An Infobiotics Workbench Conversion Tool for SBOL and SBML

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The Infobiotics Language (IBL)

① Design
② Simulation
**IBW**
④ Compilation
③ Verification

A domain specific programming language
- For synthetic biology
- Supports scalable designs through modularity
- Declarative language with Java-like syntax
- Provides declarations to
  - Design synthetic biological systems through specification
  - Define rules and rates for stochastic simulation
  - Annotate designs with verification statements
  - Annotate designs with compilation directives
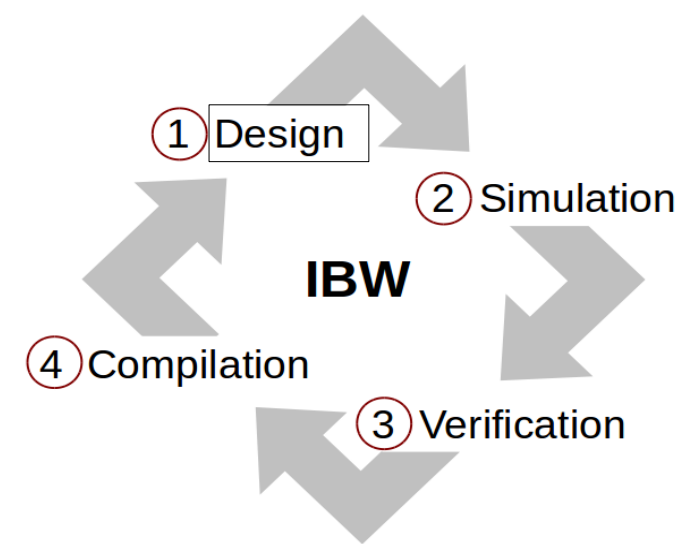
The Infobiotics Language (IBL)

Example: mRNA transcription from up-regulated promoter
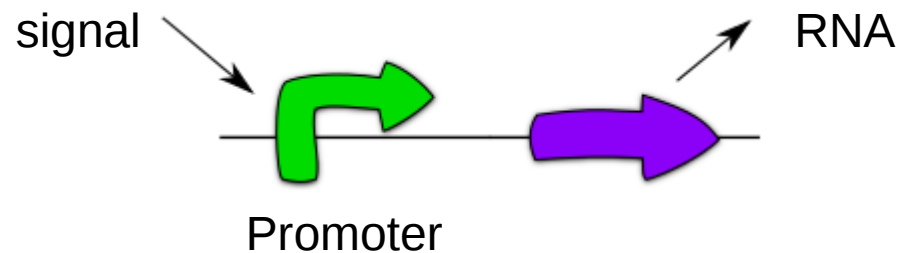
PBAD = **PROMOTER**(http://parts.igem.org/Part:BBa_I13453)
Ara   = **MOLECULE**()
rnaP   = **MOLECULE**()   parts
rna   = **RNA**()
                                                                        behavior
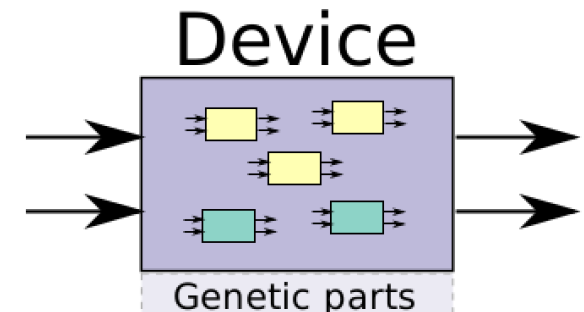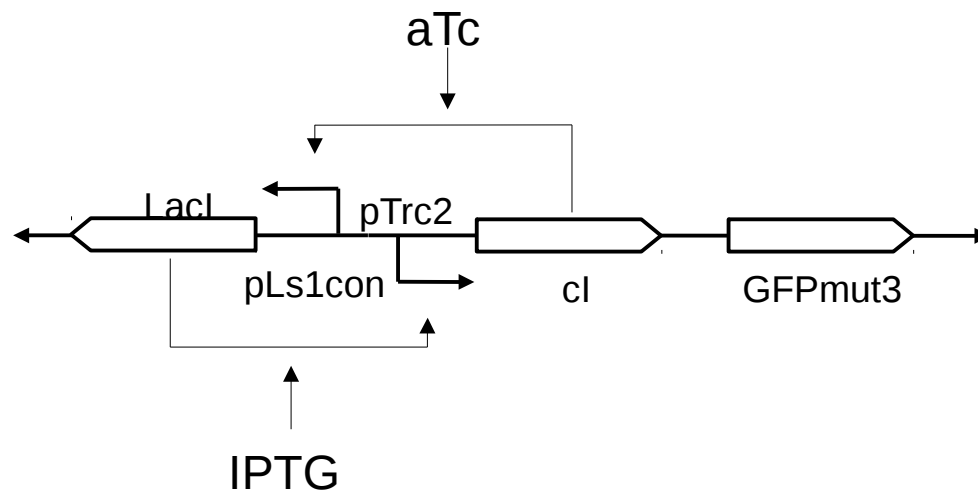**RULE** regulation: PBAD + Ara <-> PBAD~Ara
RULE transcriptionInitiation: PBAD~Ara + rnaP <-> PBAD~Ara~rnaP
RULE transcriptionStep: PBAD~Ara~rnaP -> PBAD + Ara + rnaP + rna
RULE rnaDegradation: rna ->

