statistical physics $\rightarrow$ canonical ensemble

## Hemoglobin

Often times proteins work in a cooperative fashion. For example, a protein may only function properly (fold into the proper shape) if a pair of molecules are simultaneously attached to the protein. We model this in statistical physics by assuming that the energy is not simply a linear sum of terms. One of the classical examples of a protein which behaves cooperatively is hemoglobin, the protein responsible for carrying $\mathrm{O}_{2}$ in the bloodstream. A hemoglobin molecule can bind up to $4 \mathrm{O}_{2} \mathrm{~s}$ at once, and ideally a hemoglobin molecule has either 4 or 0 oxygens (either it transports oxygen towards the cells, or is heading back to the lungs to be replenished).

We will work with a slightly simpler model for hemoglobin, which consists of a protein with 4 possible configurations, which we can label by $\left(\sigma_{1}, \sigma_{2}\right)$, with $\sigma_{i}=0(i=1,2)$ representing the state where site $i$ on the protein is unoccupied (0) or occupied (1) by oxygen. Suppose that the energy for this configuration is

$$
E=(\epsilon-\mu)\left(\sigma_{1}+\sigma_{2}\right)+J \sigma_{1} \sigma_{2}
$$

$\epsilon$ corresponds to the energy per site of attaching an oxygen, and $J$ is the "interaction energy", and the chemical potential

$$
\mu=\frac{1}{\beta} \log \frac{c}{c_{0}}
$$

where $c$ is the $\mathrm{O}_{2}$ concentration, and $c_{0}$ is a reference value.
(a) Find the partition function $Z$.
(b) If the system is at temperature $T$ (with $\beta=1 / k_{\mathrm{B}} T$ ), determine $\langle n\rangle$, if $n=\sigma_{1}+\sigma_{2}$.
(c) Find the expected value of $f_{2}=\sigma_{1} \sigma_{2}$, the fraction of proteins with both sites occupied.
(d) Determine the limiting behavior of $\langle n\rangle$ and $\left\langle f_{2}\right\rangle$, both when $c$ is very small, and when $c$ is very large.
(e) Plot $\langle n\rangle$ and $\left\langle f_{2}\right\rangle$ on the same plot, as a function of $c$ for 4 different sets of values of $\epsilon$ and $J$ : one for each possible combination of $\epsilon$ positive/negative, and $J$ positive/negative. Comment on the results.
(f) As suggested above, a biological system would likely prefer to either have this protein either bound to 0 or 2 oxygens. How should we pick $\epsilon$ and $J$ so that this is most likely?

