

Kappa practical

<http://perso.ens-lyon.fr/russell.harmer/AIV/>

Russ Harmer
LIP, CNRS & ENS Lyon

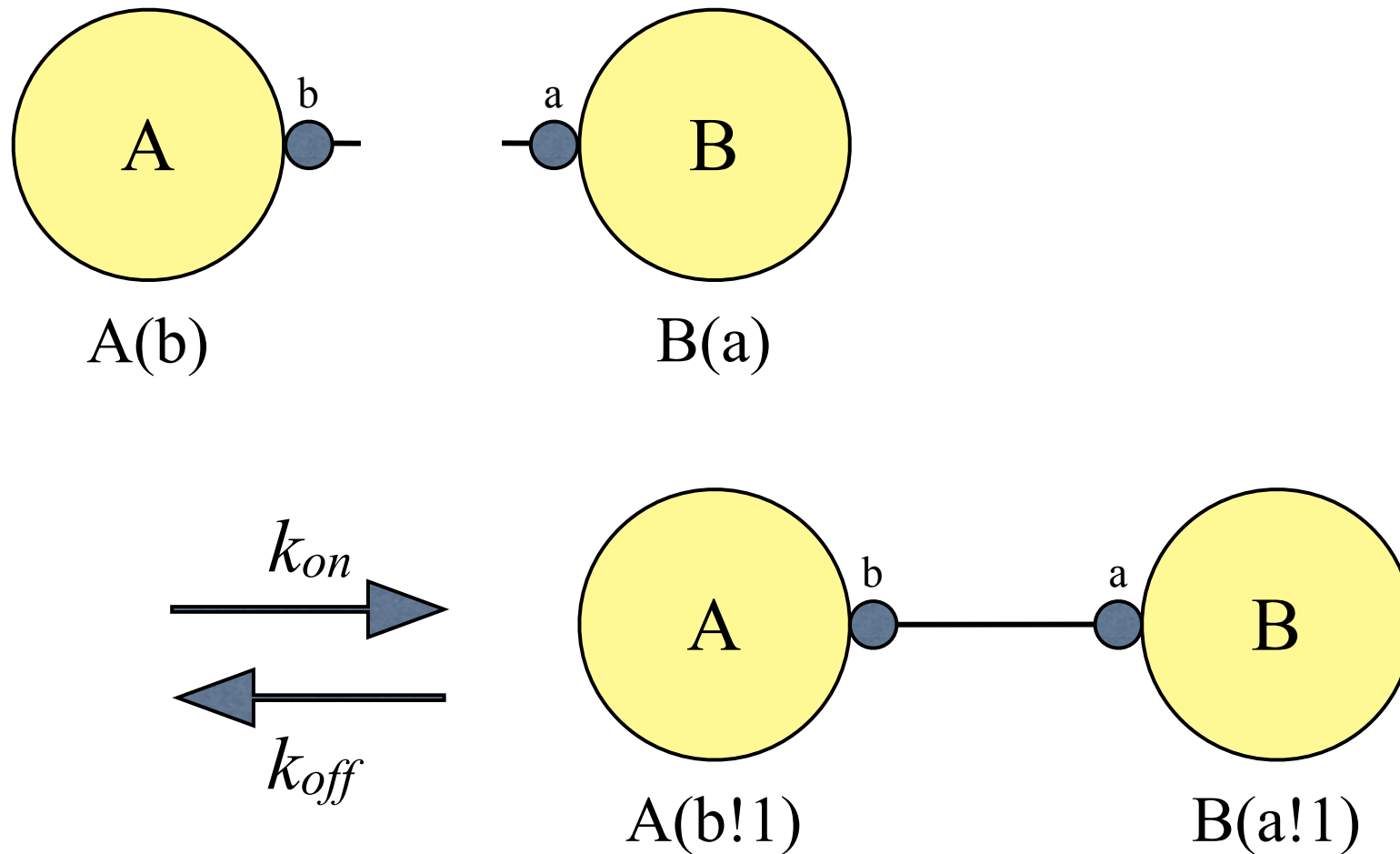
You need to be able to...

