Student Learning Assurance Report
B.S. in Biology
Department of Biology
College of Arts and Sciences
2016-2017

Scott Nunes (nunes@usfca.edu)
Brian Thornton (brthornton@usfca.edu)

Mission Statement

The core mission of the University of San Francisco is to educate students in the knowledge and skills required to succeed as professionals and as persons, while also teaching the sensitivity and values necessary to participate in a world shared by all people. The Department of Biology particularly emphasizes the core Jesuit value of advancing the freedom and responsibility to pursue truth and to follow evidence to its conclusion. In pursuit of these values, the faculty of the Department of Biology educates undergraduate students in current biological concepts, methodologies, and ethical practices in the laboratory and the natural environment to prepare them to succeed personally and professionally with the potential for advanced training in the sciences.

Last review and revision: Spring 2017.

Program Learning Outcomes

Upon graduation, students who complete the degree requirements should be able to meet the following program learning outcomes:

1) Demonstrate both in-depth and broad knowledge of the concepts that comprise the biological sciences.
2) Apply the scientific process, including designing and conducting experiments and testing hypotheses.
3) Perform laboratory, field, and analytical techniques.
4) Discuss and critically review scientific papers and prepare oral and written reports in a standard scientific format.
5) Demonstrate an awareness of the significance ethics plays in the biological sciences.

Last review and revision: Spring 2017.

Summary of Assessment Plan

- 2014-2015
    - Assessment of program learning outcome #5— *Demonstrate an awareness of the significance ethics plays in the biological sciences.*
        - Evaluation of ethics papers from BIOL 310/311-Genetics.
- 2015-2016
    - Assessment of Program Learning Outcome #3—*Perform laboratory techniques (such as light microscopy, gel electrophoresis and keeping a laboratory notebook and understanding of principles of laboratory safety).*
        - Evaluation of student work from upper division classes with a laboratory component.
        - Evaluation of equipment in laboratory courses.

        - Survey of lab techniques learned by students doing research with faculty members.
        - Survey of techniques covered in molecular biology courses with a lab component.
    - Survey of graduating seniors (indirect evidence of student achievement in program learning outcomes #1-4).
    - Note: At the suggestion of the Dean's Office, fewer courses than the seven originally planned were selected for evaluation of student work, and the survey of graduating seniors was added into the plan as indirect evidence of student achievement. We modified the plan to collect data from three courses, but one faculty member was unable to collect data, so we present data from two courses.
- **2016-2017**
    - **Assessment of Program Learning Outcome #4—*Demonstrate the ability to read, understand, and critically review scientific papers and prepare oral and written reports in a standard scientific.***
        - **Evaluation of student work from upper division classes in which students review scientific papers and prepare scientific reports**
        - **Examples of student presentations at research conferences.**
        - **Examples of published work that students contributed to as authors.**
    - **Internal review of courses and curriculum.**
    - **Survey of graduating seniors (indirect evidence of student achievement).**
- 2017-2018
    - Assessment of Program Learning Outcome #1—*Demonstrate both in-depth and broad knowledge of the concepts that comprise the biological sciences.*
        - Evaluation questions embedded in exams in foundational courses.
    - Survey of graduating seniors (indirect evidence of student achievement.
- 2018-2019
    - Assessment of Program Learning Outcome #2—*Apply the scientific process, including designing and conducting experiments and testing hypotheses*.
        - Evaluation of student work from upper division classes in which students conduct scientific experiments.
    - Survey of graduating seniors (indirect evidence of student achievement).

Academic Program Review

The last program review for the Biology Department was in 2013-2014. The department had an action plan meeting in fall of 2014. In response to the program review, the department is working to verify that ethics in science is adequately covered in the curriculum, increase representation of ecology in course offerings, diversify teaching methods, and improve assessment of the program by incorporating direct evidence of student achievement into assessment. The department has received support from the administration to improve the graduate program, increase support staff, and expand research space in the department.

Methods: Program Learning Outcome #4—Scientific Communication

—Assessment of Student Work in Upper Division Courses

Student papers were collected from two upper division courses, BIOL 356 (Developmental Biology) and BIOL 368 (Neurobiology). The papers from these courses required students to understand primary scientific literature, and explain the findings of the papers in a standard scientific format. The papers were evaluated on two criteria, compliance with the assignment (indicating proficiency in preparing a report in standard format) and literature review (indicating their level of comprehension of the source material). Each criterion was evaluated by a 3-tier rubric of excellent, satisfactory, or weak. Two faculty members evaluated the papers for each course independently. Scores were tabulated and comments were shared with the faculty for comment and discussion.

—Student Publications and Presentations

Students are encouraged to engage in research with faculty members at USF, or sometimes at nearby universities such as UCSF. Students who engage in research have opportunities to present their findings at a yearly research conference at USF, Creative Activity and Research Day (CARD), and will sometimes travel to conferences to present their work. We have collected examples of CARD abstracts, posters from conferences, and publications that students contributed to.

Methods: Survey of Graduating Seniors

Graduating seniors were asked to complete a survey with questions related to the Biology Department's program learning outcomes. The survey also allowed student to provide comments. A total of 38 students submitted responses.

Methods: Internal Review of Courses and Curriculum

—Breadth of Topics Covered in Upper Division Courses

Faculty engaged in a discussion of possibly adding a breadth requirement to upper division electives. The current system requires students to take 1 field course (a course for which more than half of the lab sessions are out in the field, using field techniques), 2 lab or field courses, and 2 courses that may be lab, field or lecture. At a mini-retreat in Spring 2016 it was noted that some universities divide their upper division courses into categories to ensure that their students cover a breadth of topics. A committee was formed to review the course coverage for our graduating students and prepare a proposal for the department to consider.

—Changes to upper division courses to better align with department goals.

At the mini-retreat in Spring 2016, the faculty had discussed replacing two upper division electives, Human Anatomy and Human Physiology, with broader courses that could better incorporate the theme of evolution as a unifying principle. Faculty

members worked on revising these courses and presented proposed changes to the department for review during the 2016-2017 academic year.

Results: Program Learning Outcome #4—Scientific Communication

—Assessment of Student Work in Upper Division Courses

Results of faculty evaluation of student papers can be seen in Appendix A. Papers were evaluated on Assignment Compliance and Literature Review on a scale from 1-10, with 10 being excellent, 6 satisfactory, and less than 6 being weak. The average scores in both categories were between 7 and 8, satisfactory. Out of the 26 papers evaluated, 3 were marked as below satisfactory by at least one evaluator, while 9 were marked as excellent in both categories by both evaluators. The comments indicated that most students followed assignment guidelines remarkably well, and evidenced a good understanding of the primary source material.

Comments by faculty indicated that for future evaluation of this topic, inclusion of oral presentation assignments would be worthwhile. These could be recorded and reviewed later by faculty other than the course instructor, provided students had been warned ahead of time that they would be evaluated in this way. Assignment length was also commented on, since one assignment was relatively lengthy (10 pages approximately) while the other was compact (2 pages max), and the students seemed to fare better with the longer assignment, perhaps also including differences in amount of faculty guidance given during the writing process. It was also commented by one evaluator that the rubric did not allow for adequate differentiation between simple description and critical understanding. Future rubrics for assessing this learning outcome should include categories to allow for better differentiation of student comprehension. Finally, it was noted by one reviewer that the degree of assignment compliance was extremely high for one course (BIOL 368) and that this likely reflected considerable guidance by the instructor, drafts and review processes, etc., and might not translate to other courses.

—Student Publications and Presentations

Examples of student work are shown in Appendix B. These represent examples of both oral and written scientific communication by students in standard scientific formats. Although these represent indirect assessments since they were not reviewed directly by faculty, they were reviewed and deemed worth of inclusion by outside parties, and as such should be included as examples of students reaching the desired learning outcome.

Results: Survey of Graduating Seniors

Student responses in the survey (Appendix C), consistent with last year's survey, indicated that students felt knowledgeable in cell, molecular, and organismal biology (program learning outcome #1) and proficient in applying the scientific method (program learning

outcome #2), performing laboratory techniques (program learning outcome #3), and evaluating the scientific literature (program outcome #4). The survey indicated that students felt knowledgeable in ecology, but less so than in other areas of biology. The survey also indicated that students felt proficient in field techniques, but not as proficient as they felt in lab techniques. Few students felt proficient in the field of Bioinformatics.

The department has continued to work toward increasing student exposure to topics in Ecology. Two tenure-track faculty were hired last year, both with backgrounds and interest in ecology. This will allow for the offering of additional sections of ecology-oriented upper division courses, particularly field courses. In addition, the department hired a Bioinformatics (and Ecology) tenure-track professor the previous year, and Bioinformatics will now be offered as a regular part of the curriculum.

Results: Internal Review of Courses and Curriculum

—Breadth of Topics Covered in Upper Division Courses

The committee reviewed the upper division course offerings and categorized them into broad areas of organismal biology, ecology, and molecular/cellular biology, and proposed a revised upper division course requirement that students take one lab/field course from each of the breadth categories, plus two additional electives of their choice. The department reviewed the upper division courses by recent graduates to see whether students were already taking courses consistent with this proposed requirement. From the previous year's graduating students, 80% had taken at least one organismal diversity lab/field course, 65.7% had taken at least one ecology lab/field course, and 74% had taken at least one molecular/cellular lab course. Given this relatively high level of compliance, and given the logistical challenges that would come from this type of curriculum change, the department opted not to pursue the breadth requirement. However, it was agreed that steps should be taken to increase exposure of students to a breadth of topics, by offering additional ecology-oriented course options, and working to ensure that ecology as a topic is better included in introductory coursework. The breadth proposal is included in Appendix D.

—Changes to upper division courses to better align with department goals.

Beginning in Fall 2017, the existing Human Physiology course (BIOL 320/321) will no longer be offered as a regular course, and the Comparative Animal Physiology course (BIOL 350), previously a lecture course, was modified to include a lab (BIOL 351) instead. Beginning in Spring 2018, the existing Human Anatomy course (365/366) will not be offered regularly, being replaced by a Comparative Anatomy course (352/353). In this way the department continues to stress a broad education in the field of Biology, rather than a human-centric approach. The revised syllabi are included in Appendix E.

Closing the Loop

- Evaluation of student papers suggests satisfactory understanding of literature and proficiency in scientific writing, however this may reflect a high degree of guidance from the instructor, and might not translate to all courses.
- Future assessment of this topic should include analysis of oral presentations, and should revise the rubric to better evaluate levels of student understanding of the material.
- The department is continuing to add Ecology content to the course offerings and will continue to evaluate student feedback on coverage of the subject.

Curriculum Maps

Curriculum maps aligning the Biology program learning outcomes with a) courses offered in the Biology curriculum and b) the USF institutional learning outcomes are presented in Appendix F.

Aggregate data for Assessment of Learning Outcome #4

	BIOL356	BIOL368	# below 6	# excellent
Assignement Compliance:	7.54	7.92	1	7
Literature Review:	7.9	8.38	2	2

Shown are averages from 2 evaluators for 13 papers from each class.
Ratings are on a scale from 0 (weak) to 10 (excellent). 6 was set as satisfactory.
The number of papers rated as below 6 by at least one evaluator is shown
The number of papers rated as excellent (above 9) by both evaluators is shown

2016-2017: Biology Department Learning Assurance: Literature Review

Criteria	Ratings			Pts
Assignment Compliance: Was thestudent prepared in accordance to the guidelines for the assignment? This would include number of sources, formatting of bibliography, assignment length, concepts covered, and any other guidelines that were in the assignment instructions.	Excellent Achievement: The paper meets all of the guidelines laid out in the assignment given to them by the instructor. 10 pts	Satisfactory Achievement: The paper meets most of the guidelines but fails to meet 1-2 relatively minor guidelines, such as length, topics covered, or formatting. 6 pts	Weak Achievement: Significant failures in meeting multiple assignment guidelines, or missing crucial guidelines that render the work inadequate. 0 pts	10 pts
Literature Review: Did the student work display critical review and understanding of primary literature? This should mean displaying both a technical understanding of the techniques described in the primary source material as well as a displayed understanding of the importance of this work.	Excellent Achievement: The student work demonstrated a critical understanding of figures, results and discussion from at least 2 primary scientific papers. This was demonstrated by accurate descriptions of experimental work done that in the reviewer's opinion displayed an understanding of both the techniques used and the importance of the work. 10 pts	Satisfactory Achievement:The student work demonstrated a critical understanding of figures, results and discussion from at least 2 primary scientific papers. The descriptions of the work displayed a decent understanding of the techniques and importance of the work, but contained some errors or did not fully explain the signficance. 6 pts	Weak Achievement: The student work did not cover primary scientific findings in enough detail to suggest an understanding of the source material. 0 pts	10 pts

Total Points: 20

Reviewer: Leslie Bach
Date Completed: 10/18/17

Work assessed	Assignment Compliance	Literature Review	Comments
1	5	7	Many grammatical errors throughout paper, missing aims and and hypothesis, missing formatting guidelines of assignment improper formatting for references and in-text citations, missing detail, some references don't seem to match text surrounding in-text citation
2	9.5	10	Minor formatting/grammatical errors; otherwise, citations are well-used and appropriate
3	7	8	No in-text citations, missing detail in experimental methods, missing figure title and reference
4	9.5	10	One minor typo, otherwise good - well-cited, well-written
5	8	8	Two references not cited in text; inconsistent formatting, one in-text reference typo, possible typo in figure legend - attention to detail lacking
6	7.5	7	One reference not cited in text, another reference cited next to statements that don't match the article; issues with verb tense and following the guidelines of the assignment
7	8	5	Some typos/inconsistencies in text; only one reference used, though that reference was interpreted well
8	8.5	9	One in-text citation not found in reference list, missing some headers, inconsistent style; figure should also have a reference
9	8	9	Some typos, need more detail
10	8	8.5	Some issues in clarity within methods section
11	8	8	Several references lack in-text citations, one in-text citation not found in reference list
12	7	7	None of the references have in-text citations, making evaluation of understanding the literature difficult; several grammatical/punctuation errors
13	9	9	One source in references not cited in text, a couple of minor punctuation errors

Reviewer: Brian Thornton
Date Completed: 19-Oct

Work assessed	Assignment Compliance	Literature Review	Comments
Paper 1, Bio 356	3	4	Extensive problems with writing, with only cursory descriptions of findings, lack of inclusion of assignment sections.
Paper 2, Bio 356	9	10	Good intro, hypothesis is not a hypothesis, well described aims, methods and expected results.
Paper 3, Bio 356	7	6	No citations in intro at all, hypothesis is not a hypothesis, some portions in methods that should be in other sections, methods not clearly organized to stated research goals,
Paper 4, Bio 356	8	10	Minor citation issue (THM quoted without attribution), hypothesis not a hypothesis, some grammar/style issues not standard for this type of writing, otherwise a solid proposal.
Paper 5, Bio 356	6	6	Citations sparse, hypothesis not a hypothesis, some word choices odd suggesting copy/replace, research method relies on a major assumption but is formally possible, only one cited research finding in text.
Paper 6, Bio 356	8	6	Some terms/genes not properly introduced, grammar/spelling issues, reasoning for methods indicates potential lack of understanding of biology of findings cited
Paper 7, Bio 356	6	5	Only one citation(?), various statements not attributed, hypothesis not a hypothesis, no clear rationale for the anticipated results.
Paper 8, Bio 356	7	10	Minor style issues, good introduction, hypothesis not a hypothesis, methods not included as their own section, some issues with tense throughout, but good understanding of literature.
Paper 9, Bio 356	9	9	Nicely written/cited intro, hypothesis not a hypothesis, some reasoning vague on how expected results lead to particular conclusions, but overall very nice analysis.
Paper 10 Bio 356	8	9	Intro well cited, but could have been expanded, hypothesis is not a hypothesis, methods could have been expanded.

