《环境与卫生科学杂志(ISSN 2413-1628)》
Journal of Environment and Health Science (ISSN 2413-1628)

ChengZhu Science™

Serial in April, 2024

ChengZhu Science Research Center Limited

(Hong Kong Registration NO. 80561228)

Journal article DOI is registered via JiangXi Province ChengZhu Environmental Engineering Company Ltd, with Crossref membership (DOI prefix 10.58473)

出版人： 刘焕 四季出版有限公司

Publisher: Liu Huan, SI JI PUBLISHING COMPANY LIMITED

ISSN 2413-1628



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Article 11. Original Review of Biodiversity Conservation Progress in China: The Theories and Cases in Practice

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Formally Published on 09/04/2024; Latest Revised on 26/06/2026.

DOI: 10.58473/JEHS0012 Retrieval from official database: www.crossref.org

Abstract

This article attempted to review the relevant theories on biodiversity conservation at three layers: ecosystem diversity, species diversity and genetic diversity, illustrated by substantial case studies which were updated in recent years and published in China. Then the new theories and its corresponding improvement in conservation methods were discussed in this article. Finally, based on the new theories discussed by this article, the modeling research project is conducted to simulate the process of the new theories by using C++ language.

Key words: Biodiversity Conservation, Ecosystem Diversity, Species Diversity, Genetic Diversity, Urban Diversity and Public Health.

This modeling project is formally registered via Open Science Framework (OSF), USA, with registration DOI: https://doi.org/10.17605/OSF.IO/7HWCM

1.Introduction

After Chinese Biodiversity Conservation Strategy and Action Planning (2010-2030) comes into force with corresponding Environment Standards, such as Environmental Standard for the Assessment of Regional Biodiversity (HJ623 -2011) and Environmental Standard on Classifying the Categories of Genetic Resources (HJ 626 -2011), evolutionary ecology study has been firstly reviewed by me according to the needs of implementing the above governance documents. In this review paper, evolutionary ecology study gives theoretical knowledge understanding the evolutionary process of biodiversity at ecosystem/community, species/population, genetics/gene layers, and the study methods of evolutionary ecology also provide the guidelines for biodiversity assessment, especially for ranking the endangered species and genetic resources [1]. However, the Chinese Biodiversity Conservation Strategy and Action Planning (2023-2030) has been renewed, so the major objectives of this review article are to update case studies firstly and then to discuss the improvement in

both theory and methods in the coming study.

One of the hot issue is that the COVID-19 epidemic disease breaks out since last biodiversity planning is worked out, so the urban biodiversity is paid more attention by this paper due to the human health effects of biodiversity. This study will focus on the relationship between the microbial biodiversity and urban ecosystem biodiversity, which will be discussed with emphasis on the pathogen impacts caused by the biodiversity degradation in the urban ecosystem. There are both direct and indirect effects of urban biodiversity on the airborne epidemic disease: firstly, the well-reserved biodiversity in microbe community of local ecosystem becomes the strong competitor against the exotic and invasive pathogens, as discussed in my another article [3], so the first objective is to measure the correlation between the biodiversity index of local airborne microbe community and urban plantation species diversity index in local scale, and then to further measure the correlation between the biodiversity index of local airborne microbe community and the density of exotic airborne epidemic pathogens. In this case, the urban plantation species diversity index becomes the direct effects on epidemic disease control; secondly, the urban plantation species diversity decreases the aerosol density in urban atmospheric environment as reported in the past case studies, which indirectly eliminates airborne pathogens density because aerosol is the major transmission pathway of airborne pathogens. Consequently, it is first to measure the correlation between the urban plantation species diversity and the aerosol density, and then it is to measure the correlation between the airborne pathogens density and the aerosol density in urban atmospheric environment at local scale. My previous articles has designed the new methods to routinely monitor the airborne pathogens in atmosphere at micro-environment scale in epidemiology study [9][10]. However, the pathogens adhering to aerosol is further paid attention at bigger scale in this article, because it is frequently reported that the fine particles ($PM_{2.5}$) are capable of transmitting at long distance [8] and pathogens may persist due to its long-time dormant nature during winter time in the transmission pathway [3], which potentially increases the epidemic disease infection at bigger scale.

2.Ecosystem Diversity

2.1.Plant community succession and plant biodiversity variation

2.1.1.Case studies

There are several research projects aiming to assess the effects of ecological restoration, degradation and natural disasters (such as extreme drought) on the variation of plant diversity indices during plant community succession period, which are considered as sensitive ecosystem types.

Table 1. Summary of plant biodiversity studies during plant community succession.

Case studies	Ecology types	Research emphasis	Diversity Indexes
[12]	Restoration of abandoned rice fields	Plant diversity variation during succession process	The α diversity indexes: Patrick species richness index (R), Shannon Wiener diversity index (H), Simpson dominance index (D), and Pielou evenness index (J); β Diversity is measured using Jaccard paired dissimilarity coefficients.
[13]	Degradation grasslands	Plant diversity variation during succession process	Both α and β diversity indexes
[14]	Reservoirs	Plant succession characteristics of phytoplankton communities under drought; water quality	Both α and β diversity indexes
[15]	Restoration of mining sites	Plant diversity variation during succession process	Both α and β diversity indexes
[16]	Restoration of mining sites	Plant diversity variation during succession process; the effect of restoration years on biodiversity; soil chemical content	Patrick richness index; Shannon Wiener diversity index, Simpson diversity index, and Pielou evenness index
[17]	Degraded Forest at three layers: tree, shrub and herbaceous	Plant diversity variation under different environmental gradient and various disturbances; Plant community succession under environmental gradient of altitude and disturbances; the correlation between biodiversity and soil conditions	Shannon Wiener index and Simpson index
[18]	Aquatic ecosystem both	Plant diversity variation by pollution control; Water	Shannon Wiener diversity index,

	before and after pollution control	quality by pollution control.	Pielou evenness index and Marglef richness index
[19]	Restoration of coal mining sites	Plant diversity variation among different restoration treatments over different plantation years.	Shannon Wiener index and Simpson index; species richness; Pielou evenness index; functional richness index; functional evenness index; functional dispersion, Rao secondary entropy, and stability coefficient

Abandoned rice fields, as the semi-natural wetland derived from natural succession, result in the significant influence on regional biodiversity. However, the changes of biodiversity in plant community on abandoned rice fields during natural succession become the gaps in research. By both field investigation and collection of historic records, the habitat of the Jingxin Wetland in the lower reaches of the Tumen River has been determined. The method of spatial series is used instead of time series to compare the vegetation of both rice fields and natural wetlands among different abandonment years. Species community is determined and the changes in plant diversity during natural succession is analyzed. The results show that there are a total of 99 species of plants in paddy fields and natural wetlands with different abandonment years, belonging to 33 families and 64 genera, which are mainly composed of wetland herbaceous plants and aquatic plants. From the perspective of community characteristics, the Jingxin Wetland is dominated by *Cyperaceae*, *Polygonaceae*, and *Poaceae* plants; As the number of abandoned years increases, the dominant species of wetland plant communities gradually approach those of natural wetland plant communities. The plant diversity in abandoned rice fields is much higher than that in natural wetlands, and decreases with the passage of succession time, thus approaching natural wetlands. However, compared with wetlands at the same latitude, abandoned rice field wetlands show a slower rate of plant succession [12].

The article takes different degradation gradient grasslands in Etuoke Banner, Inner Mongolia to conduct research, and analyzes the species types, quantities, important values and grassland degradation succession levels under different degradation succession levels. Both α diversity changes and β diversity analysis are implemented, and it is to investigate the quantitative characteristics, composition structure and diversity of plant communities in different succession stages of

degradation, and to study the composition and diversity of plant communities in different degradation succession sequences. The number of species shows an overall decreasing trend with the degradation gradient, where the importance value of species also show a trend of dispersion before concentration, and the overall community composition structure tends to become simplification development. The diversity index of α shows a gradually decreasing trend along the degradation gradient, while the Patrick index, Shannon Wiener diversity index, Simpson ecological dominance index, and Pielou evenness index of mildly degraded areas are the highest among the four degradation gradients; in severely degraded areas, the α diversity index value has reached its lowest point. From mild degradation zone - moderate degradation zone, mild degradation zone - severe degradation zone, mild degradation zone to extremely severe degradation zone, the Sørensen index of the three areas shows the significant downward trend, whereas the trend of the Cody index is opposite, showing the clear upward trend [13].

In order to understand the impact of drought on the plant succession characteristics of phytoplankton communities in reservoirs, a 2-year survey was conducted from January 2020 to December 2021 to investigate the phytoplankton community structure, as well as the water's physical and chemical indicators of the Xinfengjiang Reservoir. The results showed that the water quality of the Xinfengjiang Reservoir met the Class I standard of the Surface Water Environmental Quality Standard (GB3838-2002) both before and during the drought period in 2021. From 2020 to 2021, a total of 201 species belonging to 90 genera of 8 phyla and 191 species belonging to 86 genera in 8 phyla of phytoplankton were identified, all of which were mainly classified into the phyla *Chlorophyta*, *Cyanophyta*, *Diatoma*, *Euglenophyta*, and *Chlorophyta*. The community structure of phytoplankton was blue-green algae type before drought, but turned into green algae diatom type during drought. The average abundance of phytoplankton in 2020 and 2021 was 1.38 × 106 and 0.41 × 106 cells/L, respectively. Due to the significant reduction in exogenous nutrients, the abundance of algae during drought was lower than before drought, while during the extreme drought season, the significant reduction in precipitation leads to the declining in nutrient input into the reservoir, which limited the algal proliferation activity with high nutrient demand, resulting in temporal changes and differences in algal composition. Correlation analysis and redundancy analysis (RDA) results showed that the main environmental impact factors of floating vegetation in the reservoir before drought are NH3-N, WT, DO, TP, and SD, compared with it in drought season when the main influencing factors were changed into EC, WT, pH value, TN, CODMn, NH3-N, and SD, among which WT, SD and NH3-N were the main environmental impact factors of phytoplankton in reservoirs both before and during drought, indicating that during extreme drought periods changes in hydrology and nutrient input led to variation in the main associated factors of algae [14].

In order to explore the species diversity of plant communities during the process of community succession under the treatment of gangue, the stones left by coal seams

mining, this article uses the spatio-temporal substitution method and selects different years' plots (2a, 5a, 10a) of gangue treatment in Shuanglonggou, Tianzhu Tibetan Autonomous County, Gansu Province, compared with the control plots without the treatment of gangue. Through vegetation investigation, the characteristics of plant community succession and species diversity are analyzed and studied, and their changing patterns with the increase of gangue treatment years are revealed, which provides the scientific and theoretical basis for the management of gangue treatment for ecosystem restoration in Shuanglonggou and in its similar areas over the eastern section of Qilian Mountains [15].

The study objective of another research is to assess the effect of restoration years on plant diversity with soil chemical properties in the metal mine waste disposal sites of high-altitude, and to provide scientific guidance for in-depth exploration of plant succession trends and optimization of plant restoration processes. The slopes of 10 mining sites in the Delni Copper Mine of Golog Tibetan Autonomous Prefecture, Qinghai Province, China, ranging from 1 to 12 years' restoration period, have been chosen as the research objects. The plant species composition and diversity characteristics of the restoration sites have been investigated through sampling methods, together with soil's chemical properties tested by experiment. Four indexes of α richness, including the Patrick richness index, are identified to examine the relationship between plant diversity index and restoration years, associated with 8 characteristic indicators of soil chemicals such as total nitrogen. As the recovery period increases, natural plants continue to invade, and the number of families, genera and species of plants in the waste disposal site shows a gradually increasing trend. There are certain differences in the species composition and community characteristics among different years. The Patrick richness index of the waste disposal site shows a kind of power function growth trend with the increase of recovery years, while the Shannon Wiener diversity index, Simpson diversity index, and Pielou evenness index show the trend of increasing firstly and then decreasing with the increase of recovery years, but all of indexes follow a type of quadratic function relationship. As the recovery period of the waste dump increases, the content of total nitrogen, total phosphorus, total potassium, alkaline nitrogen and available phosphorus in the soil shows the trend of firstly increasing and then decreasing; The content of available potassium and organic matter shows a kind of power function of increasing trend, whereas the pH value shows a gradually decreasing trend. The four diversity indices of plants in the waste disposal site are positively correlated with the total nitrogen, total phosphorus, total potassium, alkaline nitrogen, available potassium, and organic matter content to varying degrees in soil, but are negatively correlated with available phosphorus and pH value. Consequently, it is concluded that when the recovery period is 12 years, the plants in the experimental area's dumping ground are still in the stage of succession and development, without reaching the stable state; There is a clear interaction between plant succession in the waste dump and soil nutrients; It is recommended to apply high nitrogen, high phosphorus, and low potassium of slow-releasing compound fertilizer for plant restoration in the

mining area's waste disposal site [16].

Another forest study focuses on the degraded forest of *Pinus armandii* at three layers (tree, shrub and herbaceous) in Shennongjia Forest Area, Hubei Province. Based on the survey of plant species and community structure in typically degraded forest plots of *Pinus armandii*, the species composition and plant diversity of three types of degraded forest, labeled as Forest A, Forest B, Forest C, are identified under different altitude gradients (medium altitude, high altitude) and disturbance conditions (pests, waterlogging) which are analyzed as environmental gradient. The trend of community succession and changes in soil's physic-chemical properties are expected to provide theoretical basis for the restoration and protection of the degraded forest ecosystem of *Pinus armandii*. The main research results are as follows: (1) A total of 53 species in 36 genera of 20 families of tree species, 47 species in 28 genera of 18 families of shrubs, and 176 species in 126 genera of 56 families of herbaceous plants have been found in the survey plots of degraded forests of *Pinus armandii*. The families with the highest amount of species in the survey site are *Asteraceae* and *Rosaceae*, with *Rosaceae* containing 35 plant species and *Asteraceae* containing 24 plant species. *P. armandii* and *Betula tilis* are the dominant tree species in the degraded forest of *P. armandii*. The dominant species in the shrub layer are *Rubus inopertus* and *Berchemia sinica*, while the dominant species in the herbaceous layer are *Dipsacus asperoides*, *Fragaria orientalis*, and *Parahelypteris nipponica;* (2) The differences in various plant diversity indices of the tree layer in degraded forests of *Pinus armandii* are not significant under different disturbance conditions and altitude gradients, while there are significant differences ($P<0.05$) in both Shannon Wiener index and Simpson index on the shrub layer in the degraded forest of *Pinus armandii*. Under insect disturbance, both Shannon Wiener index and Simpson index of the degraded forest shrub layer are significantly higher than those under waterlogging disturbance. There is significant difference ($P<0.05$) in the Simpson index of grass layer in the degraded forest *Pinus armandii* under different altitude gradients. The Simpson index of the degraded forest at high altitudes is significantly lower than that of the degraded forest at medium altitudes. Therefore, natural disturbances and the increase in altitude gradients have reduced plant diversity in the shrub and herbaceous layers of the community, to some extent; (3) According to the succession analysis trend of degraded forests of *Pinus armandii* in Shennongjia, it is to indicate that there is insufficient regeneration of *Pinus armandii* in the community, which will consequently becomes the declining species in the future, whereas *Litsea pungens*, *Crataegus wilsonii*, and *Swida macrophylla* are the progressive species in the community. It can be seen that the recent succession trend of degraded forests of *Pinus armandii* is the deciduous broad-leaved forest dominated by *C. wilsonii*, *L. pungens*, and *S. macrohuahylla*. Among them, the succession trend of degraded forests (A) infected by insect in Huashan Pine of Shennongjia will develop from the mixed forest of *P.armandii Cunninghamia lanceolata* to the mixed forest of *Carpinus turczaninowii - Bothrocaryum contraversum - L. pungens,* while the succession trend of high-altitude degraded forests (B) infected by insect will shift from the mixed forest o*f P. armandii*

- *Salix wilsonii B. tilis* to the mixed forest of *C. wilsonii Malus kansuensis* - *f. calva* Hubei *Malus hupehensis,* but the succession trend of mid-altitude degraded forests (C) that are waterlogged will evolve from the mixed forest of *P. armandii Larix kaempferi* - *C. wilsonii* Japanese larch to the mixed forest of *Ligustrum mollicum* - *Litsea cubeba* - *S. macrophylla* wet mixed forest; (4) There are significant differences in total nitrogen, hydrolyzable nitrogen, total potassium, available phosphorus and organic matter content in the soil of degraded forests of *Pinus armandii* at different altitude gradients, and the total potassium and available phosphorus content in the soil of degraded forests at mid altitude are higher than those of degraded forests at high altitude. In comparison to the environmental gradient of altitude, there are significant differences in the total nitrogen, hydrolyzable nitrogen, total phosphorus, total potassium, and available phosphorus content of degraded forests caused by the different disturbance conditions: the soil total nitrogen, hydrolyzable nitrogen, total phosphorus, and available phosphorus content of degraded forests with waterlogging are higher than those of degraded forests with insect infestations. The soil of the degraded forest of *Pinus armandii* in Shennongjia is from neutral to strongly acidic, with higher altitude indicating stronger soil acidity, while low-lying waterlogged areas are neutral soil. Overall, the soil of the degraded forest of *Pinus armandii* in Shennongjia contains higher organic matter and nitrogen content, with better soil conditions, which is conducive to the progress and succession of the plant community. The Shannon Wiener diversity index and Simpson diversity index of the shrub layer are significantly negatively correlated with soil's total phosphorus and available phosphorus content ($P<0.05$), and shows extremely significant negative correlation with soil's total potassium content ($P \leq 0.001$). Compared with the shrub layer, the correlation between the herbaceous layer and soil nutrients is stronger [17].

