Supporting Information (SI Appendix) 'Looplessness'

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CONTENTS

1 Graph ensembles

1.1 The directed configuration ensemble

This is the set of all graphs with given sequences of in- and out-degrees [1]. Using this ensemble as a null-model, we can obtain the expected numbers of paths and cycles by inserting the expected value of the adjacency matrix for large graphs, $\hat{a}_{ij} = k_i^{out} k_j^{in}/L$, in the above definitions (we shall use the notation $\hat{z}$ to refer to the expected value of a magnitude z in the directed configuration ensemble). Thus, the expected number of paths in this ensemble is

$$\hat{n}_\nu = L\alpha^{\nu-1}, \tag{1}$$

while the expected number of those paths which are cycles is

$$\hat{m}_\nu = \alpha^\nu, \tag{2}$$

where

$$\alpha = \frac{\langle k^{in} k^{out} \rangle}{\langle k \rangle}. \tag{3}$$

The branching factor α captures the correlation between the in- and out-degrees of nodes (i.e. $\alpha > \langle k \rangle$ indicates a positive correlation, with high in-degree nodes also tending to have high out-degree, while $\alpha < \langle k \rangle$ means this correlation is negative).

1.2 The basal ensemble

Let us consider the ensemble of random graphs which satisfy the following constraint: for every non-basal node, the proportion of in-coming edges which connect to basal nodes is the same. This is a sufficient condition for all non-basal nodes to have the same trophic level. More formally, if a network in this ensemble has B basal nodes, $N-B$ non-basal nodes, L edges, and L_B edges connecting to basal nodes, then every non-basal node i with in-degree k_i^{in} receives $k_i^{in} L_B/L$ edges from basal nodes and $(1-L_B/L)k_i^{in}$ from non-basal nodes. Note that this constraint does not affect the expectations obtained above for the more general directed configuration ensemble, so the expected numbers of paths and cycles are, respectively,

$$\tilde{n}_\nu = L\alpha^{\nu-1} \tag{4}$$

and

$$\tilde{m}_\nu = \alpha^\nu \tag{5}$$

(where we have used the notation $\tilde{z}$ for the expected value of a magnitude z in the basal ensemble). However, the fixed proportion of basal in-neighbours allows us also to derive expected values for several magnitudes in this ensemble, given $\{N, B, L, L_B\}$, as follows.

We recall from the main text [Eq. (4)] that the trophic level of each node i is

$$s_i = 1 + \frac{1}{k_i^{in}} \sum_j a_{ij} s_j \tag{6}$$

if is non-basal (i.e. $k_i^{in} > 0$), and $s_i = 1$ if i is basal ($k_i^{in} = 0$) [2]. Let $\tilde{s}_{nb}$ be the expected trophic level in the basal ensemble of a node given that it is not

basal. Since the expected proportion of in-neighbours which are basal, for such a node, will be L_B/L, we have from Eq. (6) that

$$\tilde{s}_{nb} = 1 + \frac{L_B + (L - L_B)\tilde{s}_{nb}}{L},$$ (7)

and so $\tilde{s}_{nb} = L/L_B + 1$. The mean trophic level of the network is therefore

$$\tilde{s} = 1 + \left(1 - \frac{B}{N}\right)\frac{L}{L_B}.$$ (8)

In the basal ensemble there will be two types of edges: those which emanate from basal nodes, with trophic difference $x = \tilde{s}_{nb} - 1$, and those between non-basal nodes, with $x = 0$. In other words, the distribution of differences will be

$$p(x) = \frac{L_B}{L}\delta\left(x - \frac{L}{L_B}\right) + \left(1 - \frac{L_B}{L}\right)\delta(x),$$ (9)

where δ is the Dirac delta function. The trophic coherence associated with this distribution is

$$\tilde{q} = \sqrt{\frac{L}{L_B} - 1}.$$ (10)

We can also obtain the expected value of α in the basal ensemble. Every node with $k^{in} \neq 0$ (i.e. every non-basal node) has in-degree $k^{in} = L/(N - B)$; and while the out-degree of such a node is not determined, the expected value is $\tilde{k}^{out} = (L - L_B)/(N - B)$. Inserting these values into Eq. (3) yields

$$\tilde{\alpha} = \frac{L - L_B}{N - B}.$$ (11)

