Contact curve based simulation of side chains from two amino acids in a protein molecule

SANGHUN JEONG, KU-JIN KIM
SCHOOL OF COMPUTER SCIENCE AND ENGINEERING

KYUNGPOOK NATIONAL UNIVERSITY, KOREA

Motivation

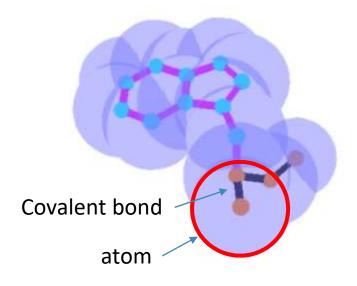
- Protein molecules have flexibility
- Simulating flexible molecules requires heavy computation efforts
- Efficient simulating method is needed
- We propose an efficient simulation method based on contact curve computation

Problem Definition

- Find a method to efficiently simulate two flexible amino acids
- Assumption
 - Fixed main chain and rotating side chains
 - Often used method for simplifying flexibility

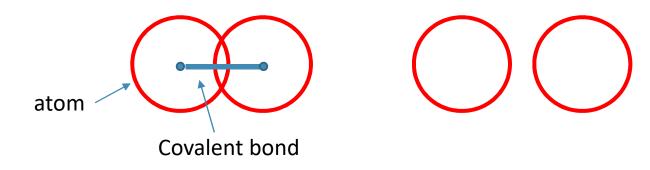
Preliminaries (1)

- A protein is composed of amino acids
- Amino acids are composed of atoms
- Each atom can be represented as van der Waals spheres
- Only covalent bonded atoms have sphere intersections

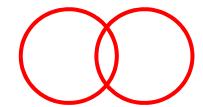


Preliminaries (2)

No collision cases

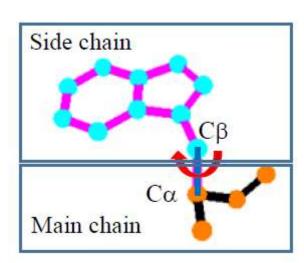


Collision case

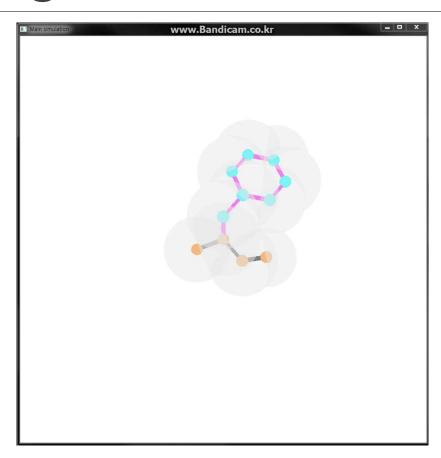


Preliminaries (3)

- An amino acid has two parts
 - Main chain
 - Side chain
- Main chain is fixed
- $^{\circ}$ Side chain rotates along the axis containing centers of C α and C β

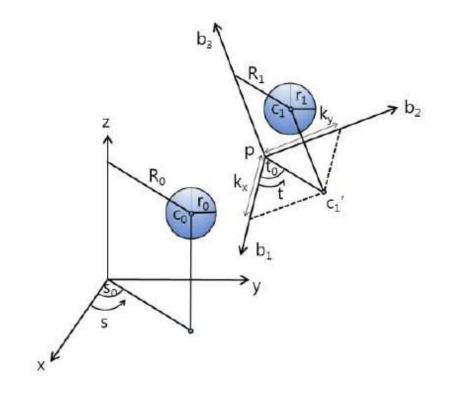


<Rotating side chain animation>



Collision region for two spheres(1)

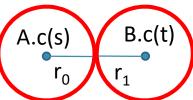
- Center location of rotating spheres A and B
 - A.c(s) = $(R_0 \cos (s + s_0), R_0 \sin (s + s_0), z_0)$
 - B.c(t) = \mathbf{p} + R₁ cos (t + t₀) \mathbf{b}_1 + R₁ sin (t + t₀) \mathbf{b}_2 + ||c₁ - c₁'|| \mathbf{b}_3



