Mathematical Modeling for Cell Biology

CellBio 24 workshop

Sunday, December 15th

In order of appearance: Stefan Hoops, Leslie Loew, Michael Blinov, Ann Cowan

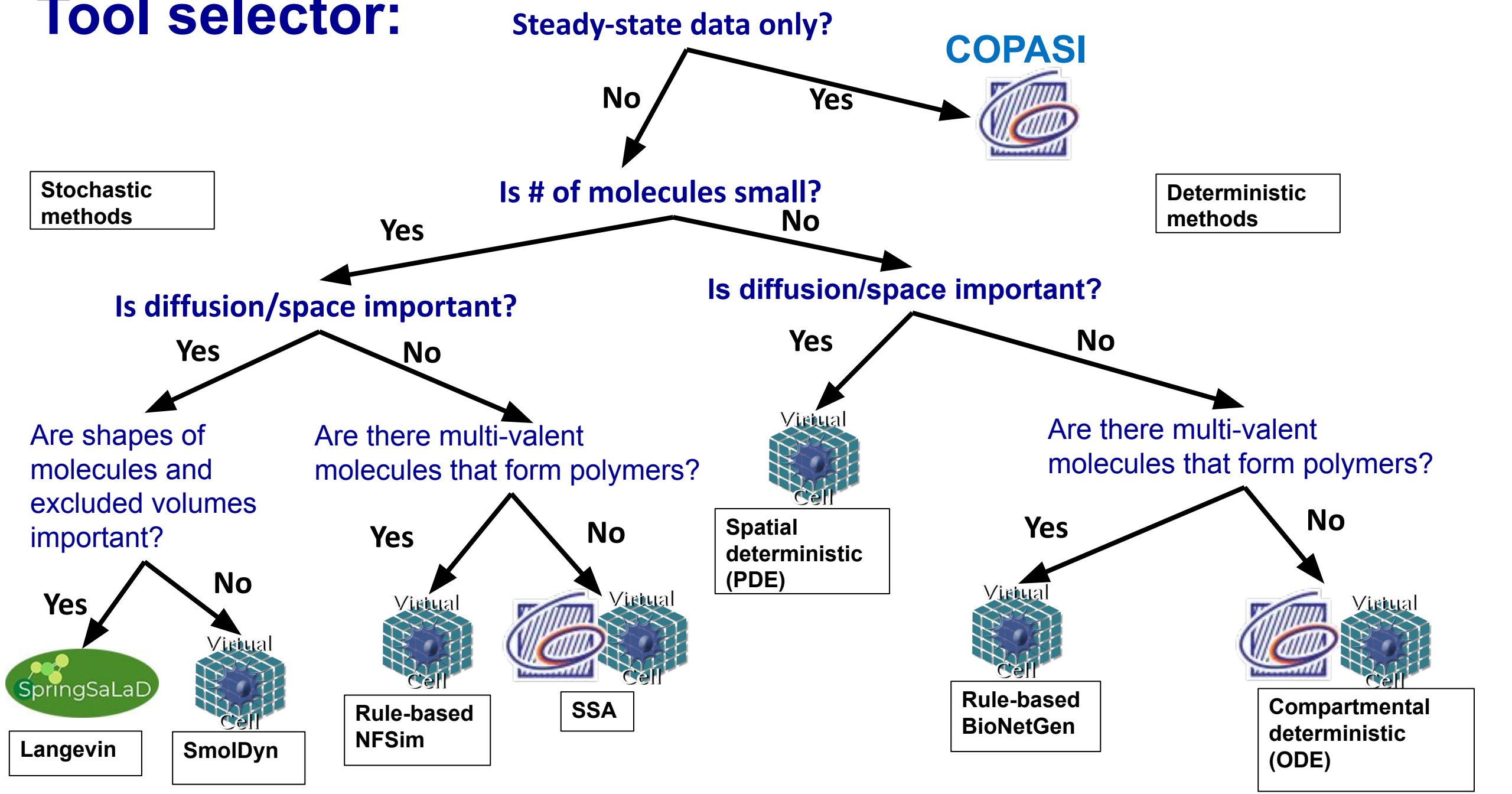
Introduce kinetic simulations, steady state analysis, parameter estimation, spatial modeling, rule-based models, demonstrating them using two modeling and simulation tools:

COPASI (http://copasi.org) and Virtual Cell (http://vcell.org).

This handout is available at: https://compcellbio.org/assets/ASCB2024.pdf

See also: https://compcellbio.org/

Tool selector:



Capabilities of our modeling tools:

METHODS	COPASI	VCell
Compartmental deterministic modeling (ODE)	✓	✓
Stochastic compartmental modeling (SSA)	✓	✓
Spatial deterministic modeling (PDE)		✓
Steady-state modeling	✓	
Stochastic differential equations (SDE)	✓	
Parameter fitting	✓	✓ **(COPASI)**
Compartmental rule-based modeling of multi-component molecules		✓ **(BioNetGen)**
Compartmental agent-based modeling of multi-component molecules		✓ **(NFsim)**
Spatial stochastic modeling		✓ **(SmolDyn)**
Spatial stochastic modeling accounting for volumes		✓ **(SpringSalad)**

Example models for today's workshop

1. **Steady-State, Time Course, and Parameter Fitting with COPASI** (Negative feedback and ultrasensitivity can bring about oscillations in the mitogen-activated protein kinase cascades) - presented by Stefan Hoops (Biomodels Database: BIOMD0000000010)
2. **Using PDEs to simulate FRAP of a biomolecular condensate** (Cowan and Loew, Biophys. J. 2023, PUBMED: 37353932 - presented by Leslie Loew (http://vcell.org/biomodel-255507058)
3. **Using ImageJ to define initial concentration distribution in reaction-diffusion simulations** (Ding et al., 2020; Current Biology; PUBMED:32155414) - presented by Michael Blinov (https://vcell.org/biomodel-169993006)
4. **Rule-based modeling defining molecules and multi-molecular species** (Nosbisch et al., 2022, JBC; PUBMED:35367415) - presented by Michael Blinov (https://vcell.org/biomodel-232498815)

Learning resources

This presentation: https://compcellbio.org/assets/ASCB2024.pdf

COPASI:

https://vcell.org/support:

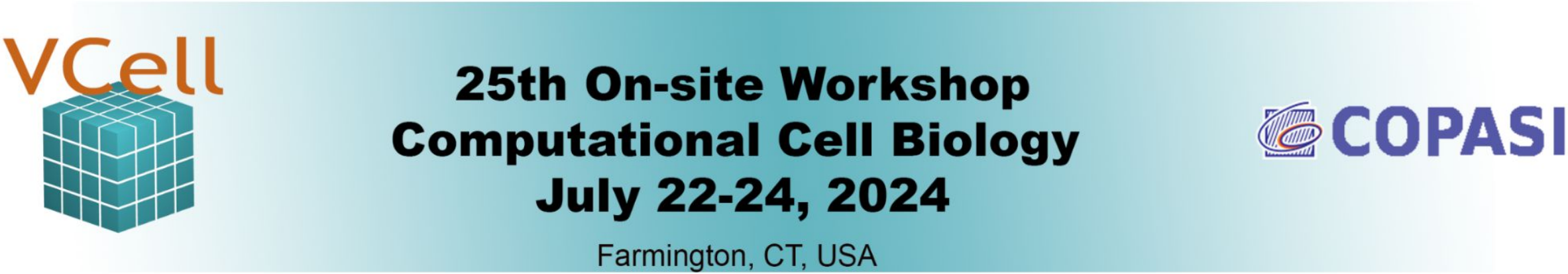
- Multiple Tutorials(including FRAP and Rule-based)
- Links to YouTube channel, CompCellBio lecture videos

Computational Cell Biology Courses

- Online Feb 24-28, 2025 https://compcellbio.org/ccbworkshop
- In person CCB Workshop, Summer 2025.

CompCellBio workshops

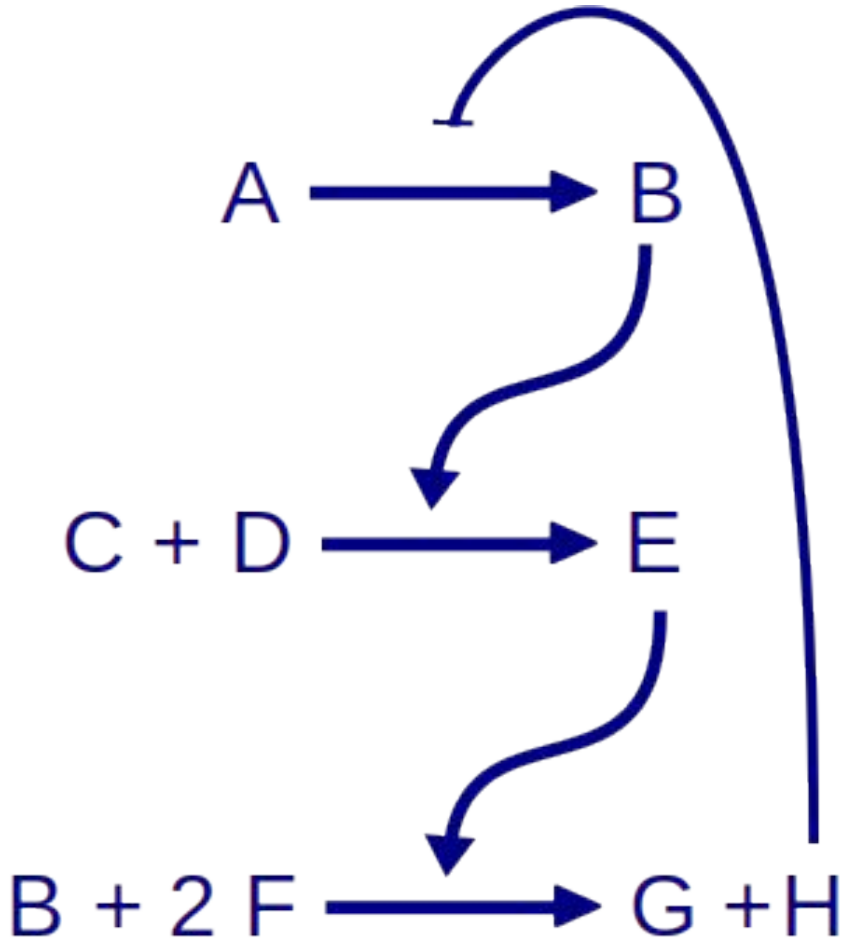
https://compcellbio.org/ccbworkshop



COPASI Capabilities

- Time course (deterministic, stochastic, and hybrid algorithm)
- Steady state
- Stoichiometric analysis of the reaction network, including mass conservation analysis and elementary flux modes.
- Optimization of arbitrary components of the model using a range of diverse algorithms.
- Parameter estimation using a range of diverse optimization algorithms. This can be done over several different experiments simultaneously, including mixtures of steady-state and time course experiments.
- Local sensitivity analysis.
- Metabolic control analysis (a special form of sensitivity analysis).
- Time scale separation analysis; this allows definition of fast and slow components of the model, in a time-dependent way.
- Analysis of stochasticity using the linear noise approximation (allows estimating variances and co-variances even in the presence of large numbers of particles).
- Cross sections, which allow to characterize non-linear dynamics properties, such as oscillations and chaos.
- Lyapunov exponents, which allows to establish if the system dynamics are chaotic.

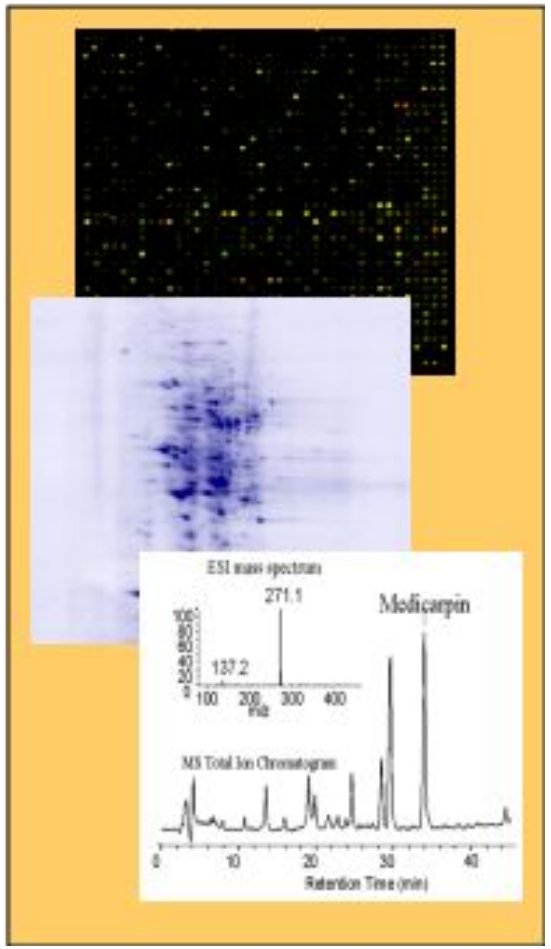
Biochemical Process



Genome

Proteome

Metabolome



Mathematical Model

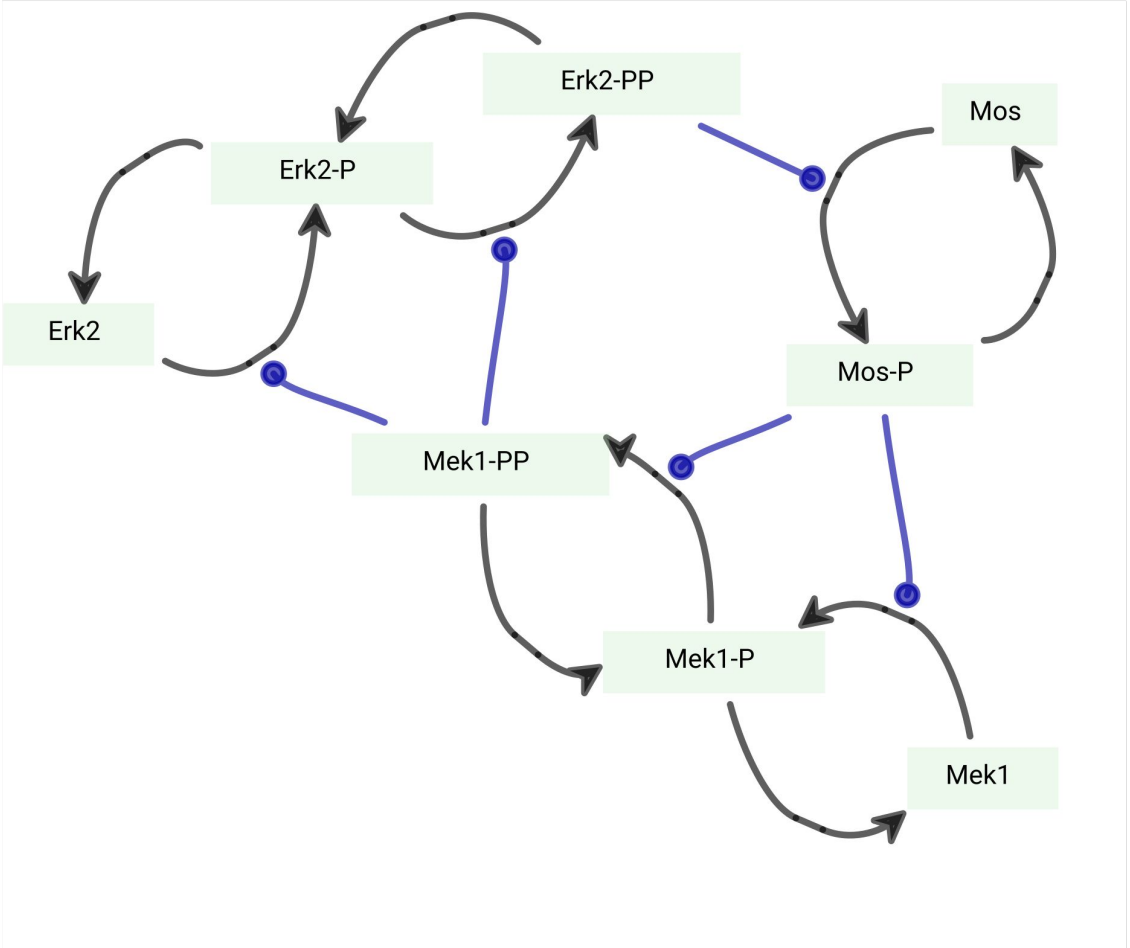
$$\begin{pmatrix} \dot{A} \\ \dot{B} \\ \dot{C} \\ \dot{D} \\ \dot{E} \\ \dot{F} \\ \dot{G} \\ \dot{H} \end{pmatrix} = \begin{pmatrix} -1 & 0 & 0 \\ 1 & 0 & -1 \\ 0 & -1 & 0 \\ 0 & -1 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & -2 \\ 0 & 0 & 1 \\ 0 & 0 & 1 \end{pmatrix} \begin{pmatrix} v_1(A, B, H) \\ v_2(B, C, D, E) \\ v_3(B, E, F, G, H) \end{pmatrix}$$

$\dot{x} = N\,v$ with: $\mathbf{x} = \begin{pmatrix} x_1 \\ x_2 \\ \dots \\ x_n \end{pmatrix}$ $\mathbf{v} = \begin{pmatrix} v_1 \\ v_2 \\ \dots \\ v_m \end{pmatrix}$