Note that this is the mean degree that would result if all basal nodes and edges emanating from basal nodes were eliminated from the network. As in the configuration ensemble, the expected proportion of paths of length ν which are cycles, in the basal ensemble, is

$$\tilde{c}_\nu = \frac{\tilde{\alpha}}{L}.$$ (12)

The basal ensemble does not include any structure which might lead to variance in the trophic levels of non-basal nodes, and so the bimodal $p(x)$ given by Eq. (9) is exact. For networks in which different non-basal nodes are connected to differing proportions of basal nodes, this expression will be a valid approximation only when the separation of the two modes of $p(x)$ is much larger than the spread about them.

1.3 Equivalence of ensembles

Let κ_i be the proportion of in-coming edges to node i which emanate from a basal node. In the directed configuration ensemble, the expectation for κ_i is $\hat{\kappa}_i = L_B/L$, $\forall i$. The basal ensemble is the subset of graphs from the directed configuration ensemble which satisfy $\kappa_i = L_B/L$, $\forall i$, exactly, not just in expectation. Thanks to this constraint, all non-basal nodes have the same trophic level, given by Eq. (7), in the basal ensemble. For finite graphs drawn from
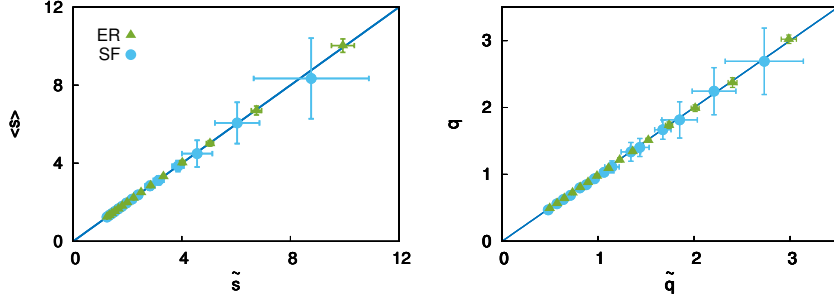
Figure S 1. Values of mean trophic level $\langle s \rangle$ (left), and incoherence parameter q (right), obtained numerically with two random graph models against the corresponding predictions for the basal ensemble, as given by Eqs. (8) and (10), respectively. The random graphs are sampled from the Erdős-Rényi ensemble (circles) with $N = 300$ and $\langle k \rangle = L/N = 10$; and from the directed configuration ensemble (triangles) with $N = 500$, $\langle k \rangle = L/N = 5$ and power-law degree sequences of exponent $\gamma = 3$. In both cases, the proportion of basal nodes, B/N, is varied from 10% (upper right hand corners) to 50% (lower left hand corners).

the directed configuration ensemble, there will be some variation in the trophic levels of non-basal nodes, leading to discrepancies with respect to the expectations of quantities such as q, α and $\langle s \rangle$. However, in the limit $N \to \infty$, with $L/N \to \infty$, expectations in the basal ensemble and the directed configuration ensemble converge, since $\kappa_i \to \hat{\kappa}_i$, $\forall i$. This suggests that the basal ensemble might provide a reasonable null model even for finite networks. In order to test this assumption numerically, we draw networks from the directed configuration and compare measured quantities with basal ensemble expectations. We note, however, that the results derived in the main text for the coherence ensemble do not depend on an equivalence between the basal ensemble and the directed configuration ensemble.

Figure S1 displays the results of Monte Carlo simulations which support the conjecture that the basal ensemble provides a good approximation to more general random graph ensembles as regards trophic structure. We consider a directed version of the Erdős-Rényi ensemble, in which L directed edges are distributed randomly among N nodes with the constraint that there must be B basal nodes. We also take the directed configuration ensemble of networks, which restricts both the in- and out-degrees of each node to specified values, and generate heavy-tailed (scale-free) networks by drawing those values from independent distributions $p(k) \sim k^{-\gamma}$, for $k = k^{in}$ and $k = k^{out}$. The left panel of Fig. S1 shows the mean trophic level $\langle s \rangle$ obtained numerically from Erdős-Rényi networks and heavy-tailed networks, as described, for varying proportions of basal nodes. This is plotted against the corresponding values given by Eq. (8) in each case. Similarly, the right panel of Fig. S1 shows the incoherence parameter q against the value given by Eq. (10), for the same networks. In both cases, the results fall very close to the $f(x) = x$ line, suggesting that the trophic structure of random graphs, regardless of their degree heterogeneity, is well approximated by the basal ensemble we have defined above.

