An Intelligent Identification Method for Urban Renewal Potential Based on Spatial Gene Theory: A Case Study of Shanghai

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1 Introduction

Urban renewal has emerged as a central governance challenge in megacities undergoing the transition from expansion-driven development to quality-oriented redevelopment. In China, the "14th Five-Year Plan" and the "Urban Renewal Regulations of Shanghai" have elevated renewal to a national strategy, emphasizing people-centered, inclusive, and resilient development. Yet, governance practices face significant hurdles in identifying renewal areas: current evaluations largely rely on qualitative assessments, static surveys, or outdated planning documents. This results in inefficiencies, misallocated resources, and unequal outcomes, particularly in complex urban environments where physical form and socioeconomic dynamics interact in unpredictable ways.

International experiences highlight that accurate spatial identification of renewal zones is fundamental for adaptive governance. For example, London delineates renewal areas through multi-dimensional monitoring reports and strategic plans, Paris employs urban observatories to track change (Desjardins 2018), while Berlin integrates renewal monitoring into city development systems (Ahlfeldt et al. 2017). These cases show that advanced tools can enhance governance by providing dynamic, evidence-based insights. In the Chinese context, however, the gap between traditional qualitative methods and the demand for precise, data-driven governance remains wide.

Against this backdrop, Chinese scholar Duan Jin first introduced the theoretical framework of "spatial genes," emphasizing that urban morphology emerges as patterned combinations accumulated over long-term interactions between natural environment and historical culture (Liu et al. 2023). Spatial genes not only reflect the uniqueness and relative stability of urban form but also profoundly shape evolutionary pathways and spatial logics across different stages of urban development. Building morphology serves as the phenotypic manifestation of spatial genes, with structural arrangements, scale systems, and layout patterns providing critical entry points for decoding the organizational logic of urban space. Because spatial genes are replicable and transmissible, morphological evolution often displays identifiable spatiotemporal trajectories, particularly evident during periods of intensive transformation such as urban renewal. Tracking building morphology dynamically during renewal processes thus offers both theoretical insight into spatial gene evolution and practical pathways for identifying areas with continuity and renewal potential.

A growing body of international and domestic research has expanded this perspective. (Delmelle 2016), for instance, treated neighborhood socioeconomic status as a phenotypic trait of spatial genes, using sequencing methods to reconstruct the trajectories of Chicago and Los Angeles neighborhoods, thereby revealing gentrification and suburban upgrading. In China, scholars have analyzed historic districts, traditional towns, and cultural landscapes through spatial gene theory, uncovering how morphological patterns encode cultural, social, and institutional logic. Much of this work draws on Conzen's urban morphology framework, which conceptualizes the city as composed of blocks, street networks, and buildings, and highlights how morphological evolution exhibits path dependence (Conzen 1960, Moudon 1997). While studies have successfully identified renewal trajectories using block-level transformations, remote sensing–based indices, or field surveys, existing approaches are often limited to static snapshots, lack standardized metrics, and remain dependent on manual classification. This restricts their ability to capture dynamic evolution in rapidly transforming megacities.

To overcome these limitations, this paper develops a four-step research framework: identify already renewed spaces, extract morphological evolution rules, construct a spatial gene atlas, and reverse-engineer renewal potential. Using the China Building Rooftop Area (CBRA) dataset, we extract morphological indicators to identify internal spatial genes of typical forms such as old urban districts and central districts, and apply a Random Forest model to analyze the driving features and spatial potential of urban renewal. Shanghai's Old City, for example, has undergone massive redevelopment over the past two decades, with less than 40% of its traditional lilong fabric preserved (Shan et al. 2022). In this context of rapid transformation, recognizing areas of morphological disruption and guiding them toward sustainable renewal has become a critical challenge in planning. With Shanghai's ambition of building a "quantum city," digital transformation and smart urban governance are accelerating. By selecting Shanghai as a case study, this research aims to integrate morphological identification with renewal strategies, enrich methods of spatial gene analysis, and explore new pathways of urban renewal under the paradigms of "digital empowerment" and "data-driven governance."