Paper 11, Bio 356	7	10	Intro well written and cited, one phantom citation, hypothesis not a hypothesis, link between methods and specific aims well stated, paper over length.
Paper 12, Bio 356	6	6	Intro not well cited, could be more concise, 3 findings not clearly stated/cited, hypothesis not a hypothesis, writing style issues ("To do so, you can…", instead of "we will"), anticipated results discuss both positive and negative results (good).
Paper 13, Bio 356	9	9	Intro uses jargon without context, hypothesis is not a hypothesis, research proposal should cover more possible outcomes for results.

General comments:

"Hypothesis is not a hypothesis" was true for all papers but one. This is likely due to assignment guidelines calling for either a hypothesis or questions in this section.

A longer assignment may have been better suited for this assessment (though more work to assess).

Reviewer: Mary Jane Niles
Date Completed: 6-Oct-17

Work assessed	Assignment Compliance	Literature Review	Comments
BIOL 368 p.1	8	9	Abstract is excellent and follows the requirements of the assignment; the Introductions (to the topic) is not scientific at all; the star PI intro is fine. Refs and Citations good. Demonstrates a solid understanding of the primary
BIOL 368 p.2	9	9	As above, the sections, citations and references follow the format, and are very good; It appears that this student has a solidd understanding of the primary literatrure, with respect to methods, results, and their significance (or lack). Still, should have defined terms / acronyms in the introduction, such as AMPA. Good comment on future work in the conclusion.
BIOL 368 p.3	9	9	Uses "encodes for" redundant: either codes for x or encodes x. Some awkwardness in writing but overall very very good.
BIOL 368 p.4	9	8	Quite good understanding of the topic and its significance. Some trouble with expression and grammar. Using "I think that" in the conclusion (several time) is not necessary.
BIOL 368 p.5	9	6	"Without uncovering the mechanisms for stroke recovery, neural repair is impossible." Maybe, neural repair therapy is impossible? Excitotoxicity rather that Exitotoxicity? Some awkwardness in expression and grammar but overall, the student has come to a satisfactory understanding of this work. Did not refer to figures by number.
BIOL 368 p.6	7	7	Perhaps more methods detail than the professor asked for, with respect to buffer consituents, for example. V. few references. Only the reviewed papers are cited. One reference is incorrect. Should define Ca transient. Addresses future directions in conclusion.
BIOL 368 p.7	7	6	Myelin is not "a protein;" Myelin is not "energy efficient" The CNS consists of (not houses) the brain and spinal cord; student uses quotations. Instructions: Please **avoid** using quotes. Does mention future work in the conclusion.
BIOL 368 p.8	9	10	Adverse effects (not affects); uses affect when effect is the proper term.
BIOL 368 p.9	9	9	Abstract has a little too much specific detail, which is addressed in the star PI introduction.
BIOL 368 p.10	8	8	A few grammar glitches and typos, background Intro could provide a little more context for the studies to be addressed. In explanations of data, the student did not refer to figure numbers.

BIOL 368 p.11	9	9	well done. Terms / acronyms defined; followed the assigned format, and appears to have a solid understanding of the figures / results and their relevance.
BIOL 368 p.12	8	9	A few grammar glitches and typos, some references oddly formatted
BIOL 368 p.13	9	9	Does not refer to figure numbers. A few grammar glitches; defines terms in the introduction.
BIOL 368 p.14	9	9	Name not redacted. Assignment calls for defining terms in the intro: hAPP genes, Aβ defined in the introduction. (Define in abstract?) Does not refer to figure numbers.

The students are remarkable in keeping to the assigned format, so assignment compliance is very high for each, in the 8-9 range.

I understand that this assignment also includes an oral presentation, at which time, no doubt, figures are presented. I found it challenging to assess the student's full understanding of figures without having the figure in front of me. So, in many cases, I looked up the paper being reviewed in order to get a better picture of student understanding. And, the assignment did not call for the student to refer to data by figure number. Perhaps that's why some did not do so.

I am guessing also that the instructor spent a great deal of time with (most?) students to elicit to these largely excellent final drafts.

Less than 10 on literature review: "critical understanding" just slightly lacking, given the rubric language and part V. of the assignment. The conclusion should include ideas of future work, although the assignment does not ask the student to critique the papers.

Note: Paper 14 was exluded from aggregate scores, since the student name was accidentally not redacted.

Reviewer: Brian Thornton
Date Completed: 19-Oct

Work assessed	Assignment Compliance	Literature Review	Comments
Paper 1, Bio 368	7	8	Intro is bit casual and personal. Technical descriptions from papers are quite good, getting at essential steps in the processes without bogging down in minute details. Figures are not referenced. Spotty definitions of terms. Did not propose future directions.
Paper 2, Bio 368	9	10	Some terminology not defined, otherwise assignment guidelines followed closely. Technical descriptions were thorough and showed good understanding, and had proposal for future directions.
Paper 3, Bio 368	9	9	Well written, follows guidelines very closely, some stylistic issues with writing, mostly minor. Did not propose future directions, otherwise literature review was thorough and in-depth.
Paper 4, Bio 368	7	9	Abstract dry, some typos/grammar errors, jargon-heavy without definitions, but thorough writeup and analysis of required figures.
Paper 5, Bio 368	7	6	No numbers on figures, never references 2nd paper, had some fairly important misunderstandings about results. Still, proficiently written and got many of the basic ideas.
Paper 6, Bio 368	8	6	Well written, style-wise, but only references main papers. Into well-meaning but ultimately distracting. Descriptions of results very detail-oriented without always capturing main point of discussion
Paper 7, Bio 368	5	8	Abstract disjointed, some issues with grammer/word choice ("CNS houses the brain and spinal cord"). Does not point out all figures used. Shows some problems with understanding of concepts, relies on terminology not well defined.

Paper 8, Bio 368	7	9	Some spelling/grammar errors, abstract mentions klotho without defining it, almost no citations beyond papers being reported on, analysis of results seems to be thorough however.
Paper 9, Bio 368	9	10	Abstract not really an abstract, but detail on figures and future directions were quite good. Would have liked description of impact of Sirtuins on gene expression.
Paper 10, Bio 368	6	7	Confusing wording in introduction, doesn't cite figures, phrases like "pre-trial epoch" are problematic, citations are sporadic, future directions were very brief
Paper 11, Bio 368	8	10	Abstract written as an introduction, not an abstract. Some grammar/spelling issues throughout, hit and miss with figure references.
Paper 12, Bio 368	8	9	"Hot topic" probably doesn't belong in an abstract, should have defined ALS in abstract, some wording issues throughout, figure citation sporadic, really good future directions in conclusion.
Paper 13, Bio 368	6	9	Abstract has info that should be in intro, citations in intro spotty, some grammar/spelling errors, figures not cited, "application of these techniques to humans is not yet popular".
Paper 14, Bio 368	8	10	Student name not redacted, will exclude from analysis. Did not cite figures, some writing style issues.

General Comments:
Papers are generally high quality, including a lot of nuanced discussion of techniques.
Some consistent issues with following assignment guidelines, but reasonable for a student population.

Infection, Genetics and Evolution 51 (2017) 46–53

Contents lists available at ScienceDirect

Infection, Genetics and Evolution

journal homepage: www.elsevier.com/locate/meegid

Research paper

Evolution of the ability to modulate host chemokine networks via gene duplication in human cytomegalovirus (HCMV)

Jessica A. Scarborough, John R. Paul, Juliet V. Spencer *

Department of Biology, University of San Francisco, Harney Science Center, 2130 Fulton Street, San Francisco, CA 94117, USA

ARTICLE INFO

Article history:
Received 19 December 2016
Received in revised form 12 March 2017
Accepted 13 March 2017
Available online 14 March 2017

Keywords:
Chemokine
Chemokine receptor
CMV
Cytomegalovirus
GPCR
G protein-coupled receptor

ABSTRACT

Human cytomegalovirus (HCMV) is a widespread pathogen that is particularly skillful at evading immune detection and defense mechanisms, largely due to extensive co-evolution with its host. One aspect of this co-evolution involves the acquisition of virally encoded G protein-coupled receptors (GPCRs) with homology to the chemokine receptor family. GPCRs are the largest family of cell surface proteins, found in organisms from yeast to humans, and they regulate a variety of cellular processes including development, sensory perception, and immune cell trafficking. The US27 and US28 genes are encoded by human and primate CMVs, but homologs are not found in the genomes of viruses infecting rodents or other species. Phylogenetic analysis was used to investigate the US27 and US28 genes, which are adjacent in the unique short (US) region of the HCMV genome, and their relationship to one another and to human chemokine receptor genes. The results indicate that both US27 and US28 share the same common ancestor with human chemokine receptor CX3CR1, suggesting that a single host gene was captured and a subsequent viral gene duplication event occurred. The US28 gene product (pUS28) has maintained the function of the ancestral gene and has the ability to bind and signal in response to CX3CL1/fractalkine, the natural ligand for CX3CR1. In contrast, pUS27 does not bind to any known chemokine ligand, and the sequence has diverged significantly, highlighted by the fact that pUS27 currently exhibits greater sequence similarity to human CCR1. While the evolutionary advantage of the gene duplication and neofunctionalization event remains unclear, the US27 and US28 genes are highly conserved among different HCMV strains and retained even in laboratory strains that have lost many virulence genes, suggesting that US27 and US28 have each evolved distinct, important functions during virus infection.

1. Introduction

1.1. The Herpesvirus family

Human cytomegalovirus (HCMV) is a member of the *Herpesviridae* family. These viruses have linear DNA genomes and share two main characteristics, the structure of the virion particle and the ability to establish lifelong latent infection of the host. Herpesviruses are highly species-specific, and more than 100 different viruses that infect mammals, birds, reptiles, amphibians, fish, and invertebrates have been identified to date (McGeoch et al., 2008). Some species are infected by multiple, distinct herpesviruses, and there are nine herpesviruses that infect humans: herpes simplex virus-1 (HSV-1), herpes simplex virus-2 (HSV-2), varicella-zoster virus (VZV), Epstein-Barr virus (EBV), human cytomegalovirus (HCMV), human herpesvirus 6A (HHV6A), human herpesvirus 6B (HHV6B), human herpesvirus 7 (HHV7), and human herpesvirus 8 (HHV8, or KSHV, Kaposi's sarcoma associated herpesvirus). Even before the evolution of *Homo sapiens*, an ancient HSV-2 jumped from chimpanzees to *Homo erectus* about 1.6 million years ago (mya), and the ancestral virus that gave rise to HSV-1 infected hominids more than 6 mya (Wertheim et al., 2014). Herpesviruses co-evolve extensively with their specific hosts, frequently through gene capture (Alcendor et al., 2009; McGeoch et al., 2006; Wang et al., 2007). The acquisition of new genes via lateral transfer not only has the potential to increase virus fitness (McGeoch et al., 2006; Wang et al., 2007) but also reduces immune recognition of the pathogen through molecular mimicry (Hughes and Friedman, 2005). Here, we investigated the relationship between two genes that encode G protein-coupled receptors (GPCRs) with immune modulating functions in the genome of HCMV.

1.2. Human cytomegalovirus (HCMV)

HCMV is a member of the *Betaherpesvirinae* sub-family and is widespread throughout the general population (Cannon et al., 2010). HCMV is adept at evading the host immune system, largely due to having

* Corresponding author.
E-mail address: jspencer@usfca.edu (J.V. Spencer).

http://dx.doi.org/10.1016/j.meegid.2017.03.013
1567-1348/

acquired many genes with homology to genes from its human host (McSharry et al., 2012a). HCMV rarely causes disease in a fit host, but more frequently, acts as an opportunistic pathogen. In healthy individuals, HCMV infection produces a strong immune response involving both the innate and adaptive systems. Despite this immune response, even immunocompetent hosts are unable to eliminate the virus or prevent the establishment of latent infection (McSharry et al., 2012b). HCMV's ability to modulate host immune responses through cytokine, chemokine, and chemokine receptor homologs plays a role in this lifelong persistence (McSharry et al., 2012b).

