

# Cytokinesis group

Ilya Kiselev, Yan Zhu, Daniel Priego,  
Naveen Kumar, Wolfram Liebermeister

# What we achieved today

## Model integration

.csv files with input/out variables are on our GitHub repository

## FtsZ polymerization submodel

Conversion SBML (from BioUML) → SBGN (in Vanted; for output to SBGN-ML)  
(information about molecule types is passed via SBO annotations)

## Cytokinesis submodel

- Random assembly of FtsZ ring (using events and binomial random variables)
- Started to prepare tests for the SBML model

# Draft model of cytokinesis

$$\text{numEdges} = \arcsin\left(\frac{\text{PI}}{\text{L}}\right)$$

diameter

callBindingEdgesStep1

```
when: start == 0 && $default.twoBent == 0
numBindingEdgesStepOne = binomialFun(numEdges, $default.oneStraight, $default.twoStraight, rateFilamentBindingMembrane)
```

bindingFirstStep

```
when: start == 0 && numBindingEdgesStepOne >= 1 && $default.twoBent == 0
even if on start
$default.oneStraight = $default.oneStraight + numBindingEdgesStepOne
start = 1
$default.MG_224_9MER_GDP = $default.MG_224_9MER_GDP - numBindingEdgesStepOne * 9
```

callBindingEdgesStepTwo

```
when: start == 1 && $default.twoBent == 0
numBindingEdgesStepTwo = binomialFun($default.oneStraight, rateFilamentBindingMembrane)
```

bindingSecondStep

```
when: start == 1 && $default.twoBent == 0 && numBindingEdgesStepTwo >= 1
$default.twoStraight = $default.twoStraight + numBindingEdgesStepTwo
$default.MG_224_9MER_GDP = $default.MG_224_9MER_GDP - numBindingEdgesStepTwo
$default.oneStraight = $default.oneStraight + numBindingEdgesStepTwo
```

callNumBentEdges

```
when: start == 1 && $default.twoStraight + $default.twoBent == numEdges
numBentEdges = binomialFun($default.twoStraight, ratePis2GtpHydrolysis)
```

bending

```
when: start == 1 && $default.twoStraight + $default.twoBent == numEdges && numBentEdges >= 1
$default.twoStraight = $default.twoStraight - numBentEdges
$default.twoBent = $default.twoBent + numBentEdges
$default.h2o = $default.h2o - 9 * numBentEdges
$default.phosphate = $default.phosphate + 9 * numBentEdges
```

callNumUnbindEdges

```
when: start == 1 && $default.twoBent + $default.oneBent == numEdges && $default.twoStraight == 0
numUnbindBentEdges = binomialFun($default.twoBent, rateFilamentDissociation)
```

unbinding

```
when: start == 1 && $default.twoBent == numEdges && $default.oneBent && $default.twoStraight == 0 && numUnbindBentEdges >= 1
$default.twoBent = $default.twoBent - numUnbindBentEdges
$default.oneBent = $default.oneBent + numUnbindBentEdgesFirstCyc
$default.MG_224_9MER_GDP = $default.MG_224_9MER_GDP + 9 * numUnbindBentEdges
```

unbinding

```
when: $default.twoStraight + null == numEdges && $default.twoStraight >= 1.0
doBinding = 0.0
doBending = 0.0
doUnbinding = 1.0
```

