



## Research on the Integration Path of Traditional Village Spatial Gene Extraction and Environmental Landscape Planning and Design

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**SUMMARY:** *Traditional villages are an important part of traditional culture, but with the process of urbanization, many traditional villages are gradually declining, and the protection and inheritance of traditional villages is a problem to be solved nowadays. This paper firstly locates the spatial type of traditional villages through spatial gene extraction methods such as element, objective law, structure and pattern extraction. Secondly, the spatial characteristics of traditional villages are summarized, the specific expressions of spatial genes are deconstructed, and the results of deconstruction are refined, so as to obtain the spatial genes of villages. Then the spatial syntax is introduced to analyze the spatial morphological features of traditional villages, construct the spatial gene map, and propose methodological countermeasures for the protection of traditional villages. Taking County G as an example, this paper mines the historical and geographical characteristics of five types of typical villages in the county city, and finds that the spatial gene richness can reflect the well-preserved degree of traditional village appearance and historical and cultural heritage, and the well-preserved degree of A2 village in the research sample is better. Based on the above research results, this paper designs the path of environmental landscape planning for traditional villages from three levels: auxiliary planning, digital quantification and digital protection. This paper expands the application path of digital technology in the revitalization of traditional village culture and provides an innovative approach to environmental landscape protection.*

**KEYWORDS:** *traditional village; spatial gene extraction; spatial syntax; environmental landscape planning; spatial gene mapping*

### 1 Introduction

Traditional villages have richer cultural and natural resources with diverse research, protection and development values, and are an important development space for rural revitalization strategy [1]. Currently, both society and the government are highly concerned about the preservation and advancement of traditional villages and cultural landscapes. As of 2024, a cumulative total of 8155 villages across six rounds have been designated as “Chinese traditional villages” [2]. In the context of globalization, the work related to traditional villages must adhere to cultural self-confidence and cultural self-awareness in order to avoid drowning in the trend of cultural convergence. With the rapid development of urbanization, modernization and informatization, all kinds of information flow, material flow and energy flow constantly invade the relatively closed environment of traditional villages, making their spatial system and social order imbalance, which triggers the blurring of the landscape connotation, spatial texture

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disorders, and the diminishing of the village culture and spirit and other problems [3, 4]. There is an immediate need to address these issues, which serve as a warning for us to focus on the physical manifestation of the cultural landscape. At the same time, we must also take into consideration non - physical structural characteristics such as the essence of the cultural heritage, the symbolic framework, and the spatial inheritance patterns. Consequently, it is of great and urgent importance to intensify the scientific investigation of research approaches regarding the form and structural traits of the cultural landscape in traditional villages.

Gene, also called genetic factor, is a biological concept, which is a basic information unit storing certain genetic information and controlling the evolution and continuation of organisms. As a result, the conceptual approach of genes is inspiring for analyzing problems in social and cultural fields, and can effectively explain the regular characteristics of human cultural evolution. Currently, academic research both at home and abroad regarding spatial genes primarily centers around three areas: the identification and extraction of spatial genes, the generation and analysis of spatial genes, and the inheritance and control of spatial genes. [5].

In terms of spatial gene identification and extraction, Hui et al. combined the landscape gene identification method, geographic concentration index and spatial sentence method to construct a traditional village cultural landscape gene chain (CLGC) identification method, and took the ancient town of Xuanzhou, Hengshan County, Hunan Province as an example, and found that the local area presented a typical trade and culture type pattern [6]. Huang and colleagues integrated remote - sensing imagery, real - time drone mapping, Geographic Information System (GIS), and spatial syntax methods. They aimed to identify and extract twelve crucial indicators across five aspects: geomorphic hydrology, boundary configuration, spatial layout, street dimensions, and building proportions. Through these efforts, they were able to quantitatively decipher the spatial characteristics or "genes" of the settlement. [7]. Wan et al. took Xuyong County in Luzhou City as an example, constructed a three-layer analytical framework of "genome - spatial elements - specific indicators" based on spatial gene theory, identified, categorized and mapped the spatial pattern of edge-type villages in southern Sichuan, and extracted the common spatial genes and differential spatial genes through cluster analysis [8]. Using Meicheng Town in the Meishan region as a case study, Xia and Chen employed the theory of landscape genes to categorize and recognize the characteristics of cultural landscapes. They integrated the hierarchical analysis approach and the fuzzy comprehensive assessment method to establish an index system for landscape gene sorting. Subsequently, they systematically extracted 16 landscape factors. [9]. Peng et al. used the theoretical framework of spatial genetics, combined with parametric methods and quantitative analysis, to explore the fundamental laws and applicable strategies of village development, and took Gulan Village as an example to put forward a development strategy for historical villages based on characteristic spatial genetics and integrating computational technology, and constructed a multidimensional research path that takes into account both protection and revitalization to promote sustainable rural development [10]. Xu et al. constructed a set of innovative research system for identifying the extrinsic features and intrinsic value of village landscape through content analysis method, which covers three levels of landscape elements and features analysis, landscape composition law exploration, landscape gene research, as well as two phases of gene extraction and gene adaptation exploration [11].

In terms of spatial gene analysis and evaluation, Yu and Mi focused on the spatial genes of villages and conducted spatial gene analysis through the mining of genetic information. They utilized the parametric platform of CityEngine to achieve digital modeling and three-dimensional visualization of spatial forms. Using the conventional village of Xiaoxi in Xiangxi as a case study, they investigated the viability of parametric technology in the integration, characteristic evaluation, optimization guidance, and management regulation of rural spatial

landscapes. [12]. Taking Goulan Yaozhai in Jiangyong County, China as an example, Gu et al. used the cultural landscape gene theory combined with GIS spatial analysis, constructed the gene information chain mapping and village classification and coding system, and analyzed its spatial distribution and organization, and found that the spatial gene distribution of the village presented a “three-core and multi-node” pattern, with obvious clustering characteristics, and the phenomenon of mismatch in spatial accessibility and density [13]. It is found that the spatial gene distribution of the village shows a pattern of “three nuclei and multiple nodes”, with obvious clustering characteristics, and the phenomenon of mismatch between spatial accessibility and density. Cai and colleagues employed a multi - scale analytical method to investigate the safeguarding and improvement of the landscape features of rural settlements in Guangdong; among them, at the macro level, GIS spatial analysis, average nearest-neighbor index and cluster analysis were utilized for parsing; at the meso level, the spatial morphology characteristics of the traditional settlements were systematically parsed; and at the micro level, fuzzy hierarchical analysis was used to quantitatively assess the landscape characteristics, and core landscape genes were extracted [14]. Zhang et al. based on the spatial gene perspective, combined with NVivo 14 qualitative analysis, Employ ArcGIS and other instruments to initiate a comprehensive assessment of the conventional Korean villages situated in the northeastern area, identified 16 spatial gene entries, and extracted 47 spatial gene fragments through the natural breakpoint method, and utilized Spearman's correlation analysis to excavate the gene sequence associations, and ultimately constructed the spatial gene atlas [15]. The spatial gene map was finally constructed by using Spearman correlation analysis. Wang and Yuan conducted statistical analysis, spatial analysis and data visualization of quantitative morphological elements of 270 typical rural settlements in Heilongjiang Province, and resolved the dominant genes, accessory genes and mutant genes in rural morphogenesis in the province [16].

