Aeon Manual

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1 What does Aeon do

AsamemberofBioDivinesuite, Aeon (Analysis & Exploration of Networks) is a parallel tool for creating, editing, and analysing parametrised Boolean network models; specifically, it provides means of analysis of model's bifurcations—qualitative changes in behaviour, which are originating in, typically small, changes of parameters. Details on the underlying theory can be found in [1].

2 Getting Aeon running

The tool implementation consists of two components: the *compute engine*, and the webbased, user-facing GUI application (the *client*). Atypical use of the tool requires a local installation of the compute engine, which is accessed from the client. The client can be also stored locally, or hosted remotely, with no change in functionality between the two cases. The online version of the client is accessible from https://biodivine.fi.muni.cz/aeon; for offline use, the client application can be downloaded from https://github.com/sybila/biodivine-aeon-client. The client application can be used to create and edit parametric models without the compute engine being installed. The client does not connect to the internet. The engine can be obtained as a pre-compiled executable (for all major desktop platforms) or as a Rust source code. Because the client is accessing the engine via http connection in which the engine acts as a server, it is possible to access the engine remotely, assuming sufficient network configuration—this is useful when the computation is delegated to a suitable powerful hardware.

	Client
online access	biodivine.fi.muni.cz/aeon/
offline download	github.com/sybila/biodivine-aeon-client/
	Engine
-	
source, executables	github.com/sybila/biodivine-aeon-server/releases/

2.1 Running pre-compiled binaries

Pre-compiled executables formultiple platforms are available athttps://github.com/sybila/biodivine-aeon-server/releases. After downloading and running the corresponding file, the engine will be accessible from the client application and ready for use. The relevant executables can be also downloaded through the links listed in the client application under the *compute engine* panel, described in Section 4.2. Preparing the executable on Linux:

\$ unzip aeon-compute-engine-linux.zip && chmod +x aeon-compute-engine

2.2 Building from source

The engine source code, written in the Rust programming language and licensed under the MIT License, is freely available for download. To compile the software, one needs to install the Rust toolchain – rustup, and download the actual source code.

- rustup https://www.rust-lang.org/tools/install
- Compute engine https://github.com/sybila/biodivine-aeon-server

When the Rust toolchain is installed following the instructions on its website, the engine can be compiled using the led command in the root of the directory. After successful compilation, running will start up the engine.

2.3 Startup

By default, the engine uses the localhost address and the port 8000 to run on. If the port is available, the engine will report the address and the port number on which it is running.

Rocket has launched from http://localhost:8000

Thedefaultserveraddressandportwillworkinmostcases;

however, should the automatic assignment fail, manual configuration is possible through the environment variables AEON_ADDR and AEON_PORT. For example, setting a different port number would look like this (on Linux/Mac):

\$ export AEON_PORT=3485

After the engine has been properly configured and it's up and running, the client will automatically establish a connection on its startup. If it is already running in the web browser, clickingon the *Connect* buttonunder the *compute engine* panelwill link the two, and thetool will be ready to be used.

3 Model description

The Aeon does use parametrised Boolean network models. A Boolean network can be seen as a directed graph

