

Quinary lattice model of secondary structures of polymers

Talk given at the Conference "Mathematical Physics. Vladimirov-90",
dedicated to the 90th anniversary of Vasilii Sergeevich Vladimirov,
Steklov Institute, Moscow, November 13-15, 2013

We construct a new model of lattice polymers and describe for this
model all possible secondary structures for sufficiently short lattice
polymers.

This model belongs to a new class of lattice models with
cooperative interaction.

S.V.Kozyrev, I.V.Volovich, Quinary lattice model of secondary
structures of polymers, Physica A, 2014, V. 393, P. 86-95.
arXiv:1206.4424

Lattice polymer (of the length N). Conformation — a sequence of vertices in the cubic lattice $\mathbb{Z}^3$, i.e. the map

$$\Gamma : \{1, \dots, N\} \rightarrow \mathbb{Z}^3,$$

without self intersections where neighbor natural numbers map to neighbor (i.e. distance one) vertices of the lattice.

Standard model of energy of lattice polymers — interaction of nearest neighbors

$$E_2(\Gamma) = - \sum_{1 \leq i < j \leq N} \delta(d(\Gamma(i), \Gamma(j))),$$

where $d(\cdot, \cdot)$ is the distance in $\mathbb{Z}^3$, $\delta(1) = 1$, $\delta(i) = 0$, $i > 1$.

does not describe secondary structures
(special preferred conformations)

A.Yu.Grosberg, A.R.Khokhlov, Giant Molecules: Here, There, and Everywhere, 2nd ed., World Scientific Publishing Company, 2010.

E.I.Shakhnovich, A.M.Gutin, Engineering of stable and fast-folding sequences of model proteins, Proc. Natl. Acad. Sci. USA, 1993, V.90, P.7195–7199.

K.F.Lau, K.A.Dill, A Lattice Statistical Mechanics Model of the Conformational and Sequence Spaces of Proteins. Macromolecules, 1989, V.22, P.3986–3997.

R.Unger, D.Harel, S.Wherland, J.L.Sussman, A 3D building blocks approach to analyzing and predicting structure of proteins. Proteins: Struct. Funct. Genet., 1989, V.5, P.355–373.

C.Micheletti, F.Seno, A.Maritan, Recurrent Oligomers in Proteins: An Optimal Scheme Reconciling Accurate and Concise Backbone Representations in Automated Folding and Design Studies, Proteins: Struct. Funct. Genet., 2000, V.40, P.662–674.

A.N.Nekrasov, Analysis of the information structure of protein sequences: a new method for analyzing the domain organization of proteins. J. Biomol. Struct. Dyn., 2004, V.21(5), P.615–624.

The quinary lattice model (a new form of cooperative interaction)

Conformation of a segment of a lattice polymer of length 5:

$$\Gamma_i = (\Gamma(i-2), \Gamma(i-1), \Gamma(i), \Gamma(i+1), \Gamma(i+2)), \quad i = 3, \dots, N-2.$$

The energy is a sum of contributions from conformations of 5-tuples

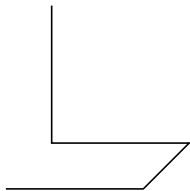
$$E_5(\Gamma) = - \sum_{i=3}^{N-2} \Phi(\Gamma_i).$$

The function Φ of conformations of 5-tuples is invariant with respect to lattice rotations and translations.

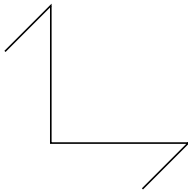
Φ is equal to zero for all conformations except conformations denoted 1 and 2 for which

$$\Phi(1) = \Phi(2) = 1.$$

Conformation 1



Conformation 2



Conformations of a lattice polymer which are minima of the energy E_5 , i.e. a conformation of any 5-tuple of neighbor monomers either of the type 1 or of the type 2 are called *minimal*.

We consider these conformations as models of secondary structures in proteins.

Examples of minimal conformations (see the next slide) — lattice models of α -helix and β -strand

The quinary lattice model possesses nontrivial secondary structures

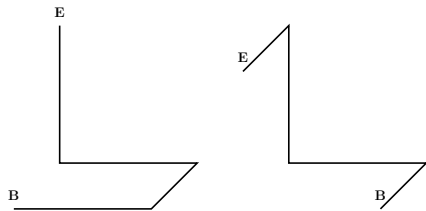
α -helix is a right lattice helix with the symmetry with respect to the rotation counterclockwise by $3\pi/2$ and translation by one upwards (according to the thumb rule).

