

too  
✓  
SBML Level 3 brief update

**Michael Hucka**

*(On behalf of many people)*

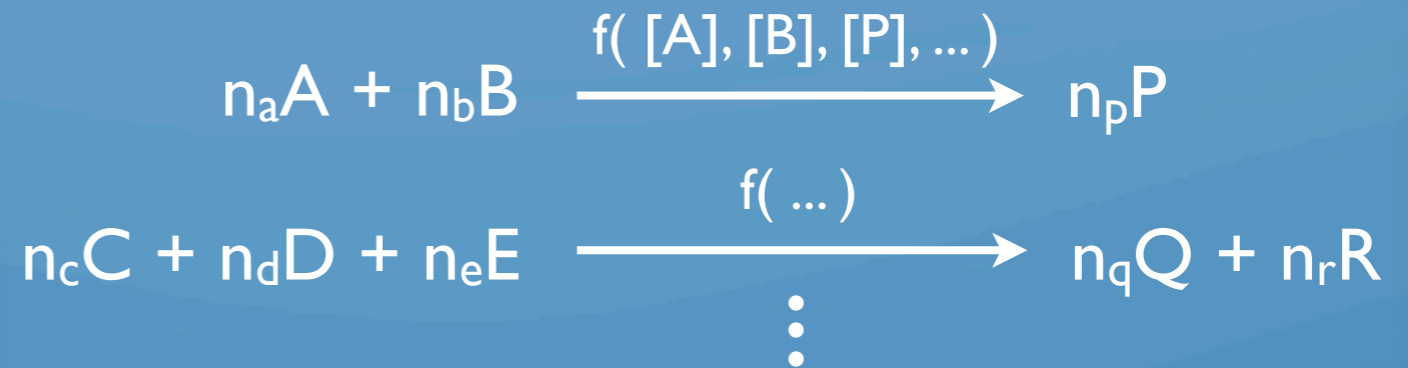
*Senior Research Fellow  
California Institute of Technology  
Pasadena, California, USA*



# SBML = Systems Biology Markup Language

- Machine-readable format for representing computational models

- Can represent processes such as (but not limited to) biochemical reactions with arbitrary rate functions



- Can include

- Compartments (i.e., where substances are located)
- Mathematical “extras” (e.g., additional assignments, ODEs, etc.)
- Discontinuous events with arbitrary triggers

- Declarative, not procedural

- Not a script for a simulation

- Not specific to a particular formalism (ODE, stochastic, ...)

# SBML is fundamentally an exchange format

- XML-based
- Lingua franca for software exchange of models
  - Not for humans to edit directly
  - Not necessarily a software system's *internal* format
  - Not suited for experimental or numerical results
- Open & free

```
<listOfSpecies>
  <species compartment="cytosol" id="ES" initia
  <species compartment="cytosol" id="P" initia
  <species compartment="cytosol" id="S" initia
  <species compartment="cytosol" id="E" initia
</listOfSpecies>
<listOfReactions>
  <reaction id="veq">
    <listOfReactants>
      <speciesReference species="E"/>
      <speciesReference species="S"/>
    </listOfReactants>
    <listOfProducts>
      <speciesReference species="ES"/>
    </listOfProducts>
    <kineticLaw>
      <math xmlns="http://www.w3.org/1998/1
        <apply>
          <times/>
          <ci>cytosol</ci>
          <apply>
            <minus/>
            <apply>
              <times/>
              <ci>kon</ci>
              <ci>E</ci>
              <ci>S</ci>
            </apply>
          </apply>
          <times/>
          <ci>koff</ci>
          <ci>ES</ci>
        </math>
      </kineticLaw>
    </reaction>
  </listOfReactions>
```