To study the changes in phytoplankton communities and water quality both before and after pollution control in Xiaoqing River, sampling surveys were conducted in the upper reaches of Xiaoqing River in 2015 (before control) and 2020 (after control) respectively. The survey results showed that in 2015 a total of 6 phyla and 35 species of phytoplankton were found in the samples, whereas in 2020 a total of 4 phyla and 31 species were identified in the samples. The paired sample t-test results showed significant variation in the species diversity and density of phytoplankton before and after pollution control. Compared to the treatment before pollution control, the relative abundance of diatoms and green algae after treatment increased by 51.6% and 13.3% respectively, while the cyanobacteria decreased by 62.9%. *Cyclotella spp*. replaced *Microcystis spp*. into the absolutely dominant species, and the community type evolved from cyanobacteria to diatoms. The results of similarity analysis and similarity percentage analysis indicated that the community characteristics in the upper reaches of the Xiaoqing River had undergone significant changes. The results of non-metric multidimensional scaling analysis showed that there were differences in community characteristics between the S2 and S3 sampling points after governance, but the community characteristics of the S4 and S1 sampling points were similar. Through redundancy analysis, it was found that after treatment, the impact of TP and

DO on phytoplankton communities was significantly weakened [18].

After pollution control, TN, NH3-N, and pH are currently the main indicators affecting community characteristics. The impact of nitrogen and phosphorus pollution on phytoplankton in the main urban area has been reduced from three sampling points of S2, S3 and S4 to sampling points S2 only. There are significant differences in the Shannon Wiener diversity index, Pielou evenness index and Marglef richness index in the upper reaches of the Xiaoqing River before and after governance, which is caused by pollution control. Overall, the water quality in the upper reaches of the Xiaoqing River after treatment is at low level with the state of α-moderate pollution, showing significant improvement compared to it before treatment [18].

In order to elucidate the evolution patterns of plant community succession and soil nutrients in the reconstruction of open-pit coal mine dumping sites in grassland areas, as well as the effects of runoff and environmental factors on plants and soil, a permanent experimental area was established in 2007 in different parts of the dumping sites of Shengli West Second Open-pit Coal Mine and Ulan Tuga Germanium Coal Open-pit Coal Mine in Xilinhot City, Inner Mongolia Autonomous Region, to conduct research on vegetation restoration and plant succession patterns. By applying principles of ecology with emphasis on restoration ecology, and using methods such as quantitative ecological statistics, this study analyzed the succession patterns of reconstructed plant communities, variations in soil nutrients, slope runoff, and climate factors. It systematically elucidated the structural characteristics and evolution patterns of reconstructed plant communities in open-pit coal mine waste disposal sites. The impact of different restoration treatments and plantation years on the biodiversity was selected to interpret in this study: during the plantation period for restoration, the diversity indexes and stability coefficient of the community showed fluctuating changes, among which the Shannon Wiener index and Simpson index showed a unimodal fluctuation increase, but the species richness showed a bimodal fluctuation decrease. The Pielou evenness index first decreased and then increased, while the functional richness index and functional evenness index showed a unimodal upward trend. The functional dispersion, Rao secondary entropy, and stability coefficient showed a downward trend. For the Shannon Wiener index, both coverage measures consistently showed significantly higher values than the control treatment. For the Simpson index, in the 11th year of planting, there was no significant difference between the two coverage measures and the control, whereas there were significant differences in other years. For species richness, the two coverage measures in the second year of planting were significantly lower than the control, but were significantly higher than the control in other years. For the Pielou evenness index in the second year of planting, there was no significant difference between the coverage treatments, while in other years the biological barrier coverage treatments were significantly higher than the other two solutions. For the functional diversity index, there was no significant difference among the measures after 2 years of plantation, while in other years both coverage treatments were significantly higher than the

control. For the stability coefficient, there was no significant difference among the measures in the second year of planting, while the biological fence coverage measures in other years were significantly higher than the other two solutions [19].

2.1.2.Discussion of plant community succession

The plant biodiversity research over the periods of plant succession has been collected and summarized in Table 1, which reveals that so far much fewer studies have shared the methods about how to analyze the evolution of plant community succession, and most of these studies give a general discussion without detailed methods. Bu et al., (2005) has selected the plant community analysis methods of both fuzzy cluster analysis and principal component analysis (PCA) to conduct the plant community classification and subsequently further identify the succession patterns of these plant communities according to the restoration periods of plant species [11]. However, this methods is only applicable on the grass and shrub species whose restoration periods can be feasibly recorded in the past, but is not applicable on the trees species with the much longer life span of restoration; in another research [17], the succession trend analysis method is based on the distribution and proportion of tree species at each layer of the forest community, which can be studied only on the recent succession trend of the forest community. However, there is no detailed information instructing how to analyze the succession trend of forest community in this article, which may rely more on the experts' experiences. For the long term succession patterns, this qualitative method that relies on the experience of experts is not applicable any more. In this article [23], the succession stage of each plant community is identified according to the age and appearance of plant, which can hardly predict its interaction of competitions between adjacent communities in future succession. Compared with my article [5], the sampling method for plant community study is described as "tree species with the point label is also recorded. In total, there are nine trees identified in each point, including the centre tree, the four nearest, and the four next nearest," and the software package implements the ordination of plant community, which attempts to eliminate the 'stress' and reveal the effectiveness of inter-object distances reflecting real similarities/dissimilarities. Through this methods that is based on the similarity of adjacent plant species in each sampling plot and calculated by the Bray-Curtis
Dissimilarity index, the plant community succession is analyzed quantitatively and conveniently according to the species's frequency-size relation, which does not rely on the collection of historic records in trees' life-long growth in the past long time, because this kind of historic restoration records is considered to be difficult for collection. The ordination philosophy of this species's frequency-size relation is easily understandable in the calculation of relative species importance for plant community classification: if the adjacent species is different from the centre tree, and the adjacent species frequency is higher or the stand size is bigger, the adjacent species are more likely to become the succession ones (or dominant species) instead of the centre tree. There are two types of inter-specific relations underlying this spatial composition pattern: firstly, the adjacent plant species are the competition species with the centre species, and the adjacent plant species may become the succession species because

they squeeze the survival space of both the centre tree and its offsprings; secondly, the adjacent plant species are the dependent species which show symbiosis with the centre tree, and the adjacent plant species would be more likely to become the dominant species, while the centre tree may tend to be the secondary species at subordinate status in this case.

2.2. Classification of plant community and ecosystem diversity

Plant community classification is the first step of identifying the plant ecosystem diversity, recognized internationally. In this grassland article [25], it is summarized that different types of grasslands are usually composed of different plants, and the differences in both dominant species and species composition between plant communities are the main basis for classifying grassland community, so it is to generally use the relative weight, relative coverage, relative height, relative abundance and relative frequency of plants as quantitative indicators for determining the dominance of different species, and the correspondingly classified grassland type is named according to the dominant species, which interact with environmental factors such as temperature, precipitation, longitude and latitude, altitude, and so on. This is also the typical analysis methods for all types of plant community classification explained by environmental factors. However, there are some shortages discussed by the grassland article, for example, in an ecosystem the composition of plant communities is similar and the species dominance is also similar, but the grassland types may be divided into several plant categories by only using dominant species to characterize. In some special cases, it is difficult to determine the dominant species in the plant community, so the grassland type can not be accurately classified. When grassland degradation is severe, the dominant species degenerate into poisonous weeds. At this time, only using plant dominant species to characterize grassland types will result in one sidedness. In addition, due to difficulties in data acquisition and limitations in quantitative techniques, there are no further development in the quantitative research based on dominant species classification so far. Instead, this article has proposed a comprehensive combination of indicators including plant dominant species, small rodents and microbes' community to classify the grassland ecosystem types as future improvement [25].

My article further proposes that because the plant community classification method is based on the relativity in dominant species indicators, the invasive plant species (usually including invasive weeds or shrubs) must be excluded from this plant community classification process, which may lead to the bias of statistics, hardly revealing the indigenous nature of ecosystem. In this case, the invasive plant species would be classified and analyzed separately. However, the invasive weeds species is different from the toxic weeds degraded from the dominant species discussed in above paragraph. If the toxic weed species is evolved from the dominant species that is the indigenous one, this is definitely the strong life signal of environmental adaptiveness for this poisonous weeds against rodents' grazing, which should be included as biodiversity conservation although this poisonous weeds may lose its economic value

for farming. There are some case studies summarized in Table 2, and it is noted that all the case studies conducted in China have selected TWINSPAN methods for quantitative classification, but the plant species importance calculation methods vary between different sampling cases, which have been compared and contrasted in this table.

Table 2. Summary of plant community classification methods and indicators used to analyze the plant community.

Cases	Classification methods	The parameters used for the classification	Indicators used to analyze the plant community
[22]	TWINSPAN	Species Importance = (Relative abundance + Relative frequency + Relative significance)/3; Relative significance is measured by the relative cross-sectional area at chest height	Plant density; The diameter at breast height (DBH); The diameter class structure of tree species; Human disturbance analysis.
[23]	TWINSPAN	Species Importance = (Relative abundance + Relative canopy coverage + Relative plant height)/3; Relative canopy coverage is estimated by the relative cross-sectional area at chest height	The diameter at breast height (DBH) structures; Plant density; Species diversity; Both functional dispersion and Rao quadratic entropy index.
[24]	TWINSPAN	Tree layer: Species Importance = (Relative abundance + Relative frequency + Relative significance)/3; Shrub and grass layer: Species Importance = (Relative abundance + Relative canopy coverage + Relative plant height)/3	Both α and β diversity indexes; The redundancy analysis (canopy density, dominant species, stand density, altitude).

This research takes the plant communities in three experiment plots as the research object, and obtains relevant basic data by using backpack LiDAR, laser rangefinder, etc. to conduct species identification, flora analysis, community classification, and community structure analysis on the plant communities of various plots. The plant community classification is conducted by using the Two-Way Indicator Species Analysis method (TWINSPAN), according to the importance of each species which is (Relative abundance + Relative frequency + Relative significance)/3. The results have

shown that: (1) 619 species of vascular plants classified into 120 families and 355 genera are found in the three sample plots, including 157 species of 120 genera belonging to 70 families in the the Pearl River source sample plot, 319 species of 224 genera belonging to 92 families in the Diaoling Mountain sample plot, and 353 species of 255 genera in 100 families in the Jizu Mountain sample plot, respectively; (2) There are 103951 surviving woody plants with DBH ⩾ 1 cm, including 24932 plants in the the Pearl River source sample plot, 25222 stands in the Diaoling Mountain sample plot, and 53797 plants in the Jizu Mountain sample plot, respectively, whose density is estimated as 2493.2 plants/ha, 3060.9 plants/ha, and 2689.9 plants/ha, respectively; (3) The total proportion of temperate flora components to all vascular plants in the sample plot group is 51.3% and 24.7% at the genus and species levels respectively, among which the proportion of Chinese endemic species accounts for 33.0%; (4) The plant communities within the sample plot can be divided into 8 formations, namely as the *Castanopsis orthacantha* formation, *C. delavayi* formation, *Lithocarpus craibianus* formation, *L. dealbatus* formation, *Pinus yunnanensis* formation, *Cyclobalanopsis delavayi* formation, *L. mairei* formation, and *Quercus senescens* formation. The Diaoling Mountain sample plot contains the most formation types, whereas the the Pearl River source sample plot has the least; (5) The diameter class structure of tree species in both Jizu Mountain and Diaoling Mountain sample plots is displayed as the inverted 'J' type, while the the Pearl River source sample plots is uni-modal; The Jizu Mountain sample plot experienced the local serious disturbance at 80 – 100 years ago, while the Diaoling Mountain sample plot experienced a general sign of light to moderate disturbance at 50 – 80 years ago, and ~~the~~ the Pearl River source sample plot experienced a covered fire disturbance at 37 years ago. It is conclude that the differences in forest formation type and diameter class structure among the sample plots mainly depend on the degree of community succession and terrain differences [22].

The Zhoushan Islands are rich in vegetation coverage that is consisted of island-specific plant communities due to the changes in island area, geographical isolation and high-intensity human interference. Based on the investigation of 30 vegetation sampling plots on Luojia Mountain Island, it is to classify their vegetation types and analyze both species and functional diversity of unique plant communities. The results show that: (1) the vegetation in Luojia Mountain Island can be divided into evergreen broad-leaved forest, evergreen deciduous broad-leaved mixed forest, evergreen shrubs, shrubs and grasslands; there are 10 population clusters or community types classified in total on the basis of dominant species and flora characteristics, which are correspondingly divided into 10 succession stages according to their age and appearance (each plant community corresponds to a kind of succession stage). These 10 plant communities include *Red Nan* Cluster, *Red Nan - Pu Tuo Zhang* Community, *Red Nan - Quan Yuan Holly* Community, *Red Nan - Mulberry* Community, *Pu Tuo Zhang - Tian Xian Guo* Community, *Liming Hai Tong* Community, *White Mouth* Community, *Wujie Mang* Community, *Mangcao* Community, and *Single leaved Manjing* Community, which are classified by using

Multi Optimality - Aggregation (Level 5) quantitative methods according to the significance of each species; (2) The diameter at breast height (DBH) structures of both the *Hongnan Putuo* camphor tree community and the *Binling Haitong* shrub exhibit an L-shaped distribution, with the highest proportion of individuals which have a DBH of 0-5 cm; (3) The average density of the *Hongnan Putuo* camphor tree community is significantly lower than that of the *Binyu Haitong* shrub ($P<0.05$), but there is no significant difference in other species diversity between any two communities ($P>0.05$); The functional dispersion and Rao quadratic entropy index of the *Hongnan Putuo* camphor community are significantly higher than those of the *Binyu Haitong* shrub ($P<0.05$). It has been found that the vegetation types on Luojia Mountain Island are rich, with complete and unique plant community structure of the island, showing high diversity in both species and ecological functions [23].

Based on the investigation data from 50 standard sampling plots, the Two-Way Indicator Species Analysis method (TWINSPAN) has been used to classify the 50 standard sampling plots into different community types; Secondly, it is to analyze the variance between different community types by using the indexes of both α-Diversity and β-Diversity, assessing the differences in plant diversity among different community types; Finally, by using redundancy analysis, it is to explore the plant diversity and the underlying influence factors of different plant communities in Zengcheng Forest Farm. The research results indicate that: (1) The plants in Zengcheng Forest Farm include 84 families, 189 genera and 270 species, which can be divided into 10 plant communities. Among them, the dominant communities are '*Huarunnan+Schima superba + light bamboo* leaf community', '*Lathyranthus chinensis+ goosefoot firewood + nine node* community', and '*Chinese fir + Schima superba + light bamboo* leaf community'; (2) There are significant differences in α-diversity between different types of plant communities. For example, in the communities of '*Chinese parasol + goosefoot firewood + black fern'* and '*Chinese fir + Schima superba + light bamboo leaves'*, the α-diversity is the most abundant, followed by the communities such as '*Huarunnan + Schima superba + light bamboo leaf* community', while the '*Eucalyptus grandis+bamboo community'* is the simplest one with the lowest α-diversity; Compared to the other communities, '*Huarunnan + Schima superba + light bamboo leaf* community' exhibits the highest β-diversity index, indicating the least inter-specific competition with other plant populations and displaying the strongest community stability; (3) According to the redundancy analysis, the canopy density and dominant tree species result in extremely significant impact on plant diversity, while stand density and altitude lead to significant impact on plant diversity as well. In summary, the comprehensive plant diversity of '*Huarunnan+Schima superba+light bamboo leaf* community' is the most abundant. By adjusting the density of advantageous tree species and optimizing the stand structure, forest management activities can transform the stand towards the direction of '*Huarunnan+Schima superba+light bamboo leaf* community', in order to further enrich plant diversity and enhance ecosystem stability [24].

2.3. Ecosystem evaluation indicators and biodiversity

There are mainly four ecological evaluation indicators summarized in this ecosystem diversity section, focusing on the quantitative methods measuring each evaluation indicator. The representative cases for each evaluation indicator are outlined in Table 3, and finally these ecological evaluation indicators are critically discussed.