The Infobiotics Language (IBL)

Devices encode functional pieces of DNA:

collection of parts,
rules, and processes
that characterize the
piece of DNA

```
operon_one = DEVICE(
    parts = [pTrc2, cI, gfpmut3],
    input = [aTc], output = [CI, GFPmut3]
) {
    mrna_LacI = RNA()  // a local "variable"

    // PROCESSES and RULES here
}
```

The Infobiotics Language (IBL)

Cells introduce compartments with physical boundaries
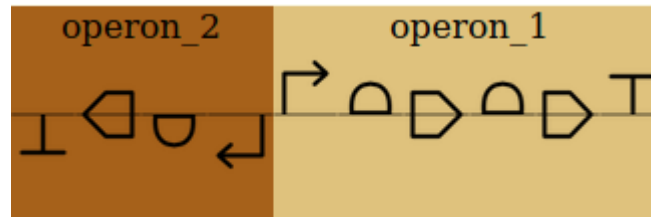
```
define Ecoli typeof CELL() {
    aTc = MOLECULE()

    RULE diffusion: aTc <-> OUTSIDE

    operon_one = DEVICE(
        parts = [pTrc2, cl, gfpmut3],
        input = [aTc], output = []
    ) {}
}
```
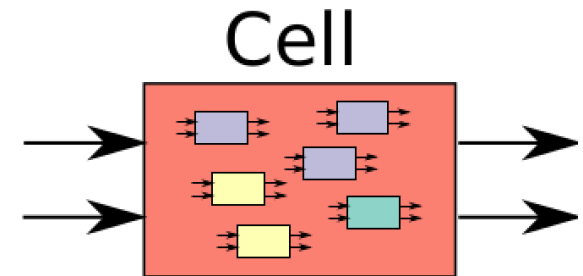