- Create and edit *plain text* files
 - TextEdit, emacs, ...
- Run the Kappa simulator from the *command line*
 - `sh> KaSim -i AB.ka -e 1000 -p 500`
- Plot the output using gnuplot
 - `gnuplot> plot "data.out" using 1:3 with lines`

I. Binding equilibrium

Binding equilibrium

<http://rulebase.org/models/binding-equilibria>



AB.ka

<http://perso.ens-lyon.fr/russell.harmer/AIV/AB.ka>

```
# agent declarations
%agent: A(b)
%agent: B(a)

# some useful variables
%var: 'fast' 10
%var: 'medium' 1
%var: 'slow' 0.1
%var: 'BND' 0.00001
%var: 'BRK' 0.1
%var: 'MOD' 0.1

# binding rule
A(b), B(a) -> A(b!0), B(a!0) @ 'BND' # * 'fast'

# unbinding rule
A(b!0), B(a!0) -> A(b), B(a) @ 'BRK' # * 'slow'

# initial state
%init: 1000 A(b)
%init: 1000 B(a)

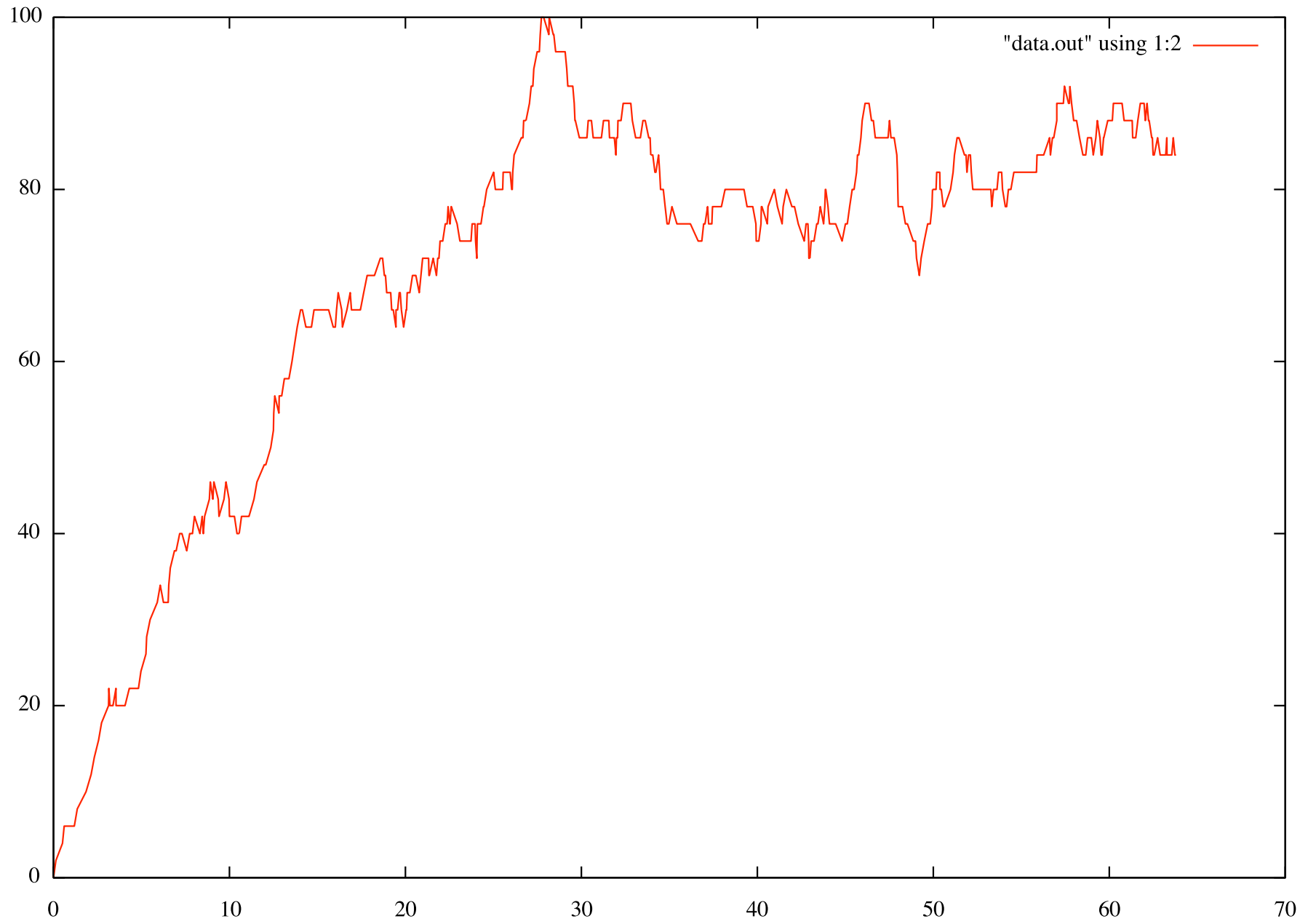
# count the number of AB complexes
%obs: 'AB' A(b!1), B(a!1)
```