2.3.1.Ecosystem resilience

Ecosystem resilience is to measure the capacity of damaged or disturbed ecosystem to restore back into its original ecosystem, which usually uses biodiversity index as the indicator in this measurement [1]. To better clarify the research scope of grassland ecosystem resilience, a grassland ecosystem resilience evaluation system on the basis of plant diversity is newly established. The grassland ecosystem resilience is quantitatively measured from three aspects: maintaining its own structure and function ability, restoration ability, and resistance ability. The resilience of the mountain meadow ecosystem in the Kanas scenic area of Xinjiang, which has been damaged by human activities, is also quantitatively evaluated, in order to provide a basis for the scientific management of the grassland ecosystem in the scenic area. The results have shown that with the increase of human activity intensity and frequency, the ability of mountain grassland ecosystems to maintain their own structure and function, as well as their restoration ability, displays as the downward trend at the levels of species diversity, functional group diversity, and community diversity respectively, and the background and buffer zones are significantly higher than the active and strongly active zones ($P<0.05$) in ecosystem resilience capacity measured by the newly designed evaluation system; The resistance ability at the level of species diversity also shows the decreasing trend with the increase of human activity intensity and frequency, and perennial plants are the main contributors to the restoration ability at the level of species diversity. However, at the levels of both functional group diversity and community diversity, due to the redundancy of functional groups and communities, the productivity of ecosystem communities have been stabilized. Consequently, although there is a downward trend, the degree and magnitude of decline trend have slowed down. This reflects the shortcomings of using the single indicator or the single organizational hierarchy of plant diversity to evaluate the resilience of grassland ecosystems, compared with the multiple indicators designed in this research. Therefore, the multi-scale grassland ecosystem resilience evaluation system avoids the bias of single indicator evaluation, making the evaluation more reasonable [26].

2.3.2.Ecosystem sustainability

Ecosystem sustainability is the intrinsic capacity of ecosystem developing its own composition, structure and function in the evolutionary process [1]. A evaluation hierarchy consisting of four element capability system is designed to assess the ecosystem sustainability, including ecological integration capacity, self-sustaining vitality ability, self-regulation capacity, and self-organization capacity. The measurement of ecological integration includes three basic contents: the diversity of

components, the structural correlations between components, and the functional processes of ecosystems. These three parts can be measured by using 14 main variables. It is noted that the diversity calculation used in this evaluation involves the broader range of components at different levels and scales of ecosystems, which can be divided into genetic diversity, biochemical diversity, species diversity, habitat (landscape) diversity, and physicochemical-environmental variability, and the measurement has the direct dependence on the selection of levels and scales in the calculation of diversity variation; The self-sustaining of an ecosystem includes two basic pathways: one is metabolic pathway that provides an inherent mechanism for the conversion of material energy in the system. The basal metabolic level and metabolic efficiency can be used to measure metabolic capacity. The second pathway is the way of conservation, which enhances the metabolic processes of the system; The measurement of ecosystem self-regulation capacity consists of three basic elements: endogenous balance (balance of interactions between components), buffering capacity (tolerance range for environmental stress or disturbance) and disturbance response capacity (system response capacity to external stress or disturbance); Self-organization capacity includes organizational maturity, efficiency of energy and resource consumption, and orderliness of evolution or succession [27].

2.3.3.Ecosystem resistance

Ecosystem resistance is the capacity of indigenous ecosystem resisting against exotic disturbance or invasive species to maintain its original structure and function [1]. Through the experimental method of simulating drought by removing the natural rainfall, the one-month drought treatment is applied at different stages of the growing season for two consecutive years to observe the ecosystem resistance of above ground biomass among different plant functional groups in grassland, as well as the recovery ability at one year after drought. The results have shown that there are differences in the impact of drought treatment on the above ground biomass between different stages of the growing season, with the greatest impact under extreme drought in the middle of the growing season, resulting in an average reduction of 47.90% in above ground biomass. Among different plant functional groups, *Poaceae* plants have the highest resistance index to drought of 1.65-2.25, while annual plants show the strongest recovery ability of 2.20-3.00, which can compensate for the decline in recovery ability of other functional groups to a certain extent [28].

The ecosystem resistance or resilience index is calculated quantitatively as:

$$RE = Log_{10}\ (A_{drt}/A_{ck} \times 100)$$

Where RE is the ecosystem resilience or resistance index, A_{drt} is the biomass of background sampling plots, A_{ck} is the biomass of treatment sampling plots [29].

However, the overall resistance and recovery ability of grasslands are still mainly

contributed by perennial apical species. Given that most ecosystems are dominated by the minority of species, it is essential to understand the functional groups to which dominant species in grassland communities belong, as well as their response to extreme climate and characteristics of recovery under extreme climate, which can provide theoretical basis for improving the functional stability of grassland ecosystems in extreme arid climates [28].

2.3.4.Ecosystem variance

Ecosystem variance is the evaluation indicator reflecting both structural and functional heterogeneity of species distribution patterns influenced by the available environment conditions [1].

Based on Landsat data from 1990 to 2020, the normalized vegetation index (NDVI) quantifying spatial heterogeneity were selected as remote sensing monitoring indicators for grassland degradation in the Kurustai grassland, to conduct the research and evaluate the degradation status of the Kurustai grassland. (1) The results showed that from 1990 to 2020, the NDVI in the central part of the study area showed an upward trend, while in the peripheral areas it showed a downward trend; The areas where grassland spatial heterogeneity was increasing were mainly concentrated in the central and southwestern regions of the study area, whereas the spatial heterogeneity of northern and southern regions was mainly decreasing. (2) The monitoring of grassland degradation showed that about 54% of grasslands had experienced degradation, but 35% of grasslands had improved, and 10% of grassland vegetation had been restored. (3) Temperature and precipitation resulted in a relatively small impact on the inter-annual variation of spatial heterogeneity in grassland, but led to a significant impact on NDVI. Precipitation was found as the main factor affecting the temporal dynamics of NDVI in the Kurustai grassland [30].

In this case study, the coefficient of variation (CV) is a statistical measure that reflects the degree of dispersion on a set of data, also known as the ‘dispersion index’. It is the ratio of standard deviation to its mean and is often used to evaluate the fluctuation of vegetation over time series. This study has quantified the spatial heterogeneity of grasslands through the coefficient of variation of NDVI, which serves as an important indicator for evaluating the growth status of grasslands. The detailed calculation method of CV based on NDVI is specified in paper [31].

Table 3. Ecological evaluation indicators and biodiversity index.

Cases	Ecological evaluation indicators	Biodiversity indexes
[26]	Ecological Resilience divided into three aspects: maintaining its own structure and function ability, restoration ability, and resistance ability.	Species diversity, functional group diversity and community diversity, including: Shannon Wiener diversity index, functional group richness, community productivity (represented by community aboveground biomass);

		ecological dominance index; group dominance index, community structure index; Coefficient of Variance.
[27]	Ecosystem sustainability includes ecological integration capacity, self-sustaining vitality ability, self-regulation capacity, and self-organization capacity.	genetic diversity, biochemical diversity, species diversity, habitat (landscape) diversity, and physicochemical-environmental variability.
[28]	Ecosystem resistance index and resilience index	The ecosystem resistance and resilience index between different plant functional groups in grassland.
[30]	Ecosystem variance	normalized vegetation index (NDVI)

2.3.5.Discussion of ecosystem evaluation theory and methods

Among these evaluation indicators, it is found that the measurement criteria for each evaluation indicator are overlapped and correlated. The case study of ecosystem sustainability is the most complex one among these case studies, which is difficult to implement quantitatively and relies much on the assessor's expertise, so the conclusion of this evaluation system may not be comparable between different ecosystem sustainability evaluation cases. Consequently, it seems not feasible to evaluate all the indicators in a case.

In my research [2], the new method of assessing both spatial and functional heterogeneity is designed, which is easier to implement in practice and it is believed that under the same level of biodiversity index, the higher spatial or functional heterogeneity, the more healthy for the ecosystem, and the other three ecological evaluation indicators (ecosystem resilience, resistance, sustainability) should be positively correlated with both spatial or functional heterogeneity indexes. In my designed method, the only criterion that relies on the assessor's expertise is the ecological functions of each species, which can be standardized officially in the future. For example, the value of a plant species for soil stabilization can be ranked according to the age of plant, soil types, geography conditions, etc, which can be guided by the national standards for the ecological assessor.

3.Species Diversity

In this species diversity section, the relevant theories with regards to the analysis of species diversity are summarized, including edge effects, inter-specific associations, rank correlation coefficient, segregation index, ecological Niche theory, illustrated by the updated and representative cases. Based the theoretical study, the plantation practice measures will be comprehensively discussed.

3.1.Theoretical conceptions of species diversity

3.1.1.Edge effects

Edge effects is the ecological zones between different plant communities influenced by the interaction between various structure and functions of plant communities [1]. ‘The edge areas between these indigenous remnants and their surrounding environment, which are typically warmer, windier, and drier than interior areas, are usually dominated by plants and animals of disturbed sites which threaten the biodiversity within indigenous remnants[41][42].’

This study focused on the grassland in the northern part of Xilingol League, typical grassland and desert grassland. Through remote sensing interpretation, field experiments and indoor analysis, the spatial pattern of land use and the ecological changes of landscape in the study area were compared at a large scale among the year 2010, 2015 and 2021. At the small scale, the spatial differentiation patterns and edge effects between different patches of severely fragmented grassland patches were explored. The aim was to analyze the change of land use and evolution direction of grassland patches in the northern part of Xilingol League, provided theoretical basis for scientific management and sustainable use of the Xilingol grassland ecosystem. The research on the edge effect between grassland patches and bare land patches showed that the biomass of grassland, typical grassland and desert grassland had been increasing with the increase of edge distance (0-3.5m). The maximum values of both species evenness and diversity index of the three types of grasslands were all found from -1 to 0 m along the edge, while the maximum value of soil AP was between -0.5 to 1m on the edge; The soil indicator of the greatest impact on vegetation community characteristics was SOM, which accounted for 76.8% and 77.6% variance in grassland and desert grasslands, respectively, but in the typical grassland the highest impact soil indicator was AP, which accounted for 51.1% variance. The performance of the three grasslands on the distance gradient was the same with high AP, AN, TN, AK, TK, which increased with the increase of biomass and showed a positive correlation; The structural equation model (SEM) established on the basis of three types of grassland community characteristics and soil indicators fitted the results of field sampling, with the fitting order: desert grassland > meadow grassland > typical grassland. The comparative fitting index (CFI) of desert grassland was 0.995, and the normative fitting index (NFI) was 0.996; in the typical grassland the CFI was 0.959, and the NFI was 0.942; in the grassland the CFI was 0.964, and the NFI was 0.947. The SEM models on the three types of grasslands all indicated that biomass was the most significantly affected indicator by edge effects, while AP and AN were the most significant indicators affecting plant species richness; The edge peaks calculated by using Euclidean distance indicated that the edge effect of vegetation community characteristics was inconsistent with soil indicators: the edge peaks of community indicators generally appeared between -1 to 0m, while the peak values of soil indicators all appeared between -0.5 to 1m [32].

3.1.2.Inter-specific association

Inter-specific association is defined as the inter-species interactions between different populations of species in spatial distribution, when the negative association is named

as segregation index reflecting competition relationship and the positive association is regarded as rank correlation coefficient revealing interdependence relationship [1].

The wild distribution of *Cephalotaxus hainanensis* is sparse, and its natural regeneration ability is weak, which is seriously threatened by human logging, resulting in a sharp decline in its population. To explore the composition and inter-specific relationships of tree species in the community of *Hainan Cephalotaxus hainanensis*, it is to analyze its endangered reasons, and to create suitable habitats for the restoration of *Hainan Cephalotaxus hainanensis* population, developing targeted conservation measures. Based on field investigations of *Hainan Cephalotaxus hainanensis* community samples in Hainan Tropical Rainforest National Park, the species diversity and flora composition of associated tree species in the community have been analyzed, by using the indexes of variance ratio method (Rv), χ^2 test, association coefficient (AC), co-occurrence percentage (PC), Pearson correlation coefficient (Rp), and Spearman rank correlation coefficient (Rs). The inter species correlation significance and its correlation strength with 16 common tree species in the *Cephalotaxus hainanensis* community have been explored. The results show that in 8 plots of 20 m × 20 m, a total of 105 tree species belonging to 78 genera and 44 families have been found, among which the flora is mainly tropical in nature, accounting for 65.9% of the total number of families; The overall correlation among the 16 common tree species shows an insignificant negative correlation (Rv=0.534, statistic W=4.27), with strong species independence; The results of the χ^2-test show that the number of negatively correlated species (41 pairs) is greater than that of positively correlated species (33 pairs), but there is no significantly correlated species in the community; There are 9 pairs of species with AC>0.67 and 7 pairs of species with PC>0.75. The connectivity between most tree species is weak, and there is only a significantly positive correlation between *Cephalotaxus hainanensis* and short medicinal peach (P=0.018); The correlation test between Rp and Rs shows that there are more significantly negative correlation pairs than significantly positive correlation pairs. There is a significantly negative correlation (P=0.027) between *Cephalotaxus hainanensis* and medicinal dog tooth flower, but the majority of pairs are not significantly correlated. According to the correlation test, both competition species and interdependence species with *Cephalotaxus hainanensis* have been revealed, which is the medicinal dog tooth flower and short medicinal peach respectively. In summary, the overall structure of the *Cephalotaxus hainanensis* community is relatively loose, and there may be frequent species succession changes, revealing that the community is still in an unstable stage, and *Cephalotaxus hainanensis* tends to survive independently. In order to alleviate the decline of the population of *Cephalotaxus hainanensis* in Hainan, the community habitat should be appropriately transformed as on-site conservation measures, and artificial replanting should be carried out to expand its population size [33].

3.1.3.Ecological Niche

Ecological Niche theory is created by the population biologists to assess the available

resources of a species for survival and development, measured by Niche Breadth(Width), as well as its around competitors competing for the available resources, indicated by Niche Overlap [1].

Huangbo (*Phellodendron amurense*) is a conservation plant species at national second level. By quantitatively analyzing the ecological niche characteristics of the main tree populations in the mixed broad-leaved forest of *Phellodendron amurense*, theoretical basis can be provided for the conservation and maintenance of species diversity of *Phellodendron amurense*. Based on the data from the 9th continuous forest resource inventory in Jilin Province, a survey has been conducted on typical plots of the mixed forest community of *Phellodendron amurense* in the Changbai Mountain area. By the calculation methods including importance value, Levins niche width, Shannon Wiener niche width, and Pianka niche overlap, the ecological niche characteristics of the main tree populations in the mixed forest of *Phellodendron amurense* have been analyzed. The results show that there are 25 broad-leaved tree species in the mixed forest of *Phellodendron amurense* in the Changbai Mountain area, accounting for 96.15% of total species, with the highest importance value in *Phellodendron amurense*; The ranking order between Levins niche width and Shannon Wiener niche width indices is basically the same. The tree species with the largest niche width all are Huangbo, followed by *Juglans mandshurica*; The ecological niche overlap values of species such as *Phellodendron amurense*, *Betula platyphylla*, *Juglans mandshurica*, and *Ulmus lobata* are relatively large, and the ecological niche width of these species shows obvious consistency with ecological niche overlap. However, there are some species with the opposite ecological niche widths against its corresponding niche overlaps, such as between species of *Quercus acutissima* and *Quercus acutissima*, *Robinia pseudoacacia*, *Tilia bassiana*, as well as between *Phellodendron* and *Pinus koraiensis*. This is related to the ecological width being influenced by multiple factors such as species' ecological habit, habitat characteristics and spatial distribution [34].

3.1.4.Discussion of theories on species diversity

The ecological niche theory is well acceptable in my article, but there are inconsistency between the statistical calculation of niche overlap and inter-specific association: the calculation of niche overlap is based on the species importance between two species in a sampling plot, but niche overlap interpretation focuses only on the competition relationship between species, ignoring the interdependence relationship between species. This would be considered as the deficiency in theoretical explanation of niche overlap. Secondly, the statistic correlation method used in inter-specific association is too mechanical, because it is believed that each sampling plot's habitat conditions vary among all the sampling plots and each sampling plot is the specific habitat for the species survival, which can be hardly revealed by the statistics of correlation calculation method. Consequently, the statistic significance level of inter-specific association calculation must not be considered in this ecological study, and the inter-specific association need to be considered as case by case in each sampling plot. For example, if the sampling plots include both deep

water depth and shallow water depth of wetland, and there are two wetland species always showing positive correlation at the deep water depth but no correlation at the shallow water depth, then the correlation calculation may show weaker or insignificant correlation when all the sampling plots are input into statistics. This statistic bias can not reveal the real nature of phenomenons in ecology.

Consequently, based on the above theoretical studies, there is Table 4 designed to analyze the population ecology.

Table 4. Design of population ecology indicators used to analyze the species diversity.

Ecological Theories	population ecology indicators	Species 1	Species 2	.....
Environmental Gradient Analysis	Geography Conditions (mainly including location, slope orientation, slope altitude, slope degree, topography, water depth for wetland species, etc)			
	Radiation			
	Precipitation			
	Soil conditions			
Inter-specific association in a specific habitat	Negative correlation reflecting competition species			
	Positive correlation reflecting interdependence species			
Ecological Niche	Niche Width			

As shown in Table 4, firstly the environmental gradient analysis is conducted to characterize the specific habitat as the available resources for species survival and development; then at the similar level of environmental gradient, the inter-specific association is analyzed to reveal both competition species and interdependence species, and all the species distribution should be analyzed under similar available resource conditions so that their association are comparable; Thirdly, Niche width calculation is conducted to reveal the broadness of spatial distribution of a species among different communities. The higher niche width, the more available resources for a species' survival, the broader distribution of a species among different communities, the broader distribution along different environmental gradient conditions as well. There is an example of this ecological niche theory application on the selection of species for wetland restoration discussed in my article [5]. My article further argues that with the development in genetic diversity study, each genetic variety of a species chooses specific habitat for distribution and survive, so the case studies illustrated in this species diversity section would be too coarse, the species' inter-specific association in the specific habitat must be analyzed as case by case.

