Visualizing and interpreting macromolecular structural models

| Time | Topic |
|---|---|
| 9:00 am – 9:15 am | • Introduction |
| | ○ What do we expect to learn from a structure? |
| | ○ How can a non-structural biologist use a structure effectively? |
| 9:15 - 9:45 | • Open access structures: The Protein Data Bank |
| | ○ What is the PDB? |
| | ○ How to navigate the PDB. |
| | ○ Structure information worth checking. |
| | ○ How to visualize structures in the browser. |
| | ○ Where to download coordinates and maps. |
| 9:45 – 10:00 | • Tools overview |
| | ○ PyMol |
| | ○ Chimera/ChimeraX |
| 10:00 – 10:45 | • PyMol hands on |
| | ○ Loading a structure. |
| | ○ Visualizing a structure. |
| | ○ Preloaded Tools: |
| | ▪ Measurements |
| | ▪ Mutagenesis |
| | ▪ Electrostatic potential maps |
| | ○ The command line. |
| | ○ Loading and visualizing maps |
| | ○ Preparing figure images. |
| 10:45 – 11:15 | • Chimera/ChimeraX hands on |
| | ○ Loading a structure. |
| | ○ Visualizing a structure. |
| | ○ The command line. |
| | ○ Loading and visualizing maps |
| | ○ Preparing figure images. |
| 11:15 – 12:00 | • AlphaFold |
| | ○ Using Google CoLab |
| | ○ Loading the structure |
| | ○ Deciding what to trust for experimental design. |
| 12:00-12:30 PM | • Lunch |
| 12:30-5PM | • Hands-on Guidance sessions (pre-registered participants) |