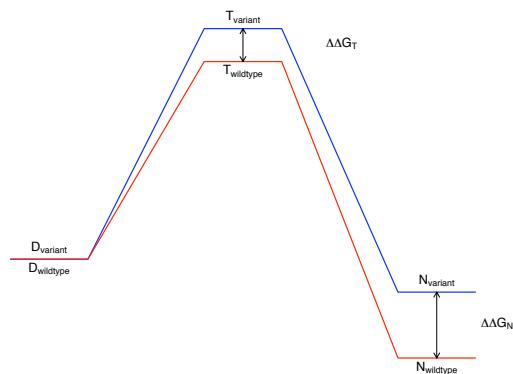


Energy Profile

On the Precision of Experimentally Determined Protein Folding Rates and Φ Values

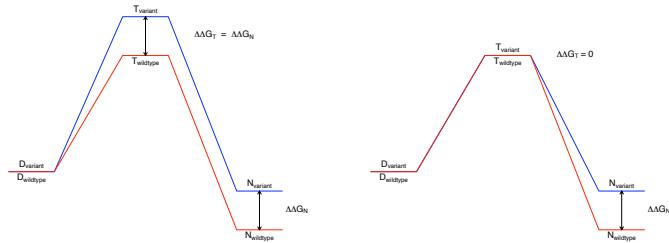
Ingo Ruczinski

Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health



→ The Φ -value is defined as the ratio $\Delta\Delta G_T / \Delta\Delta G_N$.

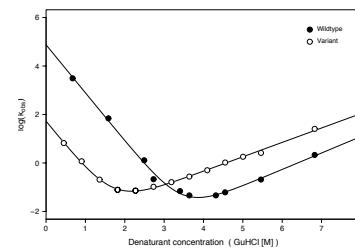
Energy Profile



- If the part of the protein that contains the variant amino acid is fully structured in the transition state, we have $\Delta\Delta G_T \approx \Delta\Delta G_N$, and hence $\Phi \approx 1$.
- If the part of the protein that contains the variant amino acid is equal in denatured and the transition state, we have $\Delta\Delta G_T \approx 0$, and hence $\Phi \approx 0$.

At least this is the idea ...

Phi-Value Estimation



$$\log(k_{\text{obs}}) = \log \left(\exp \left[\log(k_t) + m_t \times \frac{C_{\text{GuHCl}}}{RT} \right] + \exp \left[\log(k_u) + m_u \times \frac{C_{\text{GuHCl}}}{RT} \right] \right)$$

$$\Delta\Delta G_T = RT \times \left[\log(k_t^{\text{wildtype}}) - \log(k_t^{\text{variant}}) \right]$$

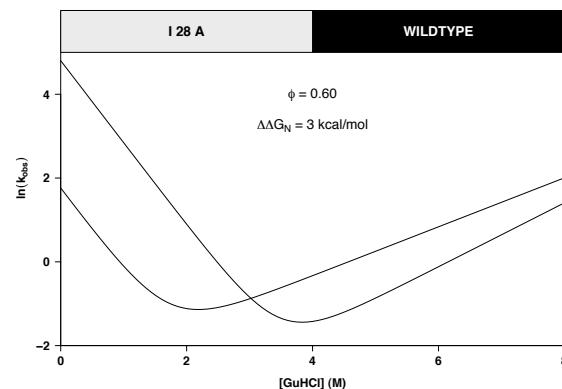
$$\Delta\Delta G_N = RT \times \left[\log(k_u^{\text{wildtype}}) - \log(k_u^{\text{variant}}) - \log(k_t^{\text{variant}}) + \log(k_u^{\text{variant}}) \right]$$

Questions

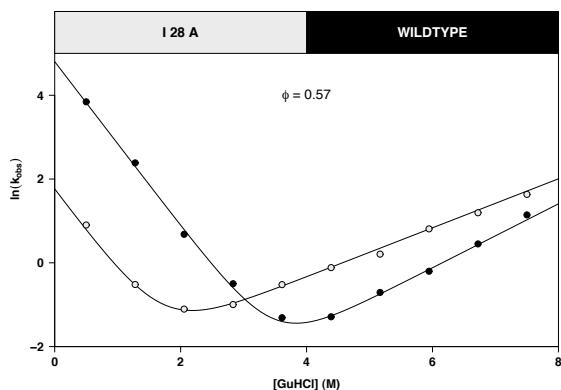
- What is the threshold for the difference in stability ($\Delta\Delta G_N$) between two variants to assure reliable estimates of Φ ?