Regarding the guidance and control of spatial gene inheritance, Zhang and Yang selected Naihegou Village in Yulin, Shaanxi as a case study. They developed a quantitative inheritance model that incorporated natural, physical, and intangible spatial elements, relying on the spatial gene theory. Moreover, they integrated GIS spatial analysis with the AHP - fuzzy comprehensive evaluation method, to identify and decipher the spatial morphology characteristics of the village and the gene inheritance, as well as to carry out a quantitative assessment [17]. From the viewpoint of "spatial genes," Nie and colleagues posited that the spatial genes of traditional villages are not just a spatial combination model but also the fundamental inheritance unit for the long - term development of the village. After that, they developed a quantitative inheritance system model for the spatial genes of traditional villages. This model disclosed the underlying logic behind the formation of the physical form of traditional villages and set up a quantitative index system for village morphology. [18]. Based on the theory of landscape gene, Wu et al. take the traditional villages in Huizhou as an example to explore the spatial characteristics of traditional villages and their inheritance and protection mechanisms, construct the landscape gene system of traditional villages and verify its scientificity, aimed at offering references for researching the spatial features of traditional villages as well as their safeguarding and inheritance [19]. Juanyu et al. introduced the DFRI base surface theory as the interface and proposed an adaptive restoration model based on the "identification - diagnosis - repair" chain activation path. They precisely identified and extracted landscape genes through multiple technical methods and regarded the protection and development of traditional villages as an organic whole, avoiding the fragmentation of protection work [20]. Wei and his work team collected and arranged data about old villages and houses in Chongqing from many different angles, which include history related aspects, geography, and society, classified and coded the cultural genes, and constructed the cultural gene maps of Chongqing traditional villages and dwellings, in order to deepen the

understanding and inheritance of the villages and dwellings cultures; moreover, through the establishment of the multi-dimensional fusion of the cultural gene maps digitization paths, we explored the archival protection, revitalization, and inheritance methods with high precision and high efficiency [21]. Zhang and Huang use the social network analysis method, the spatial gene theory and the diversity analysis method to conduct an examination of the characteristics of the architectural spatial network. Their work has the contribution to a more deep understanding of the culture value and space arrangement characteristics of old villages. Therefore, it provides a foundation for the conservation of traditional settlements and the protection of minority culture heritages[22]. In summary, the current research on spatial genetics in the field of landscape planning is still in its infancy, and most of them are based on specific geographical areas and regions, such as the traditional village clusters in Southwest China, to analyze the morphological characteristics of the traditional villages in the region as well as the background and reasons for their formation [23]. The research on traditional villages mainly focuses on the single level of space or culture, and the in-depth research on the interaction and influence among space, culture and nature still needs to be strengthened [24]. Therefore, there is an urgent need for landscape planning research to break through the limitations of a single dimension and turn to the in-depth integration of spatial, cultural and natural elements.

In this paper, the spatial characteristics of traditional villages are transformed into the traits expressed by the spatial genes of traditional villages. The spatial diversity characteristics of traditional villages are revealed by calculating the  $\alpha$  diversity index. The cultural composition elements inside different types of traditional villages are recorded and integrated to calculate the diversity of the spatial gene characteristics of traditional villages. This behavior is conducted to dig out the hereditary essence of the space artistic taste of these villages. After that, the spatial syntax, which has its root in the principles of graph theory, is utilized by people. It has the function of abstracting traditional villages into spatial parts such as spots, lines, surfaces and to carry out measurement on these spatial parts and the links that exist between them. Five kinds of villages in County G, that is, gathering type, grouping type, radial type, linear-belt type, and linear villages, are selected as the study's research objects. We have carried out deep analyses on each individual case one by one. The results of these analyses are used as the data foundation for formulating an environmental landscape planning and design strategy which depends on digital technology.

## **2 Spatial gene extraction and environmental landscape planning and design of traditional villages**

### **2.1 Traditional village spatial gene extraction methods**

#### **2.1.1 Spatial gene identification and extraction**

To carry out the identification work for the spatial genes of traditional villages, a comprehensive method is needed. We ought to integrate the natural, cultural, political, economic influences of these villages with the typical outward look and characteristics of their space features, then sum up and purify the related information. A certain spatial feature in a village may only be controlled by material space genes or non-material space genes, or it may be expressed under the joint action of material space genes and non-material space genes, and the identification of spatial genes requires full deconstruction of spatial features and in-depth excavation in order to identify spatial genes in all aspects. In the process of carrying out identification work, the below-given identification standards must be strictly followed by us. These judgment standards

contain comprehensiveness, representativeness, internal difference, external difference, local difference, and overall excellence, by referring to the principles of identification of landscape genes and cultural genes, and at the same time, taking into account the differences in spatial features between villages and the differences in spatial features within the village itself.

Spatial genes are embedded in spatial features, and the process of identifying spatial genes is to summarize the objective laws embedded in the commonality or characteristics of spatial features. The complicated degree of spatial features in traditional villages comes from the complex nature of spatial genetic components, and it is necessary to deconstruct the complex spatial features by certain methods in order to accurately identify spatial genes. Through field research and literature review, the main methods for recognizing spatial genes in this study are: element extraction, objective law extraction, structure extraction and pattern extraction. The spatial gene identification process is shown in Figure 1.

As traditional villages possess rich historical value and complete village landscape, it leads to a wide variety of spatial features with complexity. The identification of spatial genes of traditional villages is obtained based on the deconstruction and analysis of spatial features within the villages, therefore, a comprehensive and accurate extraction flow has the greatest importance for the recognition of spatial genes. The process of spatial gene identification should be as follows: firstly, locate the spatial types to be identified under different spatial scales; secondly, summarize their spatial features and deconstruct and analyze their specific forms according to the spatial gene identification method; finally, refine the identification results to obtain the spatial genes. Taking the “natural environment layer - ancient tree space” as an example, three kinds of spatial features are deconstructed and analyzed: element extraction of tree species features, ancient tree category is an important factor determining the characteristics of the tree species, from which the gene for the category of the ancient tree can be extracted; extraction of the objective rules of the landscape of the ancient tree, the spatial aesthetics attribute is a common characteristic of the ancient tree, from which the spatial aesthetics gene can be extracted; element extraction of cultural heritage, and extraction of spatial gene. Aesthetics genes are extracted from them; elements of cultural heritage are extracted from them; rituals and folklore activities take the space of ancient trees as a place, which is an important factor influencing the spatial characteristics of ancient trees, from which ritual genes and folklore genes can be extracted.

