### Statistical Physics of The Symmetric Group

Mobolaji Williams — Harvard Physics Oral Qualifying Exam— Dec. 12, 2016

### Theoretical Physics of Living Systems



*Biophysics: A Search for Principles* William Bialek

#### **Physics**







Particle Physics

Condensed Matter

Astrophysics

"All of (theoretical) physics shares a method of approach"

#### **Biology**







Microbiology

Plant Biology

Marine Biology

"All of biology shares an object of study"

What then is biological physics?

or, more specifically,

What constitutes the theoretical physics of living systems?

## Theoretical Physics of Living Systems



## Protein Folding and Design



3D-Structure

Boltzmann Weight

## Protein Folding and Design

Concrete Example:

Begin with a simple 3D structure with *N* amino acids



#### **State Space**

For simplicity, split amino acids into only polar and nonpolar residues

 $\sigma_i = \begin{cases} 1 & \text{nonpolar residue} \\ 0 & \text{polar residue} \end{cases}$ 

[Solution to design problem consists of the sequence  $\{\sigma_1, \ldots, \sigma_N\}$ ]

#### Hamiltonian

non-polar residues interact through a hydrophobic interaction for a given distance; all other contacts non-interacting

$$\mathcal{H}(\{\sigma_k\}) = rac{1}{2} \sum_{i,j} U_0 \sigma_i \sigma_j \Delta(|\vec{r}_i - \vec{r}_j|)$$
 $\Delta(r) = egin{cases} 1 & r_{ ext{low}} < r < r_{ ext{high}} \ 0 & ext{otherwise} \end{cases}$ 

 $(U_0 < 0)$ 

The stochastic solution is easy to predict

Lowest energy sequence is  $\{\sigma_i\} = \{1, \dots, 1\}$ ]

All residues are nonpolar

The polypeptide is a homopolymer?

# Protein Folding and Design

Problem with formalism:

"For virtually any target structure, the lowest energy sequence will be a homopolymer, consisting of the amino acid with the largest self-attraction"\*



**3D- Structure** 

 $I = \cdots = I = \cdots I$ 

Homopolymer?

This cannot be correct...

Suggested way forward:



New Design Question: Given a fixed number of each type of amino-acid What sequence yields the lowest energy?

Implication of New Design Question

For a chain of length N, what is the size of our state space?



### Model Building on the Polypeptide Chain

For a statistical mechanics model of protein design, we can construct a spin-like model

But it is apparent that if we assume a fixed number of amino acids of each type, our space of states consists of various **permutations** of the amino acid list

e.g., 
$$\mathcal{H}(\{\sigma_k\}) = \frac{1}{2} \sum_{i,j} U_0 \sigma_i \sigma_j \Delta(|\vec{r}_i - \vec{r}_j|)$$

i.e., 
$$|\mathcal{S}_N| \neq 20^N$$
 but  $, |\mathcal{S}_N| = \frac{N!}{n_0!n_1! \dots n_{20}!}$ 

Where are statistical mechanics models where the space of states consists of permutations?



No such models seem to exist...

...So we must build one for ourselves!

Goal: Develop a statistical physics model of permutations

#### **Simplifications**

- 1. Consider equilibrium statistical mechanics
- 2. Assume we only have one type of each unit

Our System: a chain (considered only in a single dimension) with N subunits (e.g., amino acids) which can be placed in various orderings.

e.g., 
$$\binom{N}{j} = \frac{\Gamma(N+1)}{\Gamma(j+1)\Gamma(N-j+1)}$$
$$\prod_{k=1}^{N} (1+zx_i) = \sum_{\ell=0}^{N} z^{\ell} \prod_{\ell} (x_1, x_2, \dots, x_N) \qquad d_N \equiv N! \sum_{k=0}^{N} \frac{(-1)^k}{k!}$$

 $\lim_{t\to\infty} P(\mathcal{S},t) = P^{\rm eq}(\mathcal{S})$ 

i.e.,  $n_k = 1$  so  $|\mathcal{S}_N| = N!$ 

Our Space of States: By definition, our space of states is isomorphic to the Symmetric Group.

