

Protein Structure Prediction Using Simple Genetic Algorithms

V. Sundararajan
Scientific and Engineering Computing Group
C-DAC, Pune
vsundar@cdac.in

Open Problem

There is no reliable procedure which begins with homologous model of a protein and then relaxes the structure using Molecular Dynamics to yield a conformation close to native. This is an important problem where database analysis cannot help.

Why Structure Prediction ?

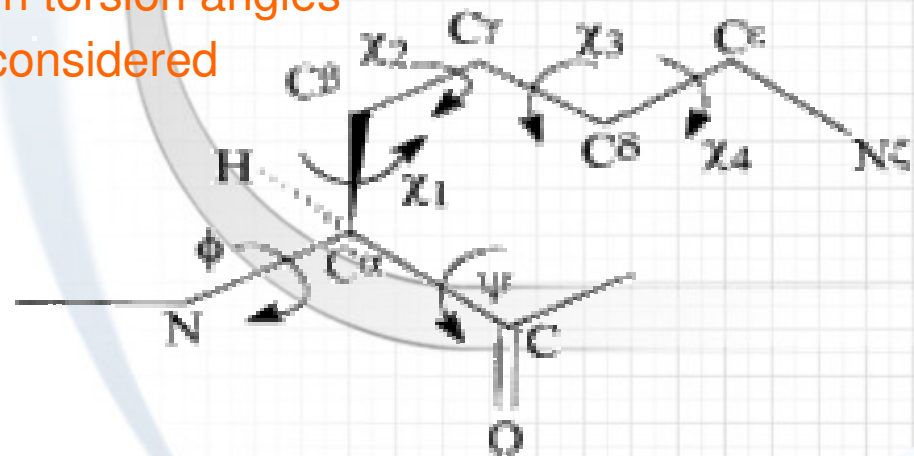
- Protein Structure prediction is one of the most challenging areas of research for the structural biologist.
- For 100 residues 4100 (or 1060) possible conformations 10 years to search the whole space assuming 1 nanosecond Per energy calculation
(Levinthal: *T. Creighton (editor), Protein Folding, W. H. Freeman (1992)*)

Why Structure Prediction ?

- Out of few lakhs protein sequences only about ten thousands have known structures (X-ray, NMR)
- Some proteins cannot be crystallized easily
- About 10% of protein sequences exhibit unrelated and unidentified folds
- It's important to evolve the structures without the help of databases
- Useful in modelling the differences between structures that databases may not facilitate

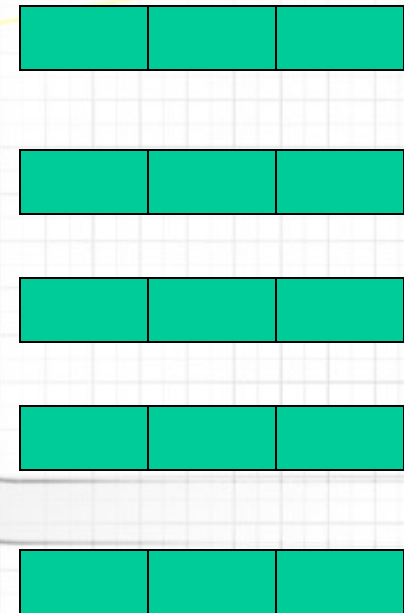
Model of Protein Structure

- Internal coordinate system restricted to torsion angle variation
- Energy = non-bond + torsion angle interactions (AMBER force field)
- Assumptions:
 - Fixed bond lengths, bond angles
 - Also fix omega and side-chain torsion angles
 - Only phi and psi angles are considered

