

# LATFOLDVEC - Manual

Martin Mann - University Freiburg

<http://www.bioinf.uni-freiburg.de/>

LATPACK Tools Package  
Version 1.8.2

## 1 Description

LATFOLDVEC models the co-translational (or vectorial) folding. This is done via a folding simulation of a periodically growing amino acid chain. Therefore, it implements a combination of a Monte-Carlo simulation utilizing a Metropolis criterion (see [4]) and a chain growth algorithm. The implementation is based on the Energy Landscape Library [5]. It supports:

1. various lattices (see Sec. 3)
2. arbitrary energy functions (see Sec. 4)
3. ...

## 2 Method

### 2.1 Co-translational Folding Simulation

**Given:**

- $S = S_1, \dots, S_n$  : monomer sequence from alphabet  $A$  to fold
- $E(S, P)$  : energy function (see Sec. 4)
- $M(L)$  : the set of neighboring structures of  $L$  in the energy landscape
- $\Delta t$  : the folding time between single chain elongations
- $N$  : the neighboring vectors of the lattice model to use

**Result:**

- $L = L_1, \dots, L_n$  : 3D coordinates of the energetically best sequential placement of  $S$  in the lattice

### Method:

The simulations follows a structure-elongating chain-growth approach in combination with a “global” folding simulation:

```

1:  $L = L_1 = (0, 0, 0)$        $\triangleright$  initialized by placing the first monomer to  $(0, 0, 0)$ 
2: for  $i = 2 \dots n$  do

3:   for  $t = 0 \dots \Delta t$  do       $\triangleright$  folding simulation of chain with length  $i$ 
4:     Select random neighbor  $m_r \in M(L)$ 
5:      $r \in [0, 1]$        $\triangleright$  get random number in interval  $[0, 1]$ 
6:     if  $(r \leq e^{-\frac{E(S, m_r) - E(S, L)}{kT}})$  then
7:        $L \leftarrow m_r$        $\triangleright$  go to neighboring structure
8:     else       $\triangleright$  keep current structure for this step
9:     end if
10:  end for

11:   $E(L) = \emptyset$        $\triangleright$  will contain all elongations of  $L$ 
12:  for all  $\vec{v} \in N$  do
13:    if  $L_{(i-1)} + \vec{v} \notin \{L_1, \dots, L_{(i-1)}\}$  then       $\triangleright$  selfavoidingness
14:       $L' \leftarrow (L_1, \dots, L_{(i-1)}, (L_{(i-1)} + \vec{v}))$ 
15:       $E(L) \leftarrow E(L) \cup \{L'\}$        $\triangleright$  store extension
16:    end if
17:  end for
18:   $Z(E(L)) = \sum_{e \in E(L)} e^{-\frac{E(S, e)}{kT}}$        $\triangleright$  partition function of  $E(L)$ 

19:  select random elongation  $e_r \in E(L)$  according to its probability
      in the ensemble of all elongations  $P(e) = \frac{e^{-\frac{E(S, e)}{kT}}}{Z(E(L))}$ 

20:   $L = e$        $\triangleright$  set choosen elongation
21: end for
22: report  $L$  with energy  $E(S, L)$ 

```

**Note:** Since we are simulating the folding of a *growing* amino acid chain, we have to ensure that the ends of the intermediate chains (namely monomer  $L_i$ ) has to have a free neighbored position that can be used for elongation. Therefore, only a reduced set of neighbored structures  $M'(L) \subseteq M(L)$  is used in line 4.

## 3 Available Lattices

Several lattice models can be used to fold a structure.

The currently supported lattice models and the corresponding neighboring vectors are:

ID	Name	Neighborhood vectors	#
SQR	Square	$\{\pm(1, 0, 0), \pm(0, 1, 0)\}$	4
CUB	Cubic	$\{\pm(1, 0, 0), \pm(0, 1, 0), \pm(0, 0, 1)\}$	6
FCC	Face Centered Cubic	$\left\{ \begin{array}{l} \pm(1, 1, 0), \pm(1, 0, 1), \pm(0, 1, 1), \\ \pm(1, -1, 0), \pm(1, 0, -1), \pm(0, 1, -1) \end{array} \right\}$	12

## 4 Energy Functions

LATFOLDVEC supports arbitrary energy functions that are based either on contacts or on distance intervals. The specification of an energy function has to be given in text format and defines the allowed sequence alphabet as well.

In general, the energy of a sequence  $S$  of length  $n$  with structure coordinates  $P$  is determined by

$$E(S, P) = \sum_{1 \leq i+1 < j \leq n} e(S_i, S_j, P_i, P_j). \quad (1)$$

Here,  $e(S_i, S_j, P_i, P_j)$  is a placeholder for the specific evaluation function that is given for the different types in the following.

### 4.1 Contact Based Energy Function

A contact based energy function for an alphabet  $A$  is defined by an energy table  $E^c : |A| \times |A| \rightarrow \mathcal{R}$  such that

$$e_c(S_i, S_j, P_i, P_j) = \begin{cases} E^c[S_i, S_j] & \text{if } P_i \text{ and } P_j \text{ are neighbored} \\ 0 & \text{else} \end{cases} \quad (2)$$

For example, a function like this was used by Lau and Dill to define the widely used HP-model [1].

#### Text File Encoding

The LATFOLDVEC text file encoding of a contact based energy function consists of two parts: the alphabet elements and the energy table. A consecutive string of the alphabet elements in the first line determines the allowed protein sequence characters (the alphabet) and the dimensions of the energy table that is read from the remaining file.

