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Title: TRuML: a translator for rule-based modeling languages

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# TRuML: A translator for rule-based modeling languages

Ryan Suderman, William S. Hlavacek

# Dynamical systems biology

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Modeling protein interaction networks traditionally done with ODEs or reaction networks

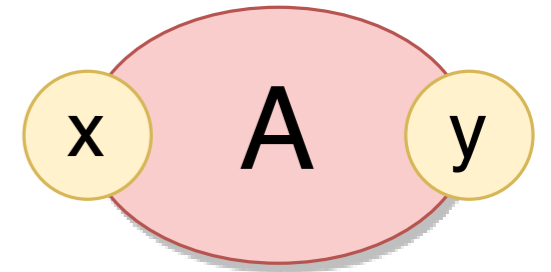
Two prominent issues:

Encoding (knowledge representation)

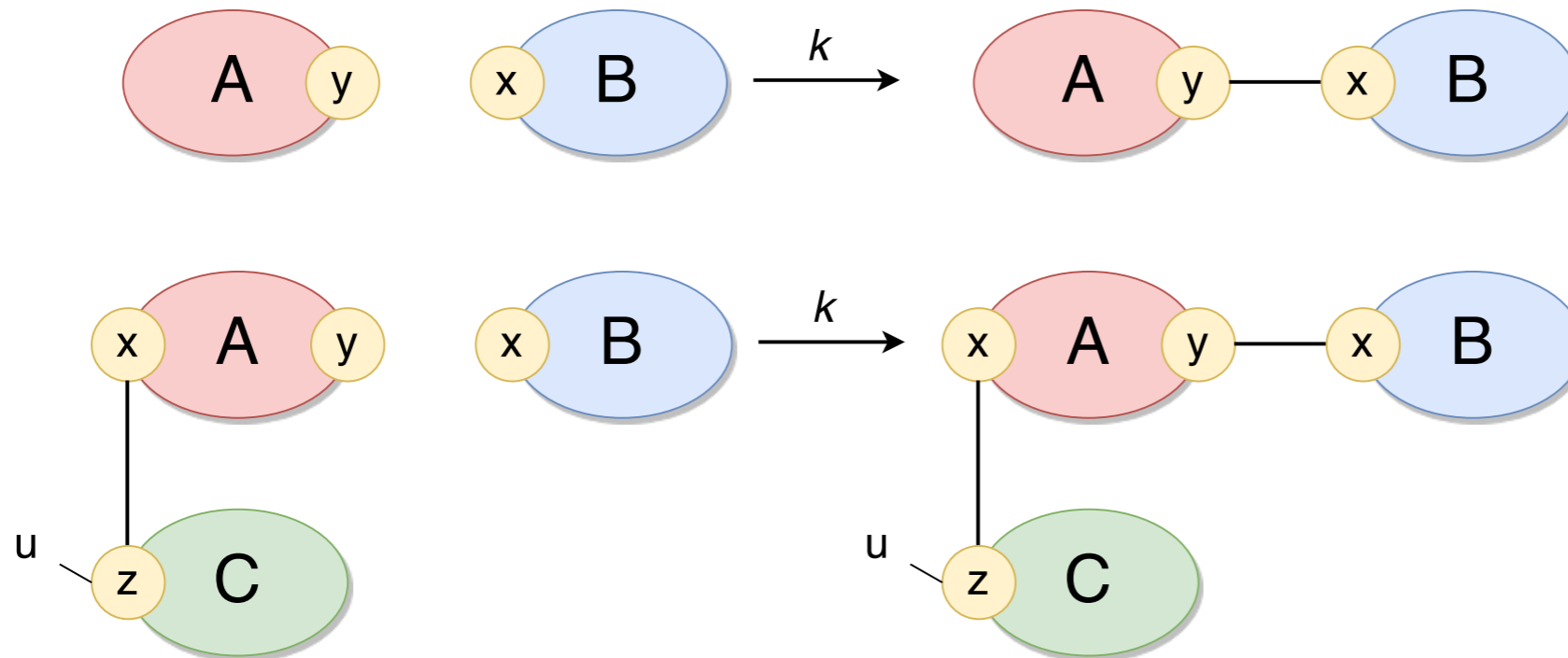
Complexity

# Rule-based modeling

“Site graphs” represent molecules/complexes



Graph-rewriting rules represent sets of reactions



Chylek, L. A., et al, (2014), WIREs: Sys Biol Med

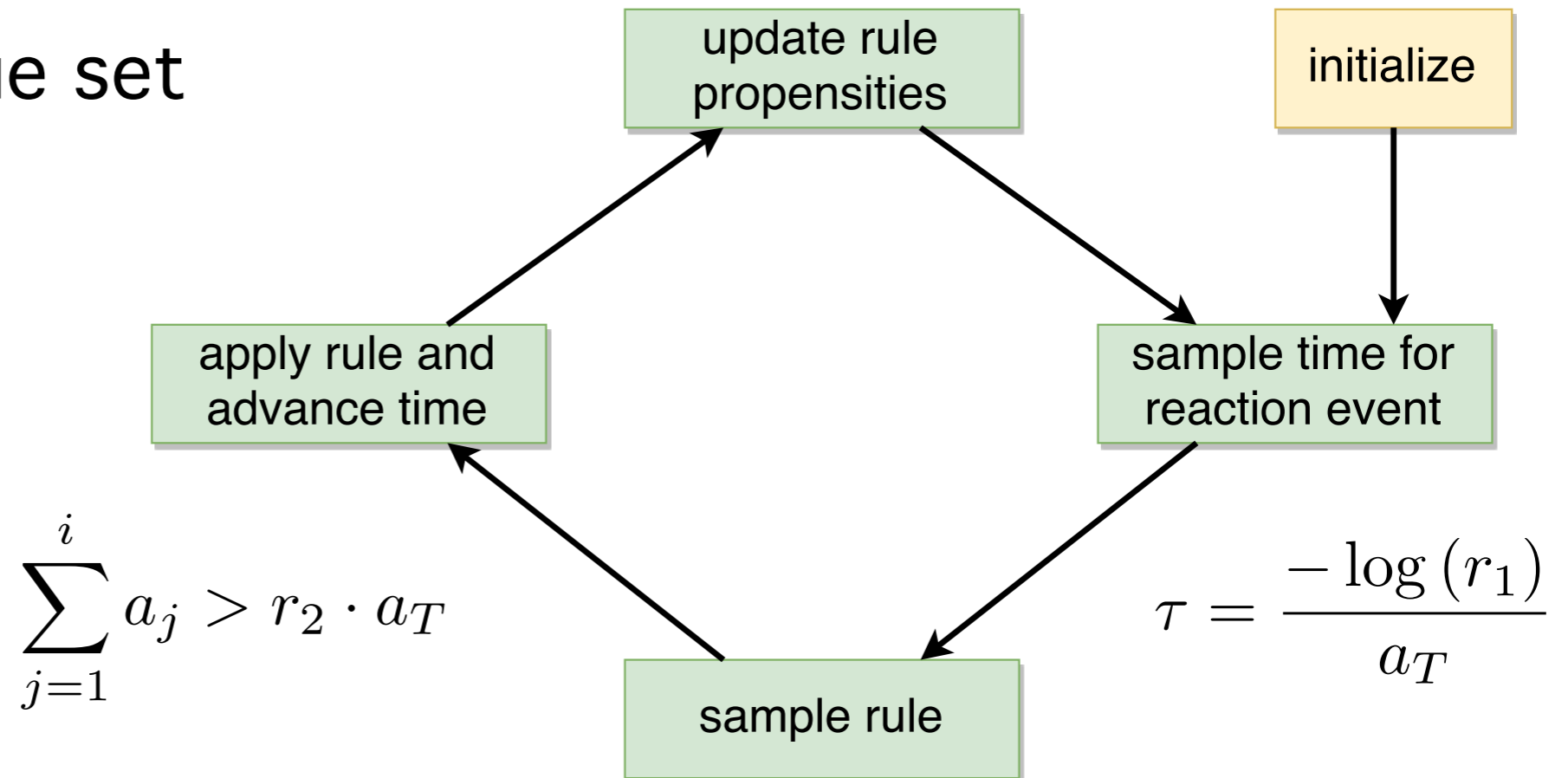
Danos, V., et al, (2007), Concur 2007

# Rule-based modeling

BioNetGen (BNGL) and Kappa languages

Both have “direct” KMC-based simulation engines

Each has a unique set of analysis tools



Danos, V., et al, (2007), LNCS

Gillespie, D. T. (2007). Ann Rev Phys Chem

Sneddon, M. W. et al, (2011), Nat Meth

$a_T$  - sum of all rules' propensities

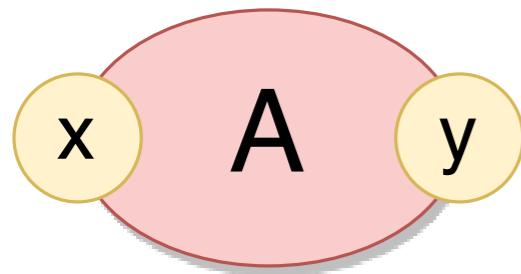
$a_i$  - the propensity of rule  $i$

# Translation

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TRuML is a tool for translating between Kappa and BNGL

