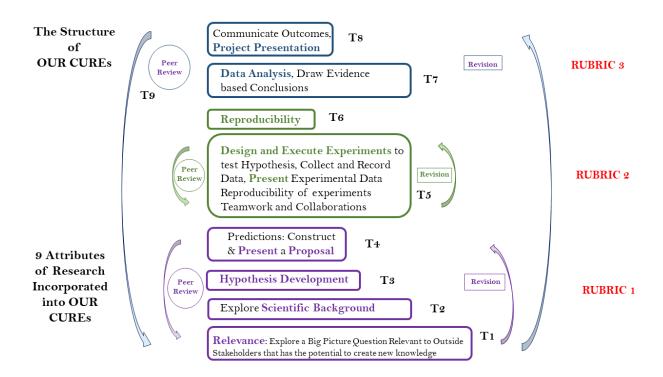
Modular CURE Generic Calendar



Week of	Pre-Lab	Activity	CURE Element
W1			Element
W2			
W3			
W4			
W5			
W6		P1: Introduction to the project, T1: Relevance, P2: PyMol and Molecular Visualization, T2 Scientific Background- Reading a paper, P3:Understanding the Model System-	Relevance, Scientific Background
W7		T3 Starting Hypothesis Development, Computational Approaches to Explore the model system The importance of record keeping:	Background and Hypothesis Development Presentation
W8		T3 continued: From Hypothesis to Prediction	Proposal Presentation

	T4: Proposal Development From Predictions to Experiments	Peer Review
W9	T5: Experimental Design and Execution : Project Related Experiments: control	Experiments and Data Analysis
W10	T5, T6 continued, Project Related Experiments- treatment situation Data Analysis and Reproducibility	Experiments and Data Analysis Reproducibilit
W11		
W12		
W13		
W14		
W15	T7, Data Analysis & Displaying Data T8, Final project presentations and discussion	Conclusions and Final Presentation Peer Review

Grading Elements in the Course are embedded throughout the Semester and consist of the following elements, aligned with the 9 essential elements of research incorporated into the course.

Relevance & Background	(presentation)	2.5%	
Hypothesis Development	(presentation)	5%	
Proposal	(presentation)	10%	Rubric 1
Experimental Design & Execution (Badges)			
Reproducibility (Lab	Record Keeping)	5%	
Data Analysis (Data Presentations)			Rubric 2
Final Project Presentation	5%		
Peer Review (of proposal and final presentation, revisions etc)			Rubric 3
NCI Foundational Concept	ts (Quizzes)	2.5%	Rubric 4

CURE Total 50%

Required Standard Labs 50%

Badges:

- Making up a Solution
 Checking Reagent Concentration
- 3. Preparing a Buffer
- 4. Titration Set up and Calculations
- 5. Measurement using TOTALS Approach

The TOTALS Approach The TOTALS Approach in Science

Try Something

Observe what happens

Think

Adjust and try again

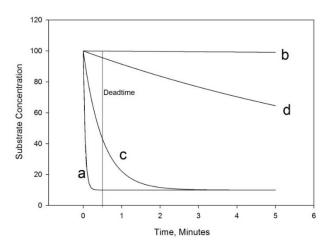
Leave Lab

Smiling and Satisfied

An Example: How do you decide how much enzyme to use? The TOTALS Approach:

When dealing with an enzyme where you do not know the specific activity, it is important to establish the correct amount of enzyme to use in assays. The trial and error approach is the only option you have. USE the **TOTALS** approach: make up your cuvette and for the first attempt at measuring the reaction, **Try some amount** (say 10µL of the enzyme solution you have) and **Observe** what happens..Then **Think**: measure the "rate"- there are three possible outcomes of this experiment.

Effects of "Deadtime" on an Assay



Too much was added (curve a or c), too little was added (curve b), or approximately the right amount was added, as shown in figure 1- curve d. After you have observed and thought about what the data told you, **Adjust** the amount of enzyme and repeat. If too much was added you can make a best guess as to how much too much from the shape of the resultant curve- if by the time you initiated the measurement the reaction was already at, or close to equilibrium (curve a) you added much too much and probably need to dilute the enzyme 50-100 fold.

If it was too much, but not way too much (curve c) maybe a 5-10 fold dilution will do. . If you added too little of the enzyme to get a reasonably measurable rate (curve b) you need to concentrate the enzyme, or simply add more volume of the enzyme until you get

reasonably measurable rate. If you added approximately the right amount the issue is whether or not it extrapolates back to the starting absorbance (usually about 0.6 in an MDH assay) at t = zero, in which case it is fine to continue with your experiment (curve d), or whether the enzyme needs some dilution- curve c- (by either adding a smaller volume- this depends upon how small a volume you are comfortable being able to add accurately, or by diluting maybe an additional 5-10 fold). At this point you can **Leave Lab Smiling**, knowing that you have established how much enzyme to use to get great initial rate data!