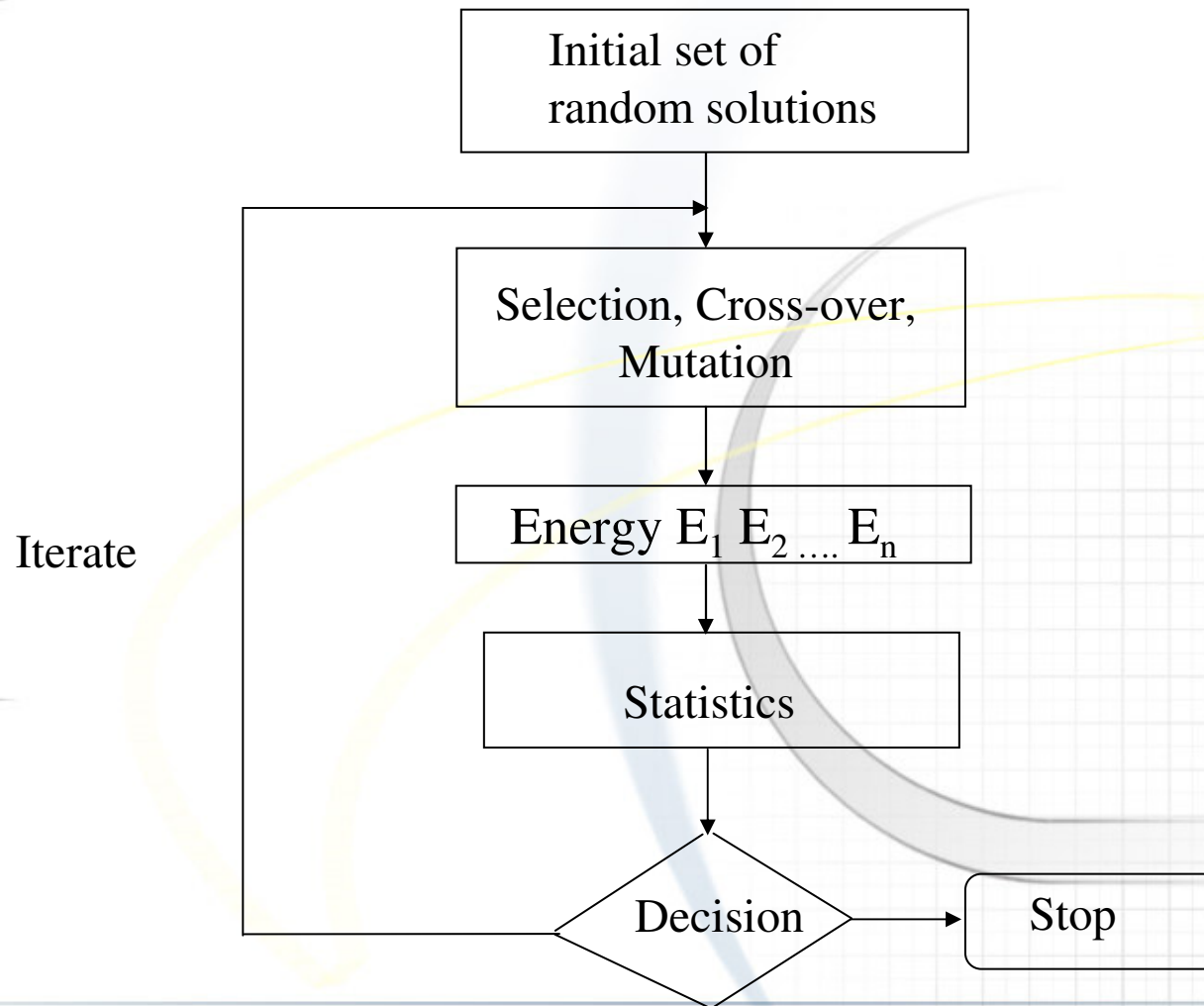


Implementation

- Torsional angles are represented by binary strings
- Choose many such randomly; each one is a possible structure
- Go through the GA procedure
- Pick up the ones that are having minimum most energy as well as few around that



Genetic Algorithms (GA)



