

# MESHI\* – a new object oriented package for molecular simulations

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\* **Meshi** – the Hebrew name of the splendid protein **silk**.

( and a tribute to CK's late cat)

# Thanks to:

- Organizers and assessors.
- My group members in BGU: Nir Kalisman, Ami Levi, Sharon Zafri-lynn, Tetyana Maxymova and Yan Gleyzer.
- The GeneFun consortium.
- The four masters : R. Elber, J. Skolnik, A. Kolinski and M. Levitt.

## Why a new package

new  
idea

Fortran/C programs dominate the field of computational structural biology. Some of them are master pieces.

- 😊 Fortran/C compilers are very well optimized.
- 😊 A huge corpus of reliable code already exists.
- 😞 Fortran/C programs are inherently hard to comprehend and not as modular as we tend to think.
- 😞 These programs tends to be oriented towards computational efficiency.

implementation



new  
idea

We believe that the most precious  
resource is developer's time.  
**Moore's law does not apply to it**

implementation

## Why Java

- ☹️ **Java is around two times slower than C++.**
- ☹️ **You always need to defend its usage.**
- 😊 **There are quite a few bugs you cannot do in Java.**
- 😊 **Java forces you to write in an object oriented fashion.**
- 😊 **One can always write the (few) computational bottlenecks in Fortran/C/assembly language.**

The modular, object oriented  
approach of MESHI.

