

The Network Basis of Pattern Formation

A Topological Atlas of Multifunctional Turing Networks

Laura Regueira López de Garayo^a and Luciano Marcon^{a,1}

This manuscript was compiled on January 27, 2025

Understanding how genetic networks can drive different self-organizing spatial behaviors remains a significant challenge. Here, we use an automated algebraic method to systematically screen for Turing networks capable of generating diverse spatial patterns from noise, including periodic static waves, traveling waves and noise-amplifying patterns. We organize these networks into a topological atlas—a higher-level graph where nodes represent Turing networks linked together when they differ by only one regulatory interaction. In this atlas, Turing networks are arranged into distinct clusters showing a remarkable correspondence between network topology and self-organizing behaviors. Using an analytical approach, we identify the specific regulatory feedbacks that characterize each behavior. Moreover, we discover that different clusters are interconnected by multifunctional networks that can transition between behaviors upon feedback modulation. Among these networks, we find a new class of multiphase Turing networks capable of altering the phase of periodic wave patterns depending on the parameters, and networks that can transition between static and oscillatory Turing behaviors. The atlas further highlights the crucial role of feedback on immobile nodes in regulating pattern formation speed and precision by canalizing system noise. Overall, our study provides a novel framework to study the evolution and development of multicellular self-organization through changes in network topology and feedback modulation. This offers insights into how genetic regulatory networks can be tuned to drive pattern formation in developmental biology and in stem cell systems like embryoids and organoids.

Turing | Self-Organization | Network Topology | Pattern-formation | Noise

Turing's reaction-diffusion model explains how uniform systems can break symmetry to generate spatial patterns. Initially proposed to explain early symmetry-breaking and morphogenesis of the embryo (1), the model was overlooked in favor of hierarchical systems such as positional information (2). Recently, interest in Turing's theory has been renewed in developmental biology (3) and for studying the self-organization of embryoids and organoids (4). Despite this resurgence, the precise genetic interactions driving different type of Turing patterns in multicellular systems remain largely unknown.

Turing proposed that cells could self-organize by exchanging substances called morphogens, which diffused between cells like hormones and interacted according to standard chemical reactions. Depending on reaction terms, morphogen systems could form six types of spatial waves categorized as stationary or oscillatory with extremely long, extremely short, or finite wavelengths (1). Patterning dynamics resembling static or oscillatory Turing patterns have been observed in various biological systems like skin appendages and limb development (5, 6). Although the key genes involved in these patterning events have been identified, understanding the interactions that drive Turing behaviors requires analysis through regulatory principles rather than chemical stoichiometry, as originally proposed by Turing.

Theoretical network screenings have systematically analyzed gene regulatory networks, identifying simple regulatory principles that promote oscillations (7) and adaptive responses (8, 9). A comprehensive screening (10) identified three-node networks capable of forming a peak of gene expression in response to a gradient. This study organized the networks into an atlas constructed as a higher-level graph of networks, where each node represented a gene regulatory topology, and edges connected topologies differing by only one interaction (10). This was a convenient approach to organizing networks in topological space, clustering similar topologies together, and identifying six minimal regulatory motifs linked to variations in underlying feed-forward logic (11). A subsequent study (12) expanded this atlas to include other patterning behaviors, finding that topological regions of different mechanisms were connected via multifunctional networks that could switch behaviors depending on parameters.

Significance Statement

By employing an automated algebraic method, Regueira and Marcon construct a topological atlas that categorizes Turing networks based on their ability to produce periodic patterns, traveling waves, or noise amplifying patterns. The atlas identifies distinct topological clusters linked by multi-functional networks that can transition between behaviors through feedback modulation. Key findings highlight how modulation of regulatory cycle strength in time or space can promote transition between static and oscillatory periodic pattern. The study also reveals the importance of feedback on immobile nodes in managing noise and influencing pattern formation. Overall the topological atlas offers a new framework for examining the evolution and development of multicellular self-organization.

Author affiliations: ^aCentro Andaluz de Biología del Desarrollo (CABD) Universidad Pablo de Olavide-CSIC-JA Carretera de Utrera Km.1 41013, Seville, Spain

LM conceived and supervised the study, LR performed the mathematical analysis and simulations, LM wrote main text, LR and LM wrote the supplementary material, methods and made the Figures.

The authors declare no competing interest.

¹To whom correspondence should be addressed. E-mail: lmarcon@upo.es

Theoretical network screenings, however, have not been traditionally applied to Turing systems. Instead, Turing systems were often studied using minimal two-species models (3, 13) due to the complexity of deriving patterning conditions for larger networks (1, 14–20). An exception to this were pioneering studies that performed a random numerical screening for all gene regulatory networks capable of spatial pattern formation (21, 22). More recently, an automated computer algebra approach was used to analyze larger Turing networks systematically, identifying minimal three- and four-node networks with one and two immobile nodes respectively (23). This was achieved by deriving analytical conditions to determine the signs of the solutions of the characteristic polynomial obtained by linear stability analysis (1, 24). These solutions relate the eigenvalue to the potential spatial patterns (wavenumbers), forming what is known as the dispersion relation. This analysis confirmed that the network’s structure depicted by the Jacobian matrix, which illustrates how substances interact around a stable state according to the linear stability analysis, effectively predicts the pattern-forming capabilities of reaction-diffusion systems (23, 25).

A subsequent study used parameter sampling for linear stability analysis of 2- and 3-node networks (26), performing numerical screening to identify parameters yielding a positive eigenvalue instead of solving analytically the linear stability analysis. While offering limited parameter coverage, this method allowed scaling up to non-minimal 3-node networks with more than six interactions. It also considered cases where all three nodes were diffusible. The model proposed that all 3-node networks reduced to two types of 2-node networks (AIJT and CAIJT), corresponding to minimal Jacobian signs for Turing patterns, referred to in (13) as Activator-Inhibitor and Substrate-Depletion systems. The study indicated greater robustness in AIJT networks, though this depended on the specific nonlinearities and the implementation of the core topologies. Indeed, in the simple linear case, these two topologies have the same parameter space size for Turing patterns (24).

Another parameter sampling approach represented each network according to the reaction terms in partial differential equations, distinguishing competitive and non-competitive interactions (27). This generated a broader network list but introduced ambiguity, as it did not clarify which terms dominate around the homogeneous steady state. For example, unlike in the Jacobian-based representation, negative linear terms were ignored in these network diagrams. This led to the proposal that five different 2-node networks can make Turing patterns, while traditional Jacobian-based methods identify only two (1, 23, 24, 26, 27). The study proposed that Turing networks are sensitive to parameter variations indicating low robustness. It also identified that core regulatory motifs such as positive feedback on diffusing nodes, diffusion-mediated negative feedback loops, and competitive interactions were prevalent in robust Turing networks (27).

While previous screenings attempted to relate Turing networks to identify regulatory principles (26, 27), they did not generate a fully connected topological atlas that mapped all networks, as achieved in (10, 12). Moreover, these studies primarily focused on Turing networks generating static periodic patterns, neglecting oscillatory patterns (23, 26, 27) and noise-amplifying networks. These networks, also known

as Turing filters, were first described in (23, 25) and later identified in (27). Turing filters meet Turing conditions but have dispersion relations that exhibit asymptotic behaviour for large wavenumbers, as first described in (16). This results in the amplification of all spatial patterning modes present in the initial conditions, leading to noisy patterns from random initial conditions (23, 27) or periodic spatial patterns from localized initial conditions (25, 28). A crucial requirement for this behaviour is the absence of a maximum eigenvalue in the dispersion relation. When the dispersion relation has a maximum eigenvalue peak, the presence of a lower positive asymptotic behaviour does not interfere with the Turing network’s ability to form patterns from noise, as initially described in (23, 25, 29) and later confirmed in (27).

In this study, we extend our previous analytical screening approach (23) to identify networks that generate both static and oscillatory Turing patterns, and also consider noise-amplifying networks. We organized these networks into a fully connected atlas, allowing transitions between Turing networks and behaviours by systematically adding or removing single interactions. By examining transitions within the atlas and exploiting the formulas from our analytical approach, we identify multiphase and multifunctional networks that switch between pattern phase relations and behaviours based on regulatory feedback changes. Additionally, we find that feedbacks on immobile nodes control noise canalization, which is crucial for pattern timing and precision.

Overall, we show that the atlas helps understand how regulatory feedback modulation in Turing networks promotes transitions between self-organizing patterning behaviors during evolution or development. This approach contributes to translate Turing’s chemical basis of morphogenesis into a framework based on regulatory network feedback, which is more suitable for studying multicellular pattern formation driven by genetic networks.

Results

We performed a comprehensive analysis to construct and understand a topological atlas of 3-node Turing networks with one immobile node. This analysis focuses on identifying networks that can generate static and oscillatory diffusion-driven patterns, as well as noise-amplifying networks. This was done in a completely algebraic manner without relying on parameter sampling and numerical simulations, but rather by deriving the conditions for the existence of positive or negative real roots λ of the characteristic polynomial $P(\lambda) = \lambda^3 + a_1(q)\lambda^2 + a_2(q)\lambda + a_3(q)$ in each network, where the coefficient (a_1, a_2, a_3) contain symbolic parameters for the rates or network cycle weights, and diffusion coefficients. More details are provided in the Material and Methods.

By examining transitions between neighbouring networks, we identify the regulatory mechanisms driving different self-organizing behaviours analytically. Our results reveals that networks with distinct behaviors are linked by Multifunctional networks capable of transitioning between behaviors depending on feedback modulation. The following sections provide details on the atlas construction and an analysis of three paths along the atlas, revealing different properties of Multifunctional networks.