Some model components can be trivially translated:



BNGL:  $A(x,y)$

Kappa: `%agent: A(x,y)`

Others require syntactic modification:

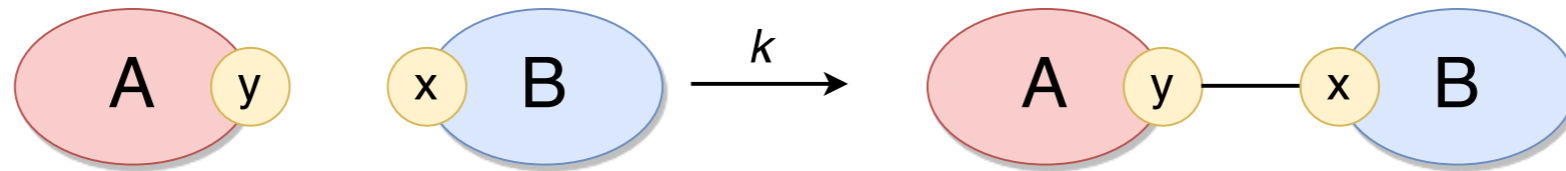
BNGL:  $x = \log_{10}(y + 1) / z$

Kappa: `%var: 'x' ([log]('y' + 1) / [log](10)) / 'z'`

# Translation

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Rules are similar syntactically, but with key differences:



Kappa:

$$A(y), B(x) \rightarrow A(y!1), B(x!1) @ \kappa$$

BNGL:

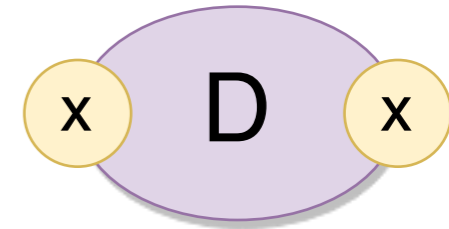
$$A(y) + B(x) \rightarrow A(y!1).B(x!1) \kappa$$



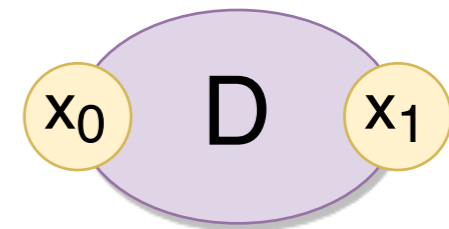
# Translating identically named sites

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BNGL allows molecules with identical sites



Kappa's formalism requires distinct site names

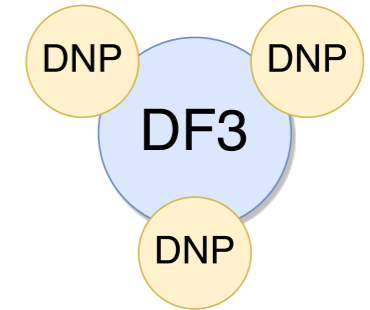
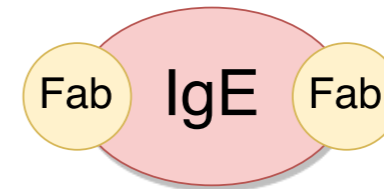


BNGL patterns involving identical sites must be expanded to accommodate Kappa's site naming conventions

# Translating identically named sites

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Consider the immune response



Two types of binding rules:

- Free DF3 binding IgE
- Bound DF3 crosslinking 2 IgEs

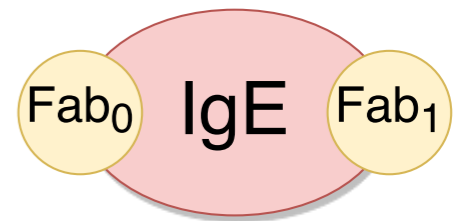
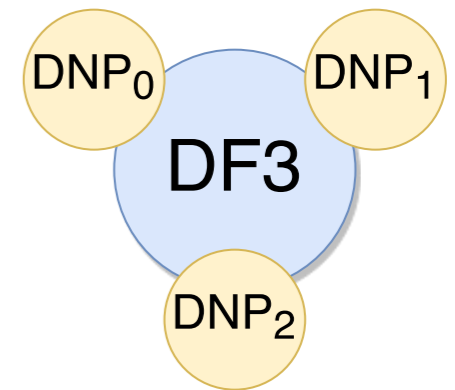
BNGL:



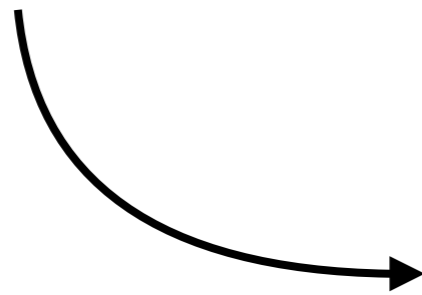
# Translating identically named sites

First, the molecule types' sites must be renamed

Patterns containing these molecule types must be combinatorially expanded



`IgE(Fab!1).DF3(DNP!1,DNP,DNP)`



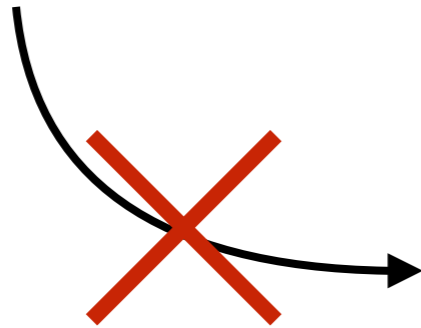
`IgE(Fab0!1),DF3(DNP0!1,DNP1,DNP2)`  
`IgE(Fab1!1),DF3(DNP0,DNP1!1,DNP2)`  
`IgE(Fab0!1),DF3(DNP0,DNP1,DNP2!1)`  
`IgE(Fab1!1),DF3(DNP0!1,DNP1,DNP2)`  
`IgE(Fab0!1),DF3(DNP0,DNP1!1,DNP2)`  
`IgE(Fab1!1),DF3(DNP0,DNP1,DNP2!1)`

# Translating identically named sites

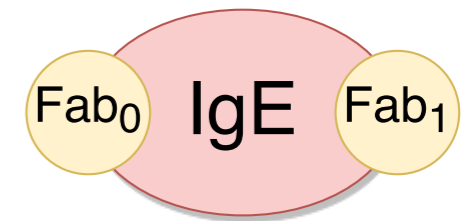
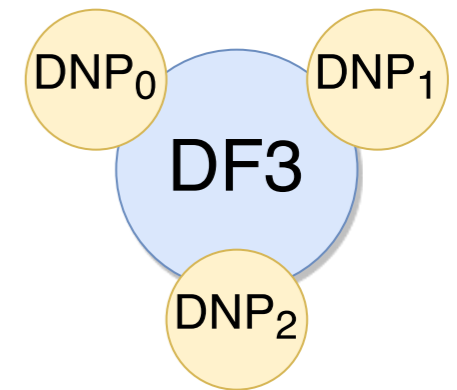
This is not sufficient for certain cases

Consider the crosslinking rule's DF3 reactant:

DF3(DNP, DNP!+)



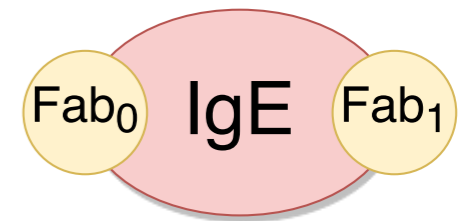
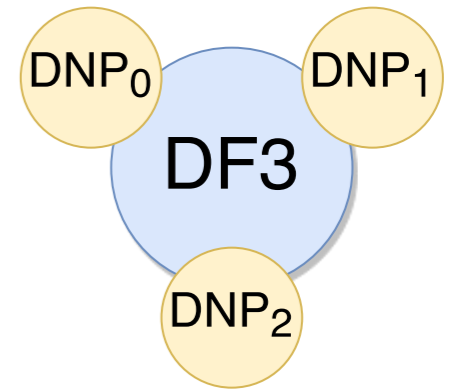
DF3(DNP0, DNP1!\_)  
DF3(DNP0, DNP2!\_)  
DF3(DNP1, DNP0!\_)  
DF3(DNP1, DNP2!\_)  
DF3(DNP2, DNP0!\_)  
DF3(DNP2, DNP1!\_)



