoint is located at the center, then x = 0, y = 0; the error is usually x = 0.01, y = 0.01).

2. Input iteration step size, usually 0.1–1.

3. Choose an iterative method: in “General iterative method,” the options are “Control iterative method” and “Vector iterative method.” Usually, “Vector iterative method” is recommended.

4. Choose an iteration start: options are “Arbitrary sort start,” “Vector sort large sample start,” and “Vector sort small sample start.” Usually, “Vector sort large sample start” is recommended.

5. Select the number of iterations of the cycle (optional): can be 1–1000. Usually, 1 is recommended.

Automatic iterative operation

To locate the “biomass abundance” synthetic variable in the target position selected by the user, the software system needs to repeatedly and automatically adjust the samples in order and run iteratively until the “target coordinate” position is found.

The biomass abundance of all samples is set to the same upper and lower limits (or several different limits)

According to the requirements of the user, the upper and lower limits of biomass abundance of different species are set at will

Definition of the parameters **η_0–η_6** in the vector iteration method (the default values of **η_i** are suitable for the data matrices with **$n \leq 100$**)

1. **η_0** is the “upper-bound adjustment coefficient.” The value of **η_0** is most commonly 2.5–5. The default value is 3. When **η_0** increases, the upper bound of the sample increases, and vice versa.

2. **η_1** is the “upper- and lower-bound adjustment coefficient.” **η_1** has a value of 0.05–0.95. The default is 0.1. When η1 increases, the ranges of the upper and lower limits of the sample are reduced, the iterative adjustment interval is narrowed, and the convergence difficulty is increased. We usually use an η1 of 0.1–0.3.

3. **η_2** is the “vector attenuation coefficient.” The value of **η_2** is usually 0.3–0.9. The default is 0.45. When **η_2** increases, the decay rate of the vector decreases and the upper bound of the sample decreases. When **η_2** = 1, the vector is not modified by decay.

4. **η_3** is the starting number of decay vectors. The value of **η_3** is usually 1–10. The default value is 1, which is the attenuation of all sample vectors. When **η_3** increases, the number of decay vectors increases, and vice versa. We usually choose **η_3** = 1.

5. **η_4** is the minimum upper bound of the sample. **η_4** is usually 1–6. The default value is 4. When **η_4** increases, the minimum upper bound of the sample iteration increases, and vice versa.

6. **η_5** is the minimum lower bound of the sample. **η_5** is generally 0.01–0.0001. The default value is 0.001. The value of **η_5** has little effect on the result of the iteration. We usually use **η_5** = 0.001.

7.η_6 is the maximum upper bound of the sample. The value of **η_6** is usually 10–50. The default is 20. When **η_6** increases, the maximum upper bound of the sample iteration increases, and vice versa. We usually use **η_6** = 15–30.

2.4.9 Model Application and Limitations

The species itself carries information about many ecological categories. The species information model was used to map the distribution of resources. Recently, statistical methods in geographic information systems have become more widely used and the uses of biological and environmental data have expanded. Thus, in addition to its applications to biogeography, species evolution, and species distributions, the models including different types of species information are also widely used for research and decision-making in areas such as climate change, biological protection, biological invasions, disease transmission, and risk control (Miller J., 2010). In paleontology, the stability of the quantitative niche and the geographic species ranges can be studied using fossil parameter models, which reveal the effects of environmental change on species distributions. In such models, C3 is used as a reference time series in combination with GIS positioning techniques; the results of these models can reflect species distribution ranges in different geological eras and can also be used to infer processes of environmental change at different time nodes (Walls and Stigall, 2011).