It depends.

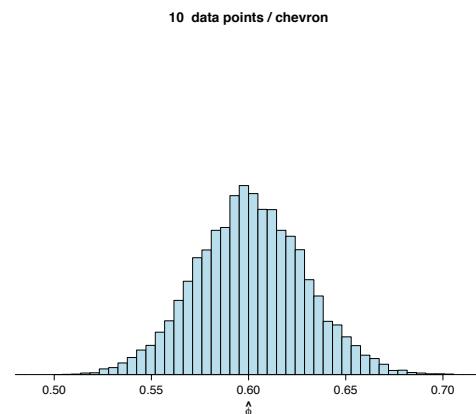
Precision



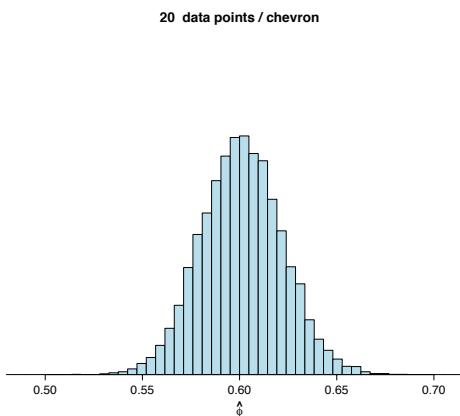
Precision



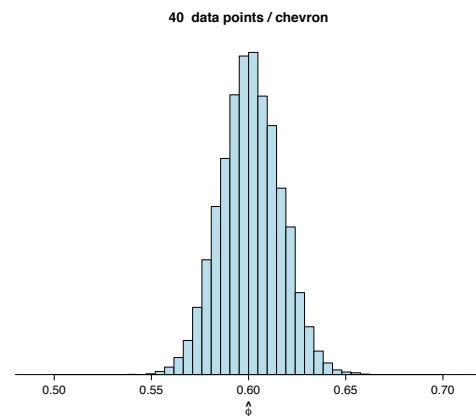
Precision



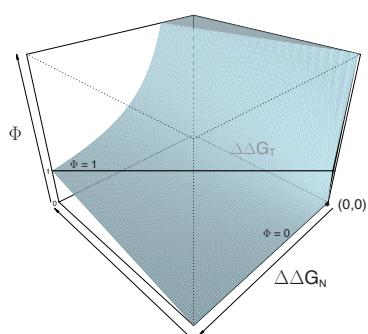
Precision



Precision



Precision

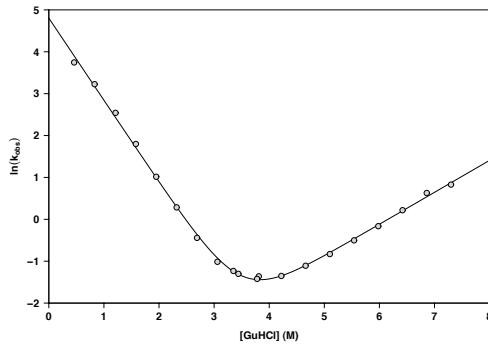


Questions

- What is the threshold for the difference in stability ($\Delta\Delta G_N$) between two variants to assure reliable estimates of Φ ?

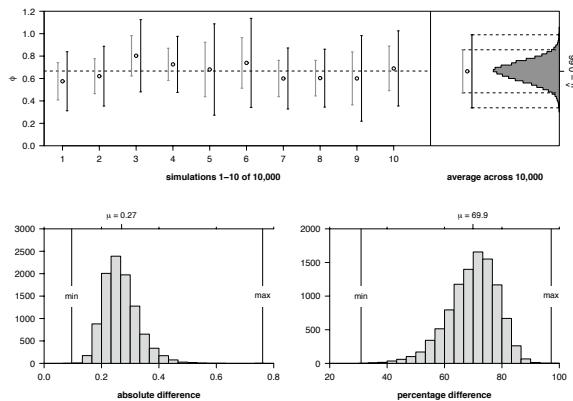
- How can we construct valid standard errors for the estimates of Φ ?