Although latent HCMV can reactivate periodically, immune competent hosts typically do not experience clinical symptoms due to strong T-cell responses (McSharry et al., 2012b; Rosa and Diamond, 2012). Immunocompromised patients, however, are much more likely to experience HCMV disease during primary infection or reactivation of latent virus (Wreghitt et al., 2003). HCMV infection is extremely serious in transplant recipients and one of the leading causes of morbidity and mortality in this highly vulnerable population (Ramanan and Razonable, 2013). Additionally, congenital infection can lead to severe birth defects, including hearing loss, mental disability, microcephaly, seizures, and other neuromuscular defects (Manicklal et al., 2013).

Recently, HCMV has been connected to increased malignancy of certain types of cancer. While HCMV is not considered an oncogenic virus, infection can contribute to increased cellular proliferation, inhibition of apoptosis, enhanced chemotaxis, and other characteristics associated with malignancy (Michaelis et al., 2009). The strongest evidence for a role of HCMV in tumor development has been seen in glioblastomas, where the virus is capable of promoting the malignant phenotype, making the HCMV a potential target in the treatment of malignant gliomas (Dziurzynski et al., 2012).

1.3. G-protein-coupled receptors (GPCRs)

HCMV's ability to establish lifelong latent infection within its host may be in part due to GPCR homologs encoded by the viral genome (Vieira et al., 1998). GPCRs are cell surface receptors, which transmit an intracellular signal upon the binding of an extracellular ligand. Humans have over 800 unique GPCRs, with a wide assortment of functional roles, yet each is similar in physical structure (Chattopadhyay, 2014). These receptors consist of a single polypeptide with seven transmembrane segments, with an N-terminus on the exterior of the cell, and the C-terminus inside the cell, typically associated with heterotrimeric G proteins or other signaling molecules (Fig. 1). Once a ligand binds and activates a GPCR, a conformational change occurs, triggering the activation of a local G-protein and leading to the dispatch of signals within the cell.

HCMV encodes at least four genes that give rise to proteins with predicted seven transmembrane domains: US27, US28, UL33, and UL78 (Chee et al., 1990). In particular, the US27 and US28 gene products (pUS27 and pUS28, respectively) exhibit homology to human chemokine receptors, a subset of the GPCR superfamily that play a crucial role in immune responses. Each chemokine receptor binds to specific chemokines, which are small secreted proteins, and regulates intracellular signaling and immune responses (Murdoch and Finn, 2000). Responses to ligand binding and G protein activation include pro-inflammatory or anti-inflammatory effects, enhanced chemotaxis, and superoxide anion production (Charo and Ransohoff, 2006). Proper functioning of these chemokine receptors is key for mediating damage from an infection or injury. Moreover, dysregulation of chemokine receptors, chemokines, and chemokine attractants is central to many inflammatory and infectious diseases, including psoriasis and allergies (Raman et al., 2011).

In addition to the seven transmembrane domains, the key hallmark features of a chemokine receptor homolog generally include: N-linked glycosylation and multiple negatively charged amino acids in the N-terminus, the capability to form a disulfide bond between the N-terminus and third extracellular loop, multiple positively charged amino acids in the third intracellular loop, conserved amino acids in the transmembrane regions, and many serine and threonine residues in the C-terminus (Beisser et al., 2008). HCMV contains several additional genes that appear to code for seven transmembrane proteins (Das and Pellett, 2007; Lesniewski et al., 2006); however, only pUS27, pUS28, and

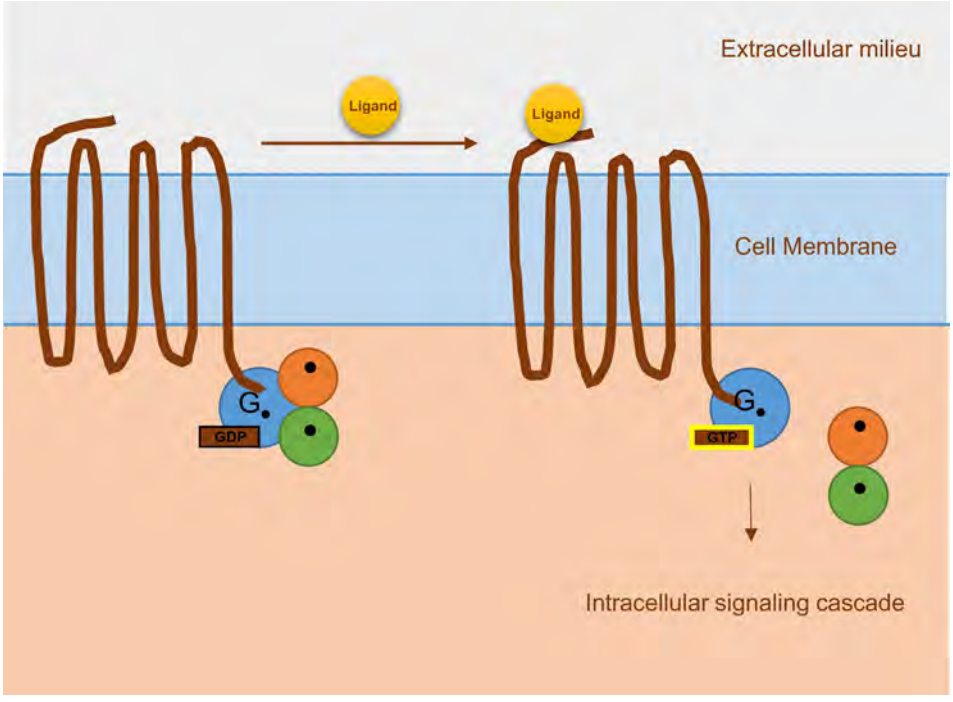


Fig. 1. Schematic diagram of GPCR activation. The GPCR is depicted in brown and has seven transmembrane segments with the amino terminus as the extracellular ligand binding domain. The carboxy-terminal tail serves as an intracellular signaling domain that binds to heterotrimeric G proteins. In response to ligand binding, the receptor undergoes a conformational change that enables the Ga protein to exchange GDP for GTP and transmit downstream signals via an intracellular signaling cascade. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

pUL33 meet the criteria for chemokine receptors, with pUS27 and pUS28 showing the greatest similarity to this receptor family.

1.4. HCMV US27 and US28

pUS27 is a putative chemokine receptor, although it has no known ligands to date (Arnolds et al., 2013). This protein can be found in intracellular vesicles and in the cell membrane of infected cells, and even within the envelope of the virus particle (McSharry et al., 2012b). US27 increases extracellular spreading of HCMV by 10-fold in fibroblasts and endothelial cells in comparison to a US27 knockout strain (O'Connor and Skenk, 2011). pUS27 may also be responsible for enhancing chemotaxis of virus-infected cells by increasing signaling through CXCR4, a human chemokine receptor (Arnolds et al., 2013). Additionally, pUS27 has been shown to increase cellular proliferation in human embryonic kidney cells (HEK293) by suppressing host negative growth regulators, although the complete underlying mechanism for this effect remains unknown (Lares et al., 2013; Tu and Spencer, 2014).

In contrast to pUS27, pUS28 is a functional chemokine receptor that is known to bind and signal in response to an extensive variety of chemokine ligands including CX_3CL1/fractalkine, CCL2/MCP-1, CCL5/RANTES, and CCL7/MCP-3 (Kuhn et al., 1995). pUS28 appears to play a key role in HCMV infection efficacy and potency, along with increased cell-to-cell spread of the virus (Noriega et al., 2014; Spiess et al., 2015). pUS28 has immune evasion properties due to its ability to internalize host chemokines, thereby decreasing the host immune system's ability to sense and respond to those chemokine signals (Beisser et al., 2002; McSharry et al., 2012b). In addition, US28 is one of a select set of genes expressed during latency, suggesting that this protein may play a role in sensing the host environment (Beisser et al., 2001; Humby and O'Connor, 2015; Mason et al., 2013).

This study examines the evolutionary history of US27 and US28, which are hypothesized to have arisen via gene duplication. Here, we performed a phylogenetic analysis confirming that US27 and US28 are paralogs that arose via a gene duplication event that occurred in an ancestral viral genome. We found that US27 and US28 likely share common ancestry with the human gene CX3CR1.

2. Materials and methods

2.1. Sequences

The pUS27 and pUS28 sequences from six different HCMV strains were analyzed: AD169, Towne, Toledo, Merlin, TR, and TB40/E. Genbank Accession numbers for the protein sequences examined in this study are as follows: US27 AD169 (ABG73076.1), US27 Towne (ABG73086.1), US27 Toledo (AAS49024.1), US27 Merlin (YP_081611.1), US27 TR (AGL96752.1), US27 TB40/E (ABV71517.1), US28 AD169 (ACL51230.1), US28 Towne (ACM48113.1), US28 Toledo (AAS49025.1), US28 Merlin (YP_081612.1), US28 TR (AGL96753.1), and US28 TB40/E (ABV71518.1).

The pUS27 and pUS28 amino acid sequences were independently searched through GenBank using the NCBI's protein Basic Local Alignment Search Tool (BLAST). This search compared the HCMV protein sequences to the entire human genome, displaying the top 100 matches by E-value (Madden, 2002). All unique chemokine receptors from this list of the top 100 matches were compiled and used for further analysis. This BLAST tool was also utilized to provide E-values between US27, US28 and their closest human chemokine receptor matches. Genbank Accession numbers for the human chemokine receptors are: CCR1 (NP_001286.1), CCR2 (AGC02843.1), CCR3 (NP_001828.1), CCR4 (NP_005499.1), CCR5 (NP_000570.1), CCR6 (NP_004358.2), CCR8 (NP_005192.1), CCR9 (AAH95516.1), CX3CR1 (NP_001328.1), CXCR3 (NP_001495.1), and CXCR4 (CAA12166.1). The outgroup used in phylogenetic analysis is a human G-protein coupled receptor that is not part of the chemokine receptor family, the Oxoeicosanoid Receptor (12NP_062545.1).

2.2. Sequence alignments

Protein alignments between HCMV strains were performed using the MUSCLE multiple sequence alignment tool, version 3.8 (Edgar, 2004), and alignment matrices were created by Clustal2.1 (Goujon et al., 2010; Larkin et al., 2007) within Geneious v. 9.1, a bioinformatics phylogenetics software, with the default settings used (Kearse et al., 2012). The alignments were then further edited by hand to replace blanks at the beginning and end of the alignment with question marks to represent missing data.

2.3. Phylogenetic analysis

Using Geneious v. 9.1, phylogenetic trees using Bayesian and maximum likelihood method were inferred to analyze the evolutionary history of the pUS27 and pUS28 proteins in relation to selected human chemokine receptors. The maximum likelihood analysis was inferred using PhyML v. 3.0 plugin (Guindon et al., 2010; Guindon and Gascuel, 2003) on the Geneious v. 9.1 software. Node values display bootstrap values (with 100 replicates) while all other settings utilized the default Geneious specifications. The Bayesian phylogenetic analysis was run utilizing the MrBayes plugin on Geneious software. A chain length of 10,100,000, subsampling frequency of 2000, and burn-in length of 1100,00 were used, with all other parameters set to default Geneious specifications (Huelsenbeck and Ronquist, 2001). Node values represent posterior probabilities of the clades.

3. Results

3.1. Protein alignments

Because there are multiple HCMV strains that have been sequenced and are used for in vitro experiments, variability in the pUS27 and pUS28 sequences among six different strains was first examined. These strains were chosen because they are prominent laboratory strains (AD169, Towne) and clinical isolates (TB40/E, Toledo, TR, Merlin) (Hosogai et al., 2015; Wilkinson et al., 2015). Sequence alignments were performed and percent identity among strains evaluated (Tables 1, 2). The results indicate that the six HCMV strains examined in this study show minimal variation within the pUS27 and pUS28 primary protein sequence. For pUS28, the lowest percent identity was between the strains TB40/E and TR (both clinical strains) with 97.46% identity match (Table 1). The closest identity was seen between AD169 and Towne, both laboratory strains that share 100% identity match within the pUS28 protein (Table 1). For pUS27, there was slightly more variation between strains (Table 2). The greatest variation was between TB40/E and Merlin, both clinical strains, with 94.74% identity match within the pUS27 protein. The closest similarity was between Towne and Toledo with a 99.45% identity match within the pUS27 protein. Thus, both genes are highly conserved among different virus strains, indicating their functions are likely beneficial for the virus.

Since the variability among strains was minimal, gross alignments used sequences from HCMV strain AD169, the first HCMV strain to be sequenced and annotated, which has been extensively used during

Table 1
HCMV pUS28 alignment percent identity matrix[a].

	TB40/E	TR	Toledo	AD169	Towne	Merlin
TB40/E	100.00	97.46	98.02	98.31	98.31	98.02
TR	97.46	100.00	99.44	98.87	98.87	98.59
Toledo	98.02	99.44	100.00	99.44	99.44	99.15
AD169	98.31	98.87	99.44	100.00	100.00	99.72
Towne	98.31	98.87	99.44	100.00	100.00	99.72
Merlin	98.02	98.59	99.15	99.72	99.72	100.00

[a] Alignment performed using the MUSCLE multiple sequence alignment tool, version 3.8 (Edgar, 2004). Matrix created using Clustal2.1 formatting.

Table 2
HCMV pUS27 alignment percent identity matrix[a].

	TB40/E	TR	Toledo	AD169	Towne	Merlin
TB40/E	100.00	98.06	95.29	98.34	95.29	94.74
TR	98.06	100.00	95.30	99.17	95.30	95.30
Toledo	95.29	95.30	100.00	95.58	99.45	98.90
AD169	98.34	99.17	95.58	100.00	95.58	95.03
Towne	95.29	95.30	99.45	95.58	100.00	98.90
Merlin	94.74	95.30	98.90	95.03	98.90	100.00

[a] Alignment performed using the MUSCLE multiple sequence alignment tool, version 3.8 (Edgar, 2004). Matrix created using Clustal2.1 formatting.

laboratory research (Wilkinson et al., 2015). A BLAST search for the most similar human chemokine receptors to pUS27 and pUS28 was performed, and alignments between complete primary protein sequences were evaluated by Expect (E) value. The closer the E-value is to zero, the more significant the match. The E-values for pUS27 and pUS28 alignments were quite low, and therefore, the results are represented as reciprocal E-value for more clear visualization of closest alignment matches. As shown in Fig. 2A, pUS27 shares the highest similarity with CCR1, although the difference between E-values for alignments of pUS27 with CCR1 and pUS27 with CCR4 (the second most closely matched to pUS27) are not significantly different. On the other hand, pUS28 shows a very strong sequence similarity to CX3CR1 in particular (Fig. 2B). The difference in alignments between pUS28 and CX3CR1 and CCR4 (the second most closely matched to both pUS27 and pUS28) is very substantial. Alignment of pUS27 and pUS28 results in an E-value of $1.0E^{-49}$ (Fig. 3). These results demonstrate that pUS27 is more similar to pUS28 than to any human chemokine receptor; however, pUS28 is more similar to CX3CR1 than to pUS27.