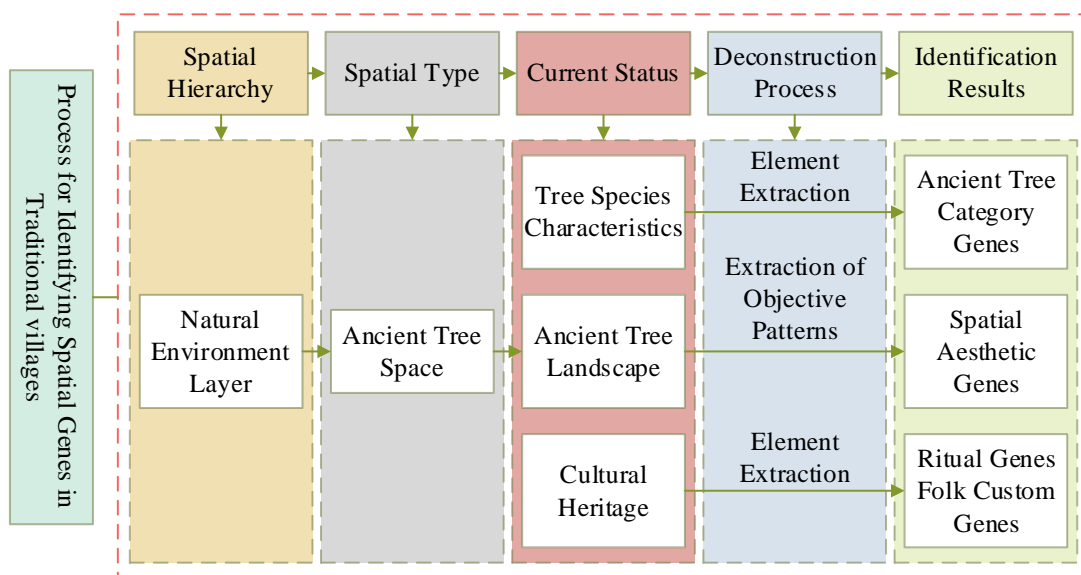


Figure 1: Spatial gene recognition process

### 2.1.2 Diversity measurement methods

$\alpha$  Diversity refers to the number of species in a community and the number and distribution of each species. There are many indices to measure  $\alpha$  diversity, commonly used such as the Maglev index, the Simpson species diversity index, the Shannon species diversity index, and the evenness measurement. In this paper, we consider each village as a complete community and each spatial gene as a species, and calculate the spatial gene (species) diversity of each village (community) and summarize its characteristics, based on the method of determining the species diversity of the community.

#### (1) Margalef

The Margalef index has the function of reflecting the abundance of spatial genes that exist in each village, that is to say, the number of spatial genes which are contained in the village. Its calculation formula is hereby given as below:

$$D_{ma} = (S - 1) / \ln N \quad (1)$$

where  $S$  is the number of spatial genes in each village;  $N$  is the number of all individuals in all spatial genes in the village.

#### (2) Shannon-Wiener

The Shannon-Wiener index has the function of describing the disorder and unpredictability of the spatial genes that are inside the village. When the quantity of spatial genes is large and the even degree of spatial gene distribution among different spatial kinds gets promotion, this therefore brings about an increase of diversity. Furthermore, a bigger numerical value of the Shannon-Wiener index therefore shows a higher degree of spatial gene diversity that is inside the village. The formula is given in the below way:

$$H' = -\sum_{i=1}^S P_i \log_2 P_i \quad (2)$$

where  $S$  is the number of spatial genes in each village;  $P_i$  is the proportion of spatial features  $n_i$  belonging to spatial category  $i$  among all spatial genes  $N$  in the village.

#### (3) Simpson

Simpson's index, also known as the dominance index, describes the probability that the number of spatial gene individuals obtained from two consecutive samples in a village belongs to the same category, furthermore, the larger the numerical value of Simpson's index, hence the larger the spatial genetic diversity that this village has. The calculation of Simpson's index uses the following formula:

$$D = 1 - \sum_{i=1}^S n_i(n_i - 1) / N(N - 1) \quad (3)$$

where  $N$  is the number of all individuals in all spatial genes in the village;  $n_i$  is the number of individuals with spatial characteristics  $i$ .

#### (4) Pielou

The uniformity index can represent that spatial genes are spread out inside each single village. In other words, it can display the uniform property of the relative content amount of each spatial gene. This index, therefore, possesses a positive correlative relationship with the abundance index that lies within the identical village. The computation formula of this thing is given in the below:

$$J = -\sum H'/\log_2 S \quad (4)$$

## 2.2 Environmental landscape planning and design based on spatial syntax

### 2.2.1 Space syntax

The spatial syntax may be said to have its origin in the basic principles of the graph theory. This theory begins its discussion from the perspective of topological analysis, and condenses traditional villages into basic spatial components which include points, lines, surfaces, and tries to describe and quantitatively delineate these elements and the relationship between them. The core concept is spatial conformation, i.e., through the ontological study of space, analyzing the relationship between it and the social and economic domains, revealing the intrinsic attributes of human activities by means of the conformation relationship, and using spatial cognition to understand spatial behavior.

The core concept of spatial syntax is spatial configuration, i.e., the interconnection of elements in a spatial system, and it is believed that urban and social spatial layout will have an impact on human activities, socialization and intensity, and that the spatial configuration of urban streets itself determines the distribution of different densities, i.e., “the configuration determines the movement”. The grouping relationship of space is the focus of the spatial syntax to understand space, and the quantitative analysis of spatial accessibility, grid characteristics and spatial structure reveals the intrinsic relationship between space, social factors and human activities.

### 2.2.2 Quantitative analysis methods for spatial syntax

In the domain of space syntax, the often utilized conformal segmentation methods include: the convex space method, the axial analysis method, the line-segment analysis approach, the visual field analysis method, the feature point approach, and so on. In this research paper, we mainly choose the axial analysis technique and the line-segment analysis method to carry out an analysis on the spatial layout of the county-seat town in [County River] County.

The axis analysis method makes the linear movement of persons in three-dimensional space become simplified into a one-dimensional linear space. In the theory of syntax, the axis stands for the small-scale space which spreads out in the direction that the axis has. This space stands for the farthest distance that an observer may look from a specific point which lies inside this space. In addition, this axis possesses two implications: one that connects to visual sensation, and the other that connects to motion modes. In the drawing of the axis map, it is required to cover the whole spatial system with the least and longest axes. In the spatial configuration, the axis lines are regarded as nodes, so there are one-to-one corresponding nodes throughout the multiple axes. According to the connection relationship between all the axes, the abstract spatial system is transformed into the configuration graphic, and quantitatively calculated by Depthmap software, which results in the spatial syntactic variable value of each axis, and the level of the spatial syntactic variable value is indicated by the warm and cold colors of the axes.