Running KaSim

- We must specify:
 - the input file: `-i`
 - the number of events *or* time: `-e` *or* `-t`
 - number of output time points: `-p`
- e.g.
 - `sh> /Applications/Kappa/KaSim -i AB.ka -e 1000 -p 500`

Displaying output

- KaSim outputs to the file data.out
 - you can change this with the -o option
- Run gnuplot from the command line
 - `sh> /opt/local/bin/gnuplot`
 - `gnuplot> set term 'x11'`
- Then
 - `gnuplot> plot "data.out" using 1:2 with lines`



"data.out" using 1:2

Questions

- Time to equilibrium?
- What does ‘equilibrium’ even mean in a stochastic setting like this?

- Run the model a second time:
 - `gnuplot> replot "data.out" using 1:2 with lines`
- Run the model for longer:
 - `sh> KaSim -i AB.ka -t 180 -p 500`

Questions

- What happens if you
 - increase the binding rate by a factor of 10 ?
 - increase the binding *and* the unbinding rate by a factor of 10 ?

Perturbations

- Modify rate constants *during* simulation !

```
%mod: [T] > 100 do 'BND' := 'BND' * 10  
%mod: [T] > 200 do 'BND' := 'BND' * 10
```

- sh> **KaSim -i AB.ka -t 300 -p 1000**

Questions

- What happens if you introduce a *conflict* ?
 - a new agent C(a)
 - rules for binding and unbinding of C to/from A
- Can you think of a way to introduce C only after A and B have reached equilibrium?

About bi-molecular rate constants

- k_{det} has dimension *conc⁻¹time⁻¹*
 - usually *M⁻¹s⁻¹* where $M = \text{mol} / l$
 - sometimes use ‘mass concentration’, e.g. *g/l*
- k_{stoch} has dimension *time⁻¹*
 - k_{det} / V has units *mol⁻¹s⁻¹*
 - $k_{stoch} = k_{det} / AV$ has units *molecule⁻¹s⁻¹*
(where $V = \text{volume in } l$ and $A = \text{Avagadro}$)

About rate constants

- For eukaryotes, $AV \sim 10^{12}$
 - typical $k_{det} \sim 10^7 - 10^9 \text{ M}^{-1}\text{s}^{-1}$
 - so typical $k_{stoch} \sim 10^{-5} - 10^{-3} \text{ molecule}^{-1}\text{s}^{-1}$
- Unbinding is volume-independent
 - $k_{det} = k_{stoch} \sim 0.1 \text{ s}^{-1}$

Rescaling (a useful trick)

- **%var: 'vol' 1.0**
- Modify birth and binding rates and variables:
A(b),B(a) -> A(b!0),B(a!0) @ 'BND'/'vol'
-> A(b) @ 'BIRTH'*'vol'
%init: 1000*'vol' A(b)
- Decreasing vol preserves system dynamics
 - increases fluctuations; speeds up simulation
- What about increasing vol ?