β -strand is symmetric with respect to translations.

Let us describe minimal conformations (secondary structures) of lattice proteins

We consider for conformations 1 and 2 their *directions*.
The beginning B and the end E of the conformations.

$\vec{1}$, $\vec{2}$ and $\overleftarrow{1}$, $\overleftarrow{2}$ — conformations 1 and 2
which are considered from B to E and from E to B correspondingly
(i.e. considered as oriented graphs).



Minimal conformation of a lattice polymer generates a sequence of symbols $\overrightarrow{1}$, $\overrightarrow{2}$, $\overleftarrow{1}$, $\overleftarrow{2}$ of conformations of 5-tuples of neighbor monomers (when we read the sequence of monomers in the polymer from the beginning to the end).

Which sequences $\Gamma_3 \Gamma_4 \dots \Gamma_{N-2}$ of the symbols $\overrightarrow{1}$, $\overrightarrow{2}$, $\overleftarrow{1}$, $\overleftarrow{2}$ can be generated by minimal conformations of a lattice polymer?

It is not always possible to combine a couple of symbols into one conformation (due to geometric restrictions).

Two consecutive 5-tuples of monomers intersect:

$$\Gamma_i = (\Gamma(i-2), \Gamma(i-1), \Gamma(i), \Gamma(i+1), \Gamma(i+2)), \dots,$$

$$\Gamma_{i+1} = \dots, (\Gamma(i-1), \Gamma(i), \Gamma(i+1), \Gamma(i+2), \Gamma(i+3)).$$

This implies the selection rules for the conformations Γ_i , Γ_{i+1} of the consecutive 5-tuples.

Lemma 1) Possible pairs of neighbor conformations of 5-tuples in the sequence $\Gamma_3\Gamma_4\ldots\Gamma_{N-2}$ related to some minimal conformation of a lattice polymer are described by the following table

	$\overrightarrow{1}$	$\overleftarrow{1}$	$\overrightarrow{2}$	$\overleftarrow{2}$
$\overrightarrow{1}$	—	+	+	—
$\overleftarrow{1}$	+	—	—	—
$\overrightarrow{2}$	—	—	—	+
$\overleftarrow{2}$	—	+	+	—

(i.e. for any pair of symbols denoted by + in the table above there exists a minimal conformation of a lattice polymer of length 6).

2) Any conformation described by a triple of symbols from $\{\overrightarrow{1}, \overrightarrow{2}, \overleftarrow{1}, \overleftarrow{2}\}$ permitted by the above table corresponds to some minimal conformation of a lattice polymer of length 7 except the triples $\overrightarrow{2}\overrightarrow{2}\overrightarrow{2}, \overleftarrow{2}\overleftarrow{2}\overleftarrow{2}..$

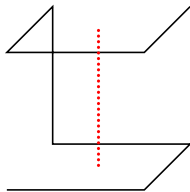
Examples

Lattice α -helix and β -strand — iterations of α and β conformations.

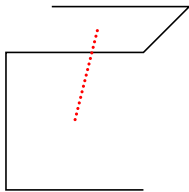
Central lines of α and β conformations
(red dotted line)

connect the centers of the corresponding faces of the cube
containing the corresponding conformation.

Conformation $\alpha = \overline{1} \overline{2} \overline{2} \overline{1}$



Conformation $\beta = \overline{1} \overline{1}$



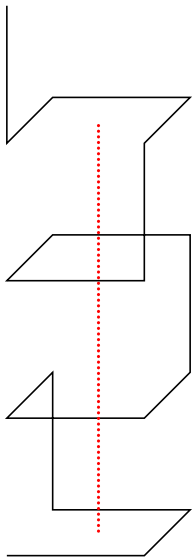
Iterations of α or iterations of β

— straight central lines,

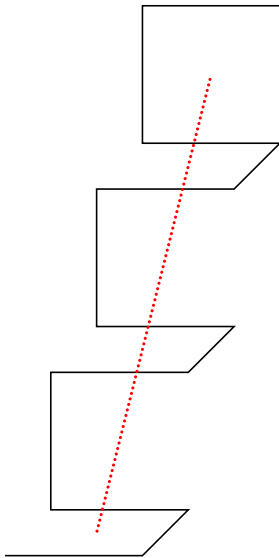
mixture of α and β

— broken central line, angle 135° .