For large-scale space, the spatial syntax usually uses the axis model to simplify the urban space into a linear spatial system, and analyzes the whole spatial system through the quantification of the axes, but due to the existence of different roles at each point where the axes intersect, the analysis results are basically accurate as a whole, but there will still be a certain degree of error. The traditional village is a meso-scale urban space with a different layout form, and the analysis of its spatial morphology characteristics requires a more accurate line segment model. The line segment model is translated on the basis of the axial model, and what

is involved in the calculation is not a straight line that is not interrupted, but each part of the line segments after interruption as the basic unit in the calculation. The  $a$  and  $b$  are involved in the calculation of the spatial network as individual elements. Compared with the axial analysis, the line segment analysis method can more accurately analyze the spatial grouping relationship by including the actual distance between the two elements, the turning distance, and the size of the corner as variables in the calculation.

### 2.2.3 Values of the main morphological variables of spatial syntax

The core function of spatial syntax is that it carries out comprehension of space. Through utilizing the syntax platform to carry out computations, one group of morphological variables which are about the spatial system is gotten by generation. These variables can directly give out description of the configurational connections among nodes and between nodes and the whole system. The variables mainly have six types that are listed below:

Connection value: it expresses the total number of other nodes which are next to a certain node inside the space structure. A higher connection numerical value expresses that the spatial penetrating ability is better. The concrete formulation is just like below:

$$c_i = k \quad (5)$$

where:  $c_i$  denotes the connection value and  $k$  is the total number of axes intersecting node  $i$ .

Selectivity: refers to the number of times a spatial node is traversed by any two other nodes in the spatial system with the shortest topological distance, which generally refers to the frequency of being selected, the higher the selectivity, the better the transportation attributes.

$$NAchoice_i = \frac{\log(ACH_x + 1)}{\log(ATD_x + 3)} \quad (6)$$

where:  $r$  identifies the topological radius,  $ACH_r$  represents the angle selection under radius  $r$ , and  $ATD_r$  represents the angle depth value under radius  $r$ .

Average depth: indicates the average value of the shortest distance from a node space to all other nodes in the space system, which can reflect the convenience of the node space to a certain extent.

$$MD_i = \frac{\sum_{j=1}^n d_{ij}}{n-i} \quad (7)$$

where:  $d_{ij}$  is the minimum distance between any two points  $i$  and  $j$  on the connection graph, and  $n$  is the total number of nodes in the connection graph.

Control degree: it represents the scope of influence which a node that is inside a spatial structure exerts on the nodes that are connected to it. This metric is got by summing up the reciprocals of the connection values of the nodes which link to the spatial position of the node. A bigger control numerical value means that this node is more easy to be reached.

$$Ctrl_i = \sum_{j=1}^k \frac{1}{c_j} \quad (8)$$

where:  $k$  is the number of nodes directly connected to the  $i$ th node,  $j(j = 1, 2, \dots, k)$  is the node directly connected to the node  $i$ , and  $c_j$  is the connection value of the  $j$ th node.

Integration degree: this shows what scope of gathering or scattering is between one space node and other space nodes in the system. Generally speaking, this measurement is utilized to depict the degree of centralization and decentralization of walkers and car flow in the space background, and the higher the degree of integration, the higher the degree of convenience of the spatial node, and the closer the connection with the whole system. In the analysis, it is often divided into global integration degree and local integration degree, global integration degree reflects the spatial relationship between the nodes in the overall spatial system, often used to analyze the dispersion of traffic flow, high global integration degree, indicating that the overall spatial connection is close, while the local integration degree indicates that the correlation between a node in the system and the nearby nodes, usually take three topological units, that is, "radius --The local integration degree is often used to describe the dispersion degree of pedestrian flow, and a high local integration degree indicates that there are more accessible neighboring spaces.

$$I_i = RRA_i = \frac{m \left( \log_2 \left( \frac{m+2}{2} - 1 \right) + 1 \right)}{(m-1)|MD_i - 1|} \quad (9)$$

where:  $MD_i$  is the average depth value,  $m$  is the total number of spatial nodes.

Intelligence: is used to describe the degree of association between local control and the whole, reflecting the difficulty of the subject to distinguish between the local and overall spatial pattern, commonly used connection value, control value, local integration and global integration one-to-one corresponding to the fit value to express, including both the degree of understanding of the behavior of the subject through the local structure to perceive the overall space, but also to reflect the degree of synergism between the local space and the overall space.

$$R^2 = \frac{\sum (c_i - \bar{c})(I_i - \bar{I})^2}{\sum (c_i - \bar{c})^2 \sum (I_i - \bar{I})^2} \quad (10)$$

where  $\bar{c}$  is the mean value of connectivity of all cell spaces and  $\bar{I}$  is the mean value of global integration of all cell spaces.

### 3 Results of spatial gene extraction and morphological quantification of traditional villages

#### 3.1 Quantitative results of village spatial patterns

In this paper, the villages with clearer and more complete spatial expressions of village streets and lanes among the five traditional villages in County G are selected as the research objects to avoid errors in syntactic parsing of the sample villages. Under this premise, A1 village, A2 village, A3 village, A4 village and A5 village are selected as the specific research cases of centralized, grouped, radial, belt and line villages respectively for the quantitative study of spatial syntax.

The depth numerical value, which expresses space reachable degree, indicates the number

of spaces that have to be passed through when one moves from a single space to another space. Owing to the fact that the depth value usually changes in accordance with the observation point, the average depth value is chosen for the analysis of the whole spatial accessibility of the village. The average depth can express the village accessibility, indicating the convenience of a certain spatial node within the whole spatial system, and the lower the average depth value indicates the stronger spatial accessibility of the node. Use syntax software to read the average depth value of each sample village, record the number of axes and the maximum, minimum and average values of the average depth value of the sample village, and plot the average depth index of the axes of the sample village as shown in Table 1.

Among these five different types of traditional villages, the highest number of axes is 157 in A3 village, the lowest number of axes is 53 in A4 village, followed by 108 in A1 village, 85 in A2 village, and 73 in A5 village respectively. In the average depth value of A1 village, A2 village, A3 village and A4 village, there is not much difference, between 4.98-5.99; the average depth value of A5 village is 8.68248, which indicates that its accessibility is the worst. Village A1 is a concentrated, traditional type village. It shows a high level of whole space cohesion, the streets and lanes are well connected, and the overall connection of the village space is relatively tight. A2 village is a group-type traditional village, the village layout is clear-cut and structured, the village has the strongest accessibility to the scenic part of Jiangwan, the spatial hierarchy from the core of the scenic area to the outside gradually decreasing, the accessibility near the northern part of Houlongshan is the worst, the overall spatial cohesion is stronger, the links are tighter. A3 village is a radiating traditional village, there is a north-east-southwest flow of the village of the waterfront landscape and the village is located in the center of the village by the Qingyan Hall and other things linked together by the cultural axis, where with the cultural main line hooked up with the cultural line. A4 village is a belt-type traditional village, the whole village space is connected by the sky street, the most accessible part is the Cao's Ancestral Hall with the lowest elevation in the middle of the village, and the village space has a strong orientation and a compact layout. A5 village is a line-type traditional village, the whole village space is connected by the sky street, the most accessible part is the Cao's Ancestral Hall with the lowest elevation in the middle of the village, and the village space has a strong orientation and a compact layout. This village is a settlement that extends in a line, passes through long time, and is made of many groups of living people. Its overall arrangement is relatively scattered. The region of the village which has the biggest accessibility is its core. Furthermore, this village displays a comparatively low level of spatial cohesion degree.

