How People Learn Meets Bioinformatics

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INTRODUCTION

More than ever, faculty must give attention not just to course content and skill development, but also to what we know about the process of learning. How People Learn: Brain, Mind, Experience, and School: Expanded Edition 2000[1] is just one resource that informs faculty about the features of teaching that maximize learning.

At Earlham College we have designed a *freshman-level, multi-week, database* laboratory exercise that has students work in small groups to trace the effect of a mutation on mRNA production, protein expression / activity, and the cellular/organismal consequences of disruption of a gene.

In addition to re-enforcing the material covered in the lecture of an introductory genetics course, this exercise introduces skills associated with using a variety of bio-informatic databases. Furthermore it is intentionally designed to incorporate our better understanding of how students learn, including:

- an increased time on task,
- engaging student's misconceptions,
- repetition of material in a new context,
- inclusion of elements of discovery,
- modeling of expert knowledge,
- personalization of material.

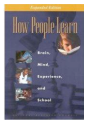
1. Committee on Developments in the Science of Learning with additional material from the Committee on Learning Research and Educational Practice and National Research Council).

SETTING

Earlham College
- o Undergraduate only
- o Liberal arts college
- o 1,200 students
- o Biology department ranks 8th in the US in the proportion of majors that obtain a PhD.

Biology 112: Cells, Genes and Inheritance
- o Introductory level
- o Majors and non-majors course
- o Total enrollment of ~90
- o Lab section size of 18-22

HOW PEOPLE LEARN



Published in 2000, How People Learn summarizes results of research on the features of teaching that promote knowledge acquisition for deep understanding and retention. Other publications[2] extend and support the conclusions.

Features Promoting Learning with Understanding	Incorporation into Assignment
Increased Time on Task	Multi-week (5) project with multiple feedback opportunities.
Engaging Misconceptions	Common misunderstandings about structure / function of gene / protein are exposed and engaged in interactions with faculty and peers.
Material in a New Context (knowledge transfer)	Students apply gene and protein content learned in lecture to new situations.
Element of Discovery, Learning as an Active Process	Faculty has limited knowledge and students become 'experts.' Students are engaged in finding, interpreting and making meaning of information.
Modeling Expert Knowledge	Interactions with faculty model extracting and interpreting information from databases. Students engage in poster session modeled after scientific meetings
Personalization of Material	Genetic nature of disease engages student's interest in health and medicine. Students chose from a list; many have personal experience.
Creating Well-Organized Knowledge Structures	Students must sort info from databases into categories.
Emphasis on Learning with Understanding	Students must tell a 'story' with the information they find; genotype to phenotype emphasis.
Formative Assessment	Students receive feedback at multiple points during the assignment period.
Assessment of Understanding	Students speak individually with faculty during the poster session; all aspects of the poster content are fair game.

2. Jensen, E. 2008. Brain Based Learning 2nd edition Corwin Press,CA; Feldman J. and D. McPhee. 2008. The Science of Leanring and the Art of Teaching. Thomson, Australia; Willis, J. 2006. Research-Based Strategies to Ignite Student Learning. ASCD, VA.

ASSIGNMENT DESCRIPTION

- Work in groups of 2-4.
- Identify information from NCBI and other databases; organize and integrate that data into poster panels.
- Follow the genotype to its phenotype for a disease by investigating:
  - Gene and transcript structure
  - Protein structure and function
  - Mutation in DNA
  - Consequence of mutation to protein/ cell/organism.
- Construct and present poster to classmates.

INFORMATION IN POSTER	SOURCE(S)
Gene Information (symbol, size, # exons, locus, transcriptional control regions)	EntrezGene, GeneCards, GeneWiki
Transcript information (length, alternative splicing?)	EntrezGene, GeneCards, ECGene
Protein Information (MW, #aa, domains, subcellular location)	Human Protein Reference Database (HPRD); PDB
Protein Function Information (Biological process, protein-protein interactions, post-translational modification, pathways)	Human Protein Reference Database (HPRD); GeneCards
Mutation (DNA change, protein-level change)	OMIM, research literature
Link Mutation to Phenotype	OMIM, GeneEntrez, GeneReviews, EntrezGene

Disease Options

The list of genes was selected from Genes and Disease in the Bookshelf at the NCBI website. In some instances, students investigated a gene/disease of their choice.

BRCA1 Breast Cancer
RB1 Retinoblastoma
WRN Werner Syndrome
ABCD1 Adrenoleukodystrophy
PIGA1 Paroxysomal Nocturnal Hemoglobinuria
MEFV Mediterranean Familial Fever
PKD1 Polycystic Kidney Disease
SMAD4 Pancreatic Cancer
SRY Gonadal Dysgenesis
DMPK Muscular Dystrophy

ASSESSMENT

FORMATIVE ASSESSMENT

Faculty or teaching assistants are critical at several points:
- Database instruction
  - We divided this into two separate sessions, one dealing with the gene/ transcript information and the other with the protein databases.
- Grading of the gene, protein and mutation panels.
  - Grading during a lab session using 20 min/group. The gene panel was due the 1st week; the protein and mutation panels were due the 2nd week.
- Final Poster Presentation
  - Each student discussed their poster with a faculty member for 4-6 minutes during a 3-hour lab session.

EVALUATIVE ASSESSMENT

- The final presentation was worth 100 points: 80 points for the poster (group grade) and 20 points for the individual discussion.
- Six true/false questions based on the project were on the final exam (see below).

PRELIMINARY ASSESSMENT OF PROJECT

Below are the questions from the final exam. The percent that answered correctly is indicated for each in red.

T F Genes typically have one or two introns. 75%

T F Many genes in the human genome are alternatively spliced. 98%

T F A disease may be caused by many different mutations in the same gene (many disease alleles). 91%

T F Deletions and insertions can occur in genes and these most often cause frame shifts. 91%

T F The Y chromosome does not get mutated because it is so small. 94%

T F We know the function of all of the proteins encoded in the human genome. 97%

None of this material was explicitly covered in class and the final exam was > 1 week following the presentation of the posters.