A simple and viable approach to estimate population trends

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Quantifying population trends and evaluating positive and negative associations between species and ecological indicators are widely employed in ecological analysis. They have practical importance for theory and ecological conservation. Standard measures of trend and association are based on deviations from the mean, and several criteria have to be fulfilled to obtain accurate results. Herein, more robust measures are presented that are based on proportional differences between observations. Trends can be calculated for metric, rank, ordinal, and binary variables. The degree of association between two different populations over time or between two rank series can also be calculated. The proposed measures of trend and association are scaled such that they range from –1 to +1, where 0 indicates that there is no monotonic association. The findings suggest that the measures possess several advantages and are applicable to a wide range of ecological contexts.

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Introduction

The magnitudes of environmental trends and ecological associations are of central concern for ecological research. Populations of individual species and the magnitude of ecological indicators can increase or decrease, and the ecological association between them can be positive or negative. Standard measures of trend and correlation use mean-deviation scores to assess if values are high or low. Using the mean as the benchmark is associated with a series of assumptions that need to be satisfied to obtain accurate results. A new approach, based on proportional differences between observations, is proposed herein. It addresses these limitations and can provide a common ground for the evaluation of trends and associations in ecological research. The quantity of interest might be population abundance. "Abundance" essentially refers to the number of individuals at a site, to biomass or coverage. To calculate abundance trends, proportional differences between abundances in a time series are used to evaluate the

fluctuation of abundances over time. For each time step in a time series, the difference proportional to abundances at later time steps F(forward), and earlier time steps B(backward) is calculated and summed up. Trend measure T is obtained by dividing the sum of both comparisons for all time steps, denoted by D, through the maximal proportional difference D_r, which is obtained by ordering abundances from the lowest to the highest.

$$\mathrm{D} = \sum \mathrm{F} + \sum \mathrm{B} = \tag{1}$$

$$\left(\left(\sum_{i=1}^{n-1} \frac{\sum \max}{z_i}\right) - \mathrm{C}\right) + \left(\mathrm{C} - \left(\sum_{i=2}^{n} \frac{\sum \min}{z_i}\right)\right), \text{ where}$$

$$\mathrm{C} = \frac{n(n-1)}{2}$$

$$\mathrm{D}_r = \sum \mathrm{F}_r + \sum \mathrm{B}_r \tag{2}$$

$$\mathrm{T} = \frac{\mathrm{D}}{\mathrm{D}_r} \tag{3}$$

Each abundance is first directly compared to the sums of later abundances for the calculation of F. Next, the number of possible pairwise comparisons C is subtracted. For B, the comparison is to the sum of observations at earlier time steps before this sum is subtracted from C. D in the numerator of Formula 3 is positive if values rise over time and negative if values get lower over time.D_r in the denominator is always positive as it is calculated for ordered abundances. However, it is D in the numerator that determines if the sign of T is positive or negative.

Bounded between -1 and 1, T measures monotonic population trends. Given that there is at least one difference between abundances, the value will be 1 if all abundances stay the same or increase from one time step to the next, and -1 if they stay the same or decrease from one time step to the next. If no monotonic association exists between abundances and time steps the value is 0. T can be used for the evaluation of trends for data of different scale types: positive-valued metric data, rank data, and binary presence/absence data. A worked example that illustrates the calculation of T is presented in Table 1, where N_t refers to the population abundances for a fictional dataset at time t and N_r to the abundances that have been ordered by magnitude. As T can only be calculated for positive values, and abundance data often contains zero values, a constant can be added to all values. To differentiate the measure from T, it is denoted T_1. These trend measures are highly robust and can measure population trends if there is a high year-to-year variability driven by cyclical dynamics and other sources of variability that are not associated with the population trend. To obtain a measure with a focus on smooth trends, T can be combined with metrics that are

based on n−1 proportional differences between the consecutive observations:

$$\mathrm{CD}_r, \mathrm{CD} = \sum_{cons} \left(\frac{|z_i - z_j|}{2z_i} + \frac{|z_i - z_j|}{2z_j} \right) \tag{4}$$

$$\mathrm{T}_2 = \frac{\mathrm{D} * \mathrm{CD}_r}{\mathrm{D}_r * \mathrm{CD}} \tag{5}$$

While CD is calculated from time-series data, CD_r is calculated from the data that has been ordered according to the magnitude of the abundances(Formula 4). The adjusted trend measure, denoted by T_2, is then obtained through a combination of the general proportional differences from Formula 3 and the consecutive differences.