(Dixon and Mortimer, Permutation Group, 1987)

"Let  $\Omega$  be an arbitrary nonempty set... The set of all permutations of  $\Omega$  forms a group, under composition of mappings, called the **symmetric group on**  $\Omega$ ."

Let's define the system more precisely and introduce a Hamiltonian.

#### System Definition:

- subunits are labeled as  $\omega_i$  with  $i = 1, \ldots, N$
- the ordering of subunits with the zero energy is  $\vec{\omega} \equiv (\omega_1, \omega_2, \dots, \omega_N)$
- an arbitrary state is  $\vec{\theta}$  where  $\vec{\theta} \in \{\operatorname{perm}(\omega_1, \omega_2, \dots, \omega_N)\} \equiv Sym(\omega)$

#### **Energy Definition:**

- The state  $\vec{\theta} = \vec{\omega}$  has zero energy and has subunits in the *correct* order. For all other states, there is an energy cost of  $\lambda_i$  for  $\theta_i \neq \omega_i$ .

$$\mathcal{H}_N(\{ heta_i\}) = \sum_{i=1}^N \lambda_i I_{ heta_i 
eq \omega_i}$$
 $I_A = egin{cases} 1 & A ext{ is true} \ 0 & A ext{ is false} \end{cases}$ 

#### **Example:** Three components

State	Energy	
$(\omega_1,\omega_2,\omega_3)$	0	-
$(\omega_2,\omega_1,\omega_3)$	$\lambda_1+\lambda_2$	
$(\omega_3,\omega_2,\omega_1)$	$\lambda_1+\lambda_3$	
$(\omega_1,\omega_3,\omega_2)$	$\lambda_2+\lambda_3$	
$(\omega_2,\omega_3,\omega_1)$	$\lambda_1 + \lambda_2 + \lambda_3$	
$(\omega_3,\omega_1,\omega_2)$	$\lambda_1 + \lambda_2 + \lambda_3$	

Note: There is a a 2-fold degeneracy for the most disordered state.

In general, for *N* subunits, the degeneracy of the most disordered state is. . .

$$d_N \equiv N! \sum_{k=0}^N \frac{(-1)^k}{k!}$$

"number of derangements": # of ways to completely reorder list

#### System Definition:

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 $I_A = \begin{cases} 1 & A \text{ is true} \\ 0 & A \text{ is false} \end{cases}$ 

Now let's compute the partition function

 $d_N \equiv N! \sum_{k=1}^{N} \frac{(-1)^k}{k!}$ 

= [Application of derangement formula, symmetric polynomials, etc.]

$$Z_N(\{\beta\lambda_i\}) = \int_0^\infty ds \, e^{-s} \prod_{\ell=1}^N \left[1 + (s-1)e^{-\beta\lambda_\ell}\right]$$

... so we can obtain a closed form expression ...

. . .but what does it mean?

#### **Energy Definition:**

- The state  $\vec{\theta} = \vec{\omega}$  has zero energy and has subunits in the *correct* order. For all other states, there is an energy cost of  $\lambda_i$  for  $\theta_i \neq \omega_i$ .

$$\mathcal{H}_N(\{ heta_i\}) = \sum_{i=1}^N \lambda_i I_{ heta_i 
eq \omega_i}$$

. .

**Partition Function:** 

$$- Z_N(\{eta\lambda_i\}) = \int_0^\infty ds \, e^{-s} \prod_{\ell=1}^N \left[1+(s-1)e^{-eta\lambda_\ell}
ight]$$

What physics is contained in this partition function?

