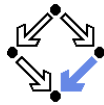


Biological Systems as Concurrent Processes

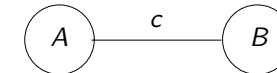
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Modeling Systems

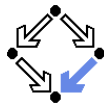
- Software/hardware systems consisting of multiple components:
 - Concurrency:** Components execute simultaneously.
 - Interaction:** Components may communicate with their neighbors.
 - Mobility:** Components may move to another neighborhood.
- May be formally modelled in some calculus.
 - E.g. π -calculus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



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

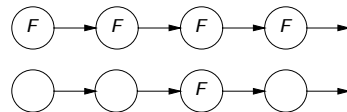
The semantics of a concurrent system is defined by its formal model.

Specifying and Verifying Systems



We may specify properties required from every possible system run.

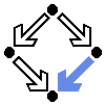
- Temporal logic:**
 - $\Box F$: “ F will always hold”.
 - $\Diamond F$: “eventually F will hold”.



- 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 π -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.

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.