Decomposing Complex Cooperative Ligand Binding into Simple Components: Connections between Microscopic and Macroscopic models.

Alexey Onufriev¹ and G. Matthias Ullmann^{2,*}

¹ Department of Computer Science, 660 McBryde Hall, Virginia Tech, Blacksburg, VA 24061. email: onufriev@cs.vt.edu; Fax: (540)-231-6075

² Structural Biology / Bioinformatics, University of Bayreuth, Universitätsstr. 30, BGI, 95447
 Bayreuth, Germany, email: Matthias.Ullmann@uni-bayreuth.de; Fax: +49-921-55-3544

submitted to J. Phys. Chem. B. January 5, 2004

Supporting Information

Details of the Derivation of Cooperativity Measure Ξ

Here we investigate how the slope at the inflection point of decoupled binding curves can be used as a measure of cooperativity. We consider two limiting cases. The maximum cooperativity is achieved if either none or all N ligands bind, i.e. only two states exist: no ligands bound or all ligands bound.

$$\langle X \rangle = \frac{N e^{-\beta (G^{\mathbf{k}} - N\mu_{\rm L})}}{1 + e^{-\beta (G^{\mathbf{k}} - N\mu_{\rm L})}} \tag{1}$$

The first and second derivative of eq 1 are given in eq 2 and 3, respectively.

$$\frac{\partial \langle X \rangle}{\partial \mu_{\rm L}} = \frac{\beta N^2 e^{-\beta (G^{\mathbf{k}} - N\mu_{\rm L})}}{(1 + e^{-\beta (G^{\mathbf{k}} - N\mu_{\rm L})})^2} \tag{2}$$

$$\frac{\partial^2 \langle X \rangle}{\partial \mu_{\rm L}^2} = \frac{\beta^2 N^3 e^{-\beta (G^{\bf k} - N\mu_{\rm L})} (1 - e^{-\beta (G^{\bf k} - N\mu_{\rm L})})}{(1 + e^{-\beta (G^{\bf k} - N\mu_{\rm L})})^3}$$
(3)

From eq 3 the inflection point μ_{I} of eq 1 is given by eq 4.

$$\frac{\partial^2 \langle X \rangle}{\partial \mu_{\rm I}^2} = 0: \qquad \mu_{\rm L} = \frac{G^{\bf k}}{N} \tag{4}$$

The slope at the inflection point is consequently given by eq 5

$$\frac{\partial \langle X \rangle(\mu_{\rm I})}{\partial \mu_{\rm L}} = \frac{\beta N^2}{4} \tag{5}$$

Eq 5 gives the maximum possible slope for a binding curve of N ligands and one receptor.

On the other extreme is a non-cooperative system of N non-interacting equivalent sites. The total binding curve of such a system is given by eq 6

$$\langle X \rangle = N \frac{e^{-\beta(G_i^\circ - \mu_{\rm L})}}{1 + e^{-\beta(G^\circ - \mu_{\rm L})}} \tag{6}$$

The first and the second derivative of eq 6 are given by eqs 7 and 8.

$$\frac{\partial \langle X \rangle}{\partial \mu_{\rm L}} = N \frac{\beta e^{-\beta (G^{\rm o} - \mu_{\rm L})}}{(1 + e^{-\beta (G^{\rm o} - \mu_{\rm L})})^2} \tag{7}$$

$$\frac{\partial^2 \langle X \rangle}{\partial \mu_{\rm L}^2} = N \frac{\beta^2 e^{-\beta (G^{\rm o} - \mu_{\rm L})} (1 - e^{-\beta (G^{\rm o} - \mu_{\rm L})})}{(1 + e^{-\beta (G^{\rm o} - \mu_{\rm L})})^3}$$
(8)

The slope at the inflection point is then given by eq 9.

$$\frac{\partial \langle X \rangle(\mu_{\rm I})}{\partial \mu_{\rm L}} = \frac{\beta N}{4} \tag{9}$$

The combination of eq 5 and eq 5 suggests the following cooperativity measure Ξ :

$$\Xi = \frac{4}{\beta N} \frac{\partial \langle X \rangle(\mu_{\rm I})}{\partial \mu_{\rm L}} \bigg|_{at \ the \ inflection \ point} \tag{10}$$

where the normalization factor is chosen so that

for non-cooperative binding: $\Xi = 1$ and for fully cooperative binding: $1 < \Xi \le N$

