



Spatial Analysis

1-A spatial autocorrelation analysis of road traffic crash by severity using Moran's I spatial statistics: A comparative study of Addis Ababa and Berlin cities

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Abstract

Methodological advancements in road safety research reveal an increasing inclination toward integrating spatial approaches in hot spot identification, spatial pattern analysis, and developing spatially lagged models. Previous studies on hot spot identification and spatial pattern analysis have overlooked crash severities and the spatial autocorrelation of crashes by severity, missing valuable insights into crash patterns and underlying factors. This study investigates the spatial autocorrelation of crash severity by taking two capital cities, Addis Ababa and Berlin, as a case study and compares patterns in low and high-income countries. The study used three-year crash data from each city. It employed the average nearest neighbor distance (ANND) method to determine the significance of spatial clustering of crash data by severity, Global Moran's I to examine the statistical significance of spatial autocorrelation, and Local Moran's I to identify significant cluster locations with High-High (HH) and Low-Low (LL) crash severity values. The ANND analysis reveals a significant clustering of crashes by severity in both cities, except in Berlin's fatal crashes. However, different Global Moran's I results were obtained for the two cities, with a strong and statistically significant value for Addis Ababa compared to Berlin. The Local Moran's I result indicates that the central business district and residential areas have LL values, while the city's outskirts exhibit HH values in Addis Ababa. With some persistent HH value locations, Berlin's HH and LL grid clusters are intermingled on the city's periphery. Socio-economic factors, road user behavior and roadway factors contribute to the difference in the result. Nevertheless, it is interesting to note the similarity of significant HH value locations on the outskirts of both cities. Finally, the results are consistent with previous studies and indicate the need for further investigation in other locations.

Keywords

Author Keywords

[Spatial autocorrelation](#)[Crash severity](#)[Spatial analysis](#)[Hot spots](#)[Spatial pattern](#)[Moran's I](#)

Keywords Plus

[KERNEL DENSITY-ESTIMATION](#)[BICYCLIST INJURY](#)

[SEVERITY](#)[SAFETY](#)[IDENTIFICATION](#)[REGRESSION](#)[RISK](#)[FREQUENCY](#)[LEVEL](#)[HETEROGENEITY](#)[PERFORMANCE](#)



Spatial Analysis

2-Research on the construction of intangible cultural heritage corridors in the Yellow River Basin based on geographic information system (GIS) technology and the minimum cumulative resistance (MCR) model

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[HERITAGE SCIENCE](#) Volume 12 Issue 1 DOI [10.1186/s40494-024-01387-y](#) Article Number 271

Published AUG 1 2024 Indexed 2024-08-08 Document Type Article

Abstract

Objectively and accurately identifying the spatial structure and protection scope of intangible cultural heritage and constructing intangible cultural heritage corridors are crucial for the comprehensive systematic protection of intangible cultural heritage and the synergistic development of the region. However, the current research on intangible cultural heritage is limited to the protection and development of intangible cultural heritage in specific locations or specific areas. Thus, systematic and holistic research perspectives are relatively limited. Therefore, this study employs geographic information system spatial analysis and the minimum cumulative resistance model to construct an intangible cultural heritage corridor in the Yellow River Basin. This study aims to establish a systematic protection method and framework for intangible cultural heritage. The results show the following: (1) The intangible cultural heritage in the Yellow River Basin has a large-scale centralized distribution and small-scale scattered distribution, which provides an important spatial basis for the construction of intangible cultural heritage corridors. (2) Overall, intangible cultural heritage corridors can be more effectively constructed in the eastern region of the Yellow River Basin than in the western region, with 84.6% of the area being suitable and 15.4% being unsuitable. (3) Based on the suitability analysis, the "18 + N" corridor system of intangible cultural heritage in the Yellow River Basin, distributed across the eastern, central and southern regions, is constructed. The major corridor has a suitable width of 60-100 km, a total length of 11,935 km, and an area of 625,976 km²-919,942 km², and can connect 634-711 intangible cultural heritage sites in series. On this basis, this study proposes a multilevel construction system for intangible cultural heritage corridors in the Yellow River Basin that integrates the "network structure-spatial scope" and "element-axis-region" levels. This approach culminates in a pattern of intangible cultural heritage protection and development in the Yellow River Basin characterized by "connecting points into lines, distributing in groups, and linking regions." This study reveals that combining geographic information system spatial analysis tools with a minimum cumulative resistance model effectively identifies potential heritage corridor networks and clarifies the hierarchical relationships of heritage element protection in the study area. This approach provides a reference model for the comprehensive protection and systematic development of intangible cultural heritage in the Yellow River Basin. Furthermore, the effectiveness and universality of this framework make it applicable to the protection and development of other similar international heritage areas.