The ecological and geographical distributions of *Rangifer tarandus* and *Cervus elaphus* during the last ice age were assessed by applying the niche model to historical fauna; this method also provided a means for the quantitative prediction of early biological distributions and community status (Svenning *et al.*, 2011). The use of trend surface analysis (TSA) to delineate regional range of species distributions, in conjunction with geographical criteria to delineate the regional range of species distributions, can reduce the impact of historical events on the parameterization of the model (Acevedo *et al.*, 2012). The main objective of species distribution modeling is to extract the important factors related to ecological models and to explain or predict changes in the development of ecological models. During the modeling process, the spatial structure data and the model parameters must be assumed, so all of the models have limitations in "distortion" and application scope; the scope of the model, as well as its autocorrelation behavior and non-stationarity, must be explained (Miller J. A., 2013).

The importance of using animal and plant data in species distribution modeling is clear, but the development of species distribution models is limited by methodology, research boundaries, and the effects of environmental factors. These factors affect the extrapolation and application functions of the model (Kéry *et al.*, 2010). The relationship between species and the environment is not a simple linear relationship. To establish a species distribution model, a clear theoretical system is necessary, including a conceptual framework for extracting data features, a mathematical analysis method (Austin, 2002; Walker and Cocks, 1991), and a method for identifying the data conditional factors and targets required for a species distribution model (Barbet-Massin *et al.*, 2012). In general, the precision of the model prediction increases with the number of samples, while prediction efficiency increases as the number of samples decreases (Stockwell and Peterson, 2002). It is also possible to develop a universal spatial modeling platform to extend the application of the model *via* the Internet (Stockwell and Peters, 1998). The taxonomy and regional distribution of a given organism are the basis of the niche of that species in the ecosystem (Batchelder *et al.*, 2002). This notion is the key to model evaluation (Peterson *et al.*, 2007). To maintain the most basic biological groups in the ecosystem, the ecosystem functions needed by human beings must probably be sustainable. The future development of science and technology is a powerful guarantee that ecosystem service functions will be changed and safeguarded.

The interpolation accuracy and transferability of the species distribution model are important features of this model. Of the models using machine learning, Maxent, the generalized Boosting method (GBM), and artificial neural networks (ANNs) show good transferability, while the genetic algorithm for rule-set prediction (GARP) and random forest (RF) models show significantly poorer extrapolation performance. Of the regression-based methods, generalized additive models (GAMs) and generalized linear models have good transferability. Three modeling techniques, Maxent, GBM, and GAM, have an ideal combination of prediction accuracy and portability (Heikkinen *et al.*, 2012).

The coexistence patterns among diverse forest species are determined by habitat-related factors and niche differentiation. In the community model, species distributions are not uniform at large spatial scales but are uniform at small spatial scales (Kraft and Ackerly, 2010). Competition theory holds that niche-like species cannot coexist; this corresponds to species classification. Instead, the concept of habitat filtering means that species with similar ecological requirements should coexist. In a real-world ecological environment, Ulrich *et al.* (2010) showed the aggregation of the species in the same genus, random species symbiosis, and cross-genus species isolation. The similar responses of congeneric species to environmental variables are the basis of stochastic symbiosis.

During the establishment of the fish community morphological model, we began with the ideal niche, considered the fish species and their taxonomic parameters in the community, and avoided many of the uncertain environmental factors involved in the actual niche. The multi-dimensional morphology of a given species was defined as the spatial conformation of the ideal niche of the species community. The spatial concept of niche and species "abundance" in the community was regarded as the ideal niche. Using the ideal niche value as a reference, the model was extended to analyze the actual niche and evaluate community succession. For example, figure 2.8 shows a two-dimensional graph of the results, with the ratio of the supplementary populations of different species as a variable based on the larval data collected in 2012. This figure shows that the "abundance" ratio factor deviates from the origin. We believe that this species' community is in an unbalanced ecological state. Although the analysis indicated that the fish community was disturbed, the analysis did not identify the target of the disturbance. Target identification requires further analysis of key factors associated with the environmental conditions of the fish habitat. Finally, matching results were obtained. These environmental factors can be further studied in a variable manner using this model. The river is a linear system, and disturbance events at certain nodes will affect the entire system. Therefore, it is important to master system information for further analysis.