# Some basics of SBML model encoding

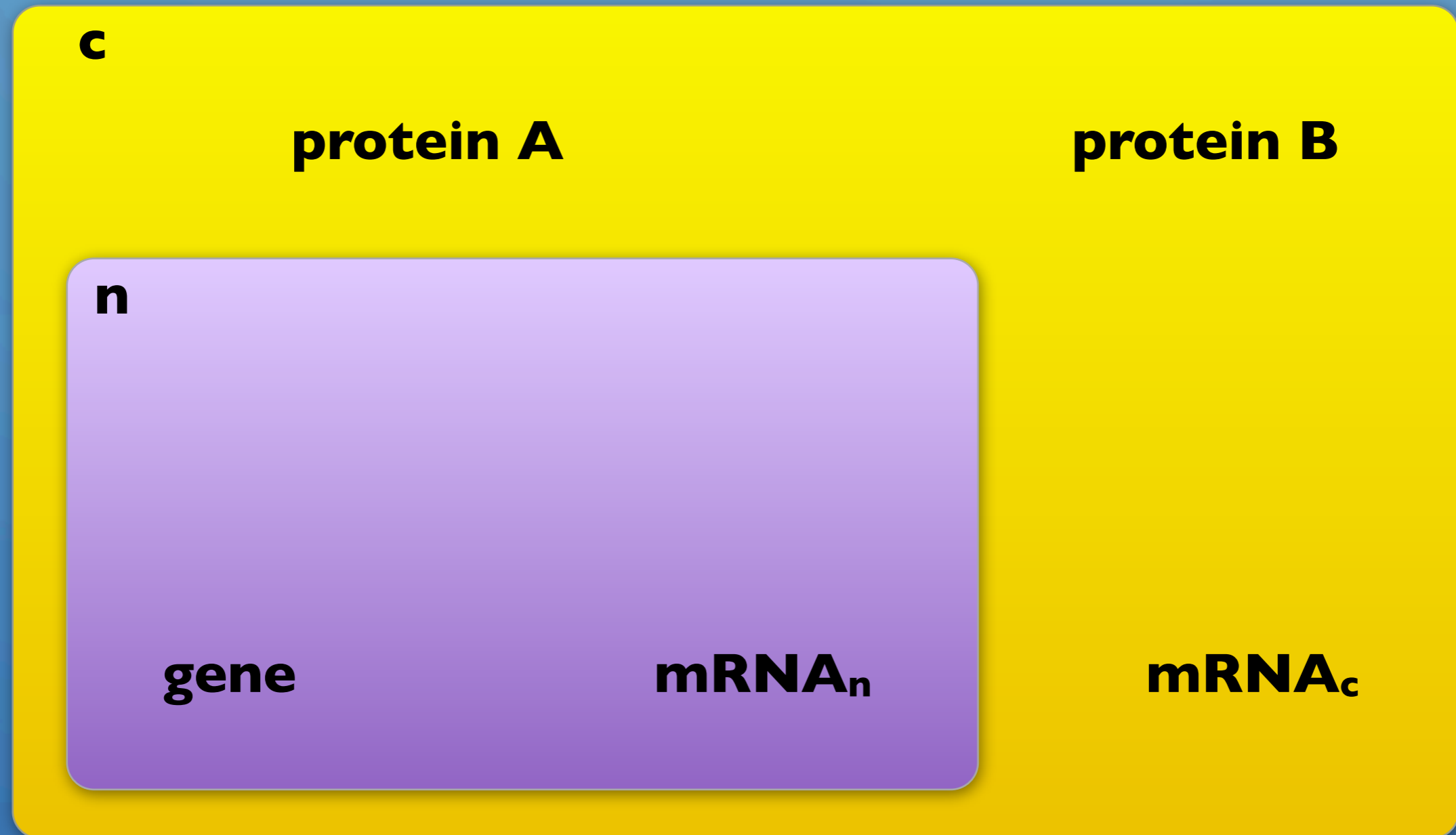
- Well-stirred compartments