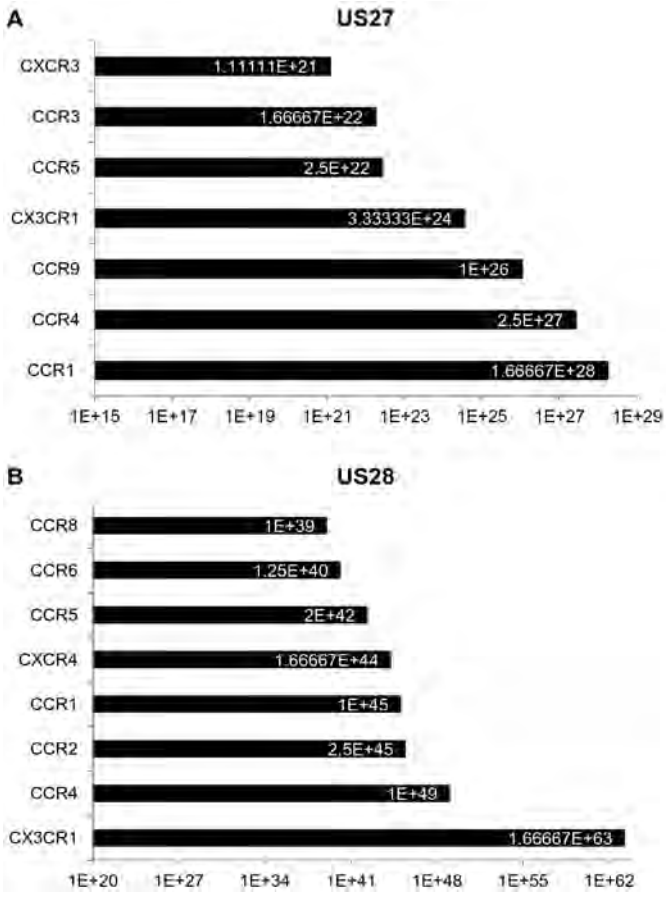


Fig. 2. pUS27 and pUS28 have high similarity to human chemokine receptors. Reciprocal of E-value from BLASTp alignment results after searching with A) pUS27 and B) pUS28.

3.2. Phylogenetic analysis

Phylogenetic analysis was used to investigate the evolutionary history of the US27 and US28 genes. A common ancestor would indicate a shared evolutionary history with the two genes evolving via a gene duplication event. If US27 and US28 had separate ancestral genes, then it is more likely that the two genes evolved via two separate gene captures between HCMV and the host DNA. The inferred maximum likelihood phylogenetic tree supports the hypothesis that US28 and US27 share a common ancestor (Fig. 4). Additionally, the common ancestor of these two viral genes shares a common ancestor with human CX3CR1. The bootstrap support values show strong support for a common ancestor between pUS27 and pUS28. There is very weak support, however, for pCX3CR1 being the closest human protein to pUS27 and pUS28's common ancestor. Bayesian phylogenetic analysis is concordant with the maximum likelihood phylogeny, showing a common ancestral gene between US28 and US27 with that viral ancestral gene sharing a common ancestral gene with human CX3CR1 (Fig. 5). The posterior probabilities are highly supportive of both US27 and US28's common ancestor and this common ancestor's relationship to CX3CR1. These results suggest that a gene capture event led to the common ancestor of US28 and US27 within the viral genome. Then, within the viral DNA, there was a subsequent gene duplication event that ultimately led to US28 and US27 evolving from one common ancestral viral gene. Both Bayesian and maximum likelihood phylogenic analysis support the notion that US27 and US28 most likely arose from a gene duplication event, and they likely share a common ancestor with human CX3CR1.

4. Discussion

Although the evolutionary history of viruses can be difficult to determine due to significant variation between strains and high rates of mutation, the evidence presented here indicates that gene duplication led to the presence of the US27 and US28 genes in the HCMV genome. Beisser et al. previously showed that US27 and US28, along with UL78, cluster with CX3CR1 in a phylogenetic tree, but the study did not evaluate the evolutionary history of the viral genes (Beisser et al., 2002). Our analyses suggest it is likely that an ancestral cytomegalovirus captured a gene from its host, then integrated this gene into its own genome. This newly integrated gene, which shares ancestry with human CX3CR1, would have then undergone a gene duplication event within the viral genome, which led to the creation US27 and US28, paralogs in the HCMV genome. The fate of duplicated genes varies, and gene loss, subfunctionalization, and neofunctionalization are some possible outcomes.

Neofunctionalization occurs when one gene from a gene duplication is constrained by selective pressure, while the other gene is not (Gibson

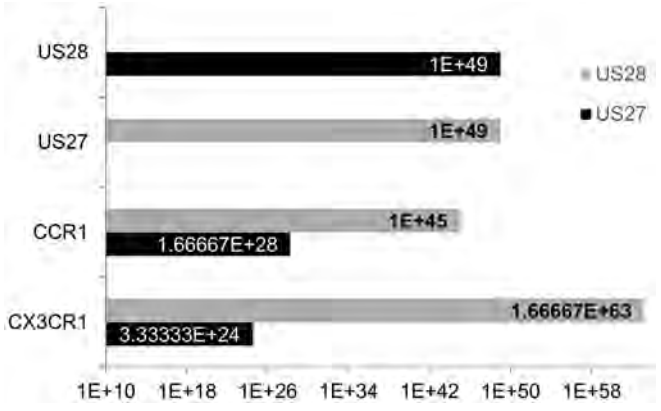


Fig. 3. Comparison of pUS27 and pUS28 alignment matches with human chemokines. Reciprocal of E-value from BLASTp alignment results for pUS27 and pUS28 with top human chemokine receptor matches and with each other.

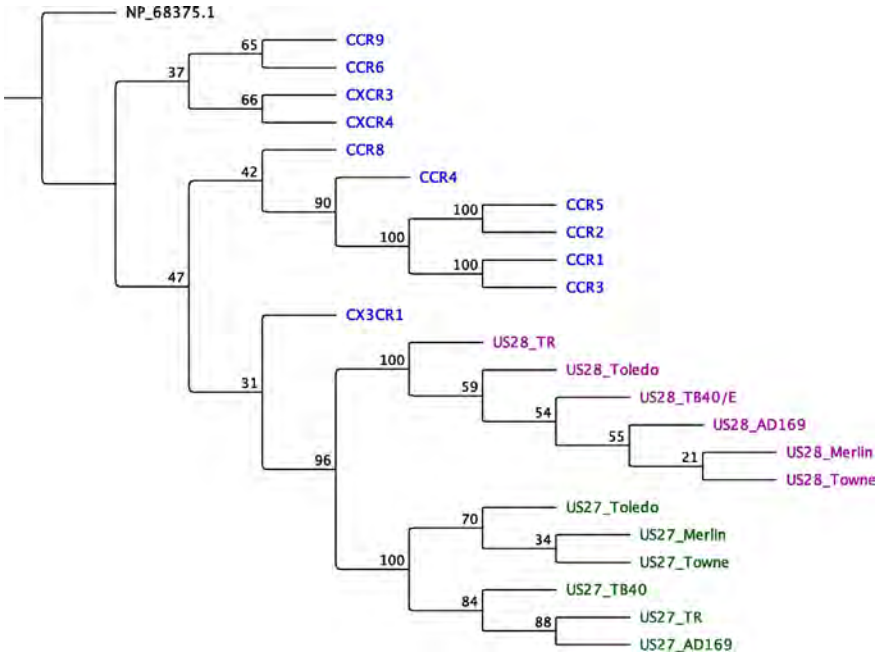


Fig. 4. Maximum likelihood phylogenetic tree of HCMV pUS27 and pUS28 and human chemokine receptors. Various strains of HCMV are shown in green (pUS27) and purple (pUS28). Human chemokine receptors are in blue. Nodes values display bootstrap values (100 replicates). Inferred using PhyML and Geneious v 8.1.3. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

and Goldberg, 2009). In the neofunctionalization scenario, one protein has a low amino acid substitution rate due to purifying selection pressure, causing it to remain more similar to its parent gene. The second gene may take on a new function because of the lack of selective pressure enables evolution of new functionalities that are beneficial to the virus (Zhang, 2003). On the other hand, subfunctionalization occurs when there is no evolutionary advantage to the extra gene copy (Zhang, 2003). With a lack of selective pressure, both genes can mutate, while keeping complementary functions of the original genes. This can be an important form of evolution because it allows enhanced evolution of specific aspects of a gene without trading off fitness for other aspects of a gene.

Because pUS28 exhibits far higher similarity to the human CX3CR1 protein than pUS27, it is likely that US27 underwent neofunctionalization after divergence. This model would propose that after gene duplication occurred, the virus could keep the functionality of pUS28, while pUS27 was less constrained and eventually gained a new function. It is notable that pUS27 does not bind any known human chemokines (Arnolds et al., 2013), but is present in the viral envelope (Margulies and Gibson, 2007) and has the ability to facilitate extracellular virus spread, as

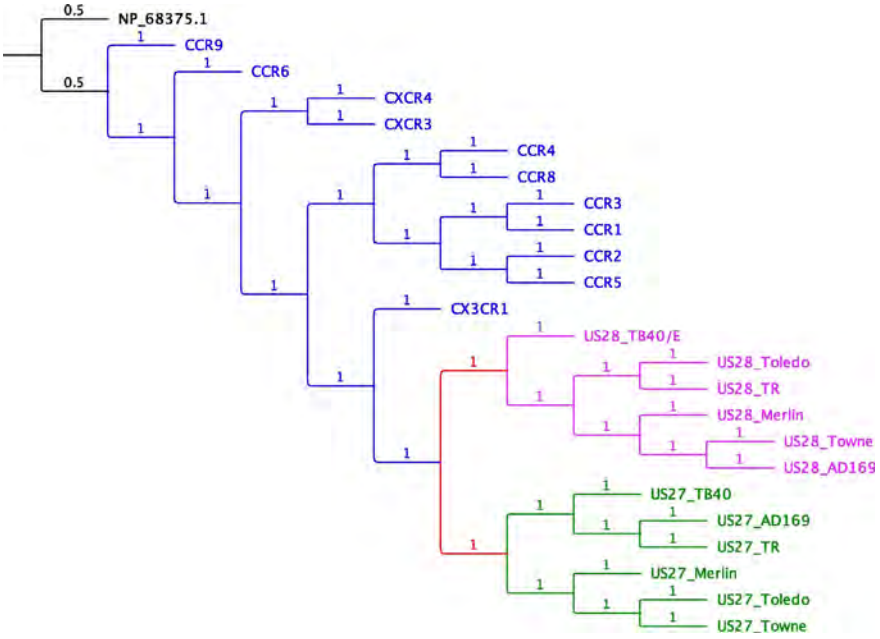


Fig. 5. Bayesian phylogenetic tree of HCMV pUS27 and pUS28 human chemokine receptors and human chemokine receptors. Various strains of HCMV are shown in green (pUS27) and purple (pUS28). Human chemokine receptors are in blue. Red indicates likely gene capture event by ancestral virus. Node values display posterior probabilities. Inferred using MrBayes and Geneious v 8.1.3. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

demonstrated by viral mutants lacking US27 that display reduced virus spreading in culture (O'Connor and Shenk, 2011). In addition, pUS27 also modulates host chemokine networks by enhancing the signaling activity of human CXCR4 (Arnolds et al., 2013), suggesting that CXCR4 may activate cellular pathways that are beneficial to HCMV. However, other possible scenarios, such as subfunctionalization, cannot be ruled out. This model would predict that the ancestral host gene had a range of functions, and after the gene duplication event, US27 and US28 each retained a different subset of the original gene's functions. This would give both US27 and US28 important but non-redundant functions, and ensure that both genes were retained in the genome. While US27 has not been evaluated in patient samples, only minimal variation in US28 sequences was found in samples from HIV-positive patients (Goffard et al., 2006) or from patients with congenital HCMV infection (Arav-Boger et al., 2002). We found that both proteins were highly conserved among a variety of laboratory and clinical strains of HCMV (Tables 1, 2), which could support the subfunctionalization model.

Other possible outcomes for duplicated genes include gene loss or regulatory differentiation (Louis, 2007). Since regulatory sequences are not transcribed into mRNA, our analyses of amino acid sequences are not sufficient for examining the differences between US27 and US28 gene regulatory patterns (Zhang, 2003). Gene loss, on the other hand, is an intriguing possibility. The genomes of green monkey cytomegalovirus (GMCMV) and Rhesus cytomegalovirus (RhCMV) each harbor five adjacent genes with homology to HCMV US28 (Alcendor et al., 2009; Hansen et al., 2003; Martin, 2000). It is conceivable that the ancestor of HCMV also had five genes and subsequently lost all but US27 and US28, which together retain all the most desirable functions of the ancestral gene. Chimpanzee cytomegalovirus also has only two GCPR genes, considered orthologs of HCMV US27 and US28 (Davison et al., 2003) Penfold et al. found that only one of the RhCMV US28 homologs genes had a ligand binding profile similar to HCMV US28 (Penfold et al., 2003), but little is known about the functions of the other genes in this cluster. Further research is necessary to understand the evolutionary advantage of the five tandem copies in GMCCMV and RhCMV, which could potentially shed light on the functions of US27 during HCMV infection.