2 Methods

The study draws on the China Building Rooftop Area (CBRA) dataset, the first multi-annual (2016–2021), high-resolution (2.5 m) building footprint dataset derived from Sentinel-2 imagery using deep learning segmentation techniques (Liu et al. 2023). This provides a dynamic foundation for monitoring morphological change across Shanghai. Six morphological indicators were extracted from building footprints: total building area, mean perimeter, building count, shape index, compactness, and orientation entropy. These indicators capture the "phenotypic traits" of spatial genes, reflecting the city's internal coding logic in physical form.

The analytical framework followed four steps:

1. Identifying renewed parcels by tracing transitions from "old urban district" (O-type) to "central urban" (C-type) building morphologies.
2. Extracting the morphological evolution rules using Gaussian Mixture Models (GMM), which cluster building morphologies into seven stable gene types.
3. Constructing a predictive model of renewal potential using Random Forest (RF), incorporating 14 variables across morphology, spatial accessibility, and socioeconomic factors.
4. Applying SHAP (Shapley Additive Explanations) to interpret variable importance, ensuring that model outputs could be understood in governance terms rather than treated as opaque algorithmic results.

Crucially, the methodology was designed not only as a technical exercise but also as a governance tool. Renewal parcels identified through spatial genes can be directly mapped to policy frameworks such as designated renewal units, urban design control zones, and district-level strategies. By offering dynamic, fine-grained insights, the method supports more inclusive and adaptive governance.

3 Results

The GMM clustering identified seven distinct spatial gene types: old urban district (O), central urban (C), near-suburban (U), suburban development (D), suburban low-density (S), rural continuous (L), and rural scattered (R). These types together reveal concentric morphological layers from central Shanghai to its peripheries, forming a gene-based typology of the city's urban fabric.

Renewal was defined as the transition from O-type to C-type morphology. Between 2016 and 2021, Shanghai's renewal areas exhibited shifting geographies: initially concentrated in the north, then spreading toward the southwest, with renewed parcels clustering in both inner-ring districts and suburban town centers. High-intensity updates occurred in central neighborhoods such as Huayang Road and Baoshan Road, while extensive renewal parcels emerged in suburban areas like Anting and Jiading.

The RF model achieved an accuracy of 88.7% on the test dataset, confirming strong predictive capacity. SHAP interpretation revealed that five variables were especially influential: total building area, mean perimeter, construction year, distance to city center, and housing price. Renewal potential was highest in areas characterized by small, fragmented parcels with poor compactness, favorable accessibility, moderate housing values, and older construction dates. Mapping results highlight a ring-shaped cluster of renewal potential between the inner and outer rings, particularly along the Suzhou Creek corridor, Huangpu River midstream, and historic districts such as Laoximen. Suburban renewal potential is concentrated in county centers like Jiangqiao, Sanlin, and Beicai, forming point-based clusters aligned with ongoing governance priorities. These spatial patterns provide clear evidence of where governance interventions may be most effective.

4 Discussion

The findings carry significant implications for governance under the theme of "tools revisited." First, the study demonstrates how data-driven tools can bridge