Standard Error



$$\ln(k_{\text{obs}}) = \log \left(\exp \left[\log(k_f) + m_f \times \frac{[\text{GuHCl}]}{RT} \right] + \exp \left[\log(k_u) + m_u \times \frac{[\text{GuHCl}]}{RT} \right] \right)$$

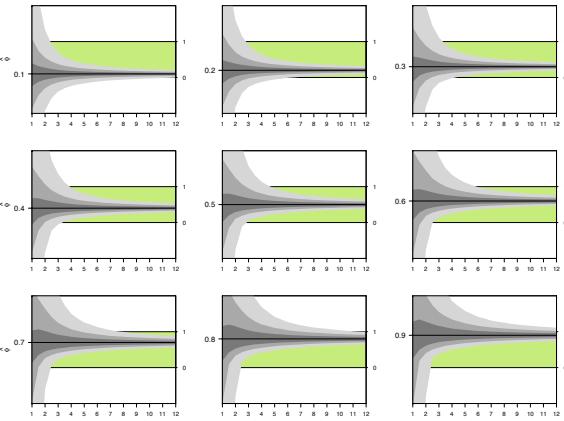
Standard Error



Standard Error

$$se(\hat{\Phi}) = |\Phi| \times \sqrt{\left(\frac{\sigma_T}{\Delta\Delta G_T} \right)^2 - 2\rho_{\Delta\Delta G} \left(\frac{\sigma_T}{\Delta\Delta G_T} \right) \left(\frac{\sigma_N}{\Delta\Delta G_N} \right) + \left(\frac{\sigma_N}{\Delta\Delta G_N} \right)^2}$$

Standard Error



Web Server

Ruczinski, Sosnick, and Plaxco
Methods for the accurate estimation of confidence intervals on experimental Φ -values.

Please read: important file format information for uploading your data. For options and output information, please read the help file.

- Upload your data: example.csv
- Specify the temperature: T = 25°C
- Specify the energy units: kcal
- Specify the comparisons: wildtype only all comparisons
- Specify the type of fit: individual fits parallel arms
- Specify the denaturant concentrations: folding rate: M - unfolding rate: M
- Specify the coverage for the Φ -value confidence intervals: 95% coverage
- Specify the number of significant digits in the output: 2 significant digits
- And they are off:

[Help](#)

Ruczinski, Sosnick, and Plaxco
Estimates for the kinetic parameters. The energies are given in kJ.

	$\log(k_f)$	$\log(k_u)$	m_f	$\log(k_f)$	$\log(k_u)$	m_u	se_{m_f}	$\Delta\Delta G_f$	$se_{\Delta\Delta G_f}$	m_u	se_{m_u}	
WT	4.80	0.06	-4.86	0.08	-0.13	1.89	0.06	23.56	0.20	-6.75	0.07	
D2A	1.75	0.06	-4.97	0.16	-2.67	0.08	1.49	0.04	10.97	0.12	-6.42	0.15
D8L	4.25	0.05	-5.05	0.08	-4.27	0.10	1.68	0.04	21.13	0.15	-6.74	0.07
I2W	4.10	0.06	-4.89	0.09	-4.34	0.13	1.71	0.06	20.94	0.19	-6.61	0.08
V5SA	4.41	0.04	-4.26	0.10	-0.81	0.08	1.75	0.04	12.94	0.12	-6.01	0.09
V5SM	4.95	0.08	-4.80	0.12	-3.22	0.15	1.77	0.06	19.99	0.22	-6.57	0.10
V5ST	4.18	0.06	-4.33	0.16	-0.78	0.10	1.80	0.05	12.30	0.16	-6.13	0.13
V5SG	4.39	0.12	-4.45	0.72	2.36	0.18	1.41	0.14	5.47	0.27	-6.86	0.62

A spread sheet with the above data for download is [here](#). The file is in csv format, which can directly be read, for example, into R and Excel.

Table 1: Estimates for the Φ values and the changes in free energy. The energies are given in kJ.

	Φ	se_{Φ}	lower	upper	$\Delta\Delta G_f$	$se_{\Delta\Delta G_f}$	$\Delta\Delta G_u$	$se_{\Delta\Delta G_u}$	P_{folding}	P_{unfold}
WT-D2A	0.60	0.02	0.56	0.64	7.56	0.20	12.59	0.37	0.20	
WT-D8L	0.56	0.11	0.33	0.80	1.36	0.20	2.43	0.40	0.40	0.13
WT-I2W	0.66	0.13	0.40	0.92	1.74	0.21	2.62	0.43	0.13	
WT-V5SA	0.09	0.02	0.06	0.12	0.96	0.18	10.62	0.37	0.12	
WT-V5SM	-0.03	0.07	-0.16	0.11	-0.10	0.24	3.57	0.47	0.14	
WT-V5ST	0.14	0.02	0.10	0.17	1.55	0.20	11.26	0.40	0.15	
WT-V5SG	0.06	0.02	0.09	0.12	0.33	0.02	18.09	0.57	0.20	

A spread sheet with the above data for download is [here](#). The file is also in csv format.