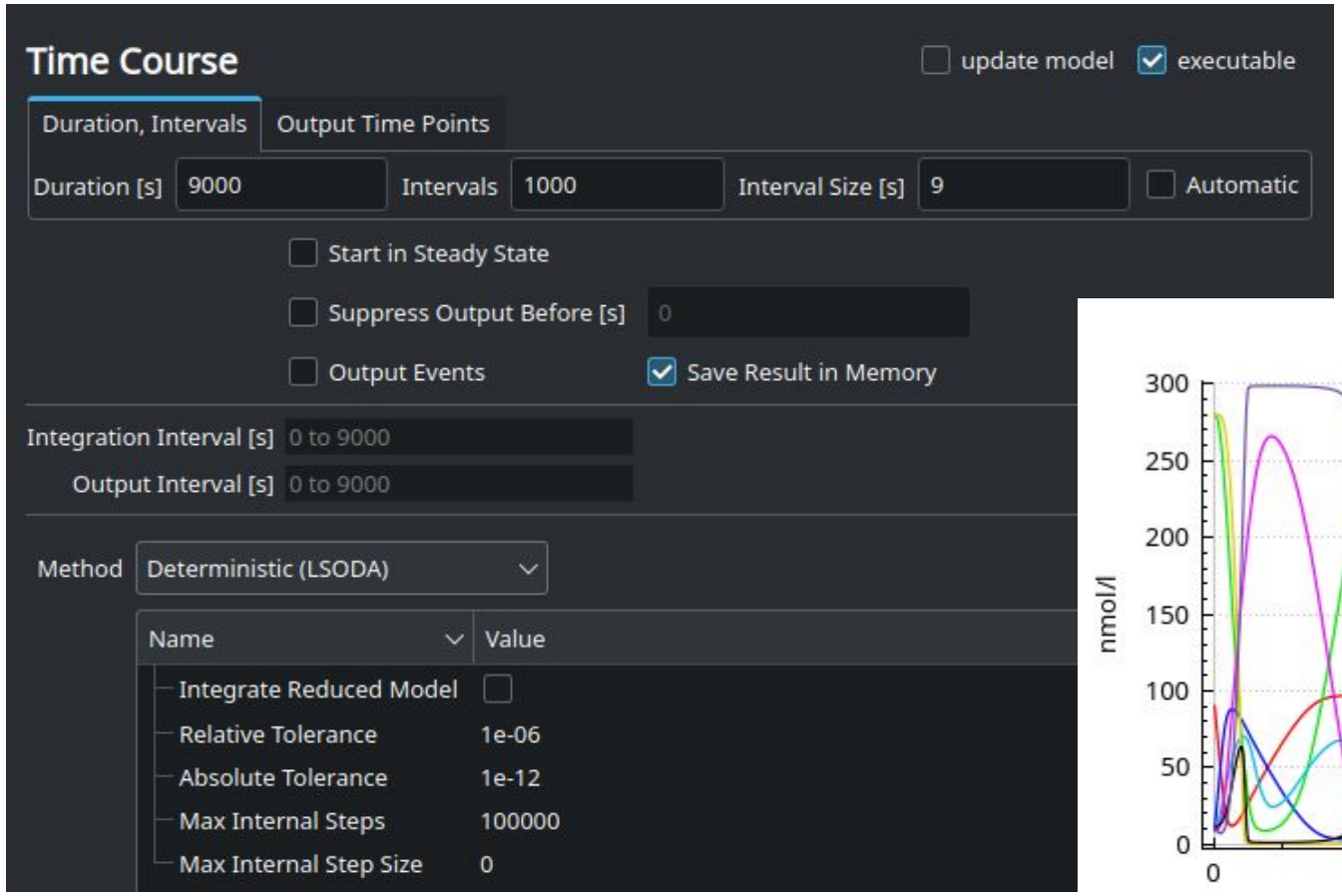
Example 1: COPASI

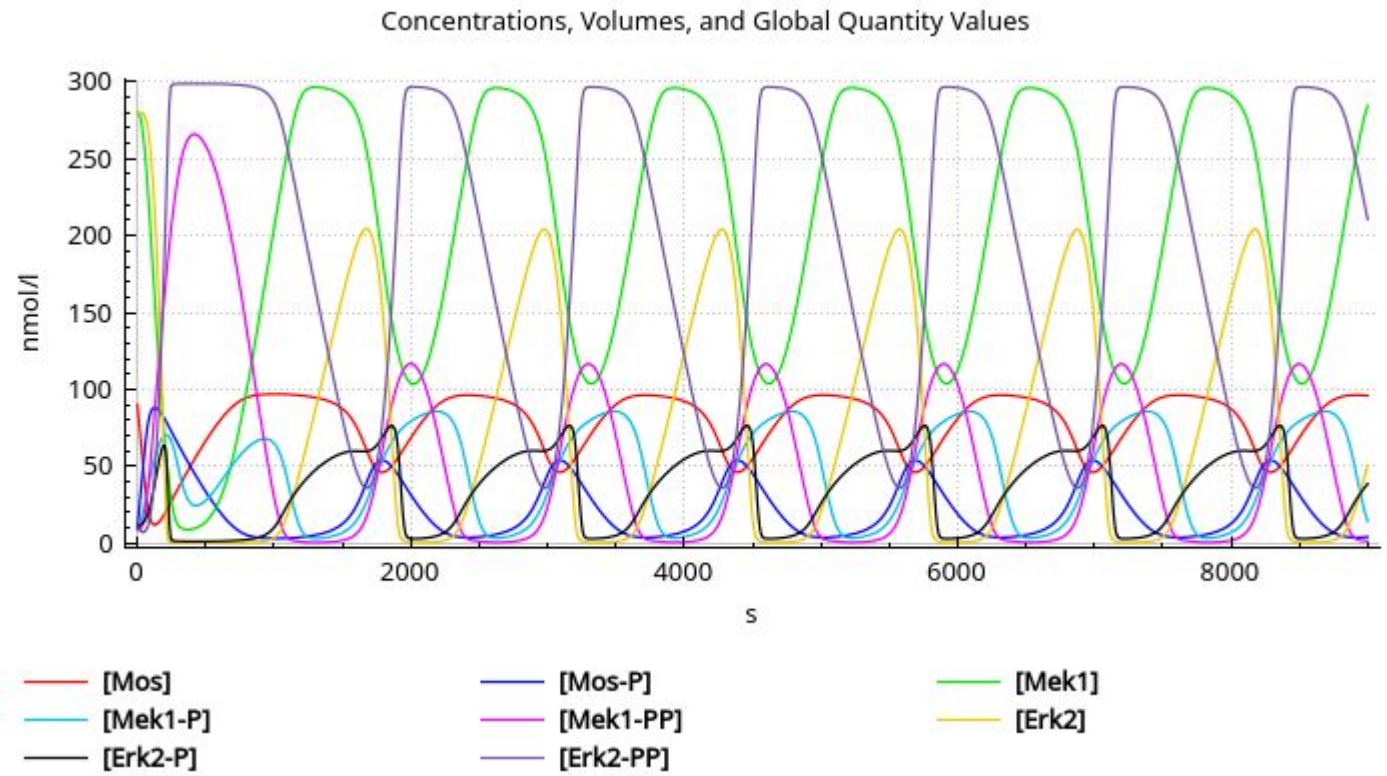
Kholodenko B. 2000: Negative feedback and ultrasensitivity can bring about oscillations in the mitogen-activated protein kinase cascades

- **Activated Mos activates Mek1**
- **Activated Mek1 activates Erk2**
- **Activated Erk2 activates Mos**

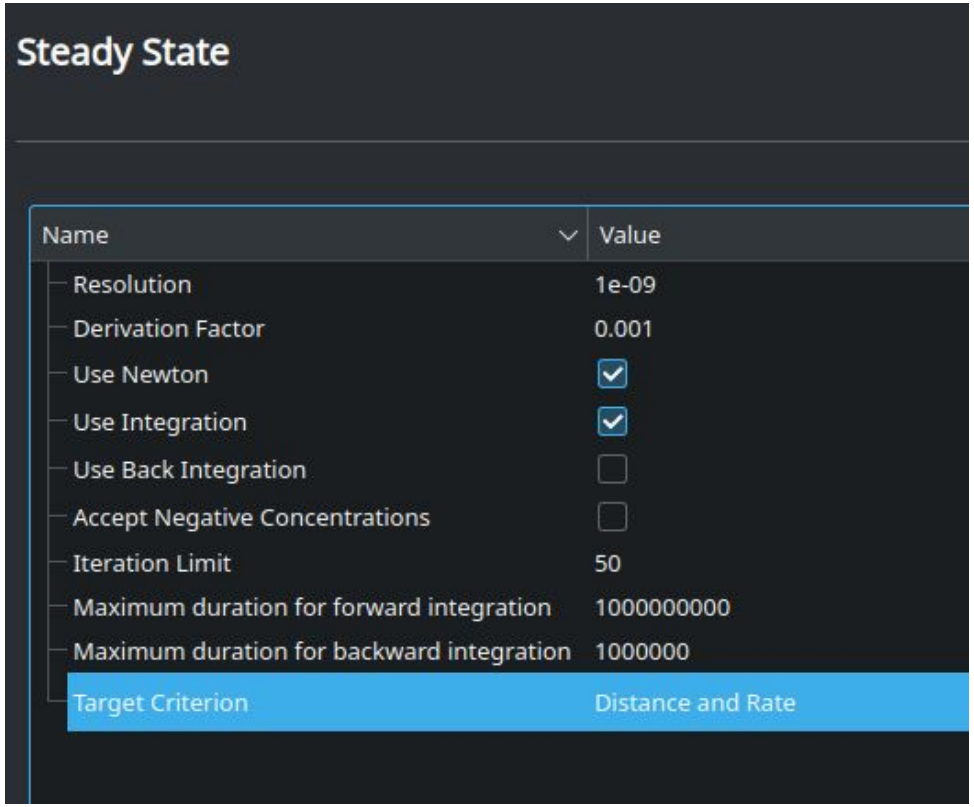


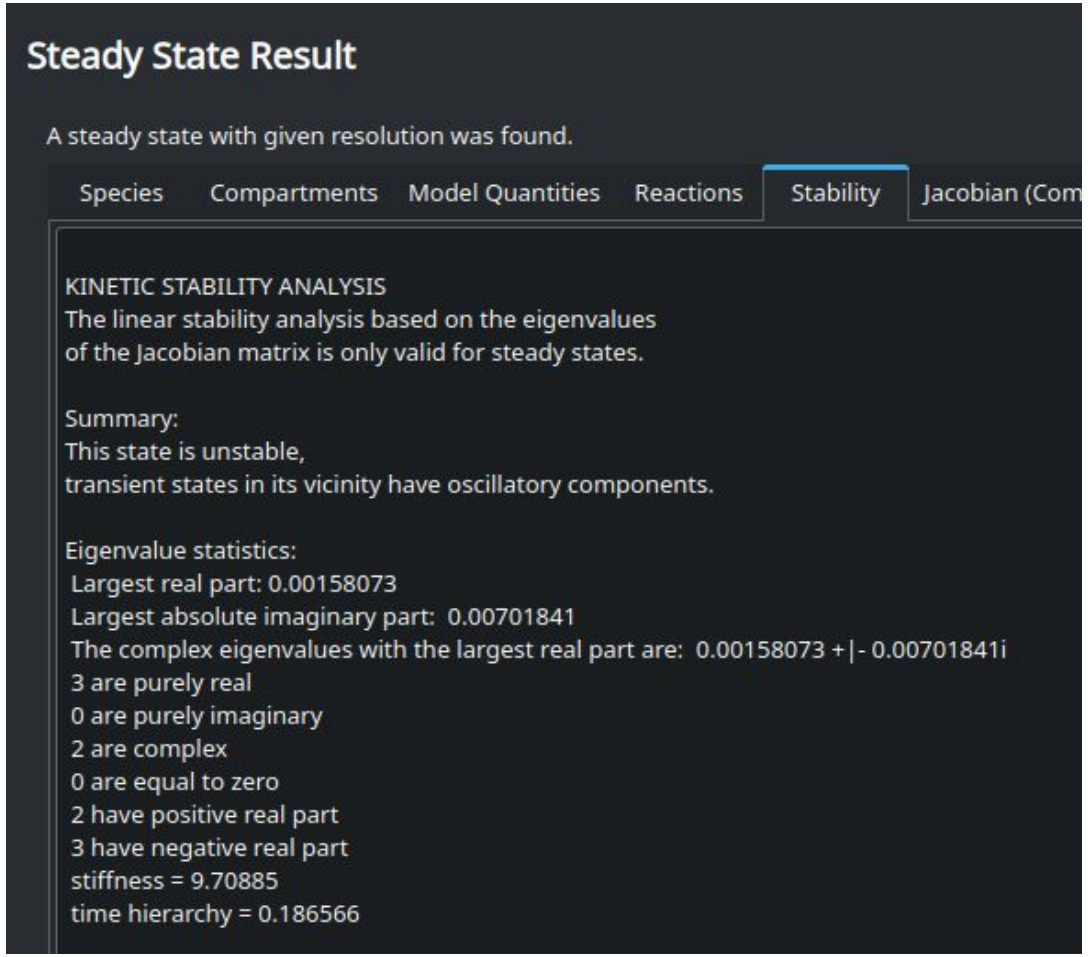
Time Course


Time Course
update model
executable
Duration, Intervals
Output Time Points
Duration [s] 9000
Intervals 1000
Interval Size [s] 9
Automatic
Start in Steady State
Suppress Output Before [s] 0
Output Events
Save Result in Memory
Integration Interval [s] 0 to 9000
Output Interval [s] 0 to 9000
Method Deterministic (LSODA)
Name
Value
Integrate Reduced Model
Relative Tolerance 1e-06
Absolute Tolerance 1e-12
Max Internal Steps 100000
Max Internal Step Size 0

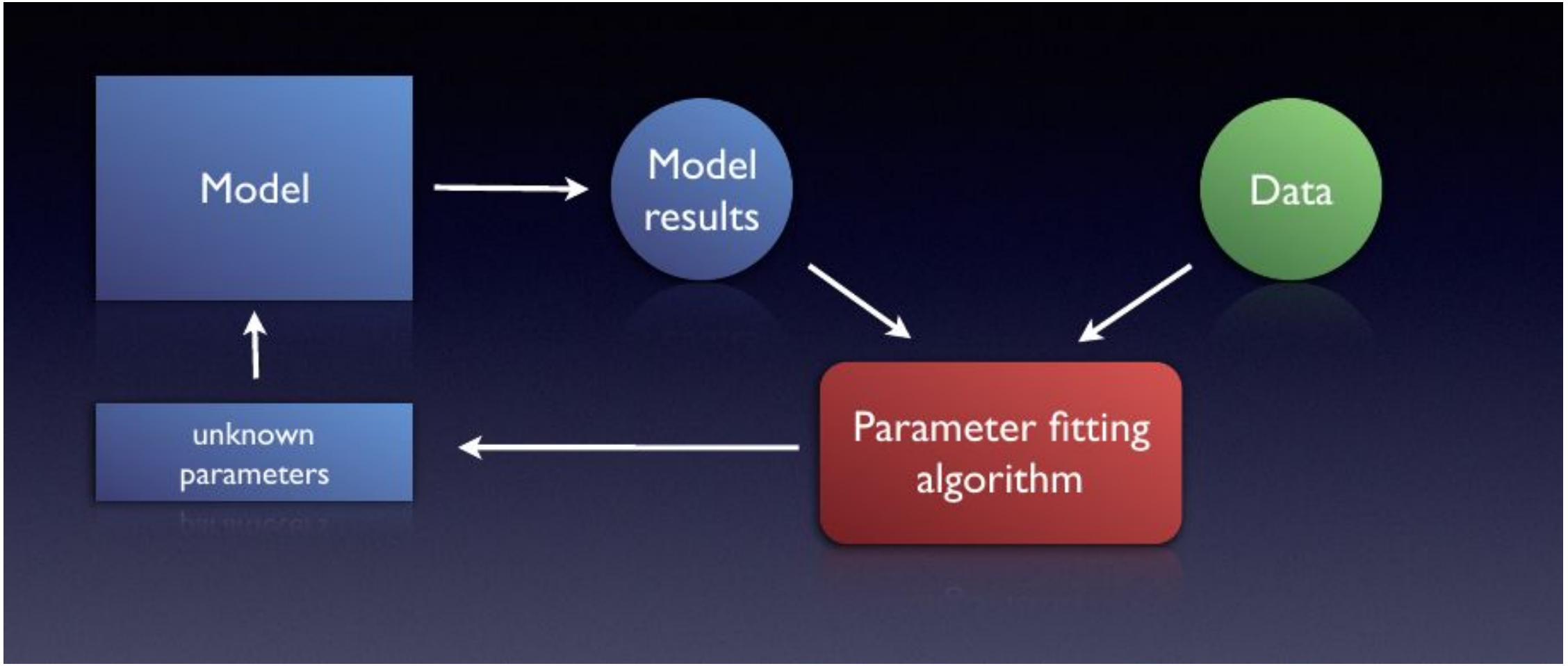

Concentrations, Volumes, and Global Quantity Values
nmol/l
300
250
200
150
100
50
0
0
2000
4000
6000
8000
s
[Mos]
[Mos-P]
[Mek1]
[Mek1-P]
[Mek1-PP]
[Erk2]
[Erk2-P]
[Erk2-PP]