**c**

**n**

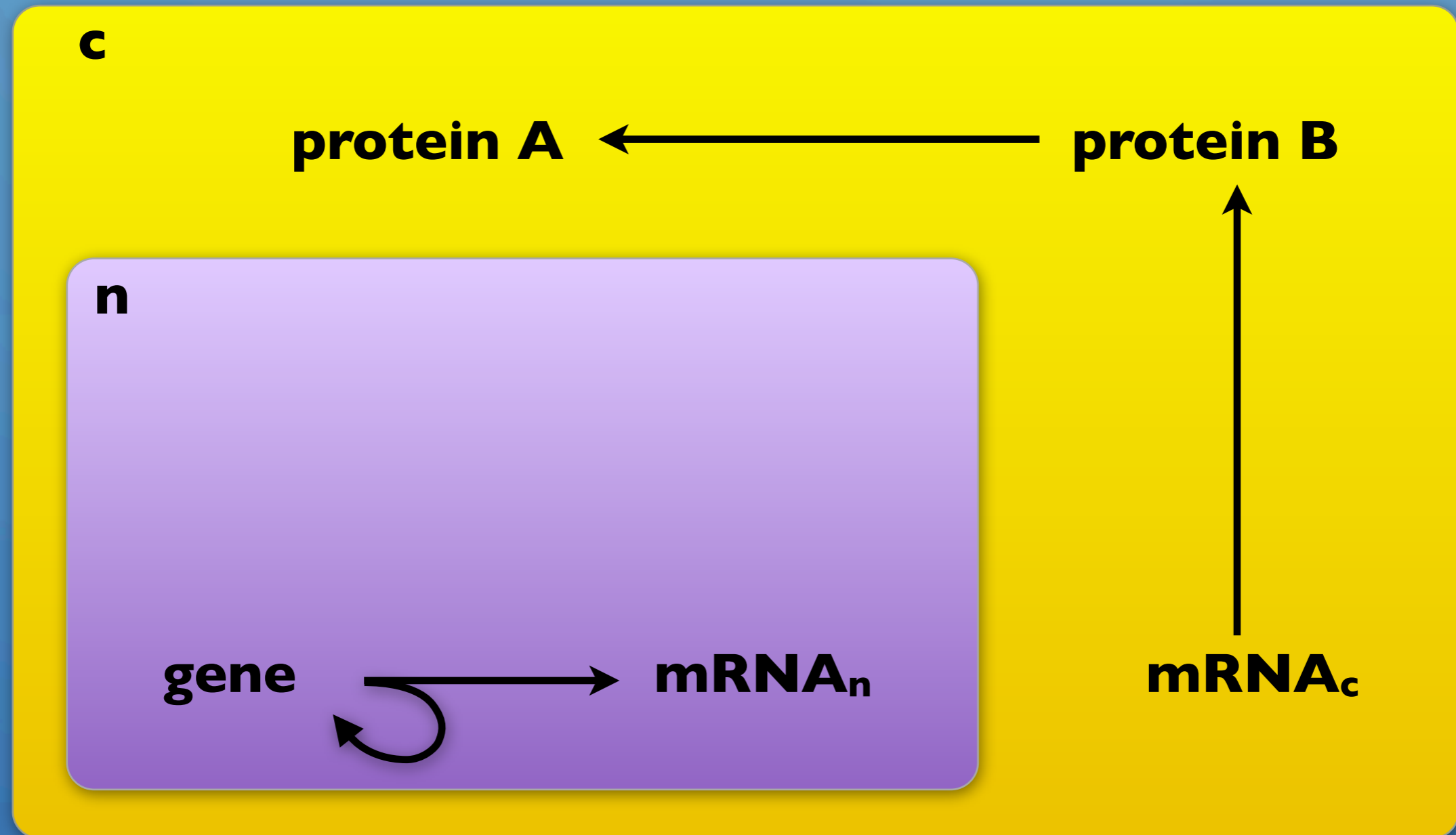
# Some basics of SBML model encoding

- Species pools are located in compartments



