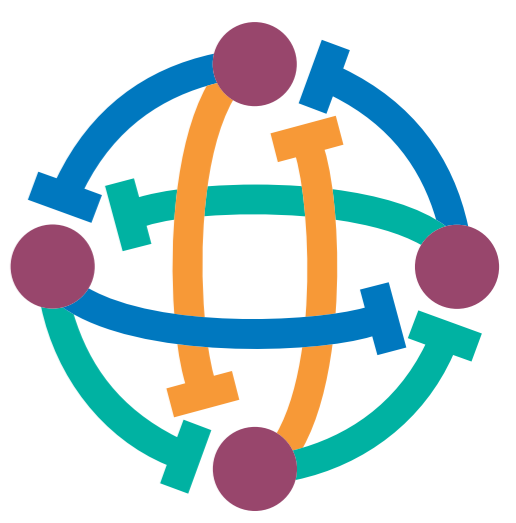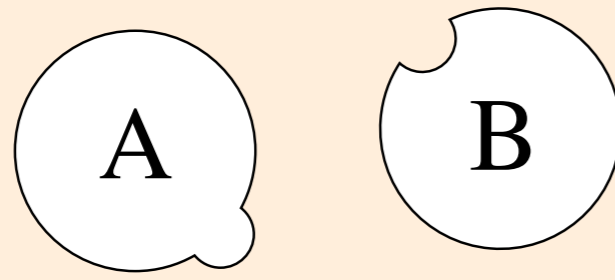# From BlenX to SBML

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Two different approaches to model biological systems

