

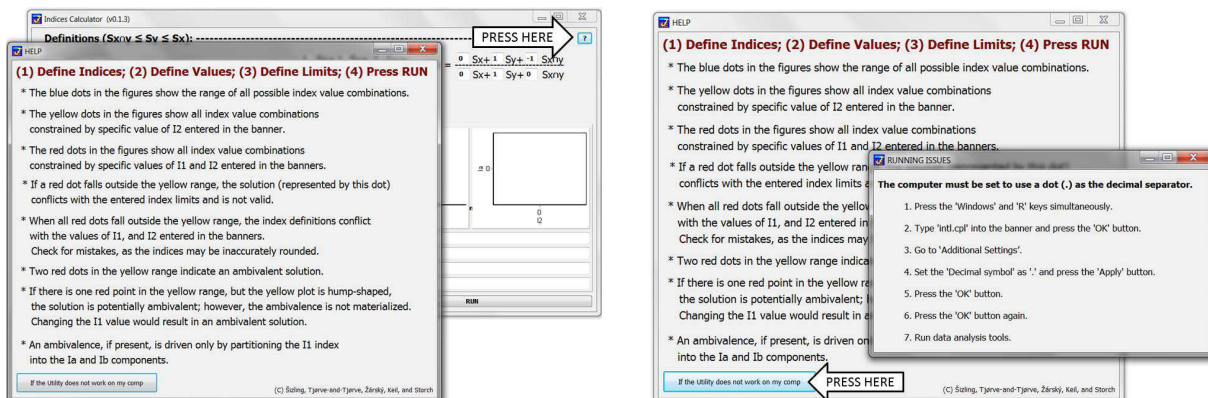



RI3: Manual for Indices Calculator

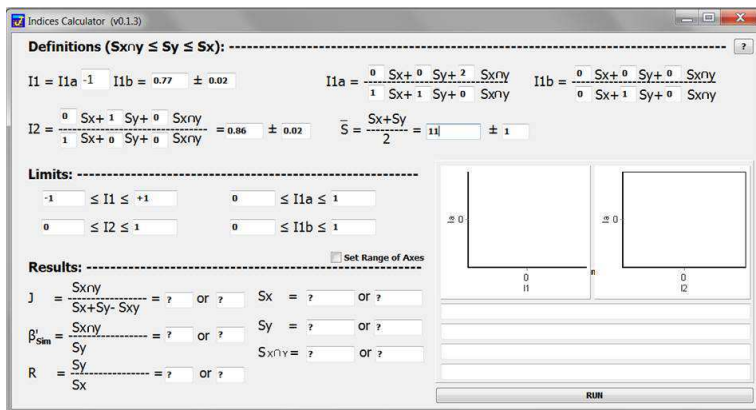
Šizling, A.L., P. Keil, E. Tjørve, K.M.C. Tjørve, J.D. Žárský, and D. Storch. 202X. Mathematically and biologically consistent framework for presence-absence indices of diversity.

The Indices Calculator converts pairwise indices based on incidences to each other and analyses their informational interdependence.

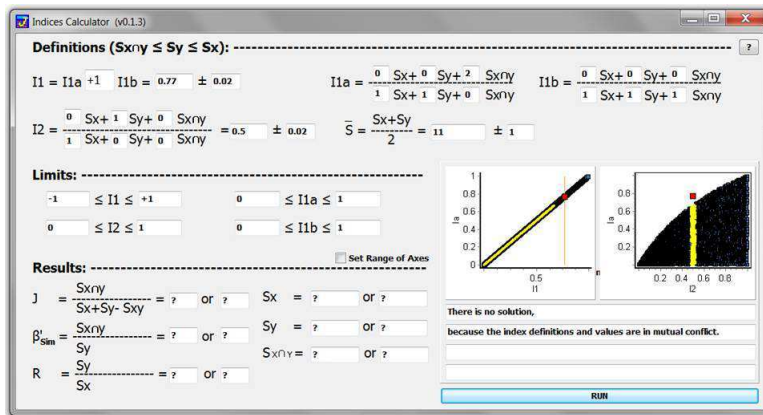
The calculator works properly only with machines that utilize a 'dot' as a decimal separator. See the help for detailed instructions.



After running the calculator (click on ) a panel appears.