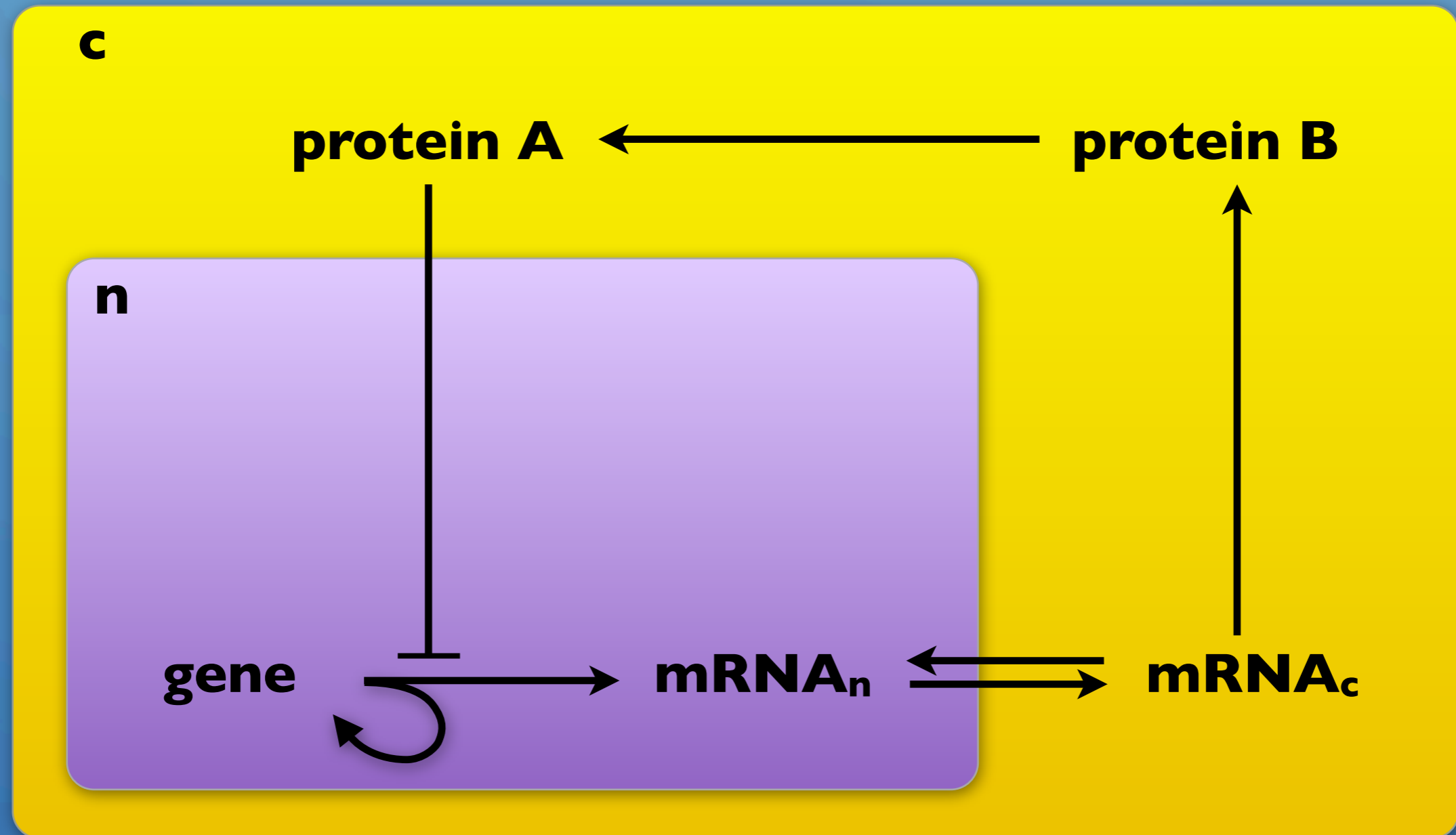
# Some basics of SBML model encoding

- Reactions can involve any species anywhere