Our analyses and published experimental evidence (Arnolds et al., 2013; Margulies and Gibson, 2007; O'Connor and Shenk, 2011) support the notion that pUS27 likely underwent neofunctionalization after a gene duplication event while US28 had greater selective pressure to retain the original gene function, keeping the amino acid substitution rate lower. Intriguingly, HCMV also encodes two adjacent chemokine genes, UL146 and UL147, which are found in clinical strains but not in laboratory strains AD169 or Towne (Cha et al., 1996; Prichard et al., 2001). UL146 is a functional chemokine that induces chemotaxis of neutrophils expressing CXCR2, but UL147 does not appear to have chemotactic ability (Penfold et al., 1999). The two genes are believed to be the result of a relatively recent gene duplication event, and evidence indicates that UL146 is the more rapidly evolving paralog (Arav-Boger et al., 2005). The UL146 gene is among the most highly variable in the HCMV genome among sequenced clinical isolates (Arav-Boger et al., 2006; Bradley et al., 2008), but no specific polymorphisms have been linked to disease outcome or severity (Arav-Boger et al., 2006; Heo et al., 2008). The loss of these genes from laboratory strains suggests they are not required for virus replication in culture but may be important during natural infection of the host, although specific roles in virulence or virus dissemination have been difficult to confirm experimentally. Like US27 and US28, the UL146 and UL147 genes are absent from the genomes of rodent CMVs commonly used for in vivo infection models. Additional work is needed to fully understand the mechanisms by which HCMV controls chemokine networks and cell migration patterns to promote virus persistence.

Both maximum likelihood and Bayesian phylogenetic analyses indicate a common ancestor between US27 and US28, suggesting that a gene duplication event within the viral genome led to their existence after capture of a host gene, and that both genes share a common ancestor with human CX3CR1. The relationships inferred for the human chemokine receptors by these analyses also make sense based on current knowledge. For example, the clades containing CCR1, CCR2, CCR3, CCR4, CCR5, and CCR8 (Figs. 4, 5) are consistent with the observation that these genes are all clustered together on human Chromosome 3, suggesting that gene duplications have played a role in the development of multiple, diverse human chemokine receptors in the human genome. The fact that these proteins formed clades in both the maximum likelihood and Bayesian phylogenies corroborates that these methods are successful at grouping together proteins that share evolutionary history.

The CX3CR1 gene, also located on Chromosome 3, codes for a chemokine receptor that binds CX3C Ligand 1 (CX3CL1), also known as fractalkine. Activation of CX3CR1 regulates cell adhesion and directed movement (Imai et al., 1997), and the binding of CX3CL1/fractalkine leads to the attraction of intraepithelial lymphocytes (Isse et al., 2005). This receptor is largely associated with expression on lymphocytes, but CX3CR1 expression has also been observed in microglial cells and macrophages, where interactions with CX3CL1/fractalkine facilitate communications with neurons (Limotala and Ransohoff, 2014). Additionally, CX3CL1/fractalkine contributes to immune function by stimulating the migration of leukocytes during both physiological and pathological conditions. This ligand can exist as either a membrane bound or isolated soluble protein (Haskell et al., 1999). When it is in a soluble state, CX3CL1/fractalkine serves an important role as chemoattractant for the CD8 + and CD4 + T cells, natural killer cells, and monocytes that express the CX3CR1 receptor. In a membrane-bound state, CX3CL1/fractalkine and CX3CR1 form strong binding interactions (Haskell et al., 1999).

The human gene CX3CR1 contains 4 exons and 3 introns (Garin et al., 2002), yet neither the US27 and US28 genes nor the GMCMV, RhCMV, and CCMV orthologs contain any introns (Rawlingson and Barrell, 1993). The exact mechanism of gene capture has not been determined; however, since US27 and US28 lack introns, one possibility is that an ancestral cytomegalovirus acquired the host gene ancestor to US27 and US28 through some retroviral intermediate, perhaps during a mixed infection (McGeoch et al., 2008). The US27 transcript was reported to be spliced within the 5′ untranslated region (Beisser et al., 2002), but the significance of this observation and any effects on US27 gene expression remain unknown.

CX3CR1 can serve as a co-receptor for entry of human immunodeficiency virus (HIV), and specific polymorphisms of CX3CR1 have been linked to an increase in susceptibility to HIV infection and more rapid progression to acquired immunodeficiency syndrome, or AIDS (Parczewski et al., 2014). There are also increased levels of CX3CR1 expression within HIV-positive monocytes (Krishnan et al., 2014). Moreover, active HCMV infection in HIV-infected patients has been connected with perpetually low CD4 + T cell counts (Munawwar and Singh, 2016). It's possible that one reason HCMV co-infection is an increased risk factor for the progression of HIV to AIDS (Munawwar and Singh, 2016; Pleskoff et al., 1997b) is that pUS28 has similar binding properties to CX3CR1 and facilitates HIV infection. In fact, pUS28 has been shown to be able to function as a co-receptor to mediate HIV entry (Pleskoff et al., 1997a). Additional investigation is needed to better understand the role of HCMV in the progression of HIV-infection to AIDS and whether cooperation between pathogens may have played a role in the acquisition of the ancestral host gene by ancient CMVs.

Manipulation of host immune responses is a critical factor for the establishment of persistent HCMV infection. pUS28 is a bona fide viral chemokine receptor that contributes to immune evasion in multiple ways, while the binding and signaling mechanisms of pUS27 remain unclear. However, there is no doubt that the US27 and US28 genes arose from a common ancestor and their protein products have developed distinct roles in the infection, spread, and persistence of HCMV.

Acknowledgements

The authors thank Dr. James Sikes for helpful discussion and critical reading of the manuscript and four anonymous reviewers for their insightful comments. This work was supported by NIH grant AI111232 (to JVS) and USF Faculty Development Funds.

References

Alcendor, D.J., Zong, J., Dolan, A., Gatherer, D., Davison, A.J., Hayward, G.S., 2009. Patterns of divergence in the vCXCL and vGPCR gene clusters in primate cytomegalovirus genomes. Virology 395, 21–32.

Arav-Boger, R., Foster, C.B., Zong, J.C., Pass, R.F., 2006. Human cytomegalovirus-encoded alpha-chemokines exhibit high sequence variability in congenitally infected newborns. J. Infect. Dis. 193, 788–791.

Arav-Boger, R., Willoughby, R.E., Pass, R.F., Zong, J.C., Jang, W.J., Alcendor, D., Hayward, G.S., 2002. Polymorphisms of the cytomegalovirus (CMV)-encoded tumor necrosis factor-alpha and beta-chemokine receptors in congenital CMV disease. J. Infect. Dis. 186, 1057–1064.

Arav-Boger, R., Zong, J.C., Foster, C.B., 2005. Loss of linkage disequilibrium and accelerated protein divergence in duplicated cytomegalovirus chemokine genes. Virus Genes 31, 65–72.

Arnolds, K.L., Lares, A.P., Spencer, J.V., 2013. The US27 gene product of human cytomegalovirus enhances signaling of host chemokine receptor CXCR4. Virology 439, 122–131.

Beisser, P.S., Goh, C.-S., Cohen, F.E., Michelson, S., 2002. Viral Chemokine Receptors and Chemokines in Human Cytomegalovirus Trafficking and Interaction with the Immune System, Viral Proteins Counteracting Host Defenses. Springer, Berlin Heidelberg, pp. 203–234.

Beisser, P.S., Laurent, L., Virelizier, J.L., Michelson, S., 2001. Human cytomegalovirus chemokine receptor gene US28 is transcribed in latently infected THP-1 monocytes. J. Virol. 75, 5949–5957.

Beisser, P.S., Lavreysen, H., Bruggeman, C.A., Vink, C., 2008. Chemokines and chemokine receptors encoded by cytomegaloviruses. Current Topics in Microbiology and Immunology. Springer Science + Business Media, pp. 221–242.

Bradley, A.J., Kovacs, I.J., Gatherer, D., Dargan, D.J., Alkharsah, K.R., Chan, P.K., Carman, W.F., Dedicoat, M., Emery, V.C., Geddes, C.C., Gerna, G., Ben-Ismaeil, B., Kaye, S., McGregor, A., Moss, P.A., Pusztai, R., Rawlinson, W.D., Scott, G.M., Wilkinson, G.W., Schulz, T.F., Davison, A.J., 2008. Genotypic analysis of two hypervariable human cytomegalovirus genes. J. Med. Virol. 80, 1615–1623.

Cannon, M.J., Schmid, D.S., Hyde, T.B., 2010. Review of cytomegalovirus seroprevalence and demographic characteristics associated with infection. Rev. Med. Virol. 20, 202–213.

Cha, T.A., Tom, E., Kemble, G.W., Duke, G.M., Mocarski, E.S., Spaete, R.R., 1996. Human cytomegalovirus clinical isolates carry at least 19 genes not found in laboratory strains. J. Virol. 70, 78–83.

Charo, I.F., Ransohoff, R.M., 2006. The many roles of chemokines and chemokine receptors in inflammation. N. Engl. J. Med. 354, 610–621.

Chattopadhyay, A., 2014. GPCRs: lipid-dependent membrane receptors that act as drug targets. Adv. Biol. 2014, 1–12.

Chee, M.S., Satchwell, S.C., Preddie, E., Weston, K.M., Barrell, B.G., 1990. Human cytomegalovirus encodes three G protein-coupled receptor homologues. Nature 344, 774–777.

Das, S., Pellett, P.E., 2007. Members of the HCMV US12 family of predicted heptaspanning membrane proteins have unique intracellular distributions, including association with the cytoplasmic virion assembly complex. Virology 361, 263–273.

Davison, A.J., Dolan, A., Akter, P., Addison, C., Dargan, D.J., Alcendor, D.J., McGeoch, D.J., Hayward, G.S., 2003. The human cytomegalovirus genome revisited: comparison with the chimpanzee cytomegalovirus genome. J. Gen. Virol. 84, 17–28.

Dziurzynski, K., Chang, S.M., Heimberger, A.B., Kalejta, R.F., McGregor Dallas, S.R., Smit, M., Soroceanu, L., Cobbs, C.S., 2012. Consensus on the role of human cytomegalovirus in glioblastoma. Neuro-Oncology 14, 246–255.

Edgar, R.C., 2004. MUSCLE: multiple sequence alignment with high accuracy and high throughput. Nucleic Acids Res. 32, 1792–1797.

Garin, A., Pellet, P., Deterre, P., Debré, P., Combadiére, C., 2002. Cloning and functional characterization of the human fractalkine receptor promoter regions. Biochem. J. 368, 753–760.

Gibson, T.A., Goldberg, D.S., 2009. Questioning the ubiquity of neofunctionalization. PLoS Comput. Biol. 5.

Goffard, A., Gault, E., Rozenberg, F., Moret, N., Hober, D., Deny, P., 2006. Comparative sequence analysis of US28 gene of human cytomegalovirus strains isolated from HIV-positive patients. Virus Genes 33, 175–181.

Goujon, M., McWilliam, H., Li, W., Valentin, F., Squizzato, S., Paern, J., Lopez, R., 2010. A new bioinformatics analysis tools framework at EMBL-EBI. Nucleic Acids Res. 38, W695–W699.

Guindon, S., Dufayard, J.-F., Lefort, V., Anisimova, M., Hordijk, W., Gascuel, O., 2010. New algorithms and methods to estimate maximum-likelihood phylogenies: assessing the performance of PhyML 3.0. Syst. Biol. 59, 307–321.

Guindon, S., Gascuel, O., 2003. A simple, fast, and accurate algorithm to estimate large phylogenies by maximum likelihood. Syst. Biol. 52, 696–704.

Hansen, S.G., Strelow, L.I., Franchi, D.C., Anders, D.G., Wong, S.W., 2003. Complete sequence and genomic analysis of rhesus cytomegalovirus. J. Virol. 77, 6620–6636.

Haskell, C.A., Cleary, M.D., Charo, I.F., 1999. Molecular uncoupling of fractalkine-mediated cell adhesion and signal transduction. Rapid flow arrest of CX3CR1-expressing cells is independent of G-protein activation. J. Biol. Chem. 274, 10053–10058.

Heo, J., Petheram, S., Demmler, G., Murph, J.R., Adler, S.P., Bale, J., Sparer, T.E., 2008. Polymorphisms within human cytomegalovirus chemokine (UL146/UL147) and cytokine receptor genes (UL144) are not predictive of sequelae in congenitally infected children. Virology 378, 86–96.

Hosogai, M., Shima, N., Nakatani, Y., Inoue, T., Iso, T., Yokoo, H., Yorifuji, H., Akiyama, H., Kishi, S., Isomura, H., 2015. Analysis of human cytomegalovirus replication in primary cultured human corneal endothelial cells. Br. J. Ophthalmol. 99, 1583–1590.

Huelsenbeck, J., Ronquist, F., 2001. MRBAYES: Bayesian inference of phylogenetic trees. Bioinformatics 17, 754–755.

Hughes, A.L., Friedman, R., 2005. Poxvirus genome evolution by gene gain and loss. Mol. Phylogenet. Evol. 35, 186–195.

Humby, M.S., O'Connor, C.M., 2015. Human cytomegalovirus US28 is important for latent infection of hematopoietic progenitor cells. J. Virol. 90, 2959–2970.

Imai, T., Hieshima, K., Haskell, C., Baba, M., Magira, M., Nishimura, M., Kakizaki, M., Takagi, S., Nomiyama, H., Schall, T.J., Yoshie, O., 1997. Identification and molecular characterization of fractalkine receptor CX3CR1, which mediates both leukocyte migration and adhesion. Arch. Immunol. Ther. Exp. 91, 521–530.

Isse, K., Harada, K., Zen, Y., Kamihira, T., Shimoda, S., Harada, M., Nakanuma, Y., 2005. Fractalkine and CX3CR1 are involved in the recruitment of intraepithelial lymphocytes of intrahepatic bile ducts. Hepatology 41, 506–516.

