

Software for SBML Today

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SBML = Systems Biology Markup Language

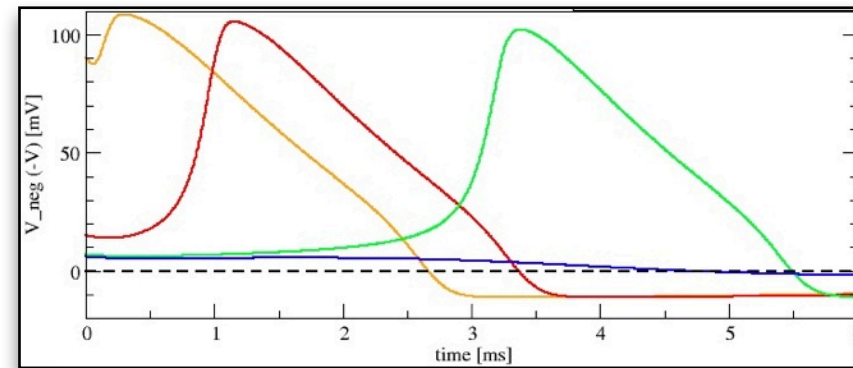
Format for **representing** computational models of biological processes

- Data structures + usage principles + serialization to XML

Neutral with respect to modeling framework

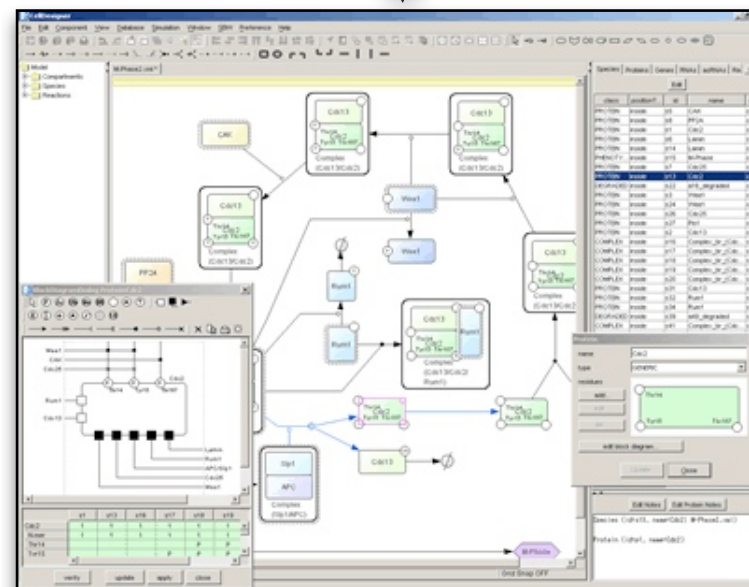
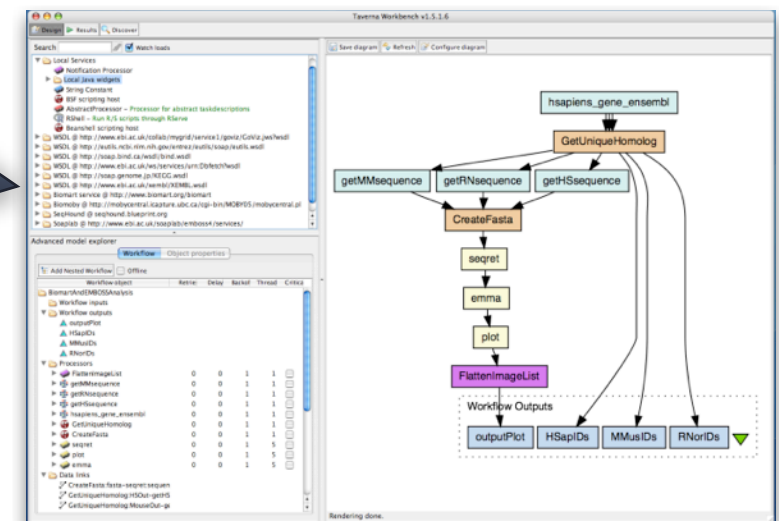
- E.g., ODE, stochastic systems, etc.

SBML is a lingua franca for software (not humans)



COPASI (4.0 Build 8)

Name	Equation
1 HXT	$GLC_0 = GLC_1$
2 HK	$GLC_1 + ATP = G6P + ADP$
3 PGI	$G6P = F6P$
4 PFK	$F6P + ATP \rightarrow F16bP + ADP; AMP F26$
5 ALD	$F16bP = DHAP + GAP$
6 TPI	$DHAP = GAP$
7 GAPDH	$GAP + NAD = BPG + NADH$
8 PGK	$BPG + ADP = P3G + ATP$
9 PGM	$P3G = P2G$
10 ENO	$P2G = PEP$
11 PYK	$PEP + ADP = PYR + ATP$
12 PDC	$PYR \rightarrow AcAld + CO_2$
13 ADH	$EtOH + NAD = AcAld + NADH$
14 ATPase	$ATP \rightarrow ADP$
15 AK	$2 * ADP = ATP + AMP$
16 G3PDH	$DHAP + NADH \rightarrow Glycerol + NAD$
17 Glycogen Branch	$G6P + ATP \rightarrow ADP + Glycogen$
18 Trehalose Branch	$2 * G6P + ATP \rightarrow ADP + Trehalose$
19 Succinate Branch	$2 * AcAld + 3 * NAD \rightarrow Succinate +$
20	



The **process** is central

- Called a “reaction” in SBML
- Participants are pools of entities (**species**)

Models can further include:

- Other constants & variables
- Compartments
- Explicit math
- Discontinuous events
- Unit definitions
- Annotations