Steady State

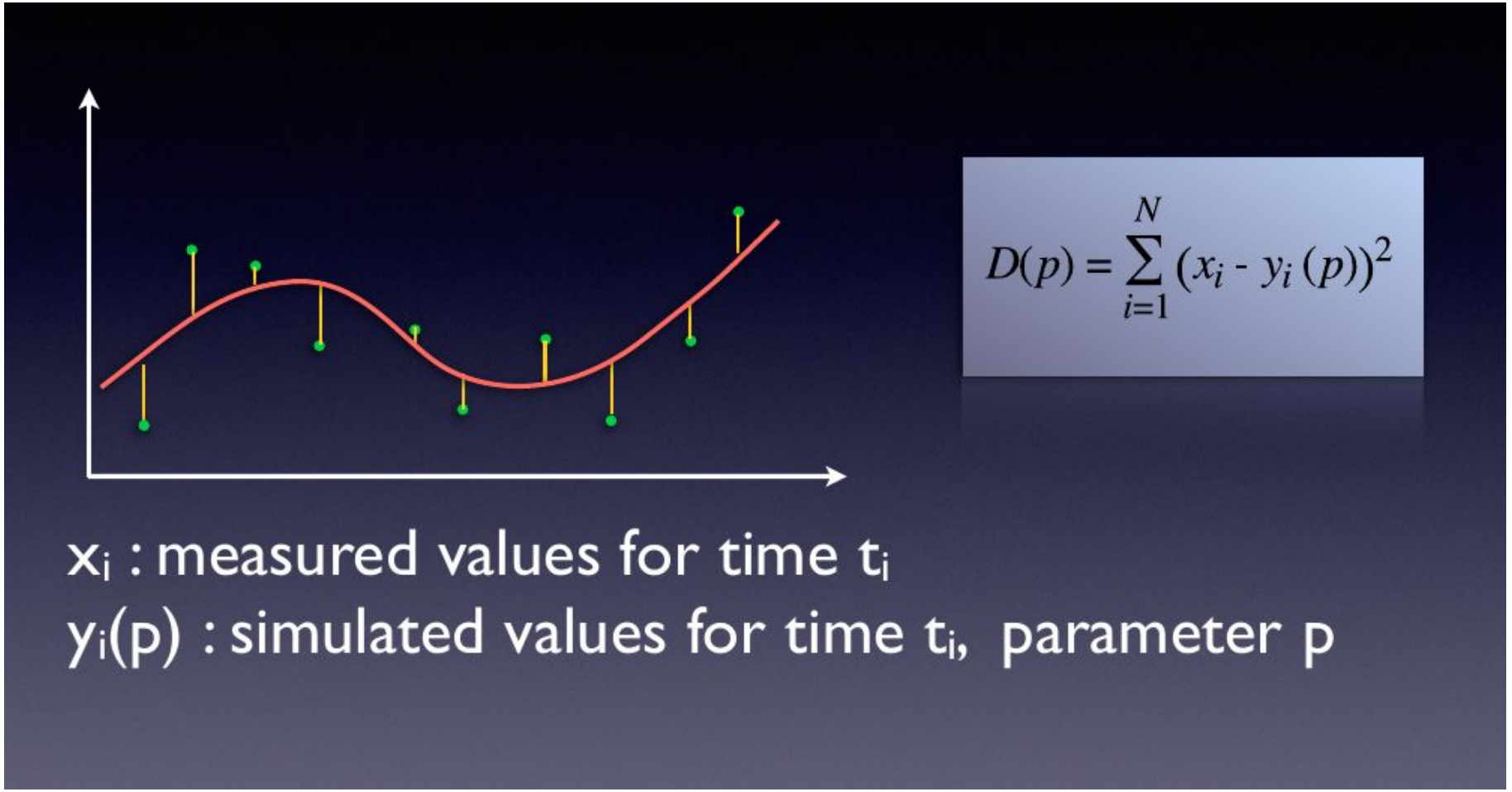




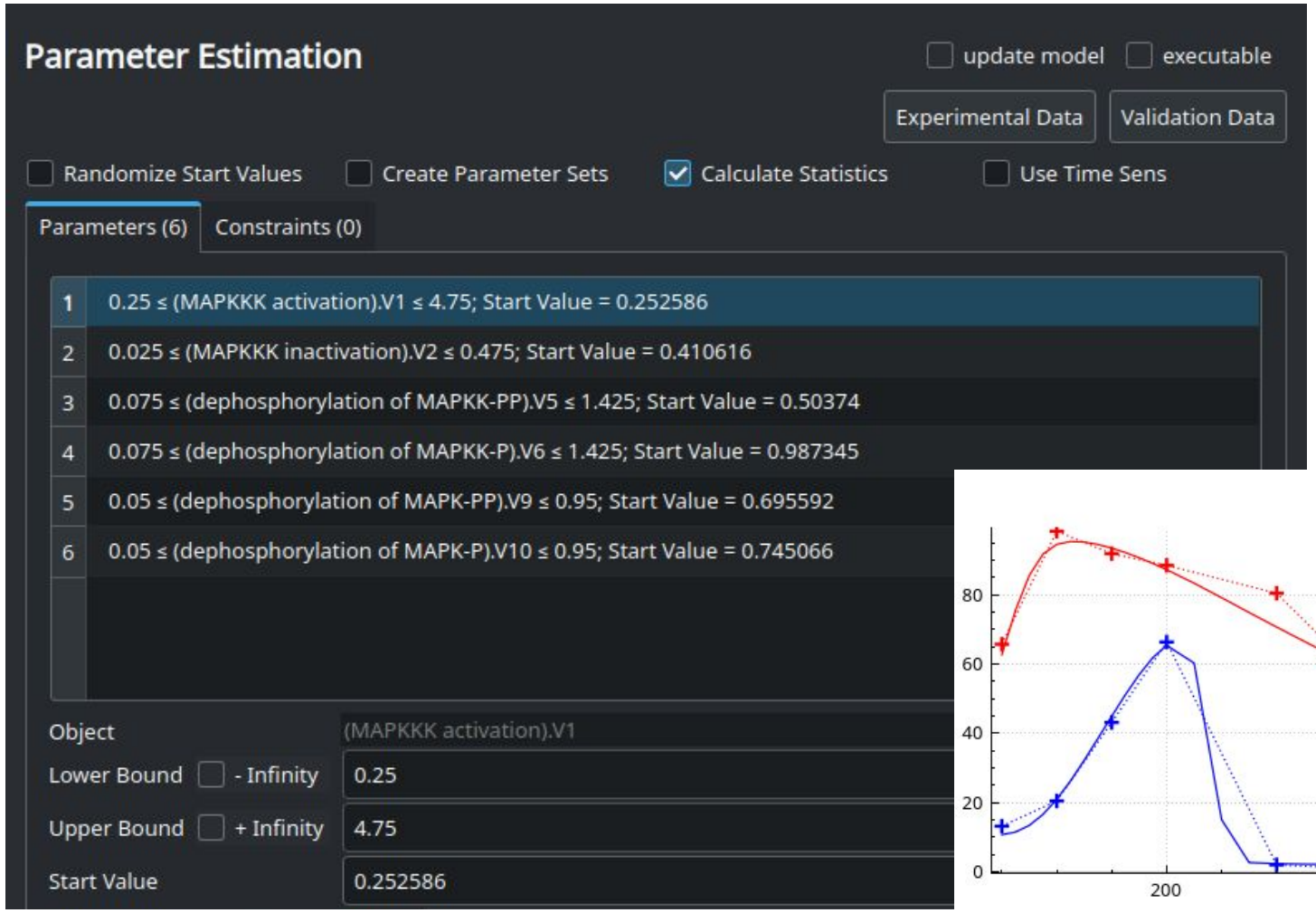
Parameter Estimation



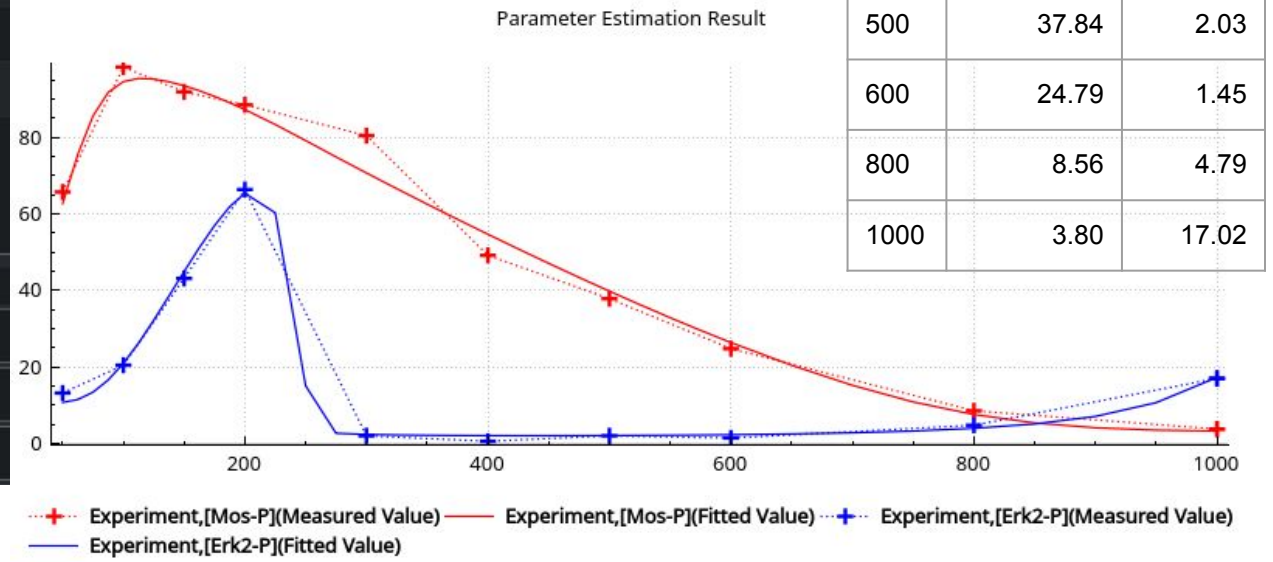
Parameter Estimation



Parameter Estimation



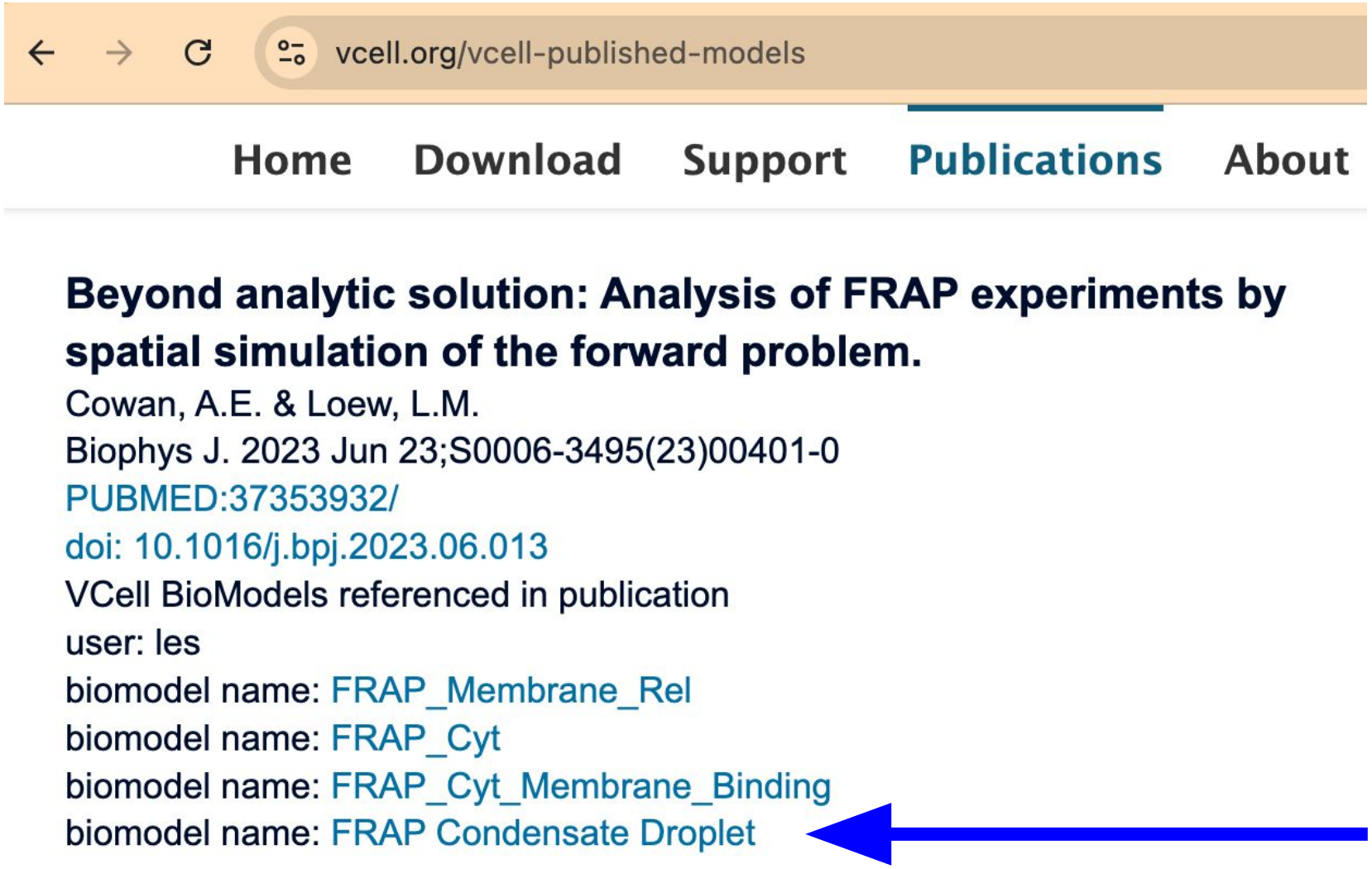
time	MAPKKK-P	MAPK-P
50	65.71	13.20
100	98.34	20.48
150	91.86	43.14
200	88.49	66.36
300	80.44	2.03
400	49.17	0.60
500	37.84	2.03
600	24.79	1.45
800	8.56	4.79
1000	3.80	17.02



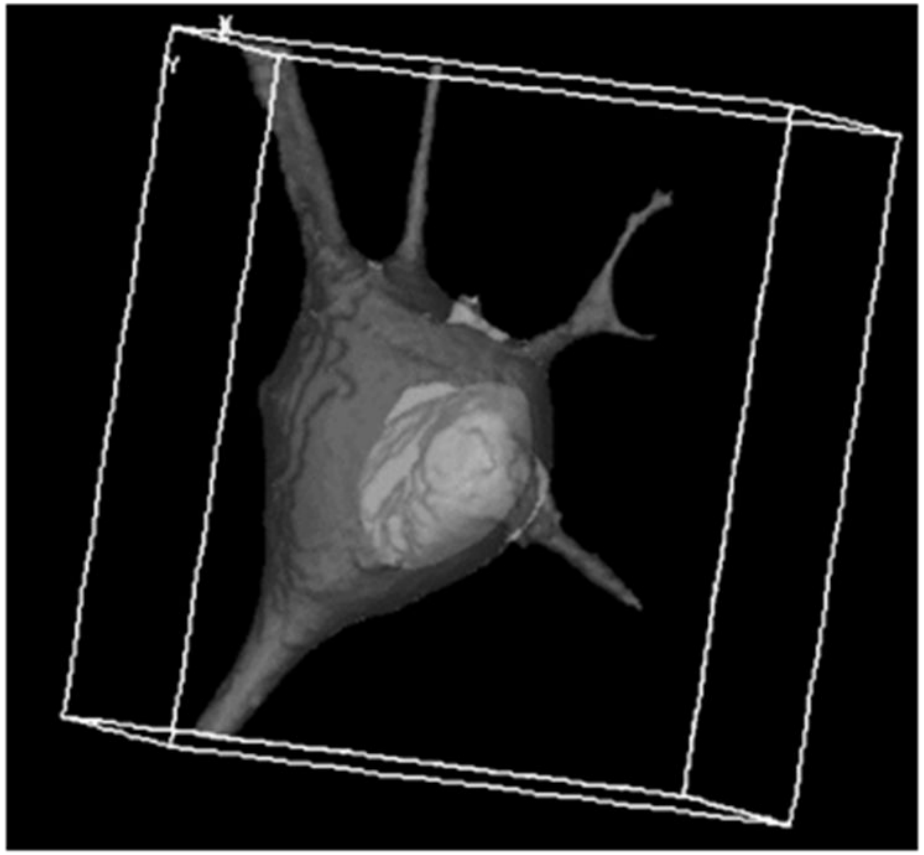
VCell Capabilities

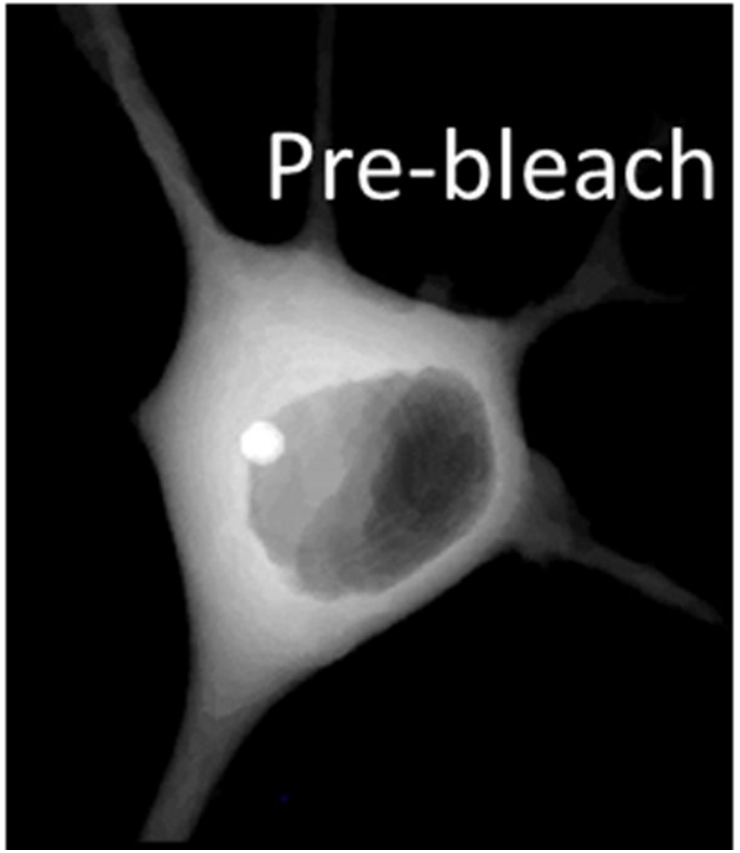
- Reaction - Diffusion - Advection - Electrophysiology
- 0, 1, 2 or 3D geometries, optionally from microscope images
- Deterministic and/or stochastic simulations
- Reaction networks or reaction rules
- Parameter scans and COPASI parameter estimation
- Database of models and model components
- Links to external model and pathway resources
- Biological Problems
  - Signaling and metabolic pathways
  - Intracellular trafficking
  - Ion channels
  - Virtual microscopy
  - Fluorescent indicators and probe redistribution

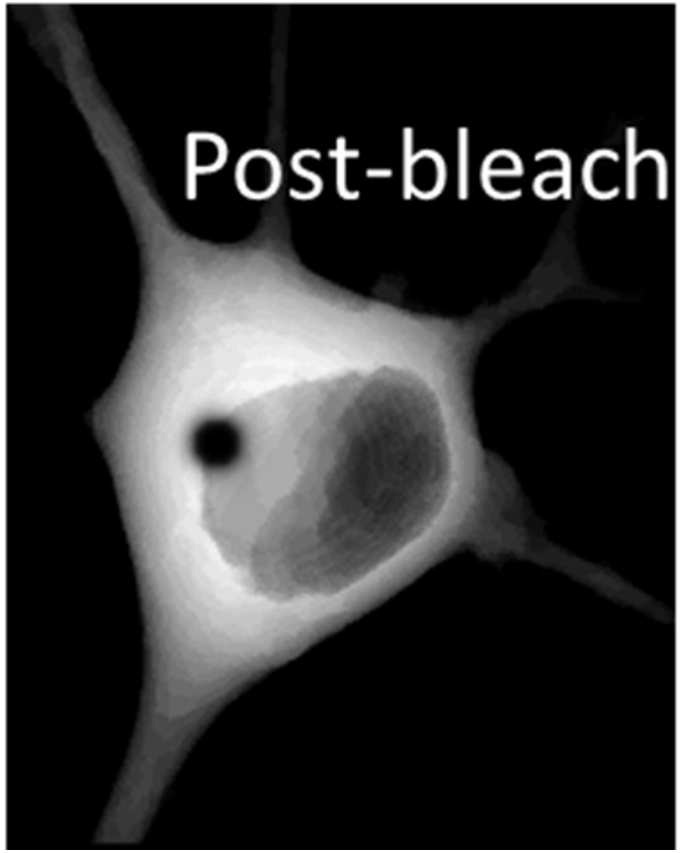
Example 2: Using PDEs to simulate FRAP of a biomolecular condensate



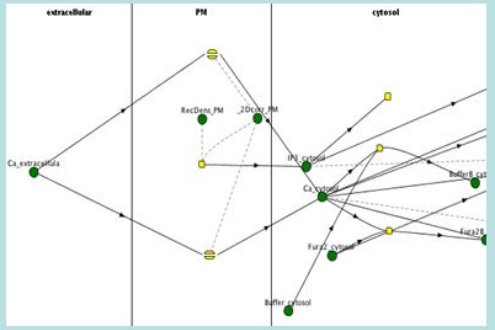
Example 2: Using PDEs to simulate FRAP of a biomolecular condensate







Physiology (Biological Mechanisms)



Reaction/Transport Network

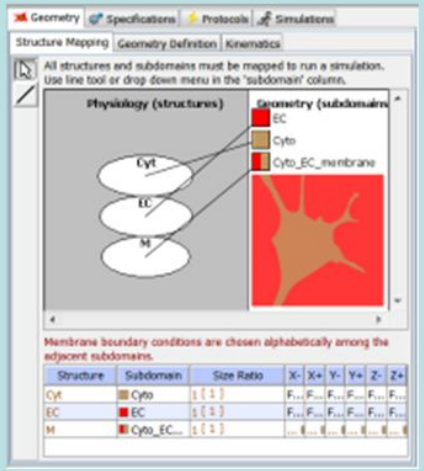
Or

Rule-based modeling (network free/agents BioNetGen)

k_{on}*(IP3_cyt)*(IP3R_mem) -k_{off}(IP3Rbound_mem)

Reaction Rate Expressions

Applications (Physical Model)



Choice of Simulation types:

Ordinary Differential Equations

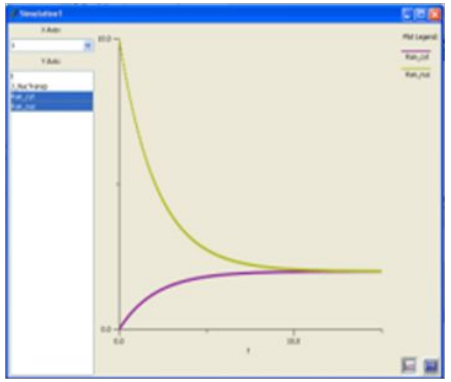
Partial Differential Equations

Non-Spatial Stochastic (Gillespie)

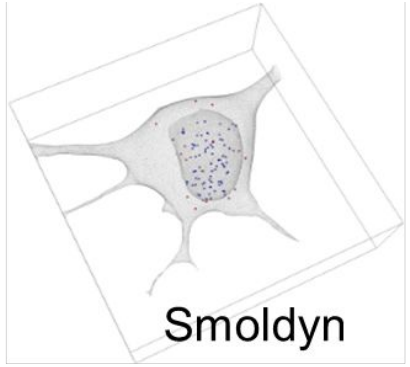
Spatial Stochastic (Smoldyn)

Hybrid Spatial Deterministic/stochastic

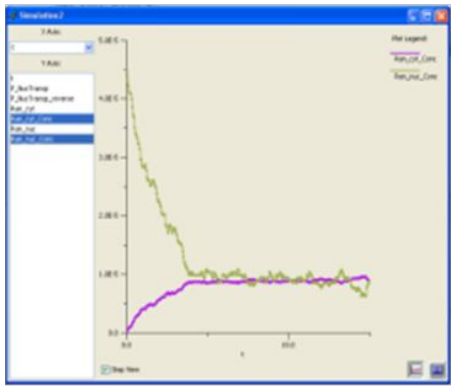
Network Free Stochastic



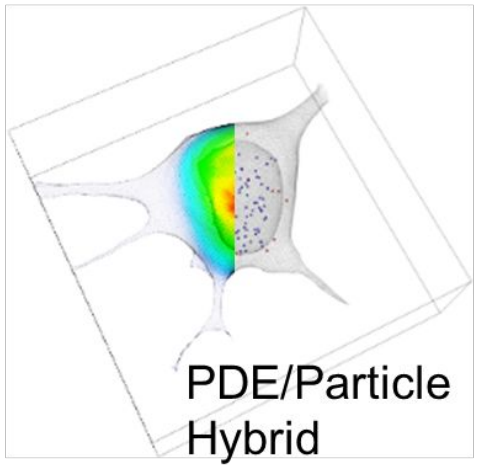
ODE



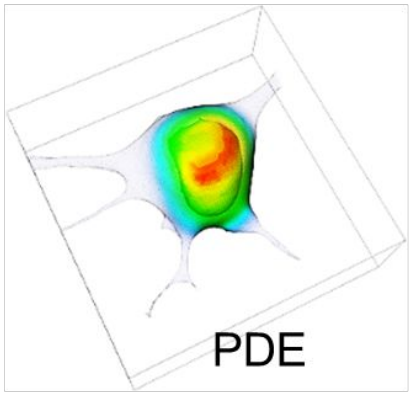
Smoldyn



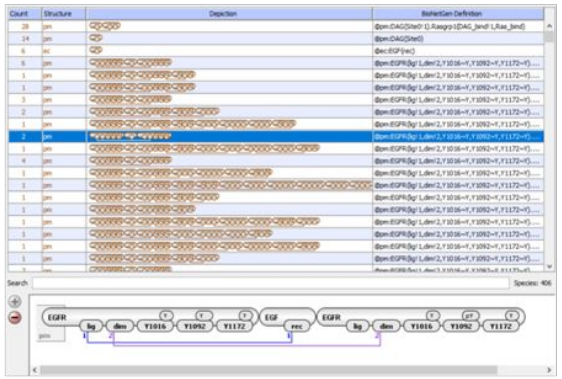
Nonspatial Stochastic (Gillespie, Hybrid)