2 Networks with self-cycles

In the main text we ignore self-edges (cycles of length one) in those networks which exhibit them; this is mainly because self-edges are not reported in all networks, the nature of self-interaction often being considered fundamentally different to that of inter-element interaction. However, for completeness we also compute the values of the leading eigenvalue λ_1, and of the loop exponent τ, defined as

$$\tau = \ln \alpha + \frac{1}{2\tilde{q}^2} - \frac{1}{2q^2}, \tag{13}$$

when self-edges are allowed, and display these values in Fig. S2 (compare with Fig. 1 of the main text). We can observe that the good fit to the expression

$$\overline{\lambda_1} = e^\tau \tag{14}$$

– Eq. (14) of the main text, where $\overline{\lambda_1}$ is the coherence ensemble expectation for λ_1 – is not significantly affected by the inclusion of self-edges. The main difference is that several of the food webs which have $\lambda_1 = 0$ when self-edges are excluded now have $\lambda_1 = 1$, as a result of cannibalism.

3 Network data

In the main text we assess the validity of our analytical results through comparisons with a set of empirically-derived directed networks. Most of these are available online, but a few of them were shared with us in private correspondence. Below we list the most relevant details for each of these networks. Table 1 is for 42 food webs, Table S2 lists eight gene regulatory networks, and Table S3 contains information on seven metabolic networks. Table S4 is for six networks of various other kinds: the neural network of *C. elegans*, a P2P file sharing network, two networks of trade between nations (one of basic manufactured good and the other of minerals) and one of concatenated English words in the book *Green Eggs and Ham*, by Dr. Seuss; the last of these was obtained from the original text for this work [3]. The adjacency matrices of these networks are available at:
http://www2.warwick.ac.uk/fac/sci/maths/people/staff/sjohnson
or upon request from the authors.

For each network, we list the number of nodes N, the number of basal nodes B, and the mean degree $\langle k \rangle$; the incoherence parameter q and its ratio to the expected value $\tilde{q}$ (low ratios mean more coherent networks than randomly expected); the mean trophic level $\langle s \rangle$ and the k^{in}-k^{out} correlation parameter α, both normalised by their expected values; the loop exponent τ, whose sign determines whether a network is in the high or low feedback regimes (see main text); the leading eigenvalue, λ_1, of the adjacency matrix; and, finally, references to the sources of the data.

