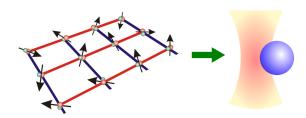
Shortcuts to adiabaticity



adiabatic quantum computing: maintaining ground state while driving a quantum system

Demirplak, Rice, JPCA (2003) Berry, J. Phys. A (2009)

Shortcuts to adiabaticity

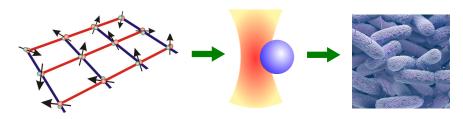


adiabatic quantum computing: maintaining ground state while driving a quantum system

Demirplak, Rice, JPCA (2003) Berry, J. Phys. A (2009) Brownian motion of bead in optical trap: maintaining instantaneous equilibrium as trap changes

Martinez et al Nature Physics (2016) Patra, Jarzynski, New. J. Phys. (2017)

Shortcuts to adiabaticity

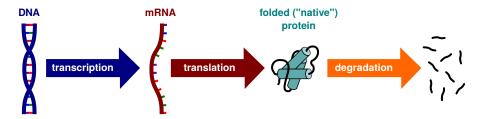


adiabatic quantum computing: maintaining ground state while driving a quantum system

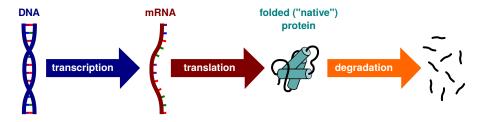
Demirplak, Rice, JPCA (2003) Berry, J. Phys. A (2009) Brownian motion of bead in optical trap: maintaining instantaneous equilibrium as trap changes

Martinez *et al* Nature Physics (2016) Patra, Jarzynski, New. J. Phys. (2017) Possible biological applications: population genetics molecular chaperones force spectroscopy

Traditional view of protein production



Traditional view of protein production

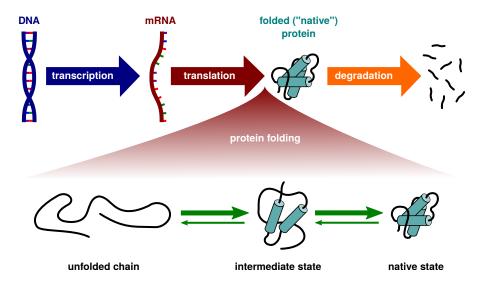


All these processes involve nonequilibrium reaction networks driven by ATP hydrolysis.

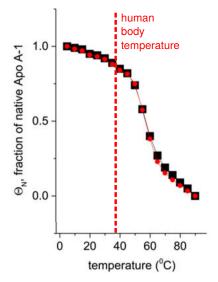
The resulting costs of expressing even a single extra protein can be evolutionarily significant for single-celled organisms.

Ilker & Hinczewski, Phys. Rev. Lett. (2019) Lynch & Marinov, Proc. Natl. Acad. Sci. (2015)

Traditional view of protein production

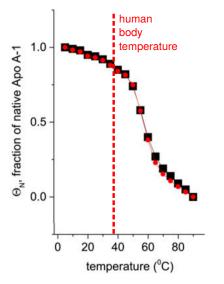


Proteins function at the cliff edge of unfolding



Seelig & Schönfeld, Q. Rev. Biophys. (2016)

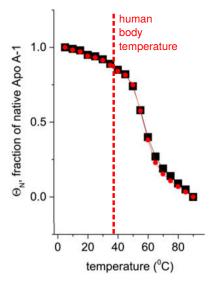
Proteins function at the cliff edge of unfolding



Being on the verge of melting gives proteins the dynamical flexibility essential for their diverse roles as enzymes.

Seelig & Schönfeld, Q. Rev. Biophys. (2016)

Proteins function at the cliff edge of unfolding

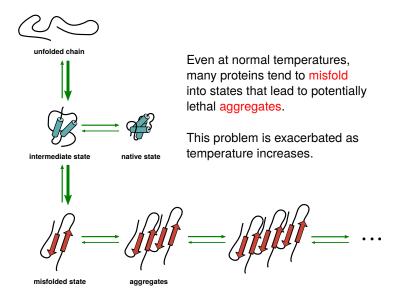


Being on the verge of melting gives proteins the dynamical flexibility essential for their diverse roles as enzymes.