Cell

collection of devices,
parts, rules, and
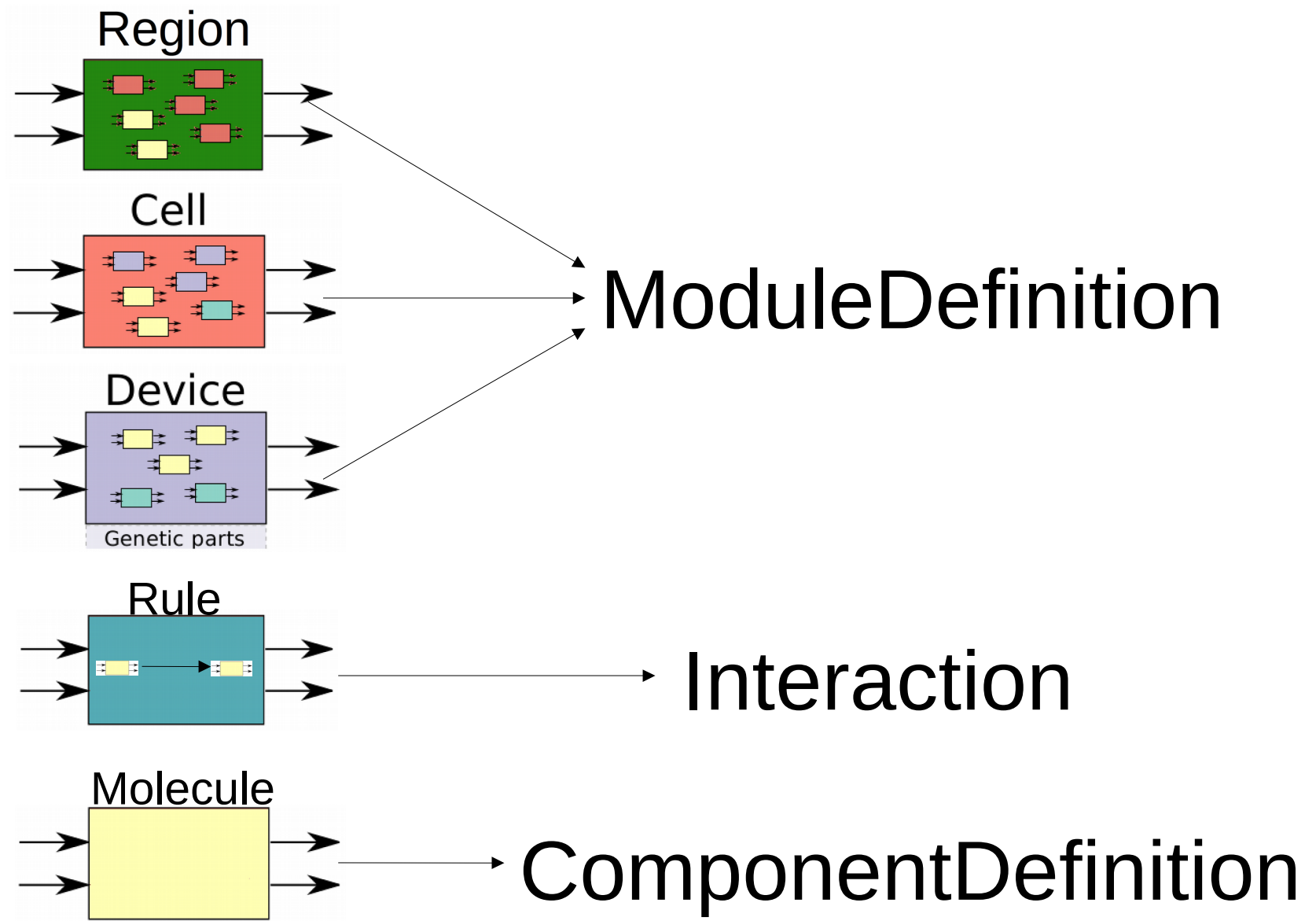processes that
characterize a cell