# Translating identically named sites

---

DF3(DNP0,DNP1!\_)  $\Rightarrow$  DF3(DNP0,DNP1!\_,DNP2!\_)  
DF3(DNP0,DNP2!\_)  $\Rightarrow$  DF3(DNP0,DNP1!\_,DNP2!\_)  
DF3(DNP1,DNP0!\_)  $\Rightarrow$  DF3(DNP0,DNP1!\_,DNP2!\_)  
DF3(DNP1,DNP2!\_)  $\Rightarrow$  DF3(DNP0,DNP1!\_,DNP2!\_)  
DF3(DNP2,DNP0!\_)  $\Rightarrow$  DF3(DNP0,DNP1!\_,DNP2!\_)  
DF3(DNP2,DNP1!\_)  $\Rightarrow$  DF3(DNP0,DNP1!\_,DNP2!\_)



Overlapping patterns cause an overestimate of a rule's propensity

Additional context is needed

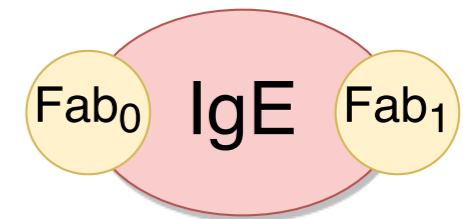
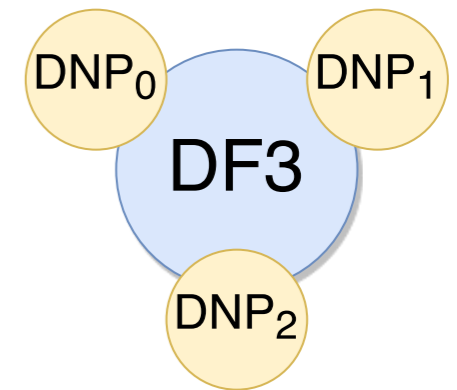
# Translating identically named sites

Generally, if multiple identical sites exist and are underspecified in a pattern:

0. Perform combinatorial expansion as before

$DF3(DNP, DNP!+)$   $\longrightarrow$

- $DF3(DNP_0, DNP_1!_)$
- $DF3(DNP_0, DNP_2!_)$
- $DF3(DNP_1, DNP_0!_)$
- $DF3(DNP_1, DNP_2!_)$
- $DF3(DNP_2, DNP_0!_)$
- $DF3(DNP_2, DNP_1!_)$



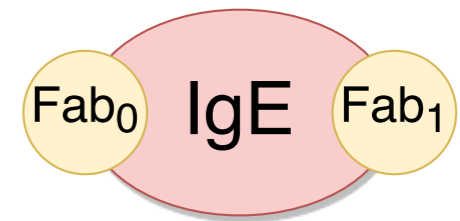
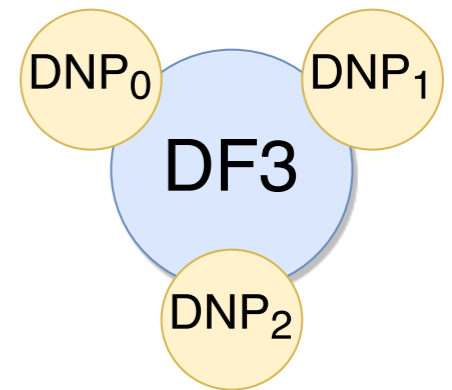
# Translating identically named sites

---

Generally, if multiple identical sites exist and are underspecified in a pattern:

0. Perform combinatorial expansion as before
1. Determine all possible states for the site in question

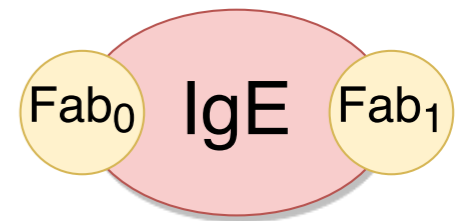
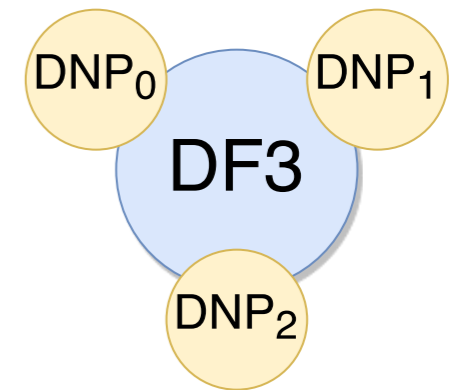
DNPN → DNPN  
DNPN!\_



# Translating identically named sites

Generally, if multiple identical sites exist and are underspecified in a pattern:

0. Perform combinatorial expansion as before
1. Determine all possible states for the site in question
2. Take product of possible states and unspecified Kappa site names for each pattern in the expansion



all sites

specified sites

unspecified sites

$$DF3(DNP0, DNP1!_) \longrightarrow \{DNP0, DNP1, DNP2\} - \{DNP0, DNP1\} = \{DNP2\}$$

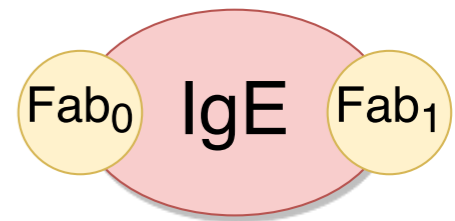
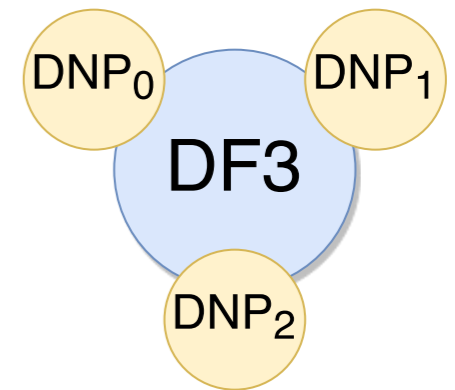
$$\{DNP2\} \times \{DNPn, DNPn!_ \} = \{DNP2, DNP2!_ \}$$



# Translating identically named sites

Generally, if multiple identical sites exist and are underspecified in a pattern:

0. Perform combinatorial expansion as before
1. Determine all possible states for the site in question
2. Take product of possible states and unspecified Kappa site names for each pattern in the expansion
3. Generate new patterns by adding all unspecified site combinations to each pattern in the expansion

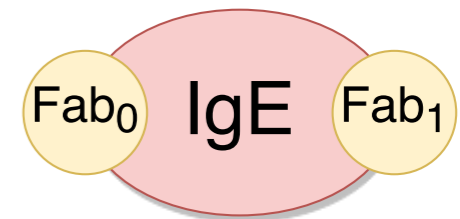
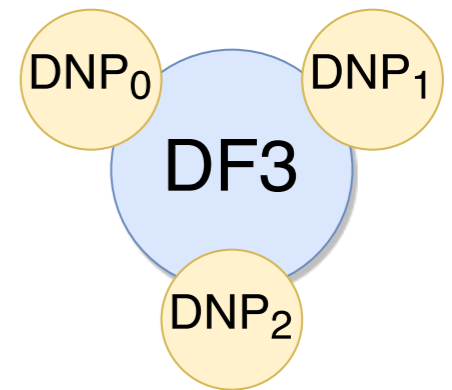


$$\text{DF3}(\text{DNP0}, \text{DNP1!}_) + \{\text{DNP2}, \text{DNP2!}_\} \longrightarrow$$
$$\{\text{DF3}(\text{DNP0}, \text{DNP1!}_, \text{DNP2}), \text{DF3}(\text{DNP0}, \text{DNP1!}_, \text{DNP2!}_)\}$$

# Translating identically named sites

Generally, if multiple identical sites exist and are underspecified in a pattern:

0. Perform combinatorial expansion as before
1. Determine all possible states for the site in question
2. Take product of possible states and unspecified Kappa site names for each pattern in the expansion
3. Generate new patterns by adding all unspecified site combinations to each pattern in the expansion
4. Prune identical patterns from list