binomialFun(nE, prob) = 0

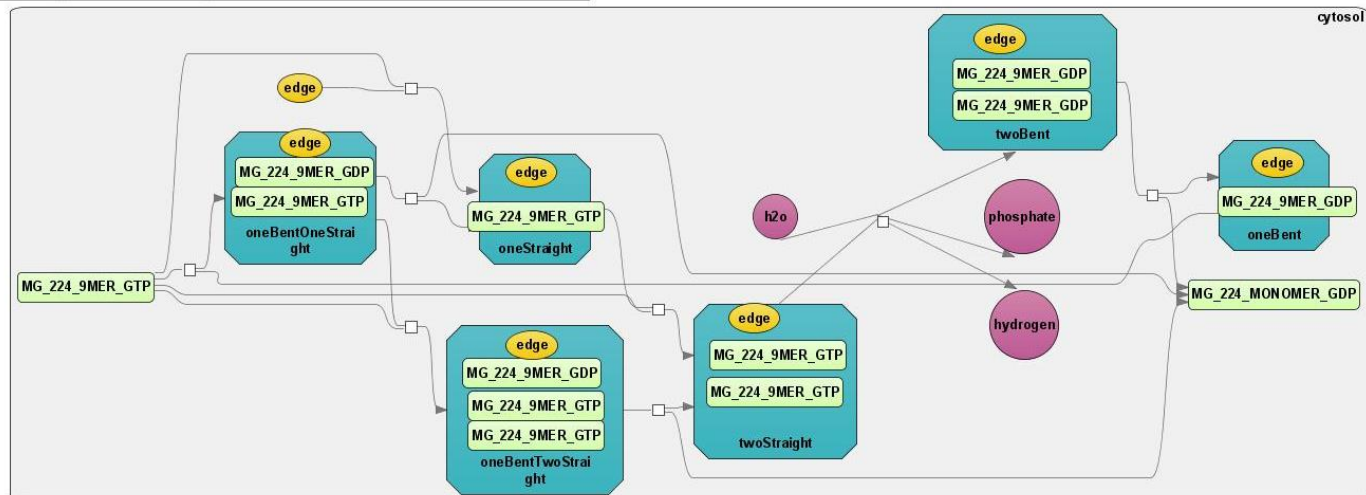
pinchFinished

```
when: false
unknown = 0.0
```

ring numEdgesTwoStraight = 0.0

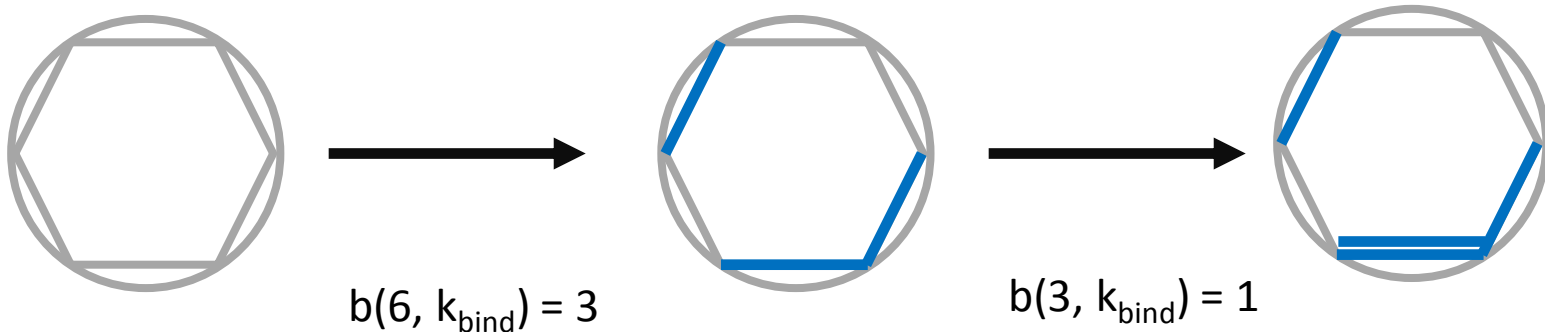
bending

```
when: false
unknown = 0.0
```



# Event-dependent transformation

$$\text{numManEdges} = \text{binomial}(\text{maxNum}, \text{rateFilamentBindingMembrane})$$



Calculate the numBindEdges  
Do binding, update the species

Calculate the numBindEdges  
Do binding, update the species

calBindingEdgesStep1

when: start == 0 && \$default.twoBent == 0

numBindingEdgesStepOne = binomialFun(numEdges - \$default.oneStraight - \$default.twoStraight, rateFilamentBindingMembrane)

bindingFirstStep

when: start == 0 && numBindingEdgesStepOne >= 1 && \$default.twoBent == 0

even if on start

\$default.oneStraight = \$default.oneStraight + numBindingEdgesStepOne

start = 1

\$default.MG<sub>224</sub><sub>9MER</sub><sub>GTP</sub> = \$default.MG<sub>224</sub><sub>9MER</sub><sub>GTP</sub> - numBindingEdgesStepOne \* 9