PDE/Particle Hybrid

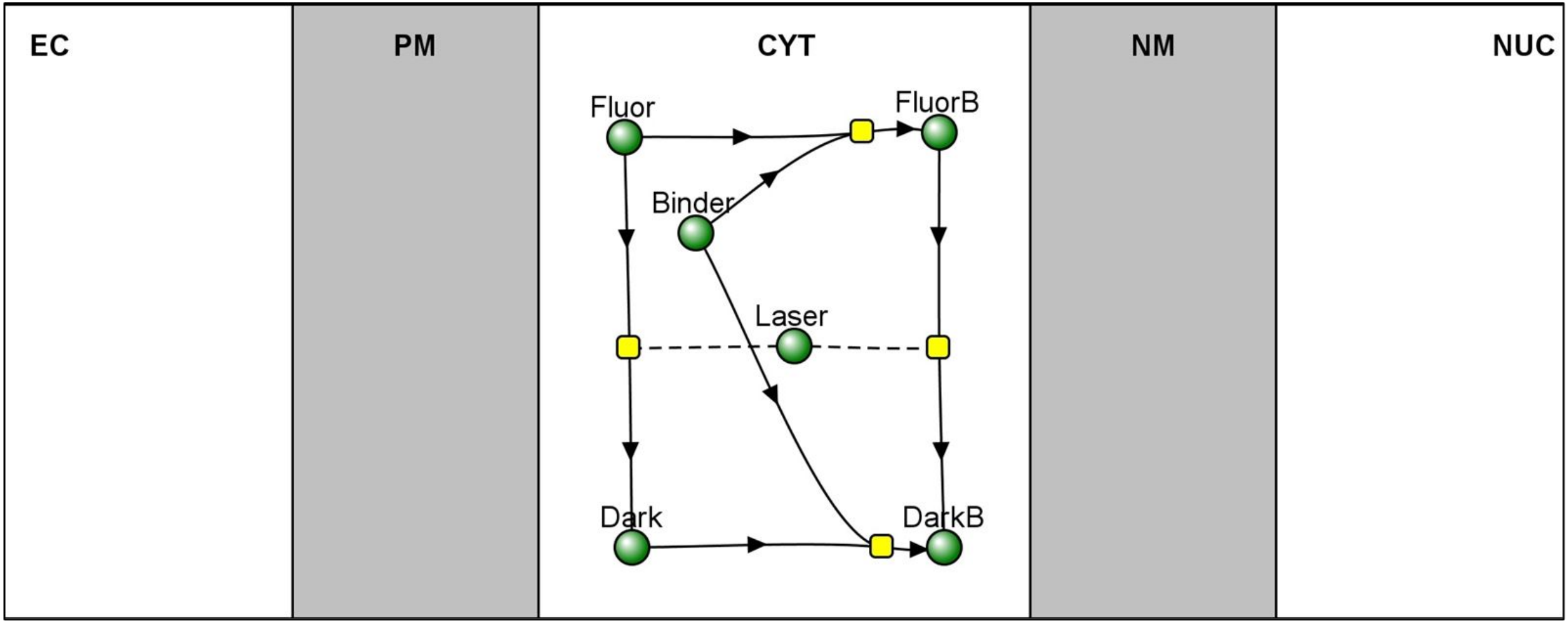


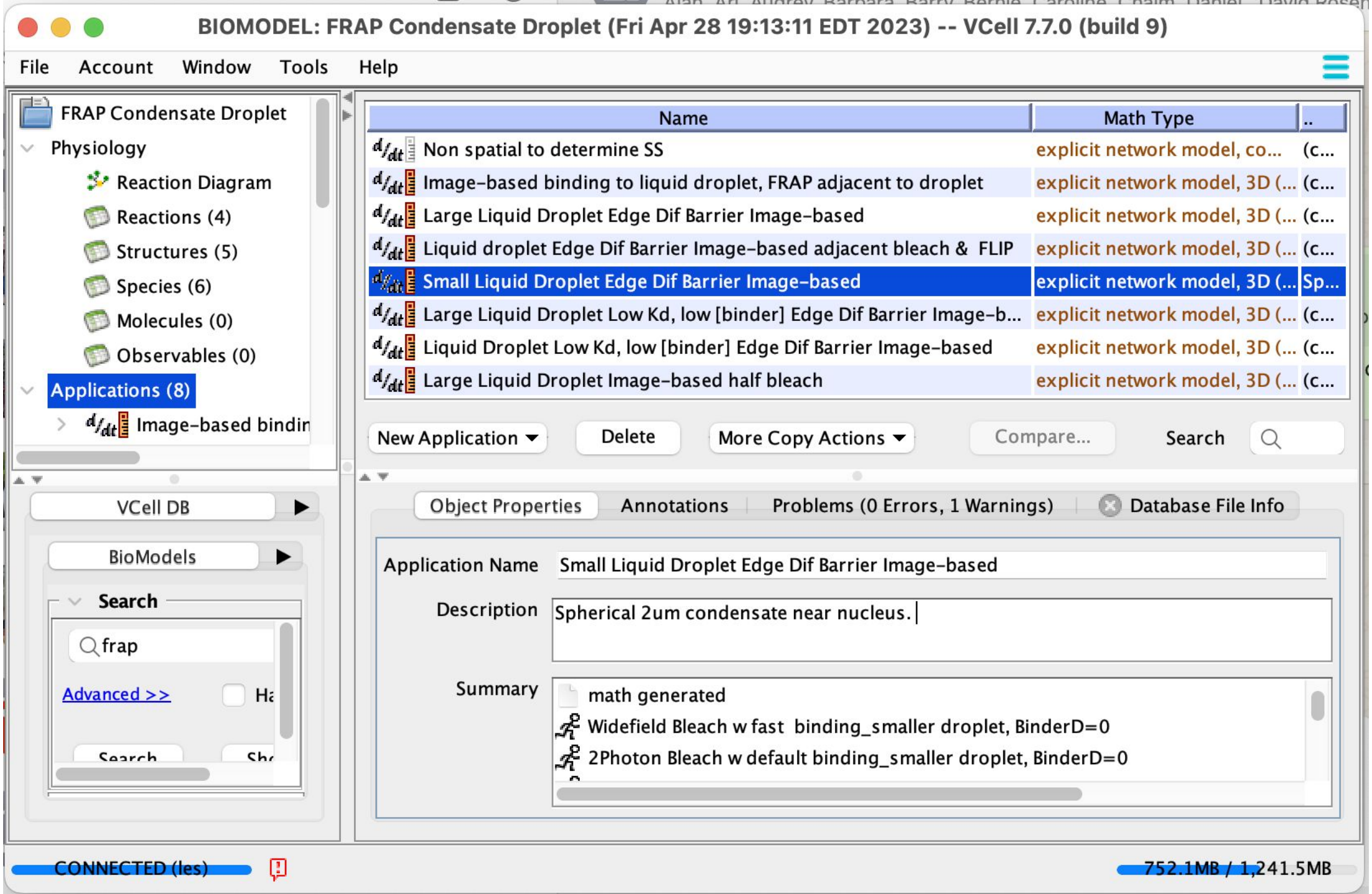
PDE

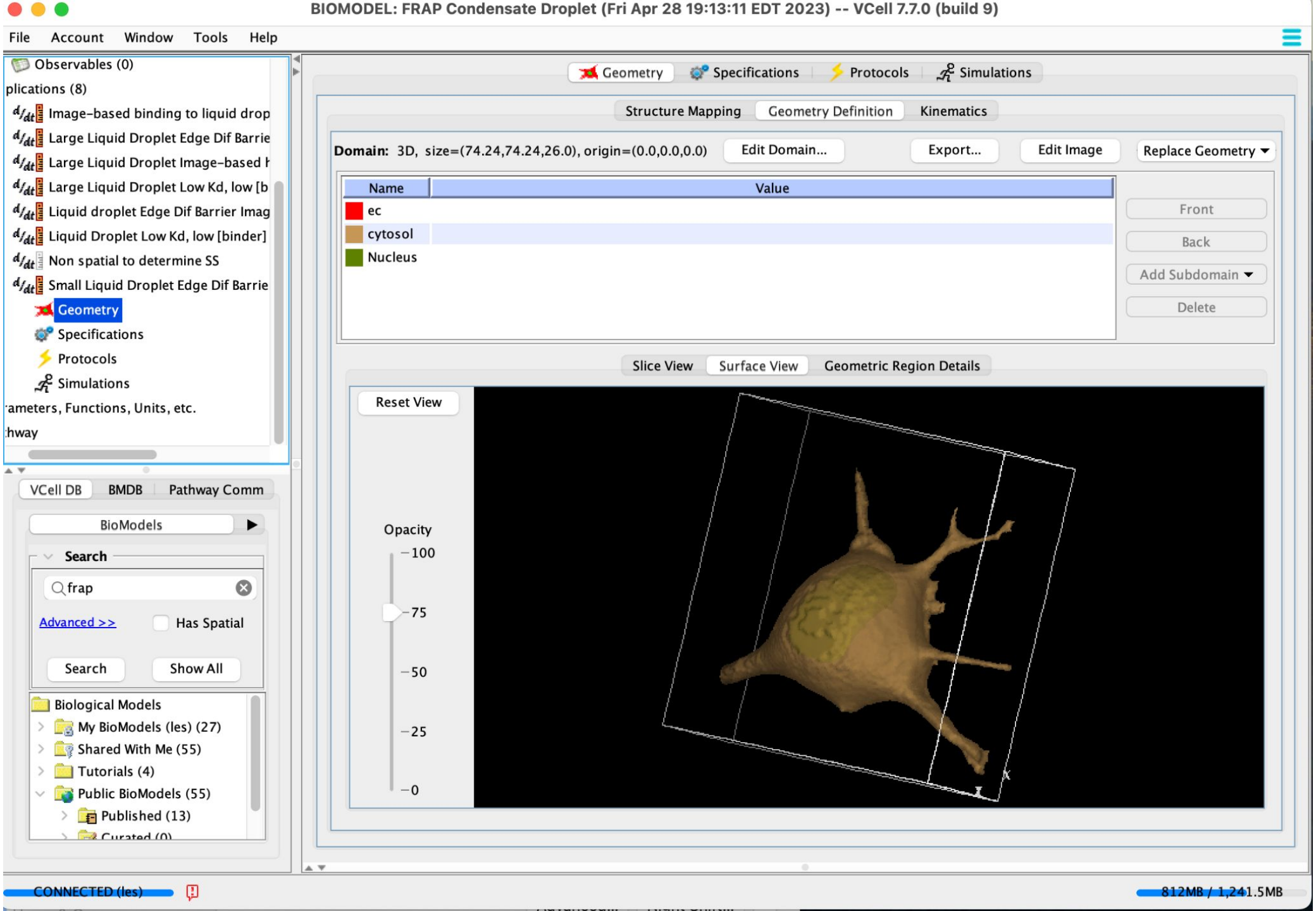


NFSim

Example 2: Using PDEs to simulate FRAP of a biomolecular condensate




BIOMODEL: FRAP Condensate Droplet (Fri Apr 28 19:13:11 EDT 2023) -- VCell 7.7.0 (build 9)
File
Account
Window
Tools
Help
FRAP Condensate Droplet
Physiology
Reaction Diagram
Reactions (4)
Structures (5)
Species (6)
Molecules (0)
Observables (0)
Applications (8)
Image-based bindin
Name
Math Type
Non spatial to determine SS
explicit network model, co...
Image-based binding to liquid droplet, FRAP adjacent to droplet
explicit network model, 3D (...
Large Liquid Droplet Edge Dif Barrier Image-based
Liquid droplet Edge Dif Barrier Image-based adjacent bleach & FLIP
Small Liquid Droplet Edge Dif Barrier Image-based
Large Liquid Droplet Low Kd, low [binder] Edge Dif Barrier Image-b...
Liquid Droplet Low Kd, low [binder] Edge Dif Barrier Image-based
Large Liquid Droplet Image-based half bleach
New Application
Delete
More Copy Actions
Compare...
Search
VCell DB
BioModels
Search
frap
Advanced >>
Object Properties
Annotations
Problems (0 Errors, 1 Warnings)
Database File Info
Application Name
Small Liquid Droplet Edge Dif Barrier Image-based
Description
Spherical 2um condensate near nucleus.
Summary
math generated
Widefield Bleach w fast binding_smaller droplet, BinderD=0
2Photon Bleach w default binding_smaller droplet, BinderD=0
CONNECTED (les)
752.1MB / 1,241.5MB


BIOMODEL: FRAP Condensate Droplet (Fri Apr 28 19:13:11 EDT 2023) -- VCell 7.7.0 (build 9)
File
Account
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Tools
Help
Observables (0)
plications (8)
Image-based binding to liquid drop
Large Liquid Droplet Edge Dif Barrie
Large Liquid Droplet Image-based I
Large Liquid Droplet Low Kd, low [b
Liquid droplet Edge Dif Barrier Imag
Liquid Droplet Low Kd, low [binder]
Non spatial to determine SS
Small Liquid Droplet Edge Dif Barrie
Geometry
Specifications
Protocols
Simulations
ameters, Functions, Units, etc.
hway
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Pathway Comm
BioModels
Search
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Advanced >>
Has Spatial
Search
Show All
Biological Models
My BioModels (les) (27)
Shared With Me (55)
Tutorials (4)
Public BioModels (55)
Published (13)
Curated (0)
Geometry
Specifications
Protocols
Simulations
Structure Mapping
Geometry Definition
Kinematics
Domain: 3D, size=(74.24,74.24,26.0), origin=(0.0,0.0,0.0)
Edit Domain...
Export...
Edit Image
Replace Geometry
Name
Value
ec
cytosol
Nucleus
Front
Back
Add Subdomain
Delete
Slice View
Surface View
Geometric Region Details
Reset View
Opacity
100
75
50
25
0
CONNECTED (les)
812MB / 1,241.5MB

Image-based binding to lic
Large Liquid Droplet Edge
Large Liquid Droplet Image
Large Liquid Droplet Low K
Liquid droplet Edge Dif Bar
Liquid Droplet Low Kd, low
Non spatial to determine S
Small Liquid Droplet Edge I
Geometry
Specifications
Protocols

VCell DB

BioModels

Search

frap

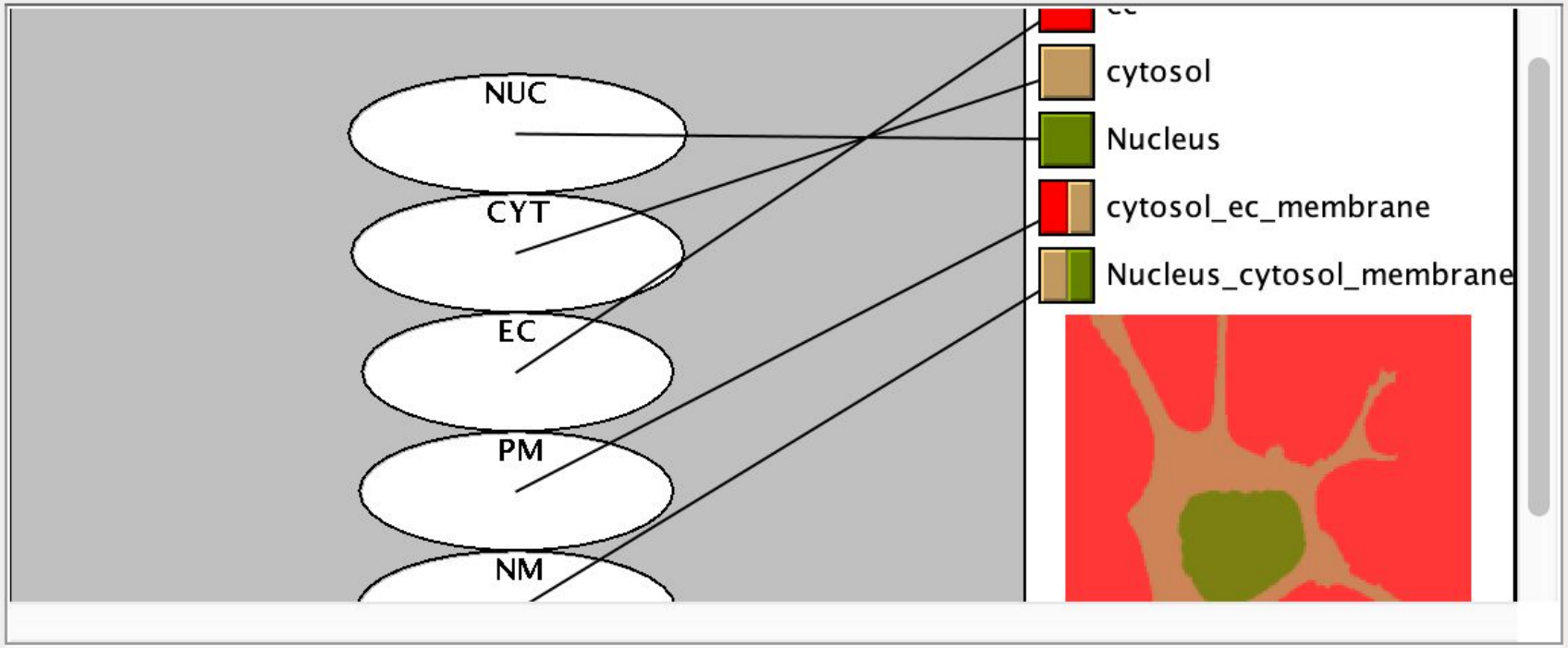
Advanced >>

Search

Geometry | Specifications | Protocols | Simulations

Structure Mapping | Geometry Definition | Kinematics

All structures and subdomains must be mapped to run a simulation. Use line tool or drop down menu in the 'subdomain' column.



Membrane boundary conditions are chosen alphabetically among the adjacent subdomains.

Structure	Subdomain	Size Ratio	X-	X+	Y-	Y+	Z-	Z+
NUC	Nucleus	1 [1]	Flux	Flux	Flux	Flux	Flux	Flux
CYT	cytosol	1 [1]	Flux	Flux	Flux	Flux	Flux	Flux
EC	ec	1 [1]	Flux	Flux	Flux	Flux	Flux	Flux

Geometry | Specifications | Protocols | Simulations

Species | Reaction | Network

Species	Structure	Depiction	Clamped	Rules	Initial Condition	Well Mixed	Diffusion Constant
Fluor	CYT				1.4462440264001468 [µM]		((((((x – 23.0) ^ 2.0) + ((y –
Dark	CYT				0.0 [µM]		((((((x – 23.0) ^ 2.0) + ((y –
Binder	CYT				(591.4462440264 * ((((x – 23.0) ^ 2.0) + ((y		(((((x – 23.0) ^ 2.0) + ((y –
FluorB	CYT				(8.553755973599845 * ((((x – 23.0) ^ 2.0)		(((((x – 23.0) ^ 2.0) + ((y –
Laser	CYT				(exp(– (((z – 10.0) ^ 2.0) / (2.0 * (sigmaaxial		0.0 [µm^2.s^{-1}]
DarkB	CYT				0.0 [µM]		(((((x – 23.0) ^ 2.0) + ((y –

Search

Object Properties | Annotations | Problems (0 Errors, 1 Warnings) | Database File Info

Description	Parameter	Expression	Units
initial concentration for FluorB	initConc	$8.553755973599845 \cdot ((((x - 23.0))^{2.0} + ((y - 39.0))^{2.0} + ((z - 13.0))^{2.0}) < 4.0)$	µM
diffusion constant for FluorB	diff	$((((x - 23.0))^{2.0} + ((y - 39.0))^{2.0} + ((z - 13.0))^{2.0}) < 4.0) \cdot BinderD$	µm^2.s^{-1}

Geometry | Specifications | Protocols | Simulations

Electrical | Events | Rate Rules | Assignment Rules | Microscope Measurements

Fluorescence Function Name fluor

Point Spread Function

(•) Z Projection

( ) Gaussian Sigma XY Sigma Z

Choose Fluorescent Species

Dark
Binder
Laser
DarkB

>>
<<

FluorB
Fluor

Geometry | Specifications | Protocols | Simulations

Simulations | Output Functions | Generated Math

Name	End Time	Output Option	Solver	Running Status	Results
No edge BarrierWidefield Bleach w fast binding_smaller droplet, BinderD=0	100.0	every 1.0 s	Fully-Impl...	completed	yes
No Edge BarrierWidefield Bleach w defalt binding_smaller droplet, BinderD=0	100.0	every 1.0 s	Fully-Impl...	completed	yes
No Edge BarrierWidefield Bleach w very slow binding_smaller droplet, Binde...	100.0	every 1.0 s	Fully-Impl...	completed	yes
Widefield Bleach w very slow binding_smaller droplet, BinderD=0	100.0	every 1.0 s	Fully-Impl...	completed	yes
Widefield Bleach w fast binding_smaller droplet, BinderD=0.1	100.0	every 1.0 s	Fully-Impl...	completed	yes
2Photon Bleach w default binding_smaller droplet, BinderD=0.1	100.0	every 1.0 s	Fully-Impl...	completed	yes
Fig. 7.B. With DropletD=1, EdgeD=0.1, kf=0.025, kr=2.5	100.0	every 1.0 s	Fully-Impl...	completed	yes
No edge BarrierWidefield Bleach w fast binding_smaller droplet, BinderD=0...	100.0	every 1.0 s	Fully-Impl...	completed	yes
Fig. 6A. DropletD=1, Fig. 6B. DropletD=0.1; for both kr=2.5, kf = 0.025, Bi...	100.0	every 1.0 s	Fully-Impl...	completed	yes
Fig. 6C. DropletD=1, Fig. 6D. DropletD=0.1; for both kr=0.025, kf = 0.000...	100.0	every 1.0 s	Fully-Impl...	completed	yes
Widefield Bleach w very slow binding_smaller droplet, BinderD=0.1	100.0	every 1.0 s	Fully-Impl...	completed	yes