An example energy file for the HPNX-model is:

HPNX
-4.0 0.0 0.0 0.0
0.0 +1.0 -1.0 0.0
0.0 -1.0 +1.0 0.0
0.0 0.0 0.0 0.0

## 4.2 Distance Interval Based Energy Function

A distance interval based energy function for an alphabet  $A$  is defined by a consecutive set of  $k$  distance intervals with the upper bounds  $d_{1\dots k}^{up}$  and an energy table  $E_{1\dots k}^i : |A| \times |A| \rightarrow \mathcal{R}$  for each of them. Given the distance to interval index function  $idx$  we define the evaluation function

$$e_i(S_i, S_j, P_i, P_j) = E_{idx(P_i, P_j)}^i[S_i, S_j] \quad (3)$$

$$idx(P_i, P_j) = \arg \min_k (|P_i - P_j| \leq d_k^{up}) \quad (4)$$

### Text File Encoding

The LATFOLDVEC text file encoding of a distance interval based energy function consists of three parts: the alphabet elements, the upper bounds of the intervals and the energy tables for the interval. A consecutive string of the alphabet elements in the first line determines the allowed protein sequence characters (the alphabet) and the dimensions of the energy tables. The second line contains a whitespace separated list of the upper interval bounds. Their number sets the number of energy tables read from the remaining file. The interval bounds are expected to be given in Ångstroems. For a correct scaling of the bounds it is necessary to give the average distance of two consecutive  $C_\alpha$ -atoms in the underlying model to LATFOLDVEC (see input parameters in Sec. 5).

An example energy file that encodes the HPNX-model using a distance interval based energy function is:

```
HPNX
3.7 3.9 999999

0.0 0.0 0.0 0.0
0.0 0.0 0.0 0.0
0.0 0.0 0.0 0.0
0.0 0.0 0.0 0.0

-4.0 0.0 0.0 0.0
0.0 +1.0 -1.0 0.0
0.0 -1.0 +1.0 0.0
0.0 0.0 0.0 0.0

0.0 0.0 0.0 0.0
0.0 0.0 0.0 0.0
0.0 0.0 0.0 0.0
0.0 0.0 0.0 0.0
```

The number 999999 is used as a placeholder for  $+\infty$ , i.e. the upper bound of the last distance interval. It is important to know that the average  $C_\alpha$ -distance in the underlying model was 3.8 Å. Therefore, the resulting interval energy function corresponds to the contact based energy function of the previous section; only distances close to the average  $C_\alpha$ -distance are taken into account.

## 5 Program Parameters

### Input

- seq** The sequence to fold globally. It has to be conform to the alphabet given by the energy file (see **-energyFile**).
- energyFile** A file that encodes the used alphabet and the specific energy function (see Sec. 4 for format details).
- energyForDist** If present, the input of **-energyFile** will be interpreted as distance interval energy function. Otherwise a contact based energy function is expected.
- energyCalphaDist** Specifies the average distance of two consecutive  $C_\alpha$ -atoms in the underlying model. This value is needed to scale the intervals of a distance interval based energy function onto the  $C_\alpha$ -distances of the lattice model in use.

### Simulation Settings

- kT** the relative temperature to calculate the Boltzmann weight for a given structure within the formula  $\exp(-E/kT)$ . Thus, the parameter  $kT$  sets the product of temperature ( $T$ ) and the energy function specific scaling constant ( $k$ ).
- maxSteps** each intermediate subchain simulation ends after this number of simulation steps before proceeding to next elongation
- minE** simulation ends if energy gets below or equal the given value
- seed** seed for random number generator (uses a system independent linear congruent generator)
- runs** number of independent folding simulations to perform

### Lattice Settings

- lat** The lattice model to use for the sequential folding. The available list of lattice identifiers is given in Sec. 3.
- moveSet** Sets the move set to use for the present lattice:
  - PullM** Pull-moves defined by Lesh et al. [2]

## Output

**-out** The output mode along the folding simulation:

**N** no additional output is done (default)

**E** the energy of the structure of each simulation step is printed

**S** structure and energy of each simulation step is given

**-outFile** Specifies where to write the output of simulations to. If equal to 'STDOUT' it is written to standard output, otherwise the given string is assumed to be the filename to write to.

**-outTiming** If present, the used cpu-time is printed.

## Miscellaneous

**-v** Give verbose output during computation.

**-vv** Give extra verbose output during computation.

**-help** Prints the available program parameters.

## 6 Contact

Martin Mann  
Bioinformatics Group  
University Freiburg, Germany

<http://www.bioinf.uni-freiburg.de/>

## References

- [1] Kit Fun Lau and Ken A. Dill: **A Lattice Statistical Mechanics Model of the Conformational and Sequence Spaces of Proteins**, *Macromolecules* 1989, **22**(10):3986–3997
- [2] Lesh, N., Mitzenmacher, M., and Whitesides, S.: **A complete and effective move set for simplified protein folding**, In *Proceedings of the seventh annual international conference on Research in computational molecular biology (RECOMB'03)* 2003, 188–195.
- [3] Madras, N. and Sokal, A. D.: **The pivot algorithm: A highly efficient Monte Carlo method for the self-avoiding walk**, *Journal of Statistical Physics* 1988, **50**, 109–186.
- [4] Mann, M., Maticzka, D., Saunders, R., and Backofen, R.: **Classifying protein-like sequences in arbitrary lattice protein models using LatPack**, *HFSP Journal* 2008, **2**(6), 396. Special issue on protein folding: experimental and theoretical approaches

- [5] Mann, M., Will, S., and Backofen, R.: **The Energy Landscape Library - A Platform for Generic Algorithms**, In *Proceedings of the 1st international Conference on Bioinformatics Research and Development (BIRD'07)* 2007, OCG **217**, 83-86.