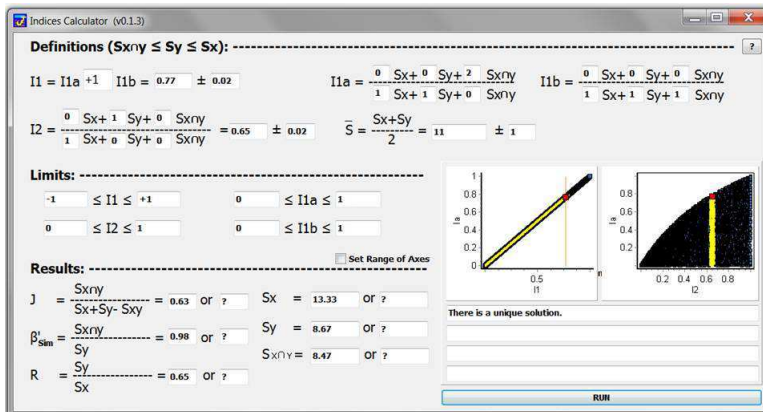


Fill the sections 'Definitions' and 'Limits'. In the pannel above 'Ia1' is defined as Sørensen similarity (see Box 1 in Šizling *et al.*, 202X). The index I1b is always zero, so the calculator will ignore the component I1b. The index I2 is species richness uniformity R . This is because $S_Y \leq S_X$ by definition. This default does not affect the generality of the process. Mean species richness is known in this example and it is set as 11. Limits are theoretical limits of the indices.



The errors should be reasonably defined (here 0.02 for indices and 1 for species richness). Too small errors may lead to the conclusion that there is no solution because index definitions and precise values on input may be in logical conflict. This conclusion may be wrong where the index values are rounded.

Press the RUN button.

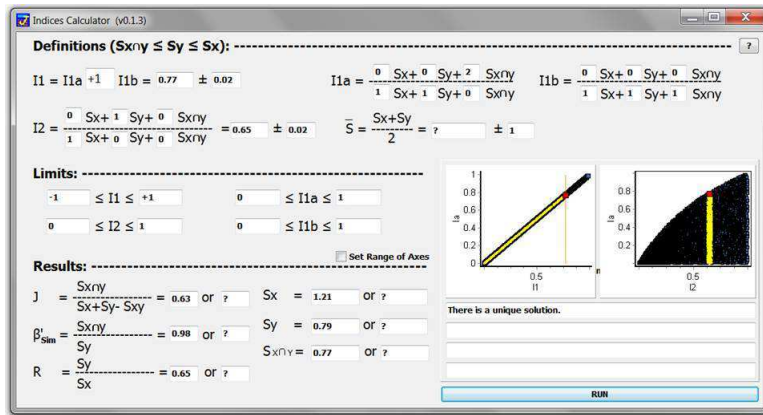


The Results section and the figures are displayed. The resulting values of Jaccard similarity, Simpson nestedness, species-richness uniformity, and S_x , S_y , $S_{X \cap Y}$ are computed as described in Box 2 (see Šizling *et al.*, 202X).

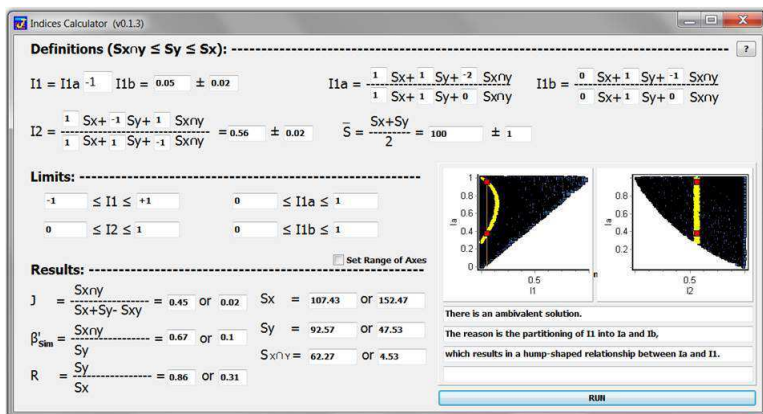
The figures and dialog boxes help to see whether there is a unique solution or not. The number of solutions is always none, one, or two. Two solutions may appear only when index $I1$ is partitioned. The reason is that additive partitioning often reduces information.

The blue area in the figures shows all possible combinations, the yellow line shows all possible combinations constrained by the value of $I2$, and the red point shows the solution constrained by both indices $I1$ and $I2$.

As a conclusion, a red point that is outside the yellow line shows a mutual logical conflict of index definitions and values of the indices.



There is no need for precise species richness, as shown on the panel above. The indices are dimensionless, which means that they are i-independent of species richness. Just write the question mark '?' or the number of one in the banner for the average species richness, \bar{S} . The resulting S_X , S_Y , and S_{XNY} displayed in the Results section are then only proportional numbers.



If $I1$ is partitioned (e.g., $I_1 = \beta_{sne}$, Baselga, 2012; $I_2 = \beta_{nps}$; Podani & Schmera, 2012), then two solutions may exist. The rationale is that if there is a partitioning (both $I1a$ and $I1b$ are defined), then Eq. 14 from Šizling et al. (202X) is employed. This equation is quadratic, therefore two different solutions may exist for partitioned indices, indicating a loss of information. Both solutions are displayed in the Results section and in the figures. The result of the determinant analysis (Theses and Evidences in R1) is shown in the dialog box.

Enjoy the Analysis