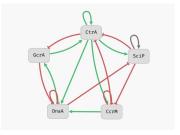
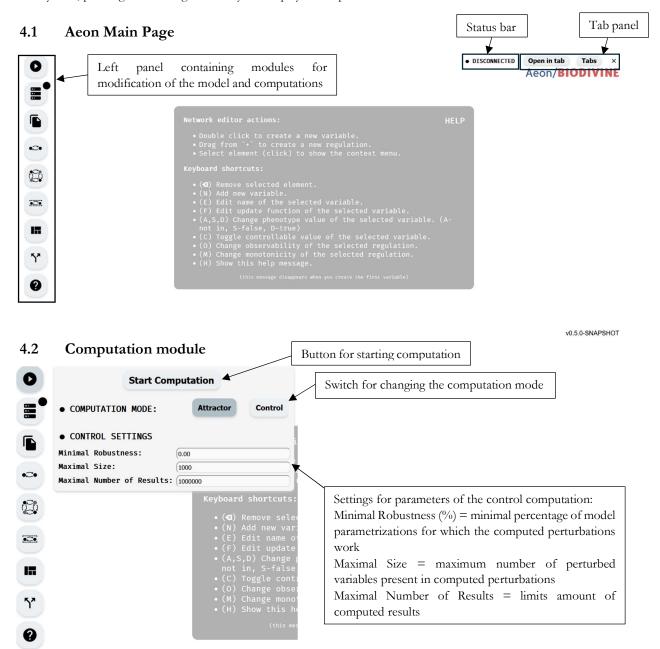
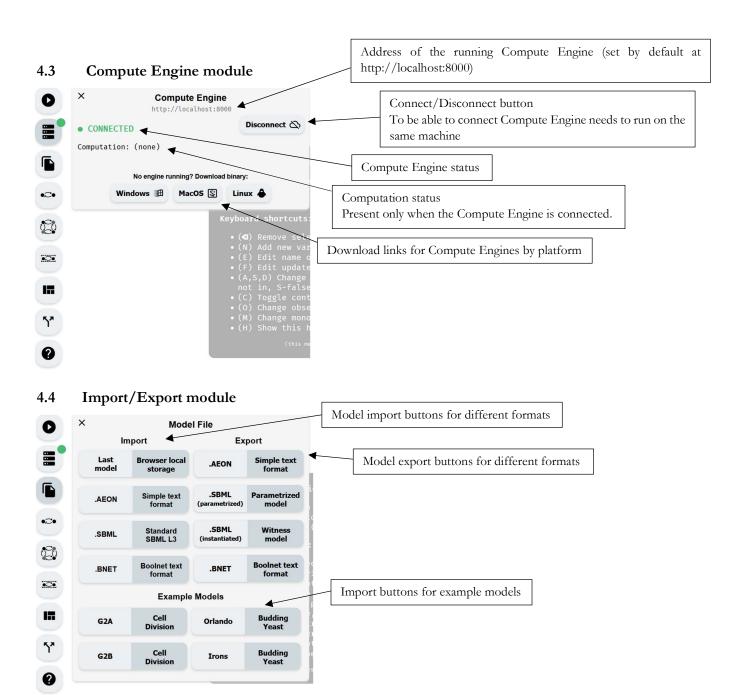


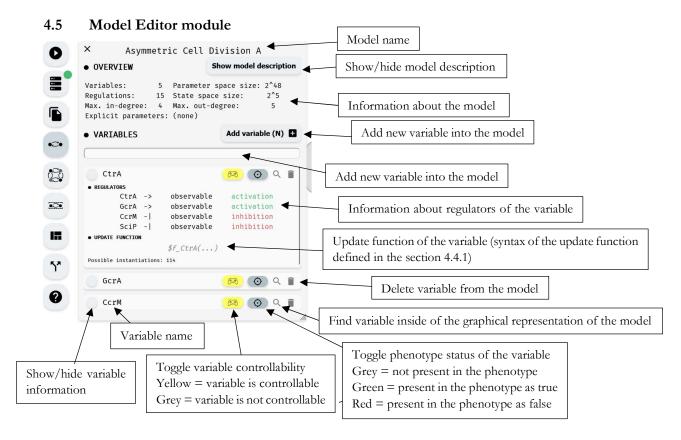
Figure 1: A simple Boolean network as displayed in Aeon- model adopted from [3].

4 Graphical user interface

The client, running in a web browser, provides a user-friendly graphical interface, that enables one to create, edit, and visualise Boolean network models on the one hand, and allows for interfacing with the engine, supervising the computation, and visualisation of the results on the other. Models are drawn and displayed on the large editor canvas. At any time, pressing and holding the H key will display the help window.





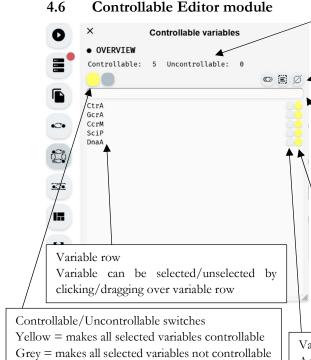


4.5.1 Computation Model format and update function syntax

Models are in this format:

Update function syntax

Only names of the can be used as function parameters.