Kearse, M., Moir, R., Wilson, A., Stones-Havas, S., Cheung, M., Sturrock, S., Buxton, S., Cooper, A., Markowitz, S., Duran, C., Thierer, T., Ashton, B., Mentijies, P., Drummond, A., 2012. Geneious basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. Bioinformatics 28, 1647–1649.

Krishnan, S., Wilson, E.M.P., Sheikh, V., Rupert, A., Mendoza, D., Yang, J., Lempicki, R., Migueles, S.A., Sereti, I., 2014. Evidence for innate immune system activation in HIV type 1–infected elite controllers. J. Infect. Dis. 209, 931–939.

Kuhn, D.E., Beall, C.J., Kolattukudy, P.E., 1995. The cytomegalovirus US28 protein binds multiple CC chemokines with high affinity. Biochem. Biophys. Res. Commun. 211, 325–330.

Lares, A.P., Tu, C.C., Spencer, J.V., 2013. The human cytomegalovirus US27 gene product enhances cell proliferation and alters cellular gene expression. Virus Res. 176, 312–320.

Larkin, M.A., Blackshields, G., Brown, N.P., Chenna, R., McGettigan, P.A., McWilliam, H., Valentin, F., Wallace, I.M., Wilm, A., Lopez, R., Thompson, J.D., Gibson, T.J., Higgins, D.G., 2007. ClustalW and ClustalX version 2.0. Bioinformatics 23, 2947–2948.

Lesniewski, M., Das, S., Skomorovska-Prokvolit, Y., Wang, F.Z., Pellett, P.E., 2006. Primate cytomegalovirus US12 gene family: a distinct and diverse clade of seven-transmembrane proteins. Virology 354, 286–298.

Limotala, C., Ransohoff, R.M., 2014. Modulating neurotoxicity through CX3CL1/CX3CR1 signaling. Front. Cell. Neurosci. 8.

Louis, E.J., 2007. Evolutionary genetics: making the most of redundancy. Nature 449, 673–674.

Madden, T., 2002. The BLAST sequence analysis tool. In: McEntyre, J., Ostell, J. (Eds.), The NCBI Handbook. National Center for Biotechnology Information, Bethesda, MD.

Manicklal, S., Emery, V.C., Lazzarotto, T., Boppana, S.B., Gupta, R.K., 2013. The "silent" global burden of congenital cytomegalovirus. Clin. Microbiol. Rev. 26, 86–102.

Margulies, B.J., Gibson, W., 2007. The chemokine receptor homologue encoded by US27 of human cytomegalovirus is heavily glycosylated and is present in infected human foreskin fibroblasts and enveloped virus particles. Virus Res. 123, 57–71.

Martin, W.J., 2000. Chemokine receptor-related genetic sequences in an African green monkey simian cytomegalovirus-derived stealth virus. Exp. Mol. Pathol. 69, 10–16.

Mason, G.M., Jackson, S., Okecha, G., Poole, E., Sissons, J.G., Sinclair, J., Wills, M.R., 2013. Human cytomegalovirus latency-associated proteins elicit immune-suppressive IL-10 producing CD4(+) T cells. PLoS Pathog. 9, e1003635.

McGeoch, D.J., Davison, A.J., Dolan, A., Gatherer, D., Sevilla-Reyes, E.E., 2008. Molecular evolution of the herpesvirales. In: Domingo, E., Parrish, C.R., Holland, J.J. (Eds.), Origin and Evolution of Viruses. Elsevier, pp. 447–475.

McGeoch, D.J., Rixon, F.J., Davison, A.J., 2006. Topics in herpesvirus genomics and evolution. Virus Res. 117, 90–104.

McSharry, B., Avdic, S., Slobedman, B., 2012a. Human cytomegalovirus encoded homologs of cytokines, chemokines and their receptors: roles in immunomodulation. Viruses 4, 2448–2470.

McSharry, B.P., Avdic, S., Slobedman, B., 2012b. Human cytomegalovirus encoded homologs of cytokines, chemokines and their receptors: roles in immunomodulation. Viruses 4, 2448–2470.

Michaelis, M., Doerr, H.W., Cinatl, J., 2009. The story of human cytomegalovirus and cancer: increasing evidence and open questions. Neoplasia 11, 1–9.

Munawwar, A., Singh, S., 2016. Human herpesviruses as Copathogens of HIV infection, their role in HIV transmission, and disease progression. J. Lab. Physicians 8, 5–18.

Murdoch, C., Finn, A., 2000. Chemokine receptors and their role in vascular biology. J. Vasc. Res. 37, 1–7.

Noriega, V., Gardner, T., Redmann, V., Bongers, G., Lira, S., Tortorella, D., 2014. Human cytomegalovirus US28 facilitates cell-to-cell viral dissemination. Viruses 6, 1202–1218.

O'Connor, C.M., Shenk, T., 2011. Human cytomegalovirus pUS27 G protein-coupled receptor homologue is required for efficient spread by the extracellular route but not for direct cell-to-cell spread. J. Virol. 85, 3700–3707.

O'Connor, C.M., Skenk, T., 2011. Human cytomegalovirus pUS27 G protein-coupled receptor homologue is required for efficient spread by the extracellular route but not for direct cell-to-cell spread. J. Virol. 85, 3700–3707.

Parczewski, M., Urbańska, A., Maciejewska, K., Clark, J., Leszczyszyn-Pynka, M., 2014. Association of chemokine receptor gene variants with HIV-1 genotype predicted tropism. HIV Med. 15, 577–586.

Penfold, M.E., Dairaghi, D.J., Duke, G.M., Saederup, N., Mocarski, E.S., Kemble, G.W., Schall, T.J., 1999. Cytomegalovirus encodes a potent alpha chemokine. Proc. Natl. Acad. Sci. U. S. A. 96, 9839–9844.

Penfold, M.E., Schmidt, T.L., Dairaghi, D.J., Barry, P.A., Schall, T.J., 2003. Characterization of the rhesus cytomegalovirus US28 locus. J. Virol. 77, 10404–10413.

Pleskoff, O., Treboute, C., Brelot, A., Heveker, N., Seman, M., Alizon, M., 1997a. Identification of a chemokine receptor encoded by human cytomegalovirus as a cofactor for HIV-1 entry. Science 276, 1874–1878.

Pleskoff, O., Tréboute, C., Brelot, A., Heveker, N., Seman, M., Alizon, M., 1997b. Identification of a chemokine receptor encoded by human cytomegalovirus as a cofactor for HIV-1 entry. Science 276, 1874–1879.

Prichard, M.N., Penfold, M.E., Duke, G.M., Spaete, R.R., Kemble, G.W., 2001. A review of genetic differences between limited and extensively passaged human cytomegalovirus strains. Rev. Med. Virol. 11, 191–200.

Raman, D., Sobolik-Delmaire, T., Richmond, A., 2011. Chemokines in health and disease. Exp. Cell Res. 317, 575–589.

Ramanan, P., Razonable, R.R., 2013. Cytomegalovirus infections in solid organ transplantation: a review. J. Infect. Chemother. 45, 260–271.

Rawlingson, W.D., Barrell, B.G., 1993. Spliced transcripts of human cytomegalovirus. J. Virol. 67, 5502–5513.

Rosa, C.L., Diamond, D.J., 2012. The immune response to human CMV. Futur. Virol. 7, 279–293.

Spiess, K., Jeppesen, M.G., Malmgaard-Clausen, M., Krzywkowski, K., Dulal, K., Cheng, T., Hjortø, G.M., Larsen, O., Burg, J.S., Jarvis, M.A., Garcia, K.C., Zhu, H., Kledal, T.N., Rosenkilde, M.M., 2015. Rationally designed chemokine-based toxin targeting the viral G protein-coupled receptor US28 potently inhibits cytomegalovirus infection in vivo. Proc. Natl. Acad. Sci. 112, 8427–8432.

Tu, C.C., Spencer, J.V., 2014. The DRY box and C-terminal domain of the human cytomegalovirus US27 gene product play a role in promoting cell growth and survival. PLoS One 9, e113427.

Vieira, J., Schall, T.J., Corey, L., Geballe, A.P., 1998. Functional analysis of the human cytomegalovirus US28 gene by insertion mutagenesis with the green fluorescent protein gene. J. Virol. 72, 8158–8165.

Wang, N., Baldi, P.F., Gaut, B.S., 2007. Phylogenetic analysis, genome evolution and the rate of gene gain in the Herpesviridae. Mol. Phylogenet. Evol. 43, 1066–1075.

Wertheim, J.O., Smith, M.D., Smith, D.M., Scheffler, K., Kosakovsky Pond, S.L., 2014. Evolutionary origins of human herpes simplex viruses 1 and 2. Mol. Biol. Evol. 31, 2356–2364.

Wilkinson, G.W.G., Davison, A.J., Tomasec, P., Fielding, C.A., Aicheler, R., Murrell, I., Seirafian, S., Wang, E.C.Y., Weekes, M., Lehner, P.J., Wilkie, G.S., Stanton, R.J., 2015. Human cytomegalovirus: taking the strain. Med. Microbiol. Immunol. 204, 273–284.

Wreghitt, T.G., Teare, E.L., Sule, O., Devi, R., Rice, P., 2003. Cytomegalovirus infection in immunocompetent patients. Clin. Infect. Dis. 37, 1603–1606.

Zhang, J., 2003. Evolution by gene duplication: an update. Trends Ecol. Evol. 18, 292–298.

Mass Extinctions Increase Evenness of Genus Diversity Across Ecological Modes

Catherine Lau
Department of Biology, University of San Francisco
cklau@usfca.edu

Introduction

In the big five mass extinctions, diversity is preferentially lost in ecological modes with greater diversity preceding these events,[1] but little is known about how diversity rebounds. Bambach et al. (2007) created the scheme of ecological modes[2] and Knope et al. (2015) used these modes as proxies for functional diversification in marine animals across time.[1] Using the Knope et al. (2015) data set, I explore the following question: **When diversity rebounds, does it recover to a similar distribution of genus diversity across ecological modes or to a more even distribution spanning different ecological modes?**

Background

The Knope et al. (2015) data set consists of the assignment of modes to 18,621 marine animal genera using Bambach's scheme, categories constructed by combinations of habitat tiering levels, motility levels, and feeding modes. Using that data, they created a heatmap (Figure 1).

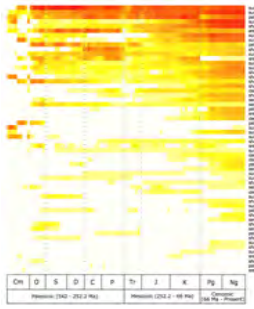


Figure 1. Heatmap of Marine Animal Genus Diversity in Ecological Modes across Time. Vertical lines represent the big five mass extinctions. Columns represent the number of genera within ecological modes at each point in time. Color intensity represents the number of genera, with yellow depicting one genus and red depicting 521 genera.

Results

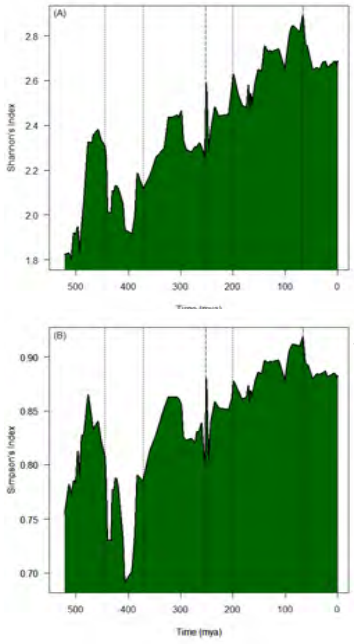


Figure 2. Evenness of Ecological Modes Steadily Increases over Time. Indices, Shannon's (A) and Simpson's (B), were plotted against time, in millions of years ago or mya, for 18,621 marine animal genera. **The indices, which represent the evenness of ecological modes, increase over time, significantly jumping after mass extinctions, depicted by the vertical lines.** While Shannon's (A) shows the increasing trend, Simpson's (B) reaffirms that evidence while showing more prominent peaks and valleys in evenness.

Discussion

The Shannon index quantifies evenness of ecological modes, accounting for both number of modes and proportion of genera in each. The Simpson index looks at an aspect of evenness by measuring the probability that two genera randomly selected at a point in time belong to different modes. While it follows the same trend as the Shannon index, the peaks and valleys in evenness are more pronounced.

During mass extinctions, there is a spike in evenness, with the most genera being lost from modes with higher genus diversity and the least being lost from those with fewer genera, decreasing the disparity in diversity among the modes. In the recovery interval, there is a rapid decline, then this increased evenness is not only maintained but continues to increase. With each subsequent mass extinction, this pattern repeats and as the disparity is continuously lessened, evenness increases over time. **When diversity rebounds, it recovers to a more even distribution spanning different ecological modes.**

Future Directions

Since this study is a first step into understanding *how* diversity rebounds, future studies should address the mechanism of *why* it tends to recover more evenly across ecological modes.

- Following each mass extinction, there is a rapid decline in evenness before evenness continues to increase. A future study would be to investigate what is causing it.
- Another study would be to examine how the functional diversification of species after mass extinctions change the trajectory of species' interactions, such as competition or predation, also causing diversification in those unaffected by the mass extinctions.

Methods

Whereas diversity index equations combine species richness and species evenness to quantify the diversity within a community, I substituted ecological modes and number of genera respectively to quantify the evenness of ecological modes for each geologic stage (~5 million year intervals) from the Cambrian Explosion (542 mya) to the present day. (Equations 1 and 2).

The Shannon index and the Simpson index were calculated for each column so that the trend could be graphed with evenness of ecological modes against time. Statistical analyses were performed in the R computer programming environment .

Equation 1. The Shannon Index

$$H = -\sum_{i=1}^{s} p_i \ln(p_i)$$

Equation 2. The Simpson Index

$$D = \sum_{i=1}^{s} (p_i)^2$$

Then, $1 - D$ is performed.

s = the number of ecological modes at a point in time
p_i = the proportion of genera in the *i*th ecological mode

References

(1) Knope, M.L., N.A. Heim, L.O. Frishkoff, and J.L. Payne. "Limited role of functional differentiation in early diversification of animals." Nature Communications (2015): 1-6.
(2) Bambach, Richard K., Andrew M. Bush, and Douglas H. Erwin. "Autecology and the Filling of Ecospace: Key Metazoan Radiations." Paleontology 50.1 (2007): 1-22.