Object Properties | Annotations | Problems (0 Errors, 1 Warnings) | Database File Info

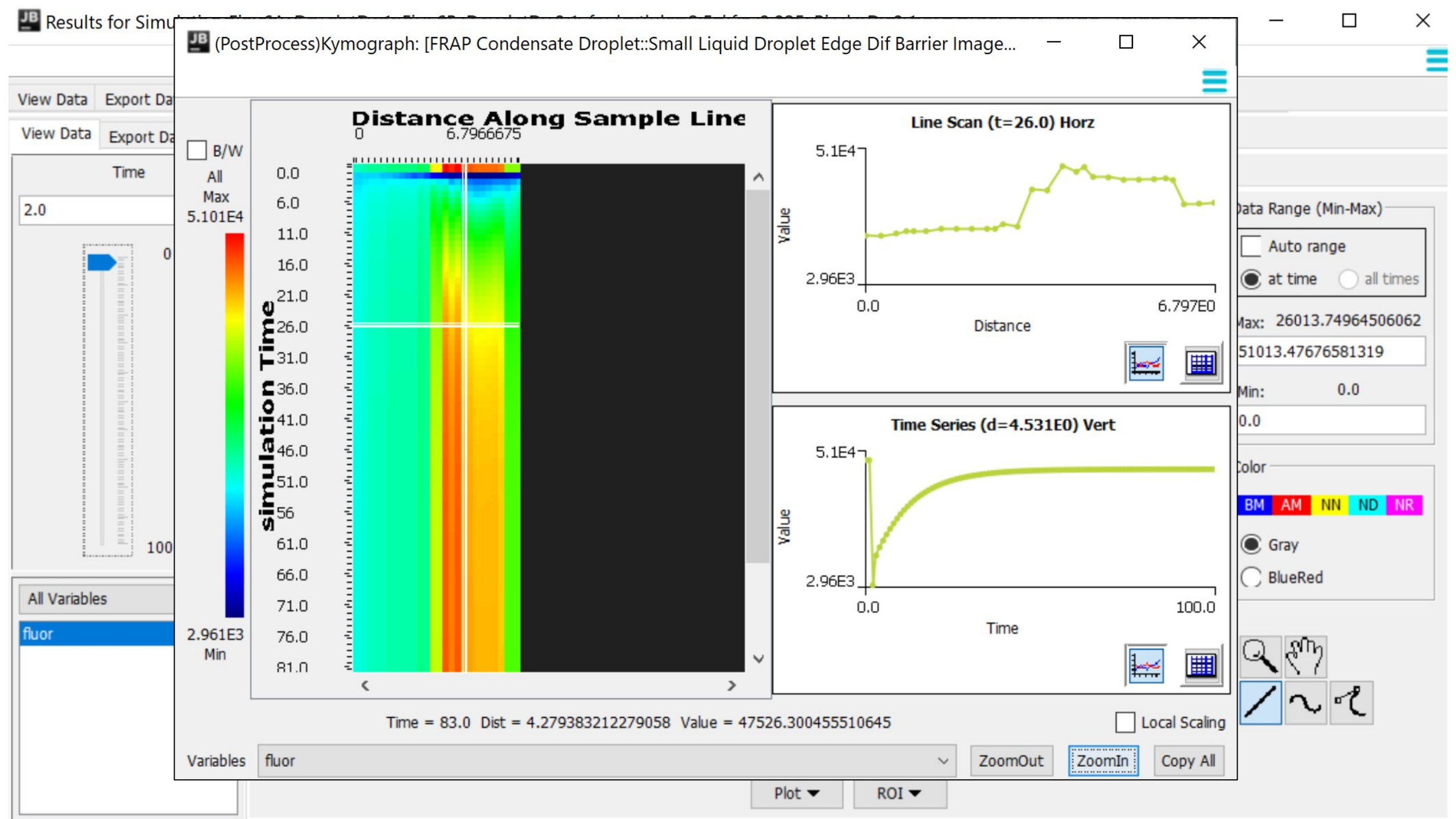
Annotation: Fig. 6A. DropletD=1, Fig. 6B. DropletD=0.1; for both kr=2.5, kf = 0.025, BinderD=0.1

Settings:

Max timestep	Output	Rel tol	Abs tol
0.1s	every 1.0 sec	1.0E-7	1.0E-9

Mesh: 256x256x35 = 2293760 elements

Geometry size: (74.24,74.24,26.0) microns


Results for Simu
(PostProcess)Kymograph: [FRAP Condensate Droplet::Small Liquid Droplet Edge Dif Barrier Image...
View Data
Export Da
Time
2.0
0
100
All Variables
fluor
B/W
All
Max
5.101E4
2.961E3
Min
Distance Along Sample Line
0
6.7966675
simulation Time
0.0
6.0
11.0
16.0
21.0
26.0
31.0
36.0
41.0
46.0
51.0
56
61.0
66.0
71.0
76.0
81.0
Line Scan (t=26.0) Horz
5.1E4
2.96E3
Value
0.0
6.797E0
Distance
Time Series (d=4.531E0) Vert
5.1E4
2.96E3
Value
0.0
100.0
Time
Time = 83.0 Dist = 4.279383212279058 Value = 47526.300455510645
Local Scaling
Variables
fluor
ZoomOut
ZoomIn
Copy All
Plot
ROI
Data Range (Min-Max)
Auto range
at time
all times
Max: 26013.74964506062
51013.47676581319
Min: 0.0
0.0
Color
BM
AM
NN
ND
NR
Gray
BlueRed

Results for Simulation Fig. 6A. DropletD=1, Fig. 6B. DropletD=0.1; for both kr=2.5, kf = 0.025, BinderD=0.1

View Data | Export Data | Post Processing Stats Data | Post Processing Image Data

Time

10.0

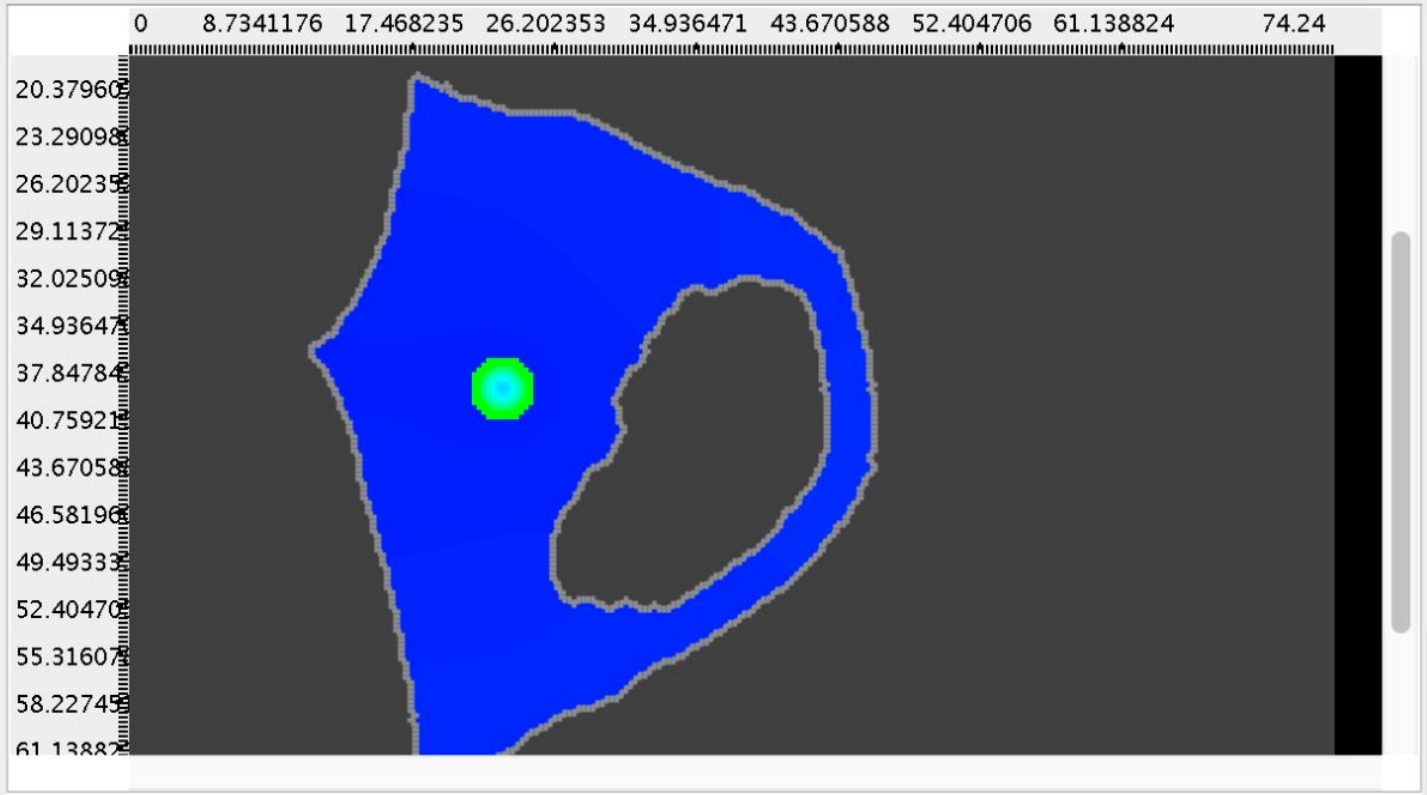
0

100

All Variables

Laser_init_uM
ROI
sobj_cytosol1_ec0_siz
sobj_Nucleus2_cytosc
TotalF
vobj_cytosol1_size

Slice View | Surface View



Info

Plot | ROI

Data Range (Min-Max)

Auto range

at time | all times (approx)

Max: 6.3579144635698635

10.0

Min: 1.251932280079312

0.0

Color

BM | AM | NN | ND | NR

Gray

BlueRed

Slice [0-34]

Z [17] = 13

Choose Parameter Values

DropletD
0.1
1.0
3.0

Example 2: Using PDEs to simulate FRAP of a biomolecular condensate

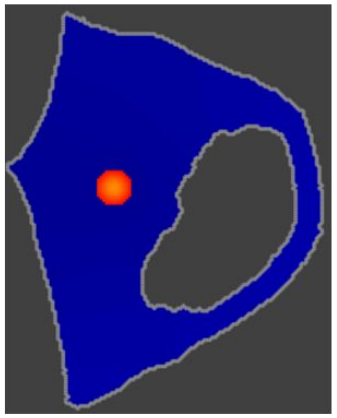
Figure 6 from Cowan and Loew, *Biophys. J.* 2023

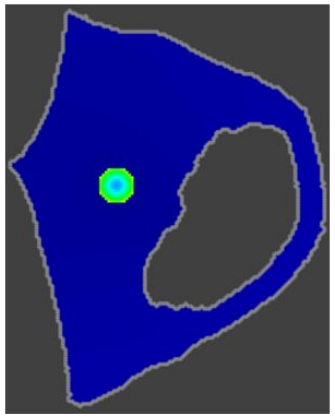
A. D=1 $\mu m^2/s$
k_r= 2.5 s^{-1}

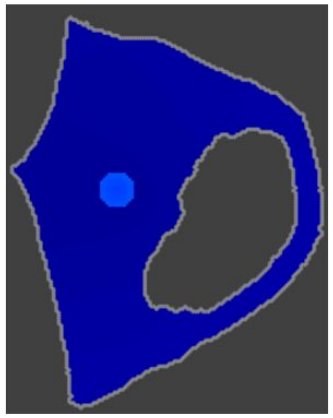
B. D=0.1 $\mu m^2/s$
k_r= 2.5 s^{-1}

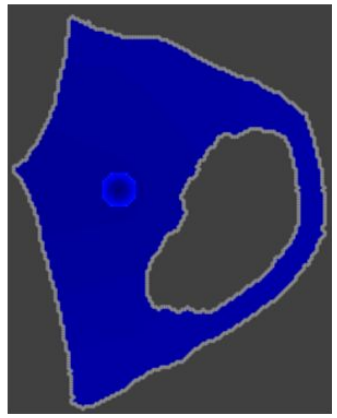
C. D=1 $\mu m^2/s$
k_r= 0.025 s^{-1}

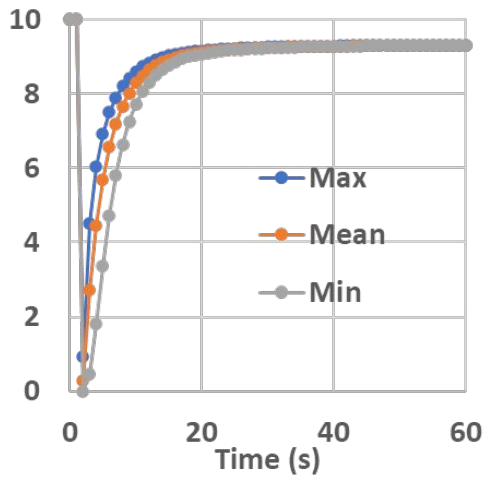
D. D=0.1 $\mu m^2/s$
k_r= 0.025 s^{-1}

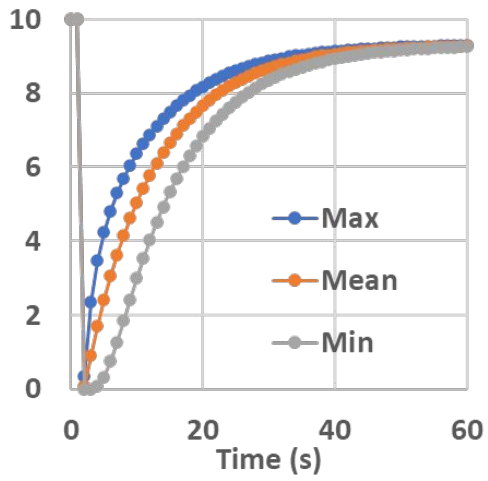


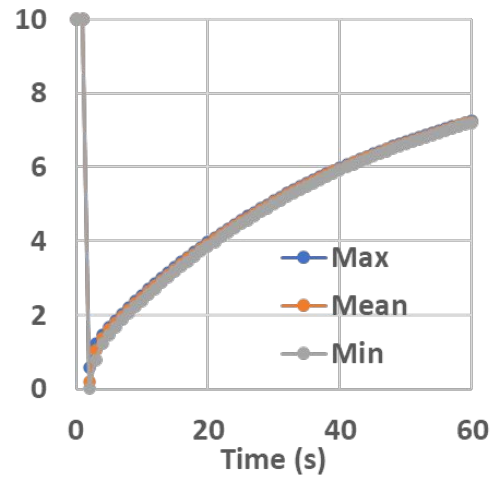


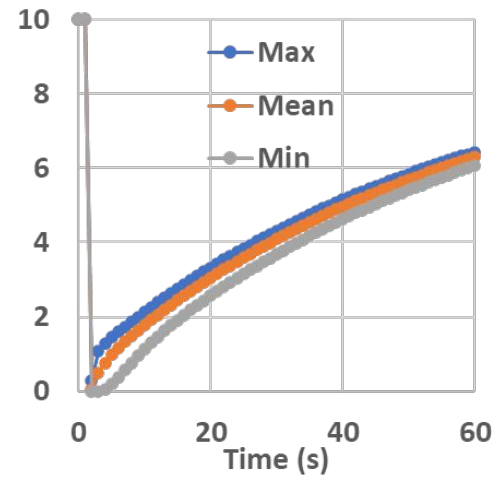






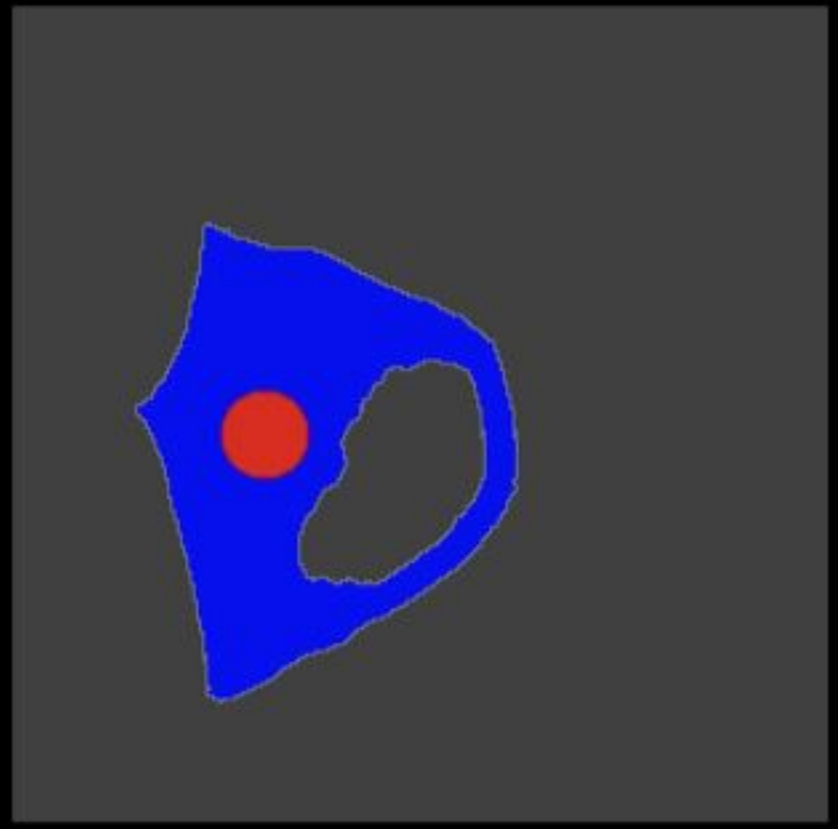






Half bleach of a large droplet (Fig. 8b)

(movie exported directly from VCell)



Simulation experiments can be directly compared to microscopy experiments to answer questions like:

is it dissociation kinetics or intradroplet viscosity that controls the dynamics of biomolecular condensates?