With further development of the ecological niche theory, the vegetation habitat which suits for endangered birds or mammal species can be limited and specific. For example, when the endangered bird species transfer from its indigenous habitat of a kind of tree species to another species of tree, these bird population will lose competitiveness once they compete with other bird species, so the conservation biology study should not only focus on the food chain theory of endangered species, but also take the competitiveness of endangered species into consideration when they are forced to move into other habitats. The indigenous habitat lose may sometimes become the main reason of a bird or mammal species turning into the endangered one. Consequently, the ecological functions would essentially include the restoration of habitats for endangered species as well. This discussion will be further illustrated by several case studies in next section.

3.2.Ecological restoration

3.2.1.Plantation measures for ecological restoration

The plantation measures for forest biodiversity conservation in New Zealand is summarized in my previous article [6], based on which this part of my article attempts to study the plantation measures from the representative Chinese case studies, given the theoretical discussion of population ecology.

3.2.2.Significance of plantation conservation in forest farm

The biodiversity conservation in artificial plantation forest is of significance due to its ecological functions such as providing essential habitats for indigenous species (including threatened species), connectivity between fragmented indigenous reserves with conservation value, and buffering function which reduce the edge effect in adjacent indigenous remnants [41].

3.2.3.Conservation of plantation forest in NZ

There are several conservation measures summarized by my previous article in NZ[6], including ‘retention of essential areas for indigenous species, maintaining the connectivity and buffering function, habitat restoration for indigenous species, improvement of harvesting process, protection of natural soil process, conservation of understorey structure, management of invasive species.’ Each measure has been described in detail in the article, which can be directly applicable on the conservation practice in China as well.

3.2.4.Conservation of plantation forest in China

So far the published articles with regards to biodiversity conservation in plantation forest are massive, but the majority of these articles are quite general, focusing on policy without detailed measures to implement in conservation management. Below there are representative and updated case studies in China selected for study purposes:

Based on the theory of forest ecosystem succession, there are several plantation

measures implemented in Saihanba Forest farm: the ultimate goal is set up to evolve from artificial plantation forest into natural forest; thinning and pruning are taken to reduce stand density, and it is to induce understory shrub and grass distribution in the forest farm, so it improves the habitat environment of animals by opening up understory channels and increasing animal accessibility; great efforts is taken to reduce the occurrence and spread of forest pests and forest fires. Through these measures, it is to gradually improve the stability of forest ecosystems, and promote the transformation of artificial forests in nature reserves towards natural forests. Therefore, the block-like mixed forest of *Pinus sylvestris* and *Picea asperata* is specially planted, and multi-layer mixed forest of different ages is cultivated. Through decades' forest management, the growth rate of single tree diameter at breast height, the richness of understory shrub species, and the growth rate of individual abundance have been significantly increased, especially solving the problems that the artificial large-scale forests of the same age in Saihanba display as mono species, decreased growth, and serious harm from pests, diseases and rodents [35].

The biodiversity conservation value has been attempted to evaluate by China currency, and the calculated methods is worked out below [36][37]:

$U_{biology} = S_{biology} \times A$

In the formula, $U_{biology}$ represents the value of forest's annual biodiversity conservation, measured by the Chinese Currency yuan/year; $S_{biology}$ is the opportunity cost of species loss per unit area, evaluated by yuan/(hm^2 · year); A is the forest area, measured in hectares [36] [37].

The Shannon Weiner index across the country of China is divided into 7 levels, each of which is assigned a certain value. According to the Shannon Weiner index, the $S_{biology}$ is divided into six classes: when the index is ≤ 1, the $S_{biology}$ is 3000 yuan/(hm^2 · year); When 1 ≤ index<2, $S_{biology}$ is 5000 yuan/(hm^2 · year); When 2 ≤ index<3, $S_{biology}$ is 10 000 yuan/(hm^2 · year); When 3 ≤ index<4, $S_{biology}$ is 20 000 yuan/(hm^2 · year); When 4 ≤ index<5, $S_{biology}$ is 30 000 yuan/(hm^2 · year); When 5 ≤ index<6, $S_{biology}$ is 40 000 yuan/(hm^2 · year); When the index is ≥ 6, the $S_{biology}$ is 50 000 yuan/(hm^2 · year) [37].

According to the evaluation methods, the total value of forest biodiversity conservation in Boshan Forest Farm is estimated as 61.658 million yuan. The value of biodiversity conservation in different types of forests is as following order: *Quercus* > *Pinus massoniana* > *Hardwood* > *Poplar* > *Robinia pseudoacacia* > *Pinus tabulaeformis* > Shrubs > Wetland pine > Chinese fir > Torch pine > *Metasequoia lanceolata* > Bamboo forest [38]. Obviously, through the economic evaluation of biodiversity conservation value, the commercial forest farms may facilitate their forest management and conservation practices.

Artificial afforestation should be based on biological theories, selecting advantageous tree species for planting and enhancing the biodiversity of forest vegetation in conservation areas. The principle of 'tree must be planted in its suitable location' is implemented, so it is to select local advantageous tree species in Gansu Province, such as black thorn, mountain willow, tea maple, etc. These local tree species have stronger environmental adaptability, even in the face of natural disasters such as drought and freezing. Ensuring these local trees' survival rate does not only improves the survival rate of the whole artificial forests, but also reduces the pressure of later forest management. After determining the tree species for artificial afforestation, scientific planting is also crucial to ensure the survival and healthy growth of seedlings. Priority should be given to areas with fertile soil and flat terrain for artificial planting tree species, while in areas with poor soil, it is advised to plant shrubs with strong vitality. Artificial afforestation should choose as many types of tree species as possible to form the more stable forest ecosystem. To enhance the resistance of forest vegetation against common pests and diseases in conservation areas, trees such as North China larch and mountain willow can be artificially planted on the hollow ground of the forest; In the valley area, it is to choose shrubs such as *moss yellow berberine* and *sea buckthorn*; In some areas with poor soil and water conditions, plants with strong vitality such as *Jinjier* can be chosen. Through continuous artificial afforestation, it is to enrich plant species in the Qilian Mountain Nature Reserve, increasing the value and stability of forest resources, and ultimately achieve sustainable development [39].

Regularly the entrance of artificial forest is closed for tree cultivation, which allows the trees in the conservation area to rest, especially for artificial forests and young forests, providing good natural growth opportunities and resulting in the positive effect on achieving forest vegetation renewal. Based on the climate characteristics of Gansu region, this regular closure of forest entrance is usually chosen to start in April, with a suitable cycle of 2-3 years. First, it is to seal off the areas with the most frequent human and animal activities, and then to seal off those critical zone where the coverage of shrub forests is around 30% only and the canopy closure of tree forests is about 0.2 [39].

The ecological restoration treatment is designed for an abandoned mine in Henan Province. According to the terrain and vegetation conditions of the mining restoration area and the on-site investigations of local residents, the vegetation restoration has selected the planting species of *Platycladus orientalis*, *Pueraria lobata*, and *Dogtail grass* seeds. A total of 1242 cypress trees are planted on the restoration platform, with the row interval and inter-plant distance of 2.00m and 2.00m, respectively. *Pueraria lobata* is planted at the foot of the slope, with the row length of 739.71m placing 370 trees. In addition to the planting of cypress trees on the periphery, the restoration platform also needs to sow *dog tail grass* seeds. The grass seed sowing area is the natural restoration area, with a specification of 40kg/hm^2 and a total sowing area of 1.95hm^2. The water consumption quota for planting *Platycladus orientalis* is

30kg/(per plant per time), and the water consumption for *Pueraria lobata* is 15kg/(per plant per time), with the maintenance period of two years. The frequency of watering, in the first month after planting, is once a day for the first 3 days, then once every 3 days for the next 4-9 days, and once every 10 days for the last 10-30 days. A total of 7 times of watering are required to ensure the survival rate of restoration plant. From the second to fourth month, watering is required at once every 20 days, and then it is to water once a month thereafter, with watering at 30 times in total [40].

3.2.5.Ecological restoration of habitats for endangered species

This section mainly summarizes the case studies on the ecological restoration of habitats for endangered species, taking conserved birds as the example:

Shiyang County in Jiangsu Province borders the Yellow Sea, which boasts unique tidal flat resources, whose ecological function serves as a crucial stopover site for migratory birds between Northeast Asia and Australia. However, excessive reclamation for aquaculture in certain areas has led to significant degradation of natural coastal wetlands, fragmentation of bird habitats, and habitat destruction, which severely disrupt birds' migration patterns and breeding capabilities, so that it is urgently necessary to implement artificial restoration measures to rebuild the wetland ecosystem and restore suitable habitats for birds. In this restoration case study based on the "core patch – stepping stone – corridor" model, there were three types of heterogeneous patches established for the restoration of bird habitat. The core patch was mainly consisted of *Suaeda salsa* beachlands, and the function was to provide habitats to black-headed gulls for foraging, resting and shelter; the stepping stones were muddy tidal flats, whose function served as feeding and resting sites for wading birds; the multifunctional corridors comprised tidal channels and ecological aquaculture areas, which ensured both ecological continuity and sustainable economic production. The detailed solutions for the three types of heterogeneous patches are as below [72]:

The *Suaeda salsa* beachland is located on the northern side of the restoration area, covering an area of approximately 95 hectares, which connected to the newly developed tidal channel. This sparse *Suaeda salsa* wetland has regained its tidal characteristics, which provides foraging grounds and habitats for black-headed gulls. Additionally, the growth of *Suaeda salsa* enhances soil’s organic matter content, which further improves soil structure and creates favorable conditions for the growth of other plants; The muddy tidal flats feature both permanent and seasonal shallow water zones: the permanent shallow zone has a water depth of 0.5–1.2 m, becoming the tidal channels connecting both eastern and western sides of the entire restoration area, and this permanent shallow zone provides suitable habitats for fish and benthic organisms, further enhancing biodiversity in the wetland ecosystem, while the seasonal shallow zone is 0 – 0.5 m in water depth and it gradually exposes to extensive mudflats, serving as vital feeding and habitat sites for wild ducks and geese during winter. The tidal channel system also facilitates water exchange and circulation,

which maintains hydrological balance in the wetland; The ecological aquaculture zone is located in the southeastern corner of the restoration area, with approximately 58 hectares. Regular cleaning of pond debris and replanting of aquatic plants are helpful to maintain ecological health. Studies have shown that wading birds also utilize the pond banks as habitats, so as to enhance bird habitats while maintaining aquaculture operations. This study has incorporated sunlit beaches and gravel banks into the ecological pond, establishing the ecological function as crucial food supply stations and resting sites along wading birds' migration routes [72].

Another adjacent study is conducted in Jiangsu Yancheng Wetland Rare Birds National Nature Reserve, which serves as a crucial stopover and wintering habitat for migratory birds along the East Asian - Australasian Flyway. From November 2022 to February 2023 (during the wintering period of migratory birds), continuous monitoring was implemented on waterbirds in the restored wetlands located at the reserve's experimental area, which collected baseline data about population sizes and community composition while analyzing habitat utilization patterns. Results revealed distinct variations in bird populations and community structures across habitats: the deep-water zone recorded the highest amount of both species (19) and individuals (18,372), whose bird communities showed lower similarity indices as compared to those in bare land, reed harvesting areas, calamus harvesting areas, and pond banks, while the shallow-water zone exhibited the highest species diversity index [73].

In this study, restoration measures were implemented in the wetland rehabilitation area of the conserved zone, and there are three types of solutions mainly including plant management (such as harvesting and removal of reeds and calamus), water level management (such as water replenishment, ditch dredging, and microtopographic shaping), and construction of a benthic food chain (such us supplementation of food resources for fish, crabs, and other migratory birds). Habitat suitability and availability are the critical factors limiting the distribution of waterbird habitats, as different waterbird species exhibit various requirements for water levels during feeding and nesting. Vegetation coverage also significantly influences waterbird habitat utilization and it is necessary to remove overly dense vegetation. The study revealed that reed wetlands after vegetation clearance became the preferred habitat for red-crowned cranes overwintering within the protected area. A total of 23,019 waterbirds were recorded during the wintering period, demonstrating that the restoration area provided suitable habitats and food resources for these birds [73].

Biodiversity conservation study is conducted on Xinbin Manchu Autonomous County, and there are mainly four problems threatening the diversity of bird community: The fragmentation of bird habitats in Xinbin Manchu Autonomous County has become increasingly degraded, and the problems are that extensive natural habitats such as forests and wetlands are divided into isolated patches reducing habitat connectivity, hindering population dispersal and limiting genetic communication among birds; Invasive species have emerged as a major threat to indigenous bird diversity, resulting

in both direct and indirect impacts through behaviors of competition, predation, and hybridization; Human activities continue to disrupt bird habitats in the local areas, including urban expansion, industrial development, and agricultural practices leading to habitat loss and fragmentation, which directly squeeze birds' living spaces; Global warming has significantly affected bird habitats, as rising temperature accelerates vegetation phenology, and alters birds' migration and breeding seasons, but food availability is limited during birds' new migration and breading period, thereby resulting in impacts on population reproduction [74].

To solve these problems, the comprehensive approach has been adopted by establishing ecological corridor networks, strengthening biological control against invasive species, reducing human activities' disruption, and enhancing habitat resilience, which enhances habitat conservation and restoration to create suitable ecological conditions for birds [74].

Identifying the distribution of potential habitats for endangered bird species' reproduction is crucial for developing effective conservation strategies. This study focused on the habitats of crested ibis (*Nipponia nippon*), which collected data from 125 nest sampling sites analyzed by nine environmental influence factors in Qinba Region, and the Maxent model was used to determine its potential reproduction distribution patterns and the key influencing factors. The results revealed that altitude, soil brightness index, slope gradient and soil greenness index were the primary environmental factors affecting breeding habitat distribution, contributing 38.1%, 18.3%, 16.4%, and 14.3% respectively to the model's results. The optimal altitude range for suitable breeding habitats ranged from 500 to 1200 meters, and the soil brightness index showed that breeding suitability decreased significantly with increased surface bareness. Breeding suitability exhibited a strong negative correlation with slope gradient. The soil greenness index indicated that breeding habitats in areas with moderate vegetation coverage resulted in the highest suitability, while its suitability declined in areas with low or high vegetation coverage [75].

Our results indicated that the area of suitable breeding habitats for the crested ibis within the study region covered 1,682.63 km², while the area of optimal breeding sites reached 432.96 km². Based on nesting density, the distribution area of suitable breeding habitats in the study region were sufficient to meet the natural expansion needs of the crested ibis population in the coming years. Reintroduction conservation of the Chinese crested ibis is also an effective approach to expand its wild population distribution and increase population size. However, without selecting appropriate habitats, reintroduced populations cannot establish long-term sustainable populations, ultimately leading to failure of reintroduction conservation efforts, so the results of this conservation study also plays the significant role in the habitat selection for reintroduction of wild crested ibis [75].

Gai et al., (2025)'s research project analyzed the bird species composition and habitat

distribution patterns in the Beijing Songshan Nature Reserve, providing theoretical foundation knowledge for bird conservation practice. Forest habitats hosted the highest amount of bird species (146 species), serving as the primary habitat type, followed by shrubland type (75 species), wetland type (60 species), residential area type (37 species), which primarily functioned as habitats for common songbirds such as the pika (*Pica serica*), great blackbird (*Corvus macrorhynchos*), and sparrow (*Passer montanus*), while bird species diversity was relatively low in bare rock habitat type and meadow habitats. The investigation revealed that 8 bird species were distributed across 4 or more habitat types, such as the Common Crow (*Corvus corone*) and Tree Lark (*Anthus hodgsoni*); 20 species were reported across 3 habitat types, such as sparrows, Yellow-bellied Lark (*Anthus rubescens*), and Yellow Wagtail (*Motacilla tschutschensis*); 86 species were identified in 2 habitat types, including Ring-necked Pheasant (*Phasianus colchicus*), Star-headed Woodpecker (*Dendrocopos canicapillus*), Great Tit, and Mountain Magpie (*Rhopophilus pekinensis*), whereas 94 species were found in only one habitat type, showing the limited ecological niche [76].

The species composition and population size of birds' community are significantly influenced by forest vegetation structure, and usually more complex forest structures provide better food resources and shelter conditions, thereby enhancing bird survival and reproduction. Within the same habitat area, the diversity of available food sources also determines bird species composition. In the study area, insectivorous and omnivorous birds constitute the majority (76.44%), whereas plant-eating birds are the exceptional (0.96%), which means that dietary resource diversity plays a prerequisite role in bird species diversity. Habitat diversity conservation is essential for supporting various ecological groups of birds, as the conserved area predominantly includes forest habitats, supplemented by shrublands, wetlands, residential areas, bare rocks, and grasslands, which collectively forms an integrated ecosystem for bird reproduction and survival. However, most bird habitats within the Reserve area exhibit narrow adaptability, with 180 species reported exclusively in only 1 or 2 habitat types. The destruction of any single habitat type results in immediate threats to birds. Therefore, prioritizing conservation of forest habitats, sufficient attention must be given to protecting other habitat types [76].