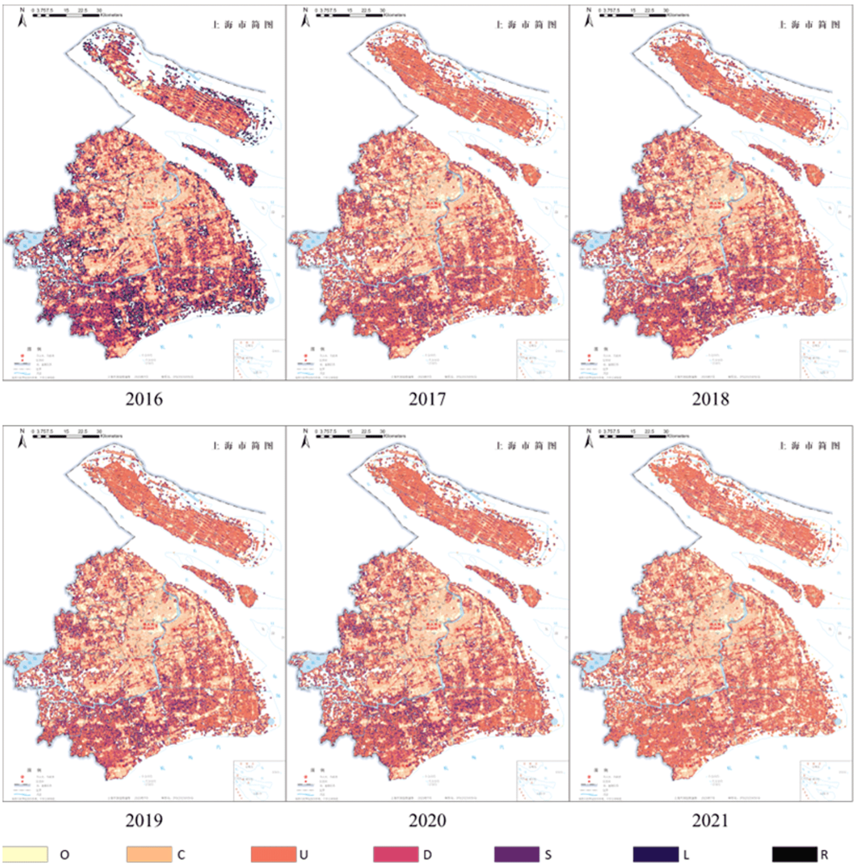

Figure 1: Spatial Distribution Map of Spatial Gene Types in Shanghai

the gap between morphological complexity and governance demands. Traditional methods of identifying renewal areas rely heavily on manual surveys or static indicators. By contrast, the spatial gene approach dynamically captures morphological transitions and provides predictive insights, enabling governments to move from reactive responses to proactive strategies. This contributes to building inclusive governance systems by improving transparency, accuracy, and accountability.

Second, the results highlight the social and economic accessibility dimensions of governance. Renewal potential is not evenly distributed: central historic neighborhoods face intense redevelopment pressures, while suburban county centers show concentrated potential. For governance, this implies the need to balance large-scale redevelopment with micro-renewal strategies to avoid exacerbating

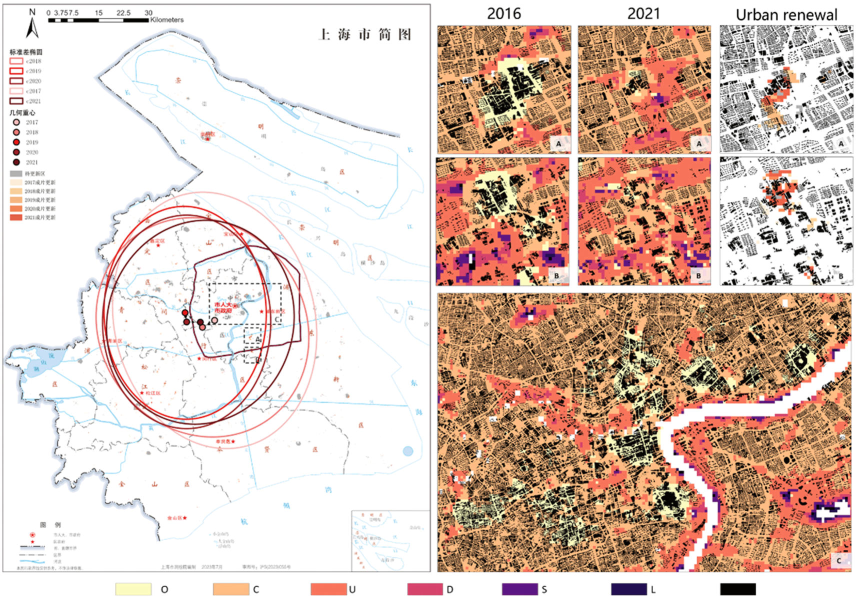

Figure 2: Urban Renewal Findings in Shanghai, 2016–2021

Figure 3: Feature Importance Distribution (Left), SHAP Beeswarm Plot (Right)