Cooperativity in the system of two interacting sites. The total binding curve is

$$\langle X \rangle = \frac{e^{-\beta(G_1^{\circ} - \mu_{\rm L})} + e^{-\beta(G_2^{\circ} - \mu_{\rm L})} + 2e^{-\beta(G_1^{\circ} + G_2^{\circ} + W - 2\mu_{\rm L})}}{1 + e^{-\beta(G_1^{\circ} - \mu_{\rm L})} + e^{-\beta(G_2^{\circ} - \mu_{\rm L})} + e^{-\beta(G_1^{\circ} - \mu_{\rm L})} + e^{-\beta(G_1^{\circ} - \mu_{\rm L})}}$$
(11)

which can be rewritten with

$$A = e^{-\beta G_1^{\circ}} + e^{-\beta G_2^{\circ}}$$

$$B = e^{-\beta (G_1^{\circ} + G_2^{\circ} + W)}$$

$$\lambda = e^{\beta \mu_{\rm L}}$$
(12)

Total binding curve

$$\langle X \rangle = \frac{A\lambda + 2B\lambda^2}{1 + A\lambda + B\lambda^2} \tag{13}$$

First derivative of the Total binding curve is

$$\frac{\partial \langle X \rangle}{\partial \mu_{\rm L}} = \frac{\beta \lambda (A + 4B\lambda + AB\lambda^2)}{(1 + A\lambda + B\lambda^2)^2} \tag{14}$$

Second derivative of the Total binding curve is

$$\frac{\partial^2 \langle X \rangle}{\partial \mu_{\rm L}^2} = \frac{\beta^2 \lambda (1 - B\lambda^2) (A - B^2\lambda + 8B\lambda + AB\lambda^2)}{(1 + A\lambda + B\lambda^2)^3} \tag{15}$$

The total binding curve has only one inflection point for cooperative binding curves

$$\mu_{\rm I} = -\frac{1}{2}\ln B = \frac{1}{2}\beta(G_1^{\rm o} + G_2^{\rm o} - W) \Longrightarrow \lambda_{\rm I} = \frac{1}{\sqrt{B}}$$
(16)

The slope of the binding curve eq 13 at its inflection point is

$$\frac{\partial \langle X \rangle}{\partial \mu_{\rm L}} \Big|_{\lambda_{\rm I}} = \frac{\beta \lambda_{\rm I} (A + 4B\lambda_{\rm I} + AB\lambda_{\rm I}^2)}{(1 + A\lambda_{\rm I} + B\lambda_{\rm I}^2)^2} = \frac{\beta (4B + 2A\sqrt{B})}{4B + 4A\sqrt{B} + A^2}$$
(17)

The cooperativity measure is then given by

$$\Xi = 2 \frac{4B + 2A\sqrt{B}}{4B + 4A\sqrt{B} + A^2} \tag{18}$$

Relation of Ξ to the Hill coefficient. For two sites one can show that Ξ is exactly equivalent to the Hill coefficient. Note, however, that this statement is generally not valid for N > 2 as seen from the examples in the current work. Let Y be saturation of the molecule, i.e.

$$Y = \frac{1}{N} \langle X \rangle \tag{19}$$

and consider only two interacting sites. The Hill coefficient n_{Hill} is defined as slope of the Y/(1-Y) curve when the receptor is half saturated.

. .

$$n_{Hill} = \frac{\partial \frac{Y}{1-Y}}{\partial \mu_{\rm L}} \quad at \quad \mu_{\rm I} = -\frac{1}{2} \ln B \to \lambda_{\rm I} = \frac{1}{\sqrt{B}}$$
(20)

From eq 11 one can find that

$$\frac{Y}{1-Y} = \frac{A\lambda + 2B\lambda^2}{2+A\lambda}$$
(21)

$$\frac{\partial \frac{Y}{1-Y}}{\partial \mu_{\rm L}} = \frac{2\lambda(A+4B\lambda+AB\lambda^2)}{(2+A\lambda)^2}$$
(22)

$$n_{Hill} = \frac{\partial \frac{Y}{1-Y}}{\partial \mu_{\rm L}}\Big|_{\mu_{\rm I}}$$
(23)

$$= \frac{2(2A\sqrt{B}+4B)}{4B+4A\sqrt{B}+A^2}$$
(24)

From comparison with eq 18 one see that

$$n_{Hill} = \Xi \ for \ N = 2. \tag{25}$$

Adair equation re-written using microscopic constants.