II. Independent binding

ABC.ka

```
%agent: A(b)
%agent: B(a,c)
%agent: C(b)
```

```
%var: 'vol' 1.0
%var: 'BND' 0.005
%var: 'BRK' 0.1
%var: 'MOD' 0.1
```

```
%var: 'nA' 1000*'vol'
%var: 'nB' 1000*'vol'
%var: 'nC' 1000*'vol'
```

```
A(b), B(a) -> A(b!0), B(a!0) @ 'BND'/'vol'
A(b!0), B(a!0) -> A(b), B(a) @ 'BRK'
B(c), C(b) -> B(c!0), C(b!0) @ 'BND'/'vol'
B(c!0), C(b!0) -> B(c), C(b) @ 'BRK'
```

```
%init: 'nA' A(b)
%init: 'nB' B(a,c)
%init: 'nC' C(b)
```

```
%obs: 'AB?' A(b!1), B(a!1)
%obs: 'ABC' A(b!1), B(a!1,c!2), C(b!2)
%obs: 'AB' 'AB?' - 'ABC'
%obs: 'total ABC' 'ABC'/'vol'
```

Questions

- What is the equilibrium level of the **ABC** complex ? What about **AB** and **BC** ?
- How do these depend on the number of **Bs** ?
 - try a few different values
 - is there a better way? (less tedious, more systematic)

Quasi-equilibrium

- Start out with no **B**s at all !