Advantages of GA

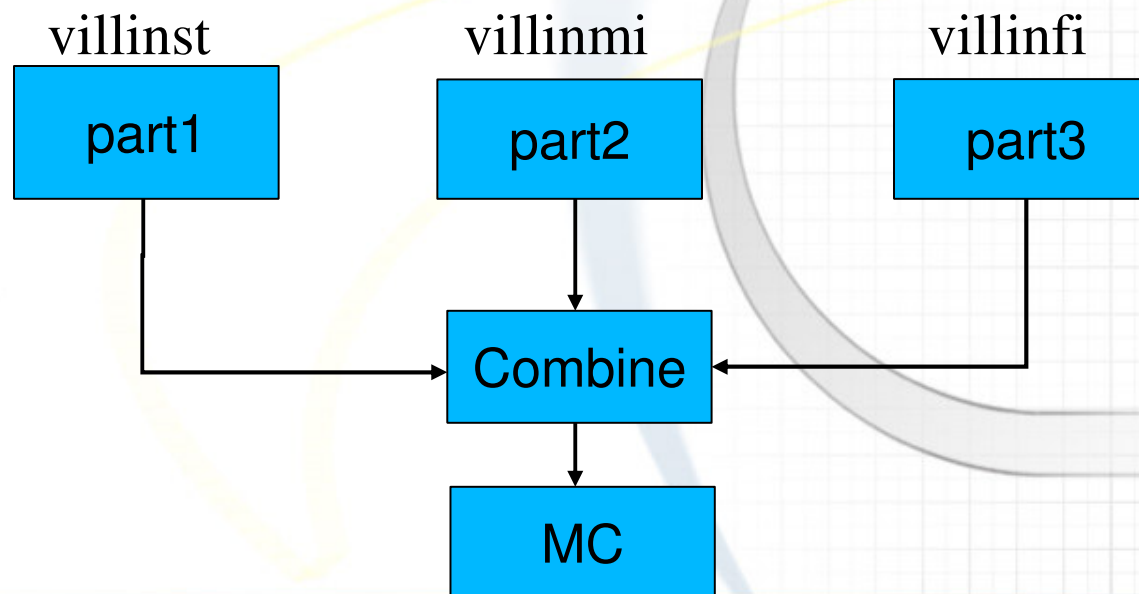
- Flexibility, robustness with global search characteristics, much less likely to get stuck on local optima
- Easy to implement
- Search from a population of points/solutions
- No derivatives, therefore can solve non-linear, discontinuous in parallel configuration
- Possible to device variety of parallel and distributed algorithms (suited both for HPC and Grid)
- Works on the representations rather than on the variables themselves

Case Study

- Simulating protein of 36 amino acids – Villin
- Simple Genetic Algorithm and Monte Carlo methods used
- To make a work flow by splitting the protein into smaller parts and execute GA codes
- Finally the full villin molecule is simulated using MC code

