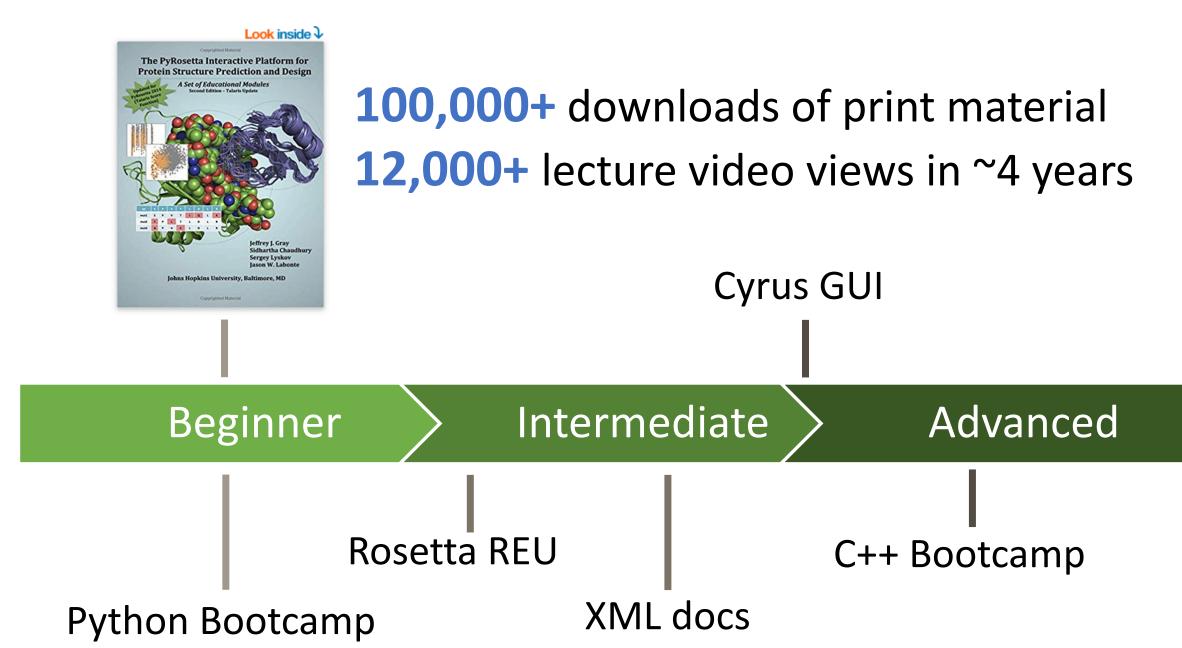


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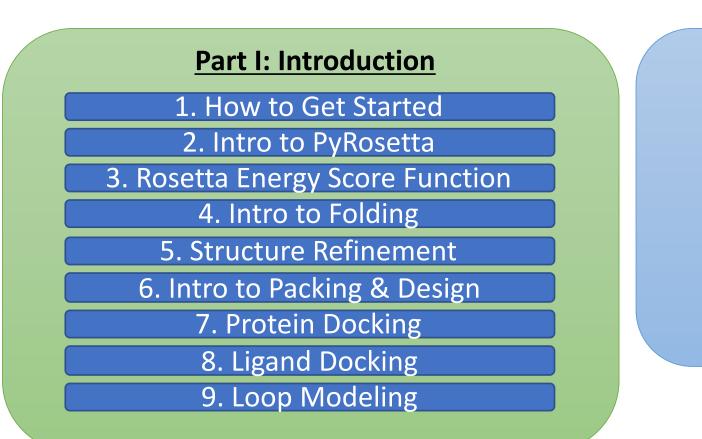
¹Johns Hopkins University, ²The Scripps Research Institute, ³University of California, Davis, ⁷University of North Carolina at Chapel Hill, ⁸Wistar Institute, ⁹Stanford University, ¹⁰Fox Chase Cancer Center, *Corresponding author: jgray@jhu.edu

Need for Interactive Teaching Material

Finding ways to train people in molecular modeling is a longstanding problem, but certain challenges remain.