Controllable/Uncontrollable variables counters

Select/unselect buttons

Left – toggles selected (unselects selected, selects unselected)

Middle – selects all variables

Right – unselects all variables

Functionality of these buttons is restricted to filtered data (for example if Filter bar contains CtrA, then middle button only selects CtrA)

Filter bar

Name of every variable in the filter has to be separated by `,` (example – CtrA, GcrA)

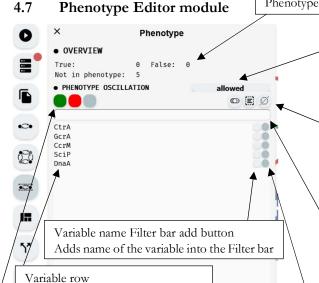
Filter also works for filtering names starting with string (for example if we write `C` into the filter, then table shows all variables starting with C)

Variable controllability indicator

Yellow = variable is controllable

Grey = variable is not controllable

Variable name Filter bar add button Adds name of the variable into the Filter bar



Phenotype status variable counters

Phenotype oscillation toggle

allowed = set phenotype may oscillate

required = set phenotype must oscillate

forbidden = set phenotype cannot oscillate

Phenotype oscillates when it repeatedly appears after some time but doesn't stay fixed to the required value forever

Select/unselect buttons

Left – toggles selected (unselects selected, selects unselected)

Middle - selects all variables

Right – unselects all variables

Functionality of these buttons is restricted to filtered data (for example if Filter bar contains CtrA, then middle button only selects CtrA)

Filter bar

Name of every variable in the filter has to be separated by `,` (example – CtrA, GcrA)

Filter also works for filtering names starting with string (for example if we write `C` into the filter, then table shows all variables starting with C)

Variable phenotype status indicator Grey = not present in the phenotype Green = present in the phenotype as true Red = present in the phenotype as false

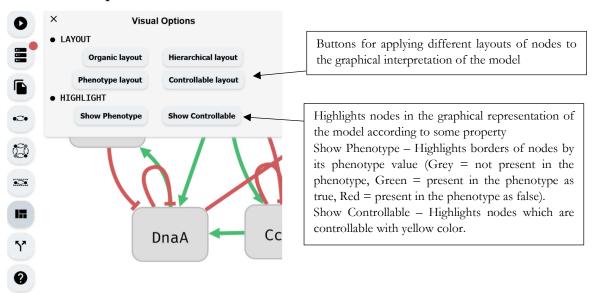
Phenotype status switches

Grey = removes all selected variables from the phenotype Green = adds all selected variables into the phenotype as true Red = adds all selected variables into the phenotype as false

Variable can be selected/unselected

by clicking/dragging over variable

4.8 Visual Options module



Examination of the bifurcation function Result

× Bifurcation Function				
	Behavior class	Witness count		
	Q	222025	<u>Witness</u>	
	•	165310	<u>Witness</u>	
	\rightleftharpoons	47407	<u>Witness</u>	
	♥ ●	18129	<u>Witness</u>	
	• •	11754	<u>Witness</u>	
	$ ightleftarrow \odot$	2305	Witness	
	QQ	748	<u>Witness</u>	
	\rightleftarrows \circlearrowleft	134	<u>Witness</u>	
	$\circlearrowleft \bullet \bullet$	44	<u>Witness</u>	
\rightleftarrows disorder $ \circlearrowleft \mbox{ oscillation } \odot \mbox{ stability}$				

Figure 4: An example of a result, representing a bifurcation function

Witness inspection Partition of the parameter space of parametrizations exhibiting the same behaviour

References

- [1] NikolaBenešetal."FormalAnalysisofQualitativeLong-TermBehaviourinParametrised Boolean Networks". In: Formal Methods and Software Engineering (ICFEM 2019). Springer, 2019, pp. 353–369.
- [2] Claudine Chaouiya et al. "SBML qualitative models: a model representation format and infrastructure to foster interactions between qualitative modelling formalisms and tools". In: BMC systems biology 7.1 (2013), p. 135.
- [3] IsmaelSánchez-Osorio, Carlos A. Hernández-Martínez, and Agustino Martínez-Antonio. "Modeling Asymmetric Cell Division in Caulobacter crescentus Using a Boolean Logic Approach". In: Asymmetric Cell Division in Development, Differentiation and Cancer. Ed. by Jean-Pierre Tassan and Jacek Z. Kubiak. Cham: Springer International Publishing, 2017, pp. 1–21.