Ecosystems are often disturbed at varying frequencies and intensities over time, and the niche of the species community is in a state of dynamic equilibrium during dynamic change. Community species structure in river systems is determined by species competition and niche allocation in time and space. Moore and Hunt (1988) studied regional species diversity, the structure of food webs, and the energy of habitats and food webs, and the results showed that communities may contain tightly coupled subunits whose numbers may increase with increasing diversity. As species diversity increases, interaction intensity decreases and the ecosystem stabilizes. Therefore, the community niche should also be in a state of dynamic equilibrium, and the occupancy rate of the species niche in the communities studied using this model should only be set to "dynamic equilibrium."

Elith and Leathwick (2009) proposed that model uncertainty could be resolved by strengthening studies of biological interactions. The species distribution model (SDMS) should be further developed to better consider biological interactions and model applications (Elith and Leathwick, 2009). The results of the basic niche and species distribution area model can be used as an indirect indicator for assessments of species distribution and abundances in response to environmental influences (Stanley and Royle, 2005). Theoretical and empirical support is necessary for ecological research (Chave, 2004). It is important to establish a standard system for ecological reconstruction, and theoretical systems must be used to guide the formation of cognitive communities. The application of phylogenetic and trait data in community studies is increasing (Ings *et al.*, 2009; Webb *et al.*, 2008).

2.5 The Modeling Software

The user interface dialog box appears on the main page of the "Morphological character niche analysis model" software. The home page of the "Help" feature includes comprehensive, systematic, and detailed guidance, as well as a description of the software.

2.5.1 Data File and Editing

2.5.1.1 Data File Format Requirements

The system has a variety of available statistical functions, and there are specific requirements for the format of the data file.

A list of the required fields follows:

Sample number (N), independent variable (factor) number (P), dependent variable (target) number (k), forecast Number (n)

Note that, for the purposes of the fish ecological research described herein, neither a target value nor a forecast number is needed, and both are thus set to 0. In addition, the forecast sample column values are not used. However, for other applications, values for these parameters may be input according to need.

“Independent Variable 1,” “Independent Variable 2,” “Independent variable 3,” …, “Independent variable P”

“Dependent variable 1,” “Dependent variable 2,” “Dependent variable 3,” …, “Dependent variable P”

“Goal 1,” “Goal 2,” “Goal 3,” …, “Goal K”

“Sample 1,” “Sample 2,” “Sample 3,” …, “Sample n”

“Forecast 1,” “Forecast 2,” “Forecast 3,” …, “Forecast n”

The help notes included in the software give the exact representations of the factor data (Xij) and target data (Yi) needed for each sample in the data matrix.

2.5.1.2 Data File Generation

① Under the system “File” menu, select “New data file.” Use the prompt box to find and edit the input data. If you do not wish to use the default factor name (or sample name), it can be changed by right-clicking the pop-up prompt.
② Use another editing software (such as Microsoft Word) to prepare the documents. Data files for six fish (samples), 22 factors, one target, and zero forecast samples follow. Please note that independent variables (factors) and dependent variables (targets) are strings and thus must be enclosed in quotation marks.

6, 22, 1, 0

“factor 1,” “factor 2,” ”factor 3,” “factor 4,” “factor 5,” “factor 6”, “factor 7”, “factor 8”, “factor 9”, “factor 10”, “factor 11”, “factor 12”, “factor 13”, “factor 14”, “factor 15”, “factor 16”, “factor 17”, “factor 18”, “factor 19”, “factor 20”, “factor 21”, “factor 22”, “target (%)”