249 **Construction of the Topological Atlas.** To construct the atlas, 311
250 we began considering only minimal 3-node Turing networks 312
251 having six regulatory interactions. We observed that changing 313
252 the sign of a single interaction in these minimal networks (e.g., 314
253 k_7 in Figure 1A) disrupts Turing behavior and it is necessary 315
254 to change the sign of two interactions simultaneously (e.g., k_2 316
255 and k_3) to maintain it, see SI Appendix. Since reconciling two 317
256 simultaneous changes with the progressive changes that may 318
257 occur during evolution is difficult, we decided to construct 319
258 the atlas alternatively by including non-minimal (extended) 320
259 networks with seven regulatory interactions. This approach 321
260 allowed us to add or remove single interactions at the time 322
261 (e.g., k_6 in Figure 1B top) while preserving Turing behavior. 323
262 This strategy resulted in a fully connected atlas where nodes 324
263 represent Turing networks that are directly connected when 325
264 differing by one interaction. Minimal networks with six edges 326
265 are represented as square nodes, while those with seven edges 327
266 are shown as circular nodes (Figure 1B), with paths in the 328
267 atlas corresponding to sequences of alternating minimal and 329
268 extended networks.

269 Node size represents the robustness to parameter changes 330
270 of the associated network, calculated as the portion of pa- 331
271 rameter space that gives rise to the self-organizing patterning 332
272 behaviors. This was determined through a multiple integral 333
273 over the defined parameter space for each network (see 334
274 Material and Methods). Node colors represent the type 335
275 of Turing behavior: static Turing waves (yellow), traveling 336
276 waves (blue), multifunctional (green), and noise amplification 337
277 (red).

278 Each network was categorized according to the sign of 340
279 the characteristic polynomial's coefficients a_1 , a_2 , and a_3 , 341
280 which predict network behavior (see Materials and Method). 342
281 If $a_3 < 0$ and λ has no maximum, the network amplifies 343
282 noise. If λ has a maximum, it corresponds to static Turing 344
283 wave patterns. Having $a_1 < 0$ or $a_2 < 0$ is a sufficient (but 345
284 not necessary) condition for networks to have a λ with a 346
285 positive complex part, giving rise to traveling waves (see 347
286 Material and Methods). Networks with both $a_3 < 0$ and 348
287 $a_1 < 0$ or $a_2 < 0$ are Multifunctional, capable of both static 349
288 and oscillatory behavior depending on parameters.

289 Our analysis revealed that the majority of networks in the 350
290 atlas generate static Turing patterns (yellow), followed by 351
291 Noise-amplifying networks (red), waves (blue), and a minority 352
292 of Multifunctional networks (green) (Figure 1C).

293 It also showed that extended networks are the majority in 353
294 each class (Figure 1D). Multifunctional networks are primarily 354
295 extended networks (green bar in Figure 1D). Analysis of the 355
296 mean robustness for each network class shows that Noise- 356
297 amplifying networks are the most robust, followed by static 357
298 Turing networks, Multifunctional networks, and Traveling 358
299 waves (Figure 1E). The atlas shows a similar proportion of 359
300 Type I and Type III networks, which can form static Turing 360
301 patterns with differential diffusion ($d > 1$) or any diffusion 361
302 value ($d \neq 0$), and a minority of Type II networks that 362
303 generate patterns for $d < 1$ (Figure 1F).

304 The analytical predictions were confirmed by numerical 363
305 simulations shown in Figure 1F-I, details provided in Material 364
306 and Methods and SI Appendix.

307 **Pattern Phase and Diffusion Constraints.** Next, we derived 365
308 an atlas with the subset of networks capable of forming static 366
309 Turing patterns (yellow nodes in Figure 1B), including Mul- 367
310

tifunctional networks capable of both static and oscillatory 311
patterns (green nodes in Figure 1B), but excluding traveling 312
waves and noise amplifiers (Figure S1).

313 For each node in this reduced atlas, we calculated the type 314
of diffusion constraint and phase relationships of the network 315
analytically. Specifically, we identified Type I networks 316
that require different diffusion rates, Type II networks that 317
allow equal diffusion rates, and Type III networks that allow 318
any combination of diffusion rates. These conditions were 319
determined based on stability conditions for homogeneous 320
steady states and diffusion-driven instability. The phase 321
relationships between periodic patterns formed by the network 322
were analyzed using the relative sign of eigenvectors, reflecting 323
four possible phases between the three reactants, as detailed 324
in the Materials and Methods section.

325 The analysis revealed that in the reduced atlas, networks 326
with similar diffusion constraints or similar phases cluster 327
in topological space (Figure 2A), suggesting that specific 328
regulatory feedbacks determine patterning constraints and 329
behavior. To characterize these regulatory feedbacks, we 330
analyzed two key transitions in the atlas, shown by boxes in 331
Figure 2A.

332 The first transition considered a Type I, a Type II, and 333
eventually a Type III network (Figure 2B). The atlas showed 334
that transitioning between a Type I and a Type III network 335
always requires passing through a 7-edge Type II network. In 336
the specific transition considered, the analytical conditions 337
for homogeneous steady-state stability and diffusion-driven 338
instability (Figure 2B) showed that adding a new interaction 339
 k_6 in the intermediate network introduces a negative feedback 340
that enlarges the homogeneous steady-state stability param- 341
eter space, transitioning from a Type I to a Type II network 342
allowing for $d \leq 1$ (Figure 2C middle). Conversely, removing 343
an interaction involved in the stability feedback (i.e., k_7) 344
enlarges the diffusion-driven instability space, making the 345
network unstable for any d (Figure 2C right), transitioning 346
from a Type II to a Type III network.

347 The second transition we studied was from a Phase 1 348
to Phase 1/3 and eventually to a Phase 3 network (Figure 349
2F). The atlas revealed that transitioning between Phase 350
1 and Phase 3, or between Phase 2 and Phase 4, always 351
requires passing through a Multiphase network capable of 352
both phases. In the specific transition considered, passing 353
from a Phase 1 to a Multiphase 1/3 network involved adding 354
the interaction k_7 , which introduces a new positive feedback. 355
Altering the strength of this feedback by increasing k_7 could 356
change the relative sign of one eigenvector, altering the 357
phase relationships of one of the reactants (Figure 2F). 358
This demonstrated that the relative strength between the 359
destabilizing positive feedbacks in the network determines 360
the phase of the network. The pie chart in Figure 2F shows the 361
parameter space percentages for each phase in the Multiphase 362
network. We also observed that not all phase transitions are 363
possible due to specific topological constraints, as Multiphase 364
networks are not found between all phase pairs. Specifically, 365
no direct transition through an intermediate Multiphase 366
network is possible between Phase 1 and 2, and between 367
Phase 3 and 4 (Figure 2A).

368 Finally, we also studied neutral transitions in the reduced 369
atlas, where the addition of interactions did not change the 370
relative pattern phase. Specifically, we explored transitions 371
372