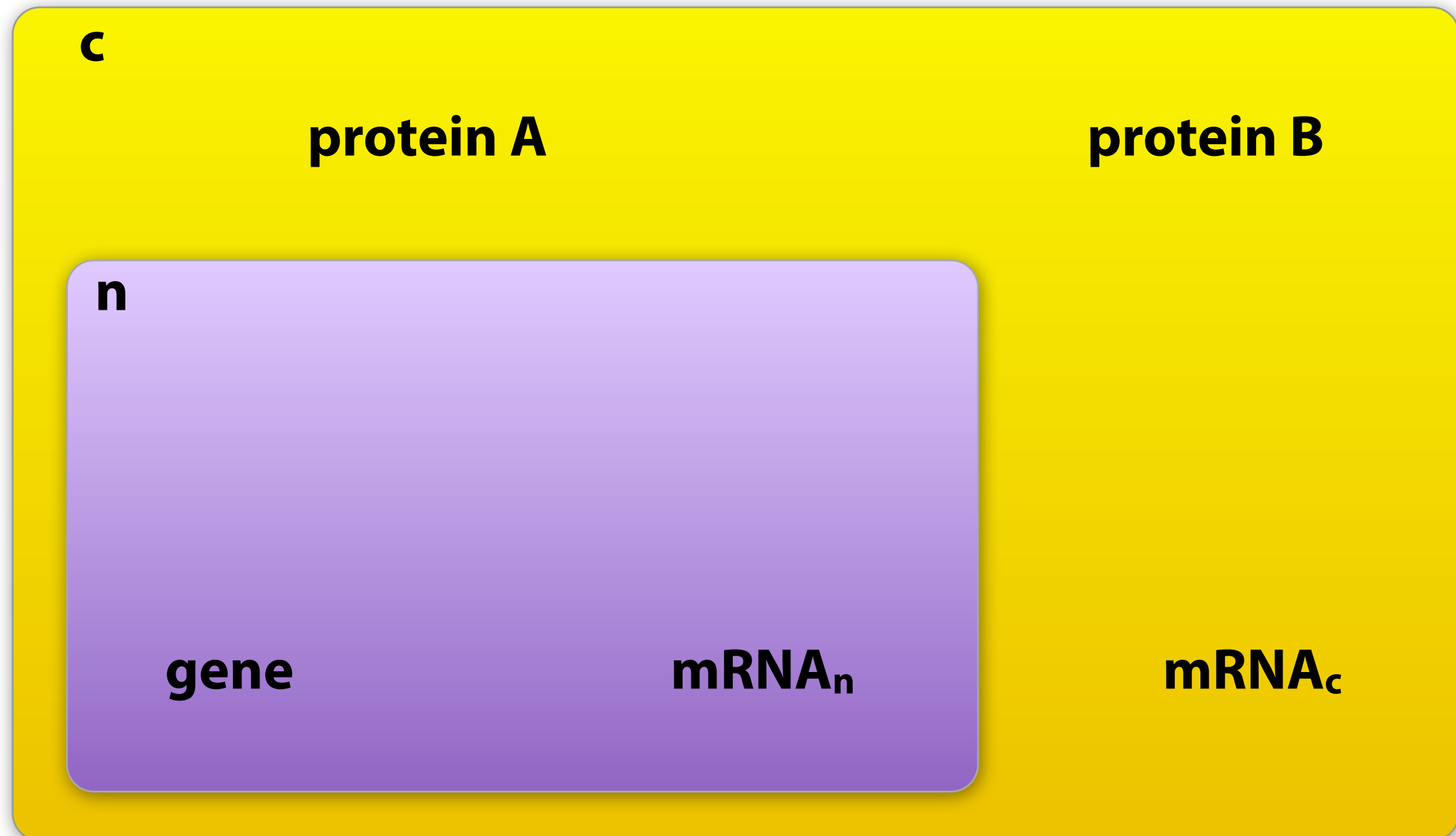
Basic SBML concepts are fairly simple

Some basics of SBML core model encoding

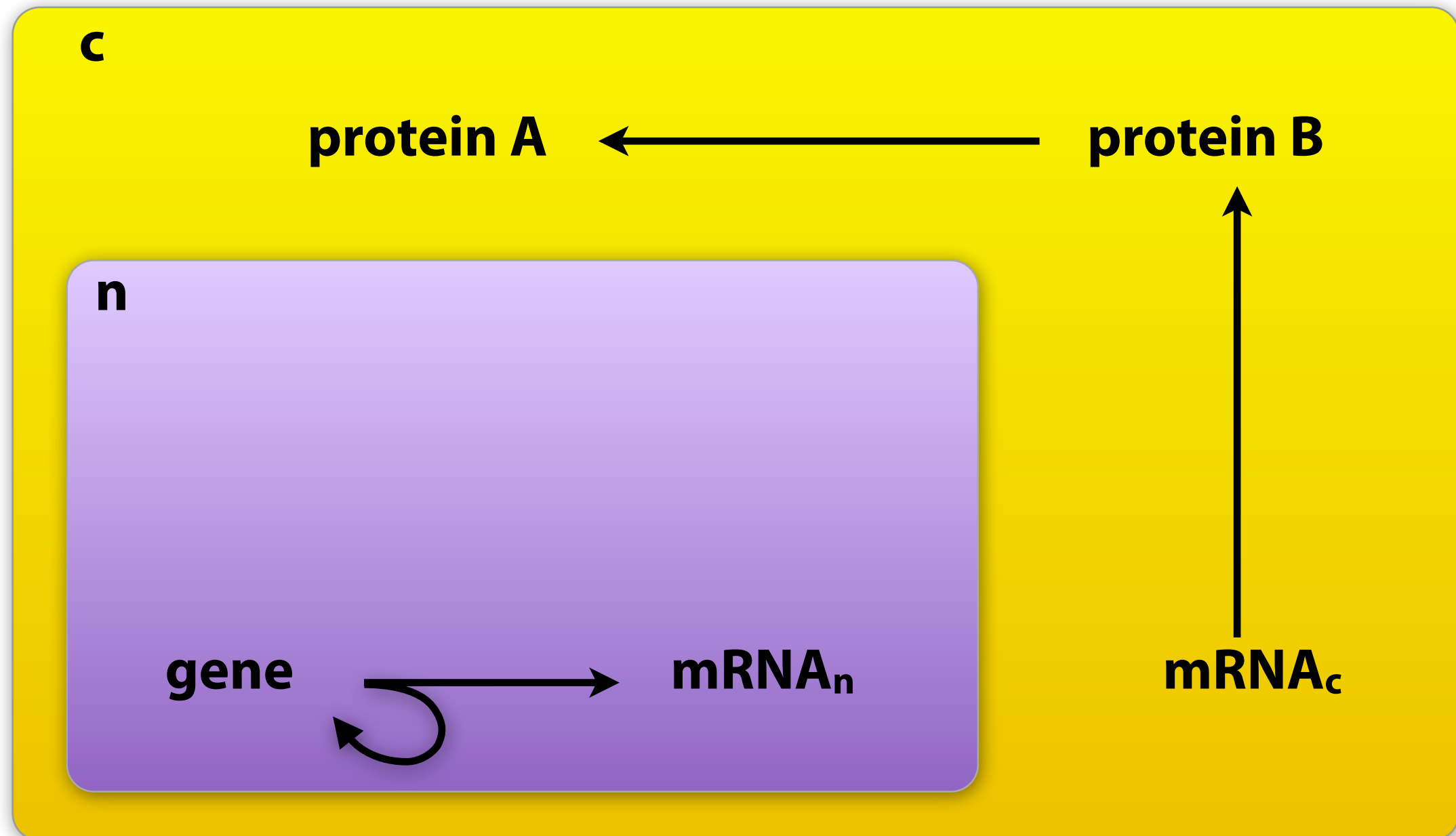
Well-stirred compartments



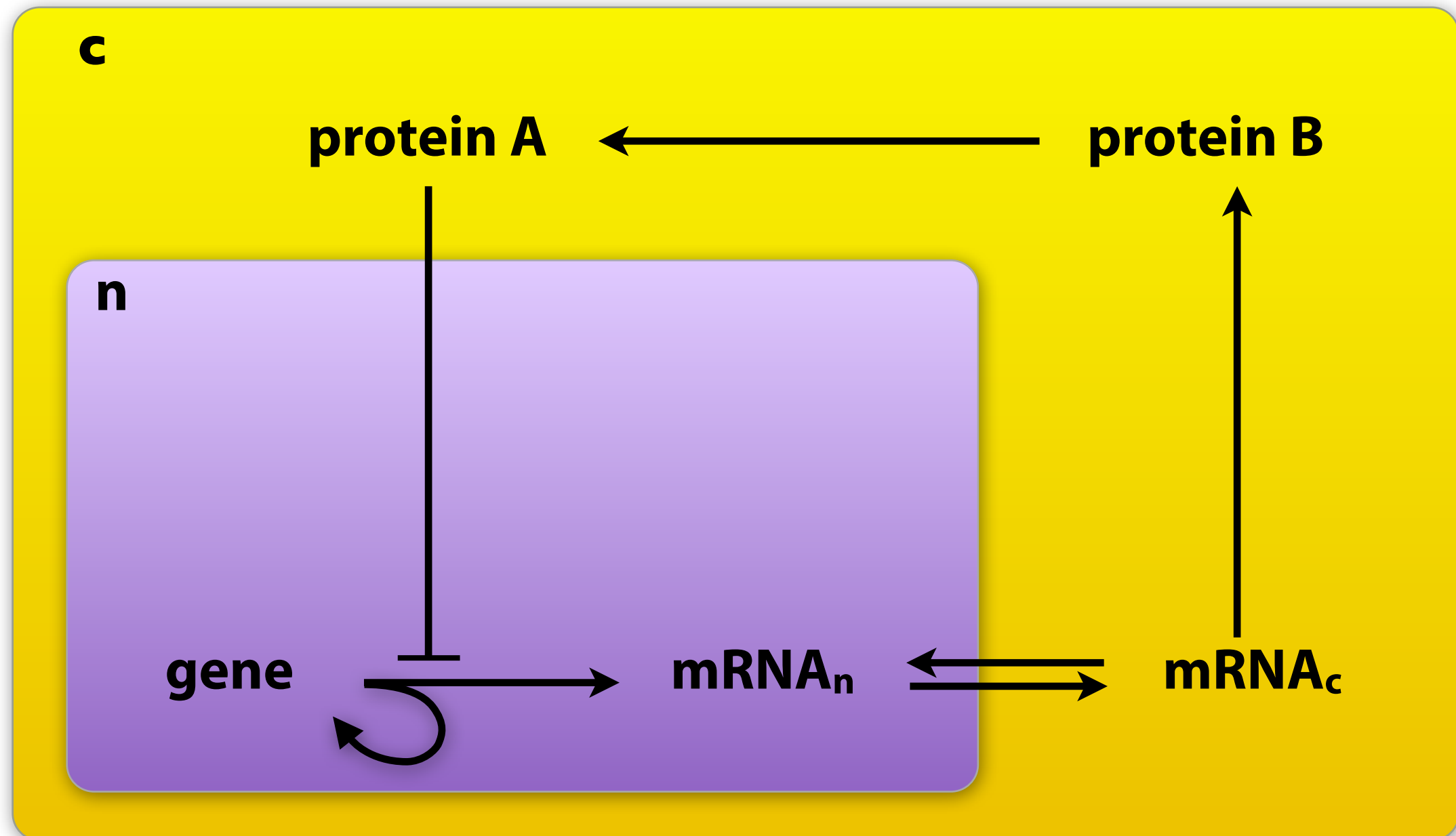
Species pools are located in compartments



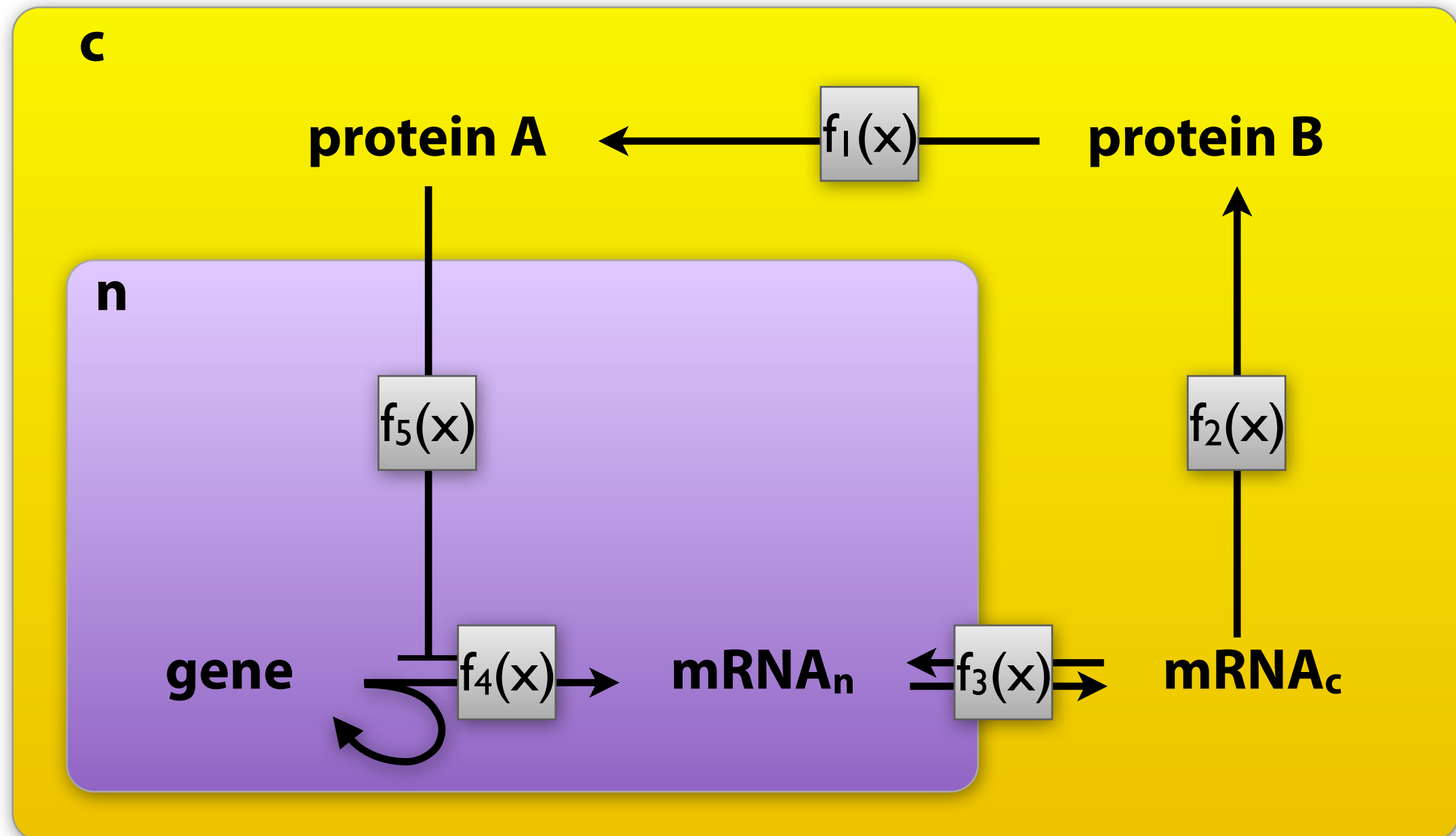
Reactions can involve any species anywhere



Reactions can cross compartment boundaries



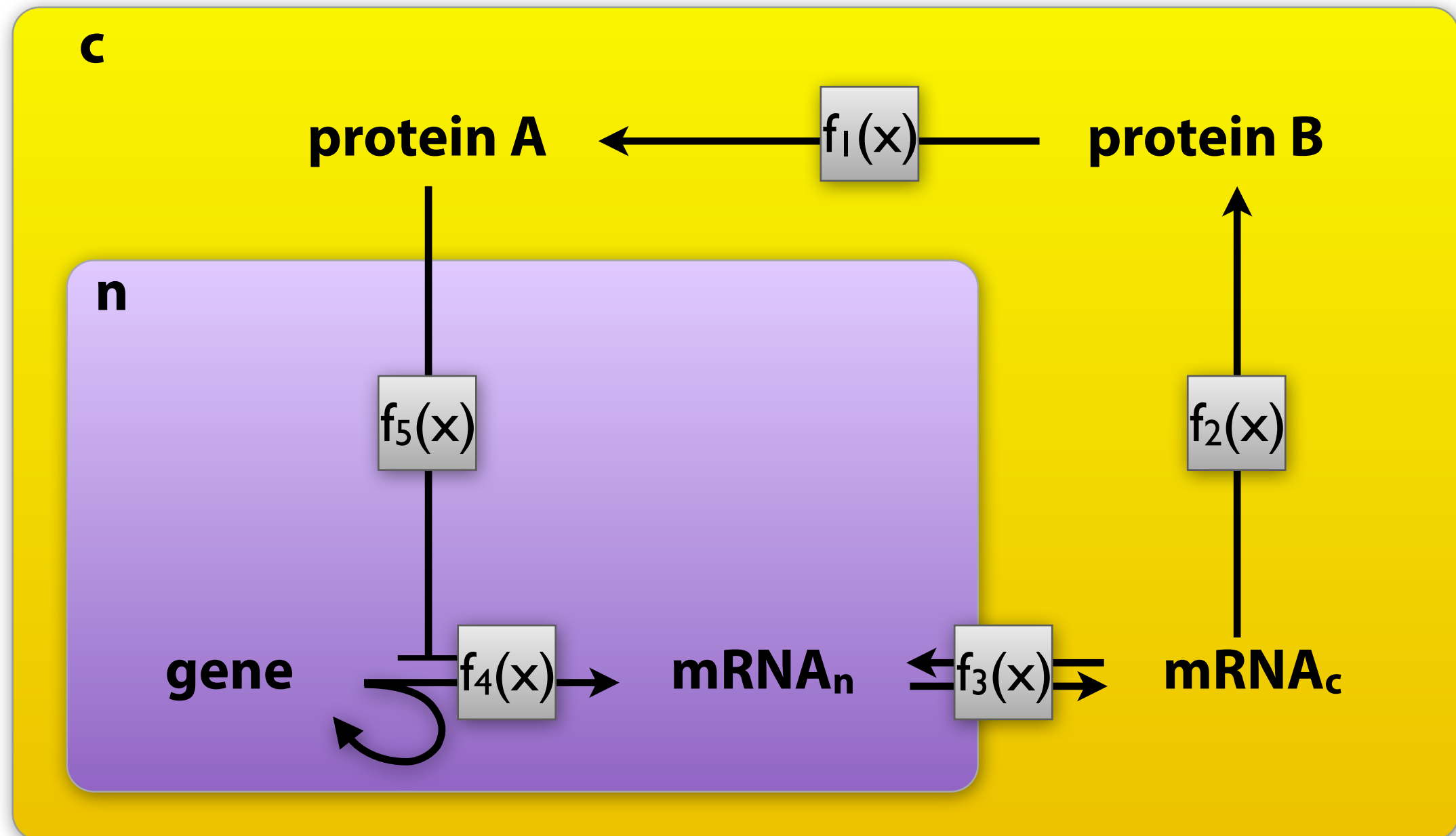
Reaction/process rates can be (almost) arbitrary formulas