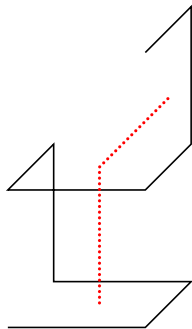
α -helix



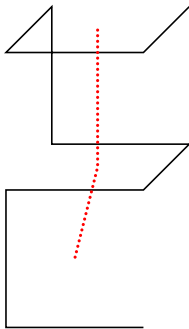
β -strand



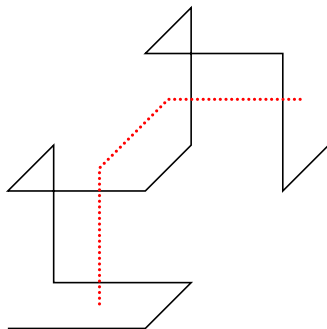
Conformation $\alpha\beta$



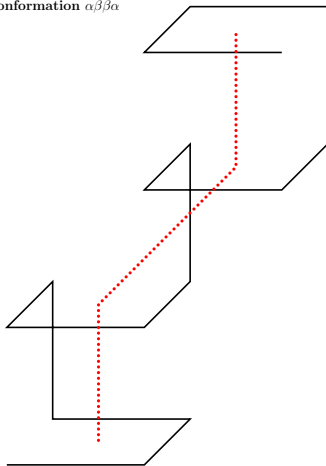
Conformation $\beta\alpha$



Conformation $\alpha\beta\alpha$



Conformation $\alpha\beta\beta\alpha$



Theorem

1) Any minimal conformation of a lattice polymer with the length $N > 6$ has the following form:

The corresponding sequence $\Gamma_3 \Gamma_4 \dots \Gamma_{N-2}$ of conformations of 5-tuples can be obtained from some sequence of α and β structures, $\alpha = \overrightarrow{1} \overrightarrow{2} \overleftarrow{2} \overleftarrow{1}$, $\beta = \overrightarrow{1} \overleftarrow{1}$ by elimination of a finite number of symbols $\overrightarrow{1}$, $\overrightarrow{2}$, $\overleftarrow{1}$, $\overleftarrow{2}$ in the beginning and the end of the sequence.

2) All conformations of a lattice polymer with the length $6 < N < 39$ obtained as above do not contain self intersections.

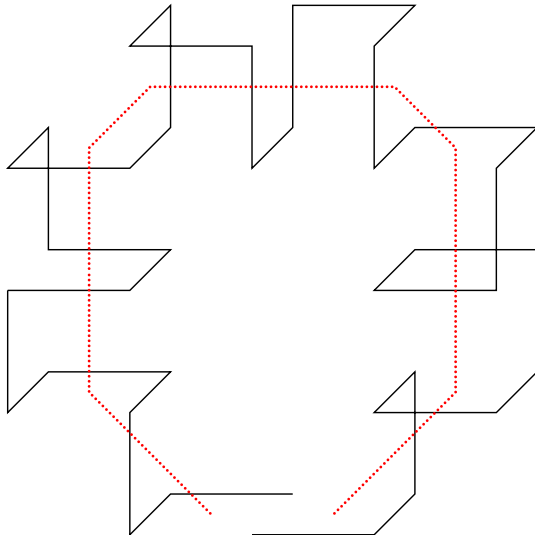
There exists a sequence of conformations of 5-tuples corresponding to the conformation of a lattice polymer of the length 39 with self-intersections.

An arbitrary minimal conformation of a lattice polymer is a combination of α and β structures,

all such combinations with the length of the polymer $6 < N < 39$ are possible.

Conformation $\overline{1}\beta\alpha\alpha\beta\alpha\alpha\beta\alpha\alpha\beta\overline{1}$ (38 vertices)

continuation possesses intersections



Conclusion

The quinary model of a lattice polymer is proposed.

New class of lattice models with cooperative interaction.

All minima of energy are combinations of lattice α -helices and β -strands.

All conformations which are energy minima for lattice polymers of length < 39 are described.

This new model allows to describe the effect of existence of secondary structures of proteins.

Relation to real proteins?