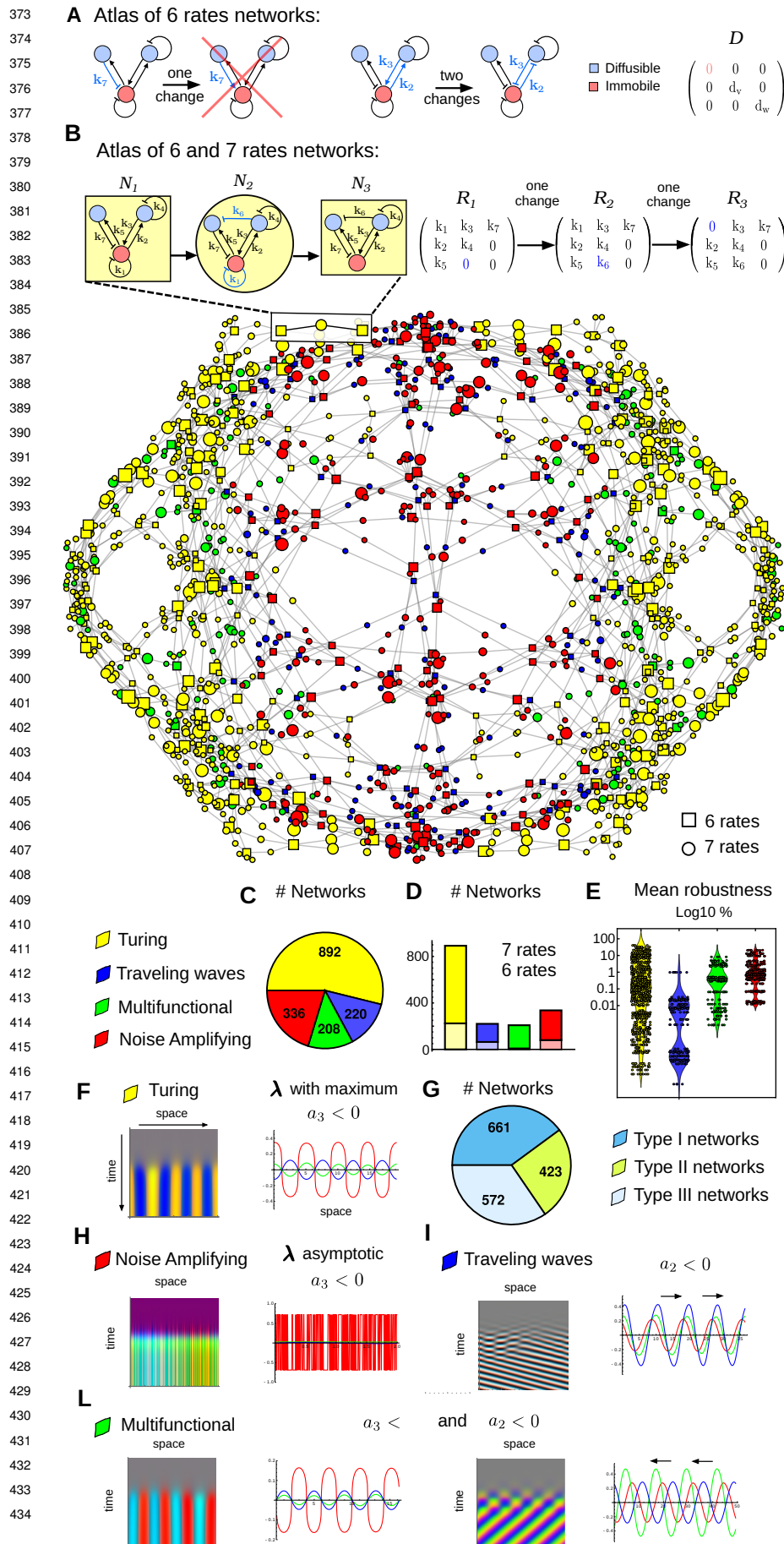


Fig. 1. Topological atlas of 3-node Turing networks

A) A minimal 3-node Turing network with 6 interactions. Changing the sign of any interaction (e.g. k_7) disrupts Turing behavior (red cross); two interactions must be changed simultaneously (e.g. k_2, k_3) to maintain Turing patterning. B) Adding a new single interaction (e.g. k_6) can maintain Turing behavior. This strategy can be used to form a topological atlas, where nodes (e.g., N_1, N_2, N_3) represent Turing networks. Nodes are connected when network differ by one interaction. Square nodes correspond to 6 edges networks (e.g., N_1, N_3), circular nodes with 7 edges (e.g., N_2). Node size is proportional to the robustness of the network to parameter changes. Node color corresponds to the Turing behaviour exhibited by the network: Static Turing waves (yellow), Traveling waves (blue), Multifunctional: static or traveling waves depending on parameters (green) and Noise Amplification (red). C) Top: pie chart shows the number of Turing networks for each behaviour. D) Number of 6 edges and 7 edges networks for each type of behaviour: 6 edges (light color) and 7 edges (dark color). Light green is very small because there are only 8 minimal networks out of 208 multifunctional networks. E) Mean network robustness to parameter space changes for each Turing behaviour. Details of the calculation are provided in Materials and Methods. The logarithmic scale emphasizes the substantial differences in robustness across networks. Turing networks (yellow) are the most robust, with up to 40% of the parameter space capable of generating a diffusion-driven instability. These are followed by Noise (red), Multifunctional (green), and Traveling Wave networks, which exhibit at most 1% of the parameter space that promote a diffusion-driven instability. F) Simulation of a static Turing pattern network identified by a positive real λ with a maximum promoted by diffusion-driven instability when the coefficient a_3 of the characteristic polynomial is negative. G) Number of Turing networks Type I (requires differential diffusivity), Type II (allow equal diffusivity) and Type III (any diffusivity). H) Simulation of a Noise Amplifying network identified by a positive real λ with an asymptotic behaviour promoted by diffusion-driven instability when $a_3 < 0$. I) Simulation of a Traveling wave network identified by a complex positive λ promoted by diffusion-driven instability when $a_1 < 0$ or $a_2 < 0$. L) Simulations of a Multi-functional network that can form static Turing waves or Traveling waves depending on parameters.

among networks that generate in-phase patterns to investigate the possible evolutionary trajectory of the Nodal-Lefty system (30), as shown in Figure S2.

Compressed Topological Atlas and Regulatory Logic. Previously, we showed that any Turing network can be partitioned into network cycles, with 3-node networks having a maximum of eight cycles (c_1 to c_8 , Figure 3A) (23, 25). We also demonstrated that Turing instability conditions can be rewritten in terms of network cycle weights and their signs (23, 25). Furthermore, networks represented by a set of cycle signs correspond to various network topologies (i.e., sets of rates $k_{1..9}$), each generating distinct phases of periodic patterns but operating according to the same cycle weight sign logic (Figure 3B) (23, 25). This property allows us to compress the atlas shown in Figure 1B into a smaller atlas, where multiple network topologies map to a single network represented in terms of cycles (Figure 3B-C). In this compressed atlas, connected nodes still represent networks differing by one interaction, introducing a new cycle, mirroring the structure of the larger atlas in Figure 1B.

As in the larger atlas, each node in the compressed atlas can still be classified into one of the behavioral classes: Turing, Traveling Waves, Multifunctional (Turing and Traveling Waves), and Noise Amplification (Figure 3C). This classification is done by studying the change of signs of the characteristic polynomial's coefficients a_1, a_2, a_3 promoted by diffusion-driven instability but written in terms of cycles c_1 to c_8 as presented in (25). This confirms the results in (25), showing that network cycles and their signs are the main determinants of the patterning capabilities of Turing networks and diffusion constrains, see also Figure S4 and SI Appendix. It also challenges previous accounts suggesting differential robustness between AIJT and CAIJT topologies (26), as we show that in linear models, these topologies have equivalent parameter space associated with the same underlying regulatory logic.

In agreement with the findings of the larger atlas in Figure 1B, we find that networks of the same type cluster together. Additionally, the compressed atlas reveals that Turing, Traveling Wave, and Noise-Amplifying networks have a similar average number of neighboring nodes (around 2.25), while Multifunctional networks have fewer connections (around 1.75), suggesting these networks may mediate connections between clusters (Figure 3D). Analysis of the neighboring node types shows that Turing networks primarily connect to other Turing networks and some Multifunctional or Noise-Amplifying networks but not to Traveling Waves. Conversely, Traveling Wave networks connect primarily to other Traveling Wave and Multifunctional or Noise-Amplifying networks but not to Turing networks. This confirms that Multifunctional networks are primarily implemented by extended networks that serve as intermediaries, connecting static Turing and Traveling Wave networks (Figure 3C). An exception is the only minimal Multifunctional network found in the compressed atlas, which is positioned at the center of a small cluster of Multifunctional networks.

By analyzing the condition for diffusion-driven instability derived in (25), we identified which cycles promote Turing instability for each network (Figure 3F-G, see also SI Appendix). Our analysis shows that in static Turing networks, it is primarily a positive cycle of length two between a

diffusible and a non-diffusible node (c_5 or c_6). For traveling wave formation, it is a positive cycle of length one on a diffusible node (c_3 or c_2). This differs from (27), which suggested that self-regulatory positive feedback on diffusing nodes are prevalent in static Turing networks. We find that Multifunctional networks, capable of forming both Turing and traveling waves, contain both types of positive cycles. Finally, noise-amplifying networks have a positive auto-regulatory feedback on the immobile node (c_1), confirming that destabilizing feedback encompassing only immobile nodes is required for an asymptotic dispersion relation (23, 25).

In the next section, we show that the compressed atlas provides a comprehensive framework for understanding how modulating regulatory feedbacks in self-organizing Turing networks can drive transitions between different patterning behaviors.

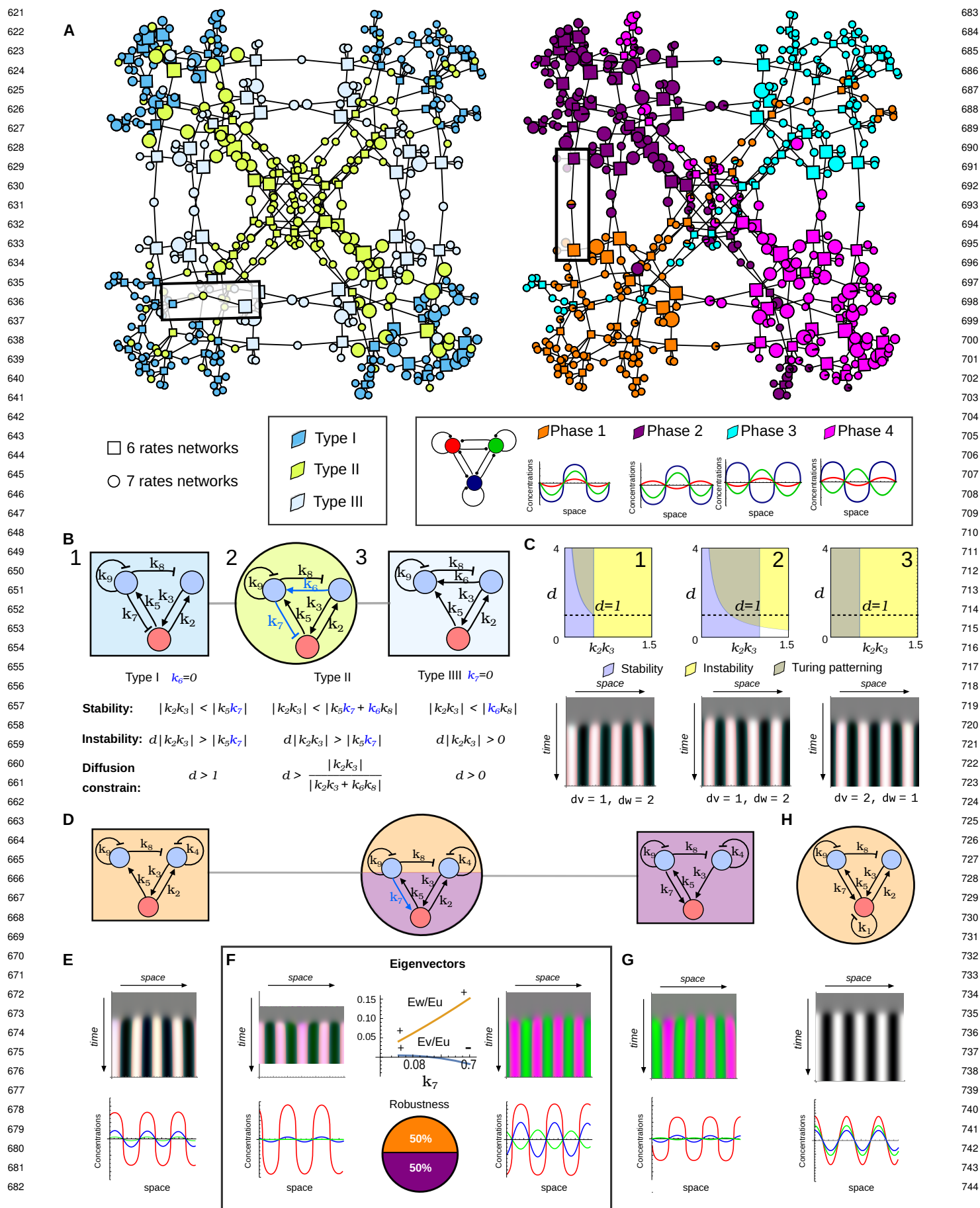
Transitions between Static Turing Patterns and Traveling Waves. To better understand how different network feedbacks control Turing patterning behaviors, we explored three trajectories in the compressed atlas.

