The Spoken Tutorial project

- Self explanatory - uses simple language

- Audio-video - uses multisensory approach

- Small duration - has better retention

- Learner-centered - learn at your own pace

- Learning by doing - learn and practice simultaneously

- Empowerment - learn a new program.

Target Group

- College teachers and students

- Research scholars

- Community at large

Workshops

The Spoken Tutorial Project Team conducts workshops on UCSF Chimera and other FOSS using Spoken Tutorials and gives certificates to those who pass an online test.

For more details, please write to
contact@spoken-tutorial.org

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Spoken Tutorials

UCSF Chimera

http://spoken-tutorial.org

Introduction

- UCSF Chimera is a program for interactive visualization and analysis of molecular structures and related data.

- It is developed by Resource for Biocomputing, Visualization and Informatics at the University of California, San Francisco.

- UCSF Chimera is a free program.

- It runs on Windows, Mac OSX and Linux operating systems.

- It is implemented in Python, with certain features coded in C++ for efficiency.

- For download and installation visit www.cgl.ucsf.edu/chimera/download.html
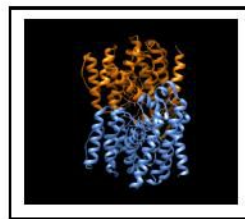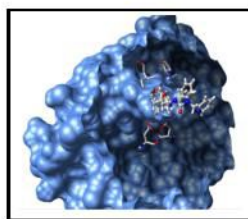
Features of UCSF Chimera

- UCSF Chimera has a powerful command line through which we can open molecules, change display, change color of residues, label atoms and remove solvent molecules.

- More than one structure can be opened on the Chimera window.

- Chimera was designed with extensibility and programmability in mind.

- Using Chimera, one can generate high-quality images and animations.

- Chimera can read molecular structures and associated data in a large number of formats.

- Images can be saved in file formats like png, jpeg, ppm, tiff, ps.

- It can directly load macromolecules from pdb website.

- More information is available at the given link.http://www.cgl.ucsf.edu/chimera

Human OX2 orexin receptor with suvorexant

DNA and Netropsin
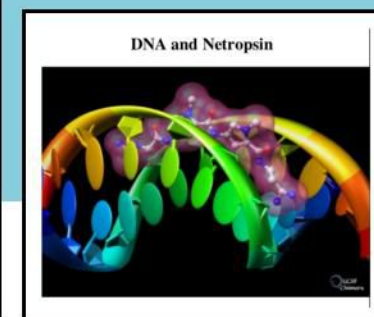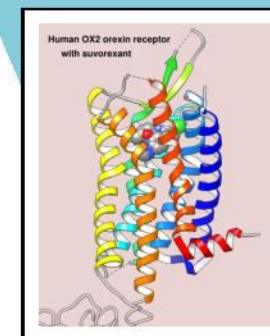
Uses of UCSF Chimera

- Ribbon structures can be loaded coloured according to the secondary structure element, i.e. strand, helix or loop.

- Display of atoms and bonds can be changed using command line.

- It can calculate and display hydrogen bonds between selected atoms.

- Molecular surface of the proteins can be shown.

- It can measure non-polar interactions in between selected atoms.

- It can superimpose structures to compare different proteins.

- It can be used in class room teaching and presentations.