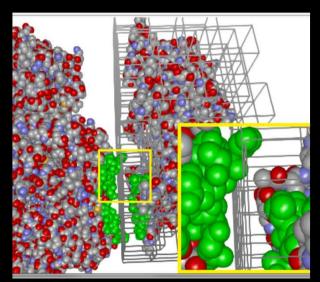
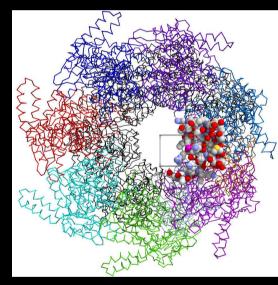
HaptiMOL: Interacting with large biomolecules using haptic feedback









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What are the benefits of using a haptic device to interact with proteins?



- Interact with three dimensional objects in 3D.
- Feel objects as the haptic probe interacts with virtual models.
- Apply forces to objects by pushing or pulling them.
- Obtain more insight into the three dimensional form of protein structure.
- Feel interaction forces during molecular docking



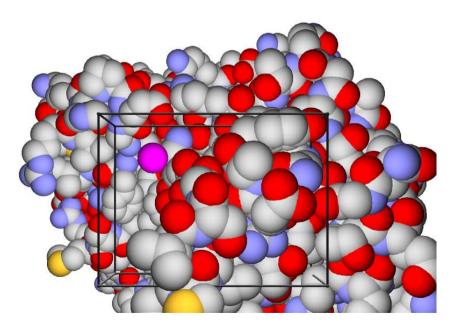




iSAS: Interactive Solvent Accessible Surface

To appreciate the 3D shape one can roll a sphere over the surface of complex structures.

The molecules are represented in space-filling mode and are rigid.



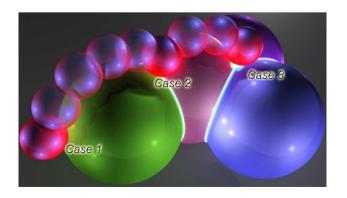
iSAS: Interactive Solvent Accessible Surface

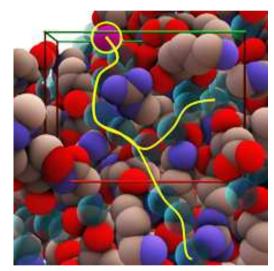


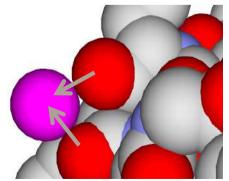
By guiding a sphere approximating a water molecule one can determine the solvent accessible surface.

The yellow lines indicate a set of crystallographic water molecules (ghost water) that you can see but not feel.

We developed a new haptic rendering algorithm for hard-sphere contacts.