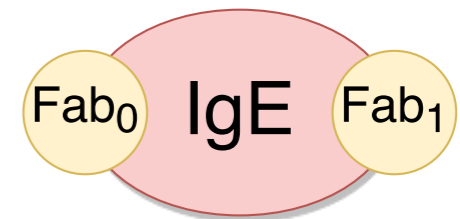
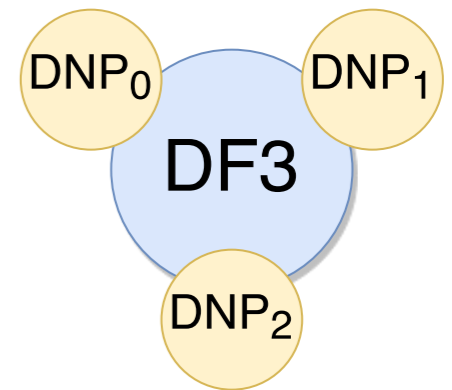


$$\begin{array}{l}
 \text{DF3(DNP, DNP!+)} \longrightarrow \\
 \text{DF3(DNP0, DNP1!_)} \\
 \text{DF3(DNP0, DNP2!_)} \\
 \text{DF3(DNP1, DNP0!_)} \\
 \text{DF3(DNP1, DNP2!_)} \\
 \text{DF3(DNP2, DNP0!_)} \\
 \text{DF3(DNP2, DNP1!_)}
 \end{array}
 \longrightarrow
 \begin{array}{l}
 \text{DF3(DNP0, DNP1!_, DNP2)} \\
 \text{DF3(DNP0, DNP1!_, DNP2!_)} \\
 \text{DF3(DNP0, DNP2!_, DNP1)} \\
 \text{DF3(DNP1, DNP0!_, DNP2!_)} \\
 \text{DF3(DNP1, DNP0!_, DNP2)} \\
 \text{DF3(DNP2, DNP0!_, DNP1!_)}
 \end{array}$$

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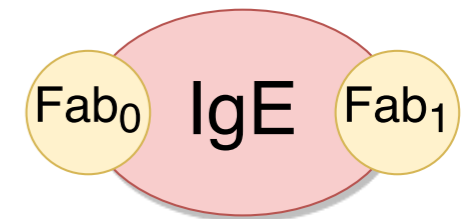
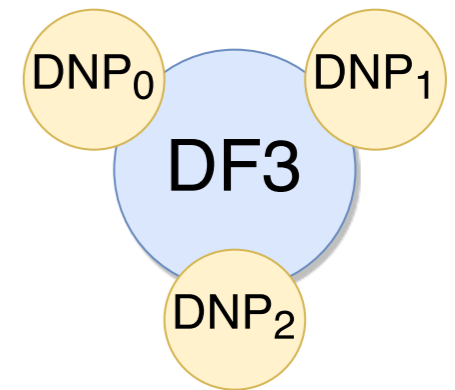


$$\text{DF3}(\text{DNP}, \text{DNP}!+) \longrightarrow
 \begin{array}{l}
 \text{DF3}(\text{DNP0}, \text{DNP1!}_) \\
 \text{DF3}(\text{DNP0}, \text{DNP2!}_) \\
 \text{DF3}(\text{DNP1}, \text{DNP0!}_) \\
 \text{DF3}(\text{DNP1}, \text{DNP2!}_) \\
 \text{DF3}(\text{DNP2}, \text{DNP0!}_) \\
 \text{DF3}(\text{DNP2}, \text{DNP1!}_)
 \end{array}
 \longrightarrow
 \begin{array}{l}
 \text{DF3}(\text{DNP0}, \text{DNP1!}_, \text{DNP2}) \\
 \text{DF3}(\text{DNP0}, \text{DNP1!}_, \text{DNP2!}_) \\
 \text{DF3}(\text{DNP0}, \text{DNP2!}_, \text{DNP1}) \\
 \text{DF3}(\text{DNP1}, \text{DNP0!}_, \text{DNP2!}_) \\
 \text{DF3}(\text{DNP1}, \text{DNP0!}_, \text{DNP2}) \\
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 \end{array}$$

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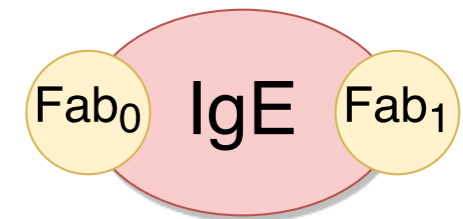
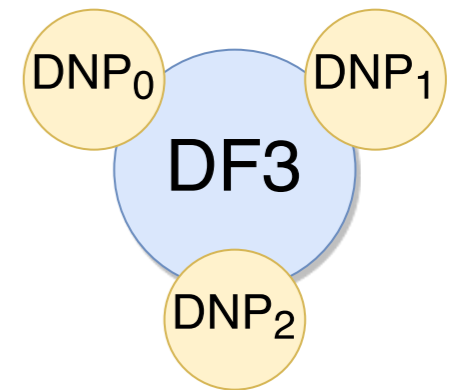


$$\begin{array}{l}
 \text{DF3}(\text{DNP}, \text{DNP}!+) \longrightarrow \begin{array}{l}
 \text{DF3}(\text{DNP0}, \text{DNP1!}_) \\
 \text{DF3}(\text{DNP0}, \text{DNP2!}_) \\
 \text{DF3}(\text{DNP1}, \text{DNP0!}_) \\
 \text{DF3}(\text{DNP1}, \text{DNP2!}_) \\
 \text{DF3}(\text{DNP2}, \text{DNP0!}_) \\
 \text{DF3}(\text{DNP2}, \text{DNP1!}_)
 \end{array} \longrightarrow \begin{array}{l}
 \text{DF3}(\text{DNP0}, \text{DNP1!}_, \text{DNP2}) \\
 \text{DF3}(\text{DNP0}, \text{DNP1!}_, \text{DNP2!}_) \\
 \text{DF3}(\text{DNP0}, \text{DNP2!}_, \text{DNP1}) \\
 \text{DF3}(\text{DNP1}, \text{DNP0!}_, \text{DNP2!}_) \\
 \text{DF3}(\text{DNP1}, \text{DNP0!}_, \text{DNP2}) \\
 \text{DF3}(\text{DNP2}, \text{DNP0!}_, \text{DNP1!}_)
 \end{array}
 \end{array}$$

# Translating identically named sites

Generally, if multiple identical sites exist and are underspecified in a pattern:

0. Perform combinatorial expansion as before
1. Determine all possible states for the site in question
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4. Prune identical patterns from list



$$\text{DF3}(\text{DNP}, \text{DNP}!+) \longrightarrow \begin{array}{l} \text{DF3}(\text{DNP0}, \text{DNP1!}_) \\ \text{DF3}(\text{DNP0}, \text{DNP2!}_) \\ \text{DF3}(\text{DNP1}, \text{DNP0!}_) \\ \text{DF3}(\text{DNP1}, \text{DNP2!}_) \\ \text{DF3}(\text{DNP2}, \text{DNP0!}_) \\ \text{DF3}(\text{DNP2}, \text{DNP1!}_) \end{array} \longrightarrow \begin{array}{l} \text{DF3}(\text{DNP0}, \text{DNP1!}_, \text{DNP2}) \\ \text{DF3}(\text{DNP0}, \text{DNP1!}_, \text{DNP2!}_) \\ \text{DF3}(\text{DNP0}, \text{DNP2!}_, \text{DNP1}) \\ \text{DF3}(\text{DNP1}, \text{DNP0!}_, \text{DNP2!}_) \\ \text{DF3}(\text{DNP1}, \text{DNP0!}_, \text{DNP2}) \\ \text{DF3}(\text{DNP2}, \text{DNP0!}_, \text{DNP1!}_) \end{array}$$

# Translating identically named sites

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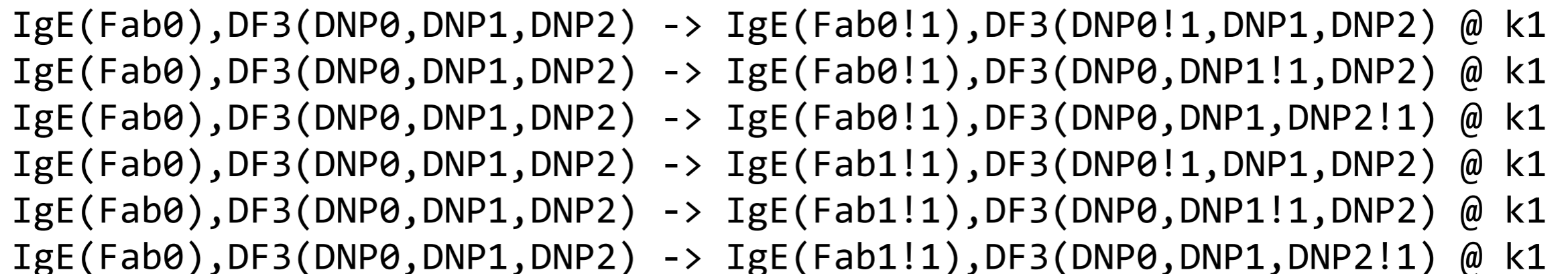
Coming back to the immune response rules

