CO-OCCURRENCE PATTERNS OF BACTERIAL AND FUNGAL COMMUNITIES ACROSS PH GRADIENT IN SALINE-ALKALINE GRASSLAND SOIL

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Abstract. Soil pH is a critical environmental parameter strongly correlating with microbial communities under various biogeochemical conditions. However, little is known about the co-occurrence pattern of microbial membership in compartments associated with different pH ranges of saline-alkaline grassland soils. To address this gap, we performed a network-based analysis using bacterial and fungal community datasets to characterize co-occurrence patterns and network topological features in four soil pH ranges in a saline-alkaline grassland. Our results indicate that the network topological features of the bacterial and fungal communities differ significantly between different pH ranges in the saline-alkaline grassland. The bacterial co-occurrence pattern in the pH range of 8.0-8.5 was more complex but less stable than that in the other pH ranges, while the fungal co-occurrence pattern had the opposite trend, being less complex but more stable in the pH range of 8.0-8.5. Our co-occurrence analysis identified 14 bacterial species (mainly *Proteobacteria* and *Chloroflexi*) and 5 fungal species (mainly in *Ascomycota*) as key taxa. Overall, our study provides insights into the effects of soil pH on microbial co-occurrence structure and identifies key microbial species in the saline-alkaline grassland of North China. These findings have practical implications for adjusting soil pH and core species to mediate soil microbial co-occurrence structure in saline-alkaline grasslands.

Keywords: microbial co-occurrence, grassland ecosystem, pH gradient, ecological interaction, microbial ecology

Introduction

Grassland, in the broader sense, is one of the largest terrestrial ecosystems on Earth, accounting for approximately a quarter of the planet's land surface area (Bengtsson et al., 2019; Wu et al., 2021). The Songnen grassland, the primary component of the northern agro-pastoral zone of China, has experienced significant land salinization and alkalinization. Soil microorganisms are a vital component of grassland ecosystems and play a crucial role in biogeochemical cycling, matter and energy conversion, and the maintenance of ecosystem functions and services (Jiang et al., 2021; Miao et al., 2020). Biogeographical distribution patterns of microbial communities have been extensively studied in various environments, and studies on microbial biogeography are rapidly being published (Lauber et al., 2009). However, the diversity and composition of microbial communities vary significantly across spatial environments, and this variation is thought to be associated with changes in various biotic or abiotic factors (Green et al., 2008; Perreault and Laforest-Lapointe, 2021). pH, as one of the critical environmental parameters in soils (Fernández-Calviño and Bååth, 2010), is strongly correlated with

microbial communities under a wide range of biogeochemical conditions (Jin and Kirk, 2018).

Soil pH primarily affects microorganisms by influencing the chemical, physical, and biological properties of the soil (Pietri and Brookes, 2008), which subsequently alters the environmental conditions necessary for their growth and survival (Bethke et al., 2011). Previous studies have examined the impact of soil pH on microbial diversity, composition (Zhalnina et al., 2015), microbial activity (Zhang et al., 2019) and microbial biomass (Malik et al., 2018). However, recent studies on the effects of soil pH on microbial processes have predominantly focused on species composition and diversity. For instance, in agricultural fields in the North China Plain, researchers observed that soil pH significantly impacted bacterial diversity and community composition (Shi et al., 2020, 2018). Yet, microbes do not exist in isolation in natural terrestrial ecosystems; they coexist with multiple species through the exchange of information, energy, and matter, thus forming complex interaction networks (de Vries et al., 2018). Recent studies have disclosed co-occurrence patterns in soil microbial communities across various terrestrial ecosystems (Ma et al., 2016). The ubiquitous cooccurrence pattern is particularly critical in understanding microbial community structure (Ma et al., 2016), providing novel insights into analyzing the relationships within the microbial community (Fan et al., 2018b), and presenting additional metrics to scrutinize niche spaces shared by community members (Ma et al., 2016). A recent study demonstrated that the modification of pH can influence the outcomes of competition between two bacterial species through a dynamic feedback loop (Shi et al., 2018). However, the composition and co-occurrence of microbial membership in different pH ranges associated with compartments of semiarid saline-alkaline grassland soils remain mostly unexplored.