Biomatter Compilation

- Compilation of DNA sequences performed by the Assistant To Genetic Compilation (ATGC)
- Completes IBL designs with terminators, spacers, RBS's
- Optionally infers RBS sequences from given desired transcription rate   (Sallis RBSCalculator)
- Arranges parts according to given constraints
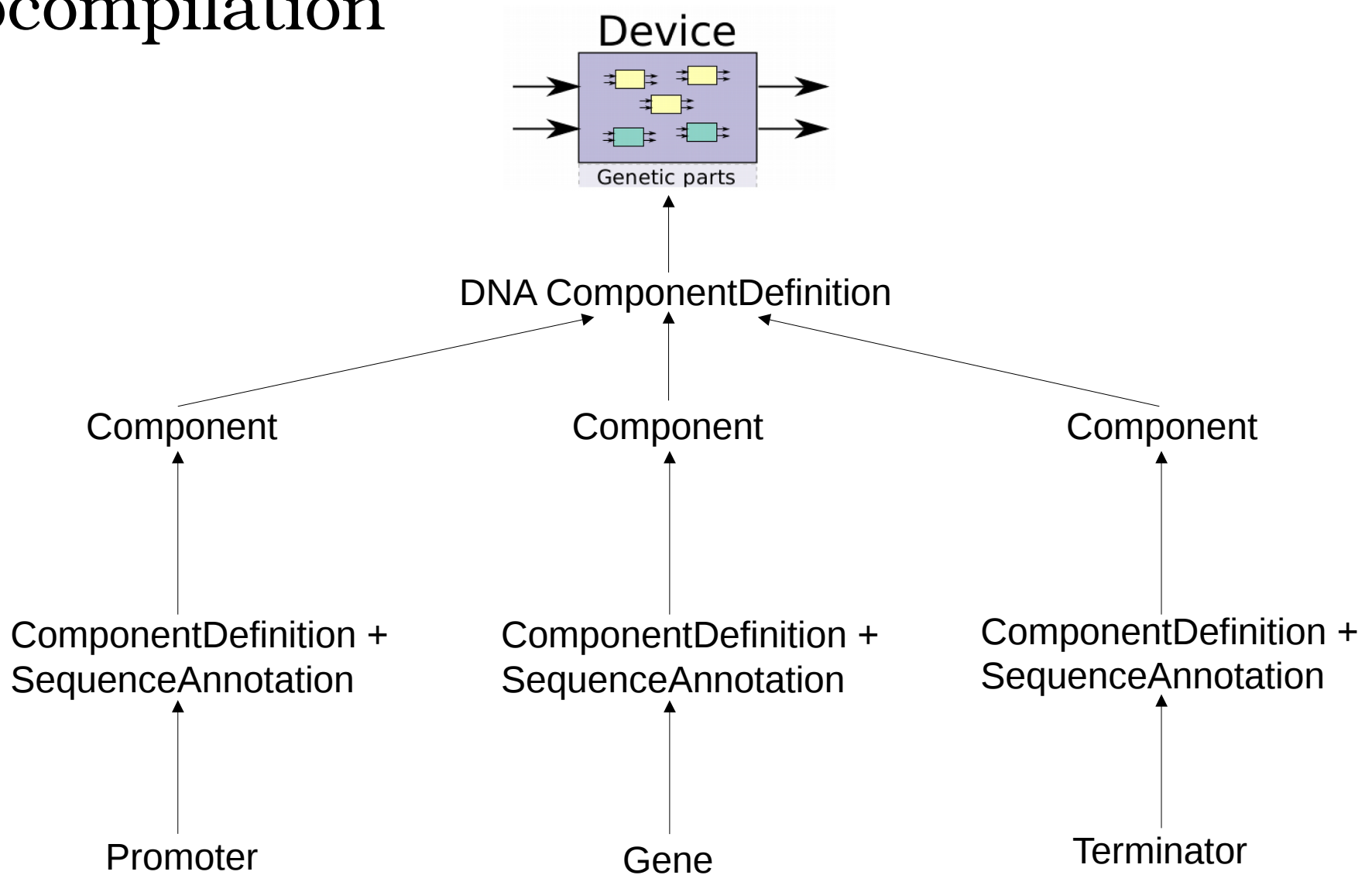- Adds cloning sites from specified library

Ladroue, C., Kalvala, S.: Constraint-based genetic compilation. In: Algorithms for Computational Biology,
LNBI, vol. 9199, pp 25-3 . Springer International, Heidelberg (2015)

# SBOL Export

SBOL – With/Without Biocompilation

Device

Genetic parts

DNA ComponentDefinition

Component

Component

Component

ComponentDefinition +
SequenceAnnotation

ComponentDefinition +
SequenceAnnotation

ComponentDefinition +
SequenceAnnotation

Promoter

Gene

Terminator

SBOL – Structural


```
define Ecoli typeof CELL() {
    aTc = MOLECULE()

    operon_one = DEVICE(
        parts = [pTrc2, cI, gfpmut3],
        input = [aTc], output = []
    ) {}
}
```

