Appendix 1

Chu-Liu/Edmonds algorithm

For a weighted directed graph G of N nodes and L links, we can produce the MWST using the Chu-Liu and Edmonds algorithm.

The procedure is:

1) For each node other than the root, select the entering link with the highest magnitude.
2) Let the selected N – 1 links be S the set of links composing the MWST.
3) If no cycle formed, G(N, S) is a MWST. Otherwise, continue.
4) For each cycle formed, contract the nodes in the cycle into a pseudo-node (k), and modify the magnitude M of each link which enters a node (j) in the cycle, from some node (i) outside the cycle, according to the following equation:
   \[ M(i,k) = M(k,j) - M(i,j) \]  \hspace{1cm} (A1)
   where M(k,j) is the magnitude of the link in the cycle ingoing the node j.
5) For each pseudo-node, select the entering link which has the smallest M.
6) Replace the link which enters the same real node in S by the new selected link.
7) If there are other cycles, goes to step 2 with the contracted graph. Else, the MWST is done.

The main idea of the algorithm is to find the replacing link(s) that produces the minimum decrease in the total magnitude to eliminate cycle(s) if any. The Eq. A1 computes the associated decrease in the magnitude substituting links. The following Fig. A1 shows an example of the algorithm.
Figure A1. (a) hypothetical weighted directed graph; (b) resulting MWST after the selection of the highest magnitude link for each node; (c) we contract the nodes in the cycle (3-4-5) in a pseudo-node; (d) according to Eq. A1 we computed the difference in magnitude between ingoing links within the pseudo-node and the ingoing link outside and to the pseudo-node (in this case, we compute $M(1,k) = M(5,3) - M(1,3) = 2$, $M(1,k) = M(3,4) - M(1,4) = 3$, $M(2,k) = M(3,4) - M(2,4) = 1$; then we select the link ingoing the pseudo-node with lower $M$, and subsequently the lowest reduction in magnitude, e.g. link from node 2 to pseudo-node; (e) we replace the link in the cycle (link 3–4) with the link outside the cycle entering from node 2 to node 4 from (link 2–4).
Figure A2. average trophic step (\(<TS>\)) for each type of tree as a function of the connectance (C) of the food web. The linear regressions are not significant: MLST (p-value = 0.5929), MWST (p-value = 0.5936), RWST (p-value = 0.4433).

Figure A3. the mean length as average trophic step (\(<TS>\)) for each type of tree and for each food web. The food web labels are indicated in Table 2 of the main paper.
Figure A4. Length of the trees (\(<TS>\)) as a function of the number of nodes (N) of the food web model. Black circle represent MWST and red triangle are the RWST. The food web models are Erdős–Rényi random graphs of N nodes (from N = 20 to N = 80) and connectance C = 0.05. The link interaction strengths are sorted from a uniform distribution in the interval (1,100). The plot is the results of 1000 simulations for each food web parameter. The RWST and the MWST show the same length in these random networks. We do not find difference in length (\(<TS>\)) between RWST and MWST (two tailed Wilcoxon test, V = 57, p = 0.47).
Figure A5. Length of the trees ($<TS>$) as function of the number of nodes (N) of the food web model. Black circle: MWST; red triangle: RWST. The food web models are Erdős–Rényi random graphs of N nodes (from N = 20 to N = 80) and connectance C = 0.05. The link interaction strengths are sorted from a normal distribution with mean = 20 and std. = 5. The plot is the results of 1000 simulations for each food web parameter. As we can see, the RWST and the MWST show the same length. No significant difference in length between RWST and MWST emerge (two tailed Wilcoxon test, V = 44, p = 0.94).
Figure A6. Length of the trees ($<\text{TS}>$) as a function of different levels of connectance. Black circle: MWST; red triangle: RWST. The food web models are Erdős–Rényi random graphs with $N = 40$. Interaction strengths are sorted from a uniform distribution in the interval (1,100). The plot is the results of 1000 simulations for each food web parameter. No significant difference in length between RWST and MWST emerged in this simulation (two tailed Wilcoxon test, $V = 18$, $p = 0.58$). Same outputs were obtained with different numbers of nodes.
Figure A7. Difference in length between MWST and RWST ($<TS>$) as function of different level of connectance. The food web models are Erdős–Rényi random graphs with $N = 40$. Interaction strengths are sorted from a uniform distribution in the interval $(1,100)$. The plot is the results of 1000 simulations for each food web parameter. No significant difference in length between RWST and MWST emerged in this simulation (two tailed Wilcoxon test, $V = 18$, $p = 0.58$).