



Commentary

Finding a dominance order most consistent with a linear hierarchy: an improved algorithm for the I&SI method

Volker S. Schmid ^{a,*}, Han de Vries ^b^a Biologie I, Universität Regensburg, Regensburg, Germany^b Department of Animal Ecology, Utrecht University, Utrecht, The Netherlands

ARTICLE INFO

Article history:

Received 30 September 2012
 Initial acceptance 15 November 2012
 Final acceptance 24 July 2013
 Available online 6 October 2013
 MS. number: 12-00753R

Keywords:

DomiCalc
 dominance ranking
 I&SI method
 inconsistent dyad
 matrix reordering technique
 nonuniqueness

To find a dominance order most consistent with a linear hierarchy, the I&SI method minimizes two criteria: first the number of inconsistencies I (i.e. number of dyads in which the lower-ranked individual dominates the higher-ranked one) and then (without increasing I) the total strength of inconsistencies SI (i.e. the sum of rank differences between individuals of inconsistent dyads or, in other words, the sum of distances of inconsistencies from the matrix diagonal). The original algorithm developed by [de Vries \(1998\)](#) to achieve this goal has two drawbacks. (1) It completely relies on the 'generalized swapping rule' (combined with partly random reordering) to decrease I , but moving single individuals' positions instead of pairwise switching them can complement the generalized swapping rule to make a more efficient algorithm. (2) It does not consider alternative orders, if more than one exists, with equally minimized I and SI values. In this paper, an improved algorithm for the I&SI method is presented. It includes: (1) more efficient searching for optimal orders; (2) consideration of all orders with equally minimized I and SI values; and (3) choice of one or more optimal orders based on correlation with a hierarchical combination of two dominance indices: primary ranking by the proportion of dominated individuals and secondary ranking by the difference between the number of dominated individuals and the number of individuals to which the focal individual is subordinate. Microsoft Excel workbooks are provided that perform the linearity test published by [de Vries \(1995\)](#) and the improved algorithm.

© 2013 The Association for the Study of Animal Behaviour. Published by Elsevier Ltd. All rights reserved.

Dominance is a widespread phenomenon in group-living animals, and many dominance hierarchies observed in nature have been found to be completely or nearly linear ([Chase et al. 2002](#); [Chase & Seitz 2011](#)). Linearity in this context means that the top-ranking individual dominates all other individuals, the one with second-highest rank dominates all individuals besides the top ranker and so on, with the lowest-ranking individual being dominated by (i.e. subordinate to) all others.

Matrix reordering methods for finding (near-)linear rank orders of individuals involved in dominance relationships have been available for a long time (reviewed by [de Vries 1998](#)). More than a decade ago, [de Vries \(1998\)](#) proposed the most recent of these procedures: the I&SI method. This method is a generalization of [Roberts's \(1990\)](#) 'flipping rule' for adjacent individuals and aims to minimize the number of inconsistencies in the data set. Inconsistencies as introduced by [Slater \(1961\)](#) are cases in which an individual dominates a groupmate with a higher rank in the

assumed linear order than this individual itself. (Accordingly, dyads in which the two individuals' relationship is consistent with the linear rank order will be called 'consistencies'.)

Individuals that form a perfectly linear hierarchy can be arranged in an order without inconsistencies. Frequently, however, data sets based on observations of group-living animals contain so-called intransitivities. These are cases in which three or more individuals form a domination circle, leading to inconsistencies that cannot be resolved, no matter how the hierarchy is ordered ([de Vries 1998](#)). Here, the I&SI method comes into play. It aims to find a nearly linear order that is most consistent with a perfectly linear order. Hence, the method is most appropriate if the assumption of linearity is statistically supported ([de Vries 1995, 1998](#)), that is, if the degree of linearity in the set of dominance relationships is significantly higher than expected on the basis of random relationships.

The I&SI method employs mainly two criteria to reorganize an interaction matrix for finally obtaining an optimal ranking order of the group members. The first criterion is a minimal number of inconsistencies, the second a minimal total strength of those inconsistencies. The strength of a single inconsistency is the absolute rank difference of the two involved individuals. 'Total strength'

* Correspondence: V. S. Schmid, Biologie I, Universität Regensburg, 93040 Regensburg, Germany.

E-mail addresses: volker.schmid@biologie.uni-regensburg.de, DomiCalc@freenet.de (V. S. Schmid).

refers to the sum of strengths of all inconsistencies present within a matrix. An optimal order fulfils both criteria, where the first has priority over the second. This means that the I&SI method aims first to minimize the number of inconsistencies (I) and then to minimize the total strength of inconsistencies (SI) without increasing I .

Appealing features of the I&SI method are that it makes fewer assumptions than many other dominance ranking methods (de Vries 1998), its robustness against sparse data and its high predictive power, although it does not make use of the whole information content of the dominance data (de Vries & Appleby 2000). Under certain conditions, the I&SI method might be inferior to other, simpler dominance analyses (Hemelrijk et al. 2005). Depending, however, on the questions studied, the I&SI method can still be considered as a useful technique and may fruitfully complement other dominance analysis methods such as David's score (Gammell et al. 2003; Vervaecke et al. 2007; de Vries 2009). Furthermore, Wittemyer & Getz (2006) suggested it could be extended by likely rank interpolation that is used to fill gaps in the data and to derive cardinal dominance strengths based on an ordinal ranking initially produced by the I&SI method.