Table 5. Summary of ecological restoration measures for habitat conservation.

Case studies	Ecological restoration measures
Shiyang County in Jiangsu Province [72]	Three types of heterogeneous patches established for the restoration of bird habitat: the core patch was mainly consisted of Suaeda salsa beachlands, and the function was to provide habitats to black-headed gulls for foraging, resting and shelter; the stepping stones were muddy tidal flats, whose function served as feeding and resting sites for wading birds; the multifunctional corridors comprised tidal channels and ecological aquaculture areas, which ensured both ecological continuity and sustainable economic production.
Jiangsu Yancheng	Plant management (such as harvesting and removal of reeds and calamus),

Wetland Rare Birds National Nature Reserve[73]	water level management (such as water replenishment, ditch dredging, and microtopographic shaping), and construction of a benthic food chain (such us supplementation of food resources for fish, crabs, and other migratory birds)
Xinbin Manchu Autonomous County[74]	Establishing ecological corridor networks, strengthening biological control against invasive species, reducing human activities' disruption, and enhancing habitat resilience,
Qinba Region [75]	Identifying the distribution of optimal habitats for the natural expansion needs of the crested ibis population and for reintroduction of wild crested ibis
Beijing Songshan Nature Reserve [76]	Conservation of habitat diversity: prioritizing conservation of forest habitats, sufficient attention must be given to protecting other habitat types; Providing the diversity of available food sources.

3.2.6.Discussion of restoration ecology

As can be seen from the above case studies, the majority of ecological restoration cases have not paid attention to the spatial and structure composition of plantation species by analyzing the inter-specific associations. Consequently, the Table 4 and the correspondingly discussion must be more reasonable and applicable on the species selection methods for plantation restoration, especially for the conservation of genetic resources with specific environmental adaptation at specific environmental gradient.

It is noted that the biodiversity conservation value of forest has been evaluated into economic value measured by the currency, and this economic value must be realized through that the evaluated conservation value can be bought or sold as a kind of financial product in the carbon trading marketplace.

Norton (1998) pointed out that plantation practice between two natural indigenous remnants should maintain the mature tree stands, which could always connect two indigenous forests, so forestry farm could plant the trees with different and consecutive age stages in rotation way [65]. My article here tries to improve this forest farm design for both conservation and economic values according to the inter-specific association theory in Figure 2 (shown in the conclusion section below): there are three kinds of indigenous species selected to plant as the mature and consecutive indigenous pathway always connecting two natural forest remnants. These three kinds of indigenous species should be the competition species (negative correlation) against each other, so that each of them may represent each different kind of plant community to increase the biodiversity, and in total three types of plant communities may be classified by the classification methods discussed in this article. However, this matrix design of Figure 2 eliminates their competition chances, to achieve their common and better growth. Then economic plant species can be planted in a rotational way, adjacently to the mature and consecutive indigenous tree stands. Of course, the selection of economic plant species should give priority to the interdependent species (positive correlation) with adjacent indigenous species. This matrix design of plantation in forest farm is also applicable on other types of forest land (even without indigenous forest remnants) to achieve higher biodiversity.

As proposed in 3.1.4 section, “with further development of the ecological niche theory, the vegetation habitat which suits for endangered birds or mammal species can be limited and specific.” This viewpoint is supported by the case studies summarized in Table 5, which provide evidences such as “180 species was reported exclusively in only 1 or 2 habitat types” and “the soil greenness index indicated that breeding habitats in areas with moderate vegetation coverage resulted in the highest suitability, while its suitability declined in areas with low or high vegetation coverage.”

It is also argued in section 3.1.4. that “the conservation biology study should not only focus on the food chain theory of endangered species, but also take the competitiveness of endangered species into consideration when they are forced to move into other habitats.” My viewpoint is further supported by the summary of case studies in Table 5, which reveals that all the case studies focus on the available resources provided by the restored habitats, but ignores the competition species against the endangered birds when they are transferred to the new restored habitats, and these competition species may not the invasive species (they would be other indigenous species competing against the endangered birds), hence becoming the new research gap in the future biodiversity monitoring for habitat restoration.

4.Genetic Diversity

4.1.Representative theories in conservation genetics

Hardy Weinberg's equiliberum law, also known as the law of genetic balance, mainly refers to the theory that under ideal conditions, the frequency of each allele and the genotype frequency of each allele are stably unchanged in the inheritance of sexual reproduction process, which means that gene balance is maintained. This ideal state must be calculated under 5 conditions: the population is large enough; individuals in the population can mate randomly; no mutation occurred; no new genes have been added; there is no natural selection [43].

Genetic distance is defined to measure the genetic variation between two species or between two sub-populations of a species, so the shorter the genetic distance, the closer the common parental generations [51]. According to the genetic distance, the evolutionary significant unit can be classified, which is considered as a sub-population of genetic variety with significant conservation value [52]. Other criteria assessing genetic diversity are summarized in Table 6, and for fully illustrating the test methods of genetic diversity, two additional cases of genetic diversity study in human population have been also selected as complement.

4.2.Case studies

In order to analyze the genetic polymorphism of Fujian yellow rabbits, micro-satellite DNA labeling technology has been used to detect the genetic variation of 25 Fujian yellow rabbits at 15 loci detected by micro-satellite. The number of alleles (Na),

effective alleles (Ne), observed heterozygosity (Ho), expected heterozygosity (He), Shannon information index (I), and polymorphic information content (PIC) are statistically analyzed. The results have showed that a total of 97 Na are detected in 15 micro-satellite loci of Fujian yellow rabbits, with Ne being 3.7414 ± 1.6414, Ho of 0.2897 ± 0.1032, He being 0.6961 ± 0.1012, I of 1.4677 ± 0.3450, and PIC being 0.6585 ± 0.1103, respectively. Among them, 7 loci are deemed as Hardy Weinberg equilibrium state (P>0.05), including micro-satellite loci 6L2H3, 7L1B10, 7L1F1, Sat12, Sol30, Sol44, INRACCDDV0344, while the loci of 6L1F10, 12L1E11, 12L4A1, 12L5A6, Sat2, Sat5, Sol33 and INRACCDDV2016 are under the unequiliberum state of Hardy Weinberg state. This result may reflect that the stability of the genetic structure in the Fujian yellow rabbit population is being disrupted. Except for the moderate polymorphism at the loci of 12L1E11 and Sol44 detected by micro-satellite, the other 13 micro-satellite loci of Fujian yellow rabbits show high polymorphism, indicating that Fujian yellow rabbits exhibit rich genetic polymorphism at these 15 microsatellite loci [44].

The availability of multi loci haplotypes provides valuable tool for genetic analysis of disease susceptibility loci (DSL), whose mapping can be achieved by detecting Hardy Weinberg imbalance (HWD) at a single locus of DNA marker in the individuals infected by disease. This article extends the HWD test to perform haplotype association analysis on DSL by detecting multiple marker loci, and investigates the statistical power of the HWD test by comparing it with the commonly used x^2 statistics. The results have shown that the HWD test results in high efficacy and is more effective than the commonly used x^2 statistics [45].

In order to understand the variation in the genetic structure among three consecutive breeding generations of *Cyprinus carpio yuanxiang*, microsatellite molecular markers have been used to assess the level of genetic diversity, gaining the knowledge of genetic structure in the population. The results have shown that a total of 116 alleles are obtained from 15 microsatellite loci in 3 generations of population, with an average of 7.73 alleles per locus. The average number of alleles per generation decreases from 7.2667 to 5.0667, and the observed heterozygosity decreases from 0.7680 to 0.7585, while the polymorphic information content decreases from 0.7634 to 0.7451, indicating that the level of genetic diversity decreases from parental generations to offspring generation. The genetic distance between adjacent generations decreases from 0.0806 to 0.0449, and correspondingly the genetic similarity increases from 0.8464 to 0.8747, showing gradually increasing trend. The coefficient of genetic differentiation (F_{st}) between adjacent generations decreases from 0.0681 to 0.0230, reflecting the low level of genetic differentiation between generations. The declined trend in genetic variation reveals that artificial breeding has led to the significant impact on the genetic structure of the *Yuanjiang carp* breeding population [46].

The objective of this study is to assess the accuracy of second-generation sequencing

technology (NGS) in detecting the allele polymorphisms at loci HLA-DRB1, DQB1, DQA1, DRB3, DRB4, DRB5, DPA1, DPB1 of random Han population in Shenzhen, which is unrelated to health, exploring the reasons for HLA-DRB1 allele loss and strategies for establishing inner quality control systems. The Mi Seq DxTM NGS platform has been used to complete HLA-II allele typing on 1 012 samples. For the difficult samples prompted by the quality control system software, it is to confirm the HLA-DRB1 homozygous samples by using PCR-SSOP or PCR-SBT methods. Results have shown that in total 45, 7, 5, 7, 17, 21, 10 and 27 alleles are detected at loci HLA-DRB1, DRB3, DRB4, DRB5, DQA1, DQB1, DPA1 and DPB1, respectively. The frequencies of both HLA-DRB1 and DQB1 loci are statistically compared with the common and confirmed HLA allele table (CWD2.4) in China, but the difference between them is not statistically significant（χ^2=12.68, P>0.05). In total 94 samples of HLA-DRB1 homozygous detected by NGS are re-tested by using PCR-SSOP method, revealing that one HLA-DRB1 allele is missed, which is confirmed by SBT method to screen that the DRB1 * 04:03 allele is missed by NGS. The HLA typing results based on the NGS-HLA typing scheme have a lower rate of ambiguous results. It can be concluded that HLA-II alleles exhibit genetic polymorphism in the Han population of unrelated-healthy donors in Shenzhen, but the independent use of NGS method in clinical tissue compatibility trials displays limitations and requires internal quality control strategies to prevent occasional allele loss events [47].

Using 59 variety resources of apple plants in Shandong Province as test materials, genomic DNA has been extracted by using an improved CTAB method. In total 25 pairs of clearly and highly polymorphic primer combinations are selected from 240 pairs of SRAP primers which are randomly combined by 15 forward primers and 16 reverse primers for the experiment. According to the total number of amplified bands, the number of polymorphic bands, and the ratio of polymorphic bands for polymorphic primers are calculated on the basis of the electrophoresis gel plot. Then it is to calculate the polymorphic information content according to the Botstein formula, including the criteria of the observed allele number (Na), effective allele number (Ne), Nei's gene diversity index (H), and Shannon's information index (I), by using POPGENE32 software to conduct genetic diversity analysis. The cluster analysis is performed by using NTSYS-pc2.10e software that is based on UPGMA method to calculate genetic similarity coefficient. Using primer pair combination method, in total 59 digital fingerprint maps of Shandong apple genetic resources are constructed. A total of 176 bands have been detected, including 158 polymorphic bands, with the polymorphism rate of 89.77%. On average, each primer combination produces 7.04 bands which include 6.31 polymorphic bands. The average number of the observed alleles, effective alleles, Nei's gene diversity index, and Shannon's information index between samples are 1.8898, 1.4945, 0.2861, and 0.4302, respectively. The UPGMA clustering results show that the similarity coefficient among 59 samples ranges from 0.6540 to 0.9829, with an average of 0.7060. Using SRAP multiple primer combination method, 59 apple germplasm resources have been

effectively distinguished, with the fingerprint maps established at the confidence probability of 99.99%. Selecting the genetic similarity coefficient of 0.7010 for classification, 59 tested apple materials can be divided into three major groups. The first group is the wild resource Mount Taishan Begonia (*Malushupehensis var. taishanensis*), which is native to Shandong Province; The second group is dominated by the begonia (*M. micromalus*) and the catalpa (*M. prunifolia*), containing a small amount of small fruit type with red flowers; The third group is dominated by the apple (*M. domestica*) and the catalpa (*M. asiatica*), with fewer amount of the crabapple (*M. micromalus*) and catalpa (*M. prunifolia*). In comparison, when the genetic similarity coefficient is set as 0.7480, the second and third groups can be divided into several small groups, with apples (*M.domestica*) clustered together. Chinese soft apples (*M.domestica subsp. chinesis*) are clustered together with most of the red flower (*M.asiatica*), and most of *M. micromalus* and *M. prunifolia* are clustered together. The clustering results are generally consistent with the morphological classification standards [48].

This study has applied both DNA marker and karyotypes marker to provide the basis for the differentiation of genetic relationships, germplasm identification, and species evolution analysis of the genus *Bupleurum*. In total 75 *Chaihu* materials are collected and 29 ribosomal DNA second internal transcription spacer (ITS2) sequences are downloaded from the GeneBank database. After proofreading and splicing the obtained sequences using CodonCode Aligner software, MEGA X is used to analyze and compare the sequences, resulting in the genetic distances both within and between species. It is to construct a system of clustering tree by the adjacency method (NJ) and predict its ITS2 secondary structure through the ITS2 database website, which is further analyzed by using 4Sale1.7.1. It is to organize the karyotype data of 13 species of *Bupleurum* plants, performing cluster analysis of similarity coefficients and calculating genetic distance of karyotypes. It is found that the maximum intra-specific genetic distance of *Bupleurum chinense* is smaller than the minimum inter specific genetic distance. The NJ tree of *Bupleurum chinense* is grouped separately, displaying good monophyletic characteristics. It is concluded that the combination of ITS2 secondary structure and NJ tree can effectively identify *Bupleurum* plants and their counterfeits. When the similarity coefficient of karyotype approaches 0.7151, 13 species of *Bupleurum* plants can be clustered into 3 major groups. Among the 13 species of *Bupleurum* genus plants, *linear leaf Bupleurum* and *purple flower large leaf Bupleurum* have the highest similarity coefficient (0.9955) but the lowest evolutionary distance (0.0045), while *long white Bupleurum* and *conical leaf Bupleurum* have the lowest similarity coefficient (0.1476) but the highest evolutionary distance (1.9135) [49].

By selecting 12 isoenzyme loci of two enzyme systems, peroxidase (POD) and esterase (EST), the isoenzyme analysis is conducted on 10 populations of two wild *chrysanthemums,* as well as on the 40 *chrysanthemum* artificial varieties with different uses. The results have shown that there are abundant genetic diversity among

wild *chrysanthemums*, medicinal *chrysanthemums*, edible *chrysanthemums*, and ornamental *chrysanthemums*, with ornamental chrysanthemums showing the highest genetic diversity. The effective allele number, proportion of polymorphic loci, expected heterozygosity, and Shannon index across all the materials are 1.654 4, 91.67%, 0.372 1, and 0.525 7, respectively. Compared with the artificial varieties, the wild chrysanthemum populations have the lowest genetic diversity, with the above four indicators of 1.389%, 50.00%, 0.228%, and 0.316%, respectively. The results of UPGMA clustering map based on genetic distance show that the evolutionary order of *chrysanthemums* is: wild *chrysanthemums* → medicinal *chrysanthemums* → edible *chrysanthemums* → ornamental *chrysanthemums*. Among them, the edible *chrysanthemum* varieties of both ‘Baoxin Tangyi Jin' and 'Jingxing Xiying' have specific E-bands of isoenzyme spectrum POD-2, while the ornamental *chrysanthemum* varieties of 'Green Water and Green Mountains' and 'Mulan Replacement' have specific O-bands of isoenzyme spectrum EST-6, which can provide evidences for variety identification and protection at the biochemical level[50].

Table 6. Summary of bio-markers and criteria in the assessment of genetic diversity.

Population of Species	Bio-Markers	Criteria in Genetic Diversity	Applications
Fujian yellow rabbits[44]	Micro-satellite DNA labeling technology	Number of alleles (Na), effective alleles (Ne), observed heterozygosity (Ho), expected heterozygosity (He), Shannon information index (I), and polymorphic information content (PIC); Hardy Weinberg state	to analyze the genetic polymorphism
Human population[45]	DNA marker	Hardy Weinberg imbalance (HWD)	genetic analysis of disease susceptibility loci (DSL)
Cyprinus carpio yuanxiang[46]	Microsatellite molecular markers	The average number of alleles; the observed heterozygosity; the polymorphic information content;the genetic distance; the genetic similarity; the coefficient of genetic differentiation (Fst)	to understand the variation in the genetic structure among three consecutive breeding generations
Han population	Second generation	The allele polymorphisms	to assess the

in Shenzhen [47]	sequencing technology (NGS); PCR-SSOP method		accuracy of second-generation sequencing technology (NGS)
59 variety resources of apple plants in Shandong Province [48]	Genomic DNA marker by using an improved CTAB method	The polymorphic information content according to the Botstein formula; The observed allele number (Na); effective allele number (Ne); Nei's gene diversity index (H); Shannon's information index (I); the polymorphism rate	Classification and identification of apple varieties in market.
Bupleurum [49]	Both DNA marker and karyotypes marker	The genetic distance; the similarity coefficient of karyotype	To identify *Bupleurum* plants and their counterfeits
Chrysanthemum [50]	The biochemistry marker: isoenzyme analysis	The effective allele number, proportion of polymorphic loci, expected heterozygosity, and Shannon index	Variety identification and protection at the biochemical level

4.3.Discussion

According to the population genetics theory [52], a sub-population of a plant species may tend to be homozygous or purity in genetic variation in a specific habitat measured by environmental gradient due to the intra-specific competition that the individuals with AA alleles expressed as stronger environmental adaptiveness in this specific habitat will suppress the individuals with Aa or aa alleles, in which A is the dominant gene and a is the recessive gene. Eventually, the individuals with AA alleles will survive instead of individuals with Aa or aa alleles, so the population's genetic variation tends to be homozygous. My article further proposes that this homozygous state or the purity in genetic variation is the stabilized or 'balanced' genetic state of a sub-population in the reproduction process. Once this sub-population is distinguished from other sub-populations by the genetic distance method, this stable and homozygous sub-population would be considered as the evolutionary significant unit. When the environmental conditions change in the long-term, this evolutionary significant unit may be replaced by other succession species. Consequently, my article theory takes the advantages of 'balanced state' in the Hardy Weinberg's equiliberum law, but it is caused by natural selections which disagrees with Hardy Weinberg's

equiliberum law. However, to achieve the ‘balanced state’ under which the alleles are stably unchanged in the inheritance of sexual reproduction process, two of pre-conditions suiting for Hardy Weinberg's equiliberum law are still applicable on my proposed theory: gene mutation seldom occurs; there is no gene communication with other sub-populations of a species due to the geographic separation among different sub-populations.