Sample classes

# Coordinates

Coordinates

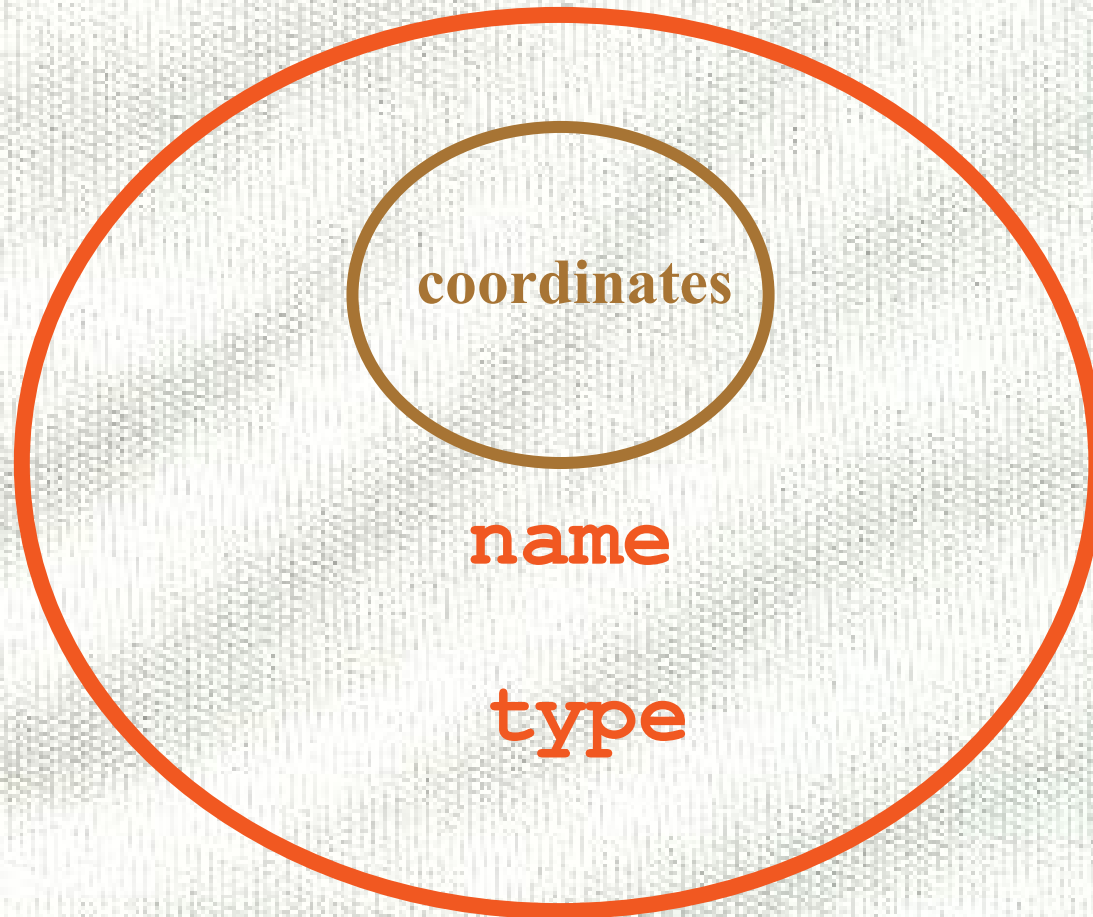
X Y Z

Forces

F<sub>X</sub> F<sub>Y</sub> F<sub>Z</sub>



# Atom







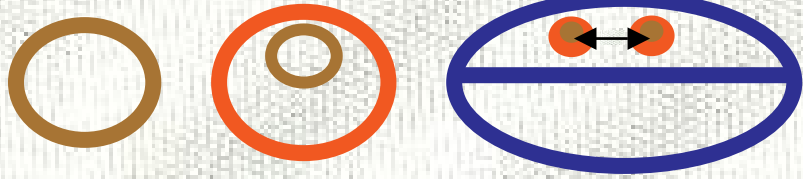
# Distance

atom1      atom2

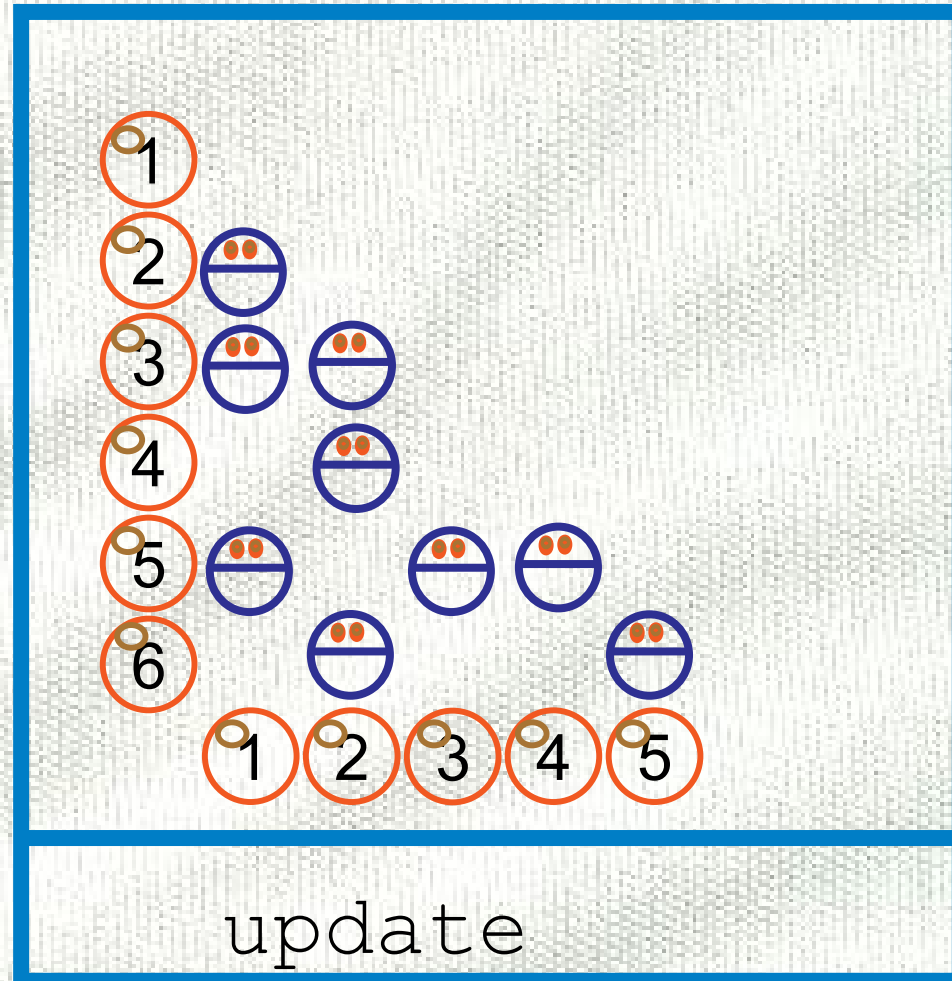
$\frac{1}{d}$        $d$        $d^2$        $\frac{\partial d}{\partial X}$        $\frac{\partial d}{\partial Y}$        $\frac{\partial d}{\partial Z}$

