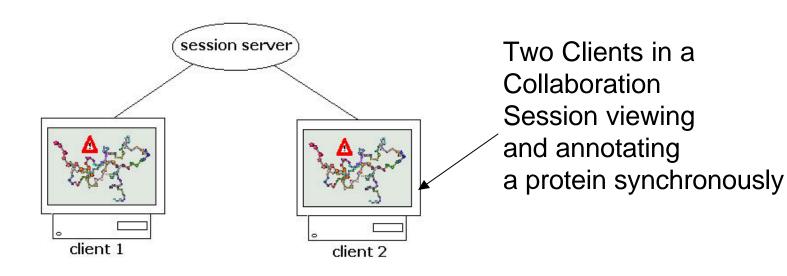
A Distributed Protein Visualization Application

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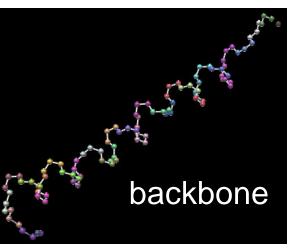
<u>OVERVIEW</u>

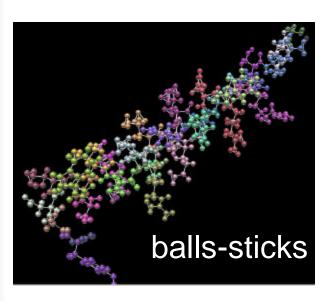
- A distributed protein visualization environment supporting collaboration by:
 - Sharing Views
 - Annotation Mechanisms
 - Sticky Notes