For the genetic breeding in selection of conservation variety, my biochemistry article has proposed that it is to select genetic variety according to the morphological markers in a specific habitat measured by environmental gradient firstly, and the major morphological markers include the yield components; then the metabolomics test is conducted to assess the biochemistry diversity that indicates the environmental adaptiveness in this specific habitat, based on the design of Matrix Xsum [53][58]; finally the combination design of both karyotypes marker and DNA sequence marker is advised in my another article [54].

To identify and classify the tree varieties growing in natural ecosystem on the basis of morphological markers (differed from the identification of varieties in experiment land), the morphological markers representing qualitative nature is selected, which is less subject to environmental condition variation in natural ecosystem. Differed from the shrubs and grass species, the yield components of tree species are chosen as: the amount of secondary branches divided from the main stem; the mean amount of tertiary branches divided from each secondary branch; the mean amount of fourth branches divided from each tertiary branch; the mean amount of flowers yielded by each fourth branch; the total amount of flowers yielded by an individual tree = the amount of secondary branches divided from the main stem × the mean amount of tertiary branches divided from each secondary branch × the mean amount of fourth branches divided from each tertiary branch × the mean amount of flowers yielded by each fourth branch. These morphological criteria of yield components would well represent the qualitative characters of tree varieties, which are consequently used for Principal Component Analysis (PCA) to identify and classify the tree varieties in wild and natural ecosystem. The amount of seeds/fruits is not selected in the yield components by my article, because the seeds/fruits yielded by each tree is easily influenced by the environmental conditions in wild ecosystem. For example, some flowers may become infertile when the tree faces environmental stress, but the amount of flowers should be relatively stable under stress conditions, which is consequently chosen as the genetic markers at morphological level. The conceptional graph of this classification method based on the new morphological markers is illustrated in Figure 1.

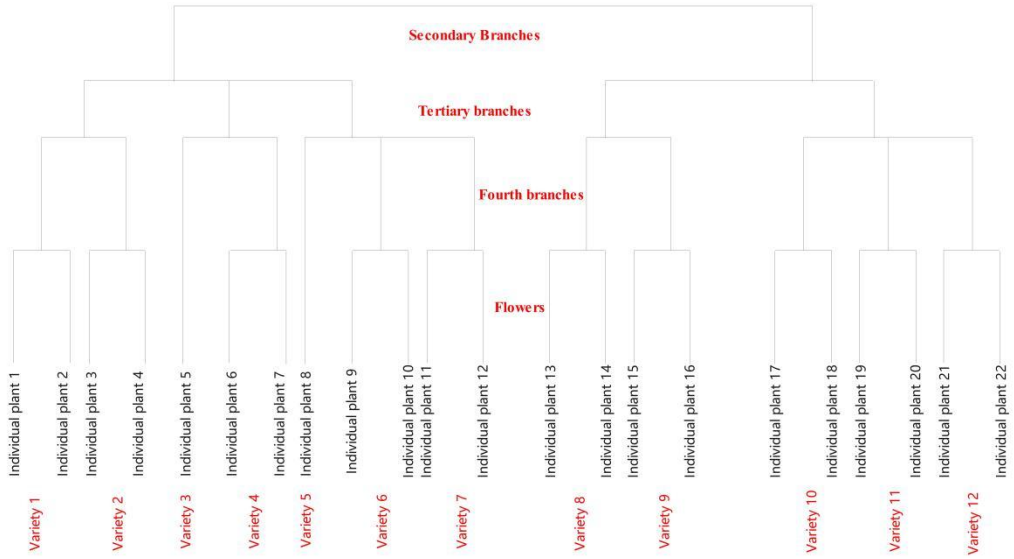

Figure 1. The classification of genetic varieties among different wild individuals in a tree species by using new morphological markers.

As can been seen from Figure 1, the classification of genetic varieties among different wild individuals is conducted in theory: the individuals are firstly classified according to different amount of secondary branches; for the individuals with the same amount of secondary branches, they are then classified according to the different amount of tertiary branches; for the individuals with the same amount of tertiary branches, they are further classified according to the different amount of fourth branches; for the individuals with the same amount of fourth branches, they are finally classified according to the different amount of flowers. However, when PCA method is conducted, the above criteria will be ranked according to the importance of each criterion in statistics, so Figure 1 is the conceptional graph only to illustrate the theory underlying the morphological markers.

It is to critically discuss the bio-informatics with regards to the classification of genetic variation by using three types of classification methods: the conceptional graph (Figure 1), PCA and multivariate cluster analysis. According to the assumed data (not list) of tree morphology for the purpose of statistic test only, classification of genetic variation is conducted by using SPSS software on the basis of both PCA and multivariate cluster analysis, compared with the conceptional graph (Figure 1), and it is found that inconsistency does happen among these three types of classification methods. Hence it is to critically discuss the bio-informatics next: Principal Component Analysis (PCA) is a statistical method to reduce the dimensions of high-dimensional variables with correlations through linear transformation, and its key philosophy is to retain the main information of variance but eliminate the correlation between variables; Multivariate cluster analysis is to classify the samples or variables according to the similarity (distance) index, aiming to maximize the

homogeneity of elements in the same category but maximize the heterogeneity of elements between categories. However, each statistics method is implemented with limitations in practice and requires expertise to interpret the statistical results and sometimes to correct the statistics bias [63].

Over the whole development stages of a tree individual, the adolescent tree individual should partition its secondary branches firstly, and then starts to partition its tertiary branches....., so the morphological markers proposed in Figure 1 reflect the time sequences of plant development. However, both PCA and multivariate cluster analysis do not take this time-sequence factor into consideration: when both statistics methods are implemented, each criterion of morphological markers is treated in parallel, which may lead to significant statistics bias, compared with the real stages of plant development.

Further more, it is argued that the classification of gene variation based on the DNA sequence marker by using the past bio-informatics methods also contains similar deficiency: the gene sequences used as bio-markers are NOT functioned in parallel, but are expressed with strict time sequences among these gene sequences' expression process, which means that one of these gene sequences must be expressed firstly before other gene sequences express. In statistics, one of the variables is definitely the determinant of other variables, but this time-sequence relation can not be simply indicated by the significance ranking, similarity or correlation calculation in bio-informatics, which should be corrected manually due to the inconsistency with the final phenotype. My another article has designed the new classification methods that the morphological markers of the whole genome molecule should be chosen firstly, and then based on the morphological marker classification, the gene sequence markers are chosen to further classify [54]. This design philosophy would also reflect the time-sequence of gene expression in cell development, to eliminate the deficiency of bio-informatics methods.

Additionally, the inter-dependent compensation mechanism is discussed among plant yield components by my article [53], so it is expected that negative correlation will be revealed among these morphological markers by the PCA method. Due to this intrinsic negative correlation among different variable, multivariate cluster analysis that is based on the similarity index may be less applicable than PCA method.

It is to clarify the conception between gene and DNA sequences by this article: my another article argues that "DNA sequencing technology does not reflect the spatial arrangement and combination information of various sequences on the genome, but the spatial arrangement and combination information of different DNA sequences in the genomes is the main contribution factor of genetic variation, because most of the gene sequences revealed by DNA primers are highly conserved sequence fragments in the evolutionary process [64]." Consequently, my article here re-defines the gene as the broader conception than DNA sequences: a gene expressed as a specific trait,

which is defined by the classical genetics theory, would be controlled by a combination of multiple DNA sequences that are located at different and non-consecutive physical positions on genome molecule, which need to be revealed by multiple different DNA loci (or DNA primers). Based on the new definition of gene, my article argues that the PCR bands detected in above case studies of this section can NOT be used to indicate the alleles, so the 'allele' interpretation is not appropriate in above genetic diversity studies. The PCR bands' mapping only reveals the genetic distance among different DNA sequences, and cannot properly reveal a specific gene defined by the classical genetics theory.

Based on this broader definition of gene, my article proposes that gene recombination does not limit to diploid sporophyte in the sexual reproduction process, but also applies on the microbes in the self-reproduction process. For example, virus may alter the spatial arrangement and combination information of existing DNA sequences (gene recombination) to adapt the changing environment in its self-reproduction process, rather than directly altering the existing DNA sequences by gene mutation. Gene mutation may be considered to be harder than gene recombination, which requires more generations' self-reproduction to occur. Consequently, the effectiveness of DNA sequencing technology may be limited in analyzing the genetic variation of a virus species in its self-reproduction process.

Although there are various DNA marker methods used to test the gene diversity, Simple Sequence Repeats (SSR) marker (also named as Microsatellite) has been implemented as Chinese National Standard such as GB/T 39917-2021 (Variety genuineness and purity testing of main crops with SSR markers—Rice), so this SSR marker technology is the only marker technology selected in my article for biodiversity conservation practice. Based on the hypothesis that the repetitive DNA sequences initiated by DNA primers are highly conserved in the evolutionary process, the genetic variation in the reproduction process is contributed by two sources: exotic source and inner source, which is classified in Table 7 below, and the theoretical discussion on this classification is further given in detail by my another article [64].

Table 7. Classification of the contribution sources for genetic variation (genetic diversity).

	Contribution sources of genetic variation	**Microbes (self-reproduction)**	**Diploid sporophyte (sexual reproduction)**	**Detectable sensitivity by DNA sequencing Technology**
Exotic sources	Gene communication between individuals in the sexual	No	Yes	Detectable

	reproduction			
	Inserting a fragment of exotic DNA sequences from host cells	Yes	No	Detectable
Inner sources	Gene recombination within the gene pool of an individual	Yes	Yes	Less Detectable
	Gene mutation on the genome molecule	Yes	Yes	Detectable

For the ‘gene recombination within the gene pool of an individual’, it means that the recombination of spatial arrangement and combination information occurs among different fragments of highly conserved DNA sequences, which are initiated by DNA primers using DNA sequencing technology, but within a fragment of highly conserved DNA sequences, the DNA sequences usually remain unchanged due to its highly conserved nature, unless it is altered by gene communication, gene mutation, or by inserting a fragment of exotic DNA sequences from host cells (such as “acquisition of human gene segments for self-modification of virus genome”[66]).

The highly conserved DNA sequence regions usually express as the essential life functions [67], and thus is chosen as Simple Sequence Repeats (SSR) marker. In comparison, the binding regions (or binding loci) between different regions of highly conserved DNA sequences would contain more active DNA sequences that are easily modified. It is deduced that these active DNA sequences in the binding regions are less detectable by DNA sequencing technology, which can be attributed to two reasons: firstly, the active DNA sequences in the binding regions are not the repetitive sequences so that they can be hardly initiated by DNA primers; secondly, the molecular weight of these active DNA loci is too tiny to be detected by the common equipment accuracy. It is further concluded that gene mutation is more likely to occur in the active binding loci, and DNA sequencing technology would be less effective in detecting this type of gene mutation, so structural biology methods would be chosen instead [20]. However, if the gene mutation occurs on the highly conserved DNA sequence regions, although this probability is much less than the active binding loci, DNA sequencing technology may turn to be more effective again. The above discussion may explain the inaccuracy in cancer cell diagnosing practice.

5.Urban Biodiversity and Human Health

5.1.Airborne pathogens

Bioaerosols are the particles of biological sources suspended in gaseous media, mainly including bacteria, fungi, viruses, and their metabolites such as endotoxins, glucans, allergens, mycotoxins, etc. The diameter range of bioaerosols particles is measured between 0.001 and 100 μm [59]. The various sampling methods of bioaerosols are chosen for comparison and contrast in the updated review study [60]. There are some representative case studies with regards to the research on the atmospheric microorganisms selected in my article below for study purpose:

Real-time fluorescence and quantitative PCR technology in combination with meta-genomic sequencing technology have been used to study the abundance of bacteria and fungi, as well as the composition characteristics of both bacterial and viral communities in the atmospheric environment of Xiamen City, and then it is to analyze the main factors including meteorological conditions, different seasons, regional and urban functional area distribution, which affect the abundance and community structure of air microorganisms. The results have found that the virus community structure in air microorganisms is easily influenced by seasonal changes, with significantly seasonal and regional differences (Adonis, $P<0.05$), but there is no difference in virus community structures among different urban functional areas. Temperature, relative humidity, and PM2.5 are the main environmental factors affecting the structure of virus communities in the air of Xiamen City [55].

Using Andersen's six level impact sampling method, 76 indoor air samples from different areas of two comprehensive hospitals have been collected and monitored for air microorganisms, and relevant air indicators (temperature, relative humidity, PM10, PM2.5, CO, CO2) are concurrently tested on site. Research has found that the common influencing factors of indoor air microbial concentration include seasonal change, temperature, relative humidity, CO2, PM10, and PM2.5 [56].

Based on traditional culture separation methods and 16S rDNA molecular biology techniques, in combination with relevant parameters in the Chinese Population Exposure Parameters Handbook (Adult Volume), the impact of population aggregation behavior on air microbial composition has been revealed. The results show that in comparison to the crowd non-gathered, the level of microbial air pollution in both locations changes from clean level to moderately polluted level during the crowd gathering. The separation and cultivation data have shown that when the population are gathered, the number of bacterial species in the air increased by 11 compared with the crowd non-gathered, and the number of fungal species increases by 5 species. In addition, there is changes in the color, morphology, humidity, physiological and biochemical characteristics of microbial colonies, while the number of pathogenic microorganisms has increased from 2 species to 9 species, among which 5 species of pathogenic microorganisms have reached BSL-2 level of high biological risk, classified into zoonotic pathogens [57].

Table 8. Summary of experiment and analysis methods chosen by above case studies.

Case study	Experiment method	Analysis method	Environmental influencing factors
[55]	Real-time fluorescence and quantitative PCR technology, based on 16S rRNA and ITS sequences	Box-plot of total atmospheric microbe abundance; α-biodiversity index; Richness index (Chao1 index); Evenness index (Pielou index); Diversity index (Shannon index); Bray-Curtis distance analysis (β-biodiversity index)	Spearman correlation with $PM_{2.5}$, PM_{10}, O_3, CO, NO_2, SO_2, WS(wind speed), T(Temperature), and RH(relative humidity);different seasons; regional and urban functional area distribution
[56]	SKC QT-30 microbial sampler; National standard for microbial monitoring: GB/T 18204.6-2013	Total atmospheric microbe abundance	Spearman correlation with $PM_{2.5}$, PM_{10}, O_3, CO, CO_2, T(Temperature), and RH (relative humidity) in both summer and winter seasons
[57]	National standard for microbial monitoring: GB/T 18204.6-2013; Observation of microbial morphology; Gram's stain; Physiological chemistry experiment, including Catalase Test, Starch Hydrolysis Test, Gelatin Liquefaction Test, Sugar Fermentation Test; 16S rDNA sequencing Tech, based on primers 27F and 1492R, ITS1 and ITS4	OLMERIANSKY equation for calculating the average microbe abundance; Comparison with NCBI database to analyze the risk level of pathogen	The impact of population aggregation behavior on air microbial composition

5.2.Discussion of research gaps in future

Urban plantation species diversity can effectively reduce the atmospheric particles, which have been frequently reported by case studies [61][62], so the effects of urban plantation diversity on epidemic disease reduction is to control the airborne bioaerosols. Especially, results of Liao Mingyu's case study reports that the

atmospheric abundance of both bacteria and fungi community is significantly positively correlated with $PM_{2.5}$, but shows insignificant correlation with PM_{10}, and the atmospheric abundance of virus community is also significantly correlated with $PM_{2.5}$ only [55]. These results support my argument proposed at the beginning of this article: the pathogens adhere to the fine aerosols ($PM_{2.5}$) which are capable of transporting in the very long distance (such as inter-continent transportation scale of fine particles [77]), so that fine aerosols would facilitate the epidemic disease infection across large regional scales, rather than limiting to local scale.

It is concluded here that there are three main reasons to explain the epidemic disease like COVID-19 virus becomes so infectious in global scale: firstly, the pathogens adhere to the fine aerosols ($PM_{2.5}$) are capable of transporting at inter-continent scale; then the virus turns to be long-time dormant after adhering to aerosols; and "the dormant nature of virus would enhance the vitality of pathogen so that pathogen increases its pathogenicity [3]."