Keywords

Author Keywords



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[Yellow River Basin](#)[Intangible cultural heritage](#)[Heritage corridor](#)[Suitability](#)[Minimum cumulative resistance model](#)

Keywords Plus

[PROVINCEPATTERN](#)

Spatial Analysis

3- Geographically weighted random forests for macro-level crash frequency prediction

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Abstract

Machine learning models such as random forests (RF) have been widely applied in the field of road safety. RF is a prominent algorithm, overcoming the limitations of using a single decision tree such as overfitting and instability. However, the traditional RF is a global concept, and thus may fail to capture spatial variability. In macrolevel analysis of road safety, the relationship between crash frequency and risk factors can vary spatially. To address this issue, we employ a modified RF algorithm, named geographically weighted random forest (GWRF). Based on the data from London at the level of Middle-super-output-area (MSOA), the predictive performances of RF and GWRF are compared using mean absolute error (MAE) and root mean square error (RMSE). Moreover, considering MSOAs are geographically connected with each other, several factors related to the discrepancies between adjacent zones are also included in the models. Our results indicate that GWRF outperforms the traditional RF and GWR when an appropriate bandwidth is selected. We further explore the effects of multicollinearity on model performance. The results show that prediction accuracy of GWRF models are not susceptible to the multicollinearity. However, the importance values of those variables with multicollinearity may reduce. Finally, and of equal importance, it is found that the importance of each explanatory variable varies across zones. The density of minor road makes the highest contribution to crash frequency in downtown area, while the crash frequency in peripheral area is more sensitive to the discrepancy of road environment between MSOAs. With such information, road safety interventions can be designed and implemented according to the locally important factors, avoiding thus general guidelines addressed for the entire city.

Keywords

Author Keywords

[Road traffic safety](#)[Random forest](#)[Spatial analysis](#)[Crash frequency prediction](#)

Keywords Plus

[NETWORK FEATURES](#)[SAFETY](#)[HETEROGENEITY](#)[SEVERITY](#)[SENSITIVITY](#)[MACHINE CONTEXT](#)[IMPACT](#)

Spatial Analysis

4-Accelerated succession in Himalayan alpine treelines under climatic warming

By Sigdel, SR (Sigdel, Shalik Ram) [1] ; Zheng, XY (Zheng, Xiangyu) [1] , [2] ; Babst, F (Babst, Flurin) [3] , [4] ; Camarero, JJ (Camarero, J. Julio) [5] ; Gao, S (Gao, Shan) [1] ; Li, XX (Li, Xiaoxia) [1] ; Lu, XM (Lu, Xiaoming) [1] ; Pandey, J (Pandey, Jayram) [1] , [2] ; Dawadi, B (Dawadi, Binod) [6] ; Sun, J (Sun, Jian) [1] ; (provided by Clarivate) Source NATURE PLANTS Volume 10 Issue 12 DOI 10.1038/s41477-024-01855-0 Published DEC 2024 Early Access NOV 2024 Indexed 2024-11-26 Document Type Article