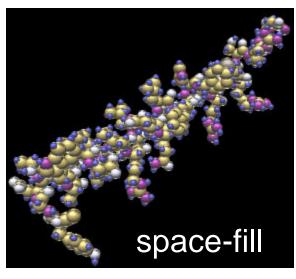


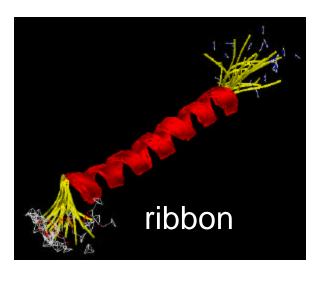
VISUALIZATION

Currently supporting four 3D model types

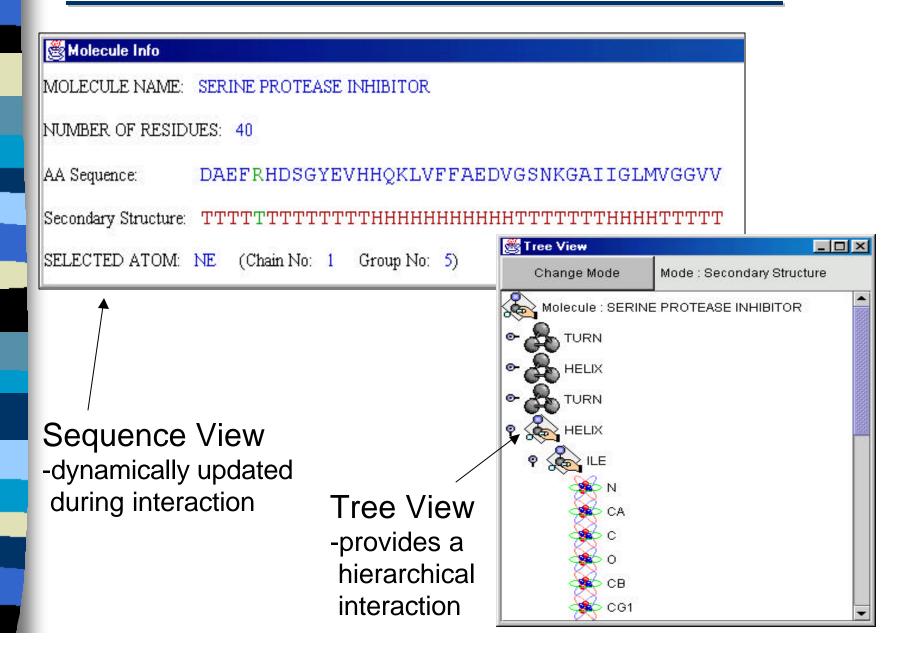








INFORMATION WINDOWS



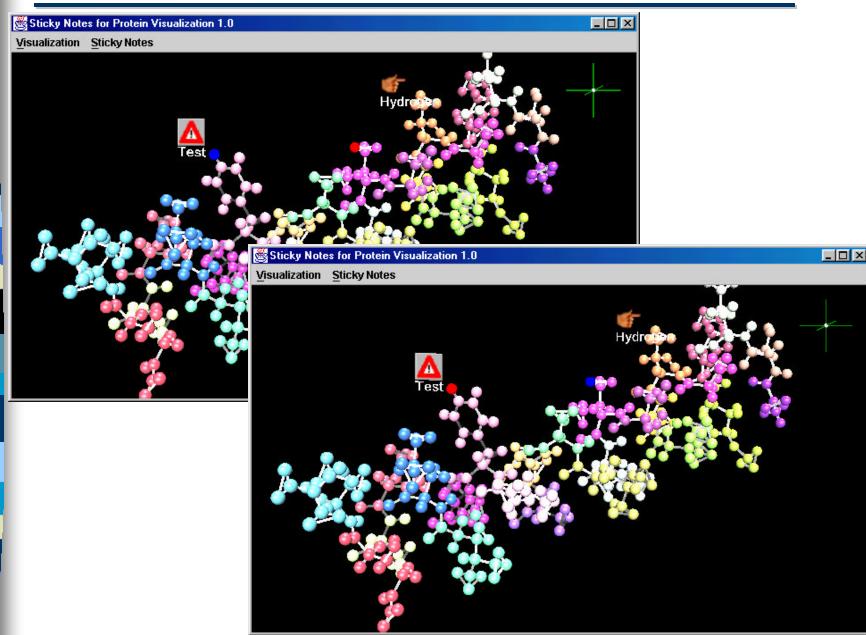
COLLABORATION

- Sharing the views
 - The 3D view of the molecule is synchronized among users.
 - Two modes exist:
 - Master-Slave: only one user is allowed to change the view. Useful for education purposes
 - Peer-peer: Any user can change the view. A Basic Locking Mechanism is implemented
- Sticky Notes
 - They provide a mechanism for annotating parts of interest

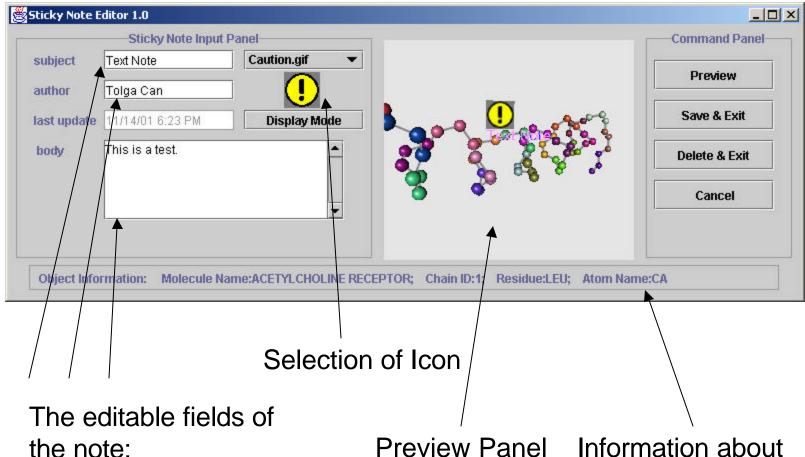
STICKY NOTES

- Annotations that attach to the underlying 3D model
- Different types of notes
 - Basic Notes (Contain Information)
 - Text Notes
 - Audio Notes
 - Advanced Notes (Perform Actions)
 - Action Notes
 - Active Notes
- Situation Awareness (Adapt to environment)
 - Adapt size so that they are always seen easily by the user
 - Adapt orientation so that they are always oriented towards the user
 - Selection of fields for display (title, author, icon, etc.)

A SNAPSHOT OF A SESSION



STICKY NOTES INTERFACE



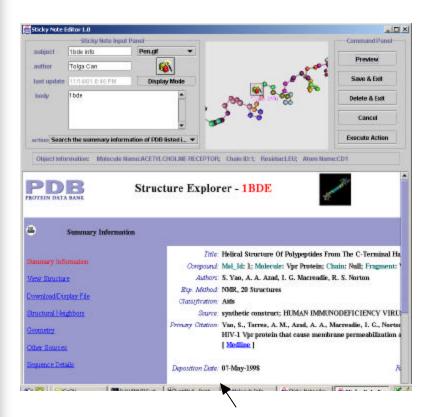
- subject
- author
- body

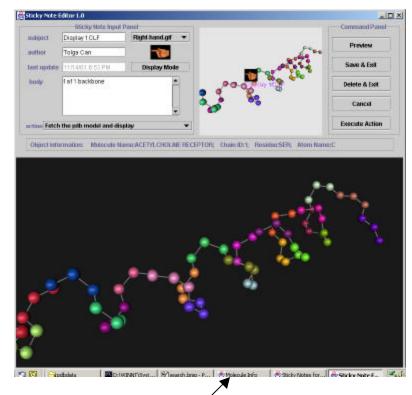
Preview Panel Information about the associated object is stored with

the note

ACTION NOTES

- Notes capable of performing actions
 - Change view point, execute an external program, etc.



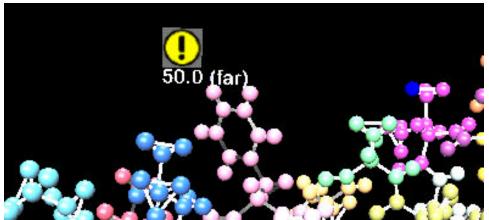


Search PDB information in PDB site

Search for another molecule and display it

ACTIVE NOTES

- Notes that monitor the environment for triggering conditions,
 - e.g. a note calculating the distance between the model and the view point



- Difference between action notes:
 - They are not user initiated, they are activated by certain environmental changes.

FUTURE WORK

- Add new 3D model types
 - Electron density map
 - Solid surface representation
- Collaborative Protein Modeling
 - Incorporating a protein folding algorithm to enable modeling a protein molecule from scratch or modifying existing proteins
- Notes Management
 - A better note browsing mechanism
 - Supporting user access rights