Figure S3 shows three example networks, one from each class: the Ythan Estuary food web [4], a metabolic network derived for *Chlamydia pneumoniae* [5], and a gene regulatory network derived for *E. coli* [6]. The height of each node on the vertical axis is proportional to its trophic level, and this visualisation is enough to show that the trophic structures of these systems can be highly informative. Note, in particular, that a network can display significant
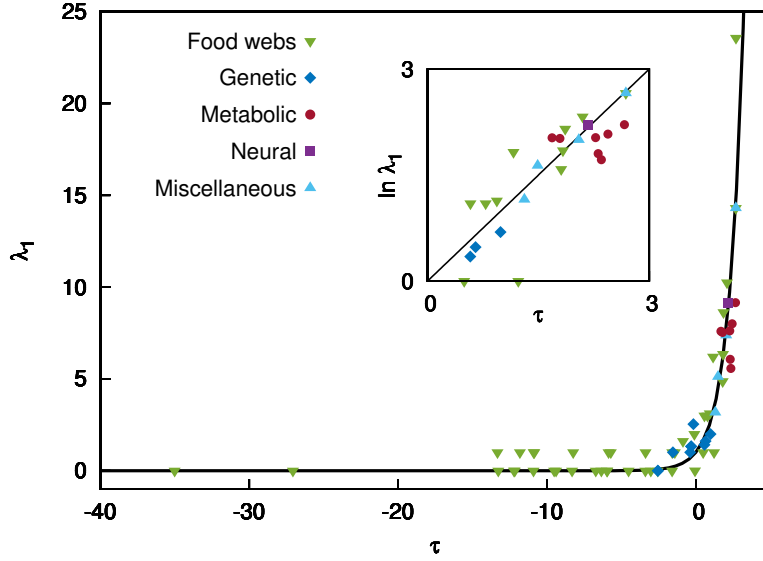
Figure S 2. Leading eigenvalues λ_1 of several directed networks when self-edges are not excluded, against τ as given by Eq. (13); symbols indicate food webs (green down-pointing triangles), gene regulatory networks (dark blue diamonds), metabolic networks (burgundy circles), a neural network (purple square), and other miscellaneous networks (light blue up-pointing triangles). Line: Expected leading eigenvalue $\overline{\lambda_1}$ in the coherence ensemble, as given by Eq. (14). Inset: Semi-log version of the positive quadrant of the main panel (Pearson's correlation coefficient: $r^2 = 0.80$). Compare with Fig. 2 of the main text, for which self-edges are excluded. Details for each network, including references, are listed in Tables S1, S2. S3 and S4 (though note that in these tables self-edges are excluded).

trophic coherence (the Ythan Estuary food web has $q/\tilde{q} = 0.15$) without all its nodes falling into clearly defined trophic levels, while it is also possible to be almost bipartite, as in the case of *E. coli*'s gene regulatory network, yet be less significantly coherent as compared to the random expectation ($q/\tilde{q} = 0.88$). These examples show that in order to determine which regime (of high or low feedback) a given system belongs to, it is insufficient to look only at trophic coherence: one must compute the loop exponent τ.

Food web	N	B	$\langle k \rangle$	q	$q/\tilde{q}$	$\langle s \rangle/\tilde{s}$	$\alpha/\tilde{\alpha}$	τ	λ_1	Ref.
Benguela Current	29	2	6.76	0.69	0.15	0.17	0.69	0.50	2	[7]
Berwick Stream	77	35	3.12	0.18	0.53	1.05	1.06	-12.21	0	[8, 9, 10]
Blackrock Stream	86	49	4.36	0.19	0.57	1.02	1.27	-9.51	0	[8, 9, 10]
Bridge Brook Lake	25	8	5.08	0.53	0.36	0.68	0.72	-0.53	1	[11]
Broad Stream	94	53	6.00	0.14	0.49	1.05	1.20	-20.10	0	[8, 9, 10]
Canton Creek	102	54	6.82	0.15	0.57	1.01	1.22	-14.52	0	[12]
Caribbean Reef	50	3	10.70	0.94	0.33	0.36	0.96	1.73	7.80	[13]
Cayman Islands	242	10	15.55	0.77	0.24	0.30	0.51	1.22	0	[14]