N_t	F	B	D	CD_t	N_r	F_r	B_r	D_r	CD_r
6	15	–	15	–	1	190	–	190	–
4	32	-0.5	31.5	0.42	2	85.5	0.5	86	0.75
2	82	-3	79	0.75	3	51	1	52	0.42
3	49	-1	48	0.42	4	34	1.5	35.5	0.29
1	179	-11	168	1.33	5	24	2	26	0.23
5	23.8	1.8	25.6	2.40	6	17.5	2.5	20	0.18
7	13	3	16	0.34	7	13	3	16	0.16
9	7.22	3.89	11.11	0.25	8	9.75	3.5	13.25	0.13
12	2.42	4.92	7.33	0.29	9	7.33	4	11.33	0.12
10	5.1	4.1	9.2	0.18	10	5.5	4.5	10	0.11
8	8.88	2.63	11.5	0.23	11	4.09	5	9.09	0.10
11	4	4.91	8.91	0.32	12	3	5.5	8.5	0.90
13	2.15	6	8.15	0.17	13	2.15	6	8.15	0.08
15	0.93	6.93	7.87	0.14	14	1.5	6.5	8	0.07
14	1.43	6.43	7.86	0.07	15	1	7	8	0.07
17	0.29	7.94	8.24	0.20	16	0.63	7.5	8.13	0.07
18	0.06	8.39	8.44	0.06	17	0.35	8	8.35	0.06
16	0.44	7.31	7.75	0.12	18	0.17	8.5	8.67	0.06
19	0.05	9	9.05	0.17	19	0.05	9	9.05	0.05
20	–	9.5	9.5	0.05	20	–	9.5	9.5	0.05
$\sum$	426.77	71.24	498.01	7.91		450.53	95	545.53	3.07

Table 1 Evaluation of general and consecutive proportional differences.

For the example presented in Table 1 measure T, is calculated 498.01/545.53=0.91, but the adjusted trend measure that also takes the consecutive differences into account is markedly lower with T_2=0.35. High values for T_2 are only possible if the trend is nearly monotonical with low fluctuations in population abundances over time that are not related to the trend. Figure 1 graphically depicts the example dataset in Table 1.

The graph for CD_r is not necessarily a straight line unless the consecutive difference is calculated for ranks, but ordering the abundances necessarily always minimizes the consecutive difference for a dataset.

On another note, V provided in Formula 6 is conceptually similar to a recently proposed measure of temporal variability (Fernandez-Martinez et al., 2018), but the former has a constant range between 0 and 1. A unit can be added to all values to avoid indetermination if there are zero counts in a time series.

$$\mathrm{V} = 1 - \left(\frac{1}{1 + \mathrm{CD}/(n-1)}\right) \tag{6}$$

Evaluating trends in presence and absence

Changes in population abundances can be measured as binary data that only assumes one of two values, i.e. "presence" and "absence", where absence is coded as 1 and presence as 2.

z_i(time)	F	B	D	z_i(ranked)	F_r	B_r	D_r
2	-2	–	-2	1	16	–	16
2	-2	0	-2	1	16	0	16
2	-2	0	-2	1	16	0	16
2	-2	0	-2	1	16	0	16
2	-2	0	-2	2	0	2	2
2	-2	0	-2	2	0	2	2
2	-2	0	-2	2	0	2	2
2	-2	0	-2	2	0	2	2
2	-2	0	-2	2	0	2	2
2	-2	0	-2	2	0	2	2
2	-2	0	-2	2	0	2	2
2	-2	0	-2	2	0	2	2
1	4	-12	-8	2	0	2	2
2	-1.5	0.5	-1	2	0	2	2
1	3	-13	-10	2	0	2	2
2	-1	1	0	2	0	2	2
1	2	-14	-12	2	0	2	2
2	-0.5	1.5	1	2	0	2	2
1	1	-15	-14	2	0	2	2
2	–	2	2	2	–	2	2
$\sum$	-17	-49	-66		64	32	96

Table 2 Evaluation of proportional differences for binary data.