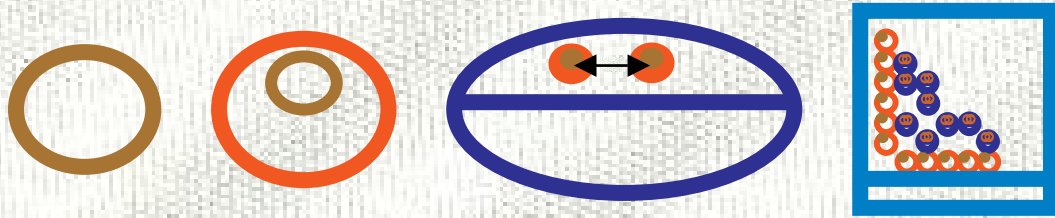
The diagram illustrates the distance between two atoms, atom1 and atom2. Atom1 is represented by a brown circle, and atom2 is represented by a brown circle inside an orange circle. A horizontal line with arrows at both ends connects the centers of the two atoms, labeled with the distance  $d$ . To the left of atom1 is the term  $\frac{1}{d}$ . Below the distance  $d$  is the term  $d^2$ . To the right of atom2 are the partial derivatives  $\frac{\partial d}{\partial X}$ ,  $\frac{\partial d}{\partial Y}$ , and  $\frac{\partial d}{\partial Z}$ .