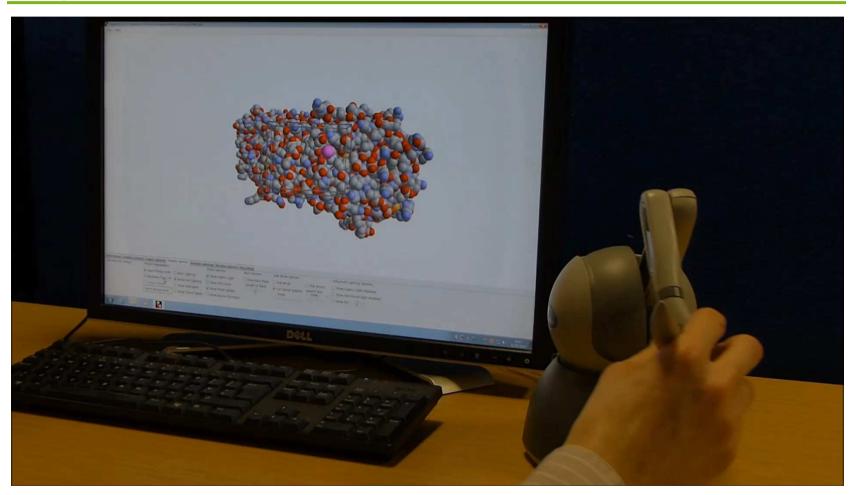








HaptiMOL iSAS

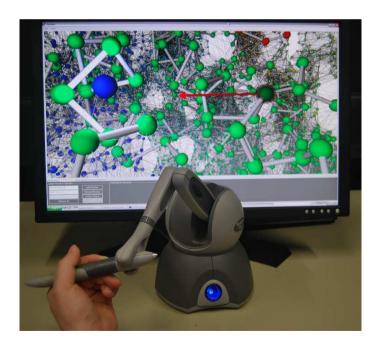


http://www.haptimol.co.uk/movies/isas_v3.wmv



Elastic Network Models

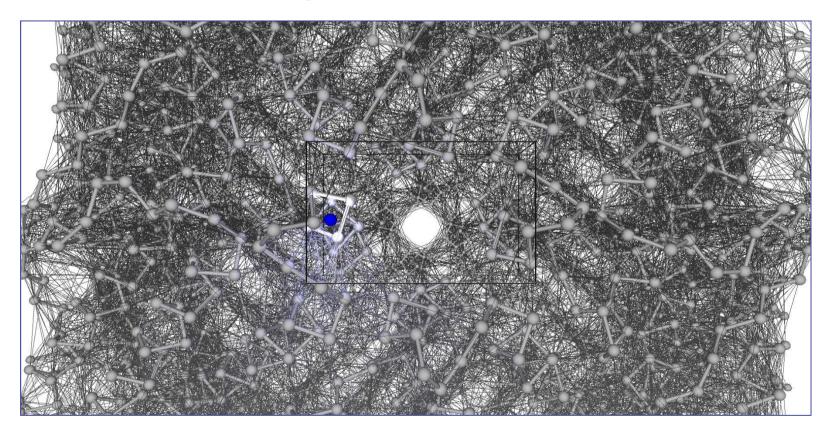
- HaptiMOL ENM enables users to apply forces to atoms in an elastic network model and to observe the resulting deformation.
- The user can apply forces to individual C_{α} atoms on the backbone by selecting them with the haptic device.





Elastic Network Models

 HaptiMOL ENM enables users to visualise the connections forming the elastic network.



Friday, 04 December 2015 www.uea.ac.uk/cmp



HaptiMOL ENM



http://www.haptimol.co.uk/movies/enmv1_movie.wmv

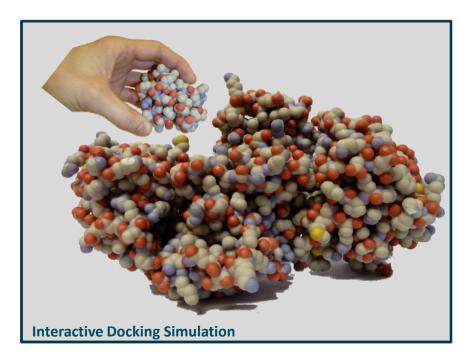


Haptic-Based Molecular Docking

- Aim: To create an immersive virtual docking environment.
 - The user interacts with the virtual molecules
 - The user senses the interaction forces
 - Can guide the molecules to their binding pose via a knowledge-guided search and selection







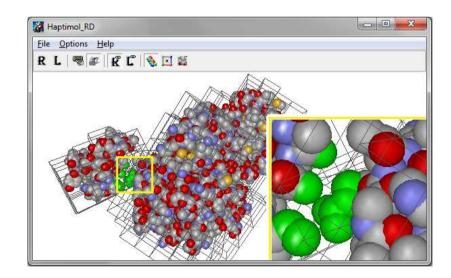
University of East Anglia

Main Issues

- Compute forces in real time, within 2ms
- Accommodate large molecules
- Support molecular flexibility

$$\vec{F}_{Tot} = \sum_{i}^{N} \sum_{j}^{M} \left[12 \frac{A_{ij}}{r_{ij}^{13}} - 6 \frac{B_{ij}}{r_{ij}^{7}} + \frac{q_{i}q_{j}}{4\pi\varepsilon\varepsilon_{0}r_{ij}^{2}} \right] \vec{\hat{r}}_{ij}$$

We investigate Spatial Partitioning approaches on the CPU and GPU to compute the interaction pairs within a cut-off distance.





HaptiMOL RD

CPU mode

- Rigid Docking for molecules up to 7000 atoms each
- Potential support for flexible docking for molecules up to 1400 atoms each

GPU mode

- Rigid docking for molecules comprising more than 200,000 atoms each
- Potential support for flexible docking with
 - RECEPTOR comprising more than 200,000 atoms
 - LIGAND comprising up to 3400 atoms (regular grid)





HaptiMOL RD

HaptiMOL RD Rigid Molecular Docking

http://www.haptimol.co.uk/movies/rd.wmv



References

- Iakovou, G., Hayward, S. and Laycock, S.D., "Adaptive GPU-accelerated force calculation for interactive rigid molecular docking using haptics", Journal of Molecular Graphics and Modelling, 2015.
- Iakovou, G., Hayward, S. and Laycock, S.D., "A real-time proximity querying algorithm for haptic-based molecular docking", Faraday Discussion 169, 2014.
- Stocks, M.B., Laycock, S.D. and Hayward, S., "Applying forces to elastic network models of large biomolecules using a haptic feedback device", Journal of Computer-Aided Molecular Design, 2011.
- Laycock, S.D., Stocks, M.B. and Hayward, S., "Navigation and exploration of large data-sets using a haptic feedback device", ACM Siggraph: Posters, 2010.
- Stocks, M.B., Hayward, S. and Laycock, S.D., "Interacting with the biomolecular solvent accessible surface via a haptic feedback device", BMC Structural Biology, 9:69, 2009.