**Autogenic Automaton**

*Documentation*

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v.1.1

**1. Setup**

The program runs under both Mac and Windows. To use, download and unpack the zip file **AA.zip** . This gives the following file structure:

* **AA.jar**: double click the icon to start the program. No further installation is required. If double-clicking doesn’t work, make sure the latest version of Java is installed on your computer (see <http://java.sun.org>)
* a folder named **img**. Contains the images used by the program
* a folder named **log**. After each simulation run, a log file is generated and put into this folder. The file format is **.cls**, which can be opened by tekst editors, spreadsheet programs (e.g. Excel) and most data analysis programs

**2. General description**

The Autogenic Automaton is a simulation program that allows a user to play around with emergent dynamics. In particular, it focuses the interplay between morphodynamics and teleodynamics in an chemical reactants environments (also known as an **autogen** or **autocell**).

Once the program is opened, the top middle panel shows three buttons (**Run**, **Stop** and **Step**), several **speed** options, and a slider to set the **temperature** (or heat). To the left are four **views** (one large, and three smaller views at the bottom) on the two-dimensional grid in which the reactions take place. The colored squares indicate the presence of a unit.

In the lower-middle of the screen are eight sliders. These are used to set the **boundary conditions**. The rightmost panel displays various **graphs** (top) and allows the user to set additional **parameters**, **reset** the simulation with different settings, **save** a log file of the current run, and shows an image of **autogenesis** (bottom).

The user interface section below describes each of these elements in more detail.

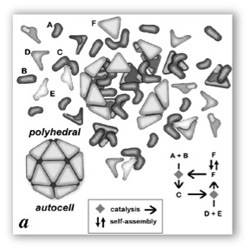
**3. User Interface**

* 1. **Grid**

A square two-dimensional grid of a given size, which can be set in the reset panel. A unit is represented by a colored square. Two units can be at the same square, though only one will be visible then. Each time step, the units move around and bounce against the edges of the grid. Different colors correspond to different unit types (Table 1). The naming conventions of types are equal to those in the Figure 1 (also displayed in the simulation).

|  |  |  |
| --- | --- | --- |
| **type** | **color** | **description** |
| A |  | reactant for B |
| B |  | reactant for A |
| C |  | catalysist |
| D |  | reactant for E |
| E |  | reactant for D |
| F |  | catalysist and containment unit |
| FF |  | autogen[[1]](#footnote-1) |

**Table 1.** Unit types and colors



**Figure 1.** Autogenesis

* 1. **Catalysis**

A mini-panel displaying a scaled down version of the grid above. When catalysis takes place, part of the map lights up red, indicating where in the grid this has occured. At times, many red dots will appear next to each other, demonstrating the localized nature of auto-catalysis.

* 1. **Crystallization**

Similar to the previous mini-map; this map lights up blue when crystallization - two or more F units collide and merge together to form an autogen - takes place.

* 1. **Decrystallization**

Similar to the previous mini-map; this map lights up black when decrystallization – an autogen breaking apart due to diffusion - takes place. Note that this breaking apart occurs regularly, but because of the high promixity of other reactants, the autogens continuous reform as well.

* 1. **Control**

Three buttons controlling the start (**Run**) and stop (**Stop**) of the current simulation. **Step** moves the simulation only one iteration forward each time it is clicked. Note that some options (such as Step and Reset) are available only when the simulation is stopped, while others (Update) can be used during a run.

**3.6 Speed**

Slows down or speeds up the simulation according to the following delays:

* Min: 1000ms per iteration
* Slow: 250ms per iteration
* Fast: 50ms per iteration
* Max: no delay[[2]](#footnote-2)

**3.7 Temperature**

The temperature controls which reactions may and may not occur, according to the boundary conditions.

**3.8 Boundary Conditions**

The sliders in this panel determine which reactions may occur under a given temperature. A reaction may occur if (and only if) both:

Temp >= BCX\_MIN

Temp <= BCX\_MAX

are both true, where X is the rule corresponding to a reaction.

The rules by which the units react can be seperated into two groups[[3]](#footnote-3):

* + 1. *Homeodynamic reactions*

These lead to stable equilibrium conditions with minimal constraint. See further Table 2a

* + 1. *Morphodynamc reactions*

These leading to far-from-equilibrium conditions with different constraints from those the homeo, due to incessant energy provided by an external heat source. See further Table 2b

|  |  |  |
| --- | --- | --- |
| **rule #** | **reactants** | **description** |
| 1 | A + B => C | colliding reactants A and B together form a new unit C |
| 2 | C => A + B | C breaks down into A and B due to diffusion |
| 3 | D + E => F | colliding reactants D and E together form a new unit F |
| 4 | F => D + E | F breaks down into D and E due to diffusion |

**Table 2a.** Homeodynamic reactions

|  |  |  |
| --- | --- | --- |
| **rule #** | **reactants** | **description** |
| 5 | A + B =F> C | reactants A, B and F collide. A and B form a new unit C; a process that is catalyzed by F |
| 6 | D + E =C> F | reactants D, E and C collide. D and E form a new unit F; a process that is catalyzed by C |
| 7 | F + F => FF | colliding reactants F and F together form a new autogen FF |
| 8 | FF + X => FFX | unit X is encapsulated by FF, where X may be one of A, B, C, D or E |

**Table 2b.** Morphodynamic reactions

Note that only the morphodynamics reactions (rule 5-8) have boundary conditions. The remaining reactions (1-4) will occur irrespective of temperature[[4]](#footnote-4).

