Abstract Behavioural Modelling
of Biochemical Networks⋆

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Abstract. This is a supplement to the tool paper of the same name submitted to the 15th Conference on Computational Methods for Systems Biology (CMSB). It contains instructions of how to obtain, compile, run and analyse the model of mRNA translation described in the paper. The instructions have been written with a Unix-based operating system such as MacOS X or Linux in mind.

1 ABS Language Resources

The main documentation resource for the ABS language and tool set is `http://abs-models.org/`, which contains the language manual as well as a number of tutorials describing in detail several aspects of developing and analysing ABS models.

2 ABS Compiler

The ABS compiler has its own public git repository at `https://github.com/abstools/abstools`. However, it is not necessary to download and build it, as a precompiled version is included with the ABS translation model below.

3 Translation Model

The translation model presented in the paper can be downloaded by cloning its git repository:

```
git clone https://github.com/rm2340/cgene.git
```

3.1   Compiling the Model

The model itself is located in the `Translation` folder. It can be compiled to native Erlang code using the provided script `compile`:

```
cd Translation
./compile
```

3.2   Executing the Model

Executing Erlang programs requires an Erlang installation, which can be obtained from `https://www.erlang-solutions.com/`. Once installed, the model can be run (simulated) as follows:

```
gen/erlang/run
```

An optional time limit can be specified using the command line option `-l`. For example, to simulate the model for 10 time units (seconds):

```
gen/erlang/run -l 10
```

4   Model Analysis

The easiest access to the ABS analysis tools is provided via the ABS "Collaboratory", a web-based ABS developing and analysis environment, as seen in Fig. 1. It can be accessed at `http://130.83.165.97:8888/ei/clients/web/`.

Note: due to a bug in the current Collaboratory implementation, the ABS models have to be uploaded in a single ABS file. This file is provided in the `onefile` folder and is named `All.abs` (it has been obtained by simply concatenating all model source files: `cat *.abs > onefile/All.abs`).

On the Collaboratory website, in the top-left pane a list of already available ABS model is displayed. To upload the ABS translation model, right-click on `User_Projects` and select `Add Remove File...`. A file dialog will appear. Click the `browse` button and in the emerging file dialog, select the file `All.abs` from the folder `Translation/onefile` on your local computer. Click `Add Files` to upload the file. Once uploaded, the ABS file content (code) will appear in the central pane and can be inspected.

To start the deadlock analysis, select the analysis type `DECO_BOOL` from the top right corner of the screen. Clicking `Apply` start the analysis. After a few seconds, the result should appear in the bottom console and resemble the following output:

```
...
Found 0 deadlock/livelock risks
Found 9 task livelock risks
Complete analysis performed in 63 ms.
done
```
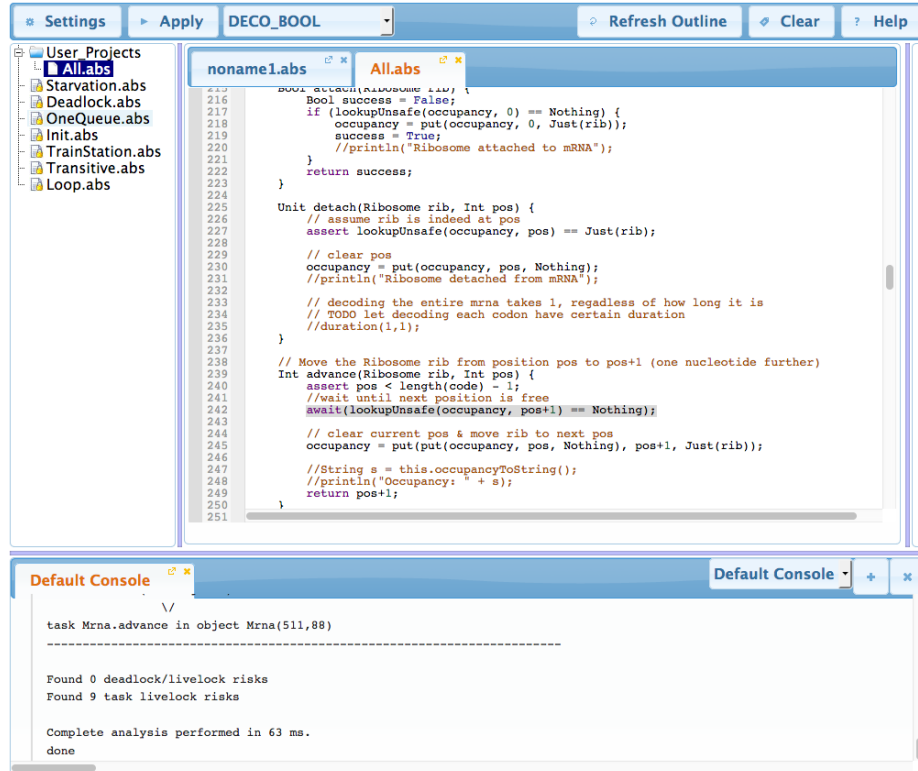
Fig. 1. Collaboratory: a web-based ABS developing and analysis environment

5   Questions

In case of questions or difficulties following these instructions, please contact the author.