Since our analysis of the compressed atlas (Figure 3F) showed that static Turing patterns are promoted by positive cycles c_5 or c_6 , which can make a_3 negative, while Traveling Waves networks are characterized by positive cycles c_2 or c_3 , which can make a_1 or a_2 negative, we first explored a trajectory involving the gain or loss of cycles c_2 and c_6 .

We chose the trajectory involving three nodes shown in Figure 4A-B. For each node, we performed symbolic linear stability analysis to study how changes in network cycles promoted transitions from static Turing patterns to Traveling Waves. Our analysis revealed that adding a positive cycle c_2 to a network that contains a positive c_6 transitions it to a Multifunctional network allowing both positive real and complex roots, shown in the bifurcation diagram in Figure 4C. Removing cycle c_6 while retaining c_2 further transitions the network to a minimal network capable of generating only Traveling Waves (Figure 4B).

In the Multifunctional network containing both c_6 and c_2 , the relative strength of these cycles controls the maximum values of the positive real and complex eigenvalues, determining the dominant behavior (Figure 4D). When $c_2 \ll c_6$, static Turing patterns dominate; conversely, when $c_2 \gg c_6$, traveling waves dominate. Numerical simulations with three parameter sets where both complex and real positive eigenvalues exist (points 1, 2, 3 in Figure 4C) confirmed that the dominant patterning behavior could be predicted by the relative maximum magnitude of the real and complex eigenvalues (Figure 4E).

To further test the predictive power of the bifurcation diagram shown in Figure 4C, we defined a trajectory within the multifunctional parameter space (green region in Figure 4C) to modulate network behavior over time (from t_0 to t_f), investigating the potential for transitioning between patterning behaviors during embryonic development. By promoting a linear reduction in c_6 strength over time (Figure 4F), the Multifunctional network first formed a static Turing pattern that then transformed into Traveling waves, highlighted by a space-time plot in Figure 4G. In a 2D domain slightly smaller than the wavelength, this modulation generated a straight stripe that propagated along its axis (Figure 4H).



683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744

745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806

807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868

Fig. 2. Reduced atlas of static Turing networks: topology determines diffusion constrains and pattern phase. A) A sub-graph of the atlas shown in Figure 1B obtained by considering only static Turing networks (yellow and green nodes). Left: Nodes are colored according to network type: Type I (blue) requires differential diffusivity, Type II (light green) can have equal diffusivity, Type III (light blue) allow for any diffusivity. The square highlights the transition shown in panel (B). Right: Nodes are colored according to the relative phase between the periodic patterns (legend below). The square highlights the network shown in panel D. Node size corresponds to robustness to parameter changes. B-C) Analysis of the transition between a Type I, Type II and Type III network shown in (A) on the left. B) A trade off between homogeneous steady state stability (stability) and diffusion-driven instability (instability) conditions determine the constrain on diffusion coefficient ratio d for the three networks (1,2,3). C) Top: graphs showing the parameter space that satisfy homogeneous steady state stability (blue) and diffusion driven instability (yellow), dash line shows equal diffusivity for $d = 1$. In Type II and Type III networks the the yellow and blue region intersect for $d < 1$. Bottom: Simulation of the networks (1,2,3) with $d = 2$, $d = 1$, and $d = 0.5$ respectively. D-G) Analysis of the Transition between a Phase1, Phase1/3 and Phase3 networks shown in (A) on the right, from left to right the transition is made by adding the interaction k_7 and loosing interaction k_2 . E) Space time plot (top) and graph (below) show that the 6 edges network shown on the left in (D) forms periodic patterns of the three reactants (u,v,w) that are in phase (Phase 1). F) The 7 edges network show in the center in (D) can form periodic patterns with two different phase depending on the strength k_7 . Left: for low values of k_7 the patterns are in phase (Phase 1), Right: for high values of k_7 the patterns of u,w (red,blue) in phase but v (green) out of phase (Phase 3) as reflected by the relative sign of the Eigen vectors (E_u, E_v, E_w). Pie chart shows that Phase 3 is more robust than Phase 1 since it is formed for 64% of the parameter space. G) The 6 edges network shown on the right in (d) forms periodic patterns Phase 3. H) Example of a 7 edges network that forms only patterns in Phase 1.

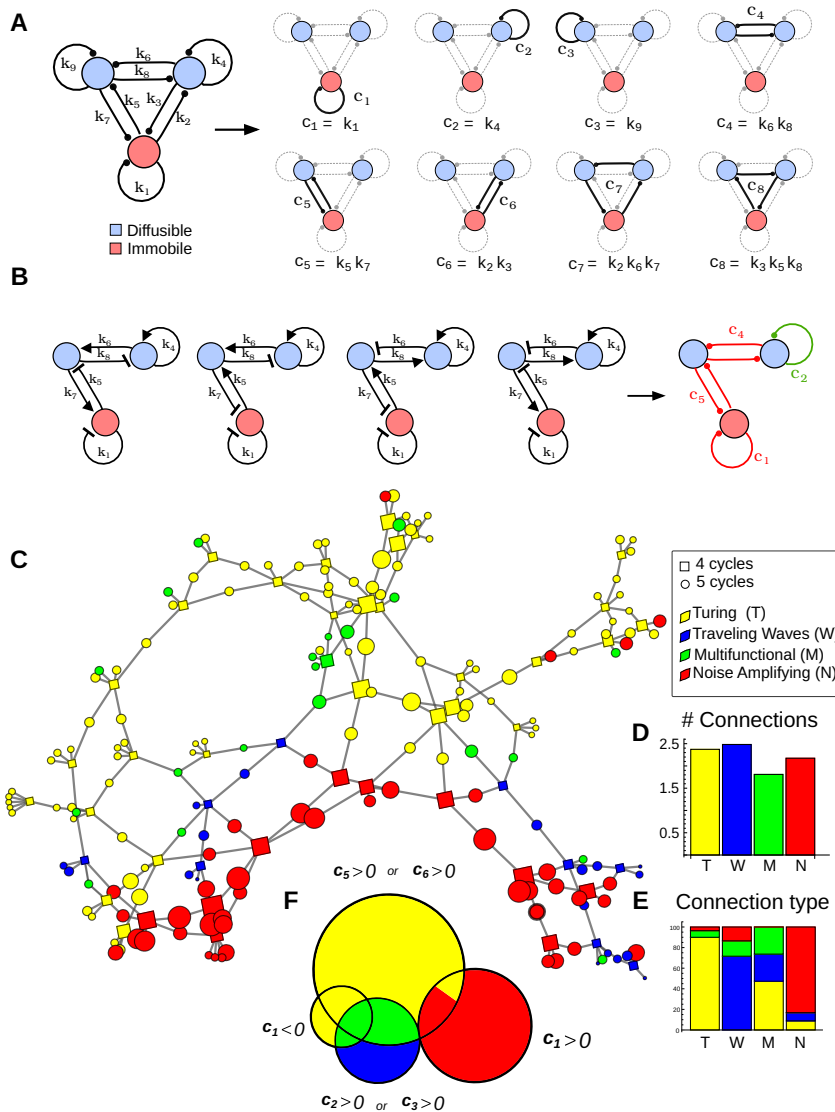


Fig. 3. Compressed topological atlas with cycle analysis. A) The different cycles ($c_1 \dots c_8$) in a three-node gene network used to analyze Turing patterning in terms of network feedbacks. B) Cycles can be used to map multiple networks to the same underlying regulatory logic (same cycle signs). The example shows four different networks ($k_1 \dots k_7$) mapped to a single network with negative cycles c_1 , c_4 , and c_5 (red) and a positive c_1 cycle (green). C) A compressed version of the atlas in Figure 1B where each node corresponds to a set of network cycles. Square nodes contain 4 cycles (6 interactions) and are connected to circular nodes with 5 cycles (7 interactions). Network colors correspond to Turing patterning behaviors: Turing (yellow, T), Traveling Waves (blue, W), Multifunctional (green, M), and Noise-Amplification (red, N). D) Average number of direct neighboring nodes per network type: Turing, Traveling Waves, and Noise-Amplifying networks have approximately 2.5 neighbors, while Multifunctional networks have approximately 1.7 neighbors. E) Proportion of neighbor types per network type: Turing nodes connect to other Turing nodes (yellow) and some Multifunctional (green) and Noise-Amplifying (red) nodes, but not to Traveling Waves (blue); Traveling Wave nodes connect primarily to other Traveling Waves (blue), Multifunctional (green), and Noise-Amplifying (red) nodes, but not to Turing networks (yellow). Multifunctional networks always mediate transitions between Turing and Traveling Wave nodes (see also panel C). F) Each circle represents networks destabilized by a specific cycle to form diffusion-driven instability. The large yellow circle corresponds to networks destabilized by $c_5 > 0$ or $c_6 > 0$, promoting static Turing patterns (yellow). The blue circles correspond to networks destabilized by $c_2 > 0$ or $c_3 > 0$, promoting Traveling Waves (blue). The red circle corresponds to networks destabilized by $c_1 > 0$, promoting Noise-Amplifying patterns (red). The small yellow circle corresponds to networks where $c_1 < 0$ contributes to destabilization, promoting static Turing patterns (yellow). Intersections between circles represent networks destabilized by two cycle types: green regions are Multifunctional networks destabilized simultaneously by $(c_5 > 0 \text{ or } c_6 > 0)$ and $(c_2 > 0 \text{ or } c_3 > 0)$. The yellow region between the yellow and red circles represents networks destabilized simultaneously by $(c_5 > 0 \text{ or } c_6 > 0)$ and $(c_1 > 0)$, promoting static Turing patterns.