# Some basics of SBML model encoding

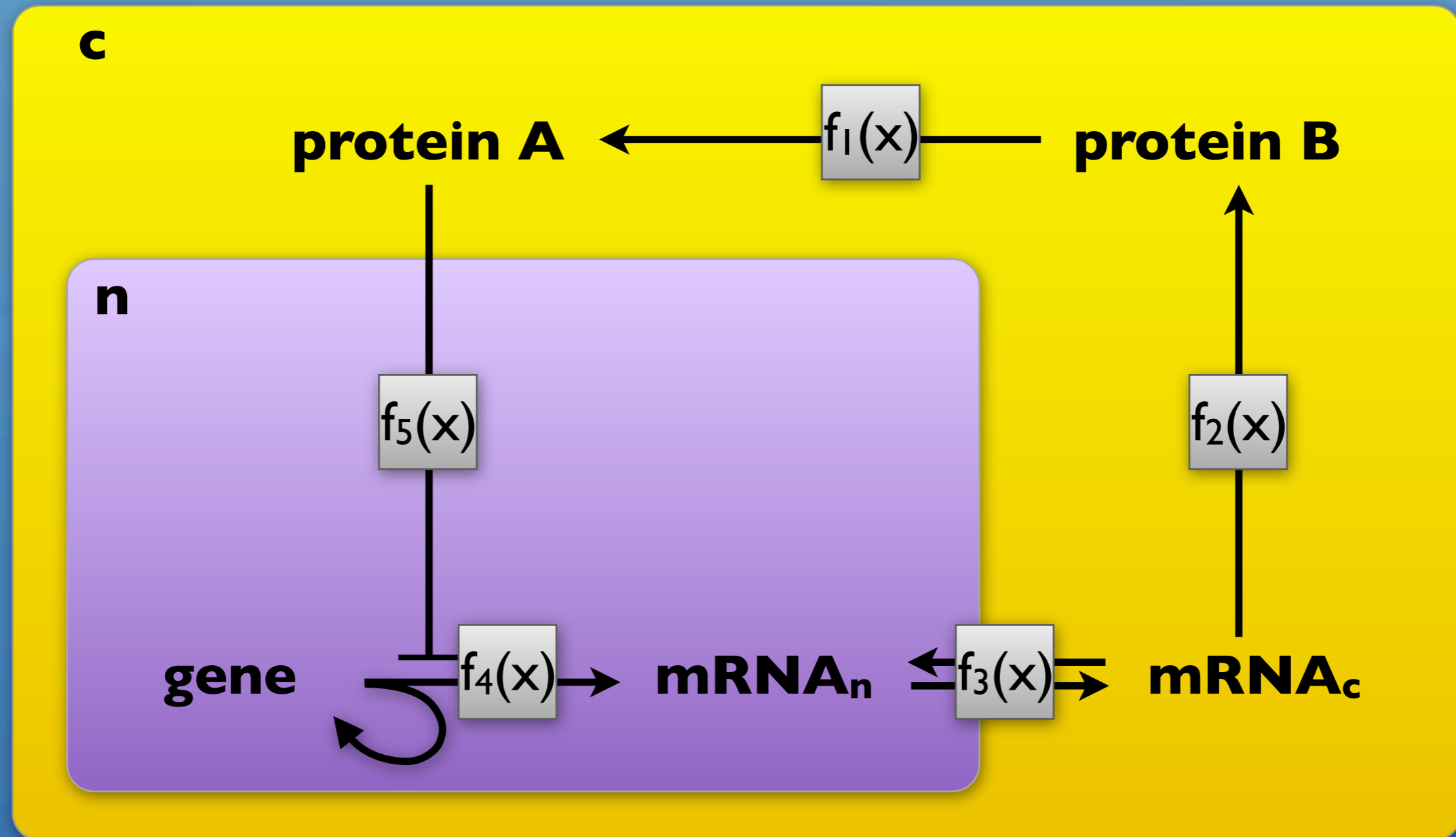
- Reactions can cross compartment boundaries