Through gathering together the average depth numerical values of the five kinds of traditional villages, therefore it is very clear that:

- 1) The village center has the strongest accessibility, and the spatial cohesion gradually decreases from the center to the surroundings.
- 2) In terms of spatial cohesion, centralized traditional villages have the strongest spatial cohesion, and linear traditional villages have the weakest cohesion.
- 3) The spiritual and cultural space of the village is easy to gather in the spatial area with strong accessibility of the village.

*Table 1: Average depth index table of each type of axis*

Mean depth value	A1 village	A2 village	A3 village	A4 village	A5 village
Axis quantity	108	85	157	53	73
Maximum value	10.87045	8.05879	9.07793	8.31998	12.36985
Minimum value	4.38887	3.51771	3.97407	3.37999	5.99996
Variance	1.21422	0.92193	1.07851	1.08144	1.60381
Mean value	5.76098	5.32369	5.98242	4.98348	8.68248

The axial maps of each type of traditional villages were imported into the spatial syntax software Depthmap to determine the integration degree (including global integration degree and local integration degree), selectability degree (including global selectability degree and local selectability degree), and to draw the quantitative indexes of each type of axial analysis, and the quantitative indexes of each type of axial analysis are shown in Table 2.

From the global integration degree of A1 village, it can be seen that the integration degree of the local space of the village is similar to that of the global integration degree. the average value of the global integration degree of A2 village is about 0.96, and the average value of the local integration degree is about 1.44. The overall accessibility of the village is high, and the spatial connection of the village is relatively close, and the layout is uniform. the shape of A3 village is similar to a windmill, and the spatial structure of the village shows that it is the group structure of multiple clusters, with the streets and lanes being interlocked, and the road system is complicated. the road system of A4 village is complex. A4 village is located in the hilly area, with large undulations in the mountainous terrain, and the architectural layout is subject to certain limitations, and the overall spatial structure of the village is relatively simple. the village structure of A4 village is relatively close, with alleys and lanes, and the utilization rate of the space is relatively high. The area with the highest global integration degree is the north-south oriented Tianjie, with a maximum global integration degree of about 1.35. The Cao Family Ancestral Hall, which is placed at the entry of the village and matches the axis of the village entry in the southeast corner, possesses a lowest whole integration degree of about 0.43, which are the main entrances and exits of the village. The local integration degree is similar to the global integration degree. A5 village is distributed in a southwest-northeast oriented linear pattern. The central main street, which runs east-west through the center of the village, exhibits a high degree of integration. The remaining component of the topological rank order of streets and lanes along the center line of the village is somewhat less obvious than the central-axis main street. When they are combined with the alleys that go along the central main axis, they connect the village and form the primary traffic network that is inside the village area.

The analysis of the integration and selectability of the five types of traditional villages can be summarized as:

1) Centralized and grouped traditional villages have the highest accessibility, good cohesion of the village, clear hierarchy of the street structure, good village orientation, and high comprehensibility of the overall space from the local space. In their village space, most of them take the ancestral hall as the center of village gathering, and combine with the surrounding streets and lanes to form the gathering point of public space.

2) Radial traditional villages are influenced by many factors, and their village space grows freely in an irregular shape. There are two or more gathering points in the village, even forming a gathering belt. The correlation between the accessibility of the village and its radial type is not strong, which indicates that besides the boundary shape index, the accessibility of the street space of traditional villages is also affected by its scale.

3) The intra-village cohesion of belt-type and line-type traditional villages is not high, and the village consists of a number of clusters together, the spatial structure of the village is more difficult to understand, the street space is crisscrossed, and a large number of secondary alleys with a low topological structure level exist.

Table 2: Quantitative index table for axis analysis

	Value	Global integration	Local conformity	Global selection	Local selection
A1 village	Maximum value	1.25638	2.34986	2564	217
	Minimum value	0.43144	0.33335	0	0
	Mean value	0.94128	1.46298	514.18211	30.23841
A2 village	Maximum value	1.56173	2.52293	2905	224
	Minimum value	0.55699	0.42242	0	0
	Mean value	0.96084	1.44462	367.51223	27.30231
A3 village	Maximum value	1.59607	2.79824	5882	324
	Minimum value	0.58762	0.33333	0	0
	Mean value	1.00200	1.57775	768.82512	37.90973
A4 village	Maximum value	1.35438	2.22569	957	124
	Minimum value	0.43067	0.33331	0	0
	Mean value	0.86471	1.27396	199.17623	19.33338
A5 village	Maximum value	0.74541	2.30198	3102	136
	Minimum value	0.32783	0.33331	0	0
	Mean value	0.50607	1.18373	561.24245	14.97121

## 3.2 Spatial genetic diversity of traditional villages

### 3.2.1 Characterization of the diversity of spatial types

According to the classification results of traditional village spatial types which this paper gives, the main spatial types of traditional villages in G County include: boundary regions, covered bridge places, farmland regions, drum tower places, square regions, building spaces, road regions, well pavilion places, woodland regions, Sa altar places, mountain regions, water system spaces, stage spaces, and walled village entrance places. For the purpose of exploring the diversity characteristics of different spatial types, Table 3 displays the diversity indices of the five sample plots.

Table 3: Different spatial types of diversity index statistics

Space type	Diversity index			
	Margalef	Shannon	Simpson	Pielou
Boundary space	3.280	1.629	0.734	0.838
Weather bridge space	5.243	2.694	0.922	0.954
Arable space	3.188	1.862	0.838	0.960
Drum space	10.673	2.931	0.945	0.943
Square space	4.516	2.277	0.875	0.924
Building space	18.591	2.983	0.947	0.850
Street space	10.070	2.555	0.915	0.909
Well space	2.153	1.540	0.735	0.782
Woodland space	2.259	1.696	0.801	0.944
Altair space	1.852	2.211	0.883	0.964
Mountain space	1.544	1.586	0.760	0.890
Drainage space	1.853	1.587	0.767	0.888
Stage space	1.953	1.750	0.810	0.896
Gate space	3.998	2.078	0.840	0.872

According to what Figure 2 shows, among the space types of traditional villages in 14 counties of region G, the Magalef richness index has an obvious overall difference. From the perspective of numerical magnitude, the index has a gradual decreasing tendency in the order of architectural space, drum tower space, street space, wind and rain bridge space, and square space. The Magalef richness index for building space achieves the maximal numerical value, attains 18.591, and the mountain space According to the actual survey results, the architectural space type presents the basic characteristics of many components, diverse forms and varieties in the composition of elements, thus increasing the richness index of this space type. Drum towers, streets and wind and rain bridges, as spatial types with an important position in traditional village culture, have different spatial styles and forms according to the economic capacity of their respective villages and the composition of their family names, and naturally become an important part of the space of the traditional villages in G County. Mountain space has the lowest richness index, and the degree of transformation of mountains is low. It reflects the basic cultural concepts of reverence for nature and harmonious coexistence with nature in traditional village culture.