Topics in The New Notebooks



Part II: Advanced

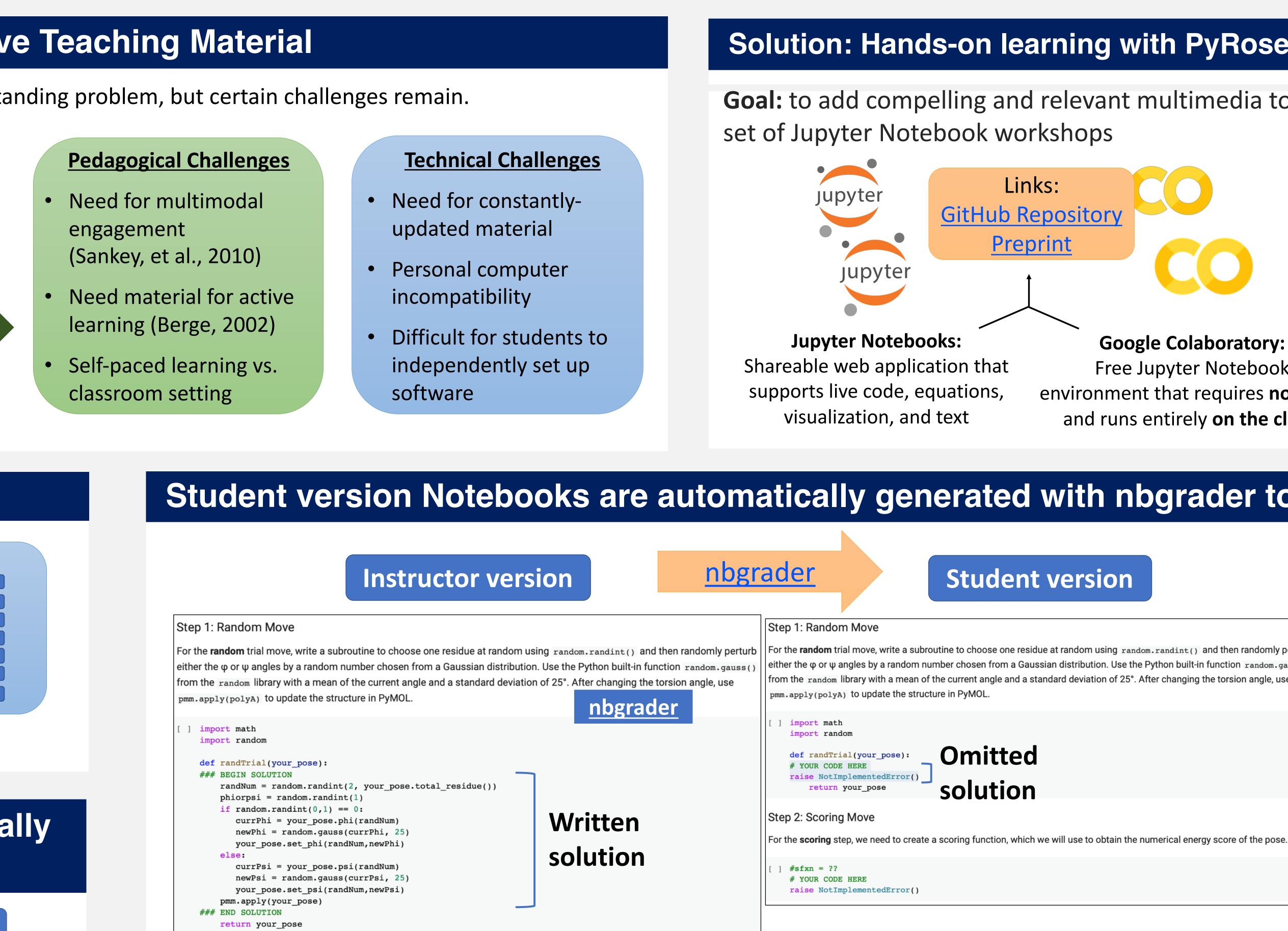
10. Working with Symmetry 11. Working with Density 12. Working with Antibodies 13. Carbohydrates 14. RNA Basics 15. Membrane Modeling