* *

For the sake of simplicity, we restrict the discussion to the N=4 ligand binding sites. We choose N=4 mainly due to the importance of the hemoglobin test case. The total ligand binding curve of a molecule that can bind N ligands of the same type is given by:

$$R + 4L \stackrel{\overline{K}_1}{\rightleftharpoons} RL + 3L \stackrel{\overline{K}_2}{\rightleftharpoons} RL_2 + 2L \stackrel{\overline{K}_3}{\rightleftharpoons} RL_3 + L \stackrel{\overline{K}_4}{\rightleftharpoons} RL_4$$
(26)

The species RL_i is the macrostate of the receptor with *i* ligands bound. The total binding curve $\langle X \rangle$ is in general described by eq 27.

$$\langle X \rangle = \frac{\mathfrak{a}_1[L] + 2 \,\mathfrak{a}_2[L]^2 + 3 \,\mathfrak{a}_3[L]^3 + 4 \,\mathfrak{a}_4[L]^4}{1 + \mathfrak{a}_1[L] + \mathfrak{a}_2[L]^2 + \mathfrak{a}_3[L]^3 + \mathfrak{a}_4[L]^4}$$
(27)

In terms of macroscopic binding constants, we have

$$\mathfrak{a}_{1} = K_{1}$$

$$\mathfrak{a}_{2} = \overline{K}_{1}\overline{K}_{2}$$

$$\mathfrak{a}_{3} = \overline{K}_{1}\overline{K}_{2}\overline{K}_{3}$$

$$\mathfrak{a}_{4} = \overline{K}_{1}\overline{K}_{2}\overline{K}_{3}\overline{K}_{4}$$
(28)

In terms of microscopic binding constants, we have

$$\begin{aligned} \mathfrak{a}_{1} &= k_{1000}^{0000} + k_{0100}^{0000} + k_{0001}^{0000} + k_{0001}^{0000} \\ \mathfrak{a}_{2} &= k_{1000}^{0000} k_{1100}^{1000} + k_{1000}^{0000} k_{1001}^{1000} + k_{0100}^{0000} k_{0110}^{0100} + k_{0100}^{0000} k_{0101}^{0100} + k_{0001}^{0000} k_{0011}^{0001} \\ \mathfrak{a}_{3} &= k_{0001}^{0000} k_{0011}^{0001} k_{0111}^{0011} + k_{0001}^{0000} k_{0001}^{0011} k_{1011}^{0011} + k_{00001}^{0000} k_{0001}^{0101} k_{1100}^{1011} + k_{1000}^{0000} k_{1100}^{1000} k_{1110}^{1000} \\ \mathfrak{a}_{4} &= k_{1000}^{0000} k_{1100}^{1000} k_{1110}^{1100} k_{1111}^{110} \end{aligned}$$

$$(29)$$

Different combinations of microscopic constants can yield the same coefficients a_i .

Adair¹⁻³ developed a model in which it is assumed that all of the ligands bind with the same affinity to the same macrostate, i.e., $k_1 = k_{1000}^{0000} = k_{0100}^{0000} \dots$, $k_2 = k_{1100}^{1000} = k_{1010}^{1000} = \dots$, etc. This assumption implies that all binding sites are equivalent. The coefficients in eq 27 are then given by

$$a_{1} = 4k_{1}$$

$$a_{2} = 6k_{1}k_{2}$$

$$a_{3} = 4k_{1}k_{2}k_{3}$$

$$a_{4} = k_{1}k_{2}k_{3}k_{4}$$
(30)

Comparing eq 28 with eq 30, one finds

$$k_{1} = \frac{1}{4}\overline{K}_{1}$$

$$k_{2} = \frac{2}{3}\overline{K}_{2}$$

$$k_{3} = \frac{3}{2}\overline{K}_{3}$$

$$k_{4} = 4\overline{K}_{4}$$

$$(31)$$

The Adair model is equivalent to eq 27 considering eq 31. Thus, the Adair model with N binding sites can always fit a binding curve of Nth degree. However, from a good fit to the Adair equation one can *not conclude* that binding constants for binding of the *i*th ligand are all equal.

References

[1] Adair, G. S. (1925) J. Biol. Chem. 63, 529-538.

- [2] Chein, J. C. W & Mayo, K. H. (1980) J. Biol. Chem. 225, 9790–9799.
- [3] Voet, D & Voet, J. G. (1995) Biochemistry. (New York), 2 edition.