update

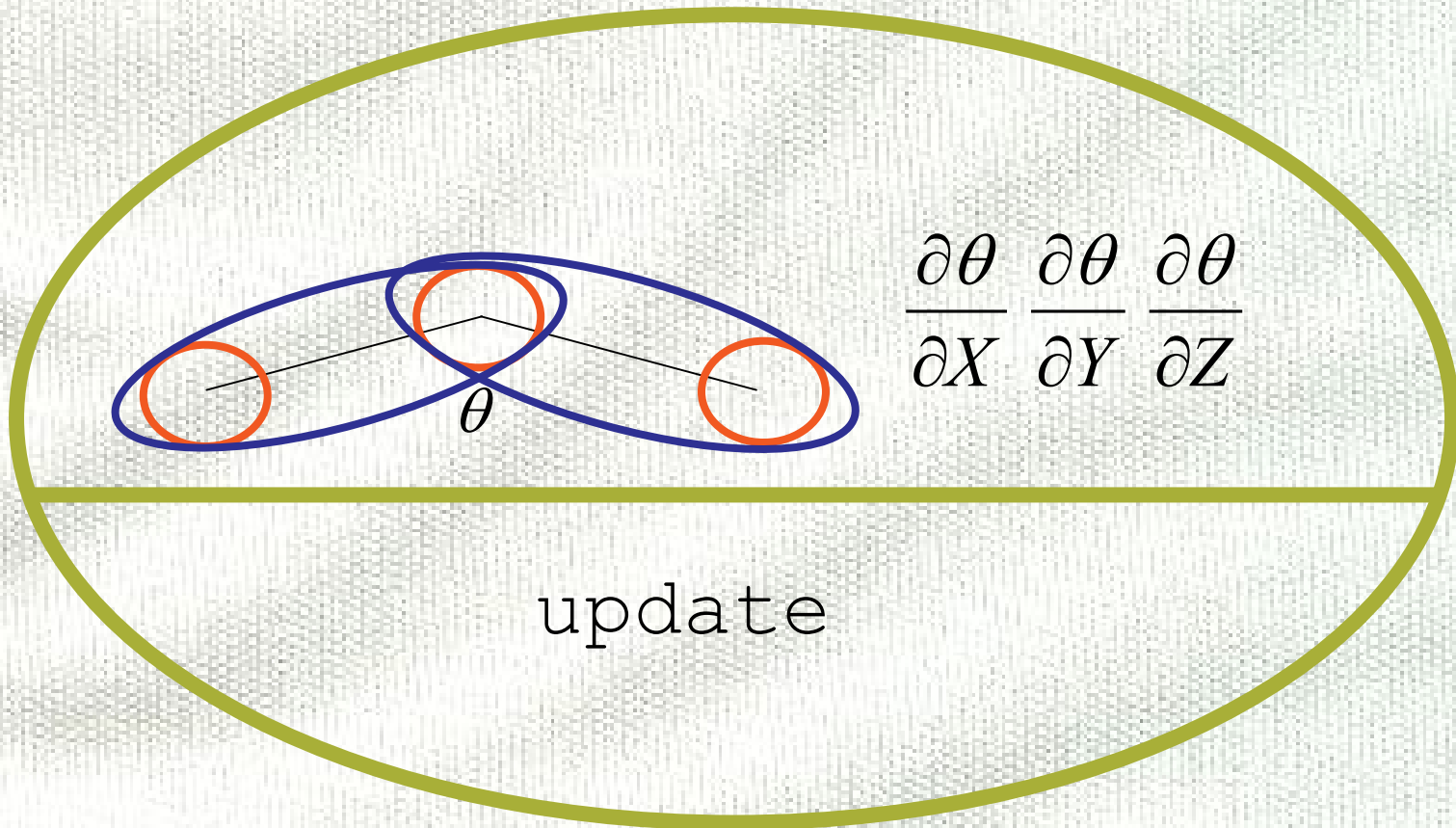


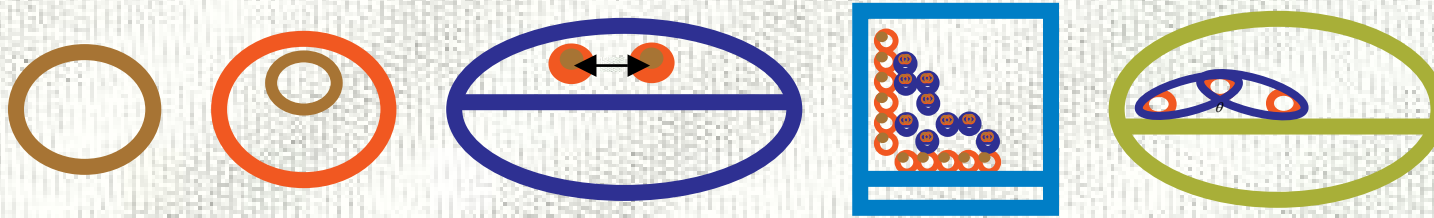
# DistanceMatrix





# Angle





# AngleEnergyElement

Atom type specific  
constants



$\bar{\theta}$

$K$

1. Evaluate  $e_{\theta} = K(\theta - \bar{\theta})^2$

2. Update **atom** forces

# AngleEnergyElement (sub-class of EnergyElement)

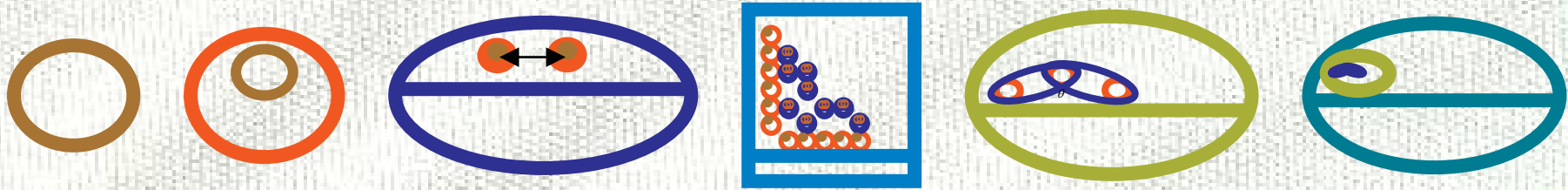
Atom type specific  
constants



$\bar{\theta}$

$K$

3.Test (inherited form  
EnergyElement).



# AngleEnergy

A list of elements



1. Evaluate  $E_{angle} = \sum_{\theta} e_{\theta}$
2. Update **atom** forces





# TotalEnergy

1. Update `DistanceMatrix`
2. Evaluate  $E_{total} = \sum_{term} e_{term}$
3. Update `atom` forces



# LBFGS

(minimizer)

A list of coordinates

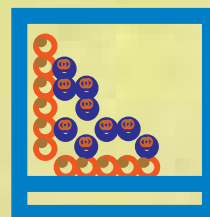


1. Update energy and forces
2. Change the coordinated according to the forces.
3. If not yet in a minimum - go to 1.



# Current Meshi projects

- ✱ Novel algorithm for non-bonded-list generation.