869 Finally, to further explore the ability of the Multifunctional
870 network, we defined a modulation over a wider range of
871 the parameter space by decreasing c_6 and increasing c_2
872 simultaneously, see the arrow from point a to b in Figure 4C.
873 This modulation transitioned from a pure Turing region (a),
874 having only a positive real eigenvalue, to a pure traveling
875 wave region (b), having only a positive complex eigenvalue.
876 Our aim was to test whether this wider modulation could
877 be promoted by a linear morphogen gradient M , driving a
878 transition between static Turing patterns to traveling waves
879 over space rather than time (Figure 4I). In agreement with our
880 predictions, one-dimensional simulations generated one peak
881 of a static Turing pattern on one side of the spatial domain
882 connected to a region of traveling waves on the opposite side
883 (Figure 4L-M). This type of modulation could be relevant
884 for several self-organizing systems such as Gastruloids (31),
885 where the modulation of different signaling pathway feedback
886 could be linked to the formation of an axis at one extreme of
887 the aggregate, transitioning into traveling waves that resemble
888 somitogenesis at the other aggregate extreme, see Figure S3.

889 We also analyzed a different type of transition between a
890 Traveling Wave and a Multifunctional network, highlighted
891 in Figure S5. As mentioned above, Static Turing Wave
892 networks are characterized by a positive destabilizing cycle
893 c_5 or c_6 that makes a_3 negative. Our analysis showed that
894 an alternative transition to Multifunctional networks can
895 be achieved by introducing a negative cycle c_1 rather than
896 c_6 , which changes the contribution of c_2 in the characteristic
897 polynomial coefficient a_3 making it negative (Figure 5C). This
898 demonstrates an alternative path to Multifunctional behavior,
899 highlighting the complex interaction between feedbacks in
900 Turing networks to transition between patterning behaviors.

901 **Transition Between Turing and Noise Amplifying Networks.** In
902 the atlas, both static Turing networks and Noise-amplifying
903 networks are predominant (Figure 1B), and direct transitions
904 are possible between these two network types (Figure 3C). As
905 shown in Figure 3F, most static Turing patterns are driven by
906 cycles $c_5 > 0$ or $c_6 > 0$, while all Noise Amplifying networks
907 have $c_1 > 0$. At the intersection of these clusters, networks
908 sometimes display normal Turing patterning behavior and
909 sometimes noise amplification. To better understand these
910 intermediate cases, we analyzed a transition in the compressed
911 atlas from a noise-amplifying network to three subsequent
912 Turing nodes, marked by changes in c_1 and gains in c_6 ,
913 highlighted by the box on the right in Figure 4A and in
914 Figure 4O.

915 In this transition, we observed that the sign and strength of
916 c_1 significantly affect the shape of the dispersion relation and
917 pattern formation capabilities (Figure 4N-O). A positive c_1
918 results in a higher asymptote for large wavenumbers, leading
919 to greater unspecific amplification of modes. Lowering c_1
920 reduces this asymptote, decreasing unspecific amplification
921 and resulting in more precise patterns.

922 In agreement with this prediction, 1D and 2D simulations
923 show that a positive c_1 promotes fast patterning with random
924 noise amplification (Figure 4P-Q). When c_1 strength is
925 smaller and coexists with c_6 , it leads to static Turing patterns
926 that are noisy and have irregular wavelengths in 2D. As c_1
927 decreases to zero, patterning slows and becomes more regular.
928 Further negative values of c_1 continue to slow down patterning
929 and improve its regularity.

931 The intuitive interpretation of these results is that the
932 self-regulatory loop c_1 on the immobile node plays a crucial
933 role in destabilizing the network because this node is not
934 subjected to the equilibrating force of diffusion. A positive
935 feedback on c_1 enhances this destabilization, while negative
936 feedbacks mitigate it. From a biological and evolutionary
937 standpoint, these findings suggest that cell autonomous
938 feedback mechanisms involving immobile nodes are essential
939 for modulating the trade-off between the speed and precision
940 of pattern formation.

941 Discussion

942 The topological atlas presented in this study offers a novel
943 framework to understand how Turing networks transition
944 between different self-organizing behaviours in multi-cellular
945 systems. Employing an automated algebraic method, we
946 identified the networks that give rise to static, oscillatory,
947 and noise-amplifying Turing patterns. This is crucial for
948 understanding self-organization during development, where
949 modulations of gene regulatory networks drive changes in
950 patterning behaviour over time or space. We systematically
951 mapped and categorized Turing networks based on their
952 topology and patterning capabilities, advancing previous
953 network screenings that focused primarily on networks that
954 generate static Turing patterns (23, 24, 26, 27).

955 A notable feature in the atlas is that minimal networks
956 (6 interactions) with different behaviours are connected
957 by extended networks (7 interactions) exhibiting hybrid
958 multifunctional behaviour. These intermediate networks can
959 display two types of self-organizing behaviours depending on
960 interaction strength.

961 This include multiphase networks that can generate peri-
962 odic Turing patterns with different phase relations between
963 reactants depending on the parameters. These networks have
964 not been described previously and may explain changes in the
965 relative phase of periodic patterns observed for self-organizing
966 patterning during embryonic development. For instance, they
967 could account for the switch between in-phase and out-of-
968 phase patterns of BMP signaling (pSmad) and Sox9 observed
969 in digit patterning, as shown in the supplementary material
970 of (6).

971 On the other hand, we used the atlas to explore topological
972 changes that are neutral from a patterning phase perspective
973 but lead to more robust Turing networks. The atlas confirmed
974 our previous proposition (23) that changes in network
975 topology can enhance the robustness of the Nodal-Lefty
976 system, where Nodal and its inhibitor Lefty are co-expressed
977 and proposed to be part of a Turing network (30). Specifically,
978 we identified a transition from a network where Lefty inhibits
979 only the receptor to an extended network where Lefty also
980 directly inhibits Nodal (Figure S2). This introduces a
981 redundant interaction and improves the network's robustness
982 to parameter changes. Similar neutral transitions in the atlas
983 could be exploited to study the possible implementation of
984 other self-organizing Turing systems during developmental.

985 Exploiting the representation of Turing conditions in terms
986 of cycles, as introduced in (25), we derived a compressed atlas,
987 where several networks with the same underlying regulatory
988 logic are mapped into one network with a set regulatory
989 cycle signs (see Figure 3B). This allowed us to identify
990 which regulatory modules (cycles signs) drive different Turing
991 patterns.