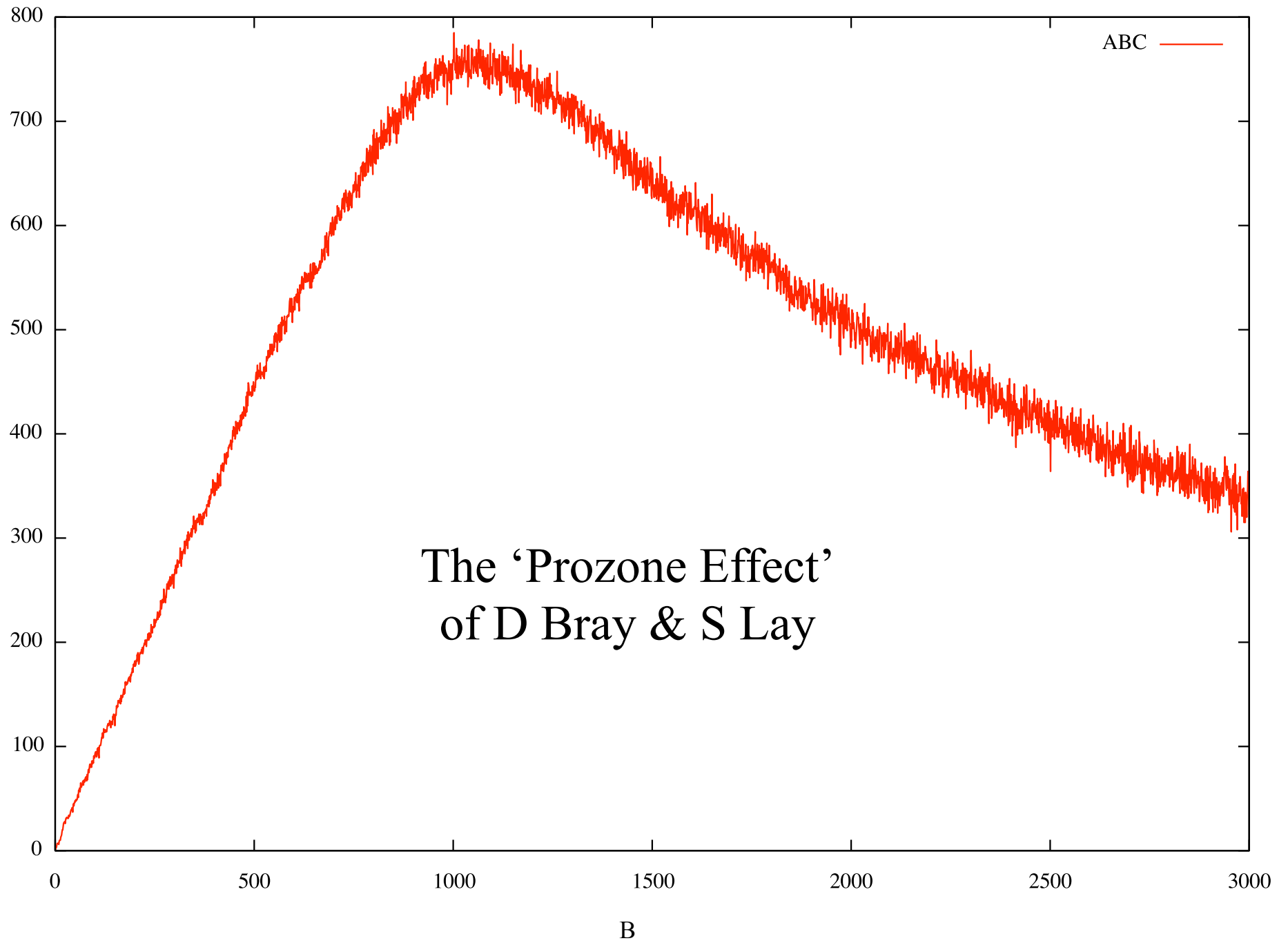
`%init: 'nA' A(b)`

`%init: 'nC' C(b)`

- Inject **B**s 1-by-1 *sufficiently slowly* ...