## 1. Rule(s) governing free DF3 binding IgE

BNGL:



Kappa:



# Translating identically named sites

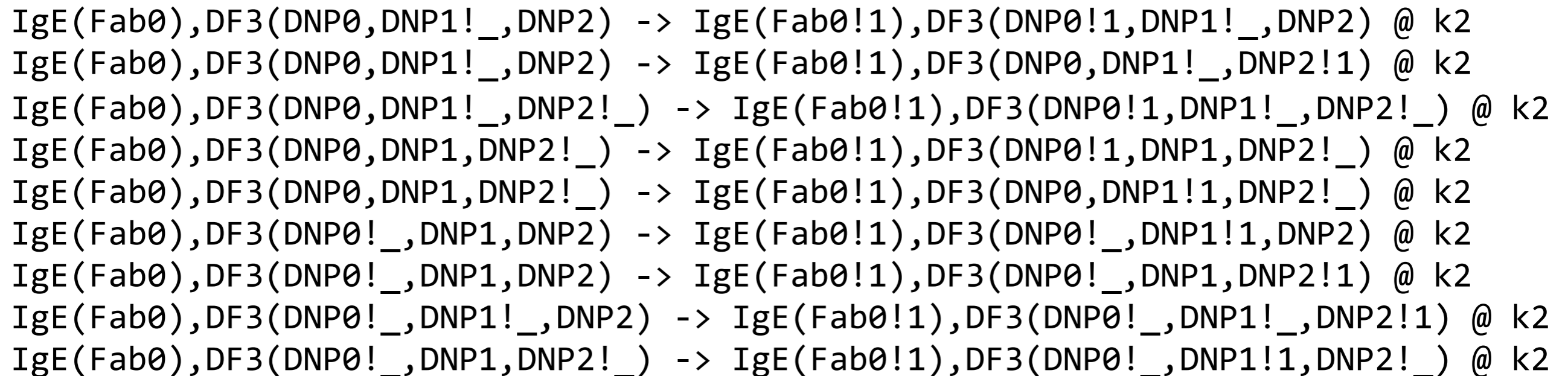
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## 2. Rule(s) governing IgE crosslinking by DF3

BNGL:



Kappa:



# Translating identically named sites

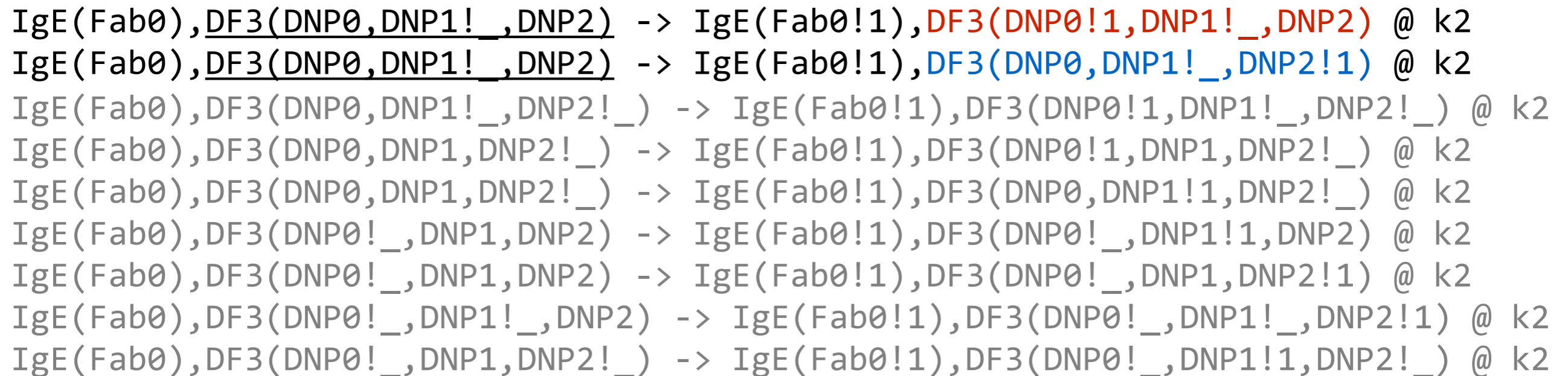
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## 2. Rule(s) governing IgE crosslinking by DF3

BNGL:



Kappa:

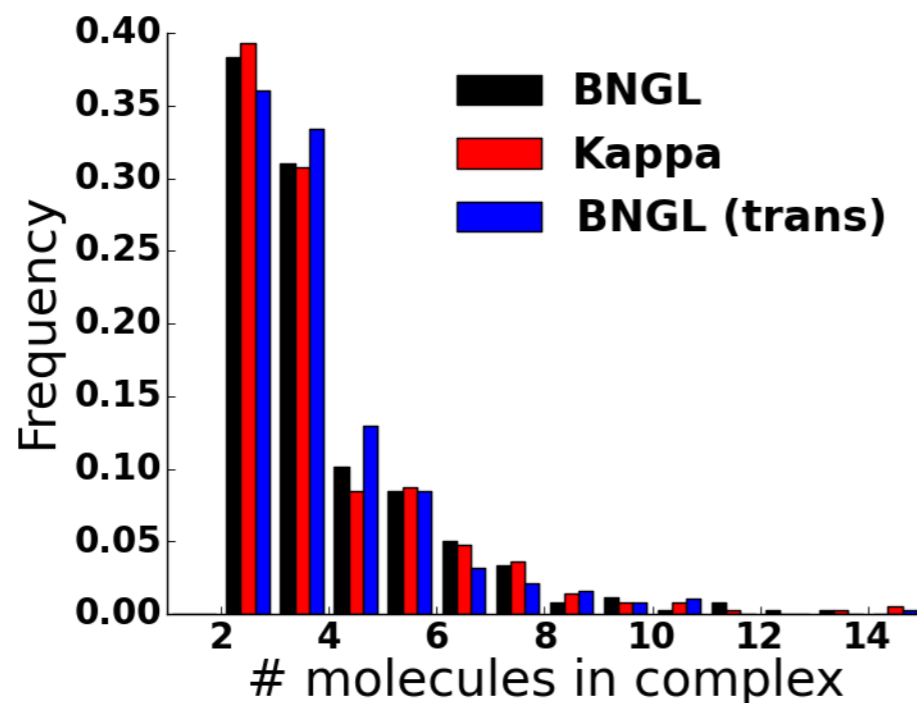
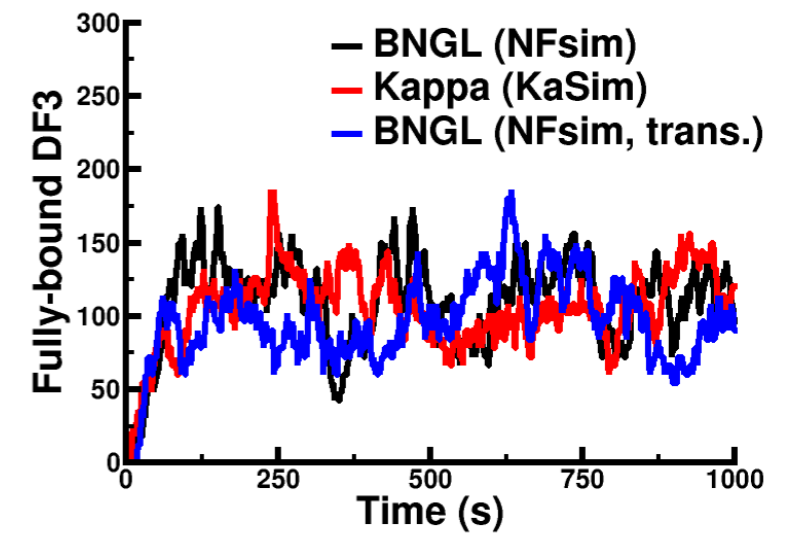
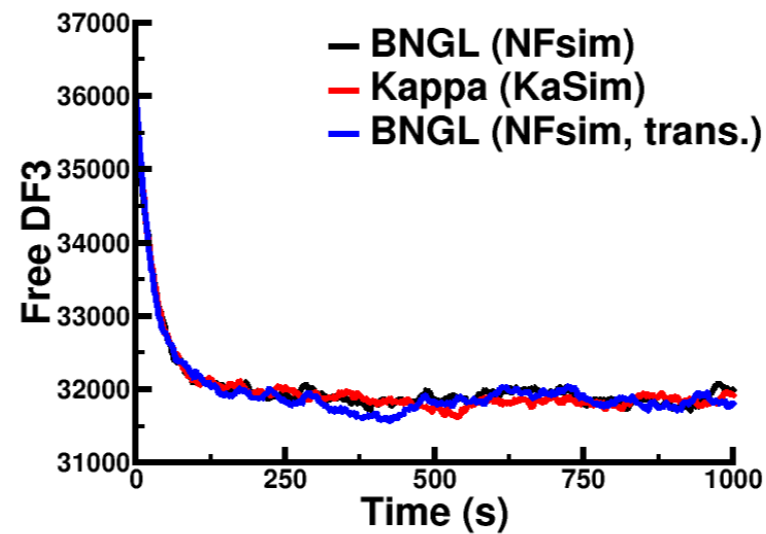