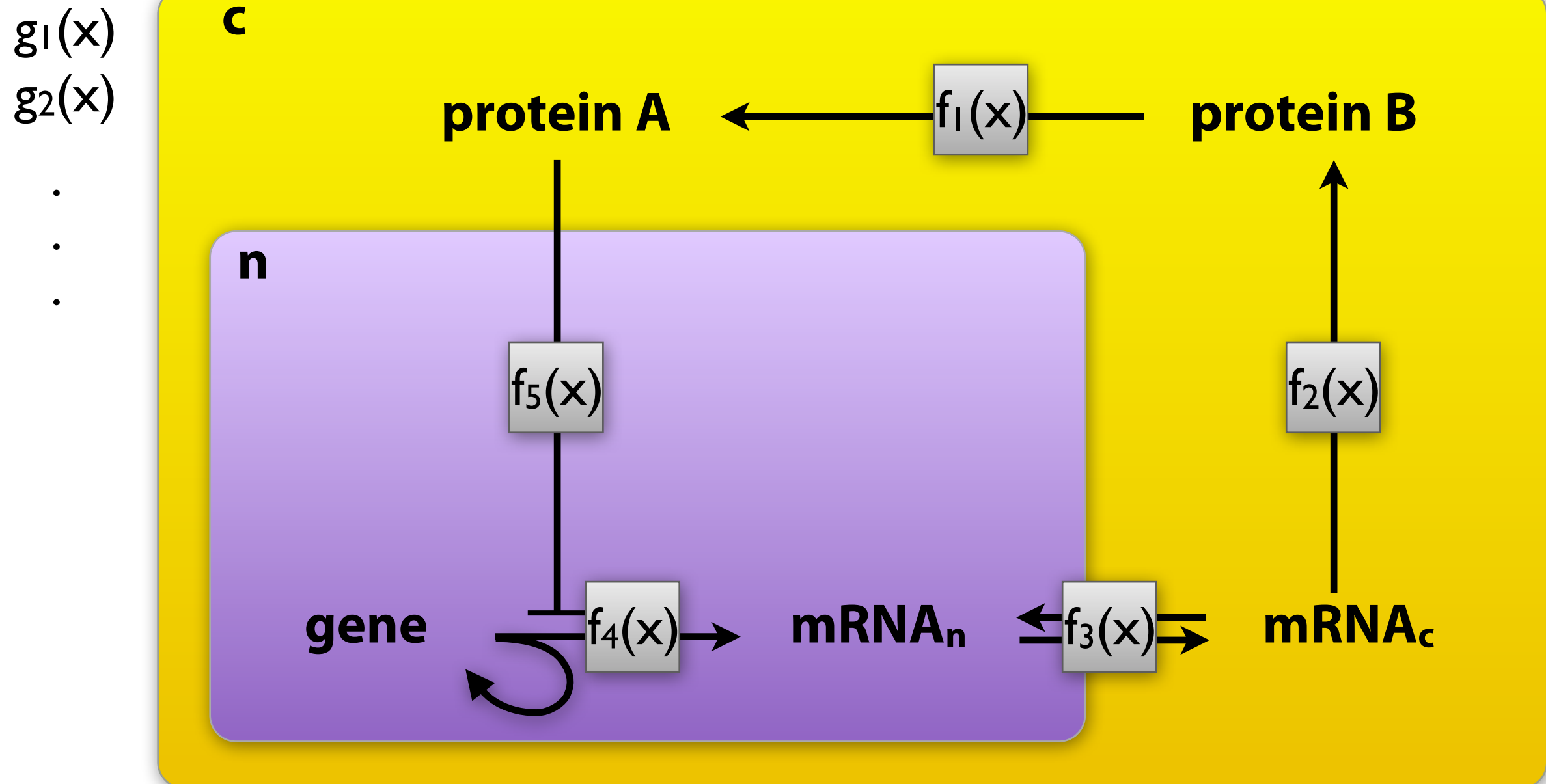
“Rules”: equations expressing relationships in addition to reaction sys.

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

·
 ·
 ·

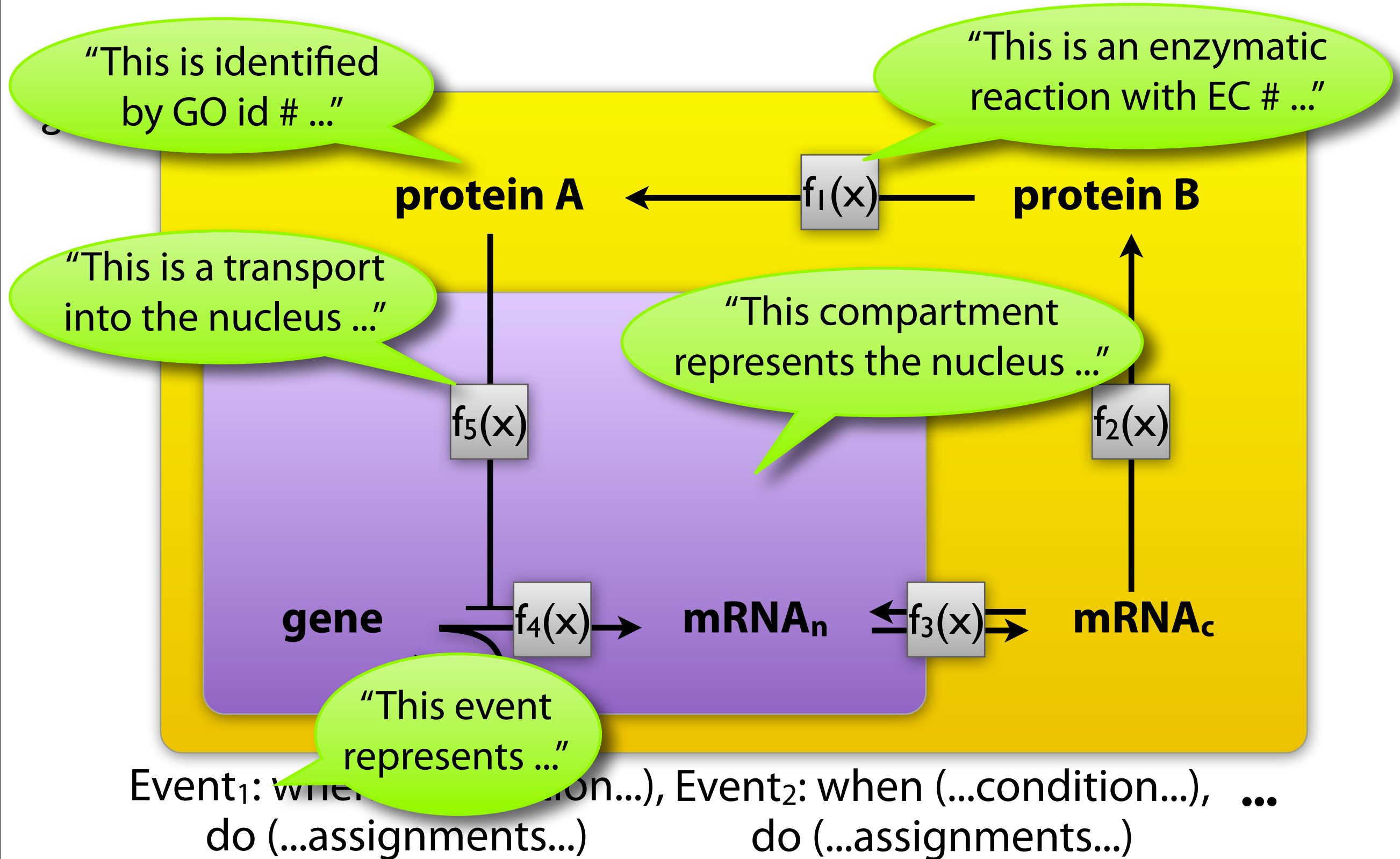


“Events”: discontinuous actions triggered by system conditions



Event₁: when (...condition...), Event₂: when (...condition...), ...
do (...assignments...) do (...assignments...)

Annotations: machine-readable semantics and links to other resources



Scope of SBML encompasses many types of models

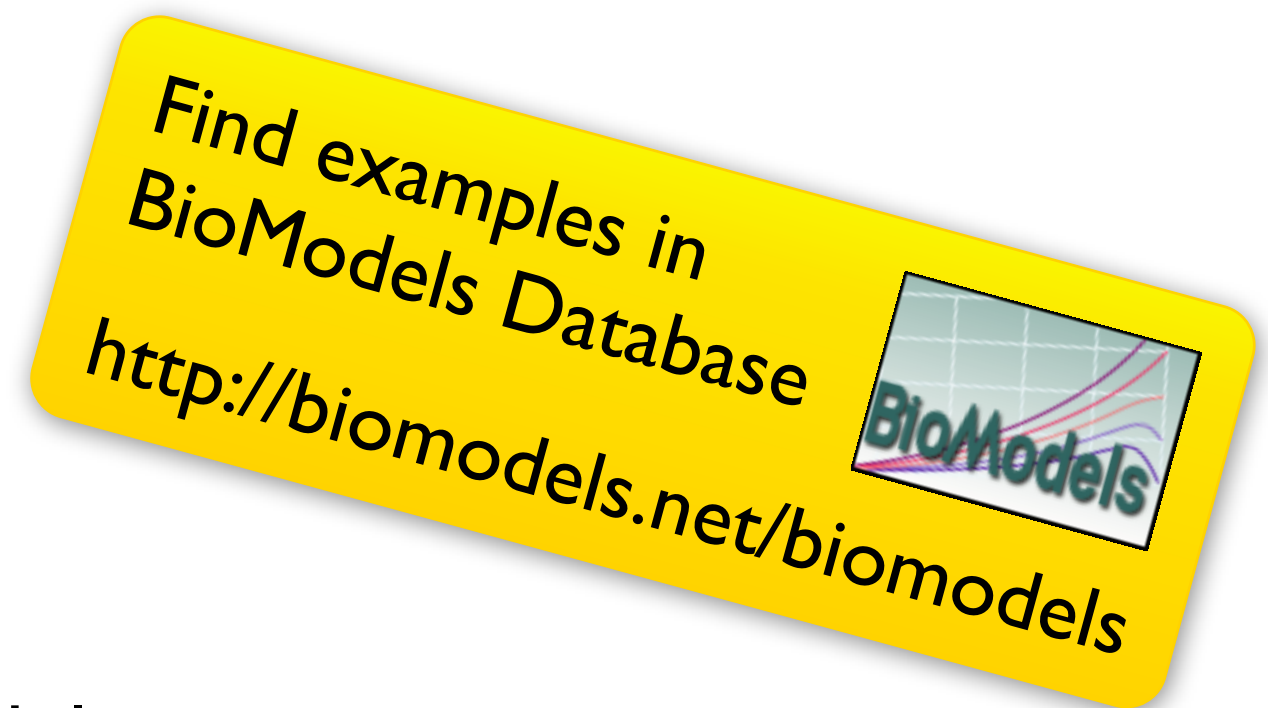
Today: spatially homogeneous models

- Metabolic network models
- Signaling pathway models
- Conductance-based models
- Neural models
- Pharmacokinetic/dynamics models
- Infectious diseases