	N	B	$\langle k \rangle$	q	$q/\tilde{q}$	$\langle s \rangle/\tilde{s}$	$\alpha/\tilde{\alpha}$	τ	λ_1	Ref.
Catlins Stream	48	14	2.29	0.20	0.41	0.98	1.00	-10.90	0	[8, 9, 10]
Chesapeake Bay	31	5	2.16	0.45	0.33	0.73	0.90	-1.81	0	[15, 16]
Coachella Valley	29	3	8.38	1.20	0.48	0.47	0.91	1.63	5.48	[17]
Coweeta 1	58	28	2.17	0.30	0.64	1.00	1.08	-3.39	0	[8, 9, 10]
Coweeta 17	71	38	2.08	0.24	0.60	1.00	1.25	-5.94	0	[8, 9, 10]
Dempsters (Au)	83	46	4.99	0.21	0.57	1.08	1.02	-7.42	0	[8, 9, 10]
Dempsters (Sp)	93	50	5.78	0.13	0.38	1.07	1.11	-27.07	0	[8, 9, 10]
Dempsters (Su)	107	50	9.02	0.27	0.57	1.05	1.04	-3.51	0.01	[8, 9, 10]
El Verde Rainforest	155	28	9.72	1.01	0.45	0.49	1.21	2.09	10.12	[18]
German Stream	84	48	4.19	0.20	0.47	1.02	1.10	-9.35	0	[8, 9, 10]
Healy Stream	96	47	6.60	0.22	0.53	1.03	1.12	-6.34	0	[8, 9, 10]
Kyeburn Stream	98	58	6.42	0.18	0.62	1.02	1.18	-9.39	0	[8, 9, 10]
LilKyeburn Stream	78	42	4.81	0.23	0.53	1.01	1.10	-5.97	0	[8, 9, 10]
Little Rock Lake	92	12	10.7	0.67	0.22	0.25	0.77	1.06	5.66	[19]
Lough Hyne	349	49	14.62	0.60	0.37	0.59	0.63	0.85	2.56	[20, 21]
Martins Stream	105	48	3.27	0.32	0.58	0.99	1.26	-2.56	0	[8, 9, 10]
Narrowdale Stream	71	28	2.17	0.23	0.50	0.98	1.17	-7.45	0	[8, 9, 10]
NE Shelf	79	2	17.44	0.73	0.13	0.10	0.71	1.57	4.32	[22]
North Col Stream	78	25	3.09	0.28	0.52	0.98	1.36	-4.52	0	[8, 9, 10]
Powder Stream	78	32	3.44	0.22	0.47	0.99	1.12	-8.32	0	[8, 9, 10]
Scotch Broom	85	1	2.58	0.40	0.14	0.30	1.20	-2.08	0	[23]
Skipwith Pond	25	1	7.56	0.61	0.15	0.16	0.64	0.20	2	[24]
St Marks Estuary	48	6	4.54	0.63	0.37	0.63	1.02	0.26	0	[25]
St Martin Island	42	6	4.88	0.59	0.32	0.54	0.79	-0.05	0.01	[26]
Stony Stream	109	61	7.59	0.15	0.55	1.03	1.16	-14.66	0	[27]
Stony Stream 2	112	63	7.41	0.15	0.55	1.04	1.18	-14.72	0	[8, 9, 10]
Sutton (Au)	80	49	4.19	0.15	0.66	1.08	1.28	-13.27	0	[8, 9, 10]
Sutton (Sp)	74	50	5.28	0.10	0.56	1.11	1.15	-35.01	0	[8, 9, 10]
Sutton (Su)	87	63	4.87	0.28	0.89	1.19	0.52	-1.59	0	[8, 9, 10]
Troy Stream	77	40	2.35	0.19	0.37	1.01	1.14	-12.16	0	[8, 9, 10]
UK Grassland	61	8	1.59	0.40	0.18	0.42	0.63	-3.03	0	[28]
Venlaw Stream	66	30	2.83	0.23	0.54	1.06	1.35	-6.72	0	[8, 9, 10]
Weddel Sea	483	61	31.71	0.72	0.55	0.75	1.17	2.63	22.91	[29]
Ythan Estuary	82	5	4.77	0.42	0.15	0.28	0.93	-1.32	1	[4]

Table S 1. Details of 42 food webs used in the main text. Columns are for number of nodes N, number of basal nodes B, mean degree $\langle k \rangle$, and incoherence parameter q; ratios of q, mean trophic level $\langle s \rangle$, and correlation parameter α to their expected values in the basal ensemble; loop exponent τ, leading eigenvalue λ_1, and references to the data sources. Many of the data are available online at:
https://www.nceas.ucsb.edu/interactionweb/html/thomps_towns.html

Gene regulatory network	N	B	$\langle k \rangle$	q	$q/\tilde{q}$	$\langle s \rangle/\tilde{s}$	$\alpha/\tilde{\alpha}$	τ	λ_1	Ref.
Human (healthy)	4071	4004	2.08	0.08	0.99	1.00	0.99	-1.54	1	[30, 31]
Human (cancer)	4049	3967	2.89	0.08	1.00	1.00	1.07	-0.16	2.54	[30, 31]
E. coli (Salgado)	1470	1316	1.98	0.23	1.03	1.00	1.21	0.65	1.62	[32, 31]