# Simulation results

The complete model also includes fully independent unbinding

BNGL to Kappa and back to BNGL translations result in identical simulation trajectories



All models also capture similar aggregate size distributions

# Additional considerations

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Include Kappa tokens and BNGL populations

Integrate SBML **multi** extension, other languages

# Acknowledgments

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People:

Bill Hlavacek  
Song Feng  
Yen Ting Lin  
Eshan Mitra  
Alex Ionkov

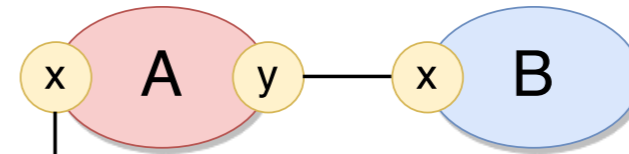
Funding:



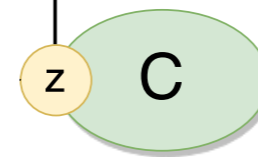
# Molecularity

BNGL operators enforce molecularity on pattern matching

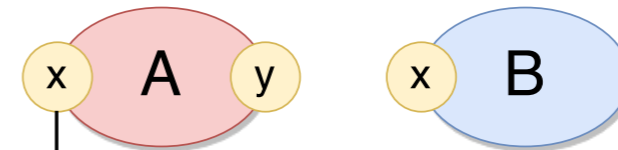
$A(x!+) \cdot B() \Rightarrow$



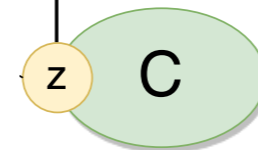
$A(x!_) , B() \Rightarrow$



$A(x!+) \cdot B() \neq />$



$A(x!+) + B() \Rightarrow$



$A(x!_) , B() \Rightarrow$

Kappa rules do not (locality)

# Grammars

## BNGL simple patterns

$\langle pattern \rangle ::= '0' \mid \langle molecule \rangle, [\{'.', \langle molecule \rangle\}]$

$\langle molecule \rangle ::= \langle bName \rangle, ['(', \langle compList \rangle ')']$

$\langle compList \rangle ::= \langle empty \rangle \mid \langle component \rangle, [\{',', \langle component \rangle\}]$

$\langle component \rangle ::= \langle bName \rangle, \langle compState \rangle, \langle compBond \rangle$

$\langle compState \rangle ::= \langle empty \rangle \mid '\sim', \langle bName \rangle$

$\langle compBond \rangle ::= \langle empty \rangle \mid '!?' \mid '!+' \mid '!', \langle integer \rangle$

## Kappa simple patterns

$\langle pattern \rangle ::= \langle empty \rangle \mid \langle agent \rangle, [\{',', \langle agent \rangle\}]$

$\langle agent \rangle ::= \langle kName \rangle, '(', \langle siteList \rangle, ')'$

$\langle siteList \rangle ::= \langle empty \rangle \mid \langle site \rangle, [\{',', \langle site \rangle\}]$

$\langle site \rangle ::= \langle kName \rangle, \langle siteState \rangle, \langle bond \rangle$

$\langle siteState \rangle ::= \langle empty \rangle \mid '\sim', \langle kName \rangle$

$\langle bond \rangle ::= \langle empty \rangle \mid '!', \langle integer \rangle \mid '!_' \mid '??'$

## Useful regular expressions

$\langle integer \rangle = [0-9]^+$

$\langle bName \rangle = [a-zA-Z][a-zA-Z_0-9]^*$

$\langle kName \rangle = [a-zA-Z][a-zA-Z_0-9+-]^*$

$\langle string \rangle = .*$

# Grammars

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## BNGL simple rules

$$\langle uniRule \rangle ::= [\langle bName \rangle, ':', \langle patternList \rangle, '->', \langle patternList \rangle, \langle ws \rangle, \langle rate \rangle, \langle newline \rangle]$$
$$\langle biRule \rangle ::= [\langle bName \rangle, ':', \langle patternList \rangle, '<->', \langle patternList \rangle, \langle ws \rangle, \langle rate \rangle, \langle rate \rangle, \langle newline \rangle]$$
$$\langle patternList \rangle ::= \langle empty \rangle \mid \langle pattern \rangle, '+', \langle patternList \rangle$$
$$\langle rate \rangle ::= ? \text{ an algebraic expression in BNGL syntax ?}$$

## Kappa simple rules

$$\langle uniRule \rangle ::= [‘‘’, \langle string \rangle, ’’], \langle pattern \rangle, '->', \langle pattern \rangle, '@', \langle rate \rangle, \langle newline \rangle]$$
$$\langle biRule \rangle ::= [‘‘’, \langle string \rangle, ’’], \langle pattern \rangle, '<->', \langle pattern \rangle, '@', \langle rate \rangle, \langle rate \rangle, \langle newline \rangle]$$
$$\langle rate \rangle ::= \langle expression \rangle, [‘{’, \langle expression \rangle ’}’]$$
$$\langle expression \rangle ::= ? \text{ an algebraic expression in Kappa syntax ?}$$

# Part of a model of pheromone signaling in baker's yeast

Readable?

Extensible?

ODE functions:

$$\frac{d[Ste2]}{dt} = -k1[\alpha - factor][Ste2] + k2[Ste2_{active}] - k7[Ste2] + \frac{k4[Ste12_{active}]^2}{k5^2 + [Ste12_{active}]^2} + k6$$

$$\frac{d[Ste2_{active}]}{dt} = k1[\alpha - factor][Ste2] - k2[Ste2_{active}] - k3[Ste2_{active}]$$

$$\frac{d[Sst2_{active}]}{dt} = \frac{k44[Ste12_{active}]^2}{k45^2 + [Ste12_{active}]^2} - k46[Sst2_{active}]$$

$$\frac{d[G]}{dt} = -k8[Ste2_{active}][G] + k15[G_{\alpha d}][G_{\beta\gamma}] + \frac{k9[Ste12_{active}]^2}{k10^2 + [Ste12_{active}]^2} - k12[G] + k11$$

$$\frac{d[G_{\alpha t}]}{dt} = k8[Ste2_{active}][G] - k13[G_{\alpha t}] - k14[G_{\alpha t}][Sst2_{active}]$$

$$\frac{d[G_{\alpha d}]}{dt} = k13[G_{\alpha t}] + k14[G_{\alpha t}][Sst2_{active}] - k15[G_{\alpha d}][G_{\beta\gamma}]$$

$$\frac{d[G_{\beta\gamma}]}{dt} = k8[Ste2_{active}][G] - k15[G_{\alpha d}][G_{\beta\gamma}] - k40[G_{\beta\gamma}][Far1pp_{out}] + k41[Far1pp_{out}G_{\beta\gamma}]_{20} - k18[G_{\beta\gamma}][Ste20] + k19[G_{\beta\gamma}Ste20]$$

$$\frac{d[Ste20]}{dt} = -k18[G_{\beta\gamma}][Ste20] + k19[G_{\beta\gamma}Ste20]$$