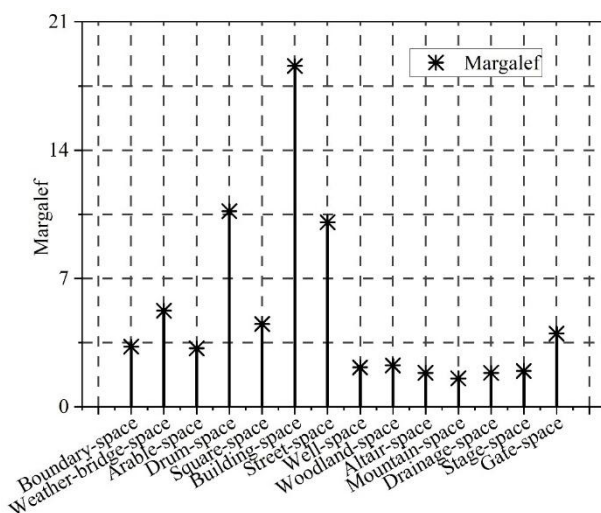


Figure 2: Magalef richness index

In the traditional village sample site, theoretically, the more spatial typology, the greater the Shannon diversity index of its spatial type, the Shannon/Simpson diversity index of different spatial types is shown in Figure 3, in the table of traditional villages in County G, the trend of the Shannon diversity index of spatial types is in line with this law, along with the big area of architecture, the space of the Drum Tower, Wind and Rain Bridge space, Simpson index represents the degree of concentration of the spatial types of traditional villages, and in the five traditional village sample plots, the trend of the Simpson diversity index of different spatial types is basically consistent with the trend of the Shannon diversity index of spatial types. The Simpson diversity index of architectural space is the largest (0.947), and the Simpson diversity index of boundary space (0.734) is the smallest.

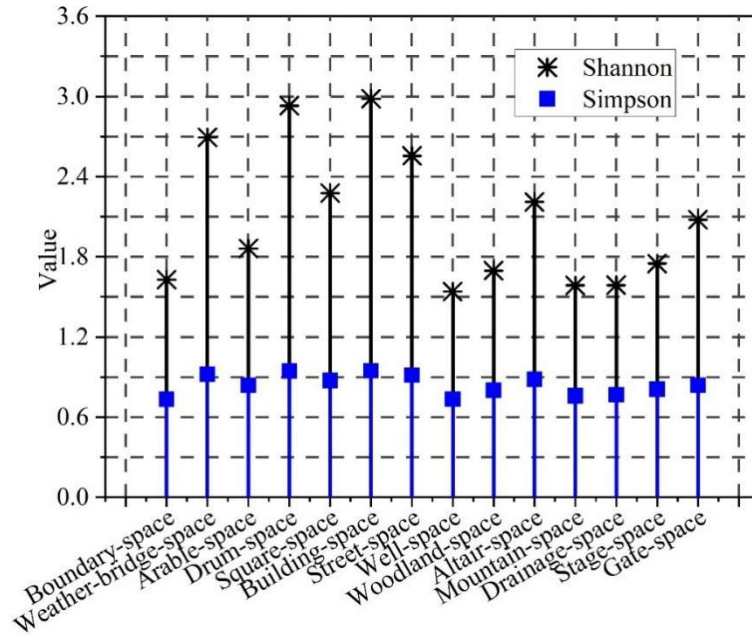


Figure 3: Shannon/Simpson index

Pielou uniformity index is shown in Figure 4, Pielou uniformity index is the degree of uniformity of distribution of different spatial types in traditional village sample plots, the uniformity index of various spatial types of traditional villages in County G has a large variability, and the highest uniformity index is the space of Satsumas (0.964), which shows that there is a universality of the distribution of the villages, and that although the activity of “Satsumas” has gradually disappeared, the Satsumas are still a necessary part of the villages in County G. The well-pavilion space has the lowest Pielou uniformity index. According to the result of actual investigation, we can find that in Village A4, the total number of existing well-pavilions is seven. On the opposite side, the other village places have already built one or two good pavilion regions. The well-pavilion place acts as an important space which villagers of G county get daily life water from. The number of well-pavilion spaces reflects the level of water requirement, hence these quantitative characteristics also reflect the overall population scale of the villages.

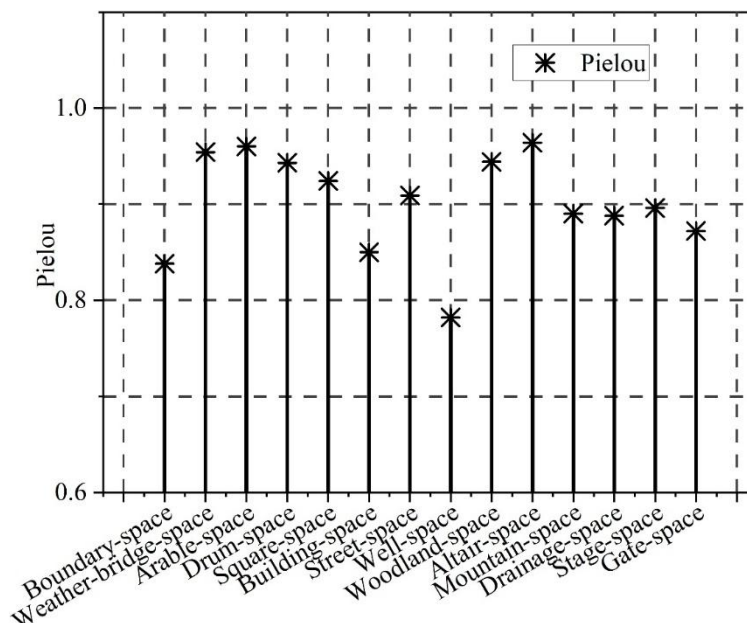


Figure 4: Pielou uniformity index

### 3.2.2 Characterization of spatial genetic diversity

For evaluating the influence that mutated genes bring to the spatial hereditary variety of traditional villages, we utilize the Traditional Village Assessment and Confirmation Index System which is published by the Ministry of Housing and Urban-Rural Development. In addition, we carry out the integration of the General Situation Materials of County G and a number of volumes on practice research works of old villages. The whole spatial genes of traditional villages in G County are divided into two big kinds: native genes and external genes. The classification principles are showed in Table 4. According to this categorization, we carry out the measurement of the related diversity indices.