For the example in Table 2, trend measure T is given by $-66/96 = -0.69$. A single divergent value at the beginning or at the end of a time series is enough, and trend measure T indicates a perfect monotonic relationship. Unbalanced data (i.e., a far larger proportion of ones than twos) is common in ecological datasets. To let T only indicate full or very high correlation if the data is also balanced it is possible to calculate the adjusted measure T′. There must be an equal number of ones and twos in the time-series, and they must be in perfect monotonical order for T′ to assume the value of 1. If the number of time steps n is even, then T′ is given by:

$$\mathrm{T}' = \mathrm{T} * \left(1 - \left|1 - \frac{\mathrm{M}}{1.5}\right|\right) \tag{7}$$

If n is an odd number, the following formula applies:

$$\mathrm{T}' = \mathrm{T} * \left(1 - \left|1 - \left(\frac{\mathrm{nM}}{((n+1) + ((n-1)/2)}\right)\right|\right) \tag{8}$$

Here M refers to the arithmetic mean of the observations that are coded as 1 and 2. For an even number of observations, the mean equals 1.5 if the data is balanced(i.e. equal number of ones and twos), and T′ will have the same value as T. For the example in Table 2, T′=−0.55. For a site with continuous *absence* for 19 time steps and then a single *presence* at the last time step T = 1, but T′ = 0.70. The same value with a negative sign is obtained for a time series with continuous *presence* for 19 time steps and *absence* at the last time step.

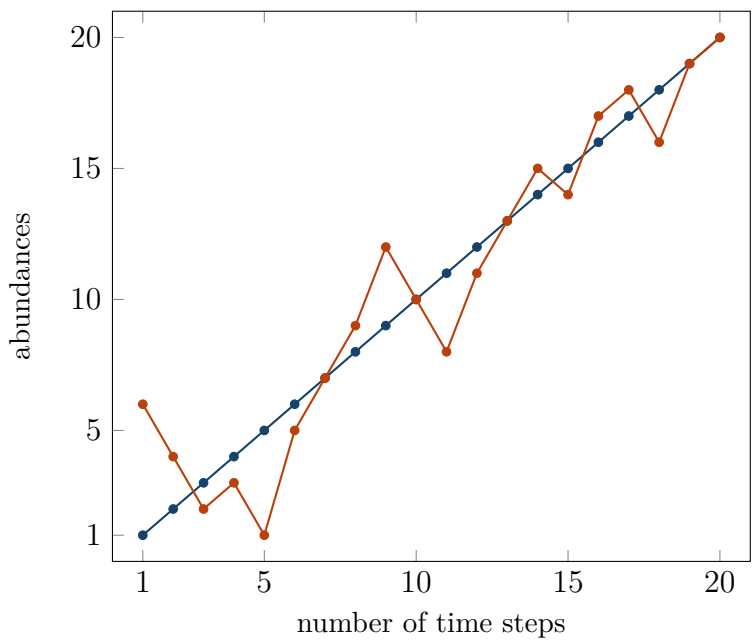

Figure 1: Unordered abundances(red) and ordered abundances(blue) of the example time series from Table 1.

Robust ecological association

The previous section illustrated a new approach to evaluate population trends that can be calculated for different data types.The order of values that represents time steps can alternatively represent a rank series, but only if there are no tied ranks and if the other variable is a different data type. If both are rank series, the result would be an inaccurate rank correlation, as the magnitude of the correlation would depend on how the roles of ordering and ordered rank series are assigned. To quantify the degree of association between two rank series, T is calculated twice.

$$\phi = \frac{\mathrm{T}_{xy} + \mathrm{T}_{yx}}{2} \tag{9}$$

Phi can also quantify the degree of association between two metric variables. To measure the degree of association between population abundances of two individual species, the approach that has been outlined above in Formulas 1,2, and 3 can be used to calculate *Phi*, but observations are ordered by the values of the other variable. T_{xy} is obtained by ordering the abundance of species X according to the abundances of species Y, i.e., taking the value of X for the lowest value of Y, then the value of X for the second-lowest value of Y, etc. until all values are ordered. Likewise, T_{yx} is obtained by ordering the abundances of species X according to the abundances of species Y. To standardize the measure to the familiar scale, the mean of T_{xy} and T_{yx} is taken. Like standard measures, *Phi* measures correlation on a scale that varies from -1 through 0 to 1. Complete monotonic correlation is expressed as either -1 or 1, whereas a value of 0 indicates that there is no monotonic association between variables. *Phi* is scale-invariant,i.e., the value remains unchanged if one or both variables are scaled by the same factor or if they are scaled by different factors. There are different methods if there are two or more observations with identical values for one of the variables. For time-series data on population abundances, the order of the abundances of the other species can be determined by chronology. If Y is ordered by X and the population abundance for X was 10 at the first and the last time step, then the value for Y at the first time step comes before the value of Y at the last time step. For non-time-series data, the mean of the two Y values that correspond to the two identical X values is calculated instead and replaces the measured values of Y.

