# BoolSim, a Graphical Interface for Open Access Boolean Network Simulations and Use in Guard Cell CO2 Signaling

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The sections of the research paper input text parsed in this audit.

Section No.	Headings	Sentences
Section: 1	ABSTRACT	12
Section: 2	Introduction	15
N/A		0

# BoolSim, a Graphical Interface for Open Access Boolean Network Simulations and Use in Guard Cell CO2 Signaling

# S1 [001] ABSTRACT

**S1 [002]** Signaling networks are at the heart of almost all biological processes.

Signaling networks are ...

- ... at the heart ...
- ... of almost all biological processes.
- **S1 [003]** Most of these networks contain a large number of components and often the connections between these components are either not known, or the rate equations that govern the dynamics of soluble signaling components are not quantified.

Most ...

- ... of these networks contain a large number ...
- ... of components ...
- ... and often the connections ...
- ... between these components are either not known, ...
- ... or the rate equations ...
- ... that govern the dynamics ...
- ... of soluble signaling components are not quantified.
- **S1 [004]** This uncertainty in network topology and parameters can make it challenging to formulate detailed mathematical models.

This uncertainty ...

- ... in network topology ...
- $\dots$  and parameters can make it challenging  $\dots$
- ... to formulate detailed mathematical models.
- **S1 [005]** Boolean networks, in which all components are either on or off, have emerged as viable alternatives to more detailed mathematical models but can be difficult to implement.

Boolean networks, ...

- ... in which all components are either ...
- ... on ...
- ... or off, ...
- ... have emerged ...
- ... as viable alternatives ...
- ... to more detailed mathematical models ...
- ... but can be difficult ...
- ... to implement.
- **S1** [006] Therefore, open source format of such models for community use is desirable.

Therefore, ...

... open source format ...

- ... of such models ... ... for community use is desirable.
- **S1 [007]** Here we present BoolSim, a freely available graphical user interface (GUI) that allows users to easily construct and analyze Boolean networks.

Here we present BoolSim, ...
... a freely available graphical user interface ...
... (GUI) ...
... that allows users ...
... to easily construct ...

**S1** [008] BoolSim can be applied to any Boolean network.

... and analyze Boolean networks.

BoolSim can be applied ... ... to any Boolean network.

**S1 [009]** We demonstrate BoolSim's application using a previously published network for abscisic acid-driven stomatal closure in Arabidopsis.

We demonstrate BoolSim's application ...
... using a previously published network ...
... for abscisic acid-driven stomatal closure ...
... in Arabidopsis.

**S1 [010]** We also show how BoolSim can be used to generate testable predictions by extending the network to include CO2 regulation of stomatal movements.

We also show how BoolSim can be used ...
... to generate testable predictions ...
... by extending the network ...
... to include CO2 regulation ...
... of stomatal movements.

**S1 [011]** Predictions of the model were experimentally tested and the model was iteratively modified based on experiments showing that ABA closes stomata even at near zero CO2 concentrations (1.5 ppm CO2).

Predictions ...
... of the model were experimentally tested ...
... and the model was iteratively modified based ...
... on experiments showing ...
... that ABA closes stomata even ...
... at near zero CO2 concentrations ...
... (1.5 ppm CO2).

**S1 [012]** One Sentence Summary This study presents an open-source, graphical interface for the simulation of Boolean networks and applies it to an abscisic acid signaling network in guard cells, extended to include input from CO2.

```
One Sentence Summary This study presents an open-source, ... ... graphical interface ... ... for the simulation ...
```

```
... of Boolean networks ...
... and applies it ...
... to an abscisic acid signaling network ...
... in guard cells, ...
... extended ...
... to include input ...
... from CO2.
```

## S2 [013] Introduction

**S2** [014] Intra-cellular signaling networks are essential in almost all biological processes.

Intra-cellular signaling networks are essential ... ... in almost all biological processes.

**S2 [015]** These networks are often complex, involving a large number of components (or nodes) that are inter-connected.

These networks are often complex, ...
... involving a large number ...
... of components ...
... (or nodes) ...

... that are inter-connected.

**S2 [016]** To gain insights into these networks, it is possible to construct mathematical models.

To gain insights ...
... into these networks, ...
... it is possible ...
... to construct mathematical models.

**S2 [017]** One of the strengths of these mathematical models is the ability to develop predictive outcomes of experimental perturbations (Phillips, 2015, Shou et al., 2015).

One ...
... of the strengths ...
... of these mathematical models is the ability ...
... to develop predictive outcomes ...
... of experimental perturbations ...
... (Phillips, 2015, ...
... Shou et al., 2015).

**S2 [018]** These perturbations can be much more easily implemented in simulations than in experiments.

These perturbations can be much more easily implemented ... ... in simulations ...

... than in experiments.

**S2 [019]** Removing or changing a component or connection between components is a trivial task in simulations but usually is a task that requires lengthy wet lab experimental procedures.

Removing ...
... or changing a component ...
... or connection ...
... between components is a trivial task ...
... in simulations ...
... but usually is a task ...
... that requires lengthy wet lab experimental procedures.

**S2 [020]** Predictions developed through models can enable narrowing the parameters for subsequent wet lab examination.

Predictions developed ...
... through models can enable narrowing the parameters ...
... for subsequent wet lab examination.

**S2 [021]** Wet lab examination, in turn, can be used to iteratively update and correct mathematical models.

Wet lab examination, ...
... in turn, ...
... can be used ...
... to iteratively update ...
... and correct mathematical models.

**S2 [022]** Furthermore, mathematical models can be used to test potential biological mechanisms or can be utilized to pinpoint the most important components of a signaling network (Brodland).

Furthermore, ...
... mathematical models can be used ...
... to test potential biological mechanisms ...
... or can be utilized ...
... to pinpoint the most important components ...
... of a signaling network ...
... (Brodland).

**S2 [023]** One way of constructing mathematical models for signaling networks is to create a rate-equation model.

One way ...
... of constructing mathematical models ...
... for signaling networks is ...
... to create a rate- equation model.

S2 [024] In such a model, the concentrations for network components can take on all real values, and their change is governed by differential equations involving rate constants and the concentration of diverse components (Melke et al., 2006, Muraro et al., 2011, Wang et al., 2017, Hills et al., 2012).

In ...
... such a model, ...

# **End of Sample Audit**

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