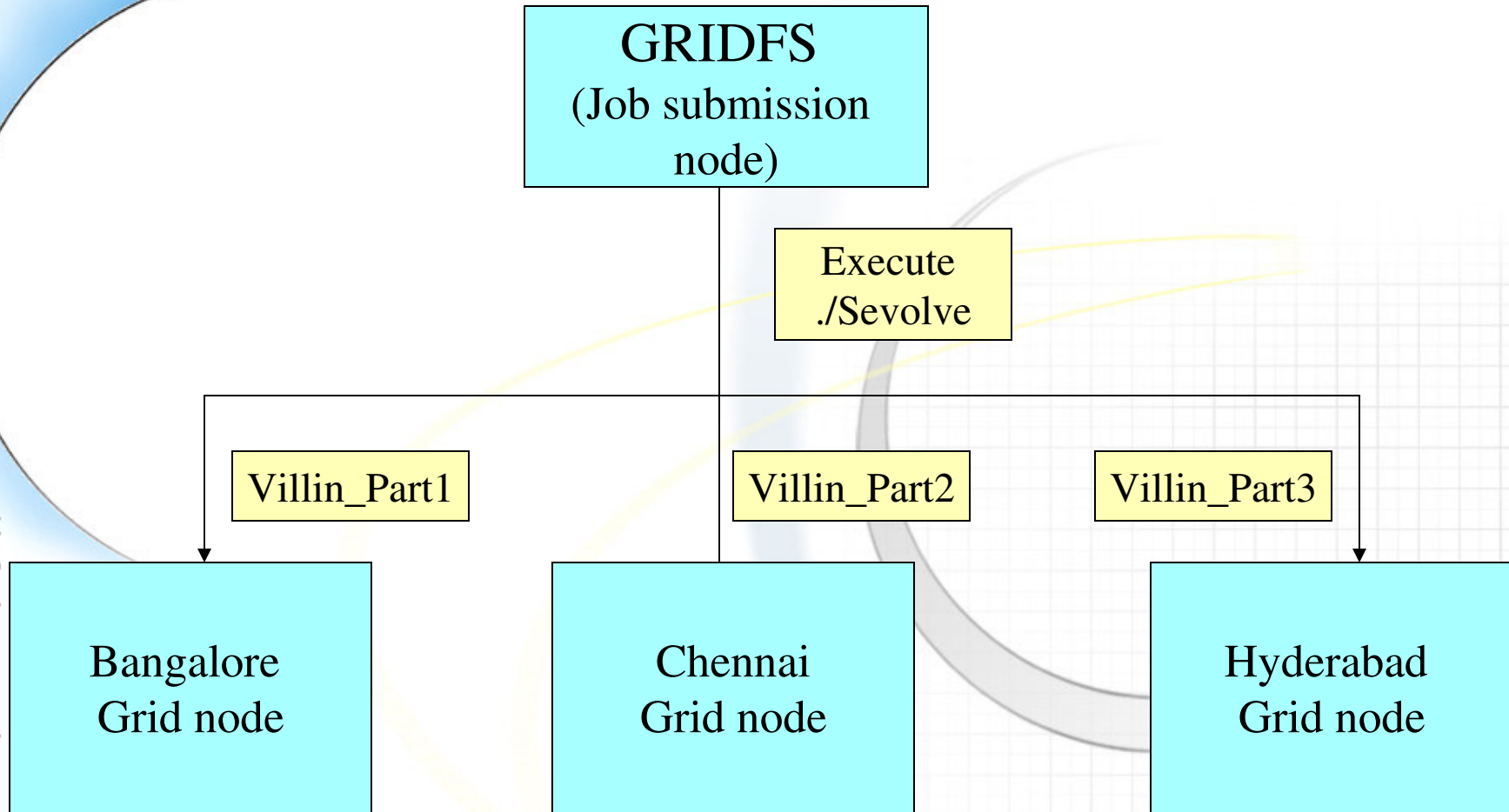
Implementation

- Implemented a simple workflow
- Parts 1 to 3 execute GA code for parts of the protein
- Advantages:
 - Reduction in Complexity
 - Possibility of concurrency



Job Submission on Grid

Workshop on Developing Applications on Grid - GARUDA



National Grid Computing Initiative - GARUDA

Submitting across Grid using RSL

```
+
(
  &(resourceManagerContact="che01/jobmanager-pbs")
  (count=1)
  (label="subjob 0")
  (environment=(GLOBUS_DUROC_SUBJOB_INDEX 0)
    (LD_LIBRARY_PATH /usr/local/globus/lib/))
  (directory="/home/garuda/garuda1/NEW_proteinmod/NEW_proteinmod/data")
  (executable="/bin/sh")
  (arguments="villin_part1.sh")

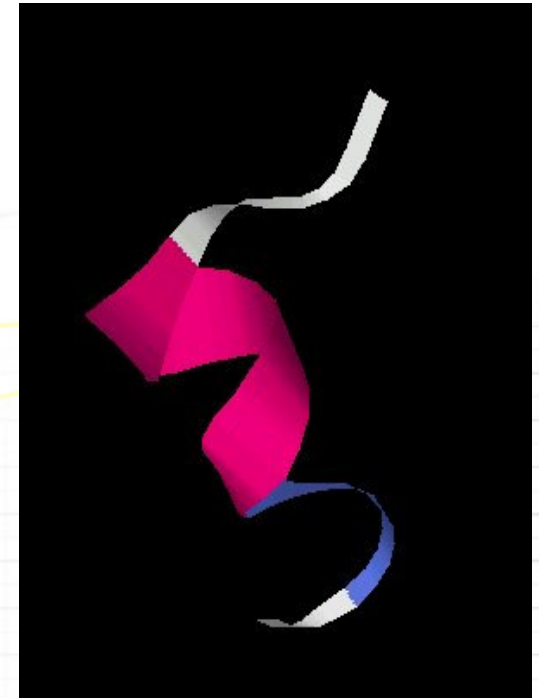
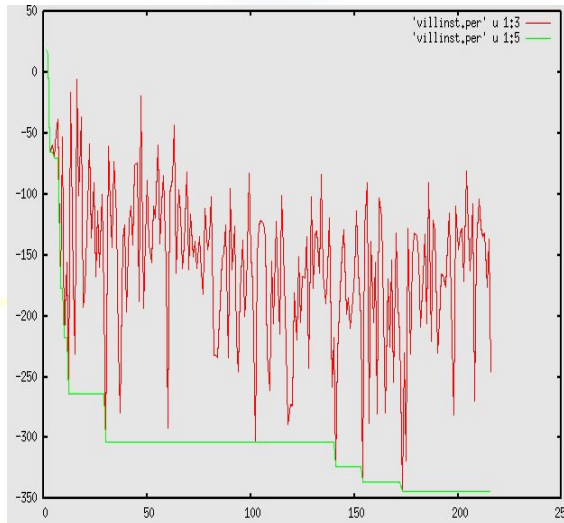
  (file_stage_out=(/home/garuda/garuda1/NEW_proteinmod/NEW_proteinmod/data
/villprt1.tar.gz $(GLOBUSRUN_GASS_URL)villprt1.tar.gz
  (stderr=vill_part1.err)
)
```

