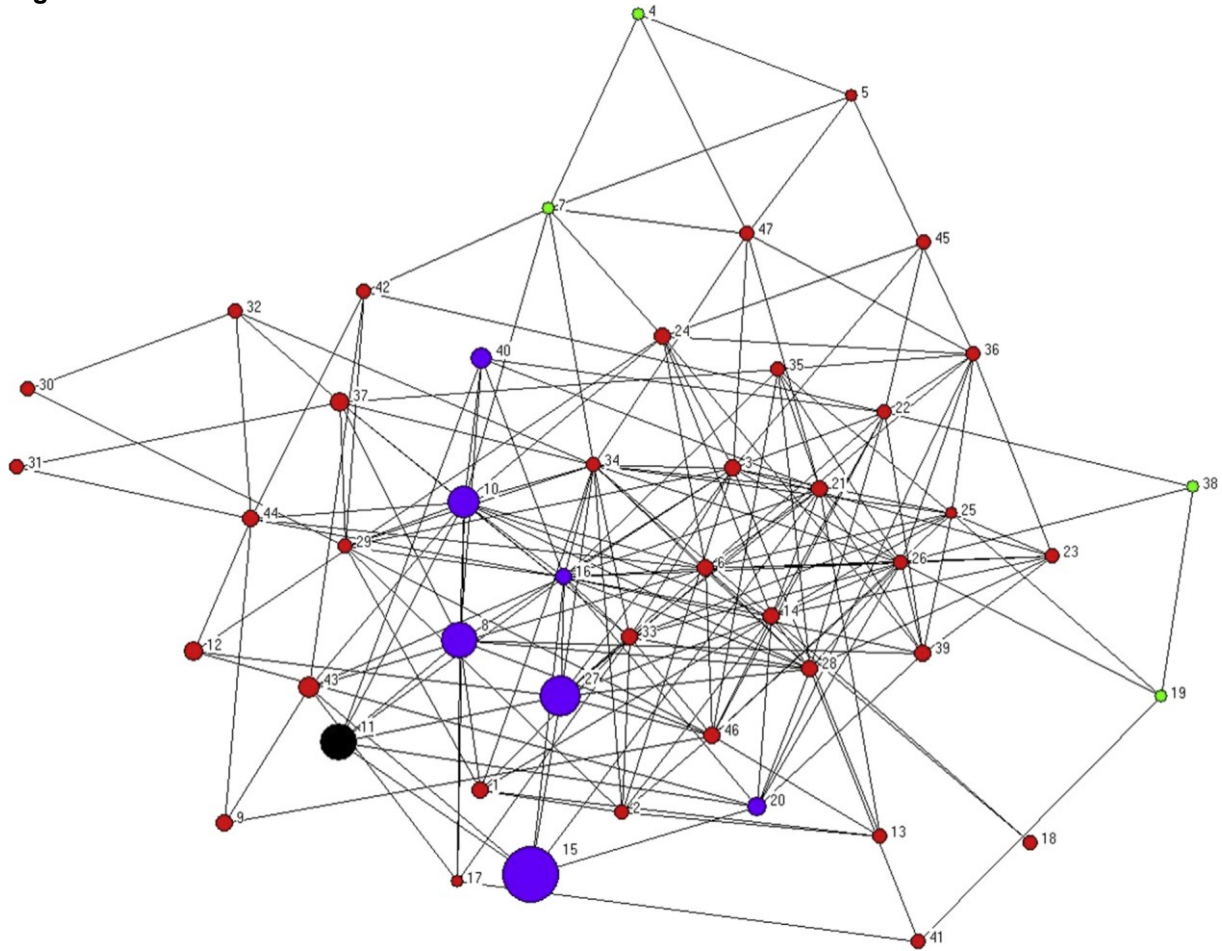**Figure 1**

Effects spreading out from a focal network node (#11 in black). The expected effects on other nodes can be assessed by network analysis, consideringonly the topology of the network [Jordán 2009]. Node size is proportional to the expected effect. Neighbors (in violet) are typically more influenced(like#15), but some of them are not so much (like #16). Nonneighbors (in red) can be influenced only by indirect effects, typically to less than neighbors: Someof them are still more strongly affected (like #43), whereas others are just weakly affected (like #17). Depending on the maximum length of indirect effects,some distant nonneighbors (in green) may not be influenced at all (like #38). Note that the red node #43 is larger than the violet node #16: In this case, asecond neighbor is more strongly affected than a (first) neighbor. This is the network of the Chesapeake Bay food web [76]