16. Running PyRosetta in Parallel

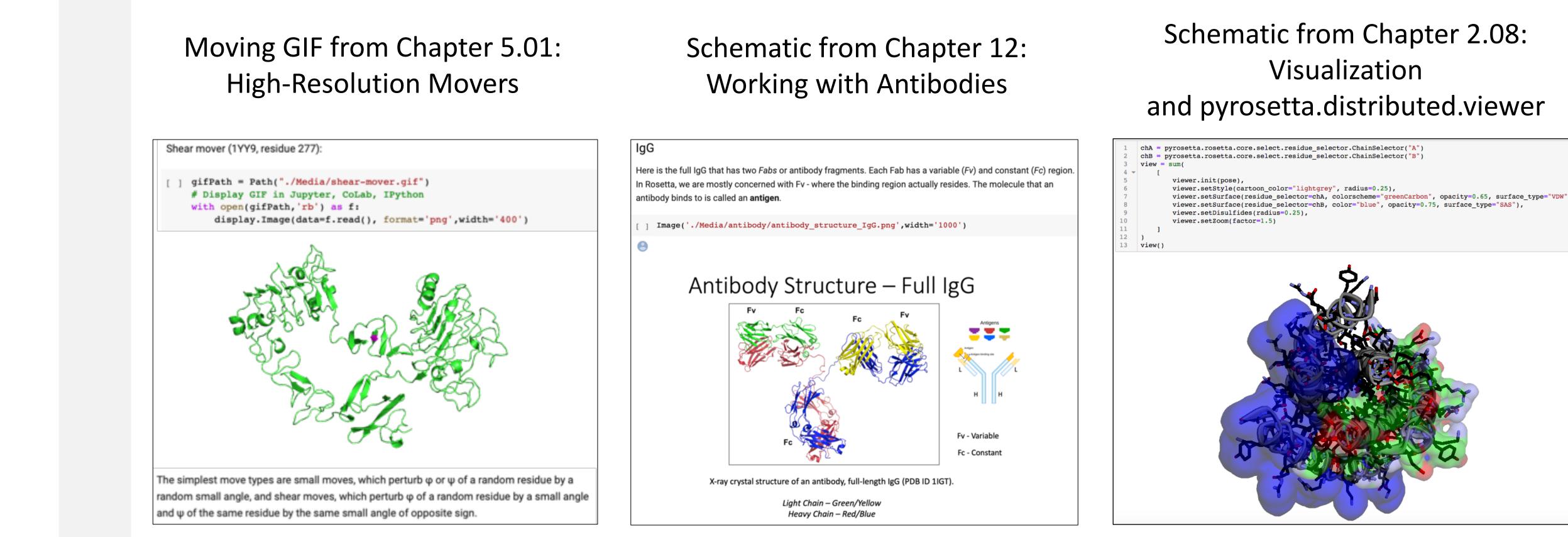
import random def randTrial(your_pose): ### BEGIN SOLUTION randNum = random.randint(2, your_pose.total_residue()) phiorpsi = random.randint(1 random.randint(0,1) == 0Keyword Index and ToC are automatically currPhi = your pose.phi(randNum) newPhi = random.gauss(currPhi, your pose.set phi(randNum,newPhi generated with nbpages tool currPsi = your pose.psi(randNum) newPsi = random.gauss(currPsi, 25 your pose.set psi(randNum, newPsi pmm.apply(your_pose) ### END SOLUTION return your_pose **ps**