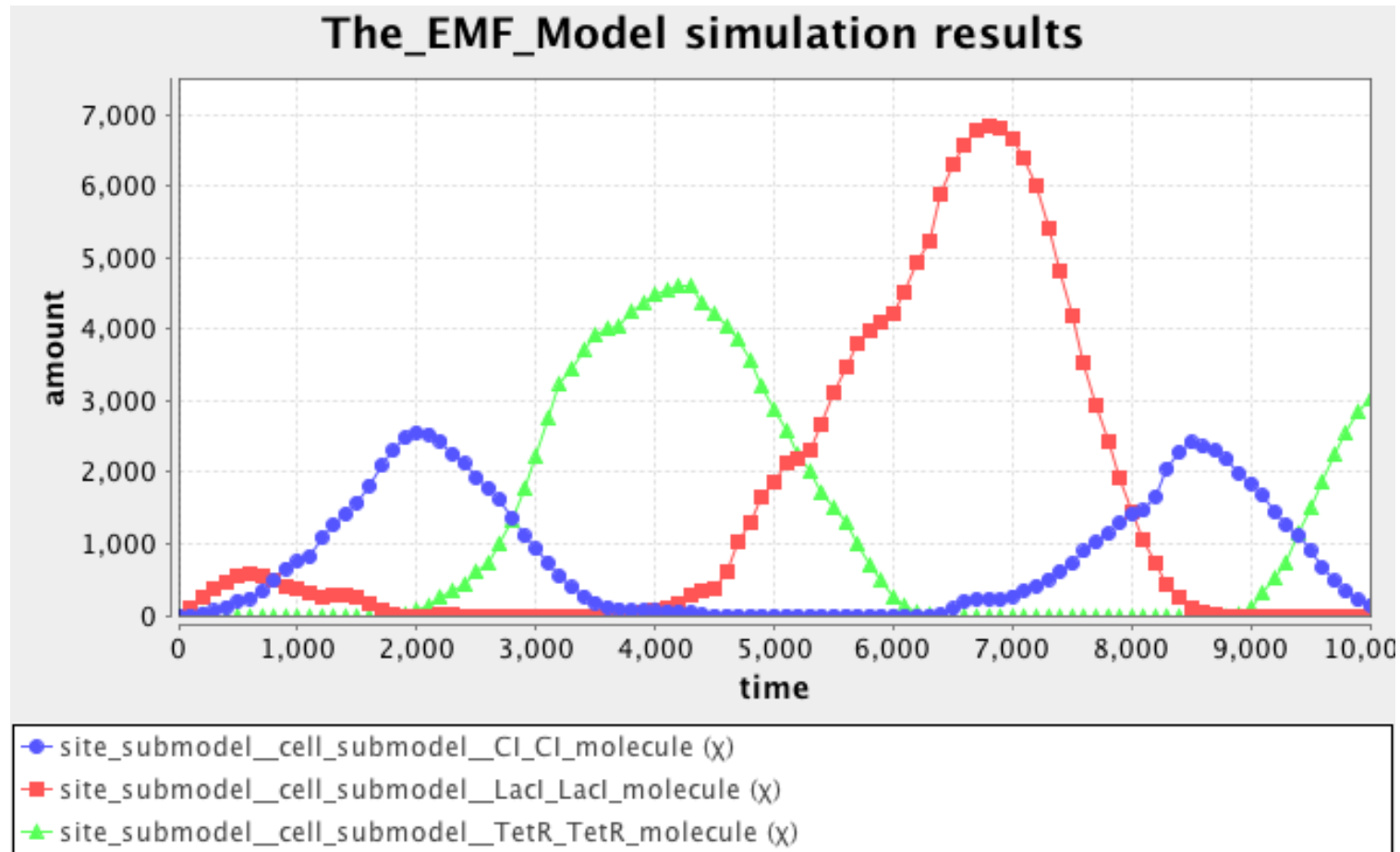# SBML Export – Flattened/Hierarchical
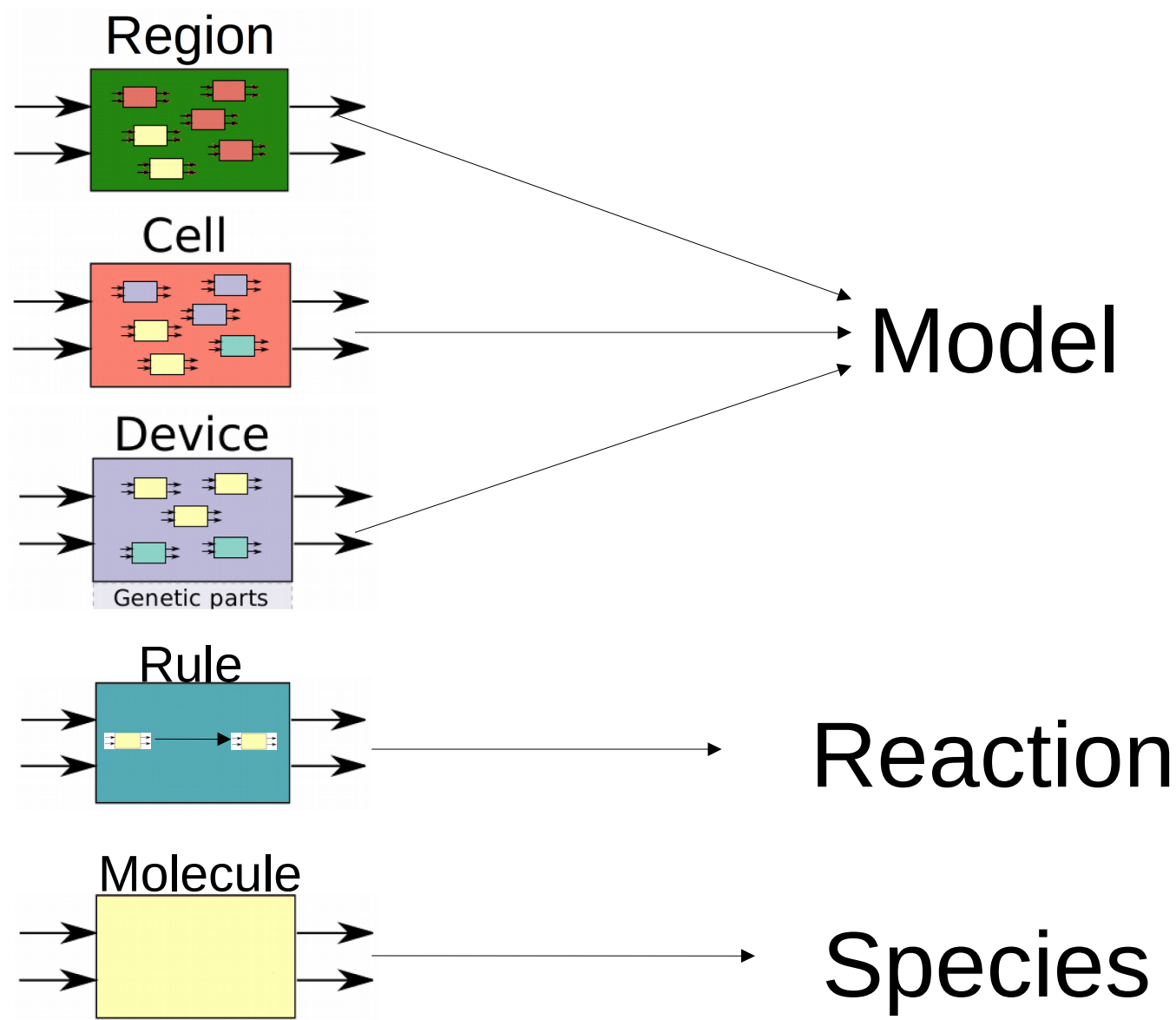
SBML – Functional