Abstract

Understanding how climate change influences succession is fundamental for predicting future forest composition. Warming is expected to accelerate species succession at their cold thermal ranges, such as alpine treelines. Here we examined how interactions and successional strategies of the early-successional birch (*Betula utilis*) and the late-successional fir (*Abies spectabilis*) affected treeline dynamics by combining plot data with an individual-based treeline model at treelines in the central Himalayas. Fir showed increasing recruitment and a higher upslope shift rate ($0.11 +/- 0.02$ m yr $^{-1}$) compared with birch ($0.06 +/- 0.03$ m yr $^{-1}$) over the past 200 years. Spatial analyses indicate strong interspecies competition when trees were young. Model outputs from various climatic scenarios indicate that fir will probably accelerate its upslope movement with warming, while birch recruitment will decline drastically, forming stable or even retreating treelines. Our findings point to accelerating successional dynamics with late-successional species rapidly outcompeting pioneer species, offering insight into future forest succession and its influences on ecosystem services.

Climate warming is accelerating successional dynamics, with late-successional species rapidly outcompeting pioneer species at Himalayan treeline ecotones, offering insight into future forest succession and its influences on ecosystem services.

Keywords

Keywords Plus

[SEEDLING RECRUITMENT](#)[SPECIES INTERACTION](#)[GLOBAL](#)

[CHANGED](#)[DYNAMICS](#)[FOREST](#)[REGENERATION](#)[FACILITATION](#)[VARIABILITY](#)[MOUNTAINS](#)[MORTALITY](#)



Spatial Analysis

5-Spatial structure and organization of the medical device industry urban network in China: evidence from specialized, refined, distinctive, and innovative firms

By Hu, F (Hu, Feng) [1] ; Yang, HJ (Yang, Huijie) [2] ; Qiu, LP (Qiu, Liping) [3] ; Wei, SB (Wei, Shaobin) [4] ; Hu, H (Hu, Hao) [5] ; Zhou, HY (Zhou, Haiyan) [6] (provided by Clarivate) Source

FRONTIERS IN PUBLIC HEALTH Volume 13 DOI 10.3389/fpubh.2025.1518327 Article Number 1518327

Published MAR 14 2025 Indexed 2025-04-04 Document Type Article

Abstract

Introduction Investigating the network of firms in a specific industry helps explain industrial location and urban functions and provides guidelines for promoting industrial restructuring and high-quality development. Methods This study develops a network model for the relationship between firms and cities based on the data of listed Specialized, Refined, Distinctive, and Innovative (SRDI) medical device manufacturing firms in China to identify the spatial distribution and influencing factors of the urban network of such firms using network analysis and GeoDetector. Results and discussion Three conclusions are obtained from the study. First, the urban network of listed SRDI medical device manufacturing firms exhibits a sparse structure, with the density decreasing from east to west, and the out-degree presenting significant spatial concentration. Suzhou, Shanghai, and Shenzhen are the core of the network power. The in-degree presents low spatial concentration. Clearly differentiated network functions are observed. Second, significant spatial differences are noted between high- and low-level linkage networks from the perspective of corporate governance structure. Third, economic level, labour costs, level of opening-up, talent base, and technological innovation capability have significant effects on the urban network of listed SRDI medical device manufacturing firms.

Keywords

Author Keywords

[specialized and sophisticated firms](#)[urban network](#)[spatial organization](#)[listed firms](#)[medical device industry](#)

Keywords Plus

[WORLD CITY NETWORK](#)[SOCIAL NETWORK](#)[CITIES](#)[EVOLUTION](#)[PATTERNS](#)[GROWTH](#)

Spatial Analysis

6-Deciphering the tumor immune microenvironment: single-cell and spatial transcriptomic insights into cervical cancer fibroblasts

