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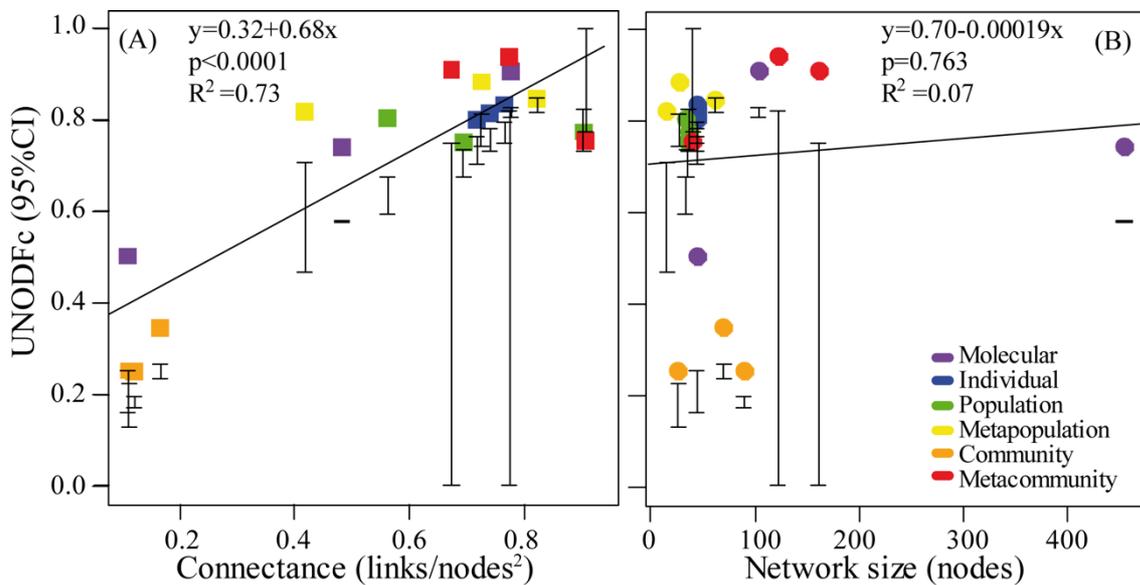
Nestedness across biological scales

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S1 Fig. Relationship between Unipartite Nestedness ($UNODF$), network connectance and

size. (A) $UNODF$ and network connectance (proportion of realized links in relation to possible

links); and (B) $UNODF$ and network size (number of nodes). A simple linear regression

suggests that $UNODF$ increases with connectance ($R^2=0.73$, $p<0.0001$) but not with size

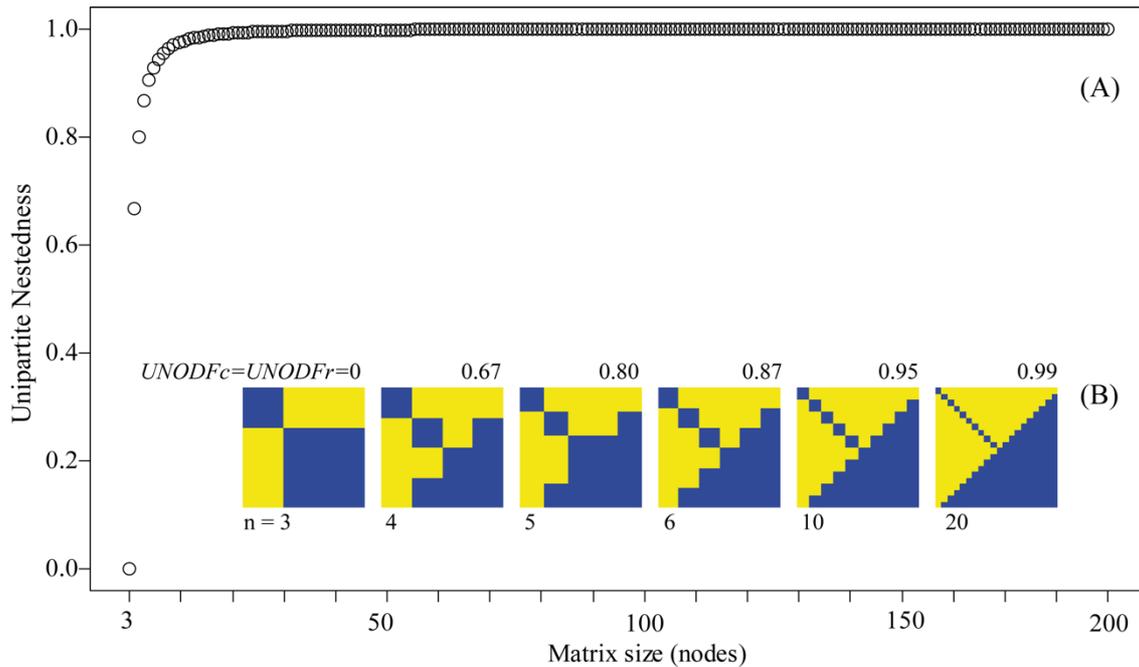
($R^2=0.07$, $p=0.763$). Colored points represent empirical nestedness value and whiskers show the