Table 4: Basic principles of local and foreign gene classification

Gene type	Basic principles of classification
Native gene	The period of formation has a certain length
	Can represent traditional production lifestyle
	There is a certain period of features and coordination with the surrounding environment
	Spatial genes have regional characteristics and can reflect cultural characteristics
Foreign gene	Lack of regional characteristics, homoqualitative severity
	The appearance and the overall landscape are different
	The formation period is shorter and has obvious modern industrial characteristics
	Lack of matching with traditional lifestyle

Table 5 shows the four indexes of Margalef richness index, Shannon diversity index, Simpson diversity index, and Pielou evenness index for the five traditional village sample sites. The calculation results show that the spatial genetic Margalef index, Shannon index, and Simpson index of traditional villages in County G are 13.966-15.477, 3.361-3.445, and 0.951-0.956, respectively; and the Pielou index is 0.691-0.743, and the diversity indices within each

sample site vary greatly, but the overall spatial The diversity indices within each site varied greatly, even so, the whole space genetic diversity indexes still keep on a comparatively high level. In special, every one of the Shannon indices was above 3.0, which therefore indicated that the spatial genetic diversity was located at a relatively plentiful degree.

Table 5: Statistics on spatial gene diversity in villages

Survey land	Margelef	Shannon	Simpson	Pielou
A1	15.302	3.413	0.955	0.718
A2	15.477	3.361	0.955	0.699
A3	13.966	3.445	0.956	0.743
A4	14.869	3.380	0.954	0.691
A5	15.212	3.371	0.951	0.703

The Pielou evenness index that belongs to traditional villages in the five sampled regions is on a comparatively low level, among which A4 village has the lowest Pielou homogeneity index of 0.691. Species homogeneity is correlated with richness, and the spatial gene abundance-homogeneity plot is shown in Fig. 5, with the blue ellipse as the 95% mean confidence interval. The richness and homogeneity indexes of A4 village are at a low level, and its diversity index is also at a low level. The richness index of A2, A1 and A5 villages is at a higher level, while the evenness index is significantly lower than that of A3. A3 village has the lowest richness index and a higher evenness index, which reflects the small number of spatial gene species within A3 village, but the overall distribution of the characteristics is more uniform.

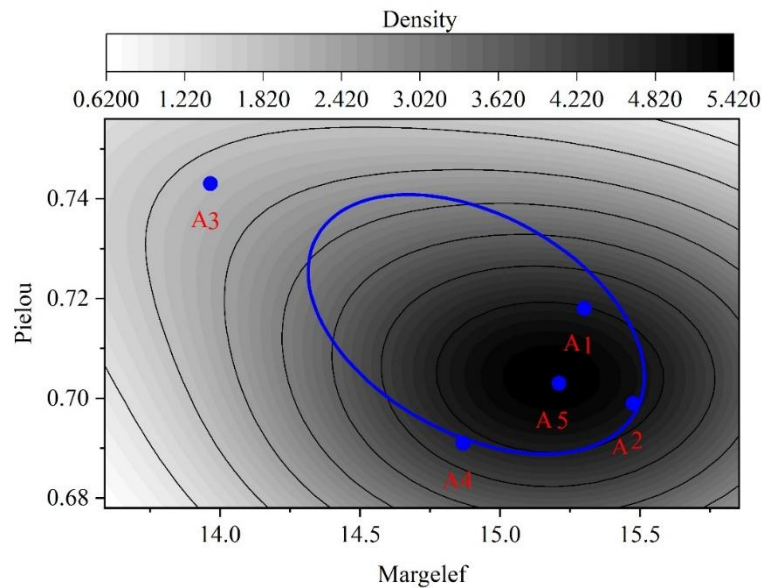


Figure 5: The richness of the sample village - the uniformity divergence

The results of the diversity indices of the two spatial gene types, indigenous and exotic, in the five sample traditional villages and the comparison with the gene diversity indices of the villages as a whole are shown in Tables 6 and 7, respectively.

The diversity calculation values of the local genes in the five collected villages are almost the same as the whole diversity calculation values of the genes, and the Pielou evenness indices of the indigenous genes of the five sample villages are all in the range of 0.65 to 0.75, and their indigenous genes have a low evenness. Among all kinds of diversity indices, the outer genetic diversity indices of Village A4 and Village A3 are in a relatively high level. However, because

there are no scientific and effective management methods, the local features of both Village A4 and Village A3 have encountered different levels of destruction. This therefore has caused a more obvious difference in outside look and characteristics when it is compared with other old-style villages.

Table 6: Local and foreign space gene richness index

Survey land	Margalef		
	Native gene	Foreign gene	Integral gene
A1	13.357	1.688	15.303
A2	14.197	1.011	15.475
A3	12.467	1.355	13.959
A4	13.495	1.144	14.871
A5	14.198	0.884	15.212

Table 7: Local and foreign spatial gene diversity index

Survey land	Shannon			Simpson			Pielou		
	Native gene	Foreign gene	Integral gene	Native gene	Foreign gene	Integral gene	Native gene	Foreign gene	Integral gene
A1	3.274	1.524	3.414	0.946	0.634	0.952	0.706	0.581	0.717
A2	3.240	1.071	3.364	0.948	0.647	0.951	0.685	0.609	0.697
A3	3.260	1.782	3.446	0.946	0.767	0.952	0.718	0.739	0.741
A4	3.189	1.805	3.382	0.943	0.791	0.954	0.670	0.752	0.697
A5	3.291	1.374	3.371	0.95	0.612	0.952	0.694	0.663	0.703

### 3.3 Construction of spatial genetic map of traditional village settlement pattern

Just like genes control the appearance of biological characters, the appearance of the spatial structure of traditional villages is also affected by genes which adjust spatial shape. Referring to the composition structure of biological genes “DNA molecule (genome)-nucleotide (gene)-base (gene locus)-protein (biological trait)”, there exists the following correspondences between genes of spatial morphology of traditional villages and biological genes. The following correspondences exist between traditional village spatial morphology genes and biological genes: ① Referring to the whole-to-part description of biological traits, colonies also include macro, meso, and micro spatial levels; ② Analogous to the different parts of biological traits, the overall spatial morphology representation of the colony is also composed of multiple colony morphology elements; ③ The gene loci control the arrangement of nucleotide molecules, and therefore control a specific trait of the organisms, and similarly, the colony covers multiple spatial sub-elements which control the overall morphology of the colony. Similarly, colonies contain multiple spatial sub-elements that control the overall morphology of the colony.

In summary, the study constructed a spatial gene description system for colonies analogous to genetics, i.e., genome, gene, locus, and trait, which correspond to the spatial research level of the colony, separately, the overall spatial shape characteristics of the colony, the spatial shape properties of the colony, and the spatial shape depiction of the colony. Spatial gene mapping is an abstract expression of complex spatial features. Among them, the connotation of the mapping with natural elements as the entry point is richer. In this paper, drawing on the human genome's expression of gene types on each chromosome and the base combination law of the constituent genes, we use the spatial parts to explain all rules that control gene combinations in

the spatial shape of colonies and the influence of natural factors. After that, we make the spatial gene drawing of the colony shape, which is shown in Figure 6.