Microbial co-occurrence network patterns have been well described for various habitats. For instance, Chen and his colleagues investigated the co-occurrence patterns of soil microbiota in the Tibetan alpine grasslands; where they found that soil pH was significantly associated with the topological features of soil microbial co-occurrence networks (Chen et al., 2021). In rhizosphere and bulk soil of wheat fields, researchers also found that soils with neutral pH had greater connectivity and stability relative to those in acidic or alkaline soils (Fan et al., 2018b). Moreover, a recent study showed that soil pH was the most important factor influencing the geographic distribution of bacterial network topology characteristics in both soybean rhizosphere and bulk soil (Zhang et al., 2018). Although soil pH has been shown to strongly influence co-occurrence networks at the various habitats (Faust et al., 2015), no attempt has yet been made to test how the species co-occurrence pattern of saline-alkaline grassland microorganisms changes with the variation of pH.

In the present study, we aimed to comprehensively assess and characterize the effects of soil pH on the co-occurrence patterns of soil microbiota in a semiarid salinealkaline grassland by conducting high-throughput sequencing (16S rRNA) and network-based analysis at 28 plots selected along a pH gradient in the ecosystem. Two hypotheses were proposed in this study. Firstly, we hypothesized that there would be significant differences in the diversity, composition, and co-occurrence topology of bacterial and fungal communities between different pH levels. Secondly, we hypothesized that the co-occurrence of bacterial and fungal networks in salinealkaline grassland ecosystems would show the same trend of change in response to variations in pH.

Materials and methods

Study site and field sampling

Our experiment was conducted in the central part of the Sonnen Steppe (Changling County, Jilin Province, China; 44°45′N, 123°45′E) (*Fig. 1*), which is situated in the East Eurasian steppe. The local climate is a typical mesothermal monsoon climate, with a mean temperature ranging from 4.6°C to 6.4°C, and annual precipitation varying from 280 to 400 mm. About 80% of rainfall events in the last 50 years (1961-2010) have occurred between June and August (Shi et al., 2019; Zhong et al., 2017).

In August 2017, we established four sites in the central part of the Sonnen Steppe (Changling County, Jilin Province, China, 44°45′N, 123°45′E) for our experiment. At each site, we set up seven 50 cm \times 50 cm plots, representing seven replicates, with 1 m distance between each plot, resulting in a total of 28 sampling plots. Soil samples were collected from each plot at a depth of 0-20 cm, and five soil cores were randomly collected and mixed to form a composite sample. All soil samples were stored in ice boxes at 4°C and immediately sent to the laboratory.



Figure 1. Location map for the study: hangling County, Jilin Province

DNA extraction and polymerase chain reaction

Soil genomic DNA was extracted from 0.5 g of soil using a Power Soil DNA Kit (Menlo Park, CA, USA). The V4 region of bacterial 16S rRNA was amplified by PCR using a primer pair (338F, 5'-ACT CCT ACG GGA GGC AGC A-3'; and 806R, 5'-GGA CTA CHV GGG TWT CTA AT-3'), while fungal Internal Transcribed Spacer primer pairs ITS1F (5'-CTT GGT CAT TTA GAG GAA GTAA-3')/ITS2R (5'- GCT GCG TTC TTC ATC GAT GC -3') were used. An equimolar amount of purified amplicons from each sample was pooled together and subjected to Illumina MiSeq sequencing at Majorbio Bio-Pharm Technology Co. Ltd. (Shanghai, China). Details on DNA extraction, quality control, and raw data processing can be found in Wang et al. (2015). Soil pH was measured in fresh soils, with a soil-to-water ratio of 1:5, using a pH monitor.

Statistical analysis

The α -diversity index (Shannon index) of bacteria and fungi was calculated by the diversity function in the "vegan" package in R (Oksanen et al., 2015). One-way ANOVA was conducted to investigate the differences in α diversity of bacteria and fungi between different ranges of pH. To explicitly test whether bacterial and fungal communities differed among different pH ranges, we performed the nonmetric multidimensional scaling (NMDS) using Bray–Curtis distances (metaNMDS function, VEGAN package) jointly with PERMANOVA (1000 permutations), applying the Adonis () function of the VEGAN package in R (Oksanen et al., 2015) on OTU data matrix.