95% confidence interval of $UNODF$ computed for theoretical networks generated using the null

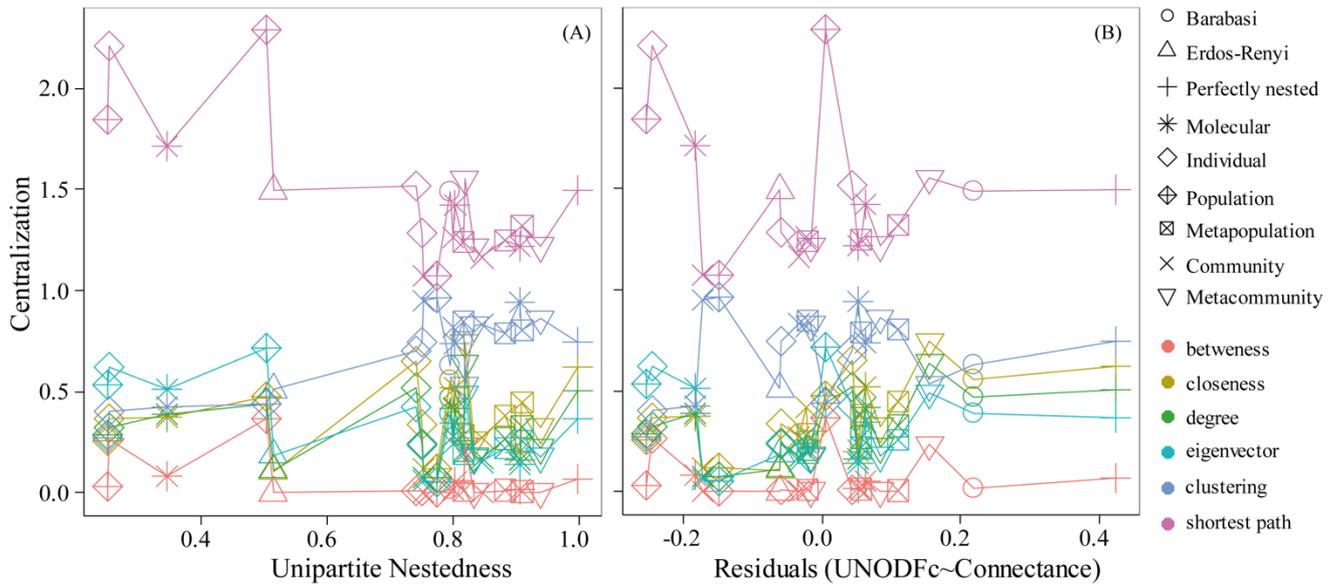
model. Values outside of the 95% Confidence Intervals are significant. Note that only

nestedness among columns ($UNODF_c$) is displayed, since for all networks (except food webs,

Community level) $UNODF_r = UNODF_c$.



S2 Fig. Relationship between Unipartite Nestedness (*UNODF*) and size of theoretical nested one-mode networks. (A) *UNODF* and size (number of nodes, n) of perfectly nested networks. (B) Adjacency binary matrices (yellow cell = 1, blue = 0) of representative small networks ($20 > n > 3$) and their respective unipartite nestedness values among columns and rows ($UNODF_r = UNODF_c$). The *UNODF* metric is sensitive to very small networks, but becomes asymptotic for networks with more than 10 nodes. Note that *UNODF* tends towards—but does not reach—1 because we considered undirected one-mode networks without nodes that interact with themselves. Therefore, the diagonal of the network adjacency matrix A is zeroed ($a_{ii}=0$). Few cases in which a node can have a link with itself include cannibalistic events in food webs. However, for the sake of generality across biological systems, these cases were disregarded here.