Development of a non-invasive liquid biopsy for detection of cmvIL-10

Alexander Shin, Margarette Mariano, and Juliet Spencer

Human cytomegalovirus (HCMV) is a prevalent type of herpes virus in our population. HCMV infection has no effect on the majority of people, but in some cases HCMV is strongly correlated with various medical outcomes, such as breast cancer. We focus on the UL111A gene product of HCMV, which encodes the secreted protein cmvIL-10. CmvIL-10 is a homolog of human cytokine IL-10 (hIL-10), which has immunosuppressive effects and promotes proliferation and invasion of breast cancer cells *in vitro.* We are measuring cmvIL-10 in human blood and have found elevated levels of cmvIL-10 in cancer patients. Here, we are investigating the adaptation of the cmvIL-10 blood test for detection of the viral cytokine in saliva and urine. We are now conducting a study of healthy donors to monitor changes in cmvIL-10 levels over time in various body fluids. The results from this small pilot project may ultimately lead to an inexpensive and non-invasive diagnostic tool for detection of breast cancer.

Human Cytomegalovirus (HCMV) is a herpesvirus that infects a majority of the world's population. There are many viral gene products that aid in virus infection and the establishment of the lifelong latency. UL111A, is a viral gene which, through alternate intron splicing, codes for two protein products cmvIL-10 and LAcmvIL-10 that mimic the structure of human interleukin-10 (hIL-10) to varying degrees. cmvIL-10 has been shown to have a wide range of physiological effects, whereas the effects of LAcmvIL-10 appear to be much more limited in scope. This study seeks to measure the expression levels of LAcmvIL-10 during lytic infection of fibroblasts, examine the dimerization patterns of hIL-10, cmvIL-10, and LAcmvIL-10, and understand the resultant signaling pathways activated by LAcmvIL-10 activity. Due to the far-reaching impact of this virus, a deeper understanding of its interactions with the host may lead to improved treatment and prevention options in the future.

Torn between two diseases: Alteration in TGFβ Signaling Prevents Diabetes but Promotes Neuropathy

VASALYA PANCHUMARTHI

UNIVERSITY OF SAN FRANCISCO

BIOLOGY MAJOR & NEUROSCIENCE, CHEMISTRY MINORS

CREATIVE ACTIVITY & RESEARCH DAY, APRIL 22ND 2016

Joy Kim
April 5, 2016

CARD Abstract

TITLE: Use of Novel Mutant Viral Proteins to Investigate Chemokine Receptor Signaling

ABSTRACT

Human Cytomegalovirus (HCMV) is a widespread pathogen that causes lifelong latent infection. HCMV rarely causes disease in healthy adults. However, immune-compromised individuals like transplant recipients and AIDS patients can suffer from life-threatening disease. HCMV encodes four G-protein coupled receptors, US27, US28, UL33, and UL78. GPCRs have seven transmembrane α-helices and play vital roles in cellular communication networks. Viral GPCRs may exploit these signaling pathways, and US27 was found to increase cellular proliferation and enhance CXCR4 signaling. Here, US27 deletion mutants are being used to define domains of the viral protein critical for impacting CXCR4 function. These results are expected to clarify how HCMV alters cell communications networks by regulating CXCR4 activity.

Virus-Host Co-evolution: Determining the Origin of Human Cytomegalovirus US27 and US28

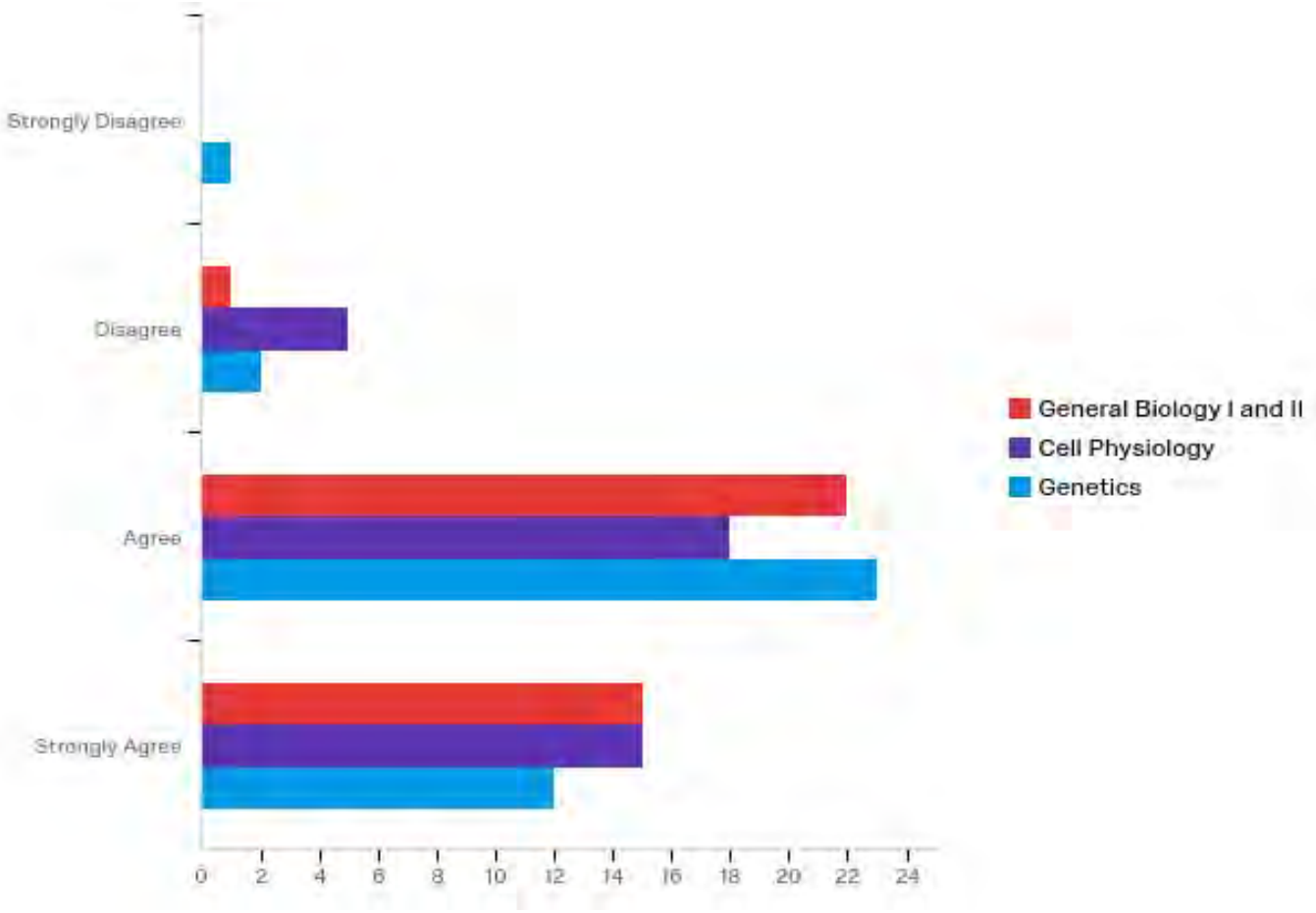
G protein-coupled receptors (GPCR) are the largest family of cell surface proteins, found in organisms from yeast to humans. Human cytomegalovirus (HCMV) is a widespread pathogen that is particularly skilled at evading immune detection and defense mechanisms, largely due to extensive co-evolution with its host's immune system. One aspect of this co-evolution involves the acquisition of four virally encoded GPCR homologs: US27, US28, UL33 and UL78. In this research, phylogenetic analysis was used to investigate the origins of the US27 and US28 genes, which are adjacent in the viral genome. The results indicate that both US27 and US28 share the same common ancestor, human chemokine receptor CX3CR1, suggesting that a single human gene was captured and a viral gene duplication event occurred. While the evolutionary purpose of the gene duplication event remains unclear, experimental evidence indicates that each gene has evolved distinct, important functions during virus infection.

Default Report

2017 Biology Graduation! Survey

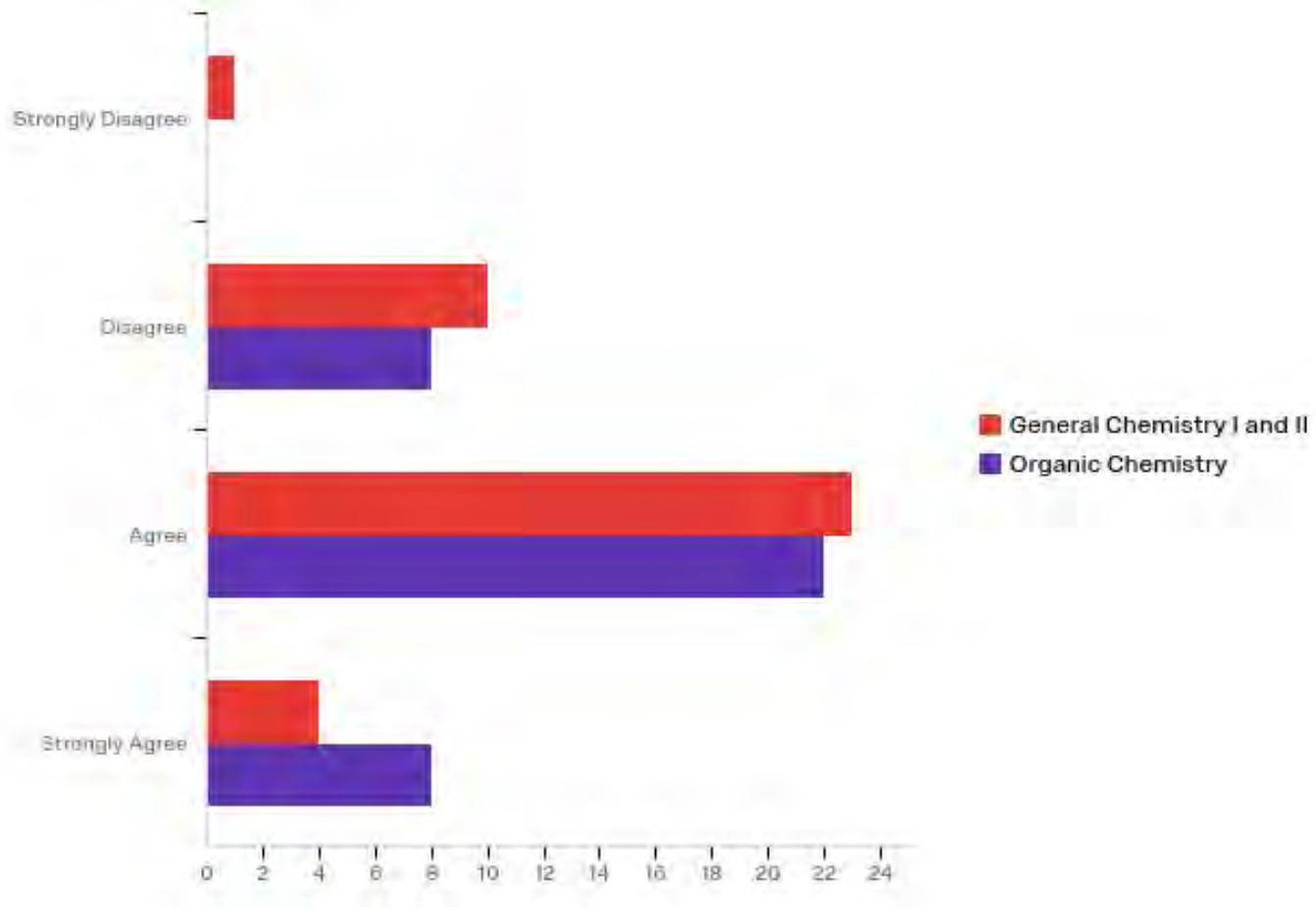
May 14th 2017, 2:30 pm PDT

Q6 - The following course/s prepared me for the biology courses that followed them.