BlenX approach: the program defines the molecules present in the initial state of the system of interest:
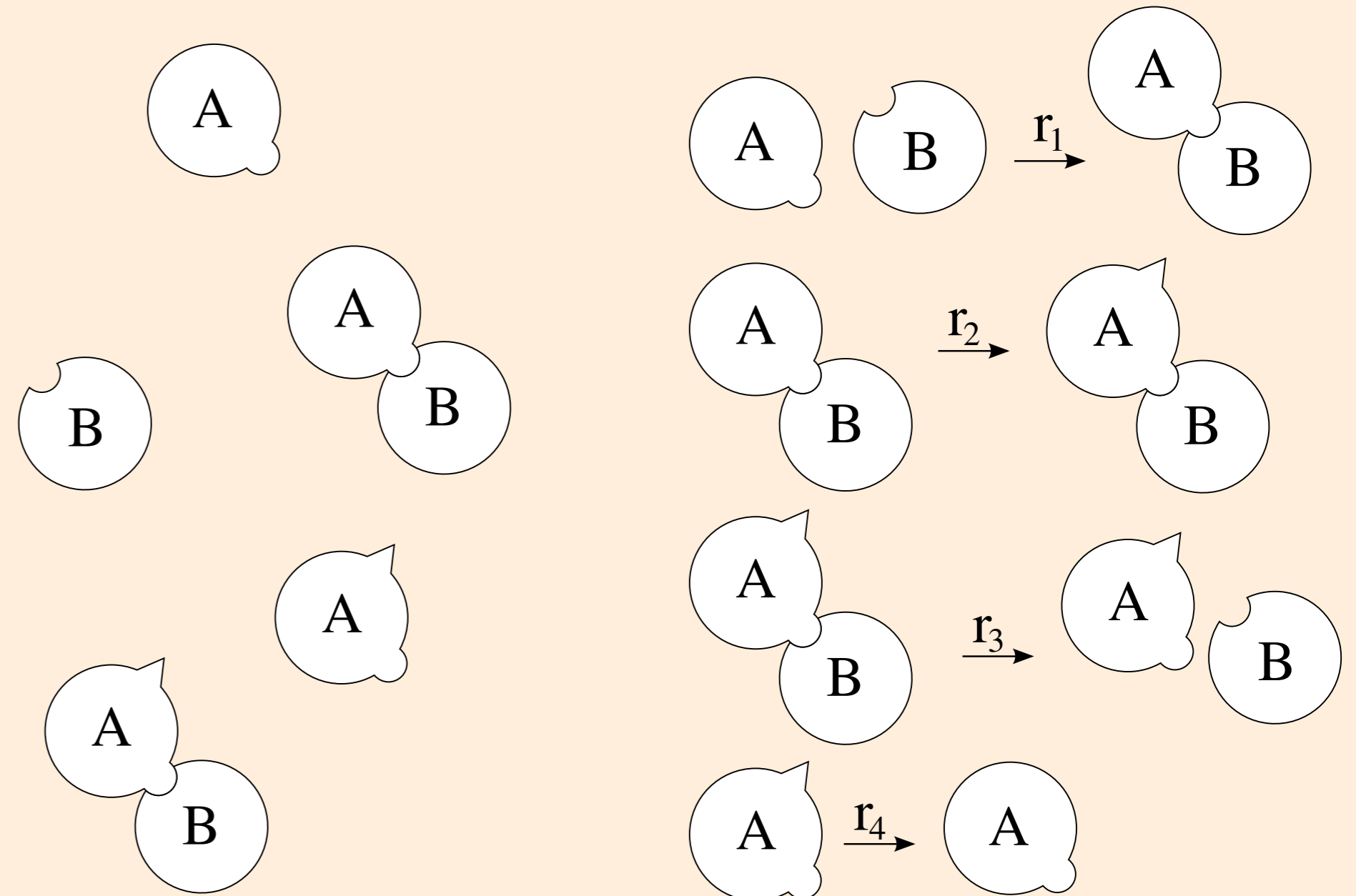
As the program runs, the molecules stochastically interact together governed by their internal processes and by their interacting capabilities giving place to reactions that create new kinds of molecules:
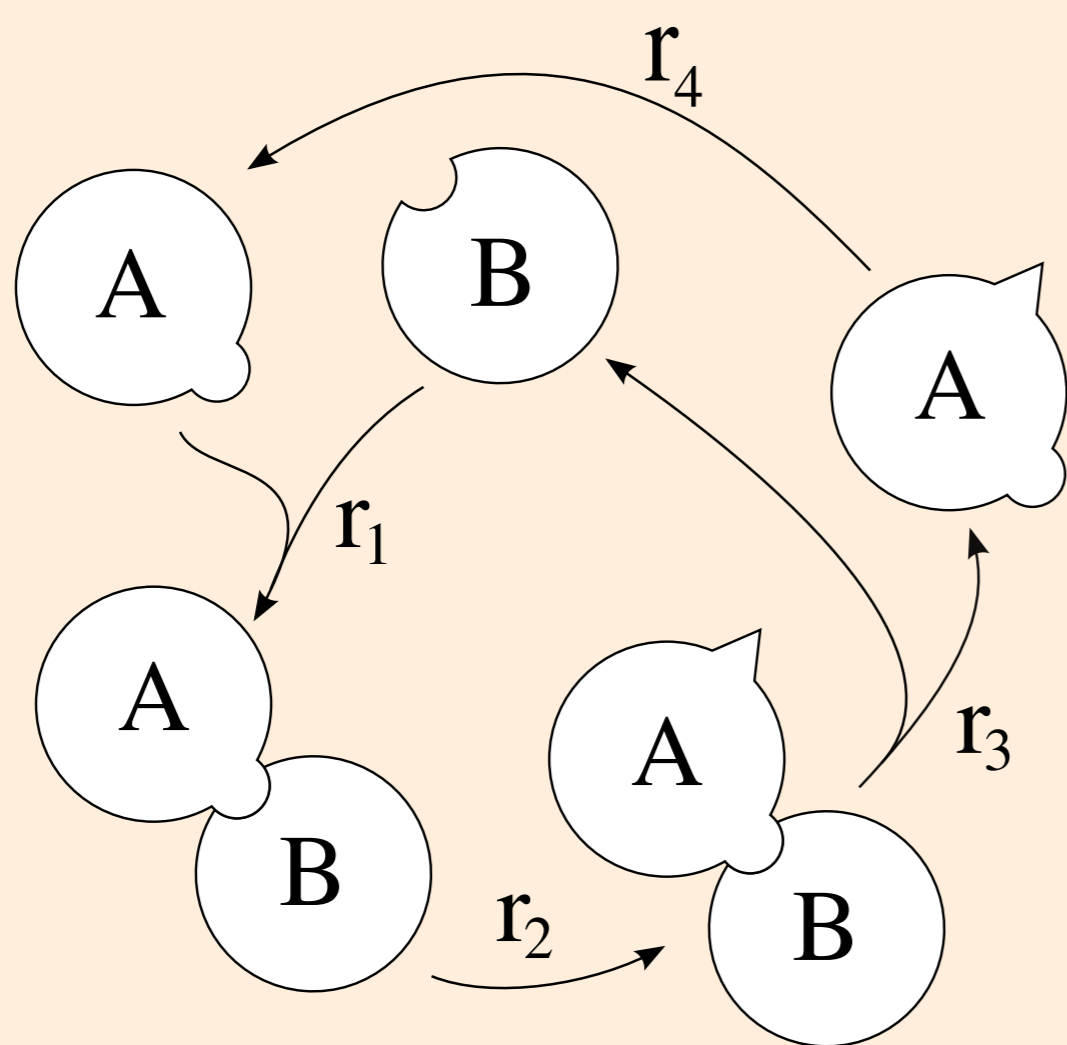
SBML approach: all the species that can appear in the system have to be defined. The same applies to the reactions that can take place:
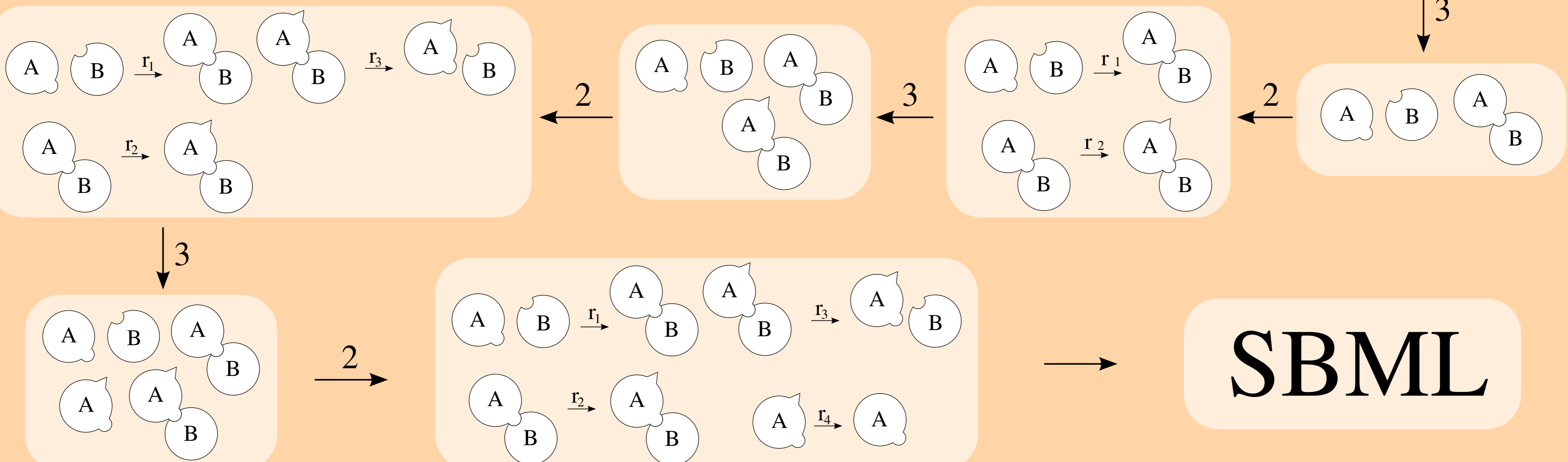
Species   Reactions

The SBML file can be read by numerous tools that perform simulation following the file specifications.

Solution to export BlenX program in SBML format

1) Read the BlenX program and find out the defined molecules

2) Make the known molecules react in order to find which reactions they can perform

3) Add molecules created by the reactions executed at the privious step to the set of the known molecules

4) If new molecules have been found at previous step go to step 2 otherwise the algorithm ends and the SBML file is created

SBML