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## Reporting Summary

Life sciences

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Statistics		
For all statistical analyse	es, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.	
n/a Confirmed		
The exact sam	ple size $(n)$ for each experimental group/condition, given as a discrete number and unit of measurement	
A statement o	n whether measurements were taken from distinct samples or whether the same sample was measured repeatedly	
	test(s) used AND whether they are one- or two-sided states should be described solely by name; describe more complex techniques in the Methods section.	
A description of	of all covariates tested	
A description of	of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons	
Y	on of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)	
	nesis testing, the test statistic (e.g. $F$ , $t$ , $r$ ) with confidence intervals, effect sizes, degrees of freedom and $P$ value noted exact values whenever suitable.	
For Bayesian a	nalysis, information on the choice of priors and Markov chain Monte Carlo settings	
For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes		
Estimates of e	ffect sizes (e.g. Cohen's $d$ , Pearson's $r$ ), indicating how they were calculated	
·	Our web collection on <u>statistics for biologists</u> contains articles on many of the points above.	
Software and c	ode	
Policy information abou	at <u>availability of computer code</u>	
Data collection	Data was generated using MATLAB version R2018B. We wrote custom MATLAB code, which we make available in Zenodo with the identifier http://dx.doi.org/10.5281/zenodo.3462156.	
Data analysis	Data was analyzed using MATLAB version R2018B. We wrote custom MATLAB code, which we make available in Zenodo with the identifier http://dx.doi.org/10.5281/zenodo.3462156.	
For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.		
Data		
<ul> <li>Accession codes, uni</li> <li>A list of figures that h</li> </ul>	nt <u>availability of data</u> nclude a <u>data availability statement</u> . This statement should provide the following information, where applicable: que identifiers, or web links for publicly available datasets nave associated raw data restrictions on data availability	
All data generated or anal	ysed during this study are included in this article and its supplementary information files.	
Field-speci	fic reporting	

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

Ecological, evolutionary & environmental sciences

Behavioural & social sciences

Human research participants

## Ecological, evolutionary & environmental sciences study design

All studies must disclose or	these points even when the disclosure is negative.
Study description	We studied the conditions for success in evolutionary games on isothermal graphs. The vast majority of our results are based on mathematical derivations and proofs, which are provided in the Supplementary Information. Additionally, there were some numerical experiments on random graphs, which were implemented using MATLAB.
Research sample	Numerical data were generated using MATLAB code, which is made available in Zenodo with the identifier http://dx.doi.org/10.5281/zenodo.3462156.
Sampling strategy	For the spatial model (Fig. 3AC), the population size is \$N=200\$, the decay parameter is \$\beta=2^{\ell/2}\$ for \$\ell=6,7,\ldots,14\$, and the number of pairing rounds is \$100,200,\ldots, 800\$. Ten random isothermal graphs were generated for each parameter combination. The clusters of points in Figure 3C correspond to different values of \$\beta\$.
	The shifted-linear preferential attachment model (Fig. 3BD) is defined as follows: Starting from a complete graph of size $\$m+1\$$ , new vertices were added one at a time, each linking to $\$m\$$ existing vertices, chosen with probability proportional to $\$k$ - $am\$$ , where $\$k\$$ is vertex degree and $\$a\$$ is a shift parameter. The process was iterated until the graph reached size $\$N=400\$$ . We used linking numbers $\$m=4,5$ ,\dots, 20 $\$$ , and shift parameter $\$a\$$ varying from 0 to 0.9 in increments of 0.05. For each combination of $\$a\$$ and $\$m\$$ , we generated ten graph topologies. For each topology generated this way, an isothermal weighting was obtained by minimizing $\$sm_{[i,j]} * m_{[i,j]} * $
Data collection	Data were generated using the MATLAB code, as written and exectued by Gabor Lippner
Timing and spatial scale	Not applicable
Data exclusions	For the preferential attachment model, graph topologies that could not be made isothermal were removed from the ensemble; such graphs arose for small \$m\$ and \$a\$ close to 1. We describe this exclusion in detail in Supplementary Note 5.
Reproducibility	All numerical data can be reproduced using the provided MATLAB code
Randomization	Not applicable
Blinding	No blinding was needed for the computer-generated data
Did the study involve fiel	d work? Yes No
Reporting fo	r specific materials, systems and methods
We require information from a	authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material,
	evant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.
Materials & experime	<del></del>
n/a Involved in the study	n/a   Involved in the study
Antibodies	ChIP-seq
Eukaryotic cell lines	
Palaeontology	MRI-based neuroimaging
Animals and other of	organisms