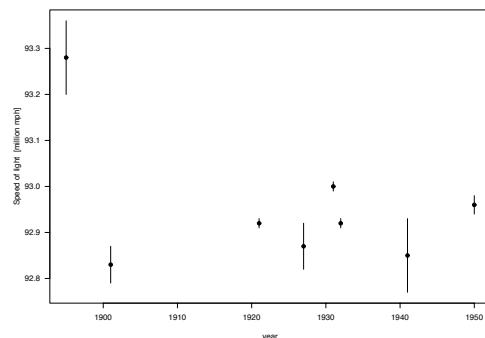
Web Server

Questions

- What is the threshold for the difference in stability ($\Delta\Delta G_N$) between two variants to assure reliable estimates of Φ ?
- How can we construct valid standard errors for the estimates of Φ ?
- How reproducible are Φ -value measurements?

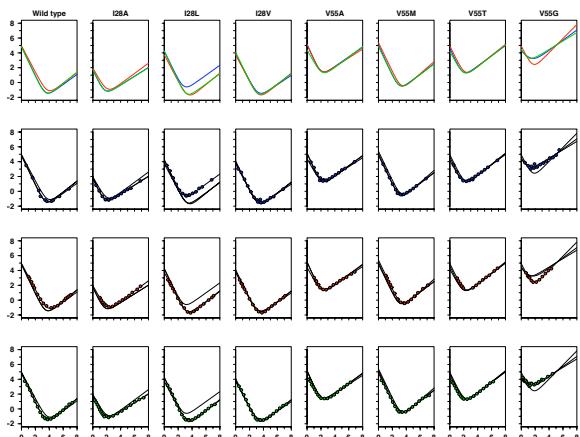
Dang...

Estimates of the speed of light, with “confidence intervals” (1895 - 1950).

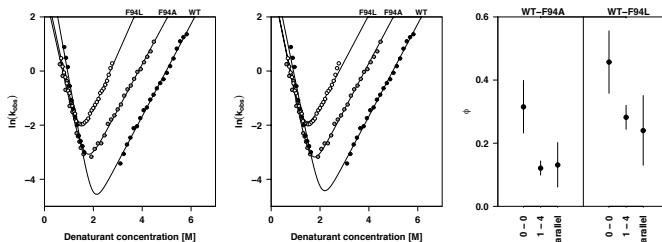


Youden (Technometrics, 1972).

Reproducibility?



Alternative Techniques



Questions

- What is the threshold for the difference in stability ($\Delta\Delta G_N$) between two variants to assure reliable estimates of Φ ?
- How can we construct valid standard errors for the estimates of Φ ?
- How reproducible are Φ -value measurements?
- What are the effects of other commonly employed techniques to calculate Φ from kinetic data?

References

- De Los Rios MA, Muralidhara BK, Wildes D, Sosnick TR, Marqusee S, Wittung-Stafshede P, Plaxco KW, Ruczinski I (2006). On the Precision of Experimentally Determined Protein Folding Rates and Phi-Values. *Protein Science*, 15(3): 553-63.
- Maxwell KL, Wildes D, Zarrine-Afsar A, De Los Rios MA, Brown AG, Friel CT, Hedberg L, Horng JC, Bona D, Miller EJ, Vallee-Belisle A, Main ER, Bemporad F, Qiu L, Teilum K, Vu ND, Edwards AM, Ruczinski I, Poulsen FM, Kragelund BB, Michnick SW, Chiti F, Bai Y, Hagen SJ, Serrano L, Oliveberg M, Raleigh DP, Wittung-Stafshede P, Radford SE, Jackson SE, Sosnick TR, Marqusee S, Davidson AR, Plaxco KW (2005). Protein Folding: Defining a Standard Set of Experimental Conditions and a Preliminary Kinetic Data Set of Two-State Proteins. *Protein Science*, 14(3): 602-16.
- Ruczinski I, Sosnick TR, Plaxco KW (2006). Methods for the Accurate Estimation of Confidence Intervals on Protein Folding Φ Values. *Protein Science* (to appear).

Acknowledgments

- UC Santa Barbara Department of Chemistry Biochemistry

Miguel de los Rios, Kevin Plaxco.

- University of Chicago Department of Chemistry

Tobin Sosnick.

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David Wildes, Susan Marqusee.

<http://biostat.jhsph.edu/~iruczins>