Reactions

- Rate law set through KineticLaw of Reaction
- Extent units: M, mM, uM, … -> SBML "items"
- Time unit: second

Replacements

- Cell Compartment replaces Device Compartments
- Cell Species replace Device Species
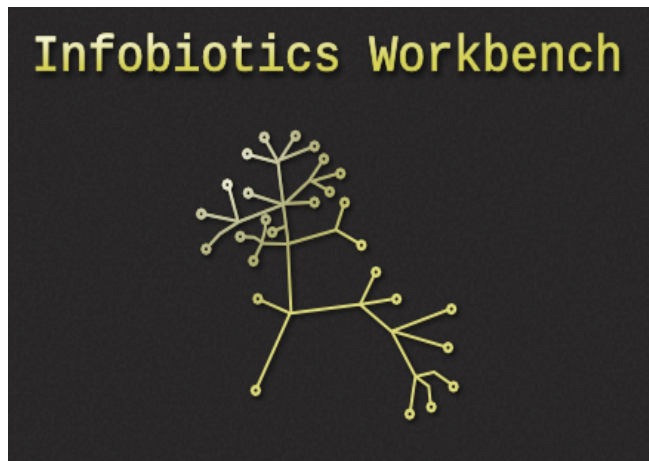
SBML – Functional

Summary

- IBW - design, simulation, and verification language
- IBL - modular language that uses Devices, Cells, and Regions
- Sequence and structure captured by SBOL
- Rates and quantities captured by SBML

The Infobiotics Workbench

http://ico2s.org/data/code/IBW-1.0.0.ova (prerelease)

Developer Team

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