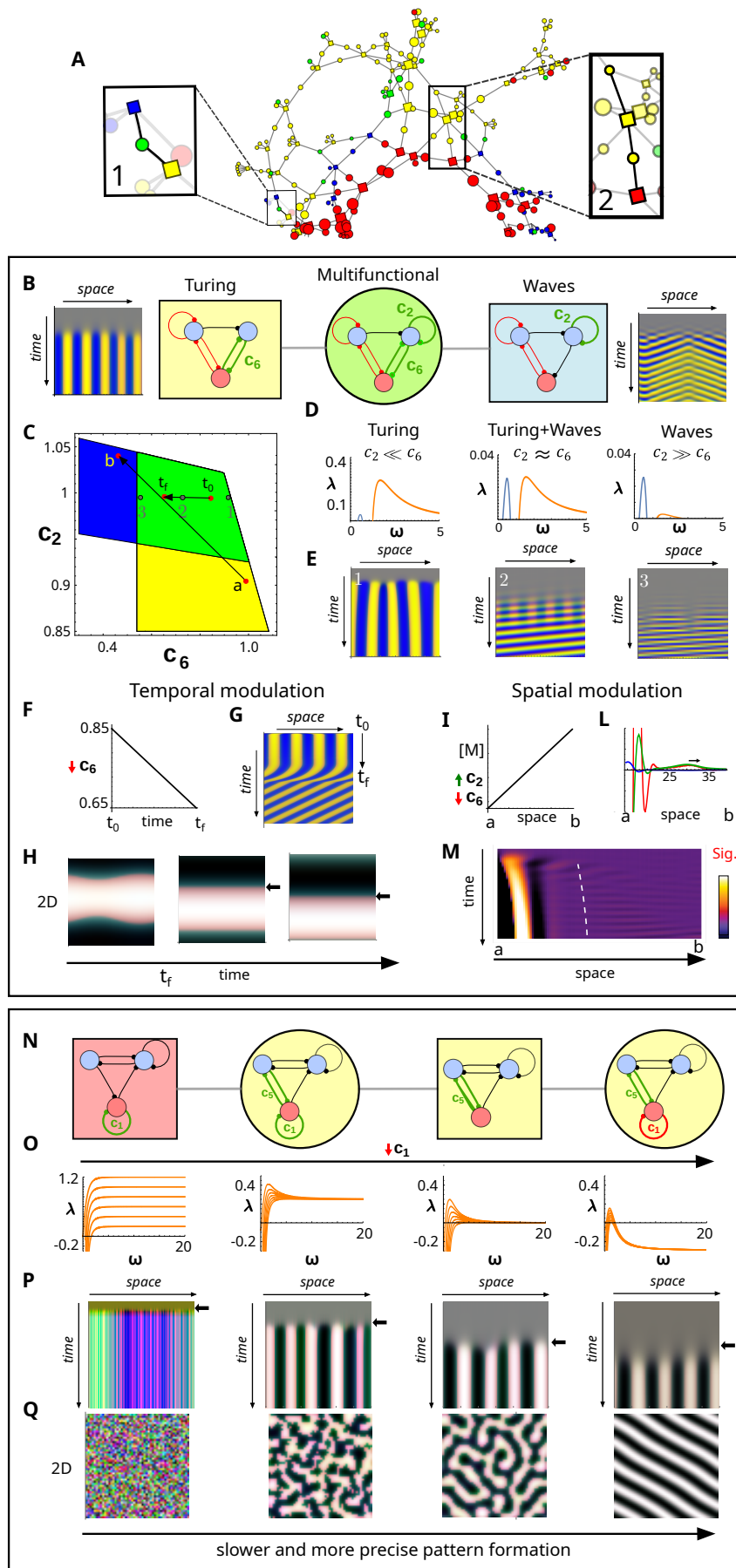


Fig. 4. Transition between Noise amplifying, Turing and Traveling Wave networks. A) The boxes highlight two transitions analyzed in detail: 1) Transition between a Turing network (yellow square), a multifunctional network (green circle), and a traveling waves network (blue square), studied in panels B-M. 2) Transition between a noise amplifying network (red square) and static Turing networks (yellow square and circles), studied in panels N-Q. B) Details of transition 1. Left: 1D Turing network (yellow square) with a destabilizing positive cycle c_6 generates a periodic static pattern (straight lines in space-time plot). Middle: addition of new cycle c_2 promotes transition from a static Turing network to a multifunctional network (green circle). Right: losing cycle c_6 promotes a transition to traveling waves driven by c_2 (diagonal lines in space-time plot). C) Parameter space associated with diffusion-driven instability for different strengths of c_2 and c_6 in the multifunctional network (green circle, panel B). The yellow region has only a positive real eigenvalue (Turing). The blue region has only a positive complex eigenvalue (Traveling Waves). The green region has both a complex and real positive eigenvalue (Turing and Waves) with points (1..3) showing parameters used in D-E, and horizontal arrow between 3 and 1 showing temporal modulation of c_6 (t_0 to t_f) simulated in panels G-H. The arrow from point a to b shows spatial modulation used for simulations in panels L-M. D) Positive real (orange) and complex (blue) eigenvalues for parameter sets (1..3). For $c_2 \ll c_6$, the positive real eigenvalue associated with Turing patterns is larger; for $c_2 \approx c_6$, both eigenvalues have similar maximums; for $c_2 \gg c_6$, the complex positive eigenvalue associated with traveling waves is larger. E) Space-time plot of simulations for parameter sets (1..3) shows the relative magnitude of the eigenvalues correctly predicts the patterning outcome. When they have equal magnitude ($c_2 \approx c_6$), both static and traveling waves coexist. F-G) A continuous linear decrease of c_6 over time (from t_0 to t_f) promotes the formation of a static Turing pattern that transforms into traveling waves (straight lines transform into diagonals in space-time plot). H) In a 2D simulation, temporal c_6 modulation promotes the formation of a stripe that begins to propagate. I-L) A linear change of c_6 and c_2 in space (from point a to b) promoted by a morphogen M drives a transition in space from static Turing pattern to traveling waves. M) This type of transition can help interpret the self-organizing patterning dynamics observed in *Gastruloids* (31). N) Details of transition 2: From left to right, a decreasing c_1 promotes transitions from a noise amplifying network ($c_1 \gg 0$, red square) to three Turing networks ($c_1 > 0$, yellow circle; $c_1 = 0$, yellow square; and $c_1 < 0$, yellow circle). O) Dispersion relations for networks in panel N with decreasing values of c_1 and varying c_5 . Ordered from left to right: noise amplifying networks with $0 < c_1 < 1.2$; Turing network with $c_1 = 0.25$ and $0 < c_5 < 1.19$; Turing network with $c_1 = 0$ and $0 < c_5 < 1.5$; and Turing network with $c_1 = -0.3$ and $1.5 < c_5 < 1.875$. In the noise amplifying case, the value of c_1 corresponds to the asymptote of the dispersion relation. In the other cases, as c_1 decreases, the dispersion relations shift towards negative values. P) 1D simulations show that as c_1 decreases, lower eigenvalues promote slower pattern formation (black cross marks later pattern appearance in space-time plots). Q) 2D simulations show that as c_1 decreases, the smaller range of modes that become unstable in practice due to the eigenvalue shifting towards negative values promotes more precise two-dimensional patterns with a characteristic wavelength.

behaviours (Figure 3F). This is significant because defining modules within Turing networks is particularly challenging due to the extensive feedback loops characteristic of these networks, where every gene seems to be connected with every other gene. It could also provide a way to reduce larger Turing networks into equivalent smaller ones, as done in (32). The cycle decomposition approach, however, extends beyond Turing systems and can be applied to any stability analysis of PDE systems with feedback.

The cycle-based atlas also confirmed that networks with different Turing behaviours are connected by extended Multifunctional networks. For instance, networks that form static Turing patterns and those that form travelling waves are connected by networks possessing two positive feedback cycles that can promote both real and complex positive eigenvalue, as shown in Figure 4B-C. Changing the strength of these cycles alters the relative magnitude between the two eigenvalues, leading to a smooth transition between static Turing patterns and oscillations, see Figure 4D-E.

An intriguing property of these Multifunctional networks is their ability to transition between behaviour over time (Figure 4F-G) promoting scenarios where the output of one self-organizing regime acts as initial conditions for the next, implementing developmental patterning dynamics driven by stigmergy, as proposed by Sasai Yoshiki (33). This can lead to more controlled self-organizing dynamics. An example is the 2D simulation shown in Figure 4H, where a multifunctional Turing network first forms a straight stripe from noise, in the regime of a static Turing pattern on a domain sized approximately as the wavelength, which then transforms into a series of travelling waves moving along the stripe's direction. Modulating the cycle strength to change self-organizing behaviour can also be relevant to investigating transitions between self-organizing regimes across tissues (Figure 4I-M), as seen in the Gastruloids presented in (31) (Figure S3).

Finally, the cycle-based atlas highlights that self-regulatory feedbacks on non-diffusible nodes play a critical role in controlling the stochasticity of pattern formation. Positive feedback on these nodes accelerates pattern formation but introduces more noise, while negative feedbacks slow down pattern formation and enhance precision, as shown in Figure 4N-Q. This reveals a fundamental mechanism by which developmental systems can balance the trade-off between speed and accuracy in pattern formation, a common challenge in many complex systems. It also highlights the mechanisms by which reaction-diffusion systems generate patterns by amplifying and filtering the periodic modes present in the initial noise of the system. Faster amplification and less filtering result in noisier patterns, while slower amplification and narrower filtering (e.g., narrow dispersion relation) produce more precise patterns.

Overall, the atlas can be used to interpret how Turing networks have evolved, providing a design space of Turing networks that evolution may have explored to reach specific configurations. Trajectories along the atlas represent possible pathways of topological changes that maintain Turing behaviour, associated with single regulatory changes, and can sequentially move from one patterning behaviour to another. Our calculation of robustness to parameter changes for each

network indicates the likelihood of these new networks being found at random.

Additionally, the atlas, though composed of different networks, can be seen as a general map of the behaviour of a large Turing network with many feedbacks. Many biological networks, especially gene regulatory networks controlling development, possess several feedbacks. In this context, the atlas highlights the feedbacks that are more important for specific behaviours in a fully connected 3 gene regulatory network. This suggests possible directions of change that can be promoted by feedback modulation in a network during development. Although changes are continuous in the atlas thanks to the presence of multifunctional states, not all paths are allowed.

Ultimately, our approach reframes Turing's original idea within a network-based framework, moving beyond the traditional chemical reaction perspective (1) towards a "network basis of pattern formation". This is a step forward to relate Turing systems with the gene networks driving self-organizing patterning during development (3). It also reveals novel network designs that can help to construct complex synthetic networks capable of transitioning between different self-organizing behaviours. Recent efforts have successfully engineered a Turing network with a 3 node regulatory logic in bacteria, achieving static patterns and demonstrating the potential for further advancements towards multifunctional capabilities (34).

In the future, we believe that our approach can be expanded to include all seven diffusion-driven instability behaviours proposed by Turing and incorporate larger networks. Given the exponential increase in analytical complexity in these systems, it would be necessary to complement our current analytical approach with numerical analysis, as done in (26, 27).

Materials and Methods

Previous studies have already proposed mathematical theorems to derive simpler analytical conditions for diffusion-driven instability in general three-reactant reaction-diffusion systems (17, 20). To simplify the conditions even further we perform a systematic automated analysis by focusing only on minimal (6 edges) and extended (7 edges) networks of three reactants, with 3 and 2 elements set to zero in the Jacobian matrix. In addition, we consider only the case where one of the three species is immobile (one element in the diagonal diffusion matrix set to zero), simplifying the conditions and broadening the criteria for diffusion-driven instability (14, 18, 23). Finally, we derived necessary and sufficient conditions for static Turing patterns and sufficient conditions for oscillatory Turing patterns by combining the Routh-Hurwitz criterion with simpler condition for the stability of three reactant system derived in (35, 36), as introduced in the supplementary material in (25). For simulations, we construct simple PDE systems from the Jacobians to simulate spatial patterning under different parameter regimes identified by the linear stability analysis.

Conditions for Stationary and Oscillatory Turing Patterns. We derived the necessary and sufficient conditions for the formation of Turing instability by analyzing the roots of the characteristic polynomial $P(\lambda) = \lambda^3 + a_1(q)\lambda^2 + a_2(q)\lambda + a_3(q)$ obtained by linear stability analysis for each network, where λ is the eigenvalue and q the wavenumber. The solution to the characteristic polynomial as a function of q is called dispersion relation. For a diffusion-driven instability to occur, the characteristic polynomial must have all negative roots for $q = 0$ (condition 1) and at least one root with a positive real part for $q > 0$ (condition 2 or 3). Necessary and sufficient conditions for the existence of a all negative roots can

1241 be derived with the Routh-Hurwitz criterion (37), as outlined in
1242 the supplementary material of (25).