"The same energy penalty for each subunit"

The partition function then simplifies to

Progress comes from a simplification:

$$Z_N(eta\lambda_0) = \int_0^\infty ds\, e^{-s} \Big(1+(s-1)e^{-eta\lambda_0}\Big)^N$$

And by steepest descent we find the free energy

$$eta F = -\ln Z_N(eta \lambda_0) \ \simeq Neta \lambda_0 - \left(e^{eta \lambda_0} - N - 1
ight) + F_0(N).$$

 $\lambda_i = \lambda_0$  for all i

And the average number of incorrect components is

$$\langle j \rangle \equiv \left\langle \sum_{i=1}^{N} I_{\theta_i \neq \omega_i} \right\rangle = \frac{\partial(\beta F)}{\partial(\beta \lambda_0)} \qquad \longrightarrow \qquad \langle j \rangle \simeq N - e^{\beta \lambda_0}$$

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We are trying to understand the physics of

$$Z_N(eta\lambda_0) = \int_0^\infty ds\, e^{-s} \Big(1+(s-1)e^{-eta\lambda_0}\Big)^N$$

 $\langle j 
angle \equiv \left\langle \sum_{i=1}^{N} I_{ heta_i 
eq \omega_i} 
ight
angle \simeq N - e^{eta \lambda_0}$ 

By considering the average number of incorrect components...

The function on the right has no constraints, but <u>the average number of incorrect components</u> <u>must be greater than 0</u>.

(Result is only valid so long as  $\langle j \rangle \ge 0.$ )



Above a certain transition temperature, there is a spectrum of states (different from "correct state") which defines the free energy minimum

This system appears to exhibit phase transitions. . .

"Average number of incorrect components"  $\langle j \rangle / N = \begin{cases} 0 & \text{for } T < T_c \\ 1 - e^{\beta \lambda_0} / N & \text{for } T > T_c \end{cases}$ 



... But we do NOT actually have a phase transition here

The **functional form** of the free energy **remains the same** above and below transition temperature...

$$F(j) = \lambda_0 j - rac{1}{eta} \ln \left[ inom{N}{j} d_j 
ight]$$



It is only the excluded region of the free energy that changes.

Qualitative argument for why there is no phase transition:

#### Modified Landau-Van Hove:

as *N* becomes large, entropy (i.e., disorder) always beats energy (i.e., order)

For the model of permutations with Hamiltonian

$$\langle j \rangle / N = \begin{cases} 0 & \text{for } T < T_c \\ 1 - e^{\beta \lambda_0} / N & \text{for } T > T_c \end{cases}$$

Interesting result, but this model is relatively simple.

#### Full Generalization:

Introduce <u>site-dependent interaction</u> terms and <u>higher-order</u> contributions to Hamiltonian:

(energy cost of incorrectness depends on **one other or two other** components.)

$$\mathcal{H}_N(\{\theta_i\}) = \lambda_0 \sum_{i=1}^N I_{\theta_i \neq \omega_i}$$

We found that above a certain amount of thermal fluctuations, the "correct ordering" (j=0) is no longer thermodynamically favored.

How would we extend it to the case where sites directly interact with one another?

$$\mathcal{H}_{N}(\{\theta_{i}\}) = \sum_{i} \lambda_{i} I_{\theta_{i} \neq \omega_{i}}$$
$$+ \frac{1}{2} \sum_{i,j} \mu_{ij} I_{\theta_{i} \neq \omega_{i}} I_{\theta_{j} \neq \omega_{j}}$$
$$+ \frac{1}{3!} \sum_{i,j,k} \tau_{ijk} I_{\theta_{i} \neq \omega_{i}} I_{\theta_{j} \neq \omega_{j}} I_{\theta_{k} \neq \omega_{k}}$$



Let's begin more simply, with <u>two terms</u> and <u>no site-dependent interactions</u>:

$$\mathcal{H}_N(\{\theta\}) = \lambda_1 \sum_{i=1}^N I_{\theta_i \neq \omega_i} + \frac{\lambda_2}{2N} \sum_{i,j=1}^N I_{\theta_i \neq \omega_i} I_{\theta_j \neq \omega_j}$$

What is the phenomenology of such a system?