Shell script: villin_part1.sh

```
#!/bin/sh
tar xvzf AAA.tar.gz
chmod ugo+x ./Sevolve
./Sevolve < vill1
tar -czf villprt1.tar.gz villprt1.*
```

Results from first part

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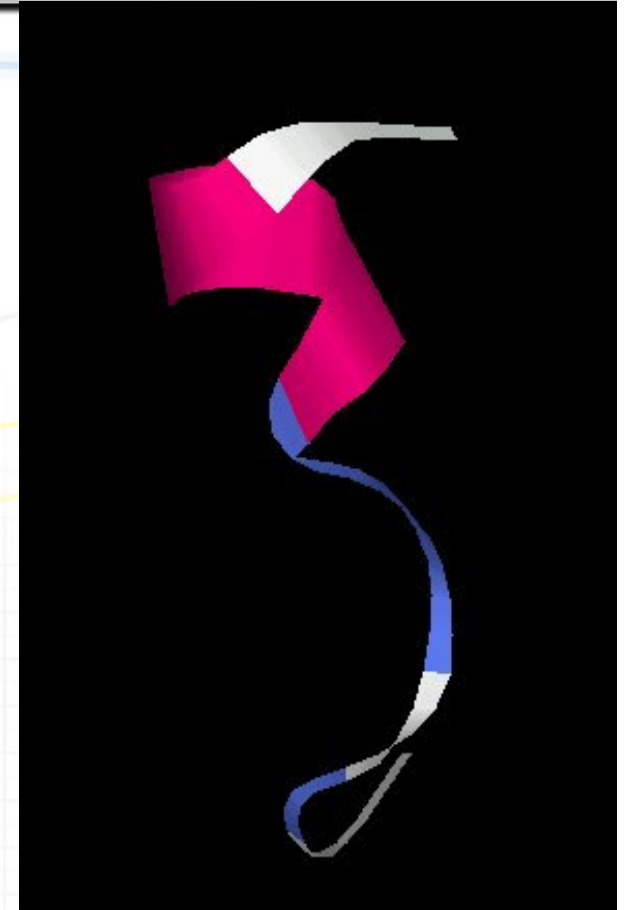
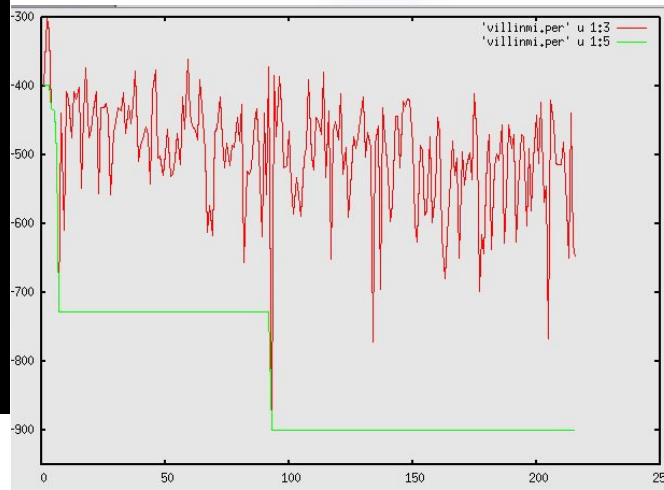
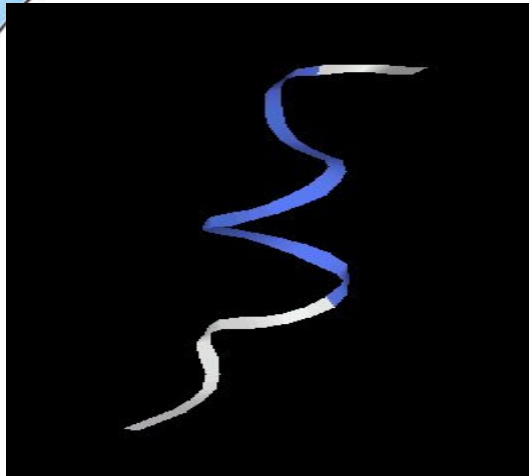