Network analysis

A network analysis was performed to explore the interactions between soil bacterial and fungal species at different pH ranges. Spearman's correlation method was used to assess the associations of bacterial and fungal species, with values having a correlation coefficient r > |0.6| and significance P < 0.05 selected for constructing co-occurrence networks. Correlation matrix analysis was carried out using the "Hmisc" package in R software. The network visualizations were created using Gephi version 0.9.3. Subnetworks were generated for every soil sample using the subgraph function in the "igraph" package in R. Topological features of each sub-network were also calculated using the igraph package and then standardized. Natural connectivity was used for the analysis of the robustness of the network structure. The stability of the network was evaluated by removing nodes from the static network to evaluate the rate of degradation of robustness (Peng and Wu, 2016).

We defined the nodes as peripherals (Zi < 2.5, Pi < 0.62), network hubs (Zi \ge 2.5 and Pi \ge 0.62), module hubs (Zi \ge 2.5 and Pi < 0.62), and connectors (Zi < 2.5, Pi \ge 0.62) definitions by Deng et al. (2012). Based on their important role in the network topology, network hubs, module hubs and connectors are identified as potential key taxa (Banerjee et al., 2016).

Results

Data sets

After filtering and removing plant-derived sequences, a total of 1,341,192 bacterial and 1,878,191 fungal sequences were obtained in this study. Using 97% sequence identity, 2928 and 863 operational taxonomic units (OTUs) were identified for the bacterial and fungal communities, respectively. The bacterial community was dominated by *Actinobacteria* (22.2%), *Alphaproteobacteria* (19.6%), *Actinobacteria* (17.3%), *Gemmatimonadetes* (5.2%), and *Gammaproteobacteria* (4.4%). On the other hand, the fungal community was mainly composed of *Sordariomycetes* (36.4%), *Zygomycota* (9.13%), *Dothideomycetes* (12.5%), *Agaricomycetes* (7.8%) and an unclassified *Ascomycota* (7.1%) (*Fig. A1*).

Soil microbial diversity and community structure

To investigate the diversity and community structure of microorganisms in salinealkaline grassland soil across different pH gradients, the samples were categorized into four groups based on their soil pH ($7.5 \sim 8.0, 8.0 \sim 8.5, 8.5 \sim 9.5, 9.5 \sim 10.0$). Analysis of alpha diversity of bacterial and fungal communities, including Shannon index, Sobs index, Ace index, and Chao index, indicated significant differences along the pH gradients. The highest bacterial and fungal diversity were observed in the pH range of $8.0 \sim 8.5$, indicating that this pH range is optimal for the majority of microbes in saline-alkaline grassland soil (*Fig. A2*).

To visualize the patterns of bacterial and fungal community structure, nonmetric multidimensional scaling (NMDS) based on Bray-Curtis distances was employed. The NMDS analysis (*Fig. 2*) indicated no significant differences in the bacterial community structure, while fungal communities at different pH ranges were clearly separated. These findings were supported by the nonparametric multivariate statistical tests (Adonis) results, which also showed highly significant differences in fungal communities among different pH ranges.



• 7.5 ~ 8.0 **A** 8.0 ~ 8.5 **B** 8.5 ~ 9.5 + 9.5 ~ 10.0

Figure 2. Non-metric multidimensional scaling (NMDS) ordination plots of the bacterial and fungal community from different ranges of pH gradient. PERMANOVA showed significant differences in soil fungal community among different pH ranges

Key characteristics of microbial networks

To investigate the co-occurrence patterns of microorganisms in the soil of saline-alkaline grasslands under different pH gradients, eight networks (four for bacteria and four for fungi) were constructed and are shown in *Figures 3* and *4*. The bacterial networks consisted of 233, 218, 225, and 239 nodes, and 3269, 1502, 2091, and 3782 links in the pH ranges of 7.5 ~ 8.0, 8.0 ~ 8.5, 8.5 ~ 9.5, 9.5 ~ 10.0 respectively. The fungal networks consisted of 150, 198, 126, and 81 nodes, and 704, 1655, 954, and 340 links, respectively. All eight networks exhibited a "small-world" nature, as indicated by their observed average path length and clustering coefficient being greater than those of their corresponding random networks (see *Table A1*). The modularity values for all eight networks were greater than 0.4, suggesting that all of them had modular structures. (*Table A1*).

