

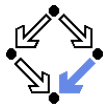
# Biological Systems as Concurrent Processes

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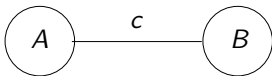
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# Modeling Systems



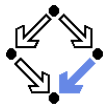
- Software/hardware systems consisting of multiple components:
  - **Concurrency:** Components execute simultaneously.
  - **Interaction:** Components may communicate with their neighbors.
  - **Mobility:** Components may move to another neighborhood.
- May be formally modelled in some calculus.
  - E.g.  $\pi$ -calculus (Milner, 1992).
- **Example:** components  $A$  and  $B$  sharing a communication channel  $c$ .



- System:  $\text{new } c (A \mid B)$ .
- Components:  $A := \bar{c}\langle a \rangle.A'$ ,  $B := c(x).B'$ .
- Interaction:  $\text{new } c (A \mid B) \rightarrow \text{new } c (A' \mid B'[a/x])$ .

The semantics of a concurrent system is defined by its formal model.

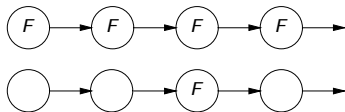
# Specifying and Verifying Systems



We may specify properties required from every possible system run.

## Temporal logic:

- $\Box F$ : “ $F$  will always hold”.
- $\Diamond F$ : “eventually  $F$  will hold”.

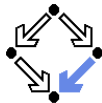


## Specification: $\Box(x > 0 \Rightarrow \Diamond x = 0)$ .

Every time  $x$  becomes greater than 0, it will become 0 again.

- **Verification:** show that every run of a system (e.g. modelled in  $\pi$ -calculus) satisfies a specification (e.g. described in temporal logic).
- **Model checking:** automatic verification a system that has only a finite number of states.

Similar techniques can be applied to biological systems.



From the BioSPI project (<http://www.wisdom.weizmann.ac.il/~biospi>):

*We employ 5 major principles in modeling biochemical processes as concurrent systems:*

- *Pathways, molecules and molecular domains as computational processes.*
- *Complementary molecular determinants as communication channels.*
- *Molecular interaction and modification as communication and change of channel names.*
- *The integrity of molecules, complexes and compartment as channels with restricted scope.*
- *The formation of complexes and translocation of molecule as extrusion of restricted channels.*

*Based on this strong correspondence between the calculus and biochemical networks, we can incrementally represent detailed information on biochemical systems in a structured, biologically faithful fashion. The resulting representations can be used in simulation, analysis and verification.*