Goal: Understand the basic physics of the "all-site-interacting" model:	$\mathcal{H}_N(\{ heta_i\}) = \lambda_1 \sum_{i=1}^N I_{ heta_i  eq \omega_i} + rac{\lambda_2}{2N} \sum_{i=1}^N I_{ heta_i  eq \omega_i} I_{ heta_j  eq \omega_j}$
of the all-site-interacting model.	i=1 $i,j=1$

We took three approaches to this end...

➤ "Landau" Free Energy

$$F_N(j,\beta) = \lambda_1 j + \frac{\lambda_2}{2N} j^2 + \frac{1}{\beta} \ln \Gamma(N-j+1) + f_0$$

► Gibbs-Feynman Inequality

$$F[\mathcal{H}] \leq F[\mathcal{H}_0] + \langle \mathcal{H} - \mathcal{H}_0 \rangle_0.$$

Method of Steepest Descent

$$Z_N(eta;\lambda_1,\lambda_2) = \sqrt{rac{N}{2\pieta|\lambda_2|}} \int_0^\infty ds \, \int_{-\infty}^\infty dx \, \left(1+(s-1)e^{-eta\lambda_1-x}
ight)^N e^{-s-Nx^2/2eta|\lambda_2|}.$$

...and all three yield the same order-parameter.

$$\frac{\overline{j}_0}{N} = 1 - \frac{1}{\beta \lambda_2} W_0 \left( \frac{\beta \lambda_2}{N} e^{\beta \lambda_1 + \beta \lambda_2} \right) + \mathcal{O} \left( \frac{1}{N} \right)$$

where  $W_0(xe^x) = x$  (for  $W_0 > -1$ )



The utility of the Landau Free Energy is that we get a qualitative picture the equilibria of the system.



Parameter Space Regions

- Ordered Region: j = 0 stable
- Order and Partial-Order Metastable Region: j = 0 and  $j = \overline{j}_0$ stable
- Order and Disorder Metastable Region: j = 0 and j = N stable
- Partially-Ordered Region:  $j = \overline{j}_0$  stable

For various parameter choices, we find

- **Disordered Region:** j = N stable

### Interacting Model

Each type of free energy function is associated with a specific region in the parameter space of the Hamiltonian



 $F_N(j,\beta)$ 

Ordered

Order-Partial-Order

### 1D Chain of Partition Functions

Equilibrium properties can be framed as a chain of partition functions

For Example If we have a Hamiltonian written in terms of the number of correct components as . . .

$$\mathcal{H}_N(\{\theta_i\}): \mathcal{E}_N(j) = \lambda j$$

Then we know that the associated partition function is . . .

$$Z_N(eta\lambda) = \int_0^\infty ds \, e^{-s} \left(1+(s-1)e^{-eta\lambda}
ight)^N$$

This partition function satisfies the identity

$$rac{\partial}{\partial eta} Z_N(eta \lambda) = -\lambda N \Big( Z_N(eta \lambda) - Z_{N-1}(eta \lambda) \Big)$$





Taking the "partition function chain" to the continuum limit we find

$$\left(\frac{\partial}{\partial\beta} + \lambda \frac{\partial}{\partial \ln \eta}\right) \mathcal{Z}(\eta, \beta \lambda) = 0$$

(with boundary condition  $\mathcal{Z}(\eta, 0) = \Gamma(\eta + 1)$ ) 18

#### 1D Chain of Partition Functions

#### **Continuum limit of Partition Function Chain**

$$\left(\frac{\partial}{\partial\beta} + \lambda \frac{\partial}{\partial \ln \eta}\right) \mathcal{Z}(\eta, \beta \lambda) = 0 \qquad \text{(with boundary condition } \mathcal{Z}(\eta, 0) = \Gamma(\eta + 1)\text{)}$$