Structure and composition of microbial networks

The study found that the co-occurrence patterns of microorganisms in saline-alkaline grassland soil vary significantly across different pH gradients. The bacterial networks showed less complexity in the pH range of $8.0 \sim 8.5$, while the fungal networks were more complex in the same pH range (*Fig. 5*). The natural connectivity in the bacterial networks was greater in the pH range of $7.5 \sim 8.0$, $8.5 \sim 9.5$, and $9.5 \sim 10.0$, indicating greater network robustness in those pH ranges. On the other hand, the natural connectivity in the fungal networks was greater in the pH range of $8.0 \sim 8.5$ and $8.5 \sim 9.5$, indicating more stable bacterial networks, but less stable fungal networks in the pH range of $8.0 \sim 8.5$.

The bacterial networks were dominated by *Proteobacteria*, *Chlorflexi*, *Actinobacteria*, *Acidobacteria*, *Firmicutes*, and *Gemmatimonadetes*, with lower proportions of *Proteobacteria* and *Chlorflexi* in the pH range of $7.5 \sim 8.0$ and $9.5 \sim 10.0$, enriched with *Firmicutes* and *Gemmatimonadetes* compared to the networks in the pH range of $8.0 \sim 8.5$ and $8.5 \sim 9.5$. The fungal networks were dominated by *Sordariomycetes*, *Dothideomycetes*, *Eurotiomycetes*, *Agaricomycetes*, *Leotiomycetes*, an unclassified *Ascomyota*, and an unclassified Fungi, with greater proportions of *Sordariomycetes*, and *Agaricomycetes* compared to the other pH ranges.



Figure 3. Co-occurrence networks of bacterial and fungal communities at OTU level across different ranges of pH gradient. The size of each node reflect their degree of connection (i.e., degree). The nodes are colored by their corresponding categories



Figure 4. Topological properties of the bacterial and fungal co-occurrence networks in different range of pH gradient. pH1: 7.5 ~ 8.0, pH2: 8.0 ~ 8.5, pH3: 8.5 ~ 9.5, pH4: 9.5 ~ 10.0. Different letters indicate the significant level at P < 0.05, determined by the nonparametric Mann–Whitney U test



Figure 5. The natural connectivity of bacterial network in different ranges of pH gradient networks in bacteria and fungi

Module hubs and connectors

To evaluate the possible topological roles of each node in the network, we use connectivity within (Zi) and among modules (Pi) to identify the roles of taxa into one of four ecological roles, included of peripherals, module hubs, network hubs or connector (*Table 1*). In the present study, most of the nodes in all bacterial and fungal networks were peripherals (>98%), and no network hubs were detect. In contrast, 11 and 5 nodes were classified as connectors in bacterial and fungal networks respectively (*Fig. 6*), 3 module hubs were detected in bacterial networks. There were 5, 5, 0 and 1 connectors in bacterial networks in the pH range of 7.5 ~ 8.0, 8.0 ~ 8.5, 8.5 ~ 9.5, 9.5 ~ 10.0, and 1, 3, 1 and 0 connectors in fungal networks, respectively. The 11 connectors in bacterial networks were distributed in various microbial Taxa, 5 belonged to *Proteobacteria*, 3 belonged to *Chloroflexi*, 2 belonged to *Actinobacteria* and 1 belonged to *Nitrospirae*. 2 connectors in fungal networks belonged to *Sordariomycetes*, 1 belonged to *Eurotiomycetes*, 1 belonged to *Dothideomycetes*, and 1 unclassified *Ascomycota*. Module hubs were only detected in bacterial community in the pH range of 8.0 ~ 8.5 (1 *Actinobacteria* and 1 *Proteobacteria*) and 9.5 ~ 10.0 (1 *Actinobacteria*).

Discussion

Although the effects of soil pH on the diversity and composition patterns of bacterial and fungal communities have been studied in a range of environmental soils, the changes in microbe interactions across different pH ranges in saline-alkaline grassland soil, particularly in alkaline grassland, remain poorly understood. In this study, we conducted a network-based analysis using combined bacterial and fungal OTU data to explore the co-occurrence patterns of microorganisms in the pH ranges of $7.5 \sim 8.0, 8.0 \sim 8.5, 8.5 \sim 9.5, 9.5 \sim 10.0$ in saline-alkaline grassland in northern China. The results showed that the co-occurrence patterns of microorganisms differed between the different pH ranges. Specifically, we found that the network complexity varied significantly among the different pH levels.