# Some basics of SBML model encoding

- Reaction/process rates can be (almost) arbitrary formulas



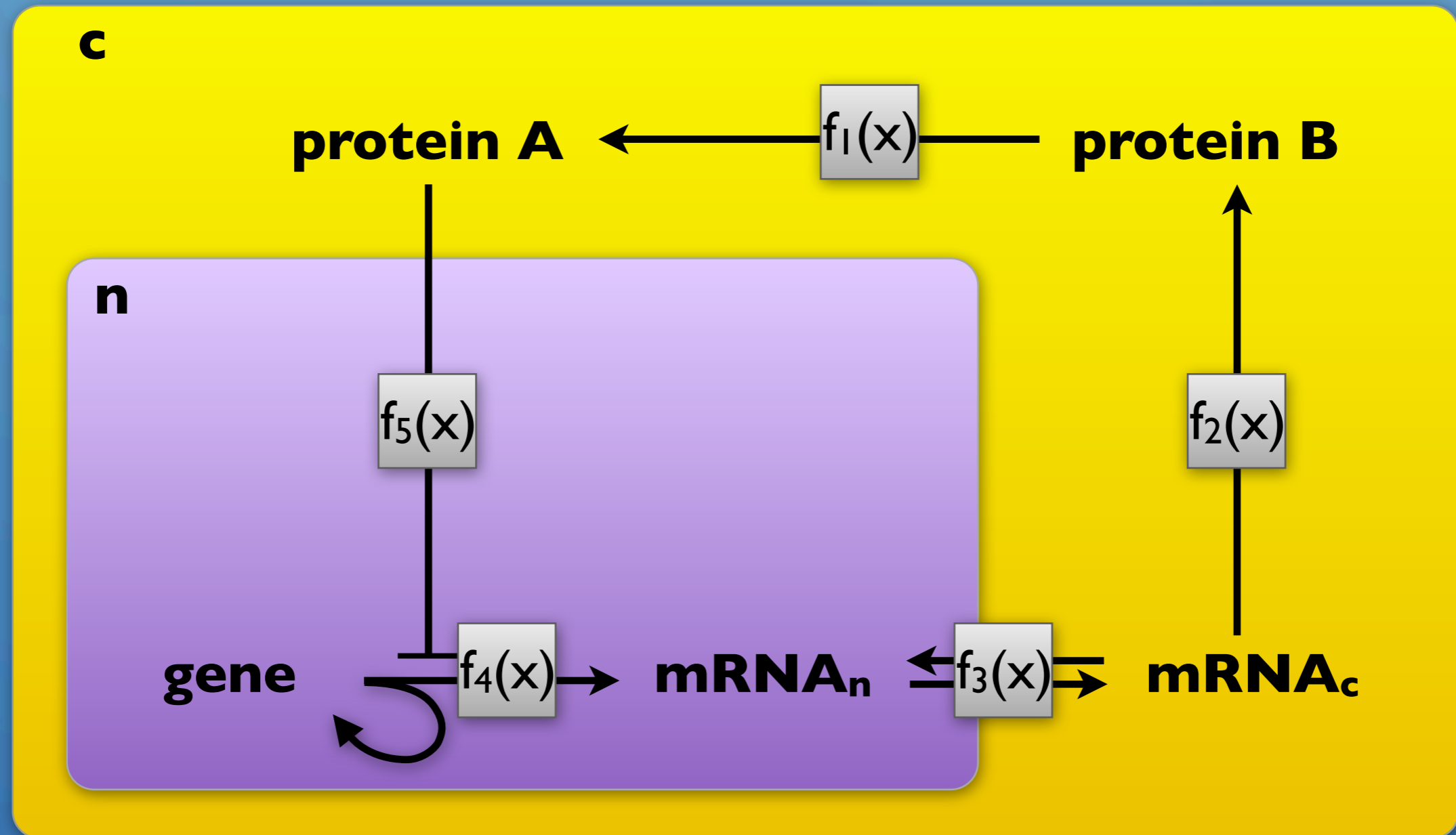


# Some basics of SBML model encoding

- “Rules”: equations expressing relationships in addition to reaction sys.