The biodiversity research methods for atmospheric microbial community have been summarized in Table 8. As can be seen from Table 8, although there are many studies conducting research on the airborne pathogens communities in the past, there is little knowledge in the inter-species interaction among these airborne pathogen communities, and especially it lacks of knowledge in which local microorganism species can compete with exotic epidemic pathogens like COVID-19 virus, which consequently needs further study according to the inter-specific association method discussed in the species diversity part of this article. It is hypothesized that more abundant diversity of local competitive microorganism species will reduce the risks in breaking out epidemic exotic pathogens, which would be influenced by urban plantation species, becoming the effects on epidemic disease control.

Additionally, my another article designs the new method of measuring the pathogen's abundance, which is based on the unique gene sequences for a specific species of pathogen and the FISH probes [9], and this new design may improve to count the concentration of a specific pathogen species in the atmospheric environment, compared with DNA sequencing Tech.

6.Ecological Modeling Project

6.1. Modeling of Net Primary Production (NPP)

6.1.1.Design Philosophy

My another article has designed a numerical model of Net Primary Production (NPP) by using Vensim Software [7]. For the improvement of the previous model, this article adopts the C++ language to edit this numerical model, contributing to the source codes, and adds the factor indicating the 'food' of vegetation, CO_2 concentration in atmosphere, to the modeling of NPP.

Firstly, it is to input the amount of plant species (variable n) in the model, and to set up the variable of Percentage for each species, which is the proportion of canopy coverage area for each species to the total plant canopy coverage area (in total 'n' amount of Percentage values).

Secondly, it is to set up the variable of Light Utilization (LU) by vegetation, and Daily Radiation (DR) is the source of Light Utilization (LU). However, not all the Daily Radiation (DR) can be utilized by vegetation creatures, so there are two limitation factors for this: when the Daily Radiation (DR) exceeds the Light Saturation Point (LSP), the excessive radiation can not be utilized again, so Valid Daily Radiation (VDR) is added in this program as: if the Daily Radiation (DR) exceeds the Light Saturation Point (LSP), the Valid Daily Radiation (VDR) is equal to Light Saturation Point (LSP), and otherwise the Valid Daily Radiation (VDR) is equal to the Daily Radiation (DR); Secondly, not all the frequencies of light wave can be utilized by vegetation, so the Ratio of Photosynthetic Active Radiation (RPAR) to the total Daily Radiation (DR) is set up for model.

Based on the satellite data, the radiation of sunlight wave absorbed by vegetation is also determined by the vegetation coverage area, so the daily Fraction of Photosynthetic Active Radiation Absorbed by plants (FPARA) is defined by this model to reflect the fraction of absorbed radiation by canopy coverage area to the total Photosynthetic Active Radiation. FPARA data can be available from Earth Resources Observation System Data Center (EROS).

Then the total Absorbed Photosynthetic Active Radiation (APAR) by plant is Valid Daily Radiation (VDR) × Ratio of Photosynthetic Active Radiation (RPAR) × Fraction of Photosynthetic Active Radiation Absorbed by plants (FPARA).

Next it is to input the Water Balance (WB) factor as a sub-model: WB = (a×Precipitation)÷(s×TDR/(s+r)), in which the variable of Precipitation is the total precipitation amount over a quarter (90 days), and TDR is the total Daily Radiation (DR) in this period. Parameters of a, s, r represent the empirical coefficient, the slope of the curve relating saturation water vapor pressure to temperature, and the psychrometric constant, respectively [7][68]. If Water Balance (WB) is more than 1, the Water Limitation Factor (WLF) is equal to 1; if Water Balance (WB) is no more than 1, the Water Limitation Factor (WLF) is equal to Water Balance (WB). Then Water Limitation Factor (WLF) will be incorporated into the final calculation of NPP, indicating the water supply effects on vegetation growth.

The variable of Light Utilization Efficiency for each species (LUEn) is calculated as: LUEn = y0 + a0 × exp(-0.5×(ln(E/x0)/b0)^2), where variable E indicates the atmospheric transmissivity (E), and parameters of y0, a0, x0, b0 are the empirical coefficients for each species estimated on the basis of field investigation data. Then the overall Light Utilization Efficiency (LUE) is the sum of LUEn × Percentage (in

total n values) for each species.

The atmospheric transmissivity (E) is utilized to indicate the proportion of irradiance reaching the top surface of vegetation canopy to the total radiation, which excludes the amount of radiation that is absorbed and scattered by the clouds and atmospheric turbidity [69]. However, my another article has proposed more specific explanation in addition to the above definition as: "The theory of atmospheric transmissivity effects on the LUE would be that atmospheric transmissivity is the indicator of the proportional utilizable radiation waves received by canopy, and other part of light waves absorbed by atmospheric gases or reflected outside the atmosphere of this planet mainly contain non-utilizable radiation waves by most vegetation species (such as UV-B and Infrared) [4]". My previous model adopts the estimation method of atmospheric transmissivity (E), based on the variable of the difference between daily maximum and minimum temperature [7][69]. However, in order to reflect the effects of atmospheric CO_2 concentration (plants' food) on NPP, this article chooses another calculation method of atmospheric transmissivity (E) proposed by Drayson (1966) [70] instead: Ev = exp (-Kv×m), where Ev is the atmospheric transmissivity at a single frequency v; m is the optical mass at pressure p; Kv is the absorption coefficient at a single frequency v. Parameters of both Kv and m can be estimated according to the interpretation of CO_2 bands data measured by satellite radiometer, with detailed calculation steps discussed by Drayson (1966) [70]. To simply the modeling process, the variable of Ev under different atmospheric pressures is calculated as: Ev = exp [-$\sum_1^P (\mathrm{Kv}\times\mathrm{m})$], where 1, 2, 3, ...P are the amount of slabs for the pressures of the boundaries (in the equation 14 of Drayson (1966) article). The final atmospheric transmissivity (E) is then calculated, based on the mean value of each Ev, and in total V amount of frequencies are given (in Drayson (1966) case study, CO_2 bands range between 12 u and 18 u).

To fit the Precipitation variable, the time scale of this model is set as 1 day (90 days in total), and the spatial scale of this model is set to hectare (ha.) for the regional scale level.

Finally the Net Primary Production (NPP) is calculated as: NPP = APAR × LUE × WLF, where APAR is the the total Absorbed Photosynthetic Active Radiation (APAR) by plant; LUE is the Light Utilization Efficiency; and WLF is the Water Limitation Factor. It is to output the final NPP in the model.

6.1.2.Data Availability

Meteorological data of precipitation and daily radiation can be obtained from the meteorological stations in each local area; The data for atmospheric transmissivity (E) calculation can be obtained from the satellite radiometer specifically for CO_2 bands, and the calculation methods is demonstrated in detail by Drayson (1966) [70]; The daily Fraction of Photosynthetic Active Radiation Absorbed by plants (FPARA) can

be available from the Earth Resources Observation System Data Center (EROS); The Ratio of Photosynthetic Active Radiation (RPAR) to the total Daily Radiation (DR) is published by articles such as an estimation of 0.45 by my previous article [7]; Light Saturation Point (LSP) for each common species may be available from published articles; Parameters of y0, a0, x0, b0 have to be estimated on the basis of site-specific field sampling data, such as article [71]; Parameters of a, s, r can be available from the published articles like paper [68].

6.1.3.Discussion

Compared with my previous model, this article adopts another method of atmospheric transmissivity (E) calculation that is based on the satellite radiometer data specifically for atmospheric CO_2 concentrations, reflecting the 'food' of plant, which may improve the accuracy in both Tech and theory understanding for the numerical modeling. However, the natural disaster factors (such as strong wind or flooding) of limiting plant growth have not been incorporated into this model, which would be easily added as a limitation factor, like the Water Limitation Factor (WLF) variable of this model.

For the parameterization (determination of parameters), there are always "the economic trade off between the field-specific parameter determined by field sampling and estimation only of parameters", as pointed out by my previous modeling article [7]. However, if the above parameters are estimated according to the similar data that have been published in the past for the purpose of cost-saving, validation of modeling must be implemented by comparing the final modeling result of NPP with field investigation or other models' results. For the estimated parameters, sensitivity analysis must be taken to analyze the risks in each parameter estimation, as my previous modeling article has argued that "the more sensitive for the model parameters, the higher inaccuracy of modeling results, because all the parameters are estimated according to the empirical data, if the parameter is very sensitive, a tiny inaccuracy in parameter estimation will lead to a big error in final results" [7].

6.1.4.Source Code (Dev-C++ 6.5 Version)

// @All rights reserved by Liu Huan. Source from: https://doi.org/10.58473/JEHS0012

```
#include <iostream>
#include <cmath>
#include <vector>
using namespace std;

int main() {
    // Definition of Variables;
    double NPP, APAR, LUE, WLF, FPARA, LU, RPAR;
    vector<double> DR(90), FPARA_daily(90), VDR(90);
```

```
double TDR, WB, Precipitation, E, Ev, Kv, LSP;
double a, s, r;
int V, P, n;

cout << "=== Calculator of NPP for multiple plant species ===" << endl;

// To input the species amount;
cout << "Please input the species amount n (integer): ";
cin >> n;

// To input the water balance parameters;
cout << "Please input the parameter a: ";
cin >> a;
cout << "Please input the parameter s: ";
cin >> s;
cout << "Please input the parameter r: ";
cin >> r;

// To input the LSP, V, P;
cout << "Please input the parameter LSP: ";
cin >> LSP;
cout << "Please input the parameter V (integer): ";
cin >> V;
cout << "Please input the parameter P (integer): ";
cin >> P;

// To input the RPAR, Precipitation;
cout << "Please input the parameter RPAR: ";
cin >> RPAR;
cout << "Please input the parameter Precipitation: ";
cin >> Precipitation;

// To input the variable of Percentage;
vector<double> Percentage(n);
cout << "\n Please intut " << n << " species' Percentage:" << endl;
for(int i = 0; i < n; i++) {
        cout << "Percentage[" << (i+1) << "]: ";
        cin >> Percentage[i];
}

// To input the 90 days' DR;
cout << "\n Please input 90 days' DR: " << endl;
for(int i = 0; i < 90; i++) {
        cout << "The" <<" "<<(i+1) <<" "<< "day's DR: ";
```

```
        cin >> DR[i];
}

// To input the 90 days' FPARA;
cout << "\n Please input 90 days' FPARA: " << endl;
for(int i = 0; i < 90; i++) {
        cout << "The" <<" "<< (i+1) <<" "<< "day's FPARA: ";
        cin >> FPARA_daily[i];
}

// To input m value under P types of different pressure;
vector<double> m_values(P);
cout << "\n Please input " << P << " amount of m value:" << endl;
for(int i = 0; i < P; i++) {
        cout << "m[" << (i+1) << "]: ";
        cin >> m_values[i];
}

// To calculate the final m that is the sum of m values (in total P amount);
double m = 0;
for(int i = 0; i < P; i++) {
        m += m_values[i];
}

// To input Kv value under V types of different frequencies;
vector<double> Kv_values(V);
vector<double> Ev_values(V);
cout << "\n Please input " << V << " amount of Kv values: " << endl;
for(int i = 0; i < V; i++) {
        cout << "Kv[" << (i+1) << "]: ";
        cin >> Kv_values[i];
}

// To calculate VDR;
for(int i = 0; i < 90; i++) {
        if(DR[i] > LSP) {
                VDR[i] = LSP;
        } else {
                VDR[i] = DR[i];
        }
}

// To calculate LU;
LU = 0;
```

```
        for(int i = 0; i < 90; i++) {
            LU += VDR[i] * FPARA_daily[i];
        }

        // To calculate TDR;
        TDR = 0;
        for(int i = 0; i < 90; i++) {
            TDR += DR[i];
        }

        // To calculate WB and WLF;
        WB = (a * Precipitation) / (s * TDR / (s + r));
        if(WB > 1) {
            WLF = 1;
        } else {
            WLF = WB;
        }

        // To calculate Ev and E;
        double Ev_sum = 0;
        for(int i = 0; i < V; i++) {
            Kv = Kv_values[i];
            Ev_values[i] = exp(-Kv * m);
            Ev_sum += Ev_values[i];
        }

        E = Ev_sum / V;

        // To calculate LUEn and LUE;
        vector<double> LUEn(n);
        LUE = 0;
        for(int i = 0; i < n; i++) {
            // To input the LUE parameters for each species;
            cout << "\n Please input the " << (i+1) << " species' LUE parameters: " <<
endl;
        double y0, a0, x0, b0;
        cout << "y0[" << (i+1) << "]: ";
        cin >> y0;
        cout << "a0[" << (i+1) << "]: ";
        cin >> a0;
        cout << "x0[" << (i+1) << "]: ";
        cin >> x0;
        cout << "b0[" << (i+1) << "]: ";
        cin >> b0;
```

```
        double ln_value = log(E / x0) / b0;
        LUEn[i] = y0 + a0 * exp(-0.5 * pow(ln_value, 2));
        LUE += LUEn[i] * Percentage[i];
        }

        // To calculate APAR and NPP;
        APAR = LU * RPAR;
        NPP = APAR * LUE * WLF;

        cout << "\n=== final results ===" << endl;
        cout << "Net Primary Production (NPP): " << NPP << endl;

        return 0;
}
```

6.2. Modeling of Plant Community Succession and Molecular Evolution

6.2.1. Design Philosophy

In section 2.1.2 of this article, my research adopts the sampling method that "tree species with the point label is also recorded, and in total there are nine trees identified in each point, including the centre tree, the four nearest, and the four next nearest." This sampling method divides the sampled trees into center samples and adjacent samples. Based on the Bray-Curtis Dissimilarity index that quantitatively analyzes the species' frequency-size relationship, the plant communities are classified and the corresponding succession between these communities are speculated. To reveal the species' frequency-size relationship, the species importance is calculated as: relative importance Xij = (relative abundance + relative frequency + relative size)/3, and the Bray-Curtis Dissimilarity index is calculated as:

$$\text{Bray-Curtis Dissimilarity index} = (\sum |Xij - Xik|)/\sum (Xij + Xik)$$

Where variables of Xij and Xik represents the relative importance of species 'i' in the sample plot 'j' and sample plot 'k', respectively.

To calculate the Bray-Curtis Dissimilarity index, the input variables of this ecological modeling include relative abundance (a[i][j][k]), relative frequency (b[i][j][k]) and relative size (c[i][j][k]). Using this 3-Dimensional array, each plant individual's coordinates is labeled in this model, and variables of 'i', 'j', 'k' indicate the 3D coordinates (longitude, latitude, and altitude respectively) of each individual. Then it is to input the species' identifier number (each plant species is given an identifier number) and sampling plot number by using this 3D array for each plant individual in each 3D coordinate point.

Because the sampling method of my research divides the sampled plants into center

samples (including the centre tree and the four nearest) and adjacent samples (the four next nearest), it is to compare these two sample plots (for example, sample plot 1 is the center sample plot and sample plot 2 is the adjacent sample plot): if the Bray-Curtis Dissimilarity index is more than D level between sample plot 1 and sample plot 2; and the dominant species between two sample plots shows negative correlation (less than -E level); and the relative importance of sample plot 1 is higher than it in sample plot 2 (or sample plot 2's relative importance is higher than sample plot 1), then the trees in sample plot 1 will invade the trees' survival space in sample plot 2 (or the trees in sample plot 2 will invade the trees' survival space in sample plot 1). Otherwise the trees in both sample plots stay in the stable state. This modeling design reflect the philosophy proposed in the section 2.1.2 of this article: "if the adjacent species is different from the centre tree, and the adjacent species frequency is higher or the stand size is bigger, the adjacent species are more likely to become the succession ones (or dominant species) instead of the centre tree. There are two types of inter-specific relations underlying this spatial composition pattern: firstly, the adjacent plant species are the competition species with the centre species, and the adjacent plant species may become the succession species because they squeeze the survival space of both the centre tree and its offsprings; secondly, the adjacent plant species are the dependent species which show symbiosis with the centre tree, and the adjacent plant species would be more likely to become the dominant species, while the centre tree may tend to be the secondary species at subordinate status in this case."

Next it is to simulate the molecular evolution between sample plots: if the dominant species is the same species between center sample plot and adjacent sample plot, then it is to input the genetic distance between the varieties of these two sample plots. If the genetic distance is more than F level, and the relative importance of sample plot 1 is higher than it in sample plot 2 (or sample plot 2's relative importance is higher than sample plot 1), then the trees in sample plot 1 will invade the trees' survival space in sample plot 2 (or the trees in sample plot 2 will invade the trees' survival space in sample plot 1). Otherwise the trees in both sample plots stay in the stable state. This modeling design reflects the intra-species competition relationship as: after several generations' evolution, the genetic distance between center sample plot and adjacent sample plot will be reduced, and the variety with higher relative importance will dominate in both sample plots, becoming the stabilized or 'balanced' genetic state of a sub-population in the reproduction process, which is proposed in the section 4.3 of this article. Finally both sample plots may be evolved into the 'evolutionary significant unit'. Please note: if the dominant species between center sample plot and adjacent sample plot are the different species, then it is to input '-1' value for the variable of genetic distance between two sample plots (the normal value of genetic distance should range from 0 to 1; '0' value represents 'cloned' one and '1' value represents 'hybridized' one; some research may choose more than '1' value of genetic distance to indicate different species, but my article does not think different species will breed, so it is to give '-1' value to indicate different species for better fitting the model).