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Time: 00:06:00
2:57 + 3:03

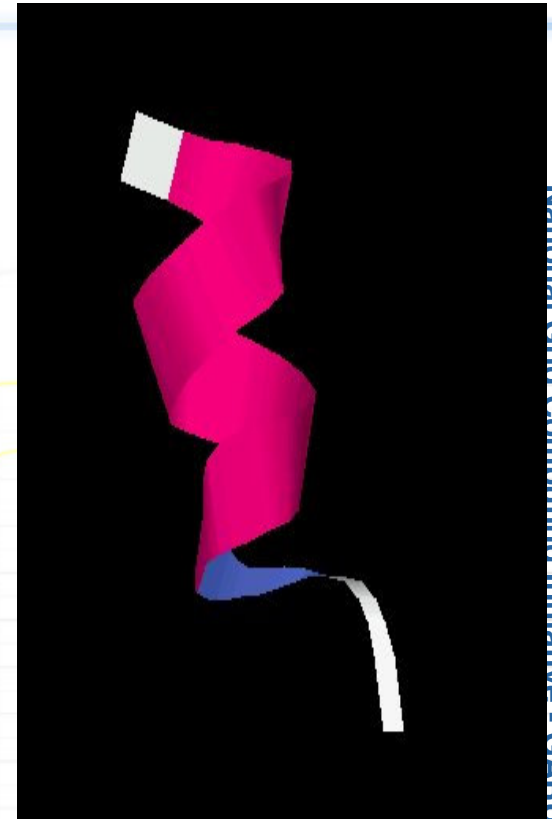
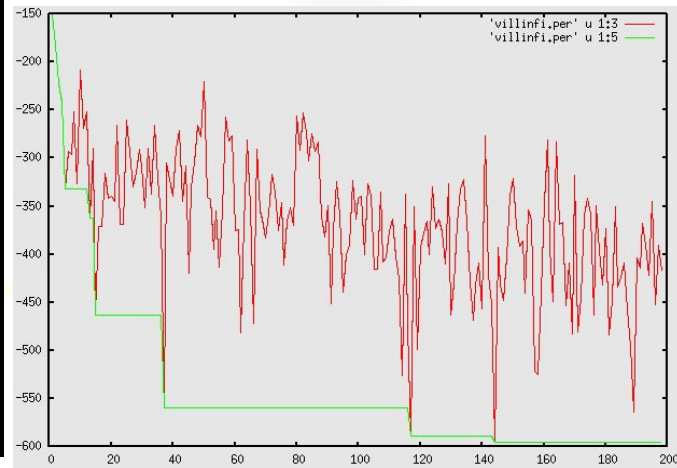
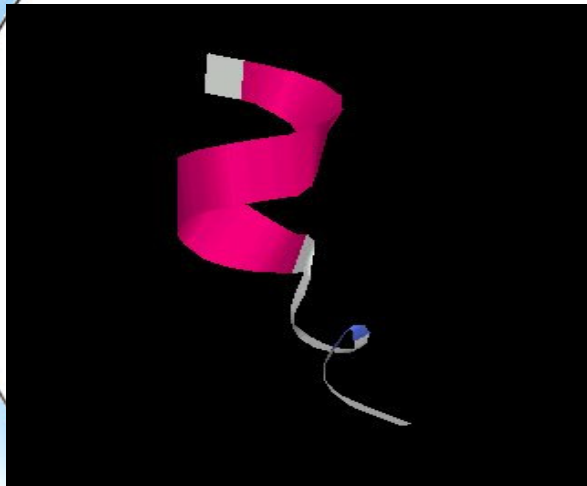
Results from second part