Figure 6. Identification of keystone taxa based on their topological roles in different pH gradient networks in bacteria and fungi. Module hubs are identified as $Zi \ge 2.5$, Pi < 0.62, connectors are identified as Zi < 2.5, $Pi \ge 0.62$

| | | Bacto | Fungi | | | | | |
|------------------------|--------|-------|-------|--------|-------|-------|--------|-------|
| | pH1 | pH2 | pH3 | pH4 | pH1 | pH2 | pH3 | pH4 |
| Links | 1104 | 389 | 850 | 1329 | 309 | 631 | 597 | 154 |
| Positive | 80.9% | 80.2% | 84.0% | 88.1% | 94.8% | 96.9% | 99.6% | 99.3% |
| Negative | 19.1% | 19.7% | 16.0% | 11.8% | 5.1% | 3.0% | 0.3% | 0.6% |
| Nodes | 214 | 208 | 214 | 221 | 124 | 177 | 107 | 66 |
| Network density | 0.048 | 0.018 | 0.037 | 0.054 | 0.041 | 0.04 | 0.105 | 0.072 |
| Average degree | 10.318 | 3.74 | 7.944 | 11.973 | 4.984 | 7.13 | 11.159 | 4.667 |
| Modularity | 0.978 | 1.134 | 0.95 | 0.798 | 0.85 | 0.866 | 0.566 | 0.858 |
| Average path length | 4.501 | 7.865 | 3.998 | 3.691 | 4.786 | 3.037 | 1.041 | 1.097 |
| Clustering coefficient | 0.697 | 0.528 | 0.62 | 0.713 | 0.72 | 0.798 | 0.936 | 0.928 |

Table 1. Bacterial and fungal network topological features at different ranges of pH

pH1: 7.5 ~ 8.0, pH2: 8.0 ~ 8.5, pH3: 8.5 ~ 9.5, pH4: 9.5 ~ 10.0

Numerous studies have demonstrated that soil pH plays a crucial role in shaping microbial diversity and community composition in terrestrial ecosystems (Delgado-Baquerizo et al., 2018; Fierer, 2017). Our study investigated the microbial diversity and co-occurrence patterns of bacteria and fungi in saline-alkaline grassland soil in northern China across different pH ranges, including 7.5 ~ 8.0, 8.0 ~ 8.5, 8.5 ~ 9.5, and 9.5 ~ 10.0. Our results showed that the highest Shannon index values for both bacteria and fungi were observed in the pH range of $8.0 \sim 8.5$, suggesting that this pH range may be optimal for most soil microbes in saline-alkaline grassland in northern China. This finding is consistent with a recent study conducted on alkaline arable lands, which reported that bacteria and fungi exhibited their highest frequency distributions of occurrence when the pH was ~8.3 in alkaline soil (Shi et al., 2021). However, it is important to note that microorganisms in soil do not exist in isolation but rather form complex networks of interactions (Zhang et al., 2018; Ritter et al., 2021). Co-occurrence patterns among soil microbiota have been extensively studied in various terrestrial ecosystem (Jiang et al., 2017; Sung et al., 2017; Chen et al., 2021). Previous studies have found that changes in pH can modify the outcome of competition between bacterial species through dynamic feedback loops (Gondal et al., 2021). Our study found that the network size and complexity differed significantly among different pH levels. Specifically, the bacterial community in the pH range of 8.0 ~ 8.5 formed significantly smaller and less complex networks than those in the pH ranges of 7.5 ~ $8.0, 8.5 \sim 9.5$, and $9.5 \sim 10.0$. In contrast, the fungal community formed larger and more complex networks in the pH range of $8.0 \sim 8.5$ than in the other pH ranges. This finding is consistent with previous studies that have reported a positive correlation between network complexity and microbial diversity, suggesting that higher diversity leads to more associations between nodes (Fan et al., 2017, 2018a; Wagg et al., 2019). Interestingly, we found that the number of network nodes and links was lower at the optimal pH range for bacteria. This is reasonable, as nutrient-rich environmental habitats maintain high microbial diversity and may not require more associations among their nodes (Faust et al., 2015; Banerjee et al., 2018; Shi et al., 2021). A larger range of OTUs can independently obtain resources from the environment (Fierer, 2017; Shi et al., 2021).