	N	B	$\langle k \rangle$	q	$q/\tilde{q}$	$\langle s \rangle/\tilde{s}$	$\alpha/\tilde{\alpha}$	τ	λ_1	Ref.
E. coli (Thieffry)	418	312	1.24	0.27	0.88	1.01	0.94	-2.54	0	[6, 33]
S. cerevisiae (Harbison)	2933	2764	2.10	0.17	0.98	1.00	1.29	-0.38	1	[34, 31]
S. cerevisiae (Costanzo)	688	557	1.57	0.25	1.04	1.00	0.81	-0.31	1.32	[35, 33]
P. aeruginosa	691	606	1.43	0.30	1.00	1.03	1.94	0.58	1.41	[36, 31]
M. tuberculosis	1624	1542	1.95	0.17	1.02	1.00	1.24	0.99	2.00	[37, 31]

Table S 2. Details of eight gene regulatory networks (GRN) used in the main text. The E. coli (Salgado) and Yeast (Harbison) are available online at: `http://wws.weizmann.ac.il/mcb/UriAlon/download/` `collection-complex-networks`. The others were shared with us by Luca Albergante, and some of them can be obtained from various websites: `http://regulondb.ccg.unam.mx/` (E. coli, Salgado); `http://younglab.wi.mit.edu/regulatory_code` (Yeast, Harbison); `http://www.genome.gov/ENCODE/` (Human, both the non-cancer GM12878 cell line and the K562 leukaemia cell line). Columns as in Table S1.

Metabolic network	N	B	$\langle k \rangle$	q	$q/\tilde{q}$	$\langle s \rangle/\tilde{s}$	$\alpha/\tilde{\alpha}$	τ	λ_1	Ref.
A. fulgidus	1267	36	2.38	13.79	1.88	2.06	4.34	2.35	7.62	[5]
M. thermoautotrophicum	1111	30	2.43	12.17	1.77	1.90	4.08	2.31	7.59	[5]
M. jannaschii	1081	32	2.40	12.47	1.86	1.98	4.00	2.27	7.53	[5]
C. pneumoniae	386	20	2.05	8.98	1.62	1.71	2.55	1.69	5.57	[5]
C. trachomatis	446	19	2.11	11.77	1.95	2.02	2.77	1.79	6.07	[5]
S. cerevisiae (yeast)	1510	43	2.54	14.61	1.73	1.82	5.54	2.66	9.15	[5]
C. elegans	1172	40	2.44	13.29	1.86	2.04	4.60	2.44	8.00	[5]

Table S 3. Details of seven metabolic networks used in the main text, downloaded from `http://www3.nd.edu/~networks/resources.htm`. Columns as in Table S1.

Network (miscellaneous)	N	B	$\langle k \rangle$	q	$q/\tilde{q}$	$\langle s \rangle/\tilde{s}$	$\alpha/\tilde{\alpha}$	τ	λ_1	Ref.
Neural (*C. elegans*)	297	3	7.90	1.49	0.42	0.39	1.42	2.17	9.15	[38, 39]
P2P (Gnutella 2008)	6301	3836	3.30	0.98	0.98	1.00	1.07	1.49	5.12	[40, 41]
Trade (manufactured goods)	24	2	12.92	4.24	1.14	1.14	1.10	2.68	14.3	[42]
Trade (minerals)	24	3	5.63	4.04	1.02	0.97	1.28	2.05	7.38	[42]
Words	50	16	2.02	2.04	1.01	1.16	1.55	1.31	3.17	[3]

