EROS-DOCK and EROS-DOCK MULTI-BODY Approach
Maria-Elisa Ruiz-Echartea, Isaure Chauvot de Beauchêne, David Ritchie

To cite this version:
Maria-Elisa Ruiz-Echartea, Isaure Chauvot de Beauchêne, David Ritchie. EROS-DOCK and EROS-DOCK MULTI-BODY Approach. CAPRI evaluation meeting, Apr 2019, Hinxton, United Kingdom. hal-02394484

HAL Id: hal-02394484
https://hal.science/hal-02394484
Submitted on 1 Sep 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L’archive ouverte pluridisciplinaire HAL, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d’enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.
EROS-DOCK
Exhaustive Protein-Protein Docking Using Branch-and-Bounds Rotational Search

Maria Elisa Ruiz Echartea
Phd Student at LORIA, Nancy, Fr.

Advisors: Isaure Chauvat de Beauchene and David W. Ritchie
Rigid Body Protein Docking Problem

- Involves sampling and scoring.
- 6 degrees of freedom.
- Docking remains as a challenging problem.
Protein Docking Using Fast Fourier Transforms

• Conventional approaches digitise proteins into 3D Cartesian grids...

• ...and use FFTs to calculate TRANSLATIONAL correlations:

BUT for docking, have to REPEAT for many rotations.
Multiple Starting Positions and Minimizations

- Atomistic or "coarse-grained" (CG) representations.
- Monte-Carlo or gradient-based techniques to search local energy minima.
A New Search Algorithm: EROS-DOCK

- The space 3D Euler angle rotations represented by a quaternion \(\pi\)-ball.
- Used previously for shape registration.
- Never used before for docking.

Defining Initial Docking Contact Poses

\textbf{Complex} \quad \begin{array}{l|c|c}
\text{Bound} & \text{Unbound} \\
\hline
\text{d/Å} & \% \text{ of} & \% \text{ of} \\
& \text{Complexes} & \text{Complexes} \\
\hline
<0.10 & 93 & 86 \\
<0.23 & 100 & 98 \\
\end{array}

• Repeat for each pair...
• Ready to look for “clash rotations”...
Branch and Bounds Search using Bead Cone Angles

- Build a list of all possible “clash cone angles”.
- Repeat for each pair ...

If $|R_a - L_b| > \sigma_{ab}$ then

$a$ and $b$ will never clash, else

$a$ and $b$ will clash.
If $\omega > \beta_{ab} + \Delta_s$ s will never clash, else s will clash.
Using the Quaternion $\pi$-Ball

- Series of sample rotations dividing the $\pi$-ball into 8 cubes.
- The sample rotations represented as nodes in a 3D “search tree” data structure.
- Angular resolution 7.5 degrees.

One Space
8 sub-spaces
8^2 sub-spaces
8^n sub-spaces

Root
$D_0 = 2\pi$

Level 1
$D_1 = \frac{2\pi}{2}$

Level 2
$D_2 = \frac{2\pi}{2^2}$

Level n
$D_n = \frac{2\pi}{2^n}$
Coloring the Search Tree and Computation of Energies

- First walk to identify spaces that lead to clash.
- Second walk to compute energies.

On average 94% of the $\pi$-ball search space is pruned
- Only 6% of orientations are used to compute energies.
Comparing EROS-DOCK With ATTRACT and ZDOCK

- 173 Docking Benchmark 4 target complexes.

- EROS-MIN uses ATTRACT minimizations for a fair comparison.
EROS Multibody Docking
The Approach

- All pairwise solutions.
- Combinatorial problem.
- Fast RMSD computational methods.

The rank is not the best yet but . . .
• The algorithm is working correctly.
Perspective

- The use of distance restraints to drive the docking.
- Improvement of the rank of good quality solutions of EROS-DOCK pairwise and multibody.
- Extend EROS-MULTIBODY to deal with a greater number of proteins.
- The use of other force fields.
thank you