6.2.2. Discussion

In this 3D model, the constants of D, E, F are assumed to be 1.00, 0.30, 0.50 in the modeling test respectively; The sample plots must be the even numbers, because the even numbers indicate how many pairs of both center sample plot and adjacent sample plot; The total amount of species is N, and then each species is given the identifier number from 0 to N-1; The total amount of sample plots are S, and then each sample plot is given the identifier number from 0 to S-1; Finally this 3D model also achieves the labeling of each species' 3D distribution in coordinates and its corresponding relative importance.

6.2.3. Source code (Dev-C++ 6.5 Version)

```
// @All rights reserved by Liu Huan. Source from: https://doi.org/10.58473/JEHS0012

#include <iostream>
#include <vector>
#include <map>
#include <iomanip>
#include <tuple>

using namespace std;

int main() {
    int I, J, K, N, S;
    const double D=1.00; double E=0.30; double F=0.50;
    cout << "=== Ecological Distribution Modeling ===" << endl;
    cout << "Input the longitude grid scale (I): ";
    cin >> I;
    cout << "Input the latitude grid scale (J): ";
    cin >> J;
    cout << "Input the altitude grid scale (K): ";
    cin >> K;
    cout << "Input the amount of vegetation species (N): ";
    cin >> N;
    cout << "Input the sample amount (S-even number): ";
    cin >> S;
    if (S % 2 != 0) {
        cout << "Error£ºsample amount 'S' must be the even number£¡" << endl;
        return 1;
    };

    vector<vector<vector<double>>> a(I, vector<vector<double>>(J, vector<double>(K)));
```

```
    vector<vector<vector<double>>> b(I, vector<vector<double>>(J, vector<double>(K)));
    vector<vector<vector<double>>> c(I, vector<vector<double>>(J, vector<double>(K)));
    vector<vector<vector<double>>> d(I, vector<vector<double>>(J, vector<double>(K)));
    vector<vector<vector<int>>> species(I, vector<vector<int>>(J, vector<int>(K)));
    vector<vector<vector<int>>> samplePlot(I, vector<vector<int>>(J, vector<int>(K)));


    cout << "\n=== Input the individual's abundance ===" << endl;
    for (int i = 0; i < I; i++) {
        for (int j = 0; j < J; j++) {
            for (int k = 0; k < K; k++) {
                cout << "abundance a[" << i << "][" << j << "][" << k << "]: ";
                cin >> a[i][j][k];
            }
        }
    }

    cout << "\n=== Input the individual's frequency ===" << endl;
    for (int i = 0; i < I; i++) {
        for (int j = 0; j < J; j++) {
            for (int k = 0; k < K; k++) {
                cout << "frequency b[" << i << "][" << j << "][" << k << "]: ";
                cin >> b[i][j][k];
            }
        }
    }

    cout << "\n=== Input the individual's relative size ===" << endl;
    for (int i = 0; i < I; i++) {
        for (int j = 0; j < J; j++) {
            for (int k = 0; k < K; k++) {
                cout << "Relative size c[" << i << "][" << j << "][" << k << "]: ";
                cin >> c[i][j][k];
            }
        }
    }

    cout << "\n=== Input the species' identifier number for each individual ===" << endl;
    cout << "Species identifier number: from 0 to " << N - 1 << endl;
```

```
    for (int i = 0; i < I; i++) {
        for (int j = 0; j < J; j++) {
            for (int k = 0; k < K; k++) {
                int n;
                cout << "Species[" << i << "][" << j << "][" << k << "]: ";
                cin >> n;
                if (n < 0 || n >= N) {
                    cout << "Error£ºSpecies identifier number must be from 0 to" << N - 1 << endl;
                    return 1;
                }
                species[i][j][k] = n;
            }
        }
    }

    cout << "\n=== Input the sample's identifier number for each individual (0-" << S - 1 << ") ===" << endl;
    for (int i = 0; i < I; i++) {
        for (int j = 0; j < J; j++) {
            for (int k = 0; k < K; k++) {
                cout << "Individual(" << i << " " << j << " " << k << ")'s sample identifier: ";
                cin >> samplePlot[i][j][k];
                if (samplePlot[i][j][k] < 0 || samplePlot[i][j][k] >= S) {
                    cout << "Error£ºthe sample's identifier number must be from 0 to " << S - 1 << endl;
                    return 1;
                }
            }
        }
    }

    // To calculate the relative importance for each individual;
    for (int i = 0; i < I; i++) {
        for (int j = 0; j < J; j++) {
            for (int k = 0; k < K; k++) {
                d[i][j][k] = (a[i][j][k] + b[i][j][k] + c[i][j][k]) / 3.0;
            }
        }
    }

    // To calculate the dissimilarity between two samples of each pair;
    double totalDissimilarity = 0.0;
```

```
    vector<double> PairDissimilarity (S) ;
    for (int samplePair = 0; samplePair < S; samplePair += 2) {

        // To calculate the dissimilarity for each species;
        for (int n = 0; n < N; n++) {
            double sumSample1 = 0.0, sumSample2 = 0.0;
            int countSample1 = 0, countSample2 = 0;

            for (int i = 0; i < I; i++) {
                for (int j = 0; j < J; j++) {
                    for (int k = 0; k < K; k++) {
                        if (species[i][j][k] == n && samplePlot[i][j][k] == samplePair) {
                            sumSample1 += d[i][j][k];
                            countSample1++;
                        }
                        if (species[i][j][k] == n && samplePlot[i][j][k] == samplePair + 1) {
                            sumSample2 += d[i][j][k];
                            countSample2++;
                        }
                    }
                }
            }
            // To calculate the dissimilarity for each pair of samples;
            if (countSample1 > 0  || countSample2 > 0) {
                double speciesDissimilarity = abs(sumSample1 - sumSample2) / (sumSample1 + sumSample2);
                totalDissimilarity += speciesDissimilarity;
                PairDissimilarity[samplePair] = totalDissimilarity;
            }
        }

        cout << "Sample" <<" "<< samplePair <<" "<< "and Sample" <<" "<< samplePair + 1 << "'s dissimilarity: " << PairDissimilarity[samplePair] << endl;
    }

    // To calculate the sum of importance for the individuals in each sample;
    vector<double> sum_importance(S, 0.0);
    for (int i = 0; i < I; i++) {
        for (int j = 0; j < J; j++) {
            for (int k = 0; k < K; k++) {
                int currentSample = samplePlot[i][j][k];
                sum_importance[currentSample] += d[i][j][k];
```

```
            }
        }
    }

    // To input the dominant species' correlation between two samples of a pair;
    vector<double> correlation(S);
    cout << "\n To input the dominant species' correlation between two samples of a pair:" << endl;
    for (int samplePair = 0; samplePair < S; samplePair += 2) {
        int sample1 = samplePair;
        int sample2 = samplePair + 1;
        cout << "Sample" <<" "<< sample1 <<" "<< "and Sample" <<" "<< sample2 << "'s correlation: ";
        cin >> correlation[samplePair];
    }

    vector<double> Genetic_Distance(S);
    cout << "\n To input the dominant species' genetic distance between two samples of a pair:" << endl;
    for (int samplePair = 0; samplePair < S; samplePair += 2) {
        int sample1 = samplePair;
        int sample2 = samplePair + 1;
        cout << "Sample" <<" "<< sample1 <<" "<< "and Sample" <<" "<< sample2 << "'s Genetic Distance: ";
        cin >> Genetic_Distance[samplePair];
    }

    // To output the sum importance for each sample;
    cout << fixed << setprecision(2);
    cout << "\n=== Each sample's sum importance ===" << endl;
    for (int s = 0; s < S; s++) {
        cout << "Sample " <<" "<< s << " 's sum importance: " << sum_importance[s] << endl;
    }

    // To analyze the succession relationship;
    cout << "\n=== To analyze the succession relationship ===" << endl;
    for (int samplePair = 0; samplePair < S; samplePair += 2) {
        int sample1 = samplePair;
        int sample2 = samplePair + 1;
        double corr = correlation[samplePair];
        double sum1 = sum_importance[sample1];
        double sum2 = sum_importance[sample2];
        double PairD = PairDissimilarity[samplePair];
```

```
        if (PairD > D) {
            if (corr < -E) {
                if (sum1 > sum2) {
                    cout << "Sample" <<" "<< sample1 <<" "<< "invade Sample"
<<" "<< sample2 << endl;
                } else if (sum2 > sum1) {
                    cout << "Sample" <<" "<< sample2 <<" "<< "invade Sample"
<<" "<< sample1 << endl;
                } else {
                    cout << "Sample" <<" "<< sample1 <<" "<< "and Sample" <<"
"<< sample2 << " " <<"Stay in Stable state" << endl;
                }
            } else {
                cout << "Sample" <<" "<< sample1 <<" "<< "and Sample" <<" "<<
sample2 << " " <<"Stay in Stable state" << endl;
            }
        } else {
                cout << "Sample" <<" "<< sample1 <<" "<< "and Sample" <<" "<<
sample2 << " " <<"Stay in Stable state" << endl;
        }

    }

    // To analyze the evolution of genetic variation£»
    cout << "\n=== To analyze the evolution of genetic variation ===" << endl;
    for (int samplePair = 0; samplePair < S; samplePair += 2) {
        int sample1 = samplePair;
        int sample2 = samplePair + 1;
        double Genetics = Genetic_Distance[samplePair];
        double sum1 = sum_importance[sample1];
        double sum2 = sum_importance[sample2];

        if (Genetics > F) {

            if (sum1 > sum2) {
                cout << "Sample" <<" "<< sample1 <<" "<< "invade Sample" <<"
"<< sample2 << endl;
            } else if (sum2 > sum1) {
                cout << "Sample" <<" "<< sample2 <<" "<< "invade Sample" <<"
"<< sample1 << endl;
            } else {
                 cout << "Sample" <<" "<< sample1 <<" "<<"and Sample" <<" "<<
sample2 << " " <<"Stay in Stable state" << endl;
```

```
            }
        } else {
            cout << "Sample" <<" "<< sample1 <<" "<<"and Sample" <<" "<<
sample2 << " " <<"Stay in Stable state" << endl;
        }
    }

    cout << "\n=== To output the sum of relative importance for each species ==="
<< endl;
    map<int, vector<tuple<int, int, int, double>>> speciesData;

    for (int i = 0; i < I; i++) {
        for (int j = 0; j < J; j++) {
            for (int k = 0; k < K; k++) {
                int n = species[i][j][k];
                speciesData[n].push_back(make_tuple(i, j, k, d[i][j][k]));
            }
        }
    }

    cout << fixed << setprecision(4);
    for (int n = 0; n < N; n++) {
        if (speciesData.find(n) != speciesData.end()) {
            cout << "\n Species " << n << " 's relative importance£¨Totally " <<
speciesData[n].size() << " individuals£©:" << endl;
            cout << "Individual (i,j,k)       ->       relative importance" << endl;
            cout << "--------------------------------" << endl;

            for (const auto& data : speciesData[n]) {
                int i = get<0>(data);
                int j = get<1>(data);
                int k = get<2>(data);
                double value = get<3>(data);
                cout << "(" << setw(2) << i << "," << setw(2) << j << "," << setw(2)
<< k << ") -> " << setw(10) << value << endl;
            }
        } else {
            cout << "\n Species " << n << " does not occur " << endl;
        }
    }

    cout << "\n=== Species distribution statistics ===" << endl;
    for (int n = 0; n < N; n++) {
        if (speciesData.find(n) != speciesData.end()) {
```

```
                int count = speciesData[n].size();
                double percentage = (count * 100.0) / (I * J * K);
                cout << "Species " << n << ": " << count << " 's position (" <<
percentage << "%)" << endl;
            }
        }

        return 0;
}
```

Acknowledgement: the basic function of source code is looked up by using DeepSeek Model, and Copilot (Github) gives the advice of structuring the models.

7.Conclusion

When Technical specification for investigation and assessment of national ecological status —— Ecosystem services assessment (HJ 1173-2021) is implemented in ecological function assessment, the ecological functions have been officially included as water conservation, soil conservation, sand storm prevention and biodiversity conservation, so the criteria for assessment of ecological function heterogeneity which is designed by my another article [2] need to be revised correspondingly, and the potential improvement has been discussed in the section 2.3.5 of this article, including carbon sink function and 3S technology which have not been included in this official guidelines but is considered to be essential in ecological function services assessment. My article of numerical modeling in carbon sink forest productivity at regional scale and another 3S technology article has prepared for this improvement [4] [7]. Consequently, in my another article assessing ecological function heterogeneity[2], the Matrix T1 and T2 should include the ecological functions of water conservation, soil conservation, sand storm prevention, biodiversity conservation (such as restoration of endangered species' habitat based on ecological niche theory), and carbon sink function. The assessment of ecological function heterogeneity does not only avoid the uniformity and mono-function of ecosystem that will be NOT sustainable in the long term process, because it is believed that the sustainability of ecosystem relies on multi ecological functions playing the organic role concurrently in the long term evolution, but also quantitatively assesses the overall index of multiple functions in ecosystem.

According to Technical specification for investigation and assessment of national ecological status——Ecosystem patterns assessment (HJ 1171-2021), different types of ecosystems need to be classified before ecosystem pattern assessment. As guided by Standard for the assessment of regional biodiversity (HJ 623-2011), the classification of different types of ecosystem is based on the unit of community. However, the methods of identifying different types of ecosystems is not included in both official guidelines. My previous article [1] has summarized the various

applications of both multivariate cluster analysis and Principal Component Analysis (PCA) on the identification and classification of different ecosystems or communities at regional or local scale. Further more, my another article has adopted a combination method of both classification and ordination analysis [5], which does not only facilitate classification of sub-ecosystem/communities at local scale, but also helps to analyze the succession patterns of different sub-ecosystems identified in the long term evolutionary process, as to compared with the case studies in article [1]. For the restoration of forest ecosystem, my previous study has reviewed the plantation methods and practices in New Zealand [6], which will be further complemented in this article on the basis of case studies in China. Further, my another article has designed the new method of species selection for plantation restoration according to the ecological niche theory [5]. Obviously, the structural pattern heterogeneity increases the ecosystem diversity with different ecological niches, which enhances the sustainability of ecosystem under the long term environmental changes and increases the resistance against the exotic and invasive species. In summary, both ecosystem function services and structure pattern assessment guidelines also becomes the main criteria of plantation engineering design. Particularly, based on the quantitative assessment of both structural and functional heterogeneity designed in my article [2], it is applicable to establish the numerical models in optimizing the plantation engineering design according to the heterogeneity index, and there is an example illustrated in Figure 2 below (Figure 2 is discussed in detail at section 3.2.6.).

In summary, both structural and functional biology theories should not only include the molecular biology studies like my articles [20][21] that have substantially discussed both structural and functional gene diversity, but should also focus on the ecosystem diversity from the theoretical understanding of both structure and function that are compulsory in biology knowledge.

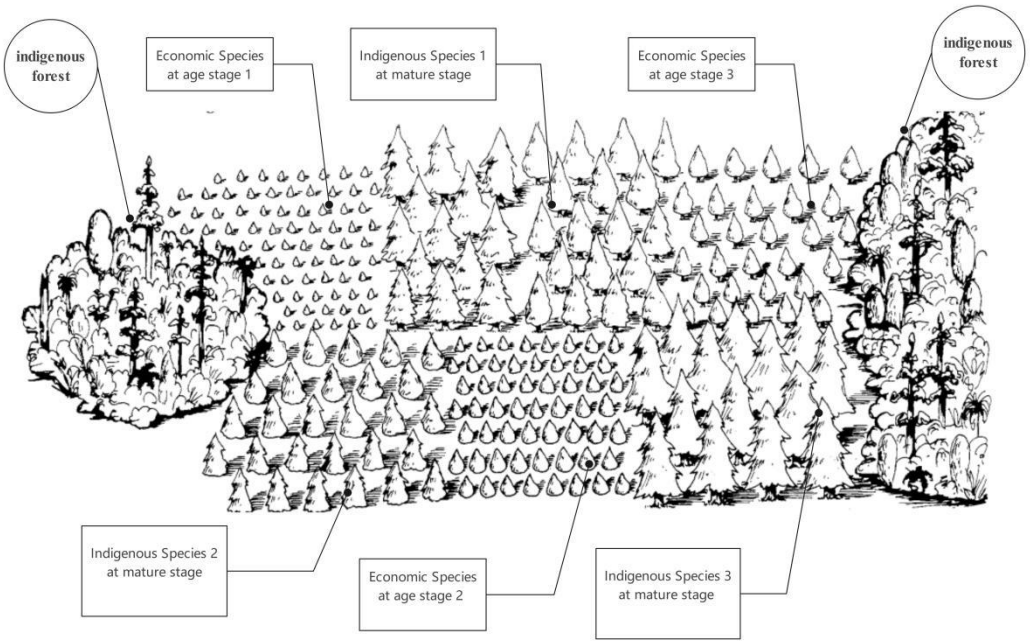

Figure 2. Plantation forest connecting two indigenous forest remnants in rotational way for both conservation and economic values. This figure is adapted on the basis of the Figure 2 (Norton, 1998)[65].

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