1243 The Routh-Hurwitz criterion is obtained by constructing the
1244 Hurwitz matrix H , which for a polynomial of the third degree is
1245 defined as:

$$1246 H = \begin{pmatrix} a_1(q) & 1 & 0 \\ a_3(q) & a_2(q) & 0 \\ 0 & 0 & a_3(q) \end{pmatrix}$$

1249 The criterion states that all roots of the polynomial have negative
1250 real parts if and only if the determinants of the leading principal
1251 minors of H are positive:

$$1252 \Delta_1(q) = a_1(q) > 0$$

$$1253 \Delta_2(q) = \begin{vmatrix} a_1(q) & 1 \\ a_3(q) & a_2(q) \end{vmatrix} = a_1(q)a_2(q) - a_3(q) > 0 \quad [1]$$

$$1254 \Delta_3(q) = \det(H) = a_3(q)\Delta_2(q) > 0 \equiv \Delta_3(q) = a_3(q) > 0$$

1256 Conversely, if any of the Hurwitz terms Δ_1, Δ_2 or Δ_3 becomes
1257 negative, the characteristic polynomial has at least one root with
1258 a positive real part. The number of roots with a positive real part
1259 in this case can further be estimated by the sign changes in the
1260 first column of the Routh array (37), which for a polynomial of
1261 degree three can be constructed as follows:

$$1262 \begin{array}{l} \lambda^3 \\ \lambda^2 \\ \lambda^1 \\ \lambda^0 \end{array} \left| \begin{array}{cc} 1 & a_2(q) \\ a_1(q) & a_3(q) \\ \frac{a_1(q)a_2(q)-a_3(q)}{a_1(q)} & 0 \\ a_3(q) & 0 \end{array} \right.$$

1266 The first column of the Routh array is:

$$1268 R_h = [1, a_1(q), \frac{a_1(q)a_2(q) - a_3(q)}{a_1(q)}, a_3(q)]$$

1270 **Stationary Turing networks.** Stationary Turing patterns occur when
1271 a single real eigenvalue becomes positive, specifically when the
1272 first column of the Routh array R_h exhibits a single sign change
1273 $R_h = [+ , + , + , -]$ for $q > 0$. This is a sufficient condition not
1274 only for the existence of a positive real root but also to guarantee
1275 that there are no other real positive roots. In section 2 of the
1276 supporting information, we demonstrate that for a third-degree
1277 polynomial this condition can be further simplified into:

$$1278 a_3(q) < 0, \quad \text{for } q > 0 \quad [2]$$

1279 which ensures that $a_1(q) > 0$ & $a_1(q)a_2(q) - a_3(q) > 0$
1280 guaranteeing that $R_h = [+ , + , + , -]$.

1281 This represents a significant simplification since analyzing all
1282 the terms in the Routh array becomes analytically impracticable
1283 in many cases.

1283 **Oscillatory Turing networks.** Oscillatory Turing patterns occur
1284 when the characteristic polynomial has a complex positive root.
1285 This is the case when R_h exhibits two sign changes, $R_h =$
1286 $[+ , - , + , +]$ or $R_h = [+ , + , - , +]$ or $R_h = [+ , - , - , +]$
1287 for $q > 0$, associated with two complex conjugate roots with a positive real
1288 part. As mentioned above, analyzing all the terms in the Routh
1289 array is often analytically impracticable. Fortunately, in section
1290 2 of the supporting information, we demonstrate that for a third-
1291 degree polynomial this condition can be further simplified into:

$$1292 a_2(q) < 0 \text{ for } q > 0 \quad [3]$$

1293 This condition simplifies the analysis considerably by guaranteeing
1294 two sign changes in the Routh array, providing necessary and suffi-
1295 cient conditions for the formation of oscillatory Turing patterns.

1295 **Multifunctional Turing Networks.** To identify multifunctional net-
1296 works capable of both oscillatory and static patterns, we require
1297 that the simplified conditions 2 and 3 can be satisfied by the
1298 network, both independently or simultaneously. The first case
1299 identifies the parameters that give rise to either a positive
1300 real eigenvalue or a positive complex eigenvalue. The second
1301 case identifies parameters that give rise to eigenvalue that can
1302 simultaneously give rise to both situation simultaneously for different
1303 wave numbers q (e.g., the green parameter space in Figure 4C). This

1303 allows us to pinpoint networks that can switch between oscillatory
1304 and static behaviours depending on parameter variations, providing
1305 a comprehensive understanding of the network's multifunctional
1306 capabilities.

1307 **Noise-amplifying Turing Networks.** If a Turing network has an
1308 eigenvalue with a positive asymptote for $q \rightarrow \infty$, a condition
1309 previously identified as necessary for the amplification of noise
1310 (23, 25), we verify whether the dispersion has a maximum above
1311 this asymptote to classify the network as noise amplifying.

1312 This verification involves obtaining parameters that satisfy
1313 diffusion-driven instability with the *FindInstance* command in
1314 Wolfram Mathematica. In the case of multifunctional network we
1315 derive parameters for both static Turing patterning and traveling
1316 wave behaviour. Starting from these parameters we derive several
1317 parameter sets by allowing one parameter to vary from its minimum
1318 to its maximum allowed values as determined by the linear stability
1319 analysis conditions. For each parameter set, we calculate the
1320 asymptote of the dispersion relation using the function *Limit*
1321 for $q \rightarrow \infty$. $\lambda(q)$. Secondly we find the maximum eigenvalue
1322 numerically using the function *FindMaximum*.

1323 If the maximum eigenvalue is lower than the limit for $q \rightarrow \infty$
1324 for all parameter sets of the network, we consider the network
1325 as a noise amplifying. Overall, we observe that if the limit is
1326 larger than the maximum, noise-amplifying networks consistently
1327 produce static patterns, regardless of the presence of a positive real
1328 root with a complex part. This supports our earlier finding that
1329 oscillatory noise-amplifying networks are only feasible in systems
1330 with four nodes (25).

1331 **Numerical Simulation.** To simulate a network, we obtained repre-
1332 sentative Jacobian values (k_1^N, \dots, k_9^N) and diffusion coefficients
1333 (d_v^N, d_w^N) that respect patterning conditions of the network N
1334 with the *FindInstance* command of Wolfram Mathematica, and
1335 construct a system of PDEs for the concentration vector $\mathbf{c} =$
1336 $(u, v, w)^T$ is given by:

$$1337 \frac{\partial \mathbf{c}}{\partial t} = J^N \mathbf{c} - \mathbf{c}^3 + D^N \nabla^2 \mathbf{c}$$

1338 where J^N is the Jacobian matrix of the network obtain by
1339 substituting the parameters (k_1^N, \dots, k_9^N) , D^N is the diagonal
1340 diffusion matrix obtained by substituting (d_v^N, d_w^N) , and \mathbf{c}^3
1341 represents cubic non-linear terms that provide saturation:

$$1342 J^N = \begin{pmatrix} k_1^N & k_2^N & k_7^N \\ k_3^N & k_4^N & k_8^N \\ k_5^N & k_6^N & k_9^N \end{pmatrix}, D^N = \begin{pmatrix} 0 & 0 & 0 \\ 0 & d_v^N & 0 \\ 0 & 0 & d_w^N \end{pmatrix}, \mathbf{c}^3 = \begin{pmatrix} u^3 \\ v^3 \\ w^3 \end{pmatrix}$$

1343 Note that J^N has 3 or 2 elements set to 0 in minimal and extended
1344 networks respectively, and u is the immobile specie with $d_u = 0$,
1345 and we consider periodic boundary conditions. This PDE systems
1346 have always one stable equilibrium at $c_0 = (u_0, v_0, w_0) = (0, 0, 0)$
1347 and generates periodic waves by diffusion-driven instability around
1348 this stable point. We begin the simulations with a random initial
1349 conditions for for all the three reactant uniformly distributed in
1350 the interval $(-0.0005, 0.0005)$ around c_0 .

1351 We perform 1D and 2D simulations using a first order finite
1352 difference scheme for space discretization and forward Euler
1353 method for time discretization, written in Wolfram Mathematica.
1354 The domain size L and total simulation T time are calculated
1355 according to the wavelength $\omega = 2\pi/q_{\max}$ and maximum
1356 eigenvalue λ_{\max} obtained from the linear stability analysis, as
1357 follows:

$$1358 L = \omega * 4 \quad T = 20/\lambda_{\max}$$

1359 with high resolution space discretization $d_s = L/300$ and time
1360 discretization $d_t = T/20^7$ to avoid numerical errors. All the
1361 simulations confirm as proposed by Turing (1) that the diffusion-
1362 driven behaviour can be correctly predicted by the linearized
1363 version of the system around steady state, while the non linear
1364 part \mathbf{c}^3 plays only a saturating effect for large deviation from
1365 equilibrium.

1366 **Network Robustness Calculation.** To assess the robustness of each
1367 network N , we quantify the volume of the parameter space that
1368

1365 satisfies the diffusion-driven conditions derived from the linear
 1366 stability analysis. This involves integrating all the diffusion-driven
 1367 instability conditions f and it is done by fixing one negative
 1368 feedback rate at -1 and one diffusion coefficient at 1, thereby
 1369 calculating the relative parameter space. The relative parameter
 1370 space volume is calculated over the ranges: 0.1 to 10 for reaction
 1371 rates k_i and 0.001 to 100 for the relative diffusion coefficient ratio
 1372 d .

1373 The robustness $R(f)$ is thus calculated as the integral over the
 1374 defined parameter space:

$$1375 R(f) = \int_0^1 \dots \int_{0.1}^{10} \int_{0.001}^{100} f(k_i, d) dk_i dd$$

1376 After obtaining $R(f)$ for each network, we standardize the
 1377 robustness values by dividing each $R(f)$ by the maximum robust-
 1378 ness value observed (i.e the most robust network), $R(f_{\max})$. The
 1379 normalized atlas robustness $r(f)$ for each network i is then given
 1380 by:

$$1381 r(f_i) = \frac{R(f_i)}{R(f_{\max})}$$

1382 The size of a node representing a network N in the atlas is
 1383 logarithmically proportional to $r(f_i)$. This approach quantifies the
 1384 likelihood of a given network achieving diffusion-driven instability
 1385 with randomly assigned parameters, and also provides a measure of
 1386 the network's robustness to parameter changes.