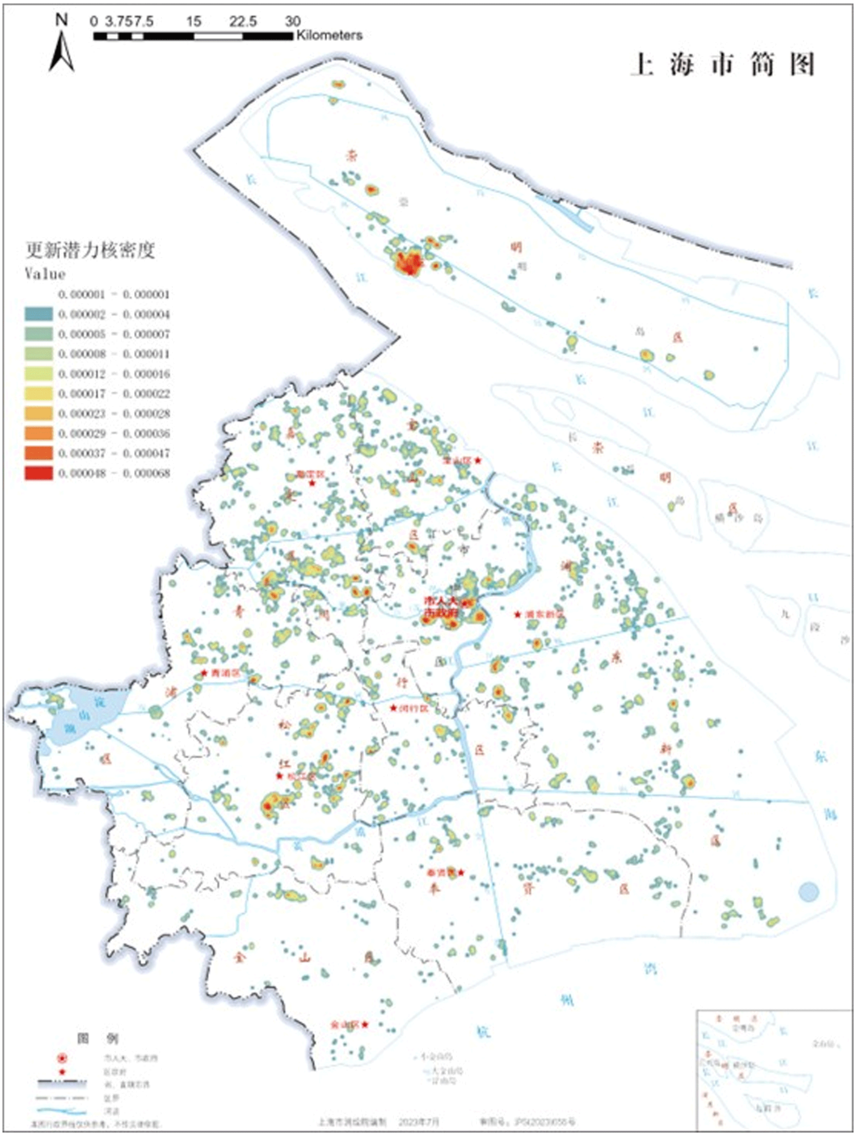

Figure 4: Kernel Density Map of Urban Renewal Potential in Shanghai

inequality. Integrating predictive results with participatory planning processes can ensure that data-driven decisions do not marginalize vulnerable groups.

Third, the study raises critical risks of algorithmic governance. While machine learning improves accuracy, it risks reinforcing biases if left unchecked. For example, "hidden renewal" forms such as functional repurposing or internal retrofits may not alter building footprints and therefore escape detection. Relying solely on morphological indicators could privilege visible, large-scale renewal while overlooking community-led, small-scale improvements. This underscores the importance of combining AI-driven identification with institutional safeguards, public participation, and cross-validation through fieldwork.

Finally, the work connects to broader debates on digital twins and quantum cities. Shanghai's ambition to develop a "quantum city" requires governance tools that integrate AI, real-time monitoring, and simulation. The spatial gene approach contributes a foundational layer for such digital governance architectures. However, ensuring that these tools enhance democratic processes rather than replace them is a pressing challenge. The future lies in hybrid governance models where data-driven tools provide evidence and foresight, while communities and institutions retain agency in decision-making.

5 Conclusion

This study develops an intelligent method for identifying urban renewal potential using spatial gene theory and machine learning. The method demonstrates strong predictive performance and reveals spatial patterns of renewal potential in Shanghai. Beyond technical contributions, the research critically reflects on how data-driven tools can support or challenge inclusive governance. By explicitly addressing both opportunities and risks, the study positions spatial gene identification not just as a methodological innovation but as a governance instrument in the era of digital transformation.

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