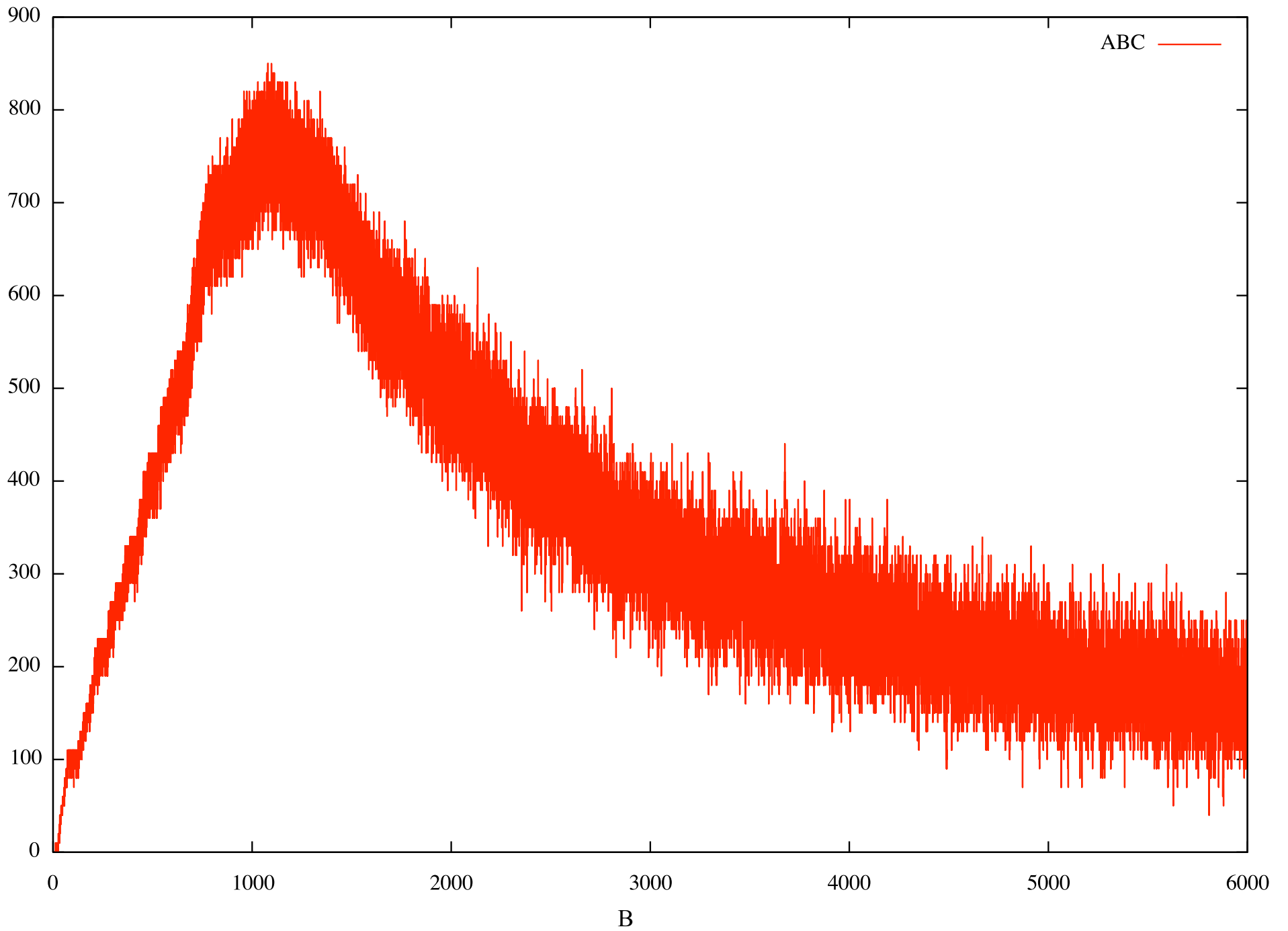
`-> B(a,c) @ 0.1`

- ... that the system re-equilibrates each time a new **B** is born !



