A Java program for non-parametric statistic comparison of community structure

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Abstract
The Java algorithm to statistically compare structure difference of two communities was presented in this study. Euclidean distance, Manhattan distance, Pearson correlation, Point correlation, quadratic correlation and Jaccard coefficient were included in the algorithm. The algorithm was used to compare rice arthropod communities in Pearl River Delta, China, and the results showed that the family composition of arthropods for Guangzhou, Zhongshan, Zuhai, and Dongguan are not significantly different.

Keywords community; structure; non-parametric test; comparison; arthropods; Java; program.

1 Introduction
The structure of community refers to species composition, population size, etc., which is formed by environment/climate conditions, and dynamic interspecific/intraspecific interactions (Damgaard, 2011; Lüi, 2011; Rai, 2011; Watts and Worner, 2011; Zhang, 2011; Zhang and Chen, 2011). Comparison of structure difference between two communities is always important. Non-parametric statistics may be used in the difference comparison (Clarke, 1993; Schoenly and Zhang, 1999). In this article a Java algorithm, based on previous studies, was presented to statistically compare between-community structure difference.

2 Algorithm
The following two algorithms are used to compare the comprehensive difference in structure composition (i.e., taxa and individual number, randomness of taxa, taxa placement, etc.) between two communities (Clark, 1993; Schoenly and Zhang, 1999).

Assume that there are $s$ taxa in both community 1 and community 2. The number of samples is $m$ in community 1 and is $n$ in community 2, in total there are $ts=m+n$ samples in combined community. Given $a_{ij}$, the individual number of taxon $i$ in sample $j$, $i=1,2,...,s$; $j=1,2,...,ts$. Calculate the distance (similarity) between sample $i$ and $j$, $i=1,2,...,ts-1$; $j=i,...,ts$. The following distance (similarity) measures, Euclidean distance, Manhattan distance, Pearson correlation, Point correlation, quadratic correlation and Jaccard coefficient can be calculated:

\[
d_{ij} = \left( \sum_{k=1}^{s} (a_{ik} - a_{jk})^2 / s \right)^{1/2}
\]

\[
d_{ij} = \sum_{k=1}^{s} |a_{ik} - a_{jk}| / s
\]

These algorithms allow for a systematic comparison of community structure, providing valuable insights into the ecological dynamics of the Pearl River Delta arthropod communities.
In the last three measures, both sample $i$ and sample $j$ take values 0 or 1, $i = 1,2,\ldots, s$. $a$ is number of both sample $i$ and sample $j$ take value 0, $b$ is number of sample $i$ takes 0 and sample $j$ takes 1, $c$ is number of sample $i$ takes 1 and sample $j$ takes 0, and $d$ is number of both sample $i$ and sample $j$ take value 1. $b_i$ is the non zero number present in sample $i$ but not in sample $j$, $b_j$ is the non zero number present in sample $j$ but not in sample $i$, $c_i$ and $c_j$ is the non zero number in sample $i$ and sample $j$ respectively, and $e$ is non zero number shared by sample $i$ and sample $j$.

Let $b_k = d_{ij}$, $i = 1,2,\ldots, ts-1$; $j = i,\ldots, ts$; $k = 1,2,\ldots,(ts*ts-ts)/2+ts-1$. Rank $b_k$ from small to large values, then re-ranked $b_k$ and its ranking value $g_k$ are thus given, $k = 1,2,\ldots,(ts*ts-ts)/2+ts-1$. For each of re-ranked $b_k$, $k = 1, 2,\ldots, (ts*ts-ts)/2+ts-1$, if its corresponding two samples belong to the same community, then let $h_k = 1$, $g_k = k$, or else let $d_k = 1$, $f_k = k$. Given the number of $h_k = 1$, is $k_p$, the number of $d_k = 1$, is $r_p$, the sum of $g_k$ is $s_p$, the sum of $f_k$ is $c_p$. Calculate $r$ measure:

$$r=4*(c_p/r_p-s_p/k_p)/(ts*(ts-1)),$$

then let $r_0=r$, i.e., observed $r$ value. Using Monte Carlo technique, randomly divide all of $d_{ij}$, $i = 1,2,\ldots, ts-1$; $j = 1,2,\ldots, ts$, into two communities with random number of samples in first community, the first community has $m_1$ samples and the second community has $ts-m_1$ samples. Let $b_k = d_{ij}'$, where $d_{ij}'$ is $d_{ij}$ after randomization, $i = 1,2,\ldots, ts-1$; $j = i,\ldots, ts$; $k = 1,2,\ldots,(ts*ts-ts)/2+ts-1$.

Repeat the above procedures from which the $r$ for this randomization can be calculated. For $v$ randomizations, record the total number of $r \geq r_0$ as $w$, and expected and standard deviation of $r$ can be derived also. Finally, calculate the $p$ value:

$$p=(w+1)/(v+1).$$

If $p$ is less than 0.05, or 0.01, then the difference of structure composition between community 1 and community 2 is statistically significant.

The algorithm is implemented as a Java program, CommStrucComp, based on JDK 1.1.8, in which several classes and an HTML file is included (http://www.iaees.org/publications/software/index.asp). In community 1 and community 2 data files, the first column is taxon ID number, and the first row is sample ID number.

3 Application

We obtained a set of data investigated in rice fields of four cities of Pearl River Delta, Guangzhou (23 samples), Zhongshan (17 samples), Zhuhai (23 samples), and Dongguan (17 samples) in September 2008 (Wei, 2010). In total 58 arthropod families were found.

Choose different distance (similarity) measures and set 1000 randomizations. The results, as indicated in Table 1, show that there is not significant difference between these cities in the arthropod composition. From $p$ values in Table 1, the family composition of arthropods between Zhuhai and Dongguan is relatively more different.
Table 1 The $p$ values for city pairs

<table>
<thead>
<tr>
<th></th>
<th>Zhongshan</th>
<th>Zhuhai</th>
<th>Dongguan</th>
<th>Guangzhou</th>
</tr>
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<tr>
<td>Euclidean</td>
<td>Zhongshan</td>
<td>0.859</td>
<td>0.566</td>
<td>0.858</td>
</tr>
<tr>
<td></td>
<td>Zhuhai</td>
<td>0.217</td>
<td>0.584</td>
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<td>Dongguan</td>
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</tr>
<tr>
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<td>0.554</td>
<td>0.864</td>
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<td>0.565</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Dongguan</td>
<td></td>
<td>0.863</td>
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<tr>
<td>Point</td>
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<td>Dongguan</td>
<td></td>
<td>0.856</td>
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</table>

References


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