### MULTIVALENCY NATURE'S ADJUSTABLE TOOL FOR CHANGING PROTEIN BINDING STRENGTH BRUNCSICS BENCE BRUNCSICS@GMAIL.COM

### **OVERVIEW**

- Protein binding
- Multivalency
- Model framework overview
  - Figuring out the model
  - Figuring out effective concentration
  - Applications



UNIVERSITY OF MINNESOTA Driven to Discover<sup>™</sup>











### **BINDING STRENGTH**

- KD-dissociation constant
  - 1nM, 1mM
- Daily dose
  - Will it be a good pill
- Multivalency can increase it significantly



### **BINDING KINETICS I**







### BINDING KINETICS II

- In steady state:  $k_{on}[R][L] = k_{off}[RL]$
- The speed of transition:

 $\begin{aligned} v_{association} &= k_{on}[R][L] \\ v_{dissociation} &= k_{off}[RL] \end{aligned}$ 

• In differential equation form:

$$\frac{d[R]}{dt} = -k_{on}[R][L] + k_{off}[RL]$$
$$\frac{d[RL]}{dt} = +k_{on}[R][L] - k_{off}[RL]$$







## MULTIVALENCY

- Multivalent molecules
  - Bivalent
  - Trivalent
  - Higher valencies
- Complexity
  - Conformations states
  - Kinetics
  - Composition homo, hetero
  - Biological functions



#### LENT EXAN ΞE ВL



Monovalent :

Multiple:

Multivalent:

association  $R_{1,1}L_1L_1$ dissociation association $R_{1,1}L_{1,1}$ 

dissociation

dissociation

 $R_{\emptyset} + L_1$ 

association $R_{1,\emptyset}L_1 + L_1$ dissociationassociation  $R_{1,\varnothing}L_{1,1}$ 

dissociation

 $R_{\varnothing,\varnothing} + L_{1,1}$ 

### FIGURING OUT ALL THE STATES



R, L,



### IDENTIFYING STATES AND TRANSITIONS

- Increasing complexity
- Notation of states:









### BINDING KINETICS II

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# ODES (OPTIONAL)

- Write an ode based on text
- You have n=10000 tasks
- Each task have 10% chance each hour to finish
- When will 95% of the tasks finish
- $\frac{dn}{dt} = -0.9n$
- Due to overheating each hour your computation is 1% slower

• 
$$\frac{dh}{dt} = 0.01$$
,  $\frac{dn}{dt} = -(0.9 + h)n$ 

- Calculate n(t) = 500
  - Math
  - Numerical

### EXAMPLE

$$\frac{d[R_{\varnothing\varnothing}]}{dt} = -2k_{on}^{1-2}[R_{\varnothing\varnothing}][L_{11}] + k_{off}^{1-2}[R_{1\varnothing}L_{11}]$$

$$\frac{d[R_{1\varnothing}L_{11}]}{dt} = +2k_{on}^{1-2}[R_{\varnothing\varnothing}][L_{11}] - k_{off}^{1-2}[R_{1\varnothing}L_{11}] - k_{on}^{2-3}[R_{1\omega}] + 2k_{off}^{2-3}[R_{11}L_{11}]$$

$$\frac{d[R_{11}L_{11}]}{dt} = +k_{on}^{2-3}[R_{1\varnothing}] - 2k_{off}^{2-3}[R_{11}L_{11}]$$

 $\begin{vmatrix} \frac{d[R_{\varnothing \varnothing}]}{dt} \\ \frac{d[R_{1} \varnothing L_{11}]}{dt} \\ \frac{d[R_{11} L_{11}]}{dt} \end{vmatrix} = \begin{vmatrix} -2k_{on}^{1-2}[L_{11}] & +k_{off}^{1-2} \\ +2k_{on}^{1-2}[L_{11}] & -k_{off}^{1-2} - k_{on}^{2-3} & +2k_{off}^{2-3} \\ +k_{on}^{2-3} & -2k_{off}^{2-3} \end{vmatrix} \begin{vmatrix} [R_{\emptyset \varnothing}] \\ [R_{10} L_{11}] \\ [R_{11} L_{11}] \end{vmatrix}$ 

 $\frac{d\boldsymbol{x}(t)}{dt} = \boldsymbol{A}(t)\boldsymbol{x}(t)$ 

State 1 - 
$$R_{go}$$
  
 $Koff^{12}$   
 $Koff^{12}$ 

# **EFFECTIVE CONCENTRATION**

## INTEGRALS

- PDF probability density function
- Integral of a PDF
- Integral the product of two PDF
- Bonus: relation between integration and derivation



### EFFECTIVE VALUES

#### for i in [1:1000]

- x = rnorm(mean=10, sd=2)
- y = rnorm(mean=7, sd=2)
- If x-y < 0.01
  - counter +=1

### for i in [1:1000]

- x = rnorm(mean=10, sd=2)
- for i in [1:eff]
  - z = runif(0,20)
  - If x-y < 0.01
    - counter +=1



## EFFECTIVE CONCENTRATION

- Effective Concentration:  $P(binding | RL) = P(binding | R, L_{C_{eff}})$
- Binding or collision probability:  $\int f_L(x) f_R(x) dx$
- Linker end-to-end PDF









## MVSIM

- Ligand and receptor parameters
  - Topology
  - Monovalent rate constants
- Ligand concentration
  - Three ligand, multiple steps
- Output
  - SPR or concentration curves
  - Microstates
  - Network representation





### MICROSTATES OF A COMPLEX SYSTEM

- Solved by ODE15s solver
- Can predict avidity, specificity
- Explanation for uncanonical behaviors
- Applicable to a wide range of multivalent interaction
- Support for protein engineering



### APPLICATION EXAMPLE – ANTIBODY DESIGN

- Bispecific antibodies
- Surface antigen concentration
- Specific targeting
- AbLec (under development)





### APPLICATION EXAMPLE – MOLECULAR SWITCHES

- Molecular switch
- Ultrasensitive reaction
- Multispecificity
- Importance of genetic switches



### SARS-COV-2 S PROTEIN RBD AND ACE2 INTERACTION

#### Multivalent Parameterization of SARS-CoV-2 and ACE2



Modeling the Efficacy of a Bivalent Neutralizing Therapeutic



MVsim-Guided Design of SARS-CoV-2 Spike Protein Inhibitors



#### MVsim generates multiphasic S protein binding response dynamics present in SPR experiment



An MVsim fitting routine extracts rate constants of RBD switching from multiphasic SPR data



### THANK YOU FOR YOUR ATTENTION!

### ODES – LETS MAKE SOMETHING SIMPLE COMPLICATED

Distance s		

$$\int \sqrt{(-g x + c1)^2 + c2} \, dx = \frac{(g x - c1) \sqrt{(c1 - g x)^2 + c2} - c2 \log \left(\sqrt{(c1 - g x)^2 + c2} + c1 - g x\right)}{2 g} + \text{constant}$$

## FRAMEWORK

- 1. Identifying unique configurations
  - Reduction by symmetry or similarity
- 2. Identifying transitions
- 3. Describing the transitions
  - Approximating the speed of transitions
- 4. Calculating time-dependent concentrations



