UCSF ChimeraX - II - Overview EM

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April 26, 2018

Contents

1 Workshop goal

In this second section we'll explore briefly electron density maps. This is usefulf for CryoEM data but also X-ray crystallography.

1.1 Learning objectives

- Open a density map
- display density
- color etc.
- Close and quit

2 Introduction

Some of the material presented here is inspired by a demonstration of **ChimeraX** by Tom Goddard (Programmer/Analyst, UCSF Resource for Biocomputing, Visualization, and Informatics) who develops the software. *YouTube* "Movie Making for cryoEM using ChimeraX."[1]

ChimeraX

Note: If you are left-handed inverting Left and Right assignments might work better for you.

Note:

`TASK`

This button will invite you to act on **suggested actions** as we go along the workshop.

[1] https://youtu.be/yOMKwCbXl0g

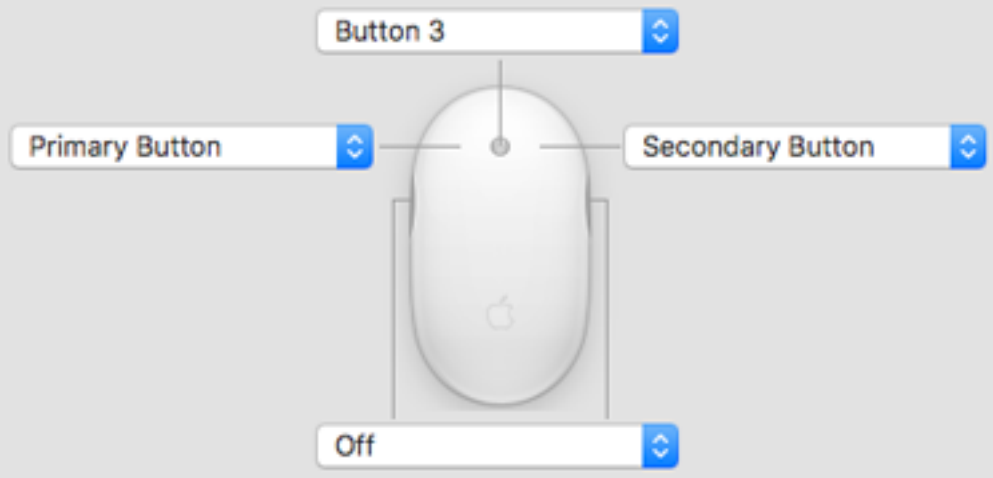

Figure 1: "***Verify mouse settings in System Preferences.***"

3 Density maps

In previous workshops we have only worked with atomic coordinates. Density maps are the primary result of experimental analysis of CryoEM and X-Ray crystallography that scientists use to build atomic coordinates if the *resolution* is adequate.

> A definition of *resolution*, in structure determinations, is the distance corresponding to the smallest observable feature: if two objects are closer than this distance, they appear as one combined blob rather than two separate objects[2] (see also embedded movie.)

4 REFERENCES

[2] http://proteopedia.org/wiki/index.php/Resolution