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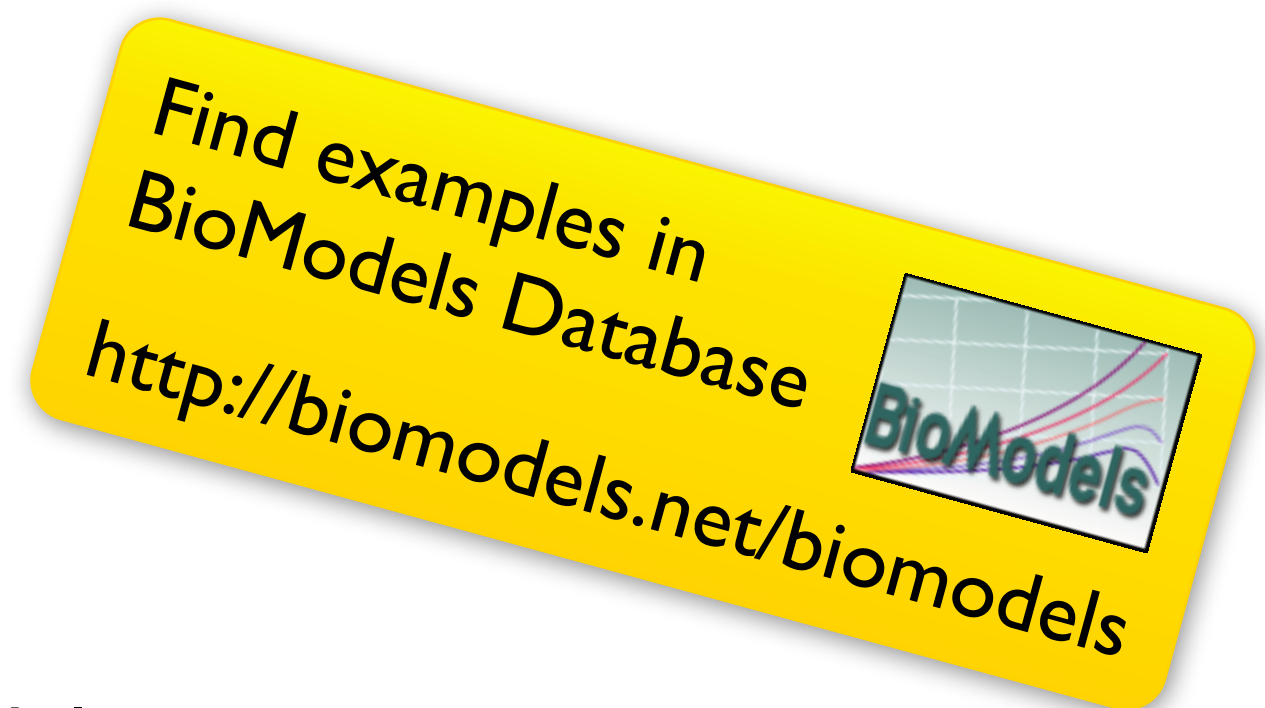
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Coming: SBML Level 3 *packages* to support other types

- E.g.: Spatially inhomogeneous models, also qualitative/logical

Scope of SBML encompasses many types of models

Where to learn more: SBML.org—the SBML portal



The screenshot shows a web browser window with the title "Main Page - SBML.org". The address bar shows "http://sbml.org/Main_Page". The page features the SBML.org logo and the title "The Systems Biology Markup Language". A navigation bar includes links for News, Documents, Downloads, Forums, Facilities, Community, Events, and About, along with a Google Site Search box. The main content area welcomes visitors to the SBML portal, describing it as a free and open interchange format for computer models of biological processes. It provides links for various user groups: "For the curious" (introduction, mailing lists), "For modelers" (software guide, BioModels Database), and "For software developers" (basic introduction, SBML specifications, libSBML). A sidebar on the right contains "SBML News" and "Community News" sections, listing recent updates and releases such as "COMBINE 2011", "SBML Test Suite updated", "PRISM 4.0 released", "MatCont 4.1 supports SBML", and "iPathways 1.1 released".

Main Page - SBML.org

http://sbml.org/Main_Page

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The Systems Biology Markup Language

News Documents Downloads Forums Facilities Community Events About

Google Site Search...

Welcome to the portal for the **Systems Biology Markup Language (SBML)**, a free and open interchange format for computer models of biological processes. SBML is useful for models of metabolism, cell signaling, and more. It has been in development by an international community since the year 2000.

For the curious
What *is* SBML? Read our [introduction](#), then perhaps browse the [mailing lists](#) to glimpse what's happening with SBML today.

For modelers
Looking for software that supports SBML? Our [software guide](#) lists over **220** systems. Are you instead looking for models? Visit [BioModels Database](#), where you can find hundreds!

For software developers
Interested in supporting SBML in your software? Read our [basic introduction](#) and then the [SBML specifications](#) to understand how to use SBML. After that, you may want to look at [libSBML](#).

No matter how you use SBML, we invite you to sign up for news updates either through our [RSS feed](#), our [Twitter feed](#), or one of the [mailing lists](#), and get involved with [community efforts](#) to help keep improving SBML. You can also call attention to your project's support of SBML by displaying the [SBML logo](#).

SBML would not have been possible without support from [multiple agencies and organizations](#), as well as intellectual contributions from many motivated individuals, including the [major contributors](#) who are shaping SBML Level 3.

SBML News

COMBINE 2011
(14 Jun. '11) Registration is now open for [COMBINE 2011](#), being held in Heidelberg, DE, on Sep. 3-7.

SBML Test Suite updated
(6 Jun. '11) Changes include addition of SBML L3v1 Core test cases, SED-ML files, and updates to the online interface.

[Older news ...](#)

Community News

PRISM 4.0 released
(3 Jul. '11) [PRISM](#) 4.0 is a probabilistic model checker that supports SBML input.

MatCont 4.1 supports SBML
(29 Jun. '11) [MatCont](#) is a MATLAB package for studying parameterized continuous and discrete dynamical systems.

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How did we gather data on the software tools?

Historically (until mid-2000's):

- Word of mouth at workshops & conferences
- Direct contact

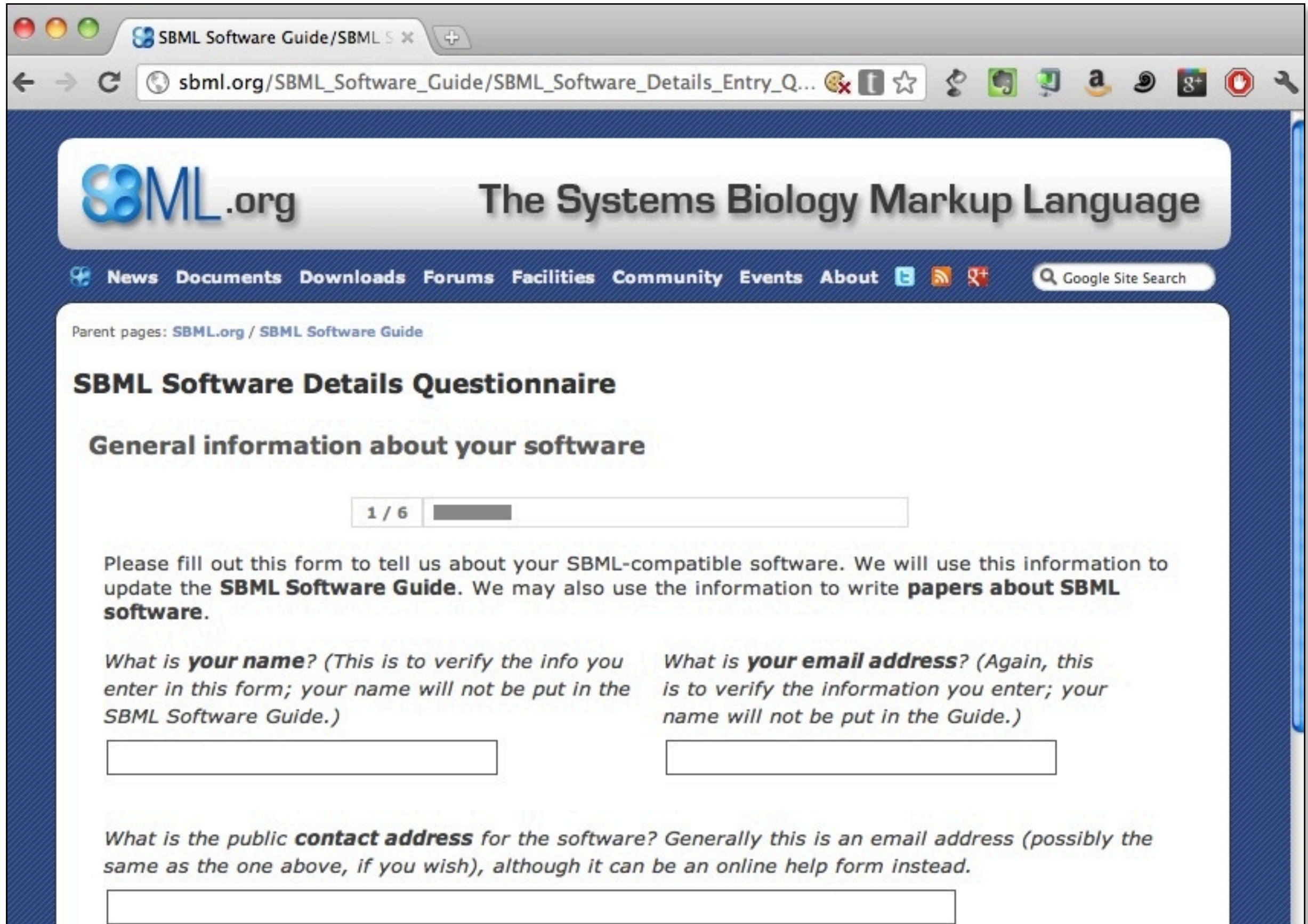
Mid/late-2000's to ~2010:

- Created electronic survey
- Citation alerts (e.g., Web of Science)

2011:

- Expanded survey
 - Basis of this talk

New version of the SBML software survey



The screenshot shows a web browser window with the address bar displaying `sbml.org/SBML_Software_Guide/SBML_Software_Details_Entry_Q...`. The page header features the SBML.org logo and the text "The Systems Biology Markup Language". A navigation bar includes links for News, Documents, Downloads, Forums, Facilities, Community, Events, and About, along with social media icons and a Google Site Search box. The main content area is titled "SBML Software Details Questionnaire" and "General information about your software". It includes a progress indicator showing "1 / 6" and a paragraph explaining the purpose of the survey. Below this, there are three input fields with corresponding labels: "What is your name?", "What is your email address?", and "What is the public contact address for the software?".

SBML Software Guide/SBML S x

sbml.org/SBML_Software_Guide/SBML_Software_Details_Entry_Q...

SBML.org The Systems Biology Markup Language

News Documents Downloads Forums Facilities Community Events About

Google Site Search

Parent pages: [SBML.org](#) / [SBML Software Guide](#)

SBML Software Details Questionnaire

General information about your software

1 / 6

Please fill out this form to tell us about your SBML-compatible software. We will use this information to update the **SBML Software Guide**. We may also use the information to write **papers about SBML software**.

What is **your name**? (This is to verify the info you enter in this form; your name will not be put in the SBML Software Guide.)

What is **your email address**? (Again, this is to verify the information you enter; your name will not be put in the Guide.)

What is the public **contact address** for the software? Generally this is an email address (possibly the same as the one above, if you wish), although it can be an online help form instead.