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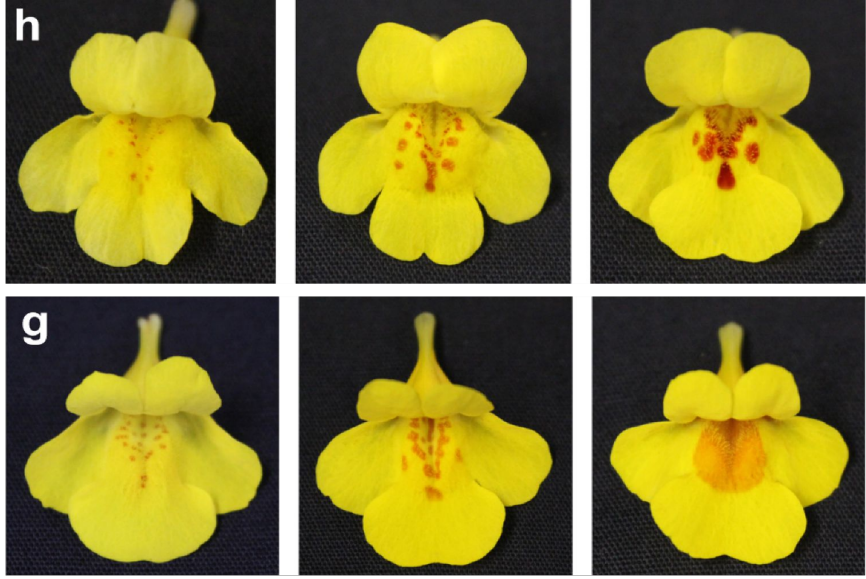
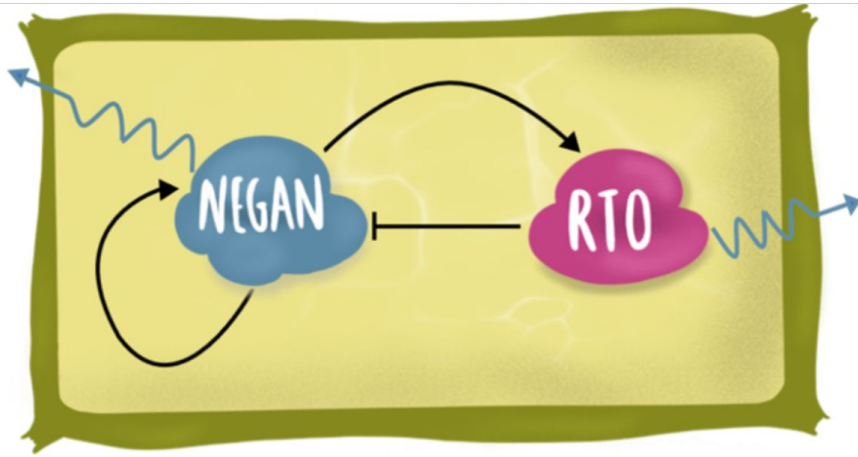
Two MYB Proteins in a Self-Organizing Activator-Inhibitor System Produce Spotted Pigmentation Patterns

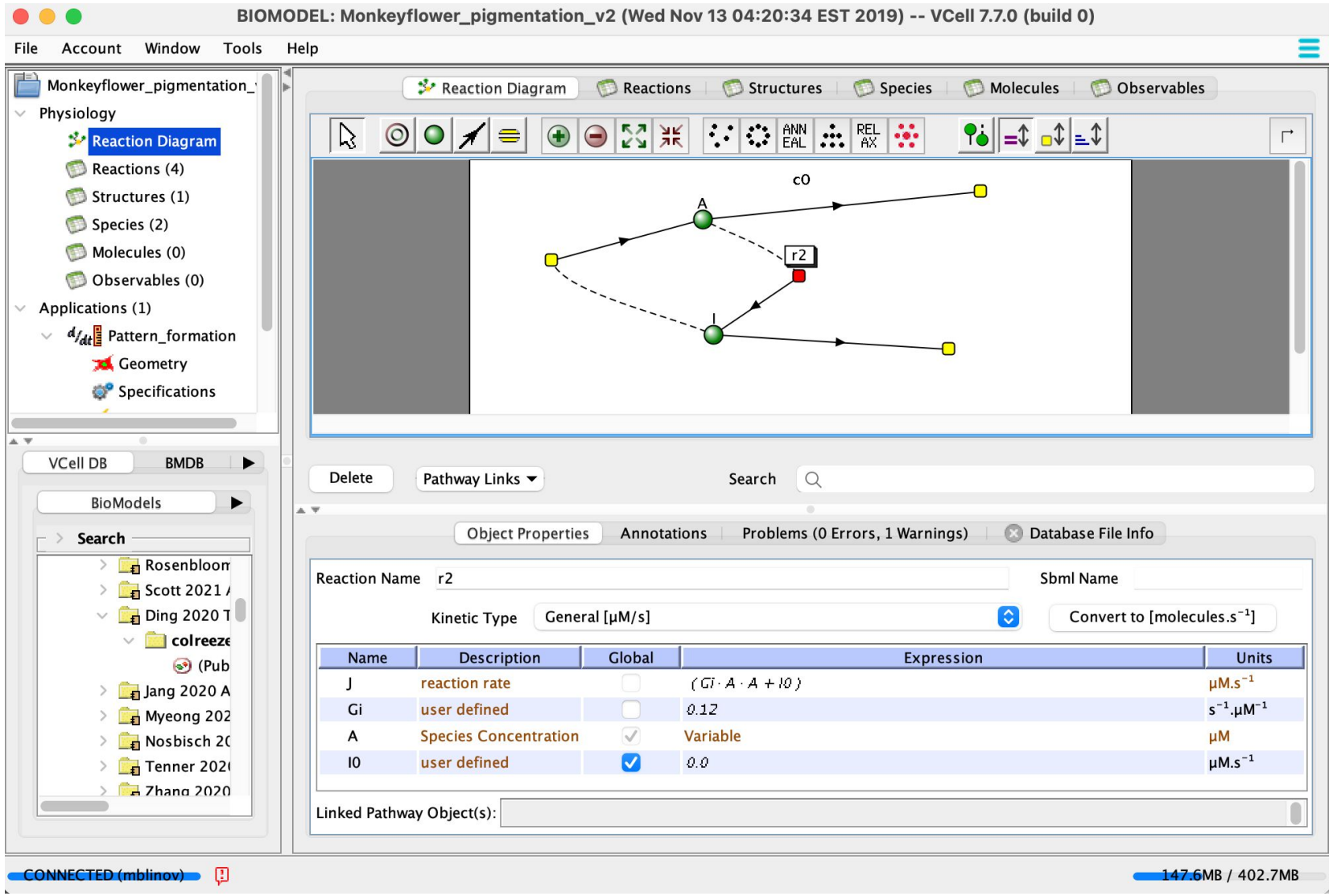
Baoqing Ding [1,9] · Erin L. Patterson [2,3,8,9] · Srinidhi V. Holalu [2,3,9] · … · Michael L. Blinov [6] · Benjamin K. Blackman [2,3,10] · Yao-Wu Yuan [1,7] … Show more



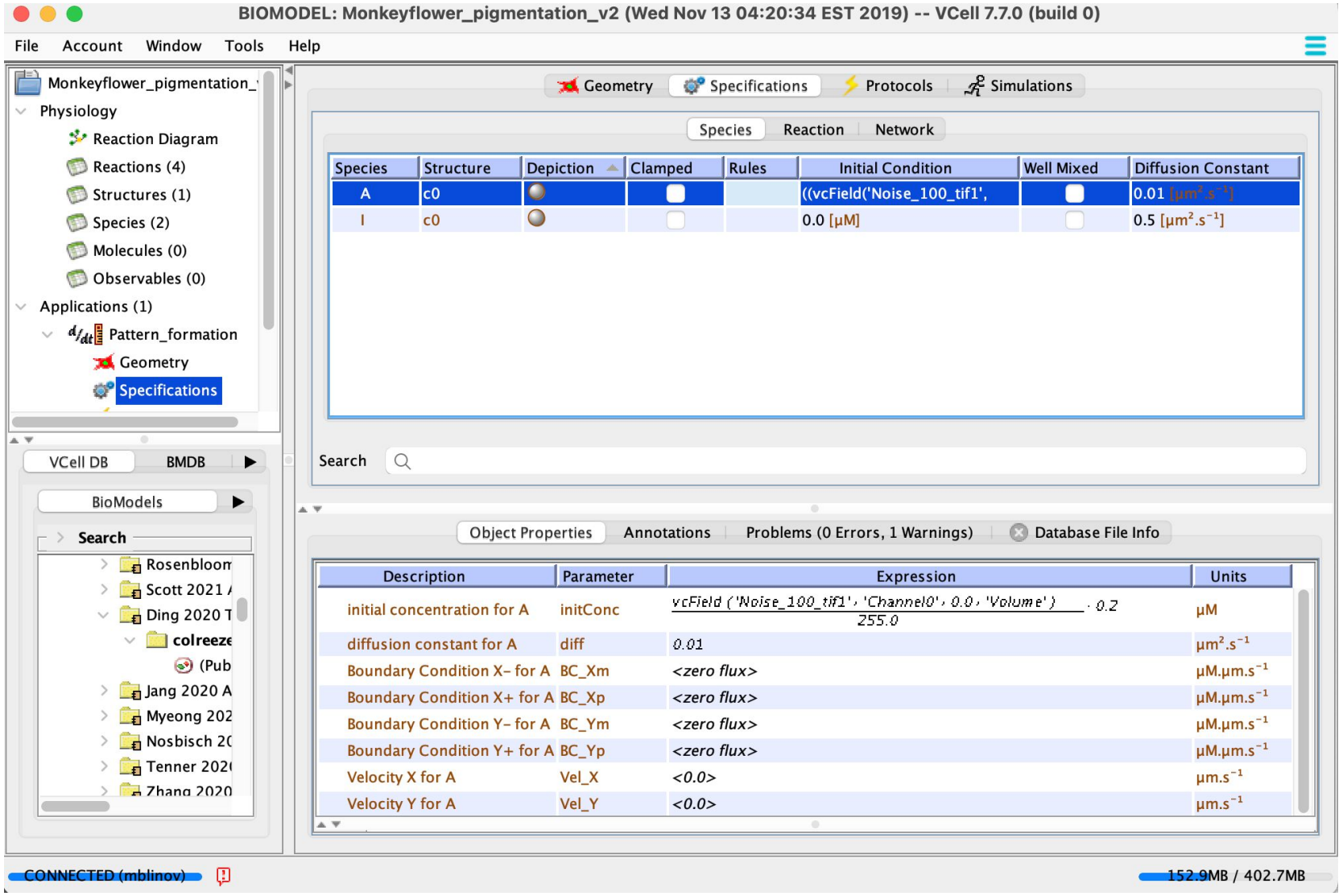


Monkeyflowers are a diverse genus of angiosperms that produce many beautiful and unique pigmentation patterns. Reaction-diffusion model with slow activator and fast repressor (Turing system) is known to generate patterns.

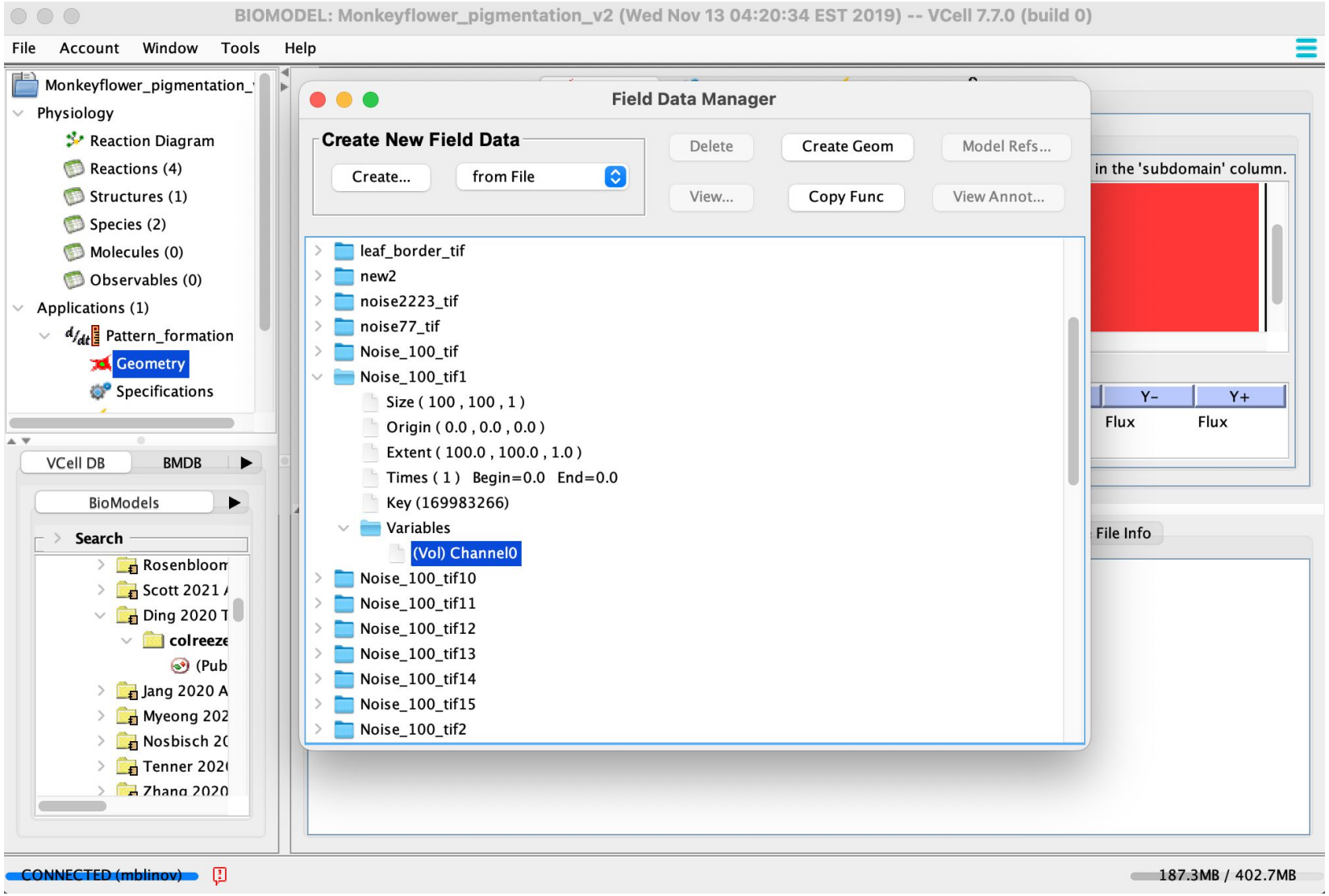
Using a simple Turing model to simulate pattern development



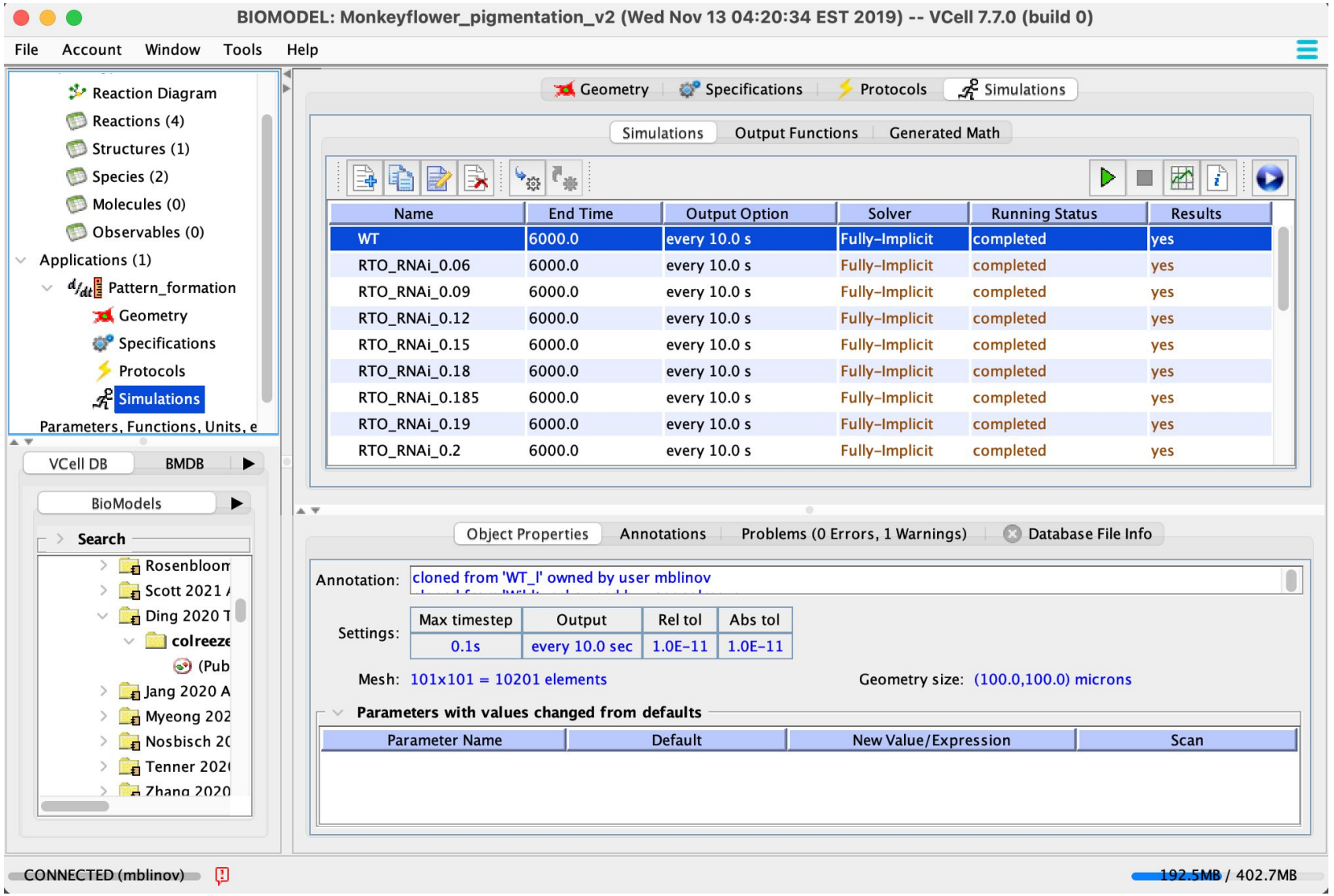
The initial species distributions can be defined from images (e.g. fluorescent image)



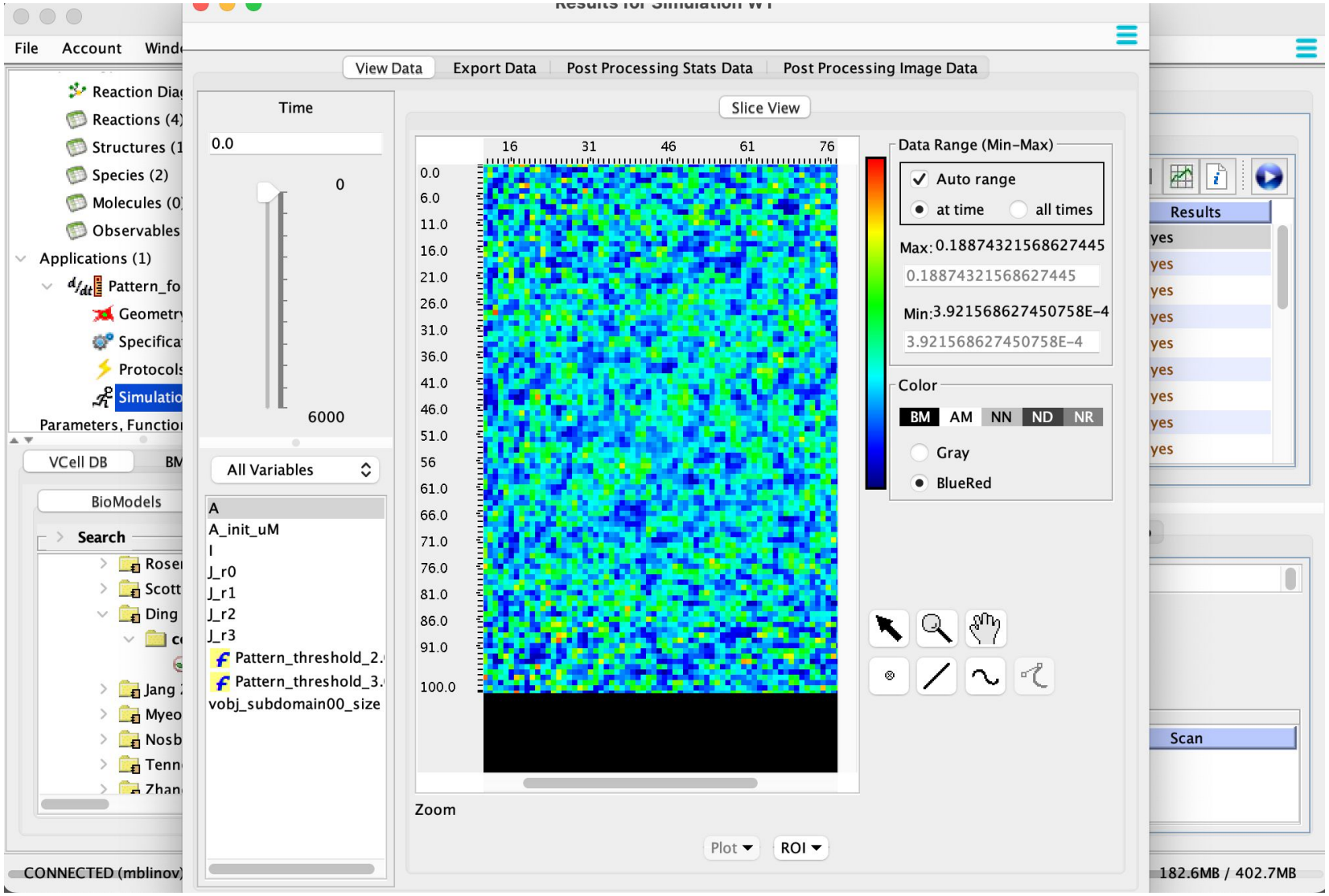
In VCell non-uniform initial distribution are called field data