Studies have demonstrated that alterations in pH can affect microbial community dynamics in terms of network size, complexity, and robustness of co-occurrence

relationships. Our findings indicate that the bacterial community in the pH range of 8.0 \sim 8.5 had the lowest network robustness, while the fungal community almost had the highest value. The optimal pH range for bacterial communities is considered to have more resource availability, which reduces competition among microbial communities (Costello et al., 2012; Fan et al., 2018b). In contrast, under poor nutrient conditions, competition among microbes can be more intense, and studies have shown that this can enhance network robustness (Foster and Bell, 2012; Coyte et al., 2015). Bacteria and fungi may have different strategies for adapting to pH variations, with dominant fungal species becoming more abundant in poor nutrient conditions and possibly outweighing less dominant species. This may reduce the robustness of co-occurrence associations, resulting in fungi having higher network robustness in the pH range of 8.0 \sim 8.5.

Topologically, network hubs/connectors, and module hubs are considered as regulators (or mediators or adaptors) and integral elements, respectively (Fan et al., 2018a; Han et al., 2004). In our study, module hubs and connectors were identified as keystone species, meaning that their elimination could potentially alter the module and network structure (Fan et al., 2018a); As such, they play a critical role in co-occurrence patterns and can be targeted for microbial regulation to enhance ecosystem function (Olesen et al., 2007). he main keystone OTUs in bacteria were from prevalent phyla such as *Proteobacteria, Actinobacteria*, and *Chloroflexi*, while those in fungal communities were from *Euryarchaeota* and *Dothideomycetes*. Keystone species are highly connected taxa that exert significant influence on other community members and are vital for maintaining ecosystem functions (Li et al., 2020). Therefore, they play a disproportionately important role in network structure relative to other taxa in the network (Olesen et al., 2007; Shi et al., 2016).

In conclusion, our study highlights the significant differences in network topological features of bacterial and fungal communities in different soil pH ranges in saline-alkaline grassland. The bacterial co-occurrence pattern in the pH range of $8.0 \sim 8.5$ was more complex but less stable than that in the other pH ranges, while the fungal co-occurrence pattern showed the opposite trend, with less complexity but greater stability in this range of pH. These findings provide novel insights into how bacterial and fungal communities in saline-alkaline grassland respond to changes in soil pH.

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Conflict of interests. The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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APPENDIX

Figure A1. Relative abundance of bacterial and fungal at Class level in each range of pH gradient



Figure A2. Changes of bacterial and fungal Shannon diversity index across different range of pH gradient. pH1: 7.5 ~ 8.0, pH2: 8.0 ~ 8.5, pH3: 8.5 ~ 9.5, pH4: 9.5 ~ 10.0

| Table A1. Topological features statistics of empirical and randomized networks in bacteria |
|--------------------------------------------------------------------------------------------|
| and fungi at different pH ranges |

| Index | Bacteria | | | | Fungi | | | |
|------------------------|--------------------------|--------------------------|--------------------------|--------------------------|--------------------------|--------------------------|--------------------------|--------------------------|
| | 7.5 ~ 8.0 | 8.0 ~ 8.5 | 8.5 ~ 9.5 | 9.5 ~ 10.0 | 7.5 ~ 8.0 | 8.0 ~ 8.5 | 8.5 ~ 9.5 | 9.5 ~ 10.0 |
| | Empirical/ randomized |
| Clustering coefficient | 0.69/0.12 | 0.53/0.05 | 0.71/0.03 | 0.71/0.06 | 0.72/0.04 | 0.94/0.04 | 0.96/0.11 | 0.93/0.04 |
| Average path length | 4.50/1.91 | 7.87/4.16 | 4.0/2.81 | 3.70/2.44 | 4.79/3.15 | 1.04/2.84 | 1.04/2.17 | 1.09/2.82 |
| Modularity | 0.98/0.26 | 0.95/0.51 | 0.80/0.32 | 0.80/0.24 | 0.85/0.41 | 0.87/0.33 | 0.57/0.24 | 0.86/0.40 |
| Network density | 0.05/0.05 | 0.02/0.02 | 0.04/0.04 | 0.04/0.05 | 0.04/0.04 | 0.04/0.04 | 0.11/0.11 | 0.07/0.07 |