General features of the survey

Online, implemented using commercial survey website

28 questions

- Mix of multiple choice and fill-in-the-blank

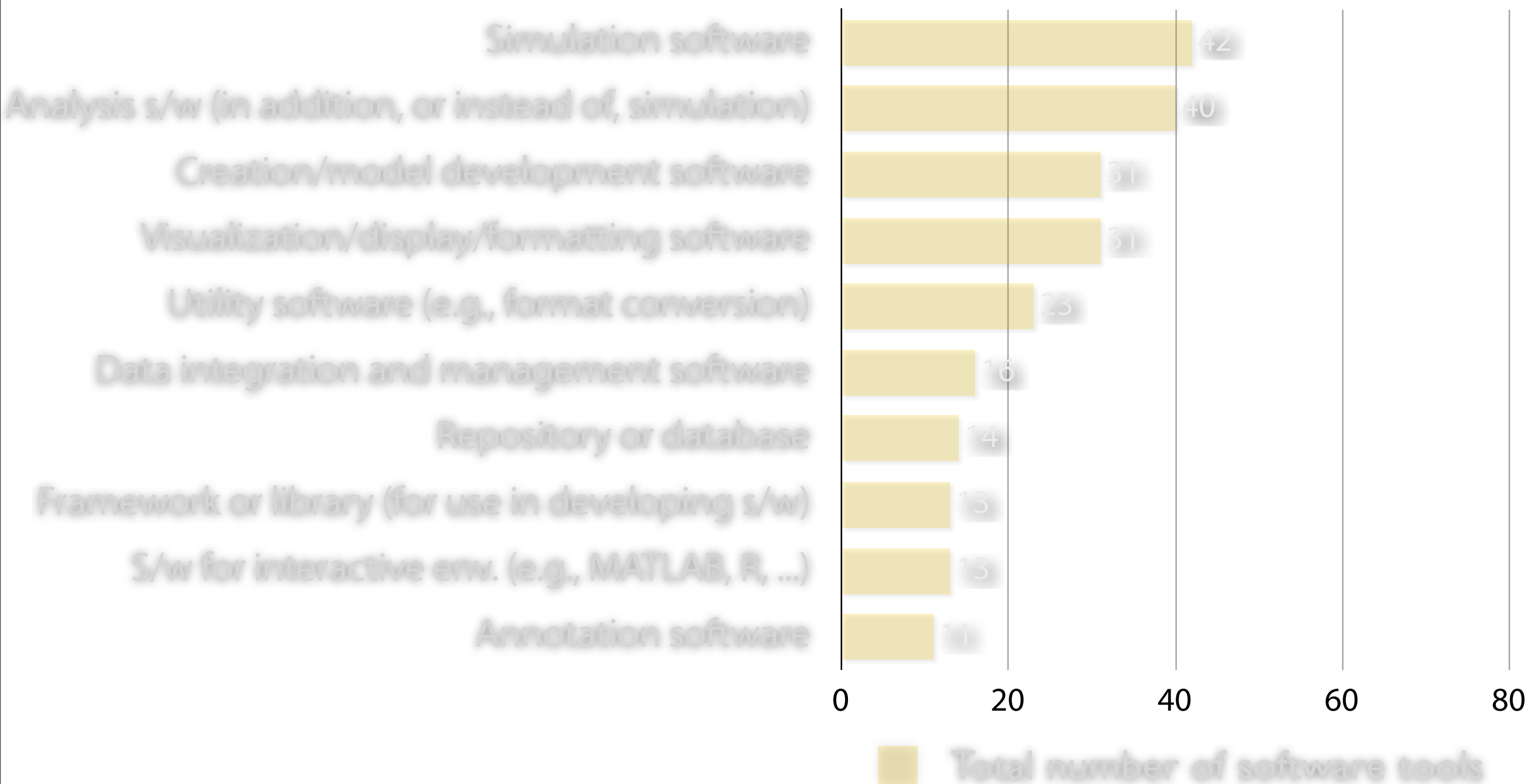
85 responses by July 2011

- Removed incomplete responses
- 81 software tools left

Avoided “corrections” to data

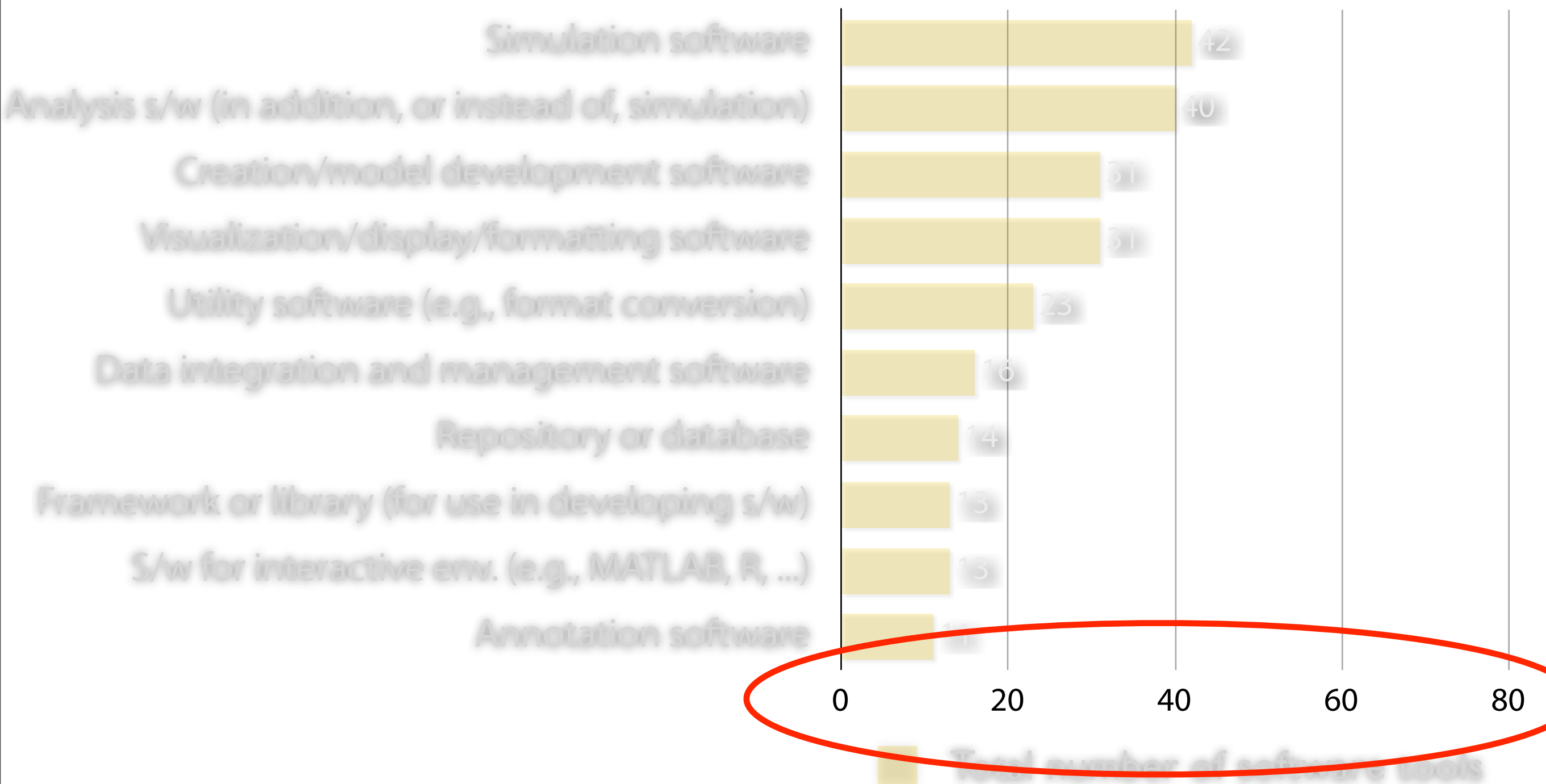
Purposes of the software systems

Question: Which of the following categories best describe your software?
(Check all that apply.)