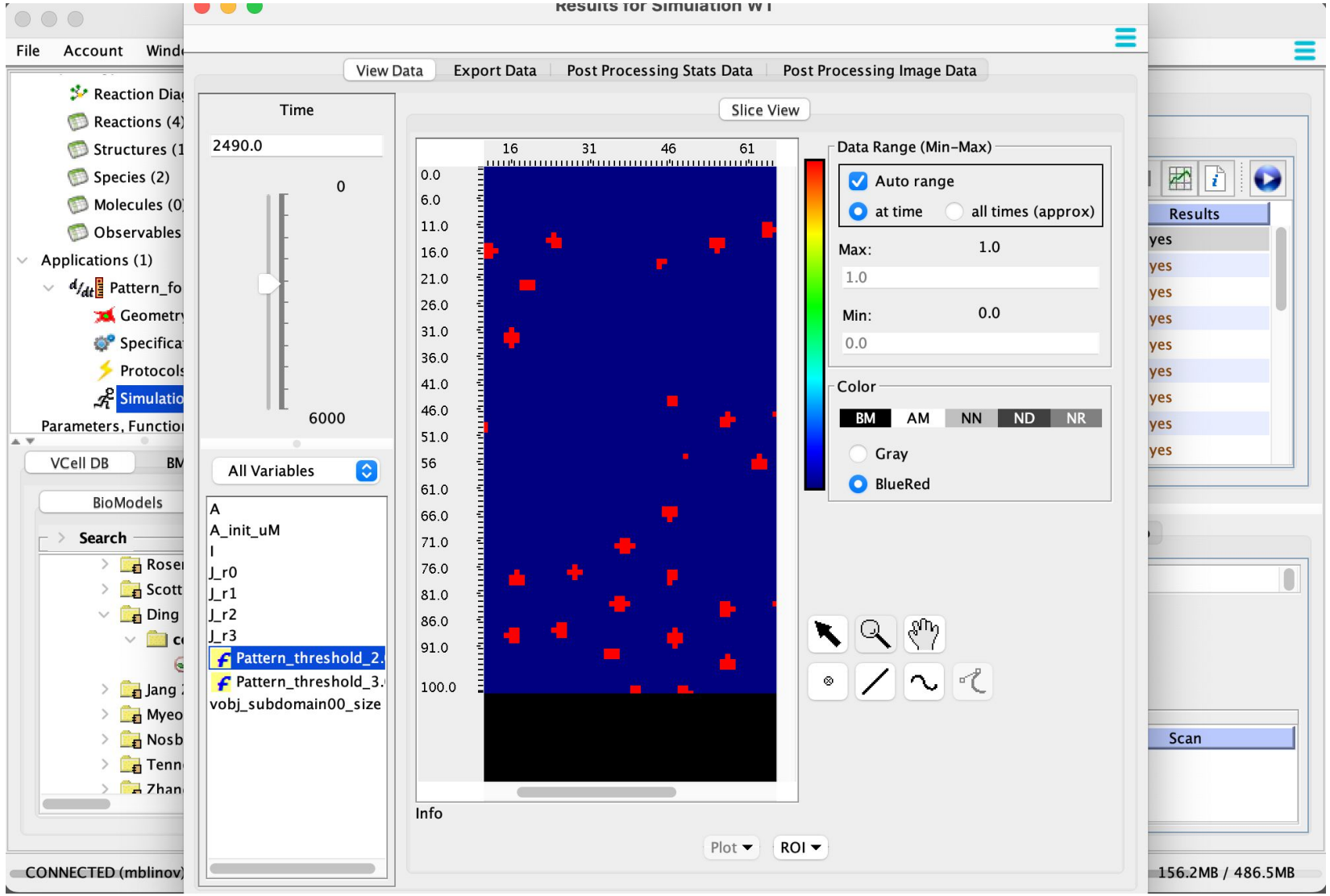
Now we demonstrate how this data is used



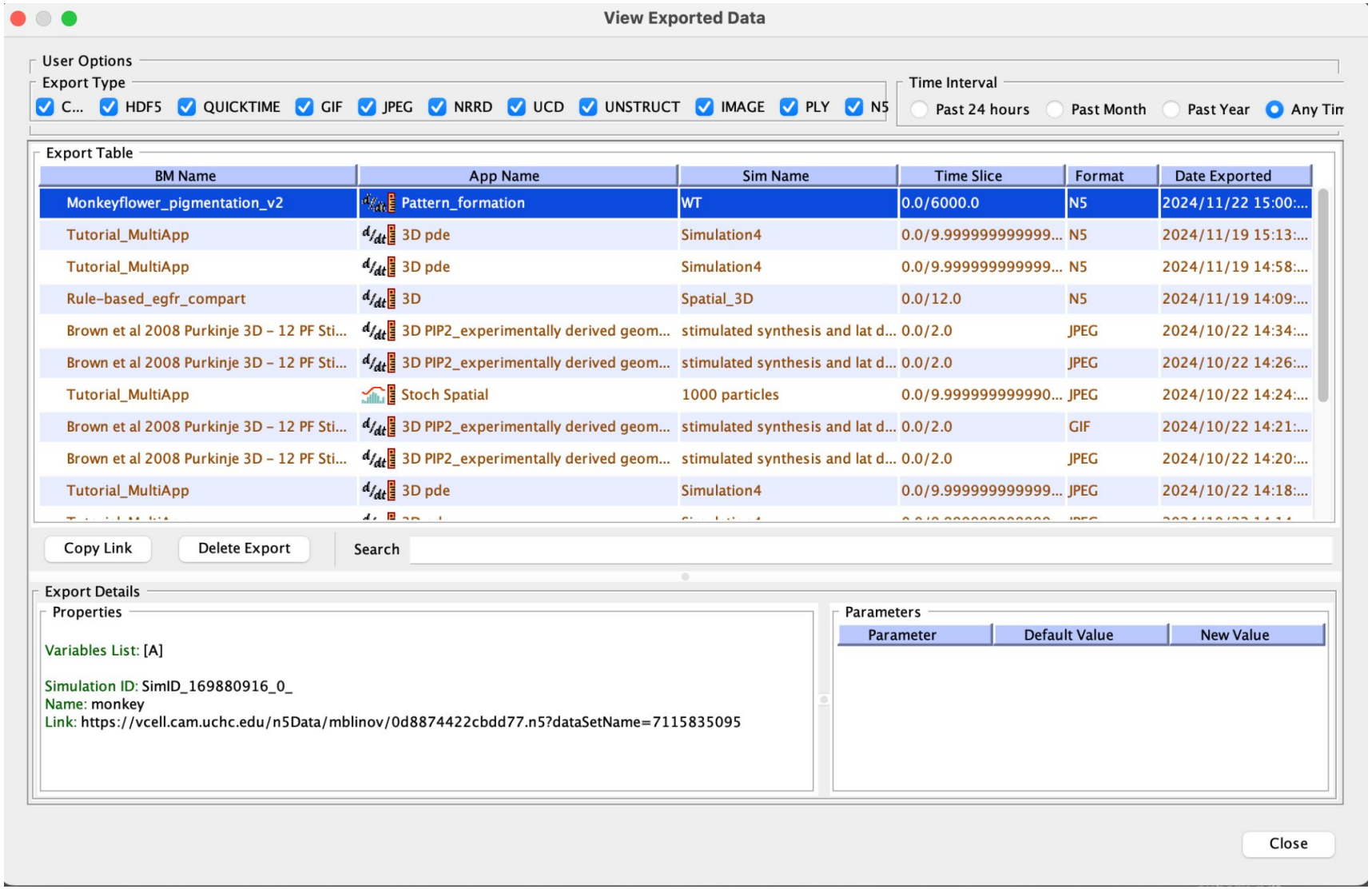
Initial condition imported from image (e.g. noise generated in ImageJ)



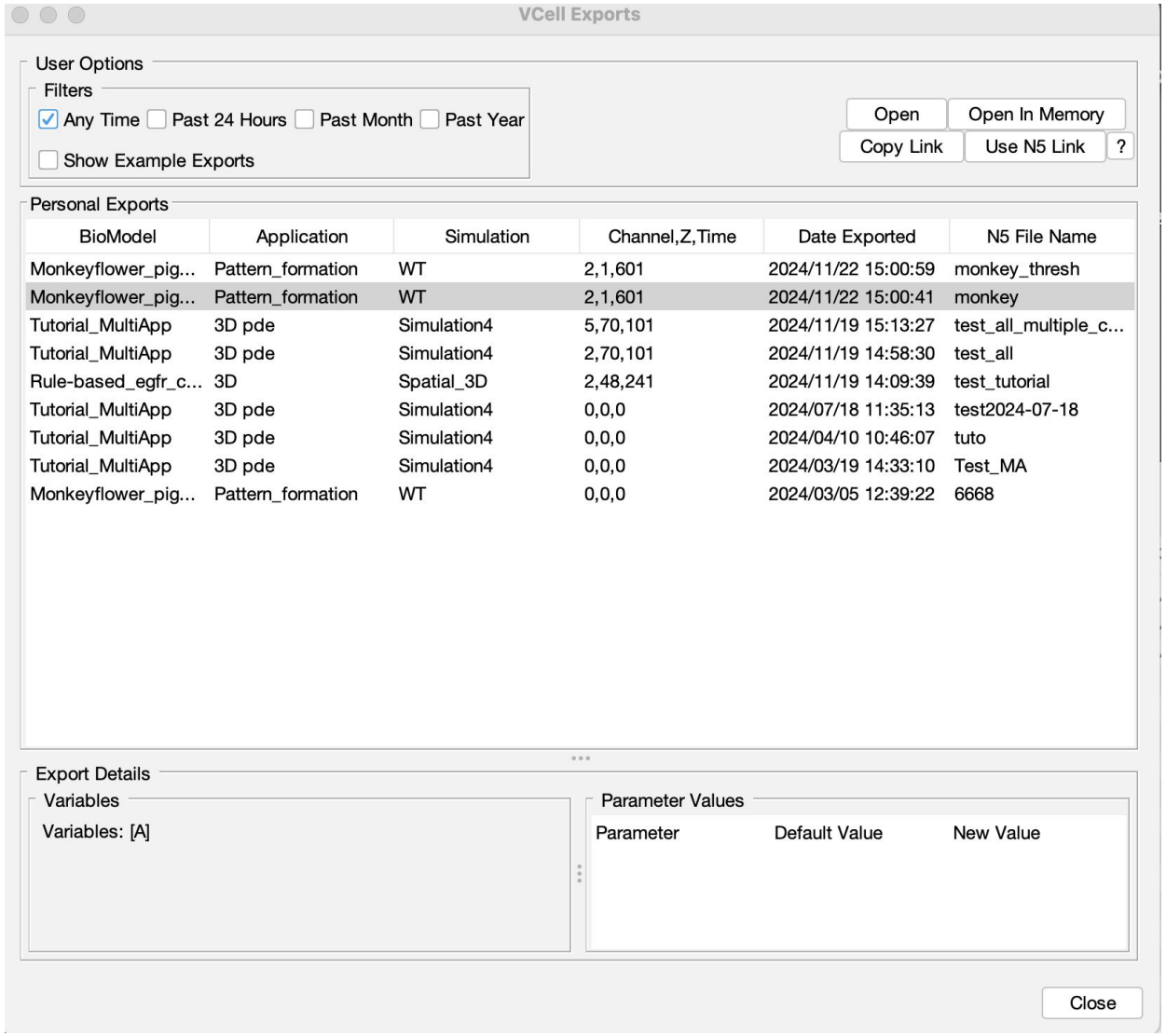
End result of the simulation



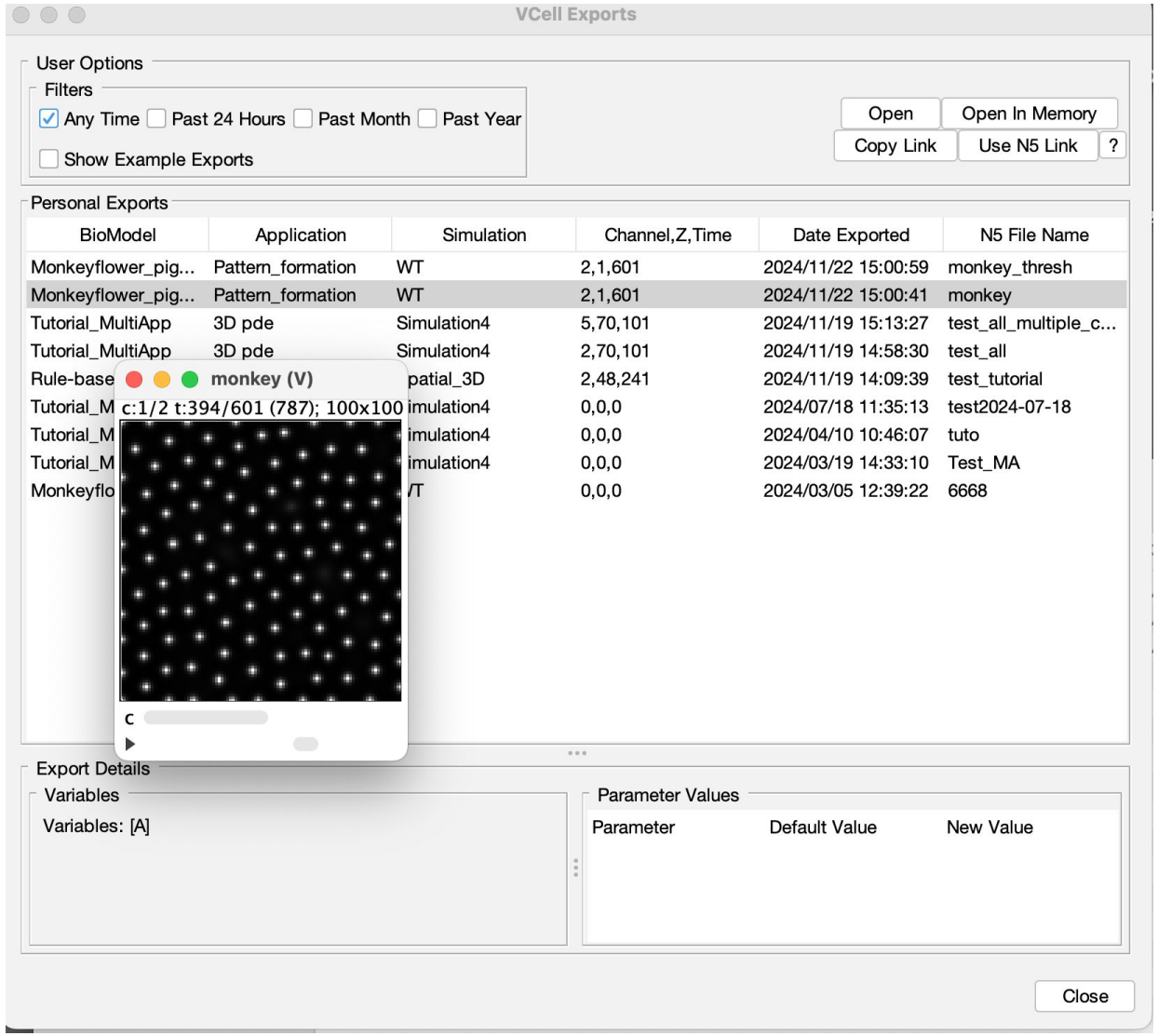
To compare with experimental data, we can export in multiple formats, including N5



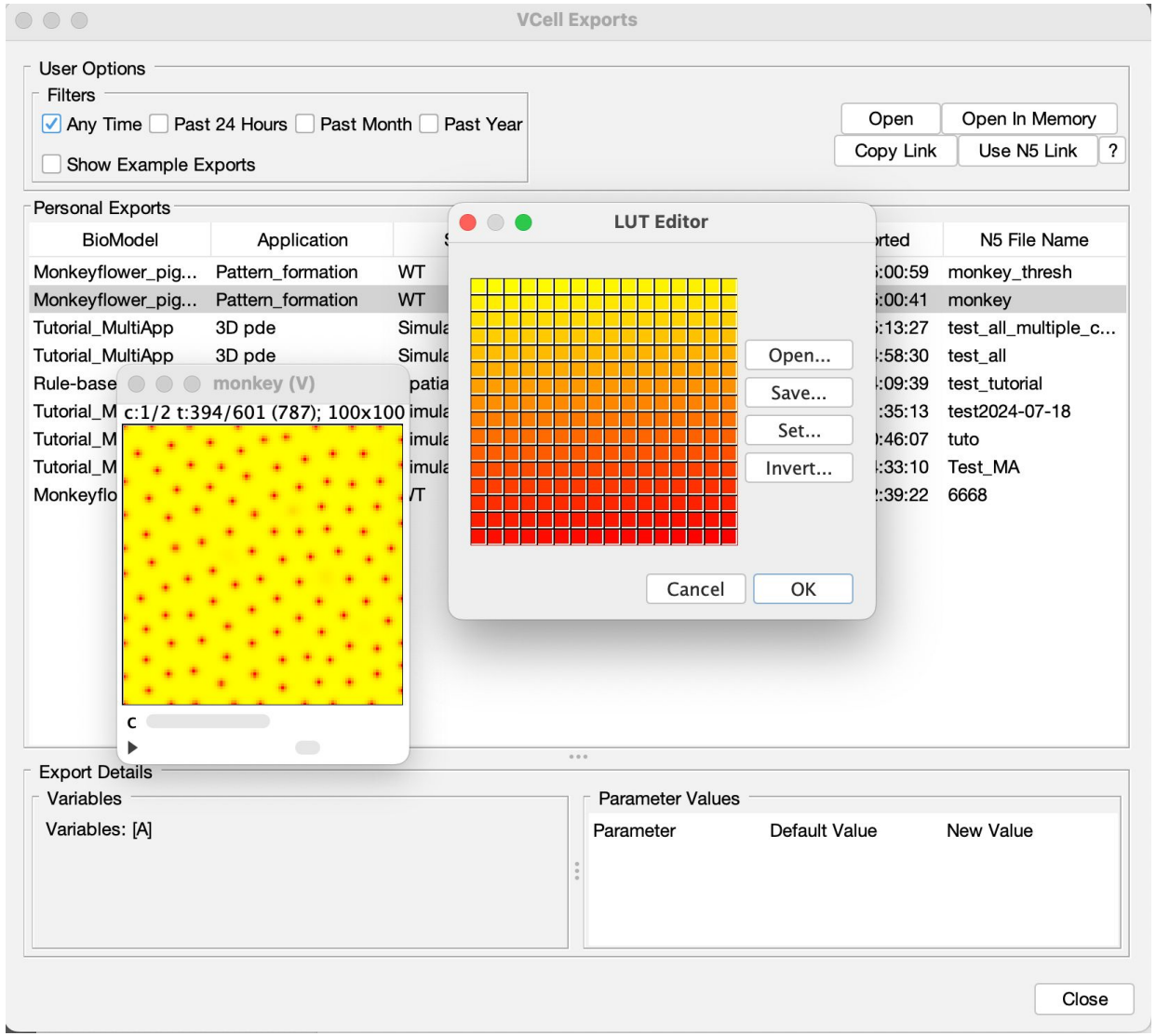
These images are accessible from FIJI/ImageJ with VCell plugin as hyperstacks

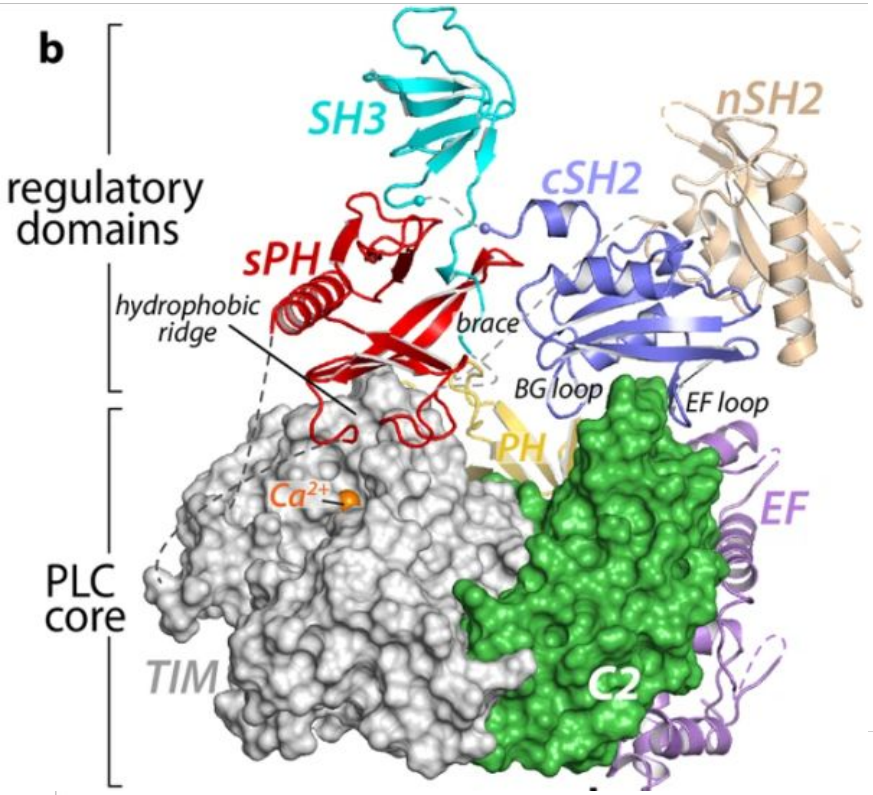


These images are accessible from FIJI/ImageJ with VCell plugin as hyperstacks



Using color LUT to compare VCell images with real data





JBC RESEARCH ARTICLE

A kinetic model of phospholipase C-γ1 linking structure-based insights to dynamics of enzyme autoinhibition and activation