Solution to PDE: 
$$\mathcal{Z}(\eta, \beta \lambda) = \Gamma(\eta e^{-\beta \lambda} + 1) = \int_0^\infty dt \, \exp\left[\eta e^{-\beta \lambda} \ln t - t\right]$$

Order Parameter:

$$\overline{j} = -\frac{\partial}{\partial(\beta\lambda)} \ln \mathcal{Z}(\eta, \beta\lambda) = \eta e^{-\beta\lambda} \psi_0(\eta e^{-\beta\lambda} + 1) \qquad * \psi_0(x) \equiv \frac{\Gamma'(x)}{\Gamma(x)}$$

By the condition 
$$\overline{j} \ge 0$$
,  
we find a transition temperature  $k_B T_c = \frac{\lambda}{\ln(\eta/\epsilon)}$  (where  $\psi_0(1+\epsilon) = 0$ )

Which is reminiscent of the discrete result

$$Z_N(\beta\lambda) = \int_0^\infty ds \, e^{-s} \left(1 + (s-1)e^{-\beta\lambda}\right)^N \quad o \quad k_B T_c = \frac{\lambda}{\ln N}$$

### 1D Chain of Partition Functions

#### **Continuum limit of Partition Function Chain**

We find a similar correspondence between

$$\mathcal{E}_N(j) = \lambda_1 j + \lambda_2 j^2$$
 and

(original permutations model)

$$\left(\frac{\partial}{\partial\beta} + \lambda_1 \frac{\partial}{\partial \ln \eta} + \lambda_2 \frac{\partial^2}{\partial \ln \eta^2}\right) \mathcal{Z}(\eta, \beta \lambda_1, \beta \lambda_2) = 0$$

(continuum model)

We can generalize these results...

Physics of original partition function of permutations	$\sim$	Physics of continuum limit of partition function chain
		Solution to
$Z_N[eta \mathcal{E}_N] = \sum_{j=0}^N g_N(j) e^{-eta \mathcal{E}_N(j)}$	$\simeq$	$\left[\frac{\partial}{\partial\beta} + \mathcal{E}\left(\eta, \frac{\partial}{\partial \ln \eta}\right)\right] \mathcal{Z}(\eta; \beta \mathcal{E}) = 0$
* $\mathcal{E}_N(j) \equiv \sum_{k=0}^M \lambda_k(N) j^k$		

Our model of permutations is connected to a PDE,...

$$Z_{N}[\beta \mathcal{E}_{N}] = \sum_{j=0}^{N} g_{N}(j) e^{-\beta \mathcal{E}_{N}(j)} \quad \rightarrow \quad \left[\frac{\partial}{\partial \beta} + \mathcal{E}\left(\eta, \frac{\partial}{\partial \ln \eta}\right)\right] \mathcal{Z}(\eta; \beta \mathcal{E}) = 0$$

#### **Transition Temperature**

...and the PDE seems to yield consistent results...

Discrete Model Continuum Model  $\lambda / \ln N$  $\lambda / \ln(\eta/\epsilon)$ 

...but what other questions could we be asking?

**Analytical Studies** (Implications of the Path Integral)

Schrödinger-Like PDE, suggest existence of...

$$K(\ln\eta,\ln\eta_1;eta\mathcal{E}) = \int \mathcal{D}[\ln\eta] \, \exp\left[-\int_0^eta deta_1 \, A(\eta,\ln\eta';eta)
ight]$$

with A an action-like function.