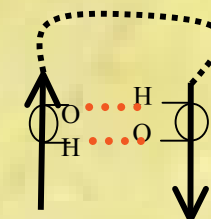


- ✱ MCMM-like stochastic optimization.

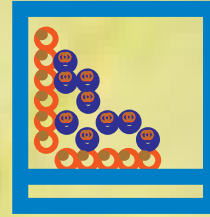


- ✱ Continues knowledge-based potential for pairs of torsion angles.

- ✱ Cooperative hydrogen-bonds potential.



generation.

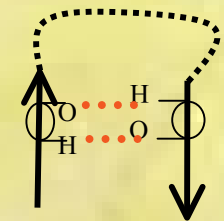


✿ MCMM-like stochastic optimization.



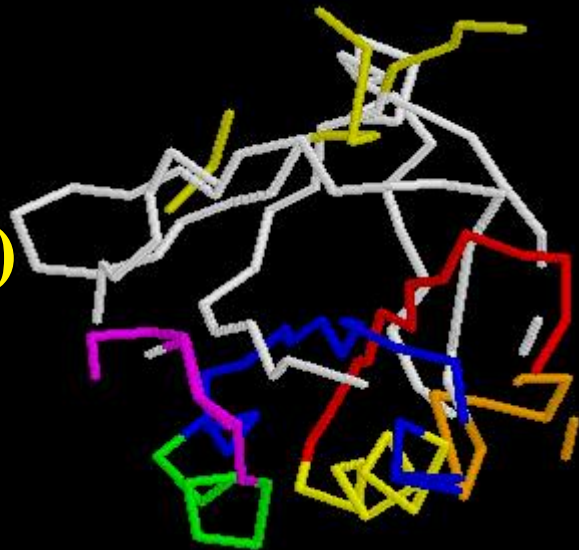
✿ Continues knowledge-based potential for pairs of torsion angles.

✿ Cooperative hydrogen-bonds potential.



✿ A refinement program for fold-recognition models.

**Shotgun**  
**12.5Å (7.4)**

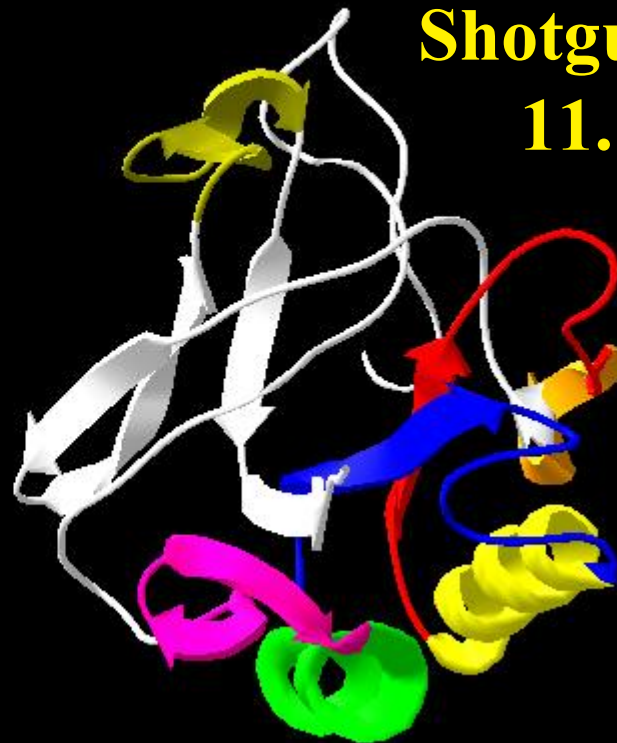


**1NXJ – T0156**

**Shotgun beautified**  
**11.1Å (6.5)Å**



**native**



[www.cs.bgu.ac.il/~meshi](http://www.cs.bgu.ac.il/~meshi)

Documentation and results are not as good as they should be, but they are (well at least the documentation) improving.