Supplemental Information

Supplemental Figure Legends

Supplemental Figure 1. Linear scaling (patch spacing *vs.* diameter). (*A*) Influence of the production coefficient ρ on the patch size and interpatch spacing in Gierer-Meinhardt patterns. Each sample point (blue) indicates a separate simulation with different ρ (decreasing from left to right). Average patch diameters and interpatch distances are linearly related. The equation of the fitted linear interpolation (red) is $y = 1.63\ x - 0.23$ ($R^2 = 0.85$, P-value $< 1 \cdot 10^{-4}$), approximating the slope of 1.65 obtained from the experimental data. The Gierer-Meinhardt model parameters were: $D_a = 0.55$, $D_h = 220$, $\mu_a = 0.18$, $\mu_h = 1.18$, $\rho_a = 0.2$, $\rho_h = 0.2$ and ρ is varied in steps of 0.006 from 0.03 to 0.144. (*B*) Influence of the diffusion coefficients on the patch size and interpatch spacing in Gierer-Meinhardt patterns. Each sample point (blue) indicates a separate simulation with a different diffusion coefficient (increasing from left to right). Average patch diameters and interpatch distances are also linearly related. The equation of the fitted linear interpolation (red) is $y = 1.7\ x - 1.1$ ($R^2 = 0.97$, P-value $< 1 \cdot 10^{-4}$). The Gierer-Meinhardt model parameters were: $D_a = 0.06 \cdot D$, $D_h = 100 \cdot D$, $\mu_a = 0.1$, $\mu_h = 0.35$, $\rho_a = 0.01$, $\rho_h = 0.015$, $\rho = 1$ and D is varied in steps of 0.06 from 1.2 to 2.34.

Supplemental Figure 2. Classification of patchy patterns. (*A,B*) Concentration profiles from a Gierer-Meinhardt pattern which is classified as patchy. *(A)* is the

activator morphogen concentration, *(B)* the inhibitor morphogen concentration of the same pattern. Bright means high morphogen concentration. *(C,D)* Activator and inhibitor morphogen concentration profiles from a pattern that is classified as non-patchy. The patterns are composed of worm-like structures. The algorithm infers that there is an inconsistency of concentration patches between the activator pattern *(C)* and the inhibitor pattern *(D)*, which is why it is classified as non-patchy. *(E,F)* Activator and inhibitor morphogen patterns which are (correctly) classified as non-patchy.

Supplemental Figure 3. Robustness of patchy patterns. Influence of deviations of the Gierer-Meinhardt model parameters on the pattern outcome. Gaussian noise of varying amplitude was added to each of the Gierer-Meinhardt model parameters. After convergence, the patterns were classified as patchy or non-patchy. The blue curve indicates the percentage of the 30 patterns that were classified as patchy, for a given standard deviation on the parameter modification noise (x-axis). The patchy patterns can be reliably generated until a standard deviation of approximately 25 % of the original template parameter is reached. Red bars correspond to the standard deviation. The original Gierer-Meinhardt model parameters were: $D_a = 0.25$, $D_h = 50$, $\mu_a = 0.3$, $\mu_h = 1$, $\rho_a = 0.05$, $\rho_h = 0.03$ and $\rho = 2$. The simulations were done in Matlab.

Supplemental Figure 4. Convergence of concentrations. This plot shows an example of the summed cellular concentration changes through time ($\sum_{i,j} |c_{ij}(t) - c_{ij}(t+1)|$). After the Turing instability drives the symmetry breaking that gives rise to a strong change in the concentration map, the difference decays over time

and the resulting patchy pattern converges to a stationary pattern.

Supplemental Movie 5. Self-organization of four patch systems. The initial precursor cell divides in the 2-dimensional plane, giving rise to several daughter cells. The cell division continues until an intracellular concentration reaches a predefined threshold, which stops the cell division. Based on this cellular plate, four mutually inhibiting Gierer-Meinhardt reaction-diffusion mechanisms lead to patchy patterns. The number of physical nodes for the simulation of the diffusion was chosen to be 60'000, located randomly and uniformly within the boundaries [-2500, 2500], [-300, 300] and [2500, 2500] in x-, y- and z-direction, respectively. The inter-object force coefficient was set to 1, the adherence coefficient to 0.01 and the somatic mass to 0.02 (in standard Cx3D units). The Gierer-Meinhardt model parameters were: $D_a = 0.001$, $D_h = 1800$, $\mu_a = 0.21$, $\mu_h = 0.355$, $\rho_a = 188$, $\rho_h = 188$ and $\rho = 720$. Repulsion coefficients between the different activators were different between different pairs, ranging from 0.05 to 0.4.

Supplemental Movie 6. Axonal growth on patch systems. Axonal growth was simulated on the cellular plate shown in supplemental movie S5. After the cells have stopped dividing and a threshold in a constantly secreted intracellular substance concentration is reached, the cells extend axons that make use of the activator substance as a guidance cue. The location of the soma determines the targeted activator type (from the totally four types). Axons that arise from cell bodies lying in a patch will make long-range projections only to the patches of its own lattice. For a clearer separation, the resulting axonal arborization of one patch system (red) is

shown in the end. Cx3D simulation parameters were the same as for the supplemental movie S5.

Supplemental Scripts 1. Matlab scripts for pattern-formation. This file contains the Matlab script patternformation_GiererMeinhardt_system.m to simulate an example Gierer-Meinhardt reaction-diffusion system. It needs the functions compute_flow_from_neighbours.m and get_topology_neighbour_indices.m, which are also included in the same file. The concentrations of the two morphogens are visualized every 50 time steps and saved every 500 time steps.

Supplemental Scripts 2. Matlab script for assessing patch size. This file contains the Matlab script compute_pattern_properties.m, which we implemented to assess the average patch size in a patchy pattern. This particular implementation is based on (Shen and Jung 2005).

Supplemental Scripts 3. Java code for diffusion and morphogen production. This file contains the main Java functions from the Cx3D scripts for the numerical computation of the reaction-diffusion processes. The extracted functions are runExtracellularDiffusion(), degradate(), diffuseEdgeAnalytically() and modifyExtracellularQuantity from PhysicalNode.java (which contains the functions essential for diffusion). The reaction part is contained in the run() functions of SimpleMorphogeneSecretor.java (for a single Gierer-Meinhardt system) and ExtendedSuperpositionSecretor.java (for multiple interacting Gierer-Meinhardt systems). Further information on the free software framework Cx3D and the source

code can be found at: http://www.ini.uzh.ch/~amw/seco/cx3d/.