Table S 4. Details of six other networks used in the main text. The network of words was obtained for this work from *Green Eggs and Ham* [3], and is available upon request from s.johnson.2@warwick.ac.uk. The other data can be found on various websites: `http://www-personal.umich.edu/~mejn/netdata/` (neural network); `https://snap.stanford.edu/data/p2p-Gnutella08.html` (P2P network); and `http://vlado.fmf.uni-lj.si/pub/networks/data/esna/metalWT.htm` (trade networks). Columns as in Table S1
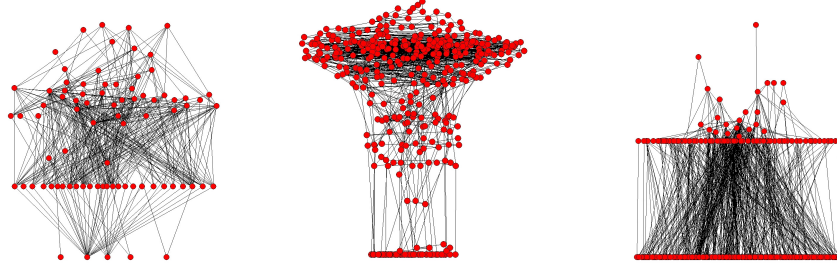
Figure S 3. Empirical networks display a rich diversity of trophic structures. Examples of three kinds of network are plotted here in such a way that the height of each node on the vertical axis is proportional to its trophic level (the scale used for each network is different because of the disparity in mean trophic level). Left: Ythan Estuary food web [4], which is significantly more trophically coherent than the random expectation ($q/\tilde{q} = 0.147$) and has no significant k^{in}-k^{out} correlations ($\alpha/\tilde{\alpha} = 0.935$); it is in the negative τ regime: $\tau = -1.319$. Centre: A network derived from observations of the *Chlamydia pneumoniae* metabolism [5], which is significantly less trophically coherent than the random expectation ($q/\tilde{q} = 1.621$), and has positive k^{in}-k^{out} correlations ($\alpha/\tilde{\alpha} = 2.550$); it is in the positive τ regime: $\tau = 1.686$. Right: A network derived from gene regulation in *E. coli* [6], which is only slightly more trophically coherent than the random expectation ($q/\tilde{q} = 0.878$) and has no significant k^{in}-k^{out} correlations ($\alpha/\tilde{\alpha} = 0.938$); it is in the negative τ regime: $\tau = -2.543$. Details for each network, including references, are listed in the tables of SI.

3.1 Green Eggs and Ham words network

We obtained the network of concatenated words from Dr Seuss's masterpiece *Green Eggs and Ham* in the following way [3]. Every node in the text was assigned a node, and a directed edge $a_{ij} = 1$ was placed whenever word i preceded word j in a sentence. Figure S4 displays this network in such a way that the height of each node on the y-axis is proportional to its trophic level. Note that the arrows we have placed between nodes in this visualisation are from the preceding word to the succeeding one, so that one can obtain sentences (some of them grammatically correct) by following the arrows. We have used colours to indicate syntactic function, as described in the caption.
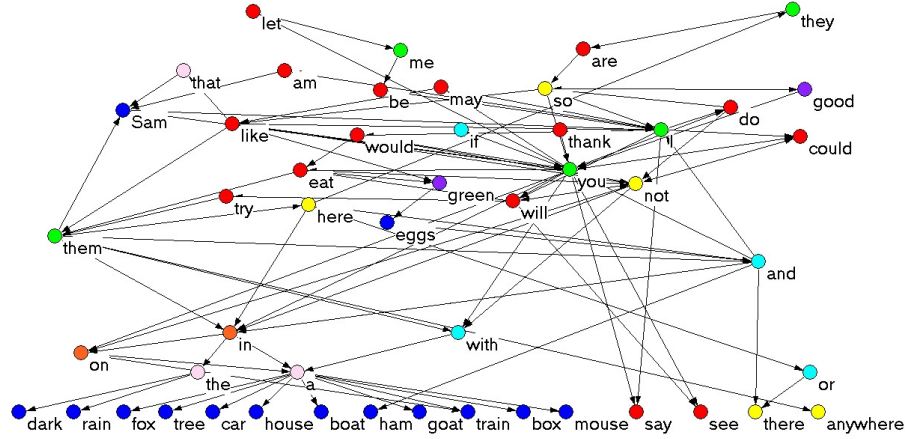
Figure S 4. Network of concatenated words from *Green Eggs and Ham*, by Dr Seuss [3]. The height of each word is proportional to its trophic level. Colours indicate syntactic function; from lowest to highest mean trophic level: nouns (blue), prepositions and conjunctions (cyan), determiners (pink), adverbs (yellow), pronouns (green), verbs (red), and adjectives (purple). When a word has more than one function, the one most common in the text is used.

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