



# Incorporating Bioinformatics into the Undergraduate Genetics Curriculum through an Authentic Research Project

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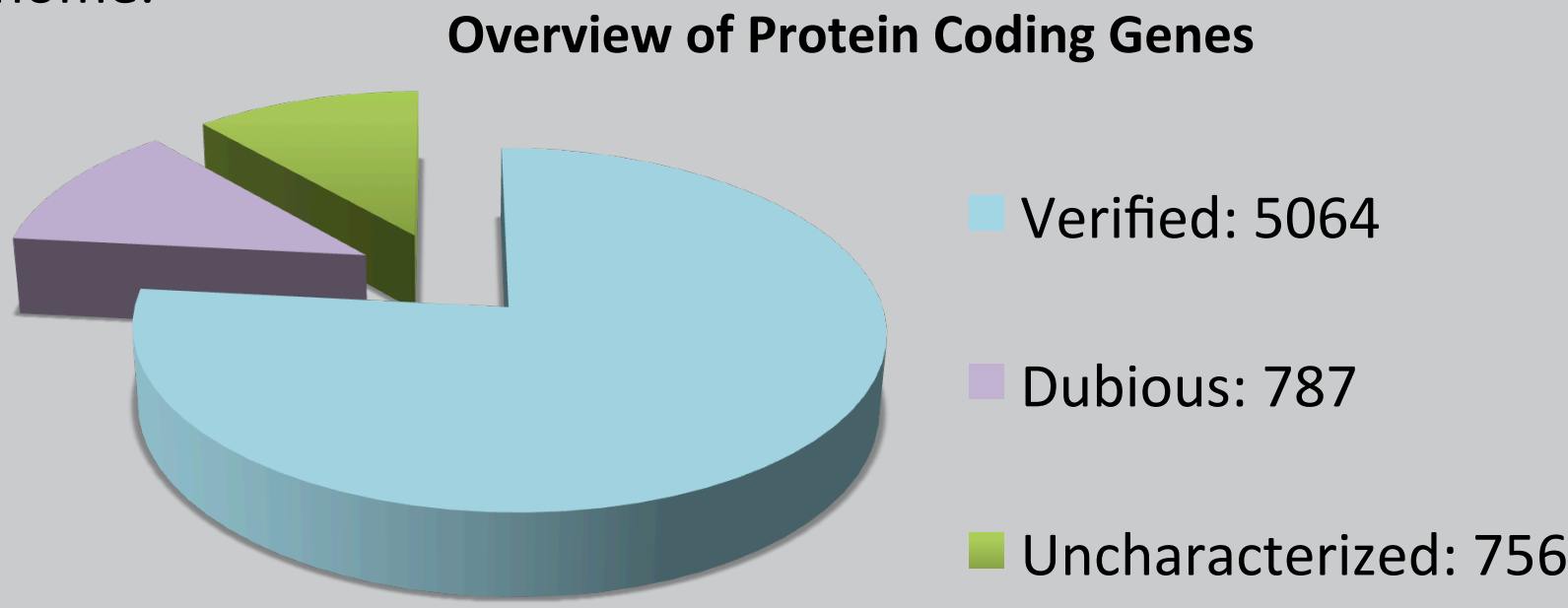


## Background

- Genomics and bioinformatics are advancing fields that are now an integral part of biological research.
- Learning current research methods and skills has many positive impacts on students (NRC 2003).
- Inquiry-based labs result in increased understanding (e.g. Lord and Orkiszewski 2006, Rissing and Cogan 2009).
- Bioinformatic and genomic approaches generate accessible and inexpensive research opportunities for undergraduates, since many of the necessary tools are online (e.g. Schaffer et al. 2010, Hingamp et al. 2008).
- Course-based research (authentic research carried out during a course rather than the apprentice model) are an ideal way to expose large numbers of students to “real science” while also increasing their knowledge of scientific concepts (Wei and Woodin 2011, AAAS 2012).
- During this course students investigate the role of *Saccharomyces cerevisiae* open reading frames designated as coding for ‘putative proteins’ within the *Saccharomyces* Genome Database.

## Bioinformatic Methods

- Students are randomly assigned a unique uncharacterized ORF from the *S. cerevisiae* genome.



- Bioinformatics analyses are conducted on individually assigned ORFs. They are setup as five modules (listed below) the students complete in- and outside of lab time. Written guides and videos help students navigate the websites and interpret data.