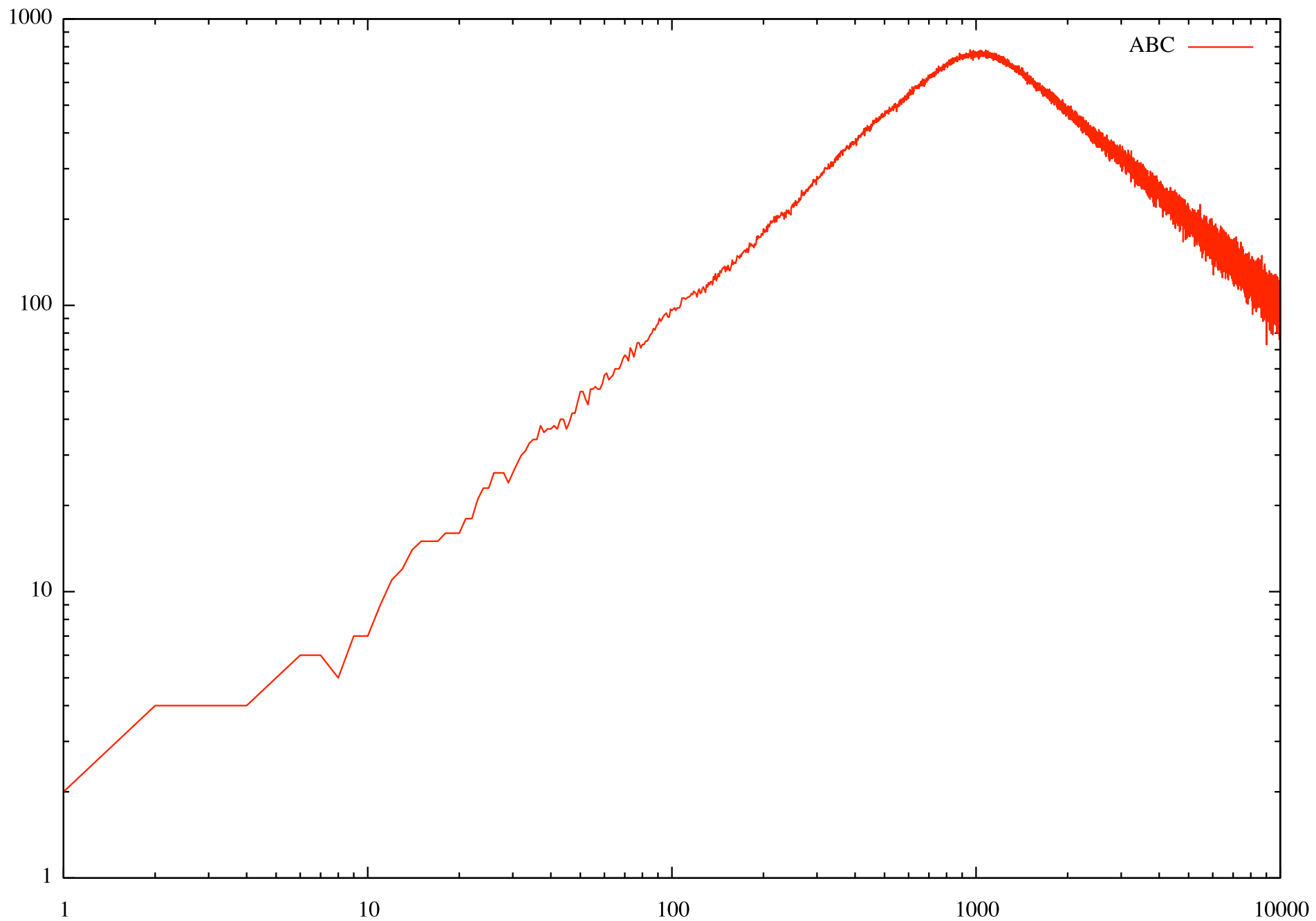
ABC

- Non-monotonic in the number of **Bs** !
 - why ?
 - where is the peak ?
- Reduce the volume to speed things up ...
 - ... but increase fluctuations
 - alternatively, rewrite the model using *tokens* ...



ABC

- Why does noise increase with the number of **Bs** ?
- A different point of view on this curve:
 - **gnuplot> set logscale xy**



ABC revisited

- Let's **refine** the 'B binds C' rule

$B(t), C(s) \rightarrow B(t!O), C(s!O) @ k$

into two *sub-cases*:

1. if 'B not bound to A', @ k_1

2. if 'B bound to A', @ k_2

- *Negative co-operativity*: $k_2 < k$ (and $k_1 > k$)
- *Positive co-operativity*: $k_1 < k$ (and $k_2 > k$)

```
%agent: A(s)
%agent: B(s,t)
%agent: C(t)
```

```
%var: 'vol' 0.1
%var: 'BND' 0.005
%var: 'BRK' 0.1
%var: 'MOD' 0.1
```

```
%var: 'nA' 1000*'vol'
%var: 'nC' 1000*'vol'
```

```
A(s), B(s,t) -> A(s!0), B(s!0,t) @ 'BND'/'vol'*10
A(s), B(s,t!_) -> A(s!0), B(s!0,t!_) @ ('BND'*10)/'vol'
A(s!0), B(s!0) -> A(s), B(s) @ 'BRK'
```

```
B(s,t), C(t) -> B(s,t!0), C(t!0) @ 'BND'/'vol'*10
B(s!_,t), C(t) -> B(s!_,t!0), C(t!0) @ ('BND'*10)/'vol'
B(t!0), C(t!0) -> B(t), C(t) @ 'BRK'
```

```
-> B(s,t) @ 0.1*'vol'
```

```
%init: 'nA' A
%init: 'nC' C
```

```
%var: 'ABC' A(s!1), B(s!1,t!2), C(t!2)
%obs: 'total ABC' 'ABC'/'vol'
%obs: 'B' B()
```

What do you think?

- How do negative and positive co-operativity impact upon the prozone effect?