Figure 2
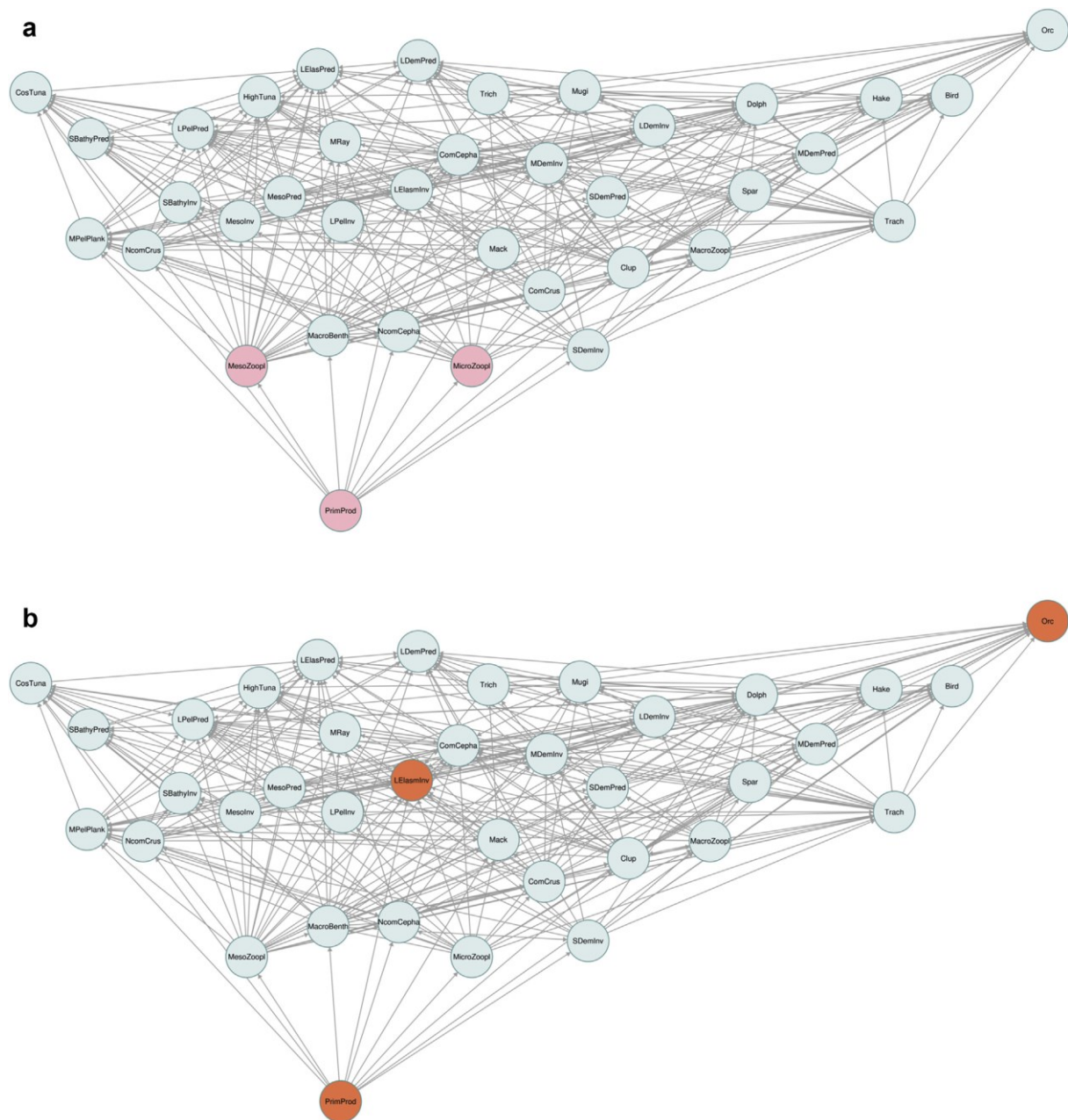
The Mauritania food web [77]. The most important network positions are calculated by closeness centrality here, and they can be identified either (a) by evaluating individual nodes or (b) by evaluating groups of nodes. The individually most central three nodes are not the same as the most central set of three nodes. Trophic groups are vertically organized according to their trophic level (TL). The organisms suggested to be keystones here are PrimProd (primary producers), MesoZoopl (mesozooplankton), and MicroZoopl (microzooplankton) according to the single-node approach (a), whereas they are PrimProd (primary producers), LElasminv (large invertebrate-eater Elasmobranchs), and Orc (orca) according to the multinode approach (b). Note that the multinode approach generally identifies a core set of species at several trophic levels, defining a core trophic chain in the food web.