$g_1(x)$   
 $g_2(x)$

•  
•  
•

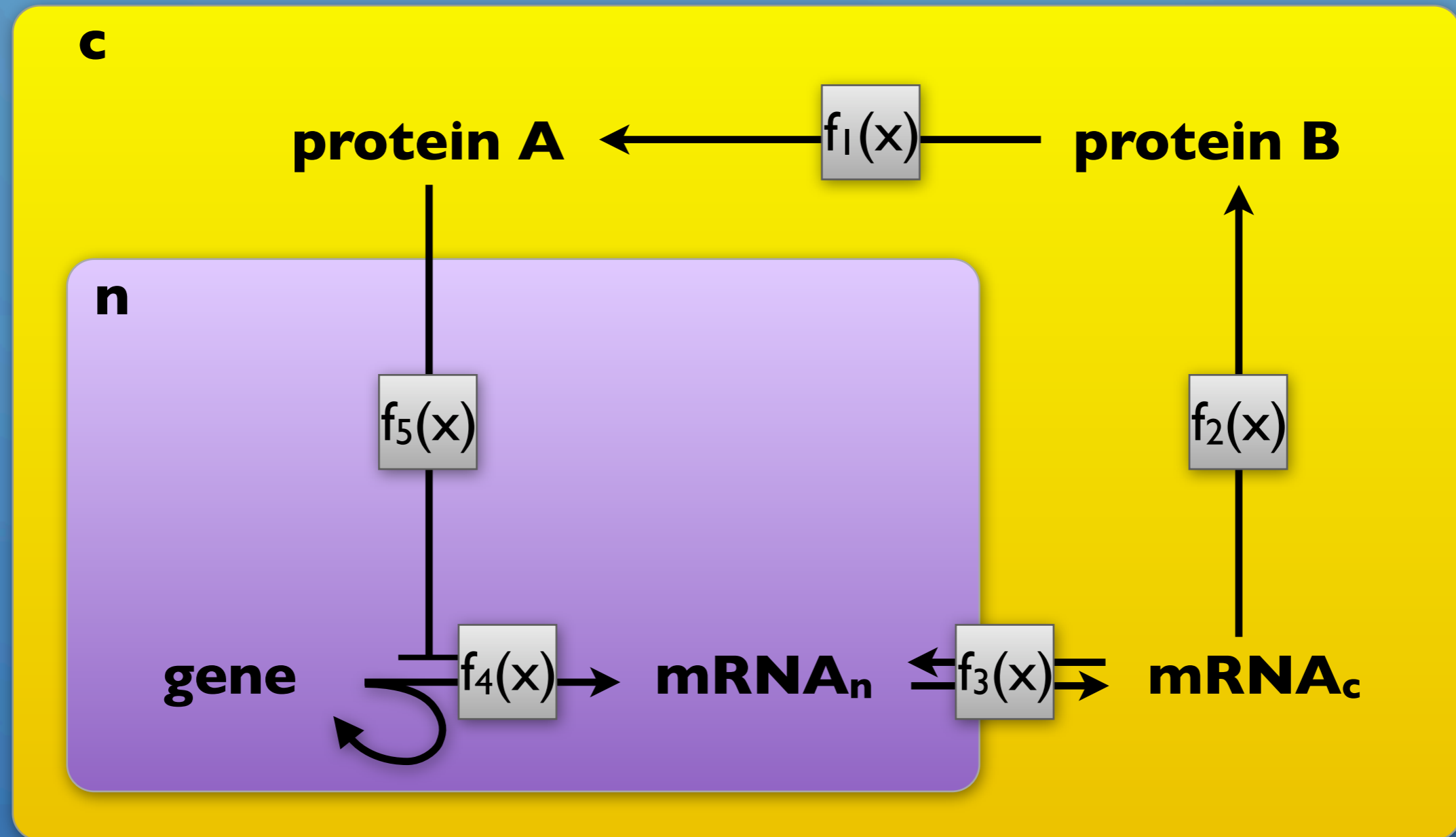


# Some basics of SBML model encoding

- “Events”: discontinuous actions triggered by system conditions

$g_1(x)$   
 $g_2(x)$

•  
•  
•



Event<sub>1</sub>: when (...condition...), do (...assignments...)  
Event<sub>2</sub>: when (...condition...), do (...assignments...)  
...

# Some basics of SBML model encoding

“This is identified by GO id # ...”

“This is an enzymatic reaction with EC # ...”