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Time: 00:22:09
19:15 + 2:54

Results from third part



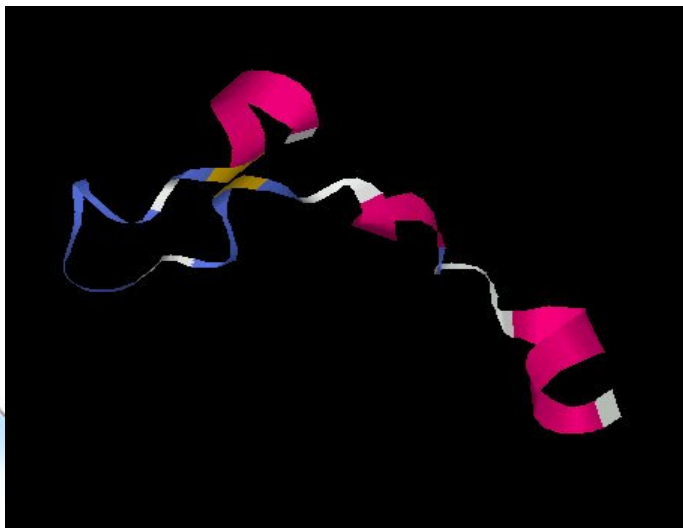
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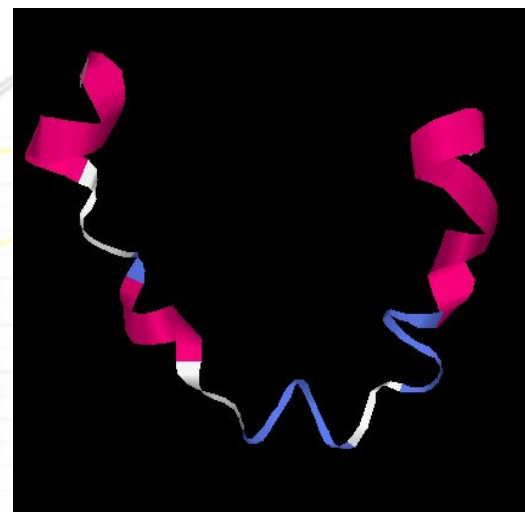
Time: 00:20:12
12:28 + 7:44