By Lin, ZH (Lin, Zhiheng) [1] ; Zhou, YW (Zhou, Youwei) [2] ; Liu, ZR (Liu, Zhenran) [2] ; Nie, WY (Nie, Wenyang) [3] ; Cao, HJ (Cao, Hengjie) [1] ; Li, SN (Li, Shengnan) [1] ; Li, XL (Li, Xuanling) [1] ; Zhu, LJ (Zhu, Lijun) [1] ; Lin, GY (Lin, Guangyao) [1] ; Ding, YY (Ding, Yanyu) [4] , [5] ; (provided by Clarivate) Source JOURNAL OF EXPERIMENTAL & CLINICAL CANCER RESEARCH Volume 44 Issue 1 DOI 10.1186/s13046-025-03432-5 Article Number 194 Published JUL 5 2025 Indexed 2025-07-09 Document Type Article

Abstract

Background Cervical cancer (CC) remains a significant global health challenge despite advancements in screening, HPV vaccination, and therapeutic strategies. Tumor heterogeneity, driven by epigenetic modifications, affects immune evasion, metastasis, and treatment response. Cancer-associated fibroblasts (CAFs) play a crucial role in CC progression and therapy resistance. Single-cell sequencing offers new insights but remains underutilized in CC research. This study integrates single-cell RNA sequencing (scRNA-seq), spatial transcriptomics, and deconvolution analysis to identify key genes and immunotherapy targets. By constructing a prognostic model and exploring the immune microenvironment, we aim to provide novel insights into CC pathogenesis and potential therapeutic strategies.

Methods We utilized scRNA-seq, spatial transcriptomics, deconvolution analysis, and pseudotime trajectory mapping to delineate fibroblast subtypes within the tumor immune microenvironment (TIME) of CC. Functional annotations, differential gene expression profiling, cell-cell communication pathways, and transcription factor networks were systematically analyzed. A prognostic model based on bulk RNA-seq data was constructed and validated through survival analysis, with correlations to immune microenvironment characteristics. Functional experiments investigated the role of SDC1, a critical mediator of fibroblast-tumor crosstalk. Additionally, Fibroblast-tumor cell co-culture systems and functional assays were employed to investigate the paracrine role of SDC1. The CAF MYH11(+) subpopulation was isolated via fluorescence-activated cell sorting (FACS). Multiplex immunofluorescence and immunohistochemical analyses were performed on both cultured cells and human cervical cancer tissue samples to characterize the spatial distribution and dynamic remodeling of MYH11 during stromal reorganization.

Results Six distinct fibroblast subtypes were identified, including the C0 MYH11 + fibroblasts, which exhibited unique roles in stemness maintenance, metabolic activity, and immune regulation. Spatial and functional analyses revealed that the C0 subtype is central to tumor-fibroblast interactions, particularly through the MDK-SDC1 signaling axis. The prognostic model incorporating fibroblast-specific markers demonstrated robust predictive power for patient survival outcomes. Additionally, *in vitro* SDC1 knockdown significantly inhibited CC cell proliferation, migration, and invasion. Fibroblasts show spatially regulated heterogeneity, with activation markers enriched in the tumor zone and MYH11 highest in normal zones, indicating dynamic stromal remodeling.

C0 MYH11 + CAF Promotes Tumor Cell Proliferation, Migration, and Inhibits Apoptosis via Soluble SDC1.

Conclusion Our results illustrate, in some ways, the possible immunomodulatory and tumor supporting roles of CAFs in CC TIME and highlight the possibility that the MDK-SDC1 pathway is a promising therapeutic target. This



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study not only promotes a partially new understanding of temporal heterogeneity in CC, but also provides a possible reference base for the development of new biomarkers and immunotherapy approaches to improve clinical outcomes.

Keywords

Author Keywords

[Cervical cancer](#)[Tumor immune microenvironment](#)[Single-cell RNA sequencing](#)[Spatial transcriptomics](#)[Cancer-associated fibroblasts](#)[SDC1](#)[Immunomodulation](#)

Keywords Plus

[EXPRESSION](#)[GROWTH](#)[RADIOTHERAPY](#)[PATHOGENESIS](#)[CARCINOMA](#)[PATHWAY](#)[GENES](#)