$g_2(x)$

**protein A**

$f_1(x)$

**protein B**

“This is a transport into the nucleus ...”

“This compartment represents the nucleus ...”

$f_5(x)$

$f_2(x)$

**gene**

$f_4(x)$

**mRNA<sub>n</sub>**

$f_3(x)$

**mRNA<sub>c</sub>**

“This event represents ...”

Event<sub>1</sub>: when (...condition...), do (...assignments...), Event<sub>2</sub>: when (...condition...), do (...assignments...), ...

# What are SBML “Levels”?

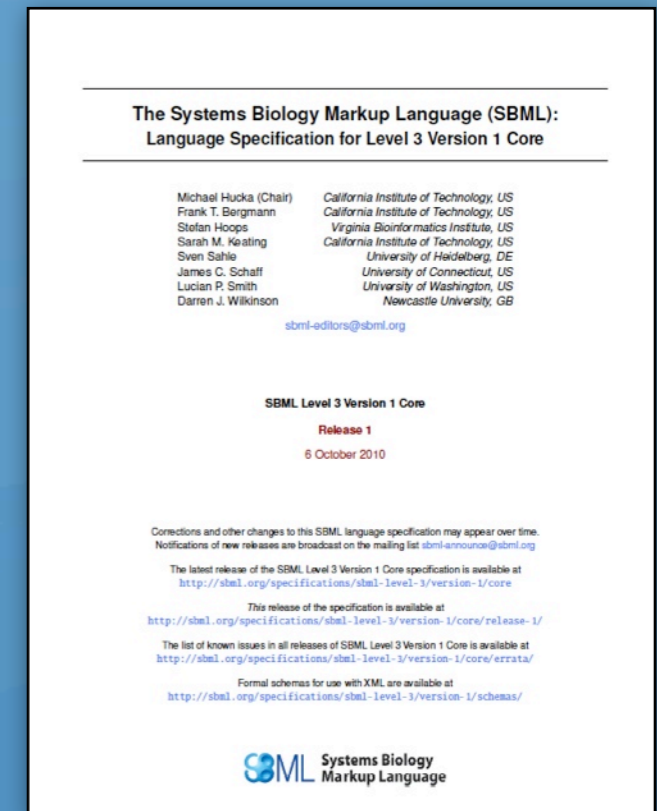
◎ Specification document available from  
<http://sbml.org/Documents>

◎ Newest: **Level 3 Version 1 Core**

◎ Oct. 2010

◎ About SBML “Levels”:

- Levels help manage significant restructuring of SBML architecture
- Levels coexist
  - E.g., Level 2 models will remain valid and exist for a long time
- A Level is *not* solely a vertical change (i.e., more features)—there is horizontal change too (i.e., changes to existing elements)



# Evolution of features took time & practical experience

Level 1	Level 2	Level 3
predefined math functions	user-defined functions	user-defined functions
text-string math notation	MathML subset	MathML subset
reserved namespaces for annotations	no reserved namespaces for annotations	no reserved namespaces for annotations
no controlled annotation scheme	RDF-based controlled annotation scheme	RDF-based controlled annotation scheme
no discrete events	discrete events	discrete events
default values defined	default values defined	no default values
monolithic	monolithic	modular

# SBML Level 3

- ◎ *SBML Level 3* is modular:
  - “Core” defines common aspects
  - “Packages” add optional features
    - Models declare which packages they use
    - Tools can tell their users which packages they support





# SBML Level 3 packages in development

Package	Specification status
Graph layout	Finalized & updated for L3; needs review
Graph rendering	Finalized & updated for L3; needs review
Multi* species	Finalized & updated for L3; needs review
Hierarchical composition	New L3 specification now under discussion
Qualitative models	Draft specification proposed
Groups	Draft specification proposed
Steady-state models	Draft specification proposed
Spatial geometry	Draft specification proposed
Annotations	Specification in development
Distribution & ranges	Past spec. proposed; needs update for final L3
Arrays & sets	Past spec. proposed; needs significant update
Spatial diffusion	No specification yet
Dynamic structures	No specification yet



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