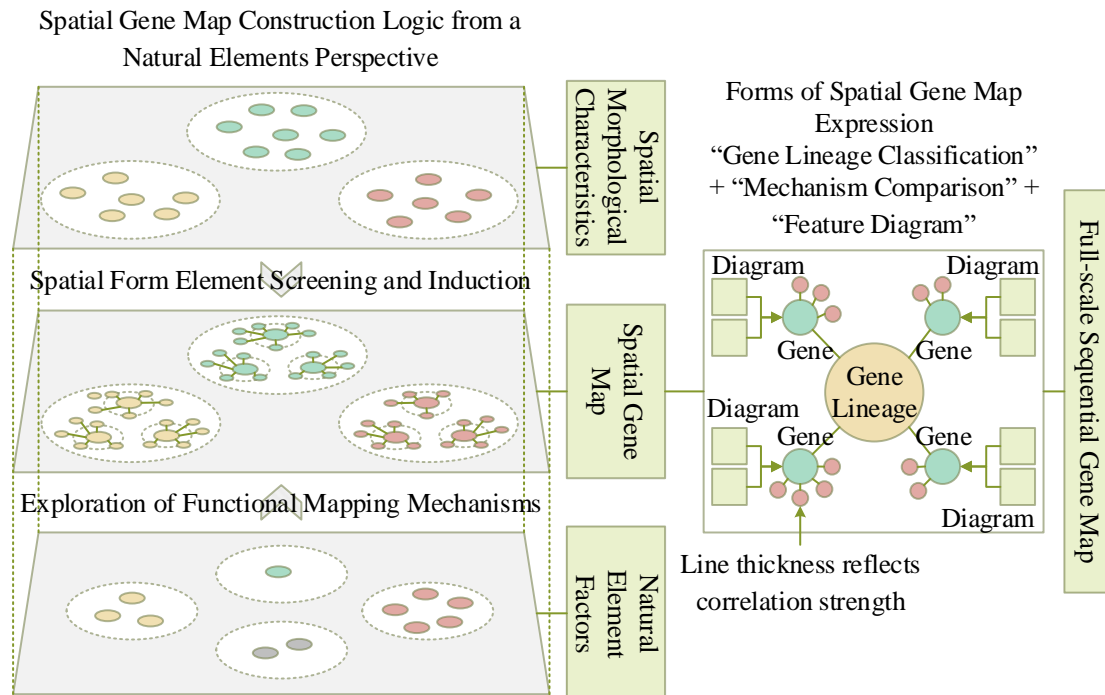


Figure 6: The spatial gene spectrum of the natural elements perspective

## 4 Application of GIS in landscape planning for traditional villages

Currently, geographic information technology is being widely used in village cultural landscape planning, which will provide landscape designers with more scientific and rational decision-making methods and promote the development of cultural heritage protection in a more modern direction.

### 4.1 Auxiliary Village Landscape Pattern Study

GIS, as a means of spatial analysis, can quantitatively assess the village landscape pattern and the sensitivity of the village landscape, help decision makers make precise descriptions of the geographic location of the village landscape and the spatial relationship between each other, and provide objective and comprehensive strategies for the optimization of the village landscape pattern. GIS has the following four main roles in the study of the village landscape pattern: (1) to classify and organize the landscape resources and establish a digital platform. (1) Classify and organize the landscape resources and establish a digital platform. (2) Evaluate the characteristics of village landscape pattern through spatial analysis. (3) To scientifically and quantitatively study the spatial distribution patterns and structural patterns of village landscapes. (4) Extract typical village landscape structures and apply them to the planning and design of village landscape.

## 4.2 Quantitative results of village spatial patterns

A landscape gene is the basic heredity unit which controls the cross-generation passing of one particular cultural landscape part, and makes it different from other cultural landscape features. On the opposite side, it also acts as the main marking symbol for these cultural landscape characteristics. The research on the concept of the landscape gene is in a quite early-stage situation. Only in the recent period has it more and more obtained the attention from scholars.

The existing landscape gene research using GIS has a set of established research system, which mainly includes the refinement, division and coding of landscape genes. Under this background, the coding of landscape genes possesses very important meaning for the follow-up researches on cultural landscapes. and scholars mostly use feature coding to distinguish different landscape genes on the basis of weighting assessment of existing cultural landscape elements, while the evaluation criteria mainly depend on the time of origin of the cultural genes, the native environment and the influence on the radiated area. On the basis of obtaining the detailed coded landscape genes in the region, GIS is utilized to construct a settlement database consisting of a geographic database and a library of characteristic elements. The spatial data are used to show the distribution of different landscape genes in space and their relationship with each other, while the attribute data differentiate various types of landscape genes.

By importing the existing data into the GIS platform, the spatial characteristics of the distribution of landscape genes can be intuitively recognized, which helps to study the existence form of cultural landscape genes, the inheritance characteristics, and the connection with the surrounding areas.

## 4.3 Participation in the digital preservation of village cultural landscapes

Digital technology has been widely used in all walks of life, three-dimensional laser scanning, virtual reality, intelligent management and other technologies have been successfully served in the protection of cultural heritage, through these digital technologies and its combination with GIS, can effectively study the spatial attribute characteristics of the village cultural landscape, and build a database to analyze the spatial information basis. After we collect together all existing research documents about digital protection of traditional villages and cultural landscapes, therefore we put forward a working plan that uses GIS to carry out digital protection research on these objects. This strategy may on the whole be divided into several phases: data evaluation, field investigation, data processing, and practical model construction.

## 5 Conclusion

This research focuses on the special methods for extracting the space genes of old villages and planning and making the environment landscape. This paper puts forward a method framework which is from the finding of spatial genes to the counting of village shape features. This frame provides a reference point for the making plan and design of the environment landscape.

The entirety spatial gene abundance of traditional villages that are in County G is comparatively high. In these villages, it is Village A2 that has the maximum value of the Margalef richness index. This is the reason that its traditional landscape and historical-cultural heritages are well kept, hence repair policies have gotten effective implementation. In all kinds of space types of traditional villages, the architecture space holds the highest Magalef richness index, which reaches 18.591. The increment of the abundance of foreign genes can cause the local genes to lose their inherent superiority. Therefore, the entirety spatial heredity diversity exponent of traditional villages still keeps on a comparatively high level. When the overall space gene multifariousness index is high, traditional villages have a bigger probability that

they can be assimilated by outer gene intrusions. This kind of condition is not beneficial to the sustainable development of these village groups. Therefore, the carrying out of monitoring on the diversity index of traditional villages can therefore provide real-time comprehension of their present development condition. This is helpful for the related departments to make policies for protecting the precious cultures and special buildings of old traditional villages.

GIS and other digital technologies are playing an increasingly important role in the planning of traditional village landscapes. This study designed a landscape planning strategy that facilitates the cultural inheritance and development of villages from three aspects, namely, assisting in the assessment of rural landscape patterns, storage and management of landscape genes, and digital conservation. The strategy not only preserves the original historical landscape and natural environment of traditional villages, but also utilizes digital technology to deeply excavate the vitality and resources of traditional villages, so that the unique traditional village culture can be sustainably developed in the long history.

## About the Author

Yue Han was born in Huludao, Liaoning, P.R. China, in 1994. She obtained a doctor's degree from a Woosuk University in South Korea. I am currently working at the School of Art and Design, Fuzhou University of Foreign Languages and Trade. My main research direction is traditional gardens and landscape design.

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