Collision region for two spheres(2)

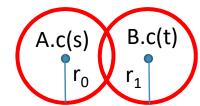
Case 1: Two spheres at (s*, t*) tangentially contact each other

$$| | A.c(s^*) - B.c(t^*) | |^2 = (r_0 + r_1)^2$$



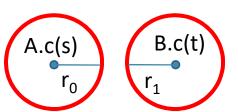
Case 2: Two spheres at (s*, t*) have an intersection each other

$$| |A.c(s^*) - B.c(t^*) | |^2 < (r_0 + r_1)^2$$

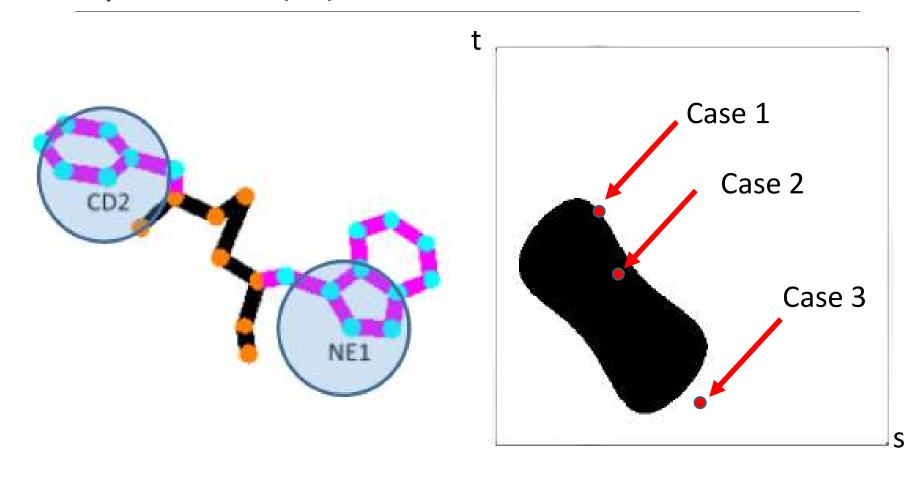


Case 3: Two spheres at (s*, t*) are apart

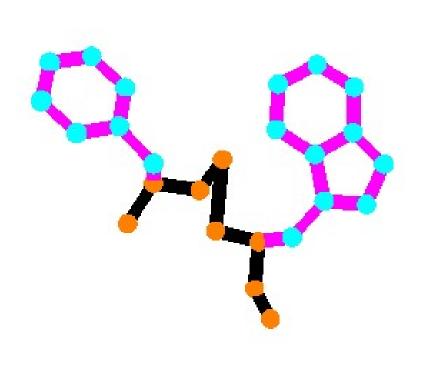
$$| |A.c(s^*) - B.c(t^*) | |^2 > (r_0 + r_1)^2$$

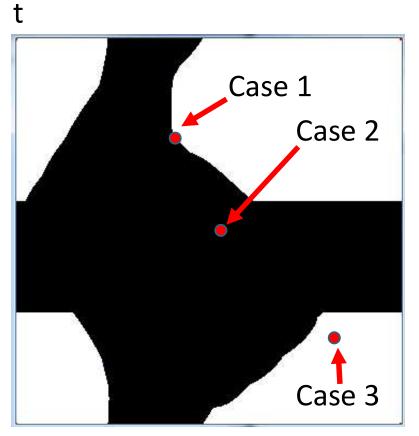


Collision region for two spheres(3)