**3.9 Graph**

This panel shows how the number of various units, temperature, and average autogen size develop over time. It is meant primarily as an indicator of how the various parameters interact to create different dynamics. For more detailed analysis, a log file that contains all this data and more can be saved, and analysed seperately with spreadsheet or analysis software (see also 3.16).

The Y-axis shows the number of units of a specific type, scaled to the maximum number of possible units. On the right side of the graph, another Y-axis with temperature values is displayed. The average autogen size scales against the former axis, with a factor 2 (e.g. average size 200 is displayed at 100), causing it to at times peak outside the axis.

The X-axis shows a time interval of the latest 100, 1.000 or 10.000 iterations (see also 3.11)

**3.10 Show**

Clicking checkboxes toggles the display of graphs. There is a checkbox for each unit type - with color that corresponds to the color in the grid – for the number of autogens, the average autogen size, and the temperature.

**3.11 Scale**

Three time scales are currently supported, showing values at the latest 100, 1.000, 10.000 iterations.

**3.12 Probabilities**

Each of the eight rules (see Tables 2a and 2b) has a probability associated with it, to allow for tweaking to induce the desired dynamics. For example with probability 0.1 for rule 1, only 1 out of every ten collisions of A and B will actually result in a merger into C.

Rules 2 and 4 are different, because they are not based on a collision but on local diffusion (breaking apart of bonds). Thus, at each iteration, for every unit C and F, it may break apart with a probability P. For this reason, P should be set at a relatively low value compared to the other probabilities.

**3.13 Reset**

When the Reset button is clicked, a new simulation starts with the given parameters for number of units, grid size and diffusion rate.

The diffusion rate is the probabillity of each unit to change direction randomly at each iteration. This is introduced to avoid biased unit movement (i.e. continuously crossing the diagonal of the grid). The default diffusion rate is set to 0.01, and may be set anywhere from 0 (only bouncing against edges) to 1 (completely randomized movement).

**3.13 Autogenesis**

An image (take from[[5]](#footnote-5)) illustrating the autogenic process (see Figure 1). The dynamic logic and naming conventions in the simulation follow those in the image.

**3.15 About**

Opens a dialog with information about the program.

**3.16 Save Log**

Opens a dialog that allows the user to save a log file of the simulation. In the current version (0.8), saving is not yet functional, but the log file is generated in a standard log folder.

**4. A Typical Run**

* Open **AA.jar**
* Press **Run**
* The units in the **grid** start to move around and react
* Note the **graph** in the right of the frame. You can change which lines to display by clicking and unclicking the **checkboxes** below the graph
* Some lines will not be visible, because they don’t have a positive value yet. Note also that the mini-displays in the bottom-left corner show no activity. This is because there are only homeodynamic processes active.
* Compare the current **temperature** (set at 10 by default) to the **boundary conditions** for the morphodynamic rules (4-8). The minimim values for each rule are well above 10.
* Increase the temperature to **40**
* This has activated rule 4. The left-most mini-display now shows where catalysis takes place, and the graph might also change as well (depending on which checkboxes are selected).
* Increase the temperature again to **50**
* Both rule 4 and 5 are active
* Increase the temperature to **75**
* Crystallization (rule 6) now is also active. The other two mini-displays show traces of where crystallization and decrystallzation (the continuous falling apart of autogens due to rule 4) occurs.
* Finally, increase the temperature to **85**. All rules are active now.
* Change the **scale** to 100, and then to 10.000. This gives a nice overview of how the changes in temperature affect the other variables
* Change the scale back to 1.000 again, and speed up the simulation to max speed
* Notice how the graph moves faster. You can still check and uncheck lines while running the simulation.
* Stop the simulation by pressing the Stop button
* Do a single iteration by pressing the Step button
* Save a log file to a desired location by pressing Save Log, or alternatively, find the log file of this run in the **log** folder
* Change the probabilities by entering different values and pressing Update and Run
* Stop the simulation and reset it with different values (i.e. with different grid size and initial units) by pressing Reset
* Play around with different boundary conditions and parameters.

1. The term *autogen* is used here, even though strictly speaking it is not necessarily a self-attractor [↑](#footnote-ref-1)
2. The speed at which the simulation runs at max setting is dependent on simulation settings - grid size and number of units especially - processor speed, available memory, and other programs running in parallel. [↑](#footnote-ref-2)
3. In a computer simulation, what constitutes a homeodynamic or morphydynamic reaction may be considered somewhat arbitrary. This discussion is, however, outside the scope of this document. [↑](#footnote-ref-3)
4. but note that their occurrence can be manipulated nevertheless, by means of the probability by which they occur (e.g. by setting this probability to zero). This can be done in the probabilities panel (3.12) [↑](#footnote-ref-4)
5. Deacon, T.W. (2005). *A general model of self-reproduction and natural selection derived from reciprocally linked self-organizing processes* [↑](#footnote-ref-5)