<u>nbpages</u>	Jupyter Notebook Workshops
• Pose Basics Keywords: pose_from_pdb(), sequence(), cleanATOM, annotated_sequence() Keyword Index Table of Contents	
 ▲ index.ipynb ☆ File Edit View Insert Runtime Tools Help Code + Text 	
PyRosetta Keyword Index • aldose • aldose • RosettaCarbohydrates • AndResidueSelector • Protein Design 2 • angle_max() • High-Resolution Movers • annotated_sequence() • Pose Basics • Antibody • Working With Antibodies • assign() • Basic Folding Algorithm • asymmetric	PyRosetta Chapter 1.0 How to Get Started • Students • Instructors • Links • PyRosetta package 1.1 PyRosetta Google Drive Setup 1.2 PyRosetta Google Drive Usage Example 1.3 How to Get PyRosetta on Your Personal Computer • Download the main necessary packages to work locally on your machine • Python 3.6 (and preferably IPython for tab-completion) • PyMOL • PyRosetta-3.6.Release Chapter 2.0 Introduction to PyRosetta 2.1 Pose Basics • Loading in a PDB File ## • Exercise 1: Inspecting pose sequences

PyRosetta Jupyter Notebooks Teach Biomolecular Structure Prediction and Design



Multimedia examples in PyRosetta Notebooks





othe	 workshops in Google Colaboratory Download <u>PyRosetta package</u> and workshops from <u>GitHub Repository</u>. Follow instructions in Chapter 1 to configure
	 PyRosetta with Google Colaboratory (~12 min). Access PyRosetta Notebooks in Google Colaboratory:
	CO Comment Com
	E + Code + Text •••• Busy
	This notebook contains material from <u>PyRosetta</u> ; content is available <u>on Github</u> .
<	< <u>Introduction to PyRosetta Contents Index Working with Pose residues</u> > CO Open in Colab
o setup loud	- Pose Basics
loud	Keywords: pose_from_pdb(), sequence(), cleanATOM, annotated_sequence()
DOI	In this lab, we will get practice working with the Pose class in PyRosetta. We will load in a protein from a PDB files, use the Pose class to learn about the geometry of the protein, make changes to this geometry, and visualize the changes easily with PyMoL and PyRosetta's PyMoLMover. On the corresponding Pose lab found on the PyRosetta website, you will find various useful commands to interrogate poses; these may come in handy for the exercises. PyRosetta Installation: The following two lines will load in the PyRosetta library and load in database files. If this does not work, please notify the professor or the TA.
	<pre>[] SHOW CODE [] from pyrosetta import *</pre>
	init() <> ▼ What is a Pose?
	The Pose class includes various types of information that describe a structure. Some of the core components include the Energies, PDBInfo,
	and Conformation. See the Rosetta3 paper to learn more: <u>https://www.sciencedirect.com/science/article/pii/B9780123812704000196</u>
	✓ Loading in a PDB File
oerturb auss() Se	Protein Data Bank (PDB) is a text file format for describing 3D molecular structures and other information. Rosetta can read in PDB files and can output them as well. In addition to PDB, mmTF and mmClF are a couple other file formats that are used with Rosetta. We will spend some time today looking at the crystal structure for the protein PafA (PDB ID: 5tj3) using Pyrosetta. PafA is an alkaline phosphatase, which removes a phosphate group from a phosphate monoester. In this structure, a modified amino acid, phosphothreonine, is used to mimic the substrate in the active site. Let's load in this structure with PyRosetta (make sure that you have the PDB file located in your current directory): cd google_drive/My\ Drive/student=notebooks/ pose = pose_from_pdb("inputs/5tj3.pdb")
	Here we are inputting the PDB file using the pose_from_pdb method. However, we can also load this structure from the internet with pose_from_rcsb("5TJ3").
	<pre>[] ### BEGIN SOLUTION pose = pose_from_pdb("inputs/5tj3.pdb") ### END SOLUTION</pre>
2.	As an example for how to use a pose, let's look at the sequence of 5TJ3: pose.sequence()
	Summary
	 Hands-on learning with PyRosetta: 1. Google Drive-based Familiar to most students
	 No local machine setup necessary
	2. Adaptable for class or independent learning
	 Interactive exercises and multimedia Easily expandable by adding more notebooks
۲.	
ſ	Links:
	GitHub Repository
	Preprint

Acknowledgements

We would like to thank the JHU Center for Educational Resources, NIH, NSF, and Rosetta Commons for funding and support. We would also like to thank Jeffrey Kantor for his advice and insight.