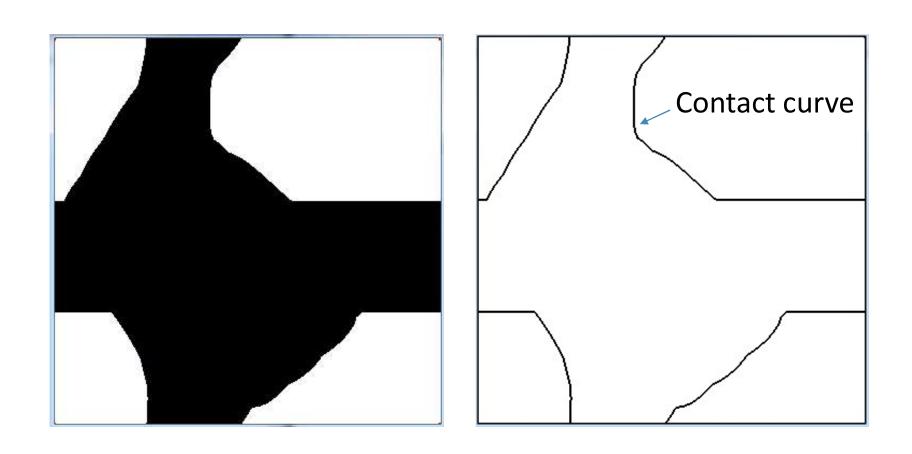
Contact curve for two amino acids (1)



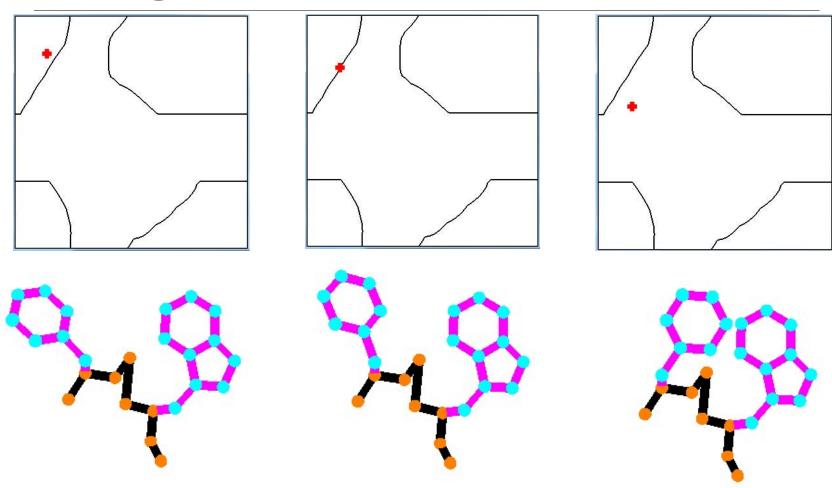


S

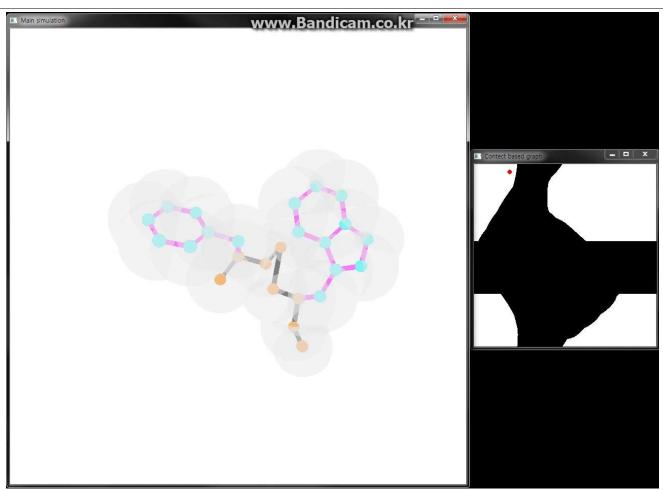
Contact curve for two amino acids (2)



Simulation along contact curve (1)



Simulation along contact curve (2)



Conclusion

- Analysis of contact configuration of two amino acids
- Computation of the contact curve
- Simulation based on the contact curve

Thank you

tkdgns3042@naver.com