$$\frac{d[G_{\beta\gamma}Ste20]}{dt} = k18[G_{\beta\gamma}][Ste20] - k19[G_{\beta\gamma}Ste20] - k16[G_{\beta\gamma}Ste20]B1 + k17C1 - k16[G_{\beta\gamma}Ste20]B2 + k17C2 - k16[G_{\beta\gamma}Ste20]B3 + k17C3 - k16[G_{\beta\gamma}Ste20]B4 + k17C4 - k16[G_{\beta\gamma}Ste20]B5 + k17C5 - k16[G_{\beta\gamma}Ste20]B6 + k17C6 - k16[G_{\beta\gamma}Ste20]B7 + k17C7 - k16[G_{\beta\gamma}Ste20]B8 + k17C8 - k16[G_{\beta\gamma}Ste20]B9 + k17C9 - k16[G_{\beta\gamma}Ste20]B10 + k17C10 - k16[G_{\beta\gamma}Ste20]B11 + k17C11 - k16[G_{\beta\gamma}Ste20]B12 + k17C12 - k16[G_{\beta\gamma}Ste20]B13 + k17C13 - k16[G_{\beta\gamma}Ste20]B14 + k17C14 - k16[G_{\beta\gamma}Ste20]B15 + k17C15 - k16[G_{\beta\gamma}Ste20]B16 + k17C16 - k16[G_{\beta\gamma}Ste20]B17 + k17C17 - k16[G_{\beta\gamma}Ste20]B18 + k17C18 - k16[G_{\beta\gamma}Ste20]B19 + k17C19 - k16[G_{\beta\gamma}Ste20]B20 + k17C20 - k16[G_{\beta\gamma}Ste20]B21 + k17C21 - k16[G_{\beta\gamma}Ste20]B22 + k17C22 - k16[G_{\beta\gamma}Ste20]B23 + k17C23 - k16[G_{\beta\gamma}Ste20]B24 + k17C24 - k16[G_{\beta\gamma}Ste20]B25 + k17C25 - k16[G_{\beta\gamma}Ste20]B26 + k17C26 - k16[G_{\beta\gamma}Ste20]B27 + k17C27$$

$$\frac{d[Ste11]}{dt} = p1_{KKK}[Ste11pMAPKKK - P] + of_{f_{KKK}}(C2+C8+C11+C12+C15+C20+C22+C23+C26+B2+B8+B11+B12+B15+B20+B22+B23+B26) - on_{KKK}[Ste11](C4+C6+C7+C1+C16+C17+C18+C19+C5+B4+B6+B7+B1+B16+B17+B18+B19+B5) - k26[Ste11][Fus3pp_{out}]$$

$$\frac{d[Ste11p]}{dt} = -a1_{KKK}[Ste11p](MAPKKK - P)_0 - [Ste11pMAPKKK - P] - [Ste11ppMAPKKK - P] + d1_{KKK}[Ste11pMAPKKK - P] + p2_{KKK}[Ste11ppMAPKKK - P]$$

$$\frac{d[Ste11pMAPKKK - P]}{dt} = a1_{KKK}[Ste11p](MAPKKK - P)_0 - [Ste11pMAPKKK - P] - [Ste11ppMAPKKK - P] - (d1_{KKK} + p1_{KKK})[Ste11pMAPKKK - P] - a2_{KKK}[Ste11pp](MAPKKK - P)_0 - [Ste11pMAPKKK - P] - [Ste11ppMAPKKK - P] + d2_{KKK}[Ste11ppMAPKKK - P] - a3_{KKK}[Ste11pp][Ste7] + (d3_{KKK} + p3_{KKK})[Ste11ppSte7] - a4_{KKK}[Ste11pp][Ste7p] + (d4_{KKK} + p4_{KKK})[Ste11ppSte7p] + * of_{f_{KKK}}(C3+C10+C9+C13+C14+C21+C24+C25+C27+B3+B10+B9+B13+B14+B21+B24+B25+B27) - * on_{KKK}[Ste11pp](C1+C4+C5+C6+C7+C16+C17+C18+C19+B1+B4+B5+B6+B7+B16+B17+B18+B19)$$

$$\frac{d[Ste7]}{dt} = -a3_{KKK}[Ste7][Ste11pp] + d3_{KKK}[Ste11ppSte7] + p1_{KKK}[Ste7pMAPKK - P] + of_{f_{KKK}}(C4+C8+C9+C16+C19+C20+C21+C23+C25+B4+B8+B9+B16+B19+B20+B21+B23+B25) - on_{KKK}[Ste7](C1+C2+C3+C6+C7+C12+C13+C14+C15+B1+B2+B3+B6+B7+B12+B13+B14+B15) - k24[Ste7][Fus3_{out}] + k25[Fus3_{out}Ste7]$$

$$\frac{d[Ste7Ste11pp]}{dt} = a3_{KKK}[Ste11pp][Ste7] - (d3_{KKK} + p3_{KKK})[Ste11ppSte7]$$

$$\frac{d[Ste7p]}{dt} = -a1_{KKK}([MAPKK - P]_0 - [Ste7pMAPKK - P] - [Ste7ppMAPKK - P])[Ste7p] + d1_{KKK}[Ste7pMAPKK - P] + p3_{KKK}[Ste11ppSte7] - a4_{KKK}[Ste7p][Ste11pp] + d4_{KKK}[Ste11ppSte7p] + p2_{KKK}[Ste7ppMAPKK - P]$$

$$\frac{d[Ste7pMAPKK - P]}{dt} = a1_{KKK}[Ste7p](MAPKK - P)_0 - [Ste7pMAPKK - P] - [Ste7ppMAPKK - P] - (d1_{KKK} + p1_{KKK})[Ste7pMAPKK - P]$$

$$\frac{d[Ste7pSte11pp]}{dt} = a4_{KKK}[Ste11pp][Ste7p] - (d4_{KKK} + p4_{KKK})[Ste11ppSte7p]$$

$$\frac{d[Ste7pp]}{dt} = -a2_{KKK}[Ste7pp](MAPKK - P)_0 - [Ste7pMAPKK - P] - [Ste7ppMAPKK - P] + d2_{KKK}[Ste7ppMAPKK - P] + p4_{KKK}[Ste11ppSte7p] - a3_{KKK}[Ste7pp][Fus3_{out}] + (d3_{KKK} + p3_{KKK})[Ste7ppFus3_{out}] - a4_{KKK}[Ste7pp][Fus3pp_{out}] + (d4_{KKK} + p4_{KKK})[Ste7ppFus3pp_{out}] + * of_{f_{KKK}}(C5+C10+C11+C17+C22+C24+B5+B10+B11+B17+B22+B24) + * of_{f_{KKK}}(C18+C26+C27+B18+B26+B27) - k27[Ste7pp]$$

$$\frac{d[Ste7ppMAPKK - P]}{dt} = a2_{KKK}[Ste7pp](MAPKK - P)_0 - [Ste7pMAPKK - P] - [Ste7ppMAPKK - P] - (d2_{KKK} + p2_{KKK})[Ste7ppMAPKK - P]$$

$$\frac{d[Fus3_{out}]}{dt} = -a3_K[Ste7pp][Fus3_{out}] + d3_K[Ste7ppFus3_{out}] + p1_K[Fus3pp_{out}MAPK - P_{out}] + of_{f_K}(C6+C12+C13+C16+C17+C20+C21+C22+C24+B6+B12+B13+B16+B17+B20+B21+B22+B24) - on_K[Fus3_{out}](C1+C2+C3+C4+C5+C8+C9+C10+C11+B1+B2+B3+B4+B5+B8+B9+B10+B11) - k24[Ste7][Fus3_{out}] + k25[Fus3_{out}Ste7] + k47[Fus3_{in}] - k48[Fus3_{out}] + \frac{k32[Ste12_{active}]^2}{k5^2 + [Ste12_{active}]^2}$$

$$\frac{d[Fus3_{out}Ste11pp]}{dt} = a3_K[Ste7pp][Fus3_{out}] - (d3_K + p3_K)[Ste7ppFus3_{out}]$$

$$\frac{d[Fus3pp_{out}]}{dt} = -a1_K[Fus3pp_{out}][MAPK - P_{out}] + d1_K[Fus3pp_{out}MAPK - P_{out}] + p3_K[Ste7ppFus3_{out}] - a4_K[Ste7pp][Fus3pp_{out}] + d4_K[Ste7ppFus3pp_{out}] + p2_K[Fus3pp_{out}MAPK - P_{out}]$$

$$\frac{d[Fus3pp_{out}MAPK - P_{out}]}{dt} = a1_K[Fus3pp_{out}][MAPK - P_{out}] - (d1_K + p1_K)[Fus3pp_{out}MAPK - P_{out}]$$