Received for publication, October 19, 2021, and in revised form, March 27, 2022 Published, Papers in Press, March 31, 2022,
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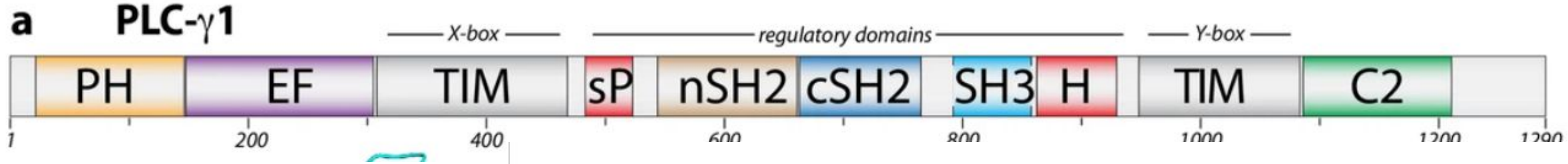
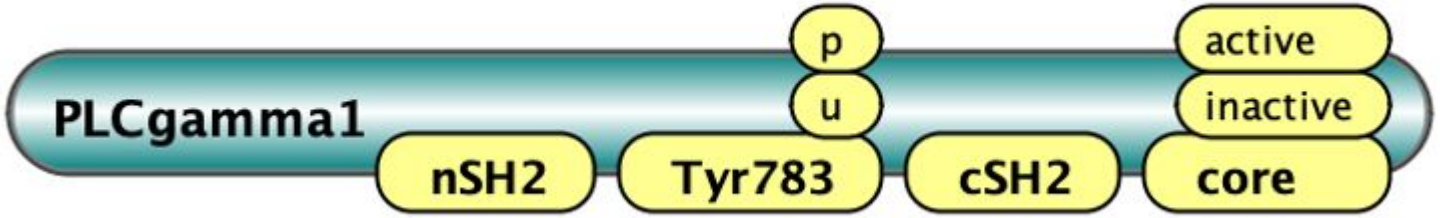
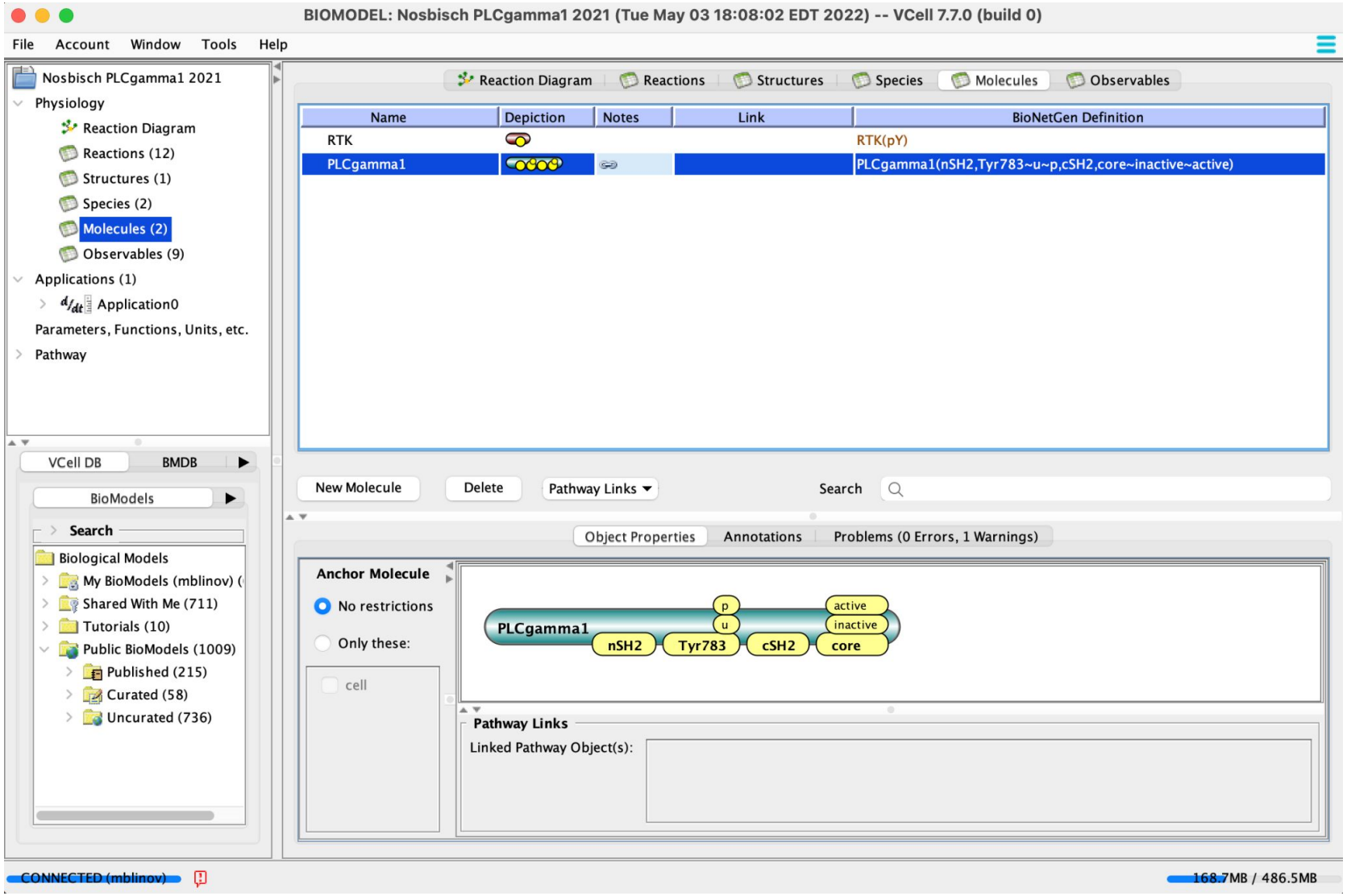
Edited by Roger Colbran





Molecules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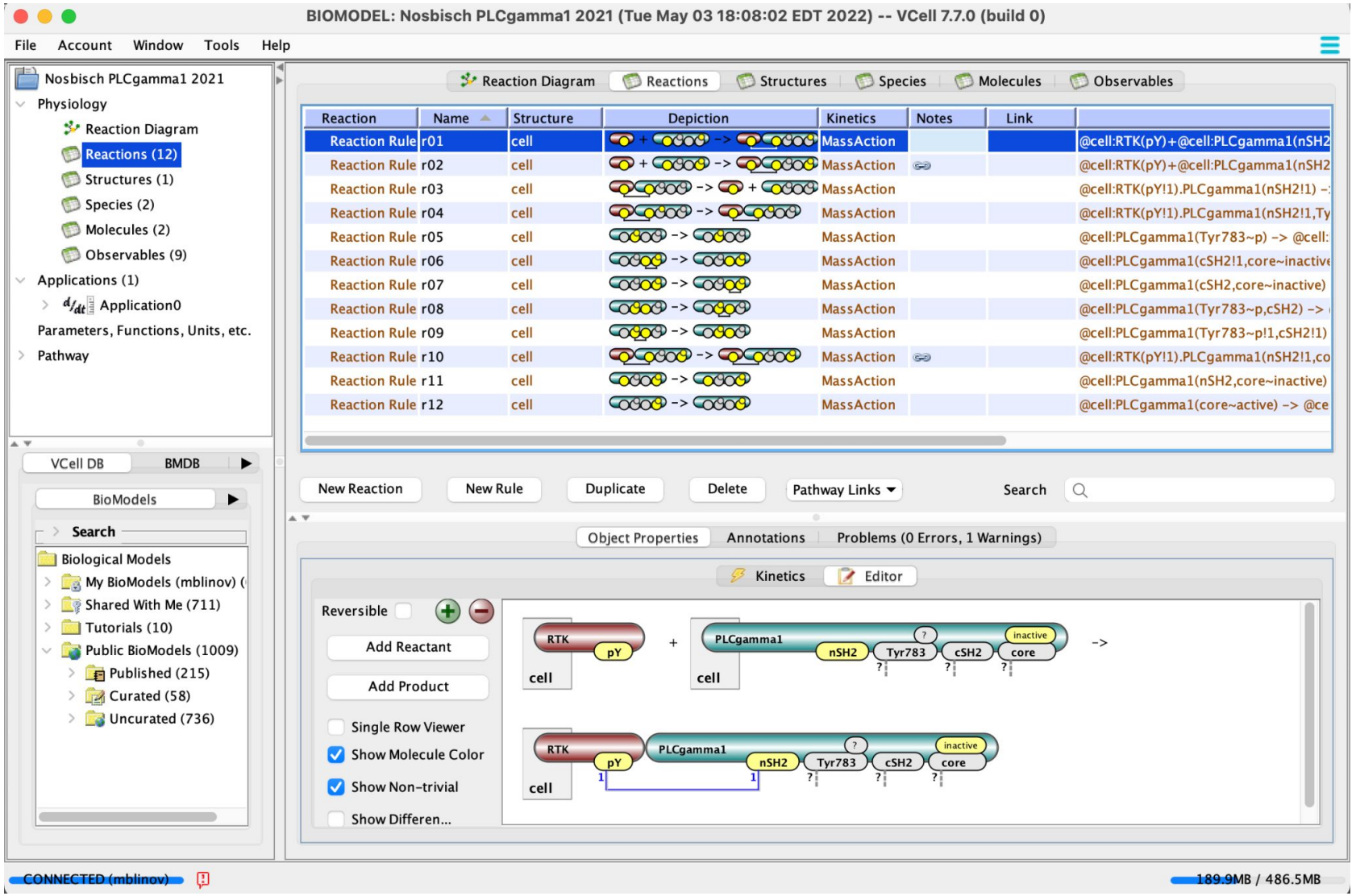
File
Account
Window
Tools
Help
Nosbisch PLCgamma1 2021
Physiology
Reaction Diagram
Reactions (12)
Structures (1)
Species (2)
Molecules (2)
Observables (9)
Applications (1)
Application0
Parameters, Functions, Units, etc.
Pathway
Reaction Diagram
Reactions
Structures
Species
Molecules
Observables
Name
Depiction
Notes
Link
BioNetGen Definition
RTK
RTK(pY)
PLCgamma1
PLCgamma1(nSH2,Tyr783~u~p,cSH2,core~inactive~active)
VCell DB
BMDB
BioModels
Search
Biological Models
My BioModels (mblinov) (
Shared With Me (711)
Tutorials (10)
Public BioModels (1009)
Published (215)
Curated (58)
Uncurated (736)
New Molecule
Delete
Pathway Links
Search
Object Properties
Annotations
Problems (0 Errors, 1 Warnings)
Anchor Molecule
No restrictions
Only these:
cell
PLCgamma1
nSH2
Tyr783
cSH2
core
p
u
active
inactive
Pathway Links
Linked Pathway Object(s):
CONNECTED (mblinov)
168.7MB / 486.5MB

Reactions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Tools
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Nosbisch PLCgamma1 2021
Physiology
Reaction Diagram
Reactions (12)
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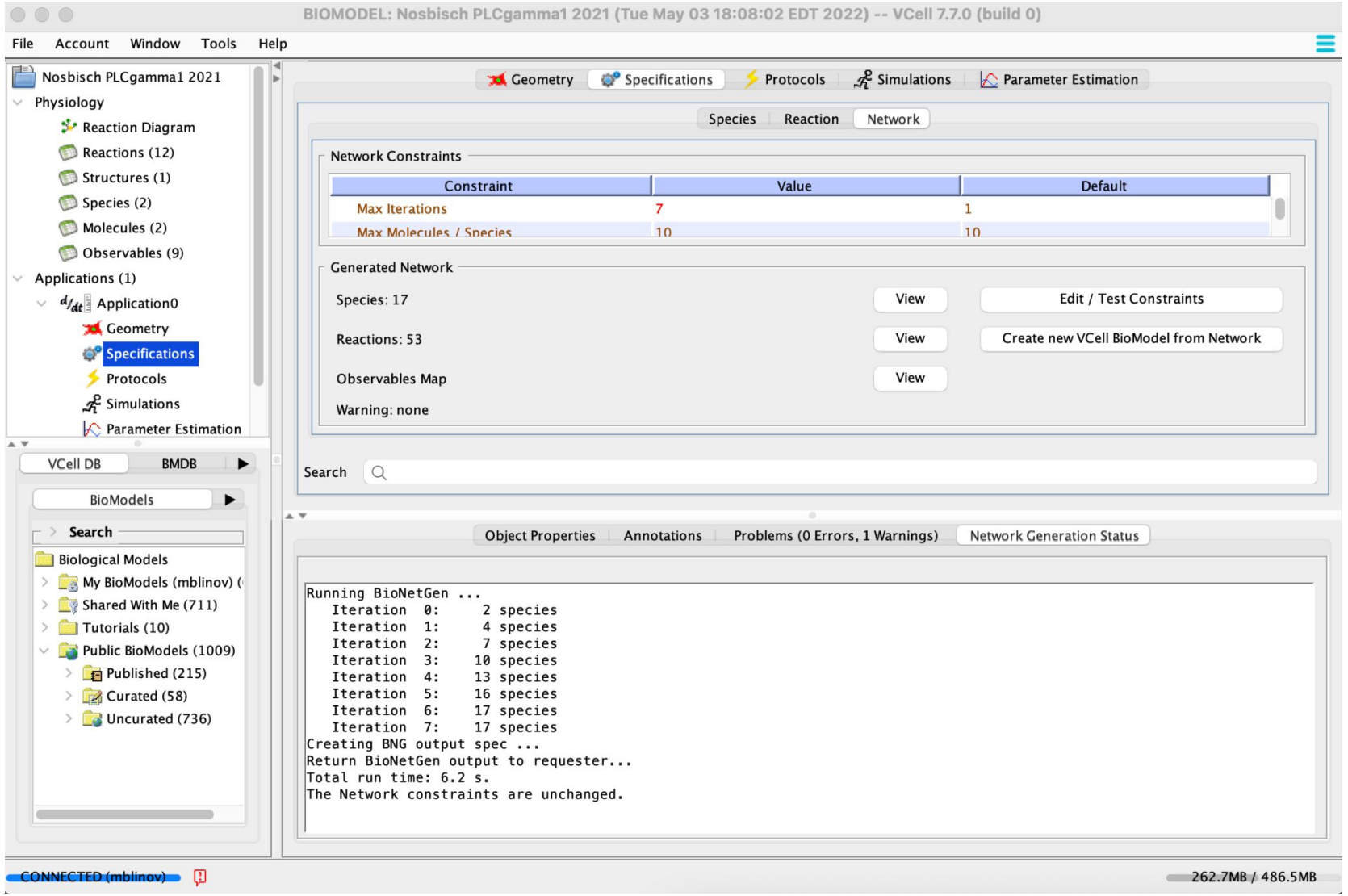
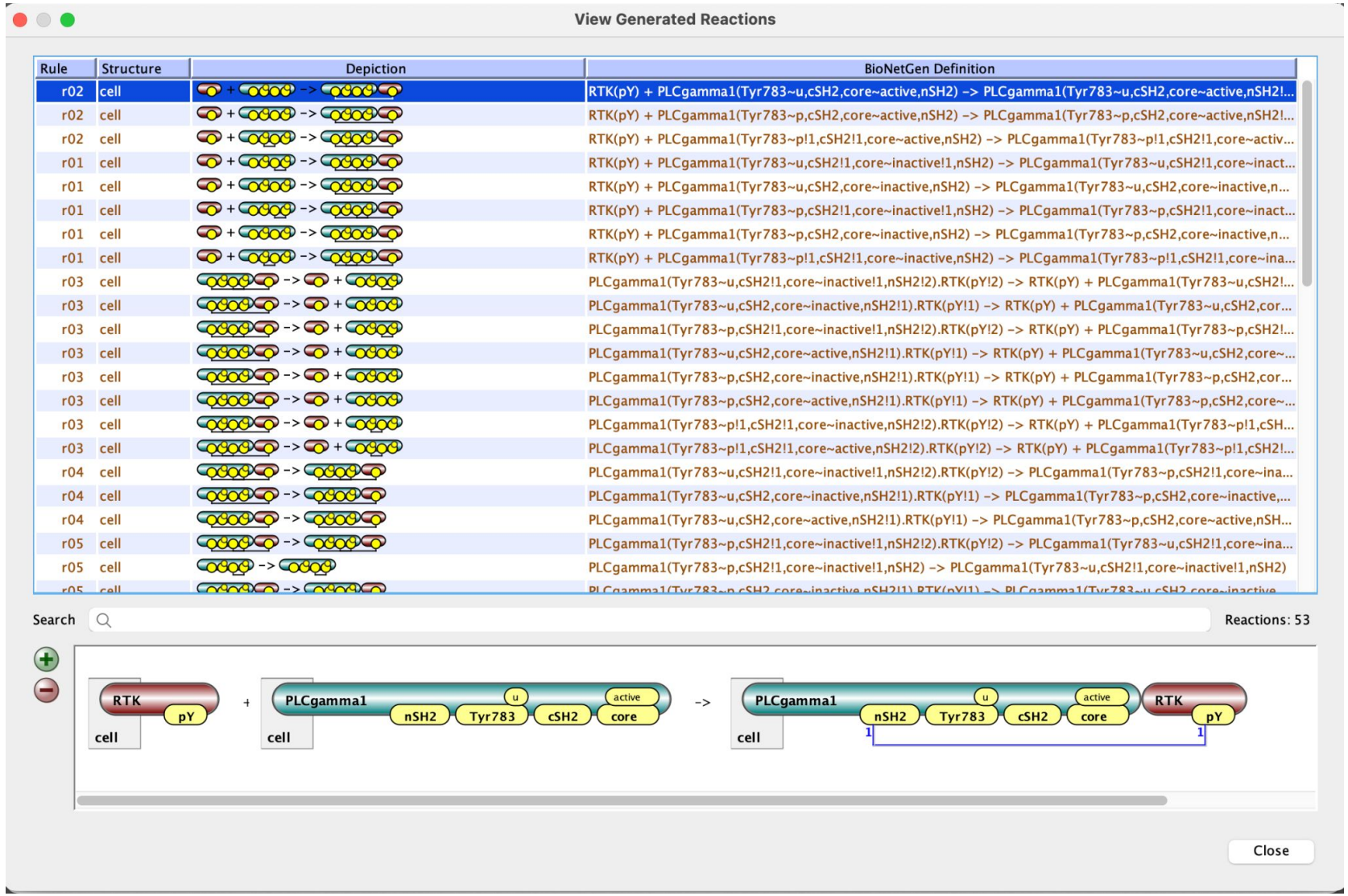
Molecules (2)
Observables (9)
Applications (1)
Application0
Parameters, Functions, Units, etc.
Pathway
Reaction Diagram
Reactions
Structures
Species
Molecules
Observables
Reaction
Name
Structure
Depiction
Kinetics
Notes
Link
Reaction Rule r01 cell MassAction @cell:RTK(pY)+@cell:PLCgamma1(nSH2
Reaction Rule r02 cell MassAction @cell:RTK(pY)+@cell:PLCgamma1(nSH2
Reaction Rule r03 cell MassAction @cell:RTK(pY!1).PLCgamma1(nSH2!1) -
Reaction Rule r04 cell MassAction @cell:RTK(pY!1).PLCgamma1(nSH2!1,Ty
Reaction Rule r05 cell MassAction @cell:PLCgamma1(Tyr783~p) -> @cell:
Reaction Rule r06 cell MassAction @cell:PLCgamma1(cSH2!1,core~inactive
Reaction Rule r07 cell MassAction @cell:PLCgamma1(cSH2,core~inactive)
Reaction Rule r08 cell MassAction @cell:PLCgamma1(Tyr783~p,cSH2) ->
Reaction Rule r09 cell MassAction @cell:PLCgamma1(Tyr783~p!1,cSH2!1)
Reaction Rule r10 cell MassAction @cell:RTK(pY!1).PLCgamma1(nSH2!1,co
Reaction Rule r11 cell MassAction @cell:PLCgamma1(nSH2,core~inactive)
Reaction Rule r12 cell MassAction @cell:PLCgamma1(core~active) -> @ce
VCell DB
BMDB
BioModels
Search
Biological Models
My BioModels (mblinov)
Shared With Me (711)
Tutorials (10)
Public BioModels (1009)
Published (215)
Curated (58)
Uncurated (736)
New Reaction
New Rule
Duplicate
Delete
Pathway Links
Search
Object Properties
Annotations
Problems (0 Errors, 1 Warnings)
Kinetics
Editor
Reversible
Add Reactant
Add Product
Single Row Viewer
Show Molecule Color
Show Non-trivial
Show Differen...
RTK
pY
cell
PLCgamma1
nSH2
Tyr783
cSH2
core
inactive
CONNECTED (mblinov)
189.9MB / 486.5MB

Network generation



Generated species and reactions



Observables