Result of the final MC program

Time : 00:05:12
1:50 + 3:22



After 5000 MC
steps

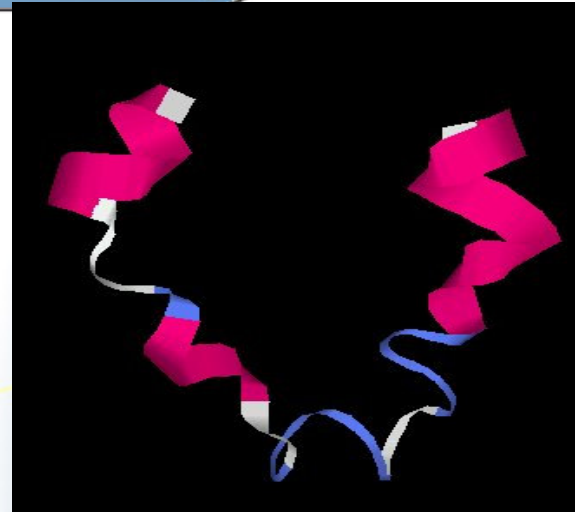


Experimental result

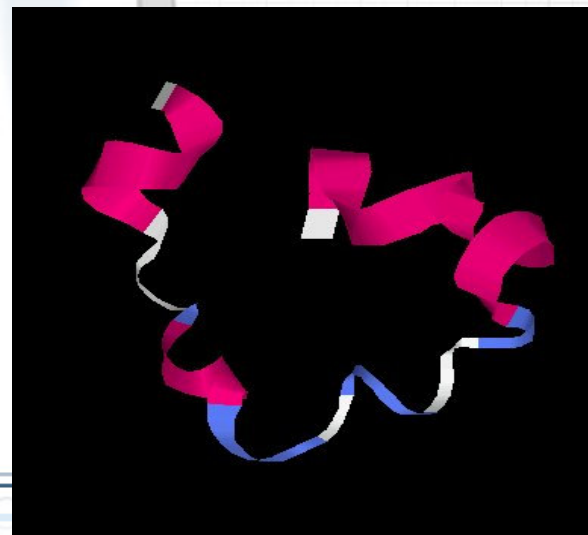


Time: 00:15:37
11:56 + 03:41

Predicted result

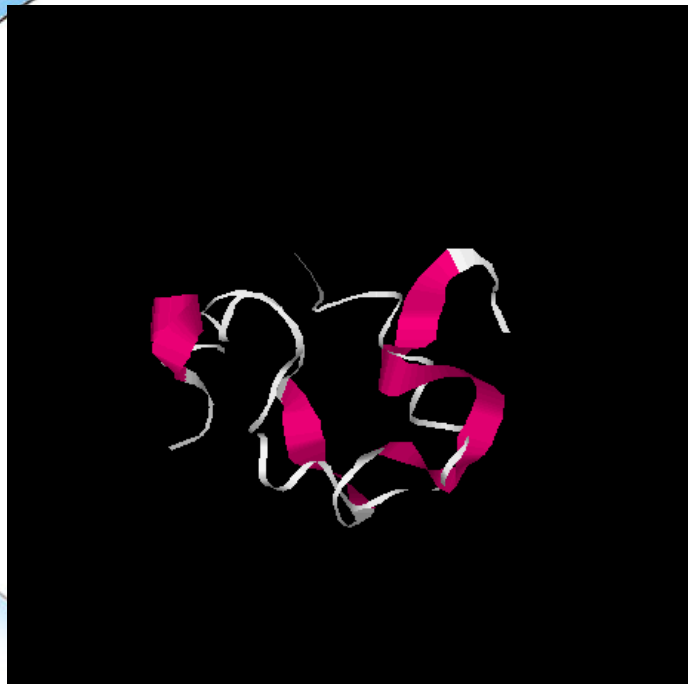


Single AA
junction

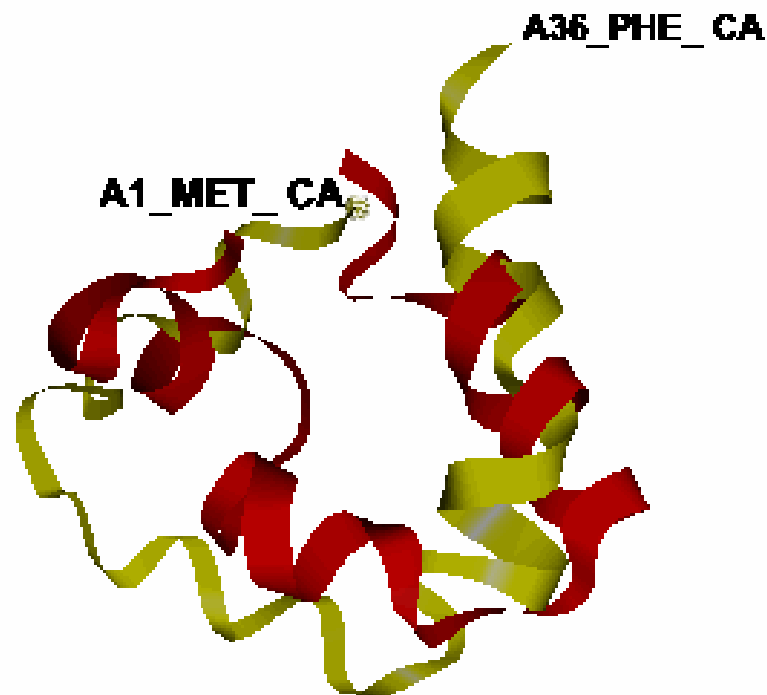


Three AA
junction

Divide & Construct method : Villin head piece



simple optimisation



Main Chain atoms aligned RMSD: 7.0900
All atoms aligned RMSD: 8.7340

Divide & Construct

What to do with Grids?

- Sequential application any where any time
- Multiple runs of applications (Monte Carlo type)
- Multiple simulations (N-body type)
- Distributed algorithms with minimal communication
- Parallel algorithms preferably on a specific cluster (but, any where)
- More effective utilisation of resources
- More effective web-services

What not to do with Grids ?

- Frequently communicating parallel codes
- A flow that has interdependencies among jobs

Bart Jacob (<http://www-128.ibm.com/developerworks/grid/library/gr-design.html>)

Conclusion

- GA converged to energies which are lower than that for the experimentally determined structure
- Major problem lies with the fitness since there are no clues to know about the native structures from the single force field function
- These methods are also highly applicable to other application areas as well