**Basic Information and Sequence-based Similarity**

- Obtain DNA and protein sequences
- BLAST
- Conserved domain database search

**Genetic and Physical Interactions**

- GeneMANIA
- SPELL

**Structure-based Evidence**

- TIGRFAM
- Pfam
- Protein Data Bank
- SUPERFAMILY
- SMART
- Multiple sequence alignment

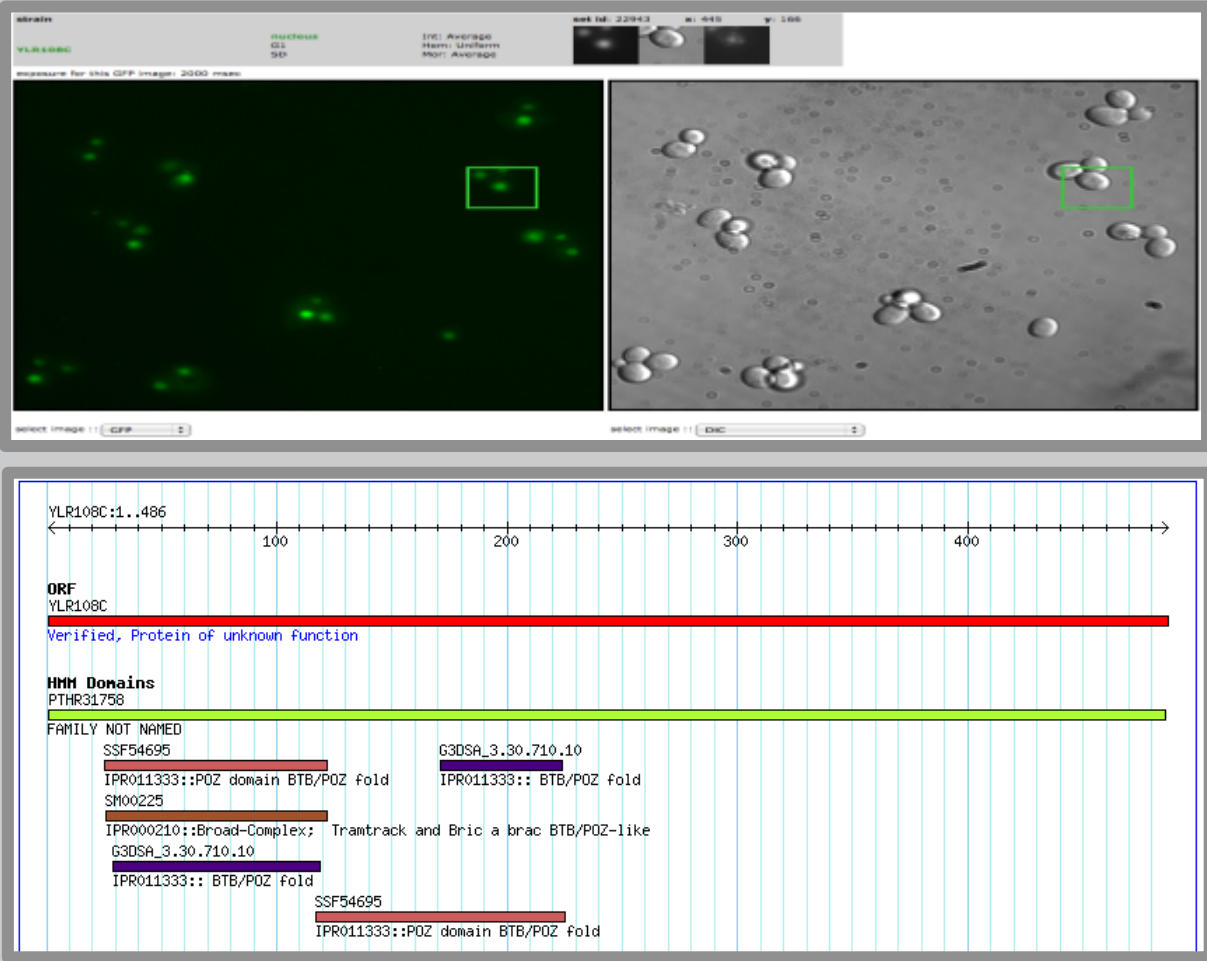