**Possible Question:** Does this yield new way to study system perturbatively? 21

Numerical Studies

Return to discrete system

$$\frac{\partial^2 \mathcal{Z}(\beta)}{\partial \eta^2} \simeq \frac{\mathcal{Z}_{i+1}^\ell - 2\mathcal{Z}_i^\ell + \mathcal{Z}_{i-1}^\ell}{\Delta n}$$

**Possible Question:** Is analyzing system with finite difference methods more efficient than standard MC methods?

(Finite Difference Methods)

### Extension: Renormalization Group

#### Steps of a Renormalization Group Transformation: Ising Model



\* Procedure allows us establish relations between original and renormalized theory (e.g. for the coupling constant)

Problem:

How do we sum over the states of half the indices when the state space cannot be factorized?

$$K' = \frac{1}{2}\ln\cosh(2K)$$

$$S_{\text{ising}} = S_1 \otimes S_2 \otimes \cdots \otimes S_N$$

1. Label half of the sites/d.o.f.s

Sum over all states
 the labeled sites can occupy

Resulting system is the "renormalized/effective theory"!

We need a new way to perform the renormalization group transformation for this system of permutations.

$$\mathcal{S}_{ ext{perm}} 
eq \mathcal{S}_1 \otimes \mathcal{S}_2 \otimes \cdots \otimes \mathcal{S}_N$$

### Extension: Permutation Glass

Similar to the Sherrington-Kirkpatrick Model, we can imagine a system of **permutations** with **quenched disorder**.

There are two choices in this direction:

1. 
$$\mathcal{H}_N(\{\theta_i\}) = \sum_{i=1}^N \lambda_i I_{\theta_i \neq \omega_j}$$
 where  $\lambda_i \sim \mathcal{N}(\lambda_0, \tilde{\lambda}^2)$  More Analogous to SK Spin glass Model  
2.  $\mathcal{H}_N(\{\theta_i\}) = \frac{1}{2} \sum_{i,j=1}^N \mu_{ij} I_{\theta_i \neq \omega_i} I_{\theta_j \neq \omega_j}$  where  $\mu_{ij} \sim \mathcal{N}(\mu_0, \tilde{\mu}^2)$ 

Mathematically more tractable,

non-trivial nature of state space

and still potentially interesting given

In either case the question is "What is the basic phenomenology of such models?"

Qualitative Features of Models of Protein Design?



### Extension: Non-Trivial Interactions



#### Extension: Kinetic Models

$Z_N(\{eta\lambda_i\})$	$k_BT_c$	$\overline{j}_0 = 1 - W_0(\cdots)$
Partition Function	Transition Temperature	"Order Parameter"

So far we've only been concerned with equilibrium physics.

How would we formulate the non-equilibrium physics of this system?

If we begin with an arbitrary ordering, how does that ordering evolve in time?

$$\underline{\omega_2} \ \underline{\omega_N} \ \cdots \ \underline{\omega_1} \ \stackrel{\text{a time } t \text{ passes}}{\Longrightarrow} \ \underline{?} \ \underline{?} \ \cdots \ \underline{?}$$

Naive Approach: Use the Master Equation (In analogy to the Kinetic Ising Model)

$$\frac{\partial}{\partial t}P_N(j,t) = \sum_{j'=0}^N P_N(j',t)w(j'\to j) - \sum_{j'=0}^N P_N(j,t)w(j\to j').$$
(j = number of incorrect components)

Example Dynamics

In each time step, we exchange two components.

$$\theta_i(t_1 + \Delta t) = \theta_k(t_1)$$
 and  $\theta_k(t_1 + \Delta t) = \theta_i(t_1)$ 

 Resulting *j* will increase/decrease or stay the same

 $j \rightarrow j, j \pm 1, j \pm 2,$ 

$$\longrightarrow$$
 What is  $\langle j(t) \rangle$ ?

# Bucking the Trend

https://imgs.xkcd.com/comics/physicists.png



LIBERAL-ARTS MAJORS MAY BE ANNOYING SOMETIMES, BUT THERE'S NOTHING MORE OBNOXIOUS THAN A PHYSICIST FIRST ENCOUNTERING A NEW SUBJECT.

# Physics can help biology



X-Ray Crystallography

mini.

#### But can biology help physics?



**DNA Structure** 

#### END

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