“*Mylopharyngodon piceus*”, “*Ctenopharyngodon idella*”, “*Hypophthalmichthys molitrix*”, “*Hypophthalmichthys nobilis*”, “*Megalobrama terminalis*”, “*Parabramis pekinensis*”, “*Xenocypris argentea*”, “*Squaliobarbus curriculus*”, “*Cirrhinus molitorella*”, “*Cyprinus carpio*”, “*Elopichthys bambusa*”, “*Ochetobius elongatus*”, “*Siniperca kneri*”, “*Sinibotia pulchra*”, “*Hemiculter leucisculus*”, “*Squalidus argentatus*”, “*Pseudolaubuca sinensis*”, “*Lcucosoma chinensis*”, “*Rhinogobius giurinus*”

2,4.5,0.01,0.01,7,8,16,8,3.9,3.8,4.6,5.6,2.4,0.95,42,6,4,43,17,17,0.01,0.01,
12.2668657

2,2,4.5,0.01,7,8,16.5,8,4.3,3.8,4,7.1,2,0.85,39,7,5,41,18,18,0.01,0.01,13.9

2,4,0.01,0.01,7,13,17,8,3.3,3.7,4.4,7.2,2.4,1.43,108,32,19,120,75,43,0.01,0.01,13.6

2,4,0.01,0.01,7,12.5,17,8,3.5,3,3.4,6.8,2.1,1.25,98,27,17,106,66,45,0.01,0.01,12.3

2,2,3,4,10,11,16.5,10.5,6.2,4.2,3.4,8.4,3.8,1.55,107,19,6,112,56,32,0.01,0.01,7.0

1,0.01,0.01,0.01,13.5,8.5,15,5,3.5,2.7,4.1,6.9,10.8,1.35,85,9,20,98,20,40,0.01,0.01,4.8

2.5.1.3 Data Editing

Using the system "File" menu, it is possible to select different secondary functions and edit the data file.

2.5.2 Run

Click on the "Analysis" menu to select different operations and access various information.

2.5.2.1 Result Information

The menu "Correspondence analysis" can be used to obtain the correlation coefficient matrix, the R-type load matrix (*i.e.*, the scatter plot of independent variables), the Q-type load matrix (*i.e.*, the scatter plot of samples), and the eigenvalues (*i.e.*, the variance contribution rates of the principal axes).

2.5.2.2 Result Graph

Select "Eigenvalue map" to obtain the relative contribution of each principal axis (principal component or principal factor) to the variance.

2.5.2.3 "Graph Analysis" Function

After selecting "Graph analysis," four types of the two-dimensional graph can be selected: "Factor and sample graph," "Factor graph," "Sample graph," and "Composition (1) + sample graph." These data can be displayed using an origin, dot-line, or vector graph.

2.5.2.4 "Adjust" Function

The "Adjust" function can be used on a two-dimensional page. After selecting "Adjust," it is possible to modify the automatic pre-iteration parameters and iteration methods that are shown on the selection page. The user can input the coordinates of the endpoint of the iteration and parameters such as the error, step length, number of cycles, and the starting order of the iteration samples.

2.5.2.5 Select the Iteration Mode

When the "Enter adjust" function is selected, an iterative mode can be chosen from three options: the common method, the constraint method, and the vector method.

2.5.2.6 Iterative Effects

Due to a large number of calculations, the page will sometimes appear to hang or freeze. This is normal. Please wait patiently. If the calculations take too long, the program may be forced to close because the iteration method and iteration parameters are not properly selected.

After the system completes the auto-tuning iteration, the iteration results will display "Up to standard" or "Not up to standard." If the parameters are suitable, the program will exit and output the result. If the parameters are not suitable, the system will return to the "Adjust" page. At this point, changes can be made to factors such as the adjustment parameters and the iteration method. Parameters should be repeatedly adjusted until the "Up to standard" message is returned.

2.5.2.7 Parameter Specification

In order to get a good iterative result, it is very important to choose the proper working parameters. In particular, the vector method has several parameters (*e.g.*, $\boldsymbol{\eta}_1$–$\boldsymbol{\eta}_6$) that can be set by the user based on experience. For the convenience of the users, these parameters have default values.