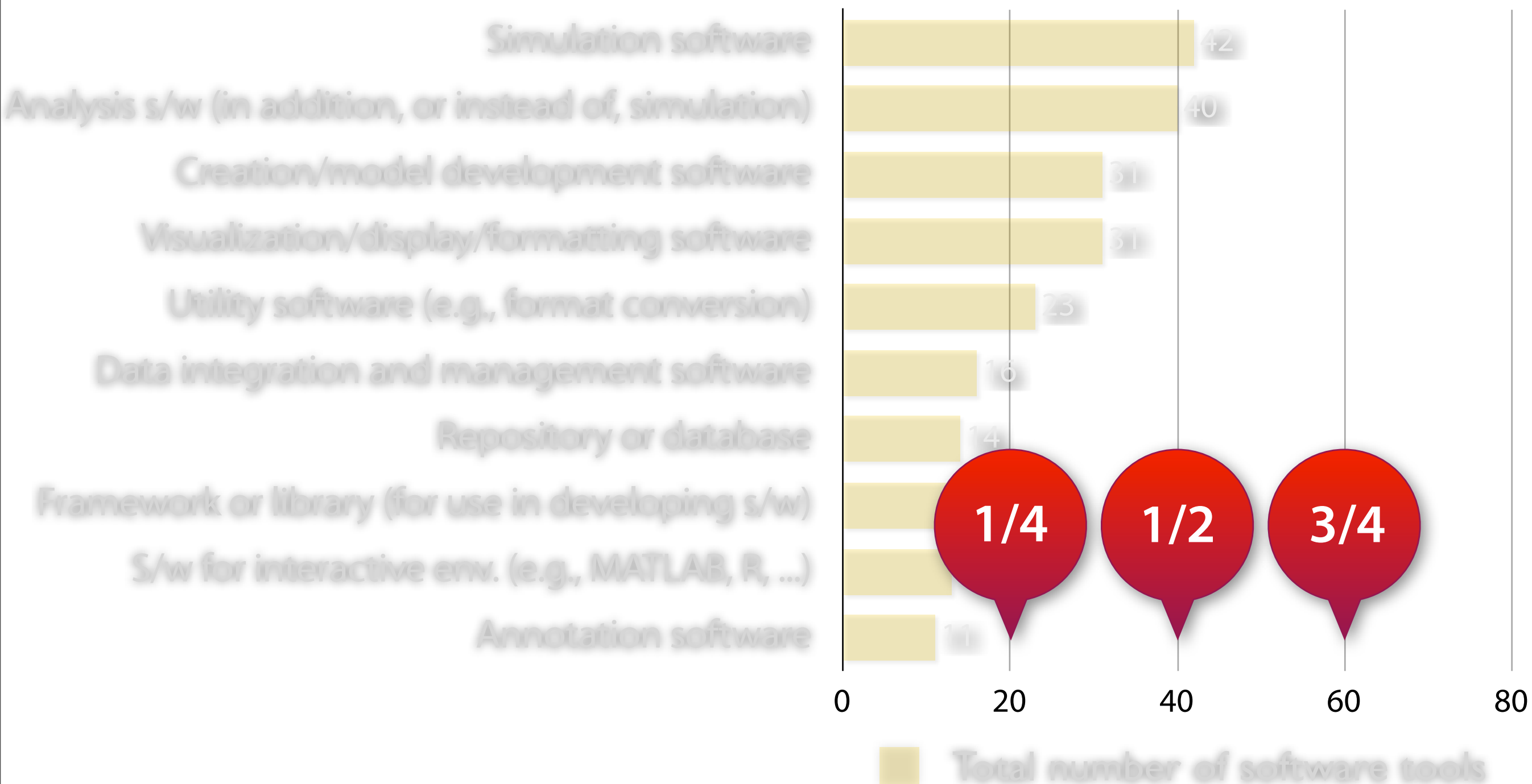
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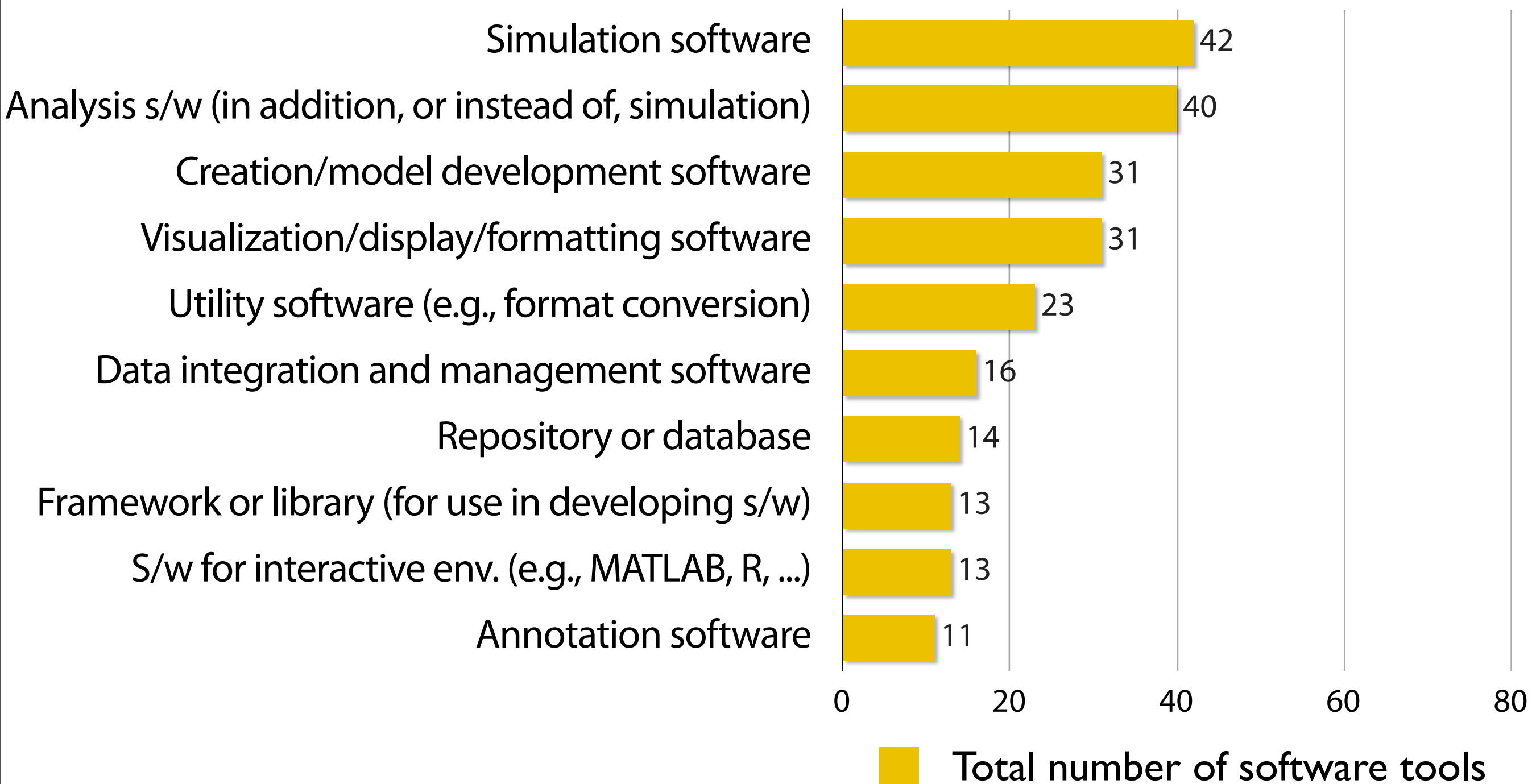
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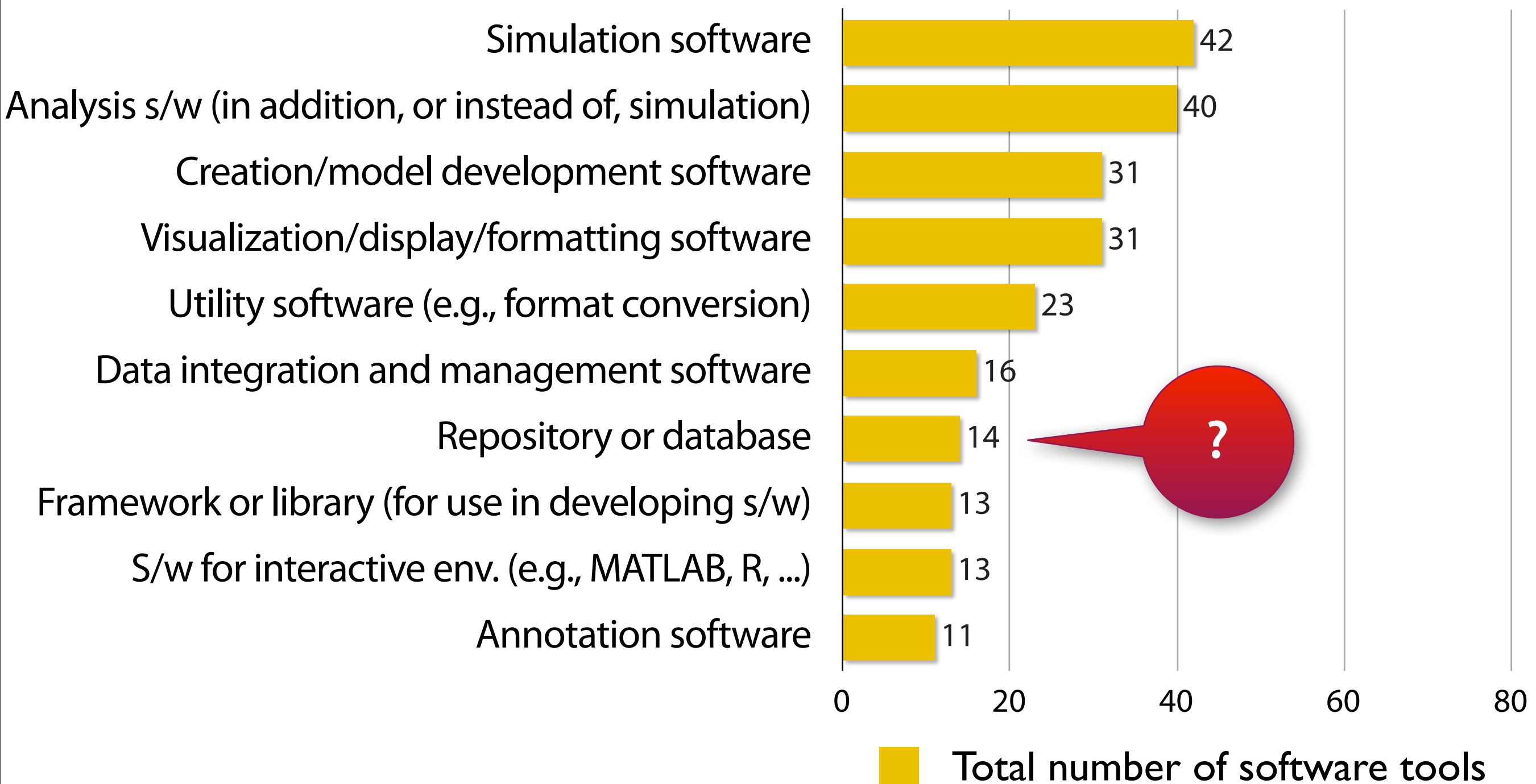
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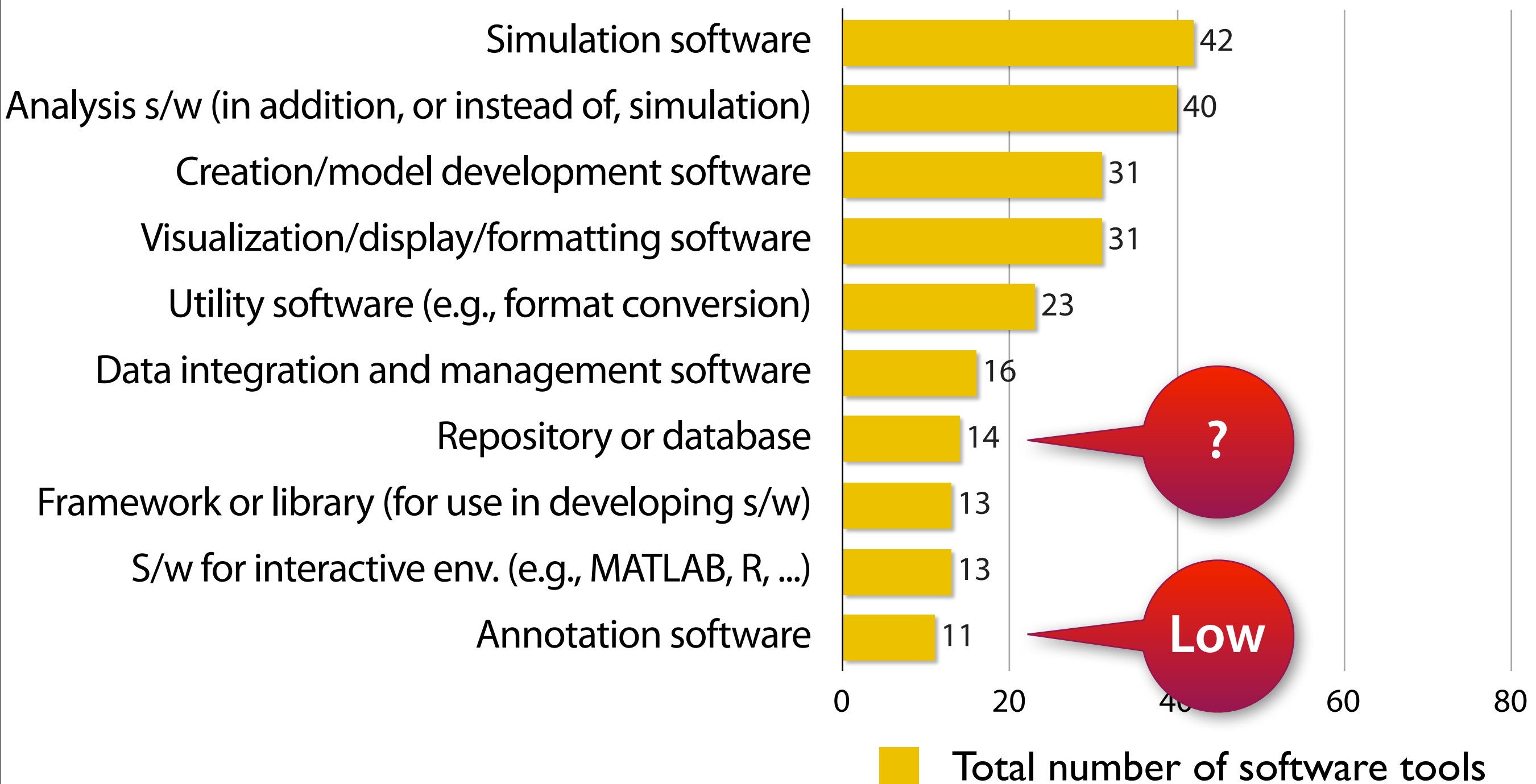
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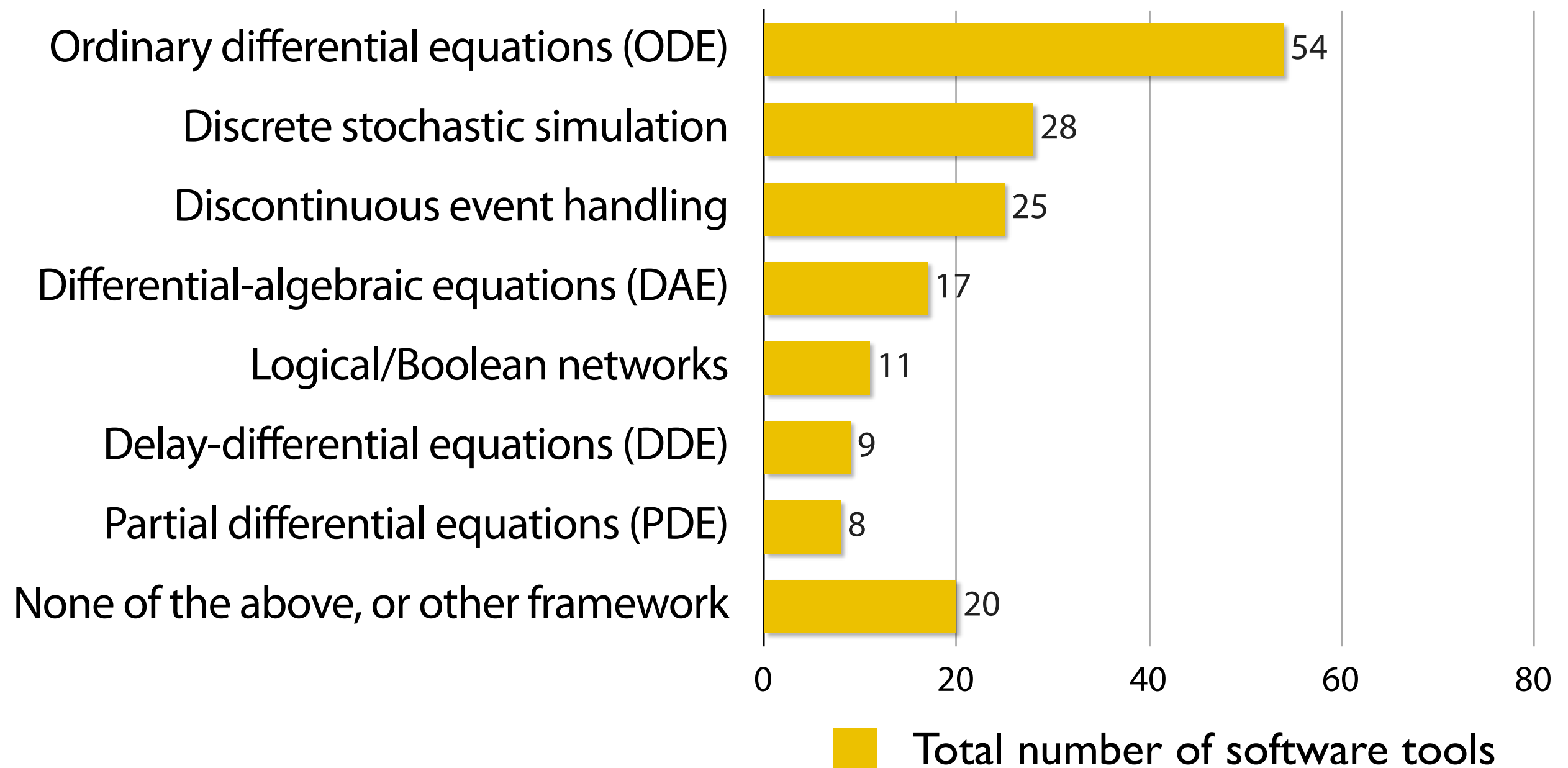
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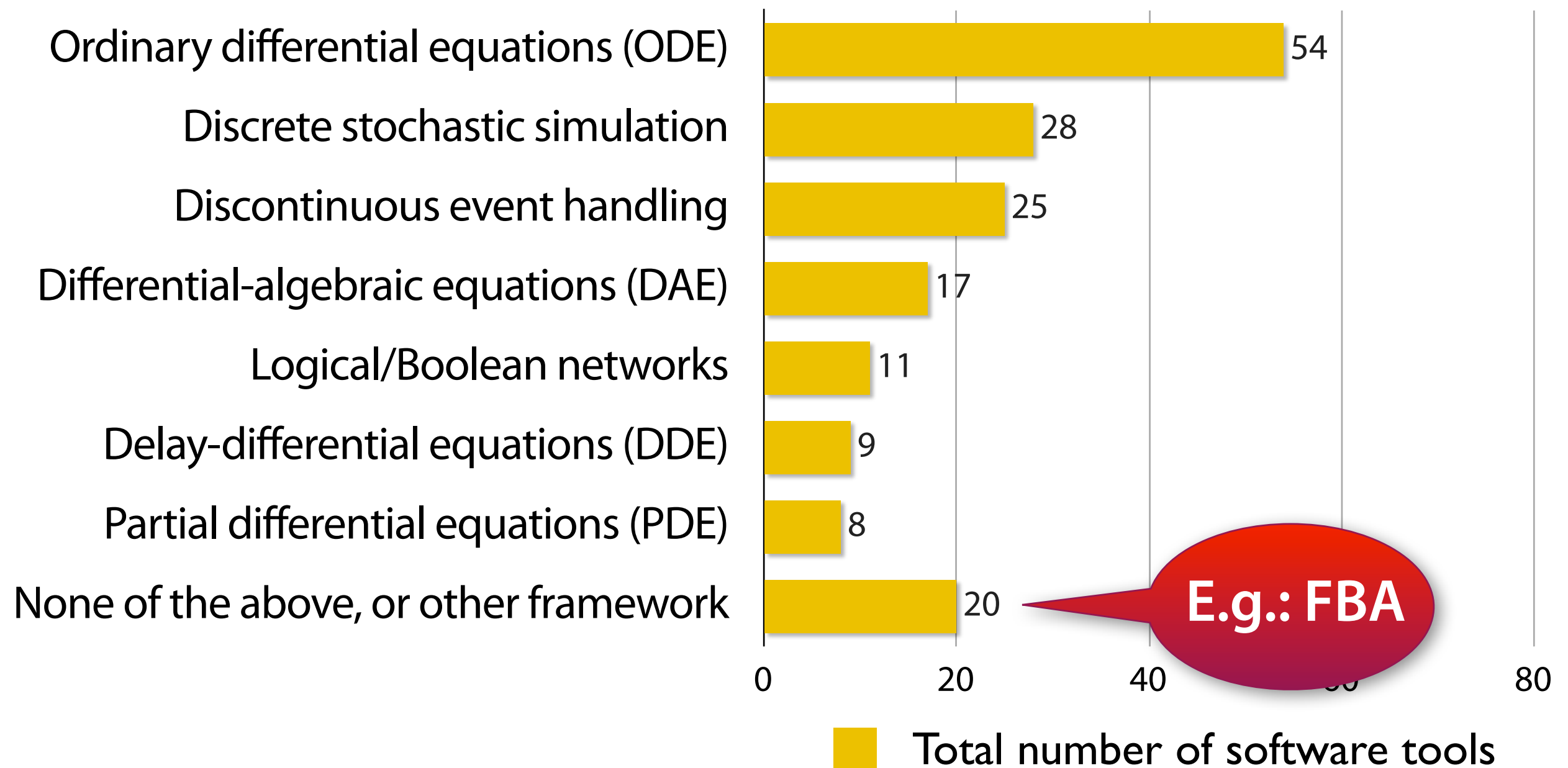
Mathematical frameworks