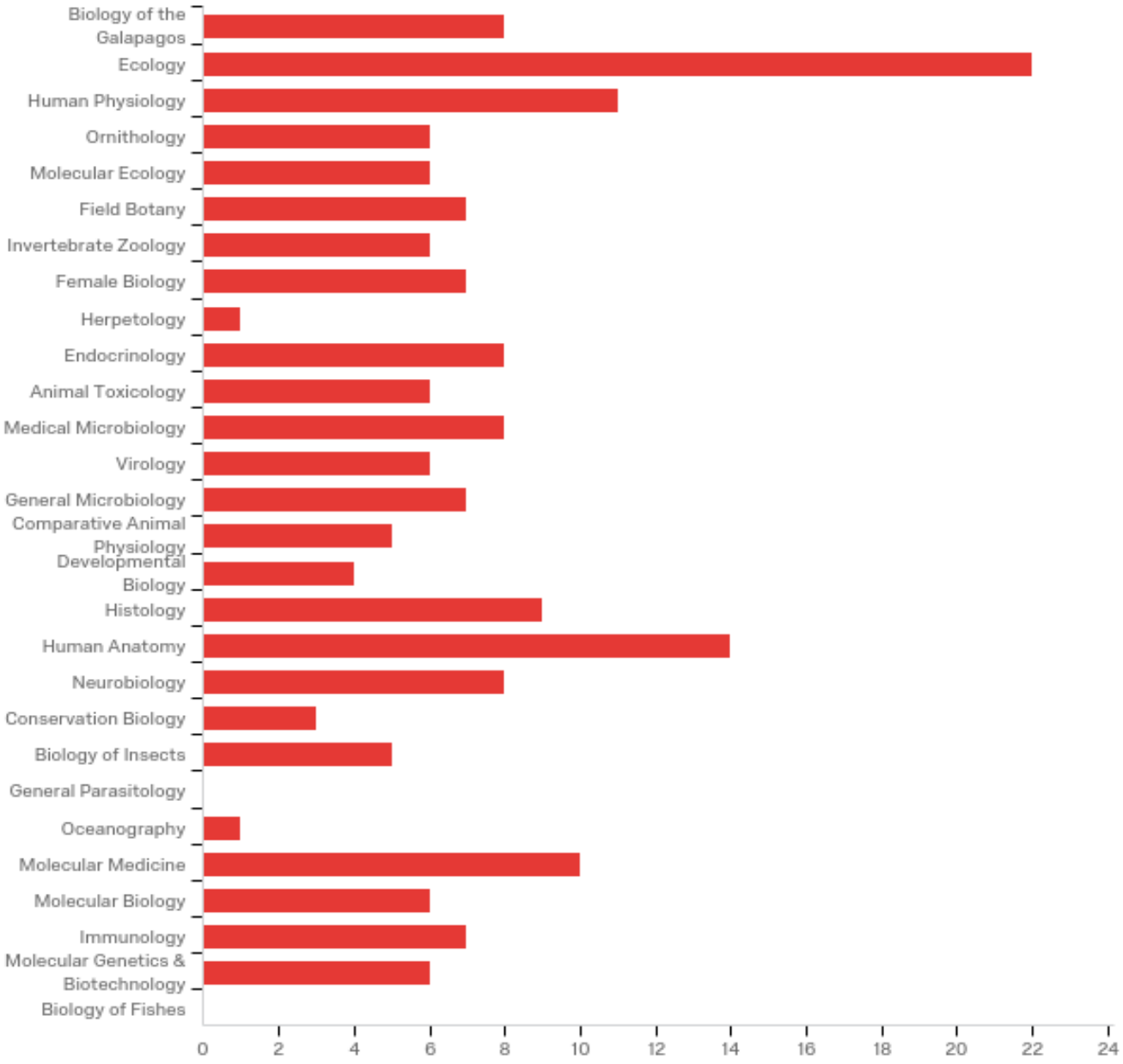
#	Question	Strongly Disagree		Disagree		Agree		Strongly Agree		Total
1	General Biology I and II	0.00%	0	2.63%	1	57.89%	22	39.47%	15	38
2	Cell Physiology	0.00%	0	13.16%	5	47.37%	18	39.47%	15	38
3	Genetics	2.63%	1	5.26%	2	60.53%	23	31.58%	12	38

Q7 - The following courses provided a foundation for my understanding of biology.



#	Question	Strongly Disagree		Disagree		Agree		Strongly Agree		Total
1	General Chemistry I and II	2.63%	1	26.32%	10	60.53%	23	10.53%	4	38
2	Organic Chemistry	0.00%	0	21.05%	8	57.89%	22	21.05%	8	38

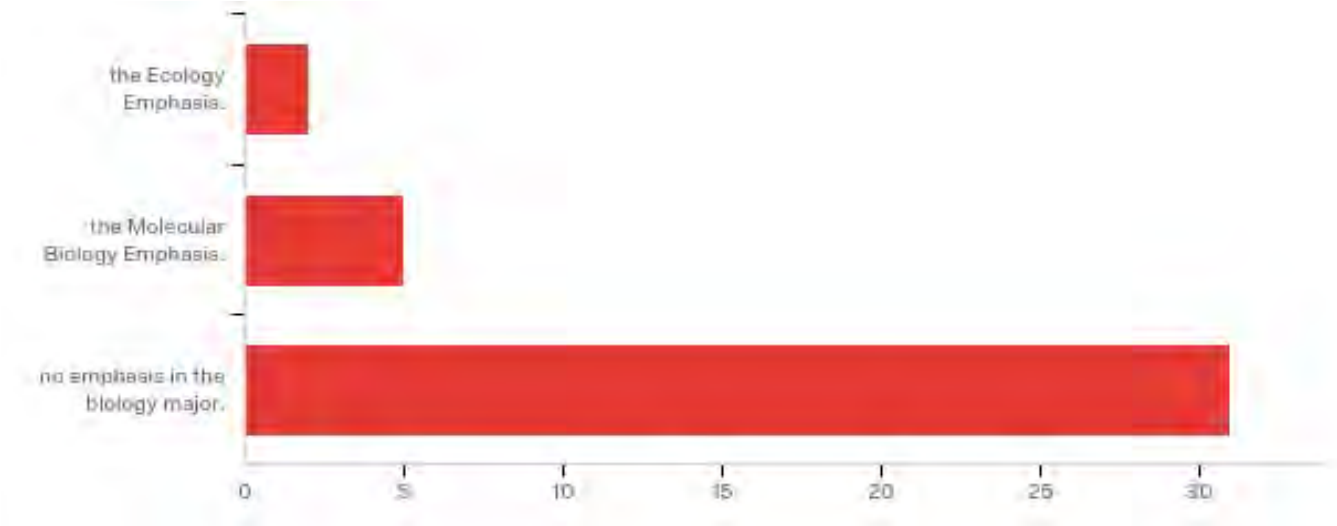
Q8 - I completed (or am currently completing) the following upper-division elective courses:



#	Answer	%	Count
1	Biology of the Galapagos	21.05%	8
2	Ecology	57.89%	22
3	Human Physiology	28.95%	11
4	Ornithology	15.79%	6
5	Molecular Ecology	15.79%	6

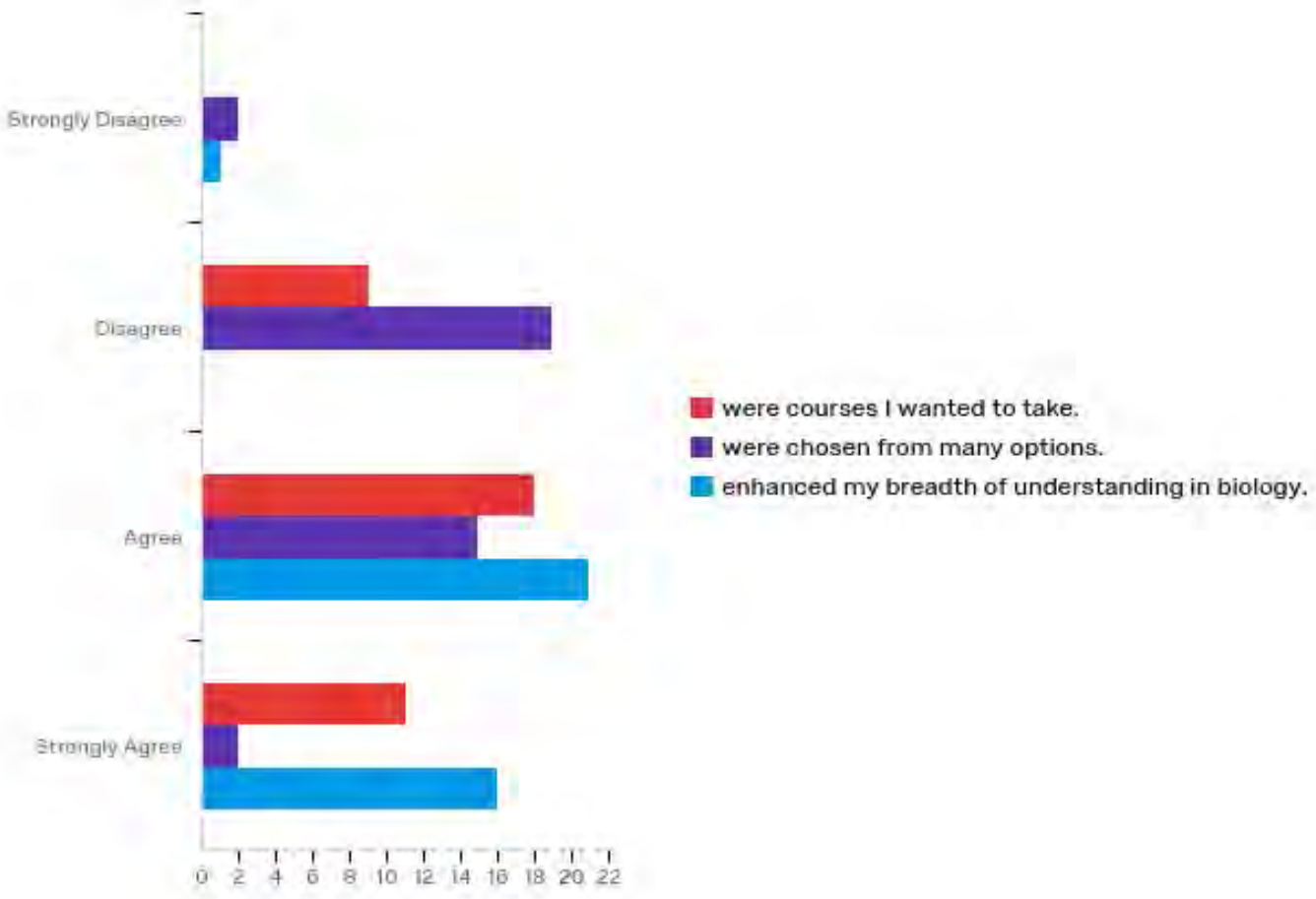
6	Field Botany	18.42%	7
7	Invertebrate Zoology	15.79%	6
8	Female Biology	18.42%	7
9	Herpetology	2.63%	1
10	Endocrinology	21.05%	8
11	Animal Toxicology	15.79%	6
12	Medical Microbiology	21.05%	8
13	Virology	15.79%	6
14	General Microbiology	18.42%	7
15	Comparative Animal Physiology	13.16%	5
16	Developmental Biology	10.53%	4
17	Histology	23.68%	9
18	Human Anatomy	36.84%	14
19	Neurobiology	21.05%	8
20	Conservation Biology	7.89%	3
21	Biology of Insects	13.16%	5
22	General Parasitology	0.00%	0
23	Oceanography	2.63%	1
24	Molecular Medicine	26.32%	10
25	Molecular Biology	15.79%	6
26	Immunology	18.42%	7
27	Molecular Genetics & Biotechnology	15.79%	6
28	Biology of Fishes	0.00%	0
	Total	100%	38

Q13 - I am completing the biology major, having declared



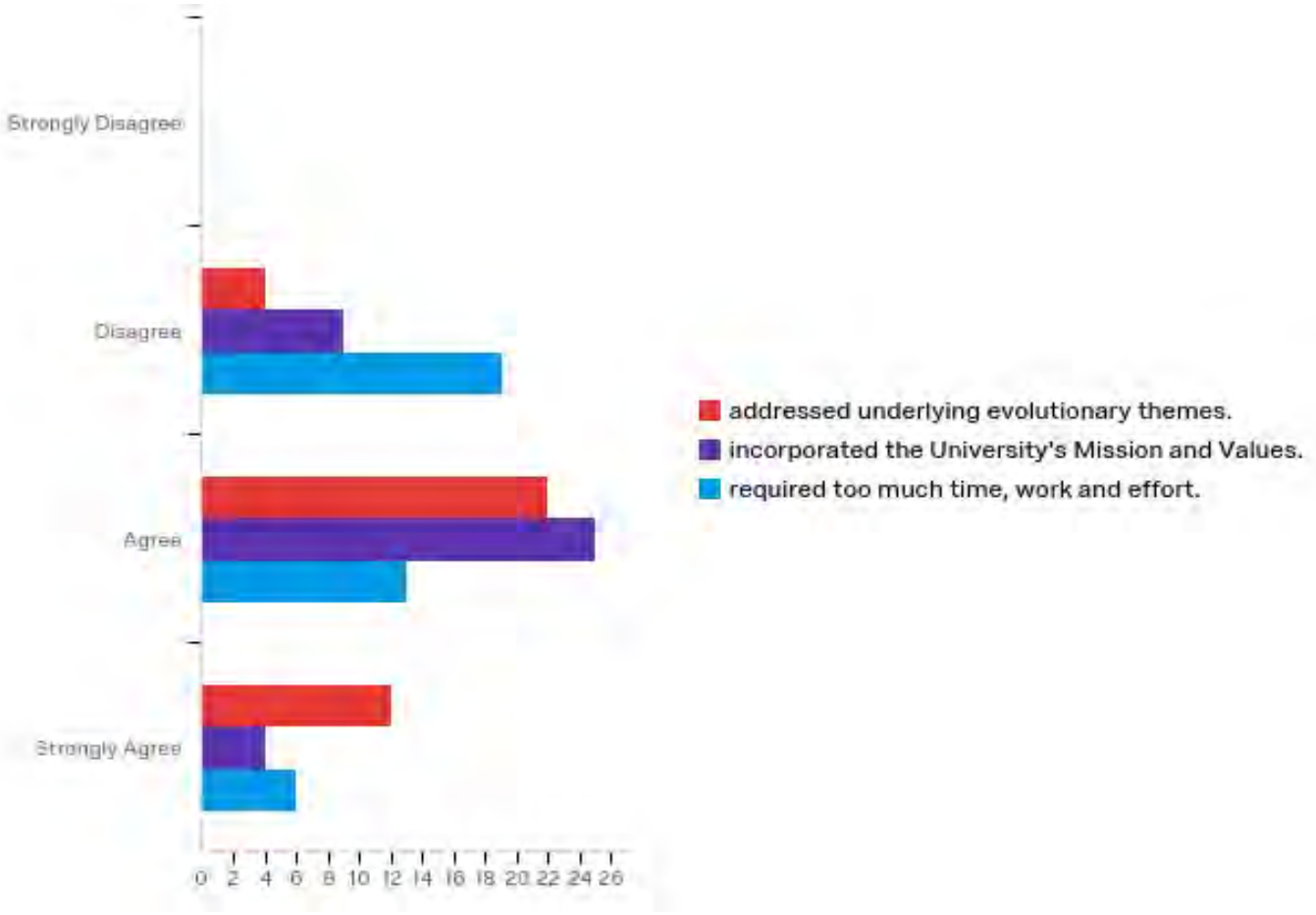
#	Answer	%	Count
1	the Ecology Emphasis.	5.26%	2
2	the Molecular Biology Emphasis.	13.16%	5
3	no emphasis in the biology major.	81.58%	31
	Total	100%	38

Q8 - The upper-division biology courses I took