A disadvantage of the I&SI method explicitly stated by de Vries & Appleby (2000) is that in some cases it may not produce unique orders. Hence, the reliability of a single order being termed 'optimal' by the I&SI method decreases with increasing gaps in the dominance interaction matrix employed. This nonuniqueness may be countered, however, by different approaches, one of which is the extension of the I&SI method devised by Wittemyer & Getz (2006). Another possibility that may be combined with the latter method is to examine as many equally I - and SI -minimized orders as possible, which is discussed in this paper.

Altogether, the I&SI method is a powerful tool to analyse dominance data. However, despite its usefulness, it might have been ignored as an analysis method because it is a rather complex procedure and was until recently only included in one software package, MatMan (Noldus Information Technology 2003; original version of MatMan is described in de Vries et al. 1993), which is only commercially available and incompatible with newer versions of Microsoft Excel. Recently an R package has been developed that includes the I&SI method (Leiva et al. 2010). To many scientists, however, the R software might be unattractive because of its command-line-based user interface. Furthermore, while the I&SI method is principally advantageous, both the efficiency and the concept of the algorithm devised by de Vries (1998) to realize the aim of that method can be improved.

In this paper, we present new reordering techniques that are assembled into a more efficient algorithm yielding extensive output, as well as a freely available software package ('DomiCalc') containing Microsoft Excel workbooks that perform the improved algorithm. Additionally, this article aims to ease understanding of the I&SI method and the principles that underlie the I&SI algorithms. Finally, by reanalysing published I&SI analyses of real data we demonstrate the advantages of the new algorithm and discuss possible consequences of such reanalyses for statistical inferences.

Many aspects presented here are discussed more extensively in the handbook of the DomiCalc package which is included in the Supplementary material. To avoid overly frequent citation of the handbook, the reader is generally referred to consult it to gain further insights.

THE ORIGINAL ALGORITHM

Based on the flipping rule for adjacent individuals presented by Roberts (1990), the 'generalized swapping rule' (de Vries 1998) searches for opportunities to exchange positions of not only adjacent but also other pairs of individuals leading to fewer

inconsistencies (I). The degree of I reduction, that is, the difference between I of the reordered matrix and I of the former matrix, is henceforth termed ΔI . Although not every swap performed by the original algorithm has a negative ΔI , the number of inconsistencies is nevertheless reliably reduced in the course of a series of swaps. The original algorithm consecutively applies the generalized swapping rule to a start matrix until it does not allow further reduction of I . The order obtained this way is saved as an intermediate result. Then, the matrix is rearranged by sequentially switching the position of each individual involved in an inconsistency (the one with the lower rank of the two individuals of that dyad) with a randomly chosen individual of higher position.

By performing this partly random repositioning, a new promising start matrix is generated to which the generalized swapping rule is applied again. The resulting new matrix is compared with the intermediate matrix: if I of the new matrix is lower, the new order is saved, replacing the former intermediate result. The same occurs if I of the new order is equal to the intermediate one and SI is lower. In any other case the hitherto present intermediate order is not replaced. Then, the partly random repositioning is again applied to the intermediate order, followed by the generalized swapping rule. This loop is repeated a number of times ('tries'). Note that these tries are not independent from each other but always applied to the best order found so far, leading to sequential improvement. More details, including a semiformal programming code, can be found in the original publication (de Vries 1998).

While the original algorithm is relatively simple and elegant it can be improved in several aspects.

(1) The generalized swapping rule may miss opportunities to decrease I directly. Frequently, after the generalized swapping rule has stopped and yields no further improvement, movements of single individuals would further reduce I (see below). Relying only on the generalized swapping rule may result in a high number of tries being necessary to find configurations with minimal I .

(2) Matrices with minimized I are not examined for opportunities to decrease SI directly without increasing I . Instead, the SI value that a matrix with minimized I has at the end of a single try is, so to say, dependent on chance. Only by comparing many tries that lead to the same minimal I is SI minimized.

(3) In the last phase, the final positioning of adjacent individuals with undecided dominance relationships is realized by comparing a numerical value that may be considered as a dominance index (see section 'Handling matrix configurations with equal I and SI '). This procedure is suboptimal because it only compares adjacent individuals, while it is possible that two or more matrices have the same I and SI values but differ in a way that does not involve reversed positions of adjacent individuals. Such cases are not accounted for.

(4) Even if different orders with minimal I and SI are compared by using a dominance index as an additional criterion, there may be two or more orders that equally fulfil all three criteria. The original algorithm does not consider this possibility but instead always presents only one order as optimal, leaving the user ignorant about the existence and frequency of other, equally optimal orders.

THE DOMINANCE SCORE TRANSFORMATION

A typical input matrix for dominance analyses contains dyadic frequencies of dominance-related behaviours (henceforth simply referred to as 'wins' and 'losses'). The core part of the new techniques for searching optimal orders presented here is a transformation of such an input matrix into a matrix providing standardized information about dyadic dominance relationships. For this purpose, we introduce a scoring system ('dominance scores') that distinguishes four relationships: domination (value 1),

Download English Version:

<https://daneshyari.com/en/article/2416498>

Download Persian Version:

<https://daneshyari.com/article/2416498>

[Daneshyari.com](https://daneshyari.com)