Question: *Regardless of whether your software provides simulation capabilities, what modeling frameworks does the package support when working with SBML files?*



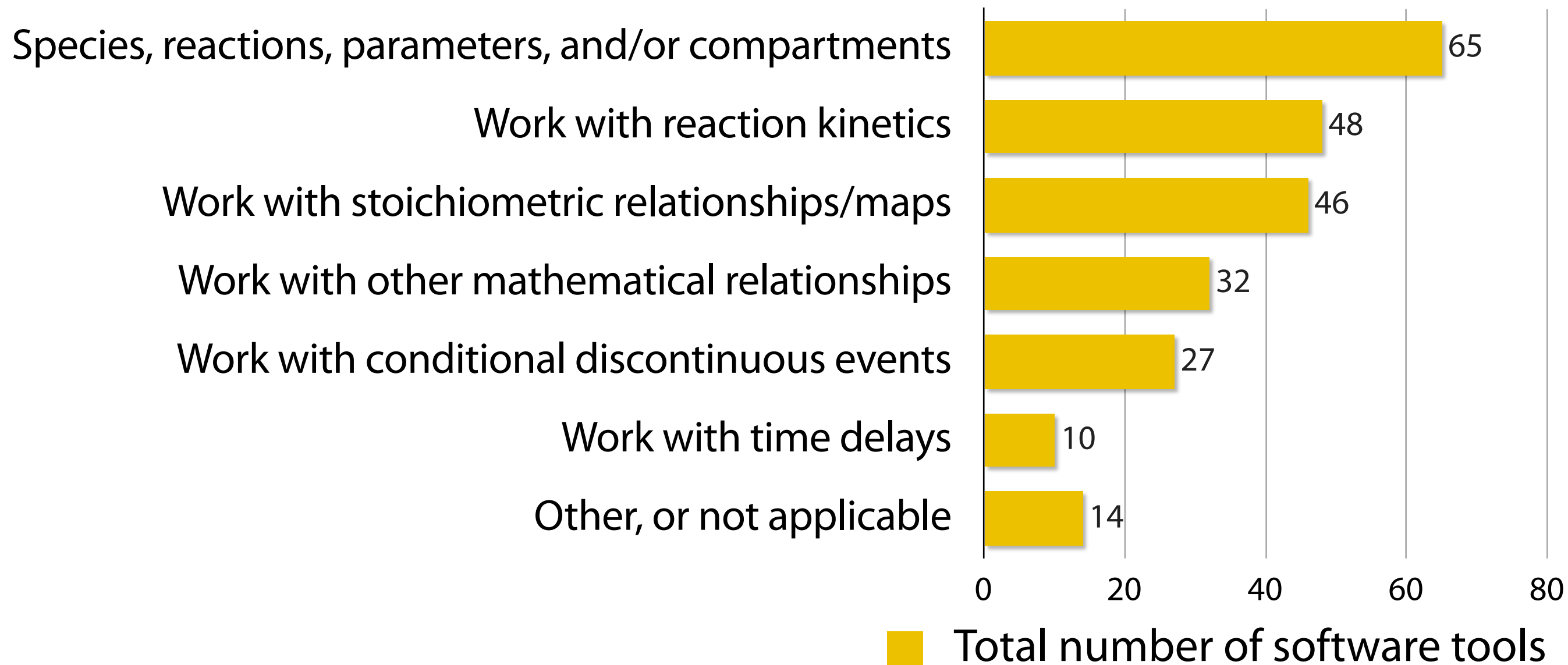
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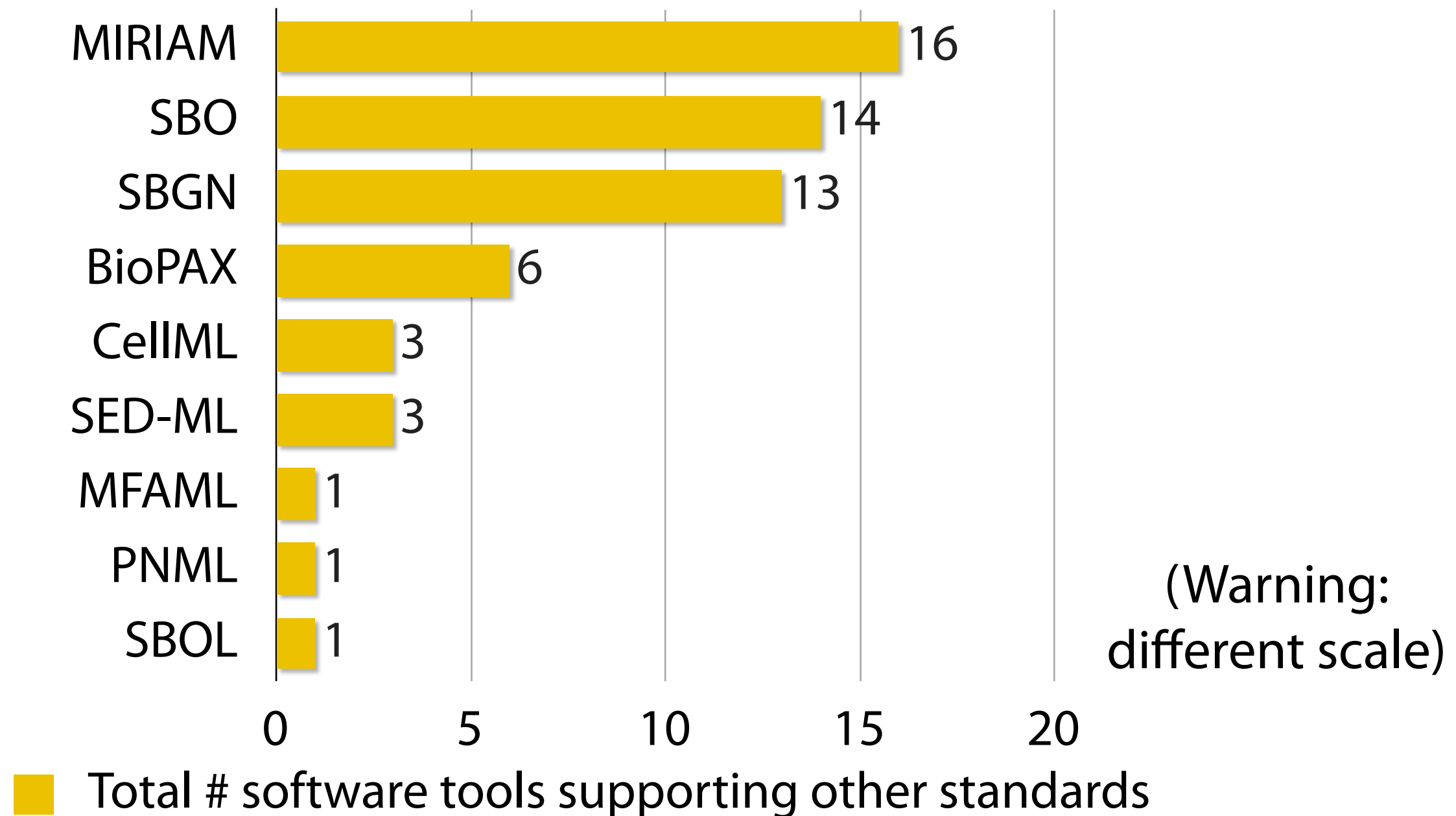
Specific SBML-specific characteristics