The degree of association between two variables is usually measured by a correlation coefficient. If both variables are metric the product-moment correlation, denoted as r, is used. It is sometimes called Pearson's correlation coefficient. This measure has various assumptions, which violated, lead to an inaccurate estimation of the association between variables. Three frequently reported assumptions are linearity, absence of outliers, and bivariate normality. They are necessary because r uses the mean as the benchmark for evaluating differences between observations. As *Phi* is calculated from

proportional differences between values, it has fewer and less-limiting assumptions. The first assumption of r is that there exists a linear relationship between variables. This is the assumption that a change in one variable changes the other variable by a fixed amount. Conversely, the assumption underlying *Phi* is a monotonic relationship between variables, if one variable increases (or decreases), the other variable also increases (or decreases). Monotonic relationships include linear relationships as a special case, but they can also accurately measure various non-linear relationships that are equally relevant for ecology. To check for types of association that are non-monotonic, plotting the data before calculating a correlation is generally recommended.

For r to be accurate, the data also cannot have outliers. A single extremely deviant value can dramatically influence its value(Campbell,2021). Such outliers typically reduce the absolute magnitude of r and simply excluding them from the dataset is not considered legitimate(Schober, 2018). To cope with the problem of outliers and other violations of normality it has been recommended to use the Spearman's correlation, denoted by r_s, or conceptually similar methods that entail the transformation of the metric data to ranks, from which the Pearson correlation is then calculated(Bishara & Hittner, 2012). *Phi* possesses the advantage that the correlation can be calculated from the actual observations as it is robust against outliers.

Another important assumption underlying r is that the variables follow a bivariate normal distribution, which implies constant variances of the residuals across all levels of X. This assumption, however, is not realistic, as even for a linear association, the absolute deviations of observations from the regression line could arguably be expected to be smaller if values are lower, and larger if values are higher. The assumption is not relevant for the proportional measure *Phi*. Despite the differences and advantages outlined above, there exists a certain degree of concurrent validity between *Phi* and r. In general, a high degree of positive association is indicated if there are no observation pairs where the abundance of species X is very high and the abundance of species Y is very low. A high negative association requires that there are no value pairs where both species have concordant high (or low) abundances. correlations between time series. Although there are marked differences between the two measures in the magnitude of the indicated association for individual datasets, the average magnitude of the correlation is similar. Attempts to apply certain cut-offs to describe the strength of the correlation can also be used for *Phi*. A classical resource on this approach is Evans (1996), and Evans's standards for correlation strength are as follows: .00 to .19 is *very weak*, .20 to .39 is *weak*, .40 to .59 is *moderate*, .60 to .79 is *strong*, and .80 to 1.00 is *very strong*. Naturally, the rules apply invariably to positive and negative values of *Phi*.

Sensitive rank correlation

Rank correlations evaluate the degree of association between two sets of ranks, e.g., two ecologists ranking the same list of individual species according to their importance for an ecosystem. A widely accepted and used measure of rank correlation is r_s, which delivers identical results to the application of the Pearson correlation to rank data if there are no tied ranks. The other frequently used measure for rank data is τ (Kendall, 1948). Both these rank correlation measures quantify the degree of the monotonic relationship between two rank series; if there are outliers in the data, they are also used on originally metric data. Although r_s and τ are widely accepted, it has been reported that they lack sensitivity to top ranks. Higher ranks(first, second, and so on) are often considered more important than lower ranks. If a rank correlation is calculated for two sets of 30 ranks, and if all other rank pairs are the same(i.e. both second, third, etc.), but the highest and lowest ranks for both series are paired, the conventional measures of rank correlation indicate relatively high correlations (r_s=0.63, τ=0.73).In contrast, *Phi* indicates a much lower correlation of 0.23. For the example, this represents diametrically opposing views on which species is the most and least important for an ecosystem. The effect of such a large difference between the first and last ranks decreases with the length of the rank series. The sensitivity to the association between top ranks can also be observed in less idealized rank series. Corrections of standard measures have been described that make them more sensitive, and these are known as Weighted Rank Correlations (see, Dancelli, 2013). *Phi* needs no correction to be sensitive.

Code availability

Excel workbooks and Jupyter Notebooks with code used for analyses are available at `https://github.com/FT81/better-trend`

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