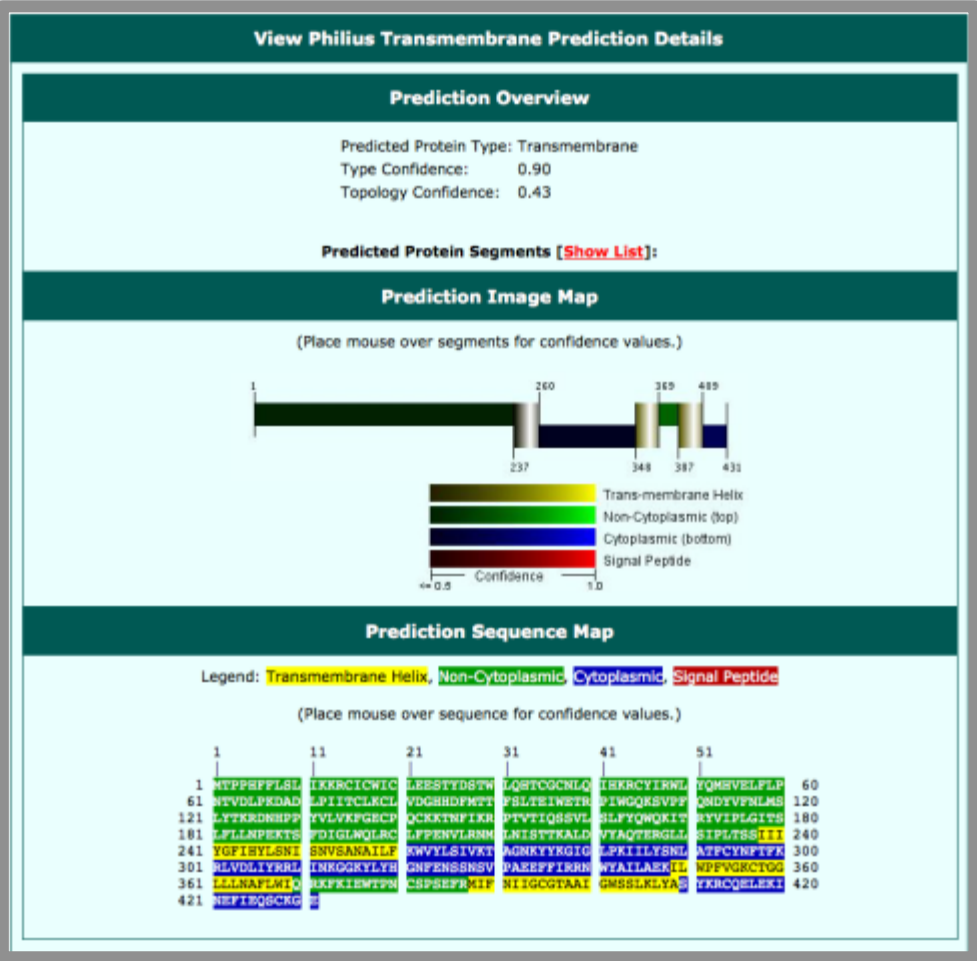
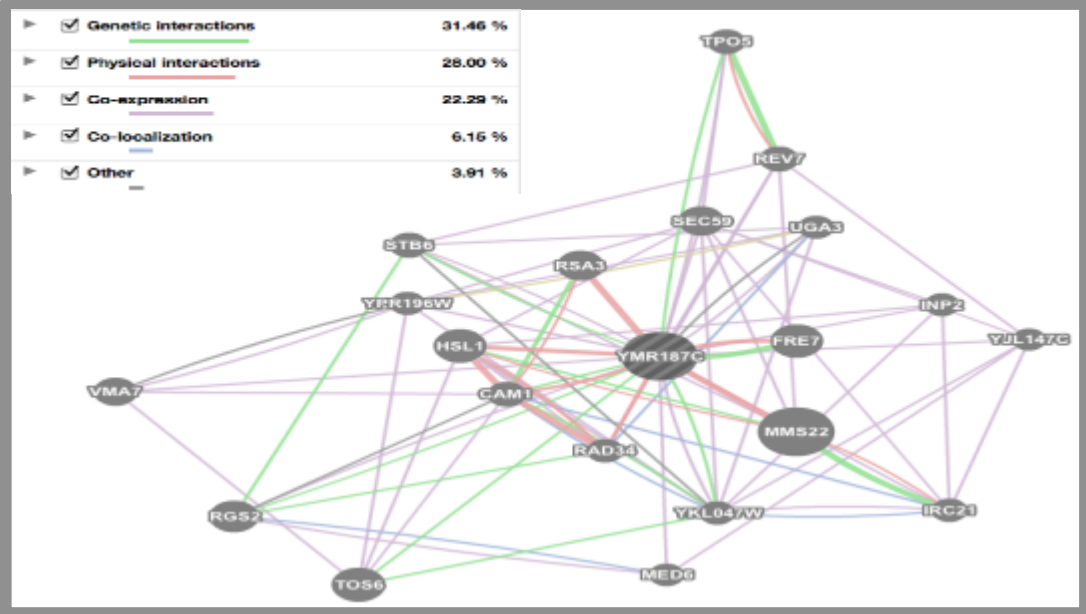
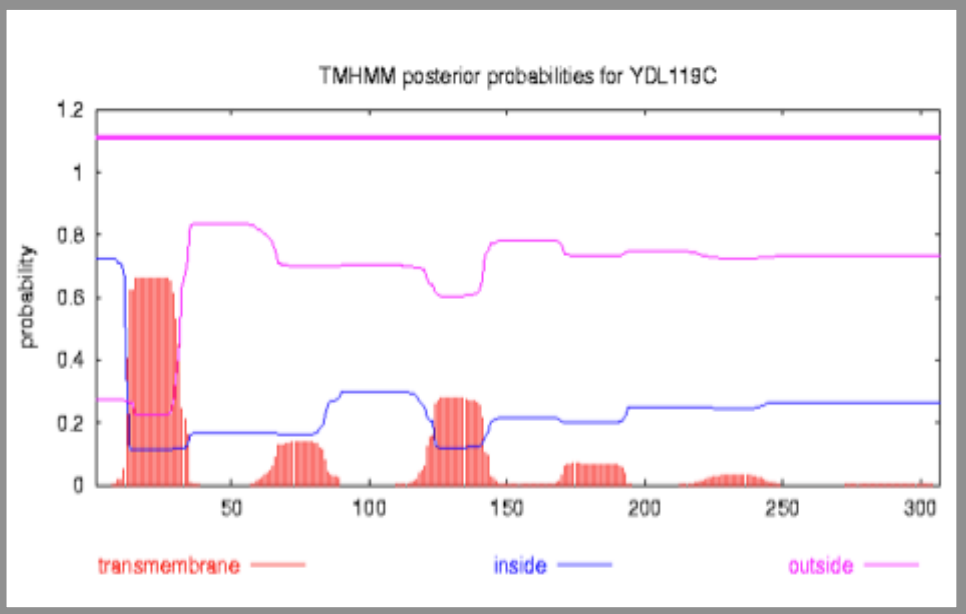
**Cellular Localization Data**