Question: *Which features of SBML can your software recognize and act on?*

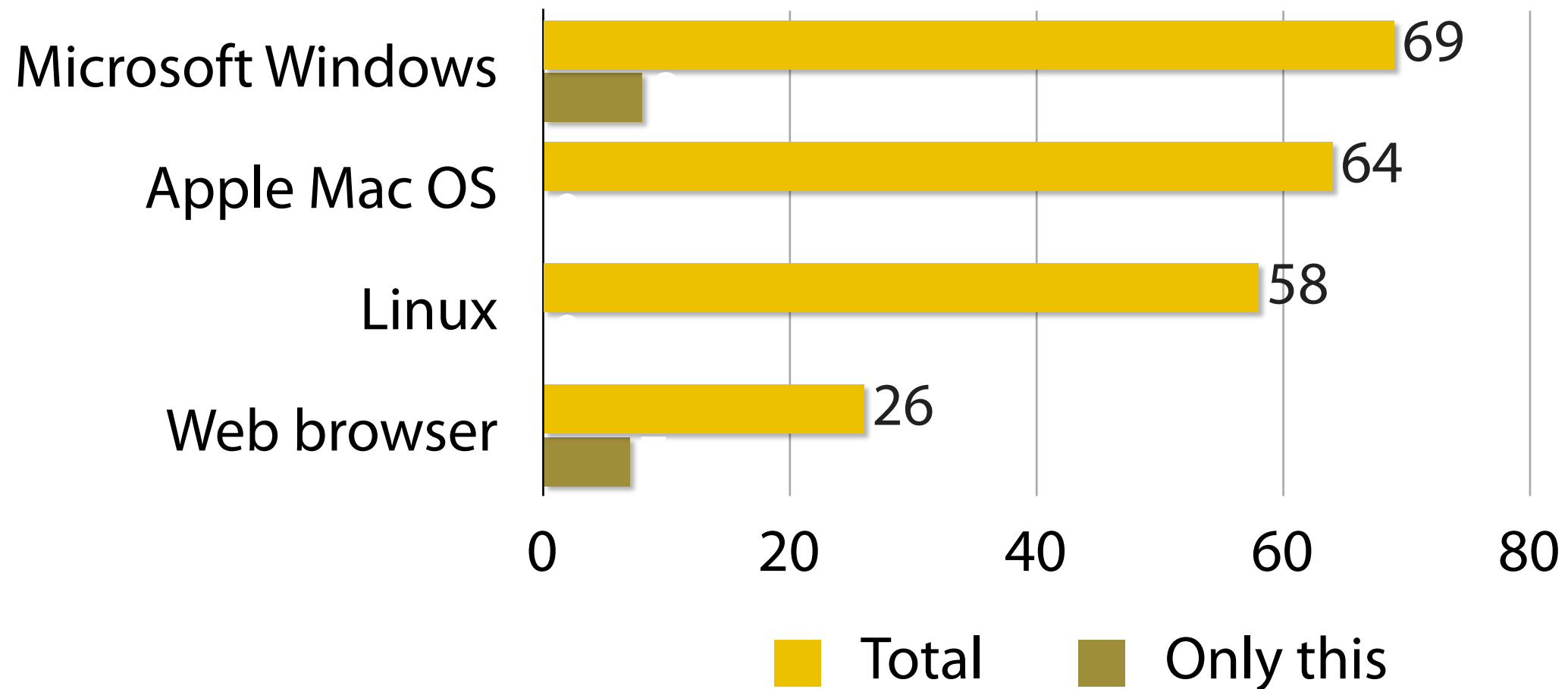


Other supported standards

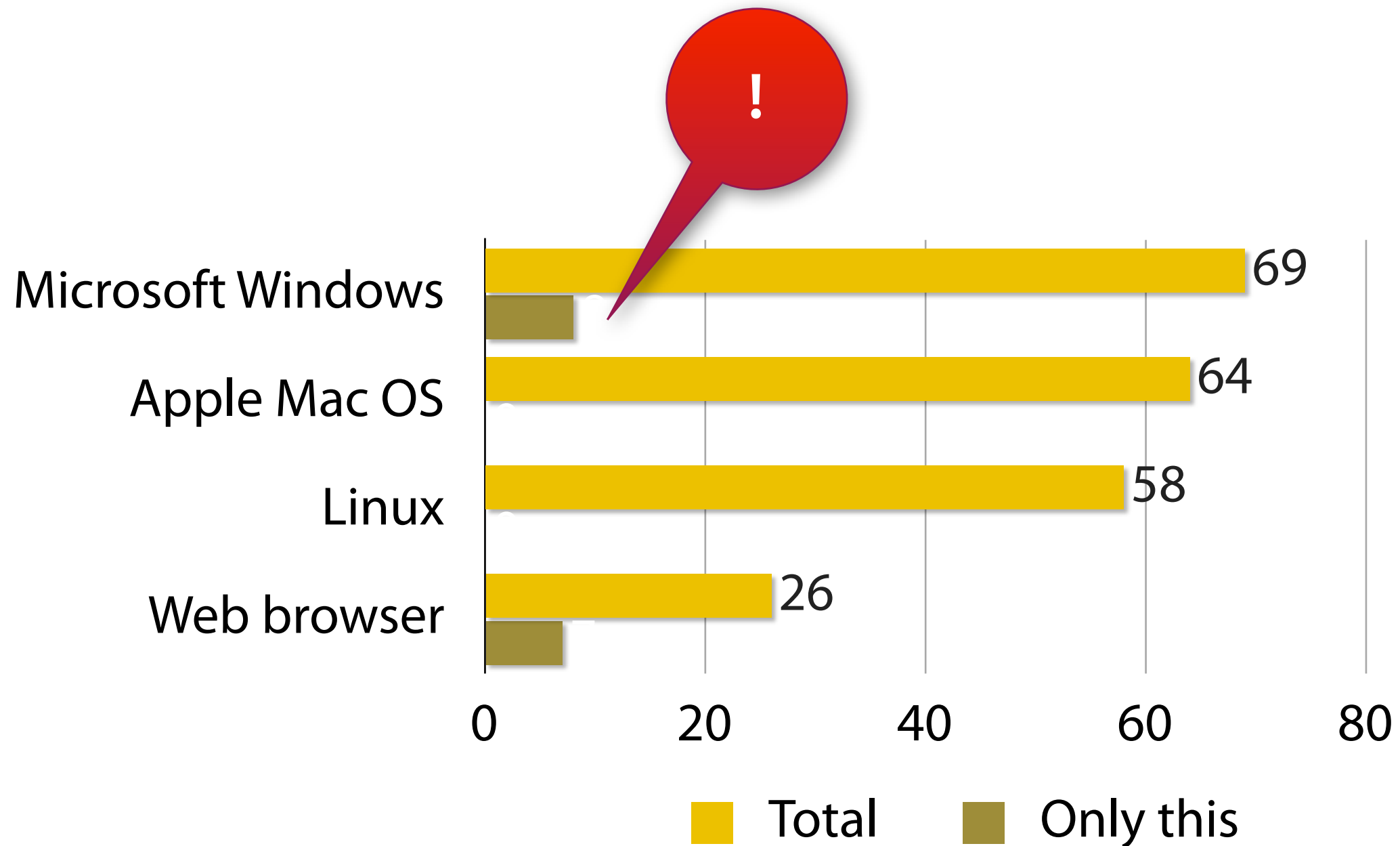
Question: *Which other standards does your software support?*



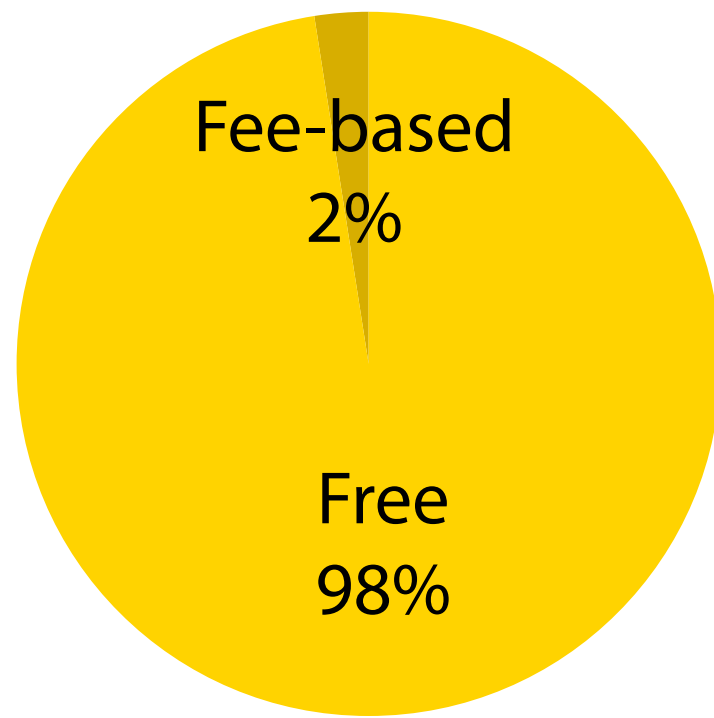
Operating systems supported by the 81 tools



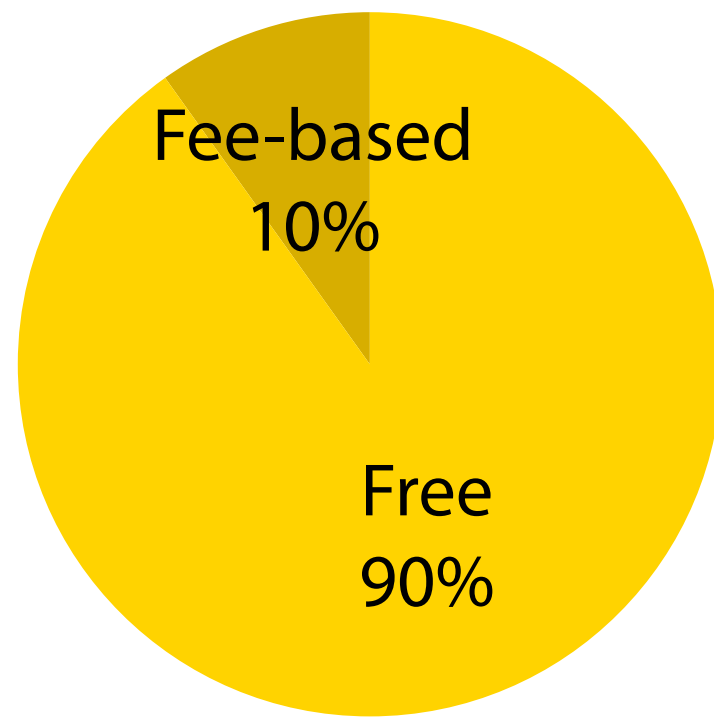
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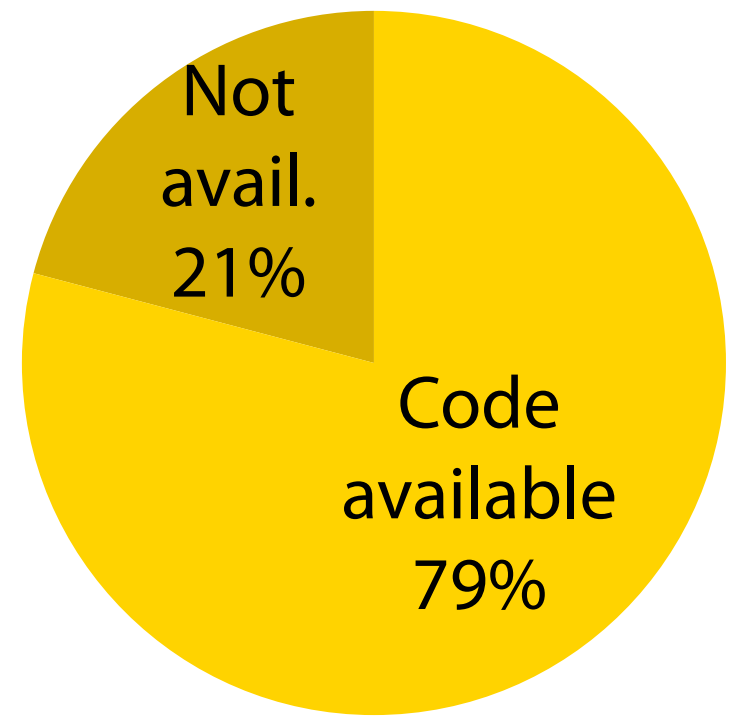
Availability of software



Fees for
academics



Fees for non-
academics



Is source code
available?

Final impressions

Some pleasing results

- Large variety, including tools with features SBML can't yet represent
 - Hopefully stands as testament to SBML's utility
- Nearly **80% are open source**

Some disappointing results

- Low response turnout: 85 vs 230 tools in matrix
- Low support for MIRIAM

National Institute of General Medical Sciences (USA)

European Molecular Biology Laboratory (EMBL)

ELIXIR (UK)

Beckman Institute, Caltech (USA)

Keio University (Japan)

JST ERATO Kitano Symbiotic Systems Project (Japan) (to 2003)

JST ERATO-SORST Program (Japan)

International Joint Research Program of NEDO (Japan)

Japanese Ministry of Agriculture

Japanese Ministry of Educ., Culture, Sports, Science and Tech.

BBSRC (UK)

National Science Foundation (USA)

DARPA IPTO Bio-SPIICE Bio-Computation Program (USA)

Air Force Office of Scientific Research (USA)

STRI, University of Hertfordshire (UK)

Molecular Sciences Institute (USA)



Attendees at SBML 10th Anniversary Symposium, Edinburgh, 2010

A huge **thank you** to the community