$$\frac{d[Fus3pp_{out}Ste7pp]}{dt} = a4_K[Ste7pp][Fus3pp_{out}] - (d4_K + p4_K)[Ste7ppFus3pp_{out}]$$

$$\frac{d[Fus3pp_{out}]}{dt} = -a2_K[Fus3pp_{out}][MAPK - P_{out}] + d2_K[Fus3pp_{out}MAPK - P_{out}] + p4_K[Ste7ppFus3pp_{out}] + * of_{f_K}(C7+C14+C15+C18+C19+C23+C25+C26+C27+B7+B14+B15+B18+B19+B23+B25+B26+B27) + k49[Fus3pp_{in}] - k50[Fus3pp_{out}]$$

$$\frac{d[Fus3pp_{out}MAPK - P_{out}]}{dt} = a2_K[Fus3pp_{out}][MAPK - P_{out}] - (d2_K + p2_K)[Fus3pp_{out}MAPK - P_{out}]$$

$$\frac{d[MAPK - P_{out}]}{dt} = -a1_K[Fus3pp_{out}][MAPK - P_{out}] + (d1_K + p1_K)[Fus3pp_{out}MAPK - P_{out}] - a2_K[Fus3pp_{out}][MAPK - P_{out}] + (p2_K + d2_K)[Fus3pp_{out}MAPK - P_{out}] + \frac{k31[Ste12_{active}]^2}{k5^2 + [Ste12_{active}]^2}$$

$$\frac{d[Fus3_{out}Ste7]}{dt} = k24[Ste7][Fus3_{out}] - k25[Fus3_{out}Ste7]$$

Shao, D., et al, (2006), Biophys J

# Dynamical systems biology

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Modeling protein interaction networks traditionally done with ODEs or reaction networks

Two prominent issues:

Encoding (knowledge representation)



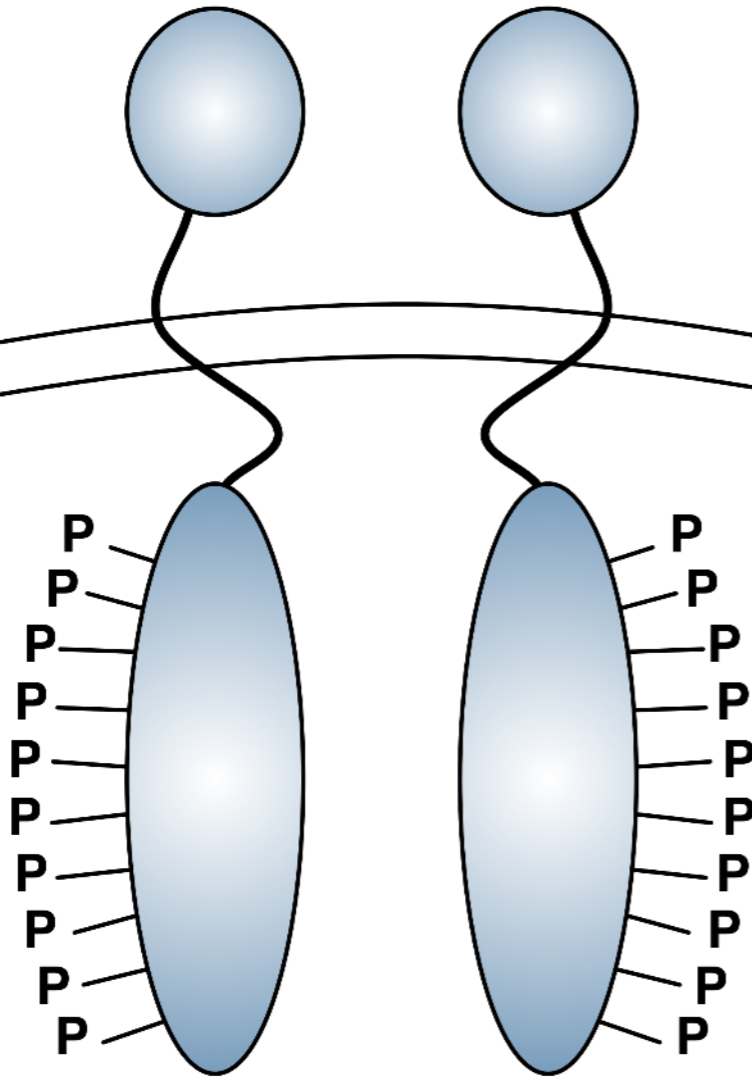
# Combinatorial complexity

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PDGF receptor

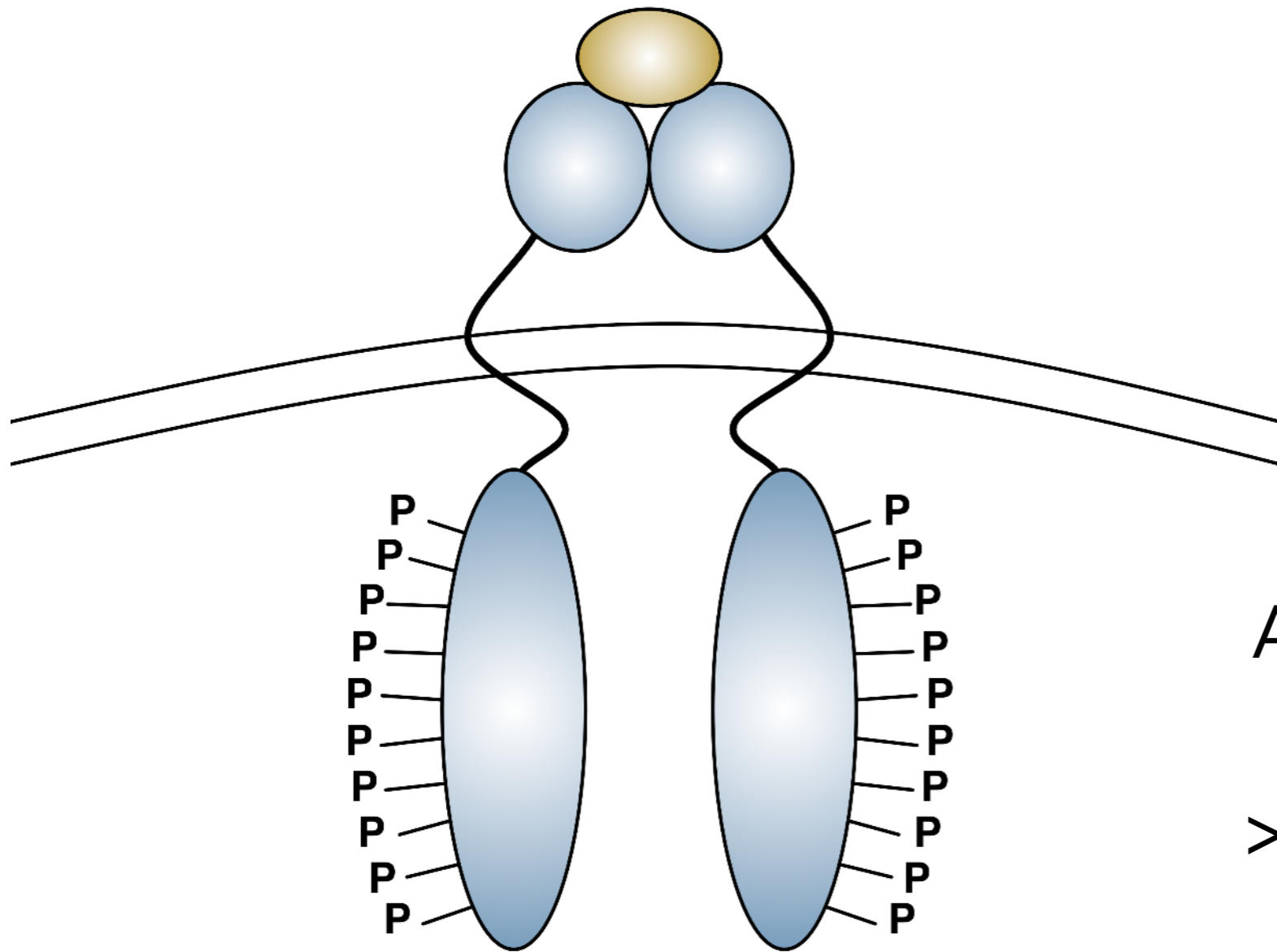
10 phosphorylation sites

$2^{10}$  possible states



# Combinatorial complexity

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PDGF receptor

10 phosphorylation sites

$2^{10}$  possible states

Active receptor dimerizes

>500,000 possible states