1387 **Diffusion Constrains.** As introduced in (23), Turing networks with
 1388 an immobile specie exhibit distinct types of diffusion constraints
 1389 for pattern-forming conditions. These constraints are categorized
 1390 as follows: Type I networks require differential diffusivity, Type II
 1391 networks allow equal diffusivity, and Type III networks have no
 1392 specific diffusivity constraints.

1393 The classification of network types is derived by checking
 1394 whether the diffusion-driven instability conditions can be satisfied
 1395 in the following cases:

- 1396 Type I, $d_v > d_w \vee d_w > d_v$
 1397 Type II, $d_v = d_w$
 1398 Type III, $\forall d_v \forall d_w$

1399 **Pattern Phase.** The relative phase pattern generated by each net-
 1400 works, which can be categorized into four distinct configurations:

- 1401 Phase 1: All three nodes in-phase
 1402 Phase 2: Node v out-of-phase, u and w in-phase
 1403 Phase 3: Node u out-of-phase, v and w in-phase
 1404 Phase 4: Node w out-of-phase, u and v in-phase

1405 To predict the pattern phase generated by a network, we do not
 1406 perform numerical simulations, instead we analyze the relative sign
 1407 of the eigenvectors associated with the eigenvalue that promote
 1408 diffusion-driven instability.

1409 For a given network, we first we obtain a set of parameters
 1410 $(k_1 \dots k_9)$ with the *FindInstance* command in Wolfram Mathematica
 1411 that satisfy the diffusion-driven instability conditions. We let
 1412 each parameter k_i to change within diffusion-driven instability
 1413 range and calculate in each case the eigenvectors $E(\lambda(q_{\max})) =$
 1414 $(E_u(q_{\max}), E_v(q_{\max}), E_w(q_{\max}))$ associated with the positive eigen-
 1415 value values. For each case we calculate the relative signs of the
 1416 eigenvectors as:

$$1417 E_{u,u} = \frac{E_u(q_{\max})}{E_u(q_{\max})} = 1, E_{v,u} = \frac{E_v(q_{\max})}{E_u(q_{\max})}, E_{w,u} = \frac{E_w(q_{\max})}{E_u(q_{\max})}$$

1418 The relative sign of the phase vector $\varphi = (E_{v,u}, E_{w,u})$
 1419 determines the phase of the periodic patterns:

- 1420 Phase 1, $\varphi_1 : \varphi = (+, +)$ Phase 2, $\varphi_2 : \varphi = (-, +)$
 1421 Phase 3, $\varphi_3 : \varphi = (-, -)$ Phase 4, $\varphi_4 : \varphi = (+, -)$

1422 The eigenvectors can be plotted as a function of k_i to identify
 1423 Multiphase networks, as shown in Figure 2F.

ACKNOWLEDGMENTS. We would like to thank Xavier Diego
 1424 for the useful discussions that inspired this project and Isaac
 1425 Salazar-Ciudad for providing critical feedback.

1. A Turing. The chemical basis of morphogenesis. *Philos. Transactions Royal Soc. London. Ser. B, Biol. Sci.* **237**, 37–72 (1952). 1430
2. J Green, J Sharpe, Positional information and reaction-diffusion: two big ideas in developmental biology combine. *Development* **142**, 1203–1211 (2015). 1431
3. L Marcon, J Sharpe, Turing patterns in development: what about the horse part? *Curr. opinion genetics & development* **22**, 578–584 (2012). 1432
4. K Ishihara, EM Tanaka, Spontaneous symmetry breaking and pattern formation of organoids. *Curr. Opin. Syst. Biol.* **11**, 123–128 (2018). 1433
5. MC Milinkovitch, E Jahanbakhsh, S Zakany, The unreasonable effectiveness of reaction diffusion in vertebrate skin color patterning. *Annu. Rev. Cell Dev. Biol.* **39**, 145–174 (2023). 1434
6. J Raspopovic, L Marcon, L Russo, J Sharpe, Digit patterning is controlled by a bmp-sox9-wnt turing network modulated by morphogen gradients. *Science* **345**, 566–570 (2014). 1435
7. ML Woods, M Leon, R Perez-Carrasco, CP Barnes, A statistical approach reveals designs for the most robust stochastic gene oscillators. *ACS synthetic biology* **5**, 459–470 (2016). 1436
8. L Goentoro, O Shoval, MW Kirschner, U Alon, The incoherent feedforward loop can provide fold-change detection in gene regulation. *Mol. cell* **36**, 894–899 (2009). 1437
9. M Adler, P Szekeley, A Mayo, U Alon, Optimal regulatory circuit topologies for fold-change detection. *Cell systems* **4**, 171–181 (2017). 1438
10. J Cotterell, J Sharpe, An atlas of gene regulatory networks reveals multiple three-gene mechanisms for interpreting morphogen gradients. *Mol. systems biology* **6**, 425 (2010). 1439
11. A Munteanu, J Cotterell, RV Solé, J Sharpe, Design principles of stripe-forming motifs: the role of positive feedback. *Sci. Reports* **4**, 5003 (2014). 1440
12. A Jiménez, J Cotterell, A Munteanu, J Sharpe, A spectrum of modularity in multi-functional gene circuits. *Mol. systems biology* **13**, 925 (2017). 1441
13. A Gierer, H Meinhardt, A theory of biological pattern formation. *Kybernetik* **12**, 30–39 (1972). 1442
14. V Klika, RE Baker, D Headon, EA Gaffney, The influence of receptor-mediated interactions on reaction-diffusion mechanisms of cellular self-organisation. *Bull. mathematical biology* **74**, 935–957 (2012). 1443
15. EM Rauch, MM Millonas, The role of trans-membrane signal transduction in turing-type cellular pattern formation. *J. theoretical biology* **226**, 401–407 (2004). 1444
16. HG Othmer, L Scriven, Interactions of reaction and diffusion in open systems. *Ind. & Eng. Chem. Fundamentals* **8**, 302–313 (1969). 1445
17. K White, C Gilligan, Spatial heterogeneity in three species, plant–parasite–hyperparasite, systems. *Philos. Transactions Royal Soc. London. Ser. B: Biol. Sci.* **353**, 543–557 (1998). 1446
18. K Korvasová, E Gaffney, P Maini, M Ferreira, V Klika, Investigating the turing conditions for diffusion-driven instability in the presence of a binding immobile substrate. *J. theoretical biology* **367**, 286–295 (2015). 1447
19. H Qian, JD Murray, A simple method of parameter space determination for diffusion-driven instability with three species. *Appl. mathematics letters* **14**, 405–411 (2001). 1448
20. RA Satnoianu, M Menzinger, PK Maini, Turing instabilities in general systems. *J. mathematical biology* **41**, 493–512 (2000). 1449
21. I Salazar-Ciudad, J Garcia-Fernández, RV Solé, Gene networks capable of pattern formation: from induction to reaction–diffusion. *J. theoretical biology* **205**, 587–603 (2000). 1450
22. I Salazar-Ciudad, S Newman, R Solé, Phenotypic and dynamical transitions in model genetic networks i. emergence of patterns and genotype-phenotype relationships. *Evol. & development* **3**, 84–94 (2001). 1451
23. L Marcon, X Diego, J Sharpe, P Müller, High-throughput mathematical analysis identifies turing networks for patterning with equally diffusing signals. *Elife* **5**, e14022 (2016). 1452
24. J Murray, *Mathematical Biology II: Spatial Models and Biomedical Applications*. (Springer, (2003). 1453
25. X Diego, L Marcon, P Müller, J Sharpe, Key features of turing systems are determined purely by network topology. *Phys. Rev. X* **8**, 021071 (2018). 1454
26. MM Zheng, B Shao, Q Ouyang, Identifying network topologies that can generate turing pattern. *J. theoretical biology* **408**, 88–96 (2016). 1455
27. NS Scholes, D Schroerr, M Isalan, MP Stumpf, A comprehensive network atlas reveals that turing patterns are common but not robust. *Cell systems* **9**, 243–257 (2019). 1456
28. S Wang, J Garcia-Ojalvo, MB Elowitz, Periodic spatial patterning with a single morphogen. *Cell Syst.* **13**, 1033–1047.e7 (2022). 1457
29. S Smith, N Dalchau, Beyond activator-inhibitor networks: the generalised turing mechanism (2018). 1458
30. R Sakuma, et al., Inhibition of nodal signalling by lefty mediated through interaction with common receptors and efficient diffusion. *Genes to Cells* **7**, 401–412 (2002). 1459
31. SC van den Brink, et al., Single-cell and spatial transcriptomics reveal somitogenesis in gastruloids. *Nature* **582**, 405–409 (2020). 1460
32. S Smith, N Dalchau, Model reduction enables turing instability analysis of large reaction–diffusion models. *J. The Royal Soc. Interface* **15**, 20170805 (2018). 1461
33. Y Sasai, Cytosystems dynamics in self-organization of tissue architecture. *Nature* **493**, 318–326 (2013). 1462
34. J Tica, et al., A three-node turing gene circuit forms periodic spatial patterns in bacteria. *bioRxiv* (2023). 1463
35. G Cross, Three types of matrix stability. *Linear algebra its applications* **20**, 253–263 (1978). 1464
36. R Satnoianu, P van den Driessche, Some remarks on matrix stability with application to turing instability. *Linear algebra its applications* **398**, 69–74 (2005). 1465
37. F Gantmacher, Applications of the theory of matrices, interscience publ. *New York* (1959). 1466