- Transmembrane helices hidden Markov models
- SignalP
- Philius
- TargetP
- NucPred
- Yeast Protein Localization Database

**Gene Deletion Phenotypes**

- PROPHECY
- Yeast Fitness Database

- Students submit module data online for instructor review.
- Structured group discussions regarding their data are held at two points during the semester. This allows students to compare results and interpretations, increasing their confidence.
- Primary literature articles are frequently referenced as unfamiliar enzymatic pathways, cellular processes, and/or assays are encountered.

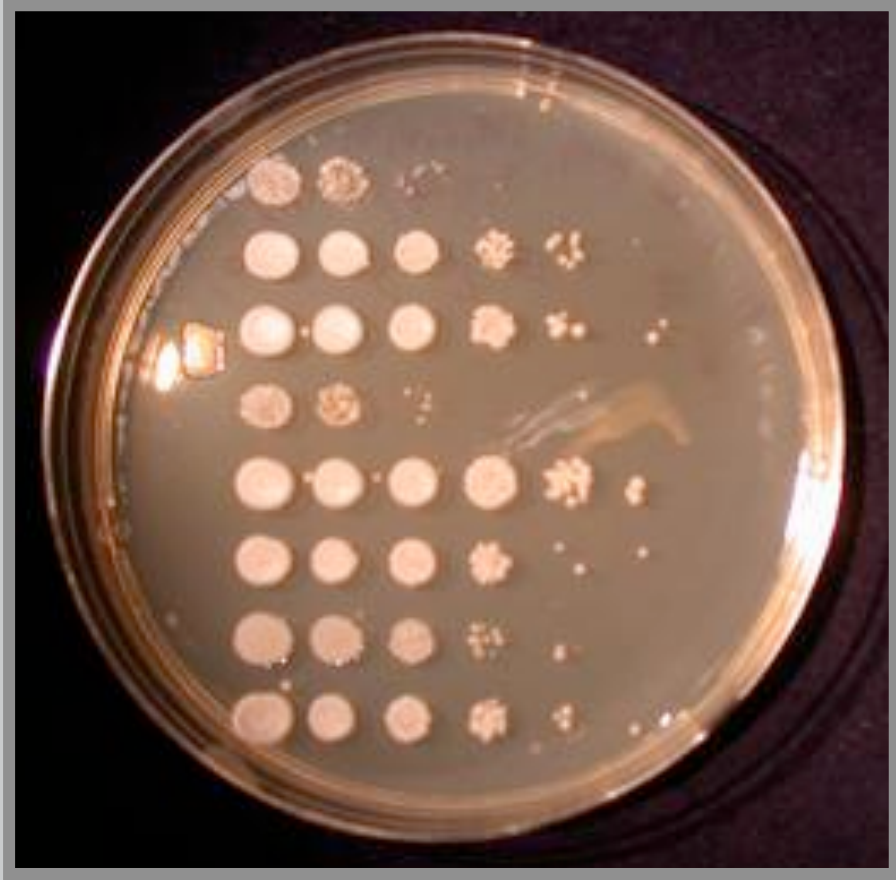
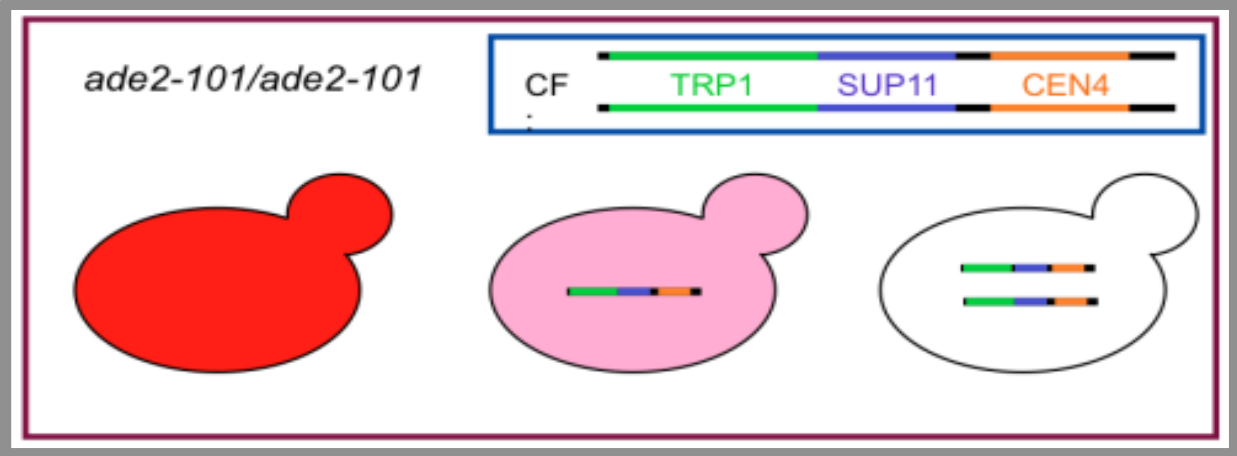


## Creation of Deletion Strain

- Student incorporate wet-lab experiments with their bioinformatics based functional predictions; generating knockout strains for their gene of interest and learning classic genetics techniques.
- Primers are designed, by students, in order to create a KanMX based knockout cassette via PCR.
- Individual knockout cassettes are transformed, by students, into a yeast strain capable of assessing genome stability. Deletant strains are assessed for phenotypic differences due to loss of the gene of interest.

## Phenotypic Assays

- Morphology
- Sugar usage
- Growth temperature
- Sensitivity to UV
- Genomic instability



## Student Final Products & Assessment

- The project culminates in a brief presentation by each student in which they summarize the most important evidence collected for the role of their gene product in the cell. Students also submit a final written report.
- Presentations by students is conducted similar to a research symposium with question and answer periods.
- Assessment based on data interpretation and integration of data from both the bioinformatics and wet-lab approaches.
- Genes demonstrating roles in genomic stability may be incorporated into ongoing research in the Strome Lab at NKU.

## Results

- Students apply genetic (and additional biological) concepts to an authentic research question; challenging them to analyze and synthesize data from various sources.
- Approximately 100 students each year benefit from this experience with a variety of bioinformatics tools.
- Instructors report increased engagement relative to “cook-book” experiments.
- Majority of students (74%) felt that they learned more from this project than other lab projects.
- The vast majority of the students indicate the research was challenging (93%) and that they are better prepared to take on investigating a problem without a known solution as a result of the project (82%).
- 83% of students think that having an understanding of the capabilities of the bioinformatics databases and programs will benefit them in the future.
- Future work will focus on increasing student skills in data interpretation and establishing a sustainable model of the project.

## Acknowledgements

- NKU Biological Sciences Department and Faculty Development Programs
- Bio349: Genetics student participants