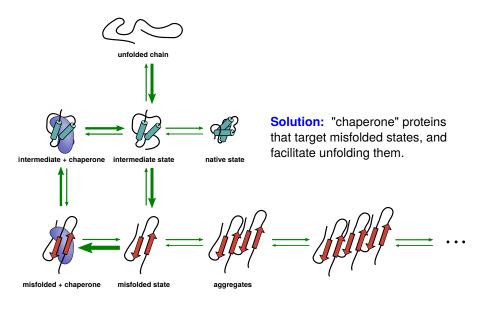
But it also makes them highly vulnerable to changes in temperature (even of a few degrees): heat shock.

Seelig & Schönfeld, Q. Rev. Biophys. (2016)

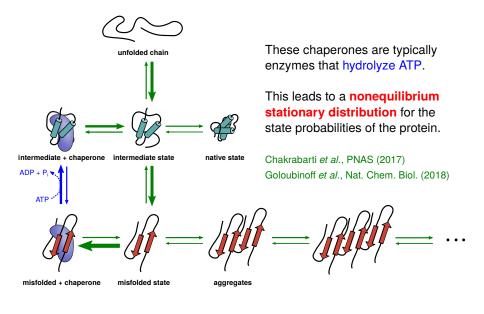
Constant threats: misfolding and aggregation

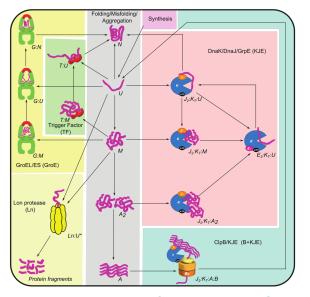


Constant threats: misfolding and aggregation



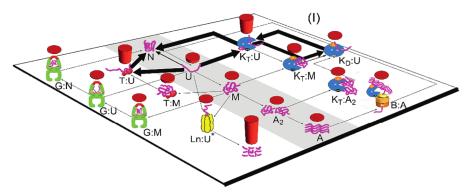
Constant threats: misfolding and aggregation





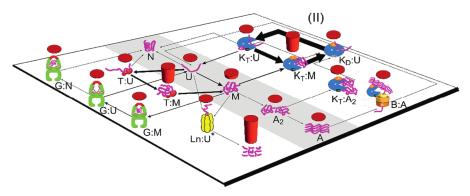
E. coli chaperone network: Santra et al., PNAS (2017)

Different classes of proteins interact primarily with different chaperone sub-systems:



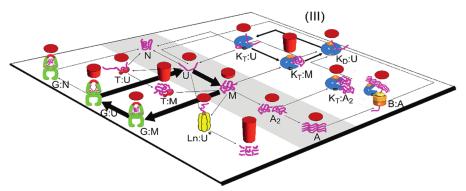
Santra et al., PNAS (2017)

Different classes of proteins interact primarily with different chaperone sub-systems:



Santra et al., PNAS (2017)

Different classes of proteins interact primarily with different chaperone sub-systems:



Santra et al., PNAS (2017)

Under optimal growth conditions, chaperones are nearly fully occupied by "patient" proteins: spare capacity is too energetically costly.

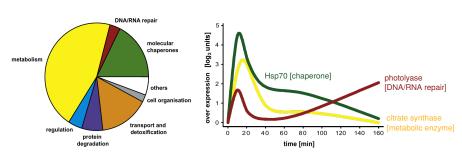
Heat shock

What happens when the cell enters a higher temperature environment?

Heat shock

What happens when the cell enters a higher temperature environment?

Functional classes of upregulated genes in yeast after a heat shock from 25°C to 35°C over 10 min (out of total of 91 genes upregulated by more than 2.8x):

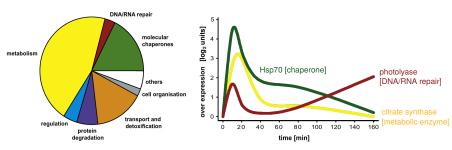


[Richter et al., Molec. Cell (2010)]

Heat shock

What happens when the cell enters a higher temperature environment?

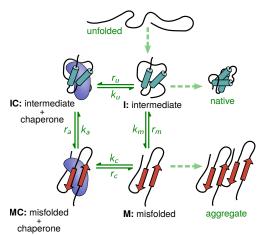
Functional classes of upregulated genes in yeast after a heat shock from 25°C to 35°C over 10 min (out of total of 91 genes upregulated by more than 2.8x):



[Richter et al., Molec. Cell (2010)]

Can we understand this upregulation of chaperones using ideas from thermodynamic control?

Markov model for chaperone-protein interaction



Using separation of timescales we can construct a simplified Markov model for a protein that tends to misfold under heat shock, focusing on four key states.