S3 Fig. Network metrics describing the centralization of the network and Unipartite

Nestedness (*UNODF*) in one-mode networks. Centralization is measured here by 6 metrics

(colored lines) for both theoretical (perfectly nested, Barabási, Erdős-Rényi) and empirical

networks (three examples for each of the six biological levels: molecular, individual,

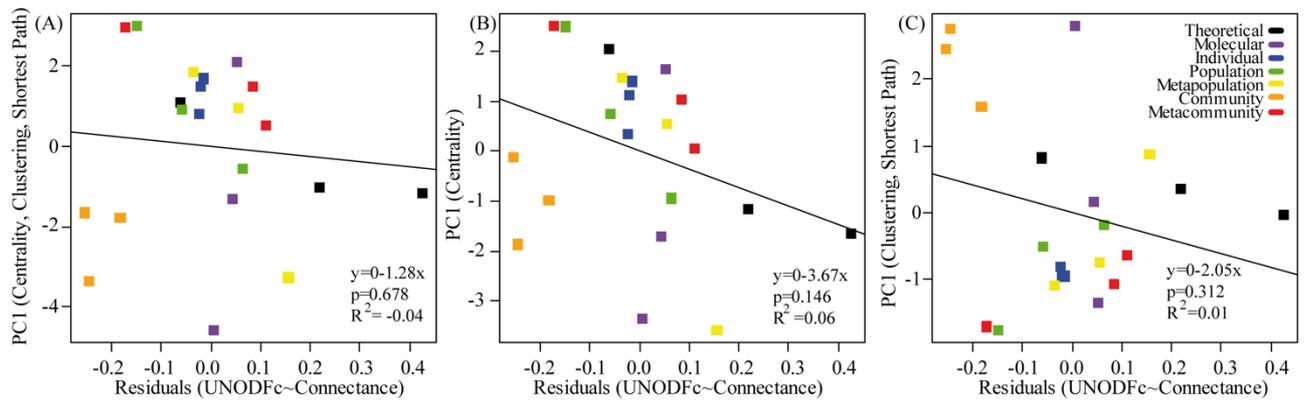
population, metapopulation, community, metacommunity; see S1 Table). In (A) the x-axis

corresponds to the Unipartite Nestedness metric defined in the main text. In (B), x-axis contains

the residuals of the linear regression between Unipartite Nestedness and network connectance (proportion of realized links in relation to possible links) given the positive relationship between them (see Fig 2, S4 Fig). We found no relationship between nestedness and centralization

metrics, suggesting that *UNODF* captures a distinct topological pattern (see also, S4 Fig).

Samples are connected simply to make it easier to read the trajectories of each metric.



S4 Fig. Relationship between Unipartite Nestedness (*UNODF*) and network centralization,

as given by a simple linear model. Here, we corrected *UNODF* for network connectance using

the residuals of the regression between *UNODF* and connectance; see S5 Fig. Centralization

was described using the first principal component to summarize (A) all 6 centralization metrics,

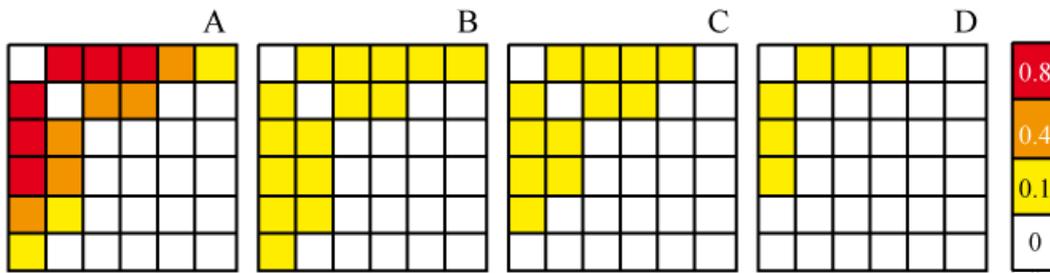
(B) the centrality metrics (degree, betweenness, closeness, eigenvector centrality) and (C) small-

world properties (Clustering coefficient and shortest path length). In all cases, the metrics were

not related to *UNODF* (All metrics: $R^2 = -0.04$, $p = 0.678$; Centrality: $R^2 = 0.06$, $p = 0.146$; Small

world: $R^2 = 0.01$, $p = 0.312$), suggesting that *UNODF* captured a topological feature of one-mode

network different than centralized networks or with small world properties.



S5 Fig. Methodological approach to define a binary interaction in weighted networks.

Color code corresponds to the strength of the interaction between elements. Hypothetical square adjacency matrices in which (A) the interactions between elements of a one-mode network are filtered off according to cut-offs (x) that range from 0.1 to 0.9 in interaction weights, here illustrated by $x > 0$ (B), $x \geq 0.4$ (C), and $x \geq 0.8$ (D). The hypothetical matrices are symmetric ($a_{ij} = a_{ji}$) and an element of a network does not have a link with itself (diagonal $a_{ii} = 0$). Overall, our findings showed that distinct biological systems across scales can have a primary backbone nested structure, but the detection of nested patterns is sensitive to the way we look to the network, i. e., whether considering only the set of strong interactions, or including weak interactions as well. As our findings suggest a relation between nestedness and connectance (S1 Fig), the choice of the link weight threshold used to define an interaction influences the emergence of the pattern: if too permissive, the network is almost fully connected; if too restrictive, the network dismantles into disconnected components as, by reducing the number of interactions, the overlap between nested subsets decrease. Importantly, the interaction strength is not directly related to its biological importance. Weak links are crucial to biological systems, such as occur for infrequent protein [1] and social interactions [2]. Therefore, nestedness is likely to be detected in well-characterized systems whose interactions among the elements are well known and estimated on comprehensive data.

S1 Table. Characterization of the 18 systems encompassing six levels of organization considered in this study and the biological entities or processes depicted by their network representation.

	Biological system	Level of organization	Nodes	Interaction	Weighted links	Network size (nodes)	Connectance (realized/ possible links)	Main References
1	Yeast spliceosome proteins	Molecular	proteins	physical association	Experimental evidence for interaction	103	0.78	[3]
2	<i>Caenorhabditis elegans</i> genes	Molecular	target genes	shared interactions with query genes	Simpson index	454	0.48	[4,5]
3	Yeast nuclear exosome proteins	Molecular	proteins	physical association	Experimental evidence for interaction	44	0.10	[6,7]
4	Cranium morphology of human males	Individual	anatomical landmarks (morphometric variables)	correlations between cranial measurements	Pearson's correlation	44	0.73	[8]
5	Cranium morphology of human females	Individual	anatomical landmarks (morphometric variables)	correlations between cranial measurements	Pearson's correlation	44	0.71	[8]
6	Cranium morphology of human males in Europe	Individual	anatomical landmarks (morphometric variables)	correlations between cranial measurements	Pearson's correlation	44	0.76	[8]
7	Guiana dolphin society	Population	individuals	social relationship	Half-weight association index	33	0.56	[9]
8	Bottlenose dolphin society	Population	individuals	social relationship	Half-weight association index	35	0.69	[10]

9	Spotted hyena social clan	Population	individuals	social relationship	Half-weight association index	35	0.62	[11-13]
10	Insular frog populations	Meta population	population	Genetic similarity	1-R _{ST} total allelic variance	27	0.72	[14,15]
11	Global human populations	Meta population	population	Genetic similarity	1-R _{ST} total allelic variance	62	0.82	[16,17]
12	Insular sparrow populations	Meta population	population	Genetic similarity	1-R _{ST} total allelic variance	15	0.41	[18,19]
13	Food web of the Mangrove estuary in wet season	Community	species	Trophic	Energy transfer	70	0.16	[20]
14	Food web of the Narragansett Bay estuary	Community	species	Trophic	Energy transfer	26	0.11	[21]
15	Food web of the Florida Bay in dry season.	Community	species	Trophic	Energy transfer	89	0.12	[20]
16	Reef fishes communities in a biogeographical region	Meta community	genera	Co-occurrence in sampled sites	Bray-Curtis similarity	158	0.18	[22]
17	Reef fishes communities in a biogeographical region	Meta community	functional group (length+ diet)	Co-occurrence in sampled sites	Bray-Curtis similarity	39	0.46	[22]
18	Reef fishes communities in a biogeographical region	Meta community	functional group (length+ diet+ mobility+ school size)	Co-occurrence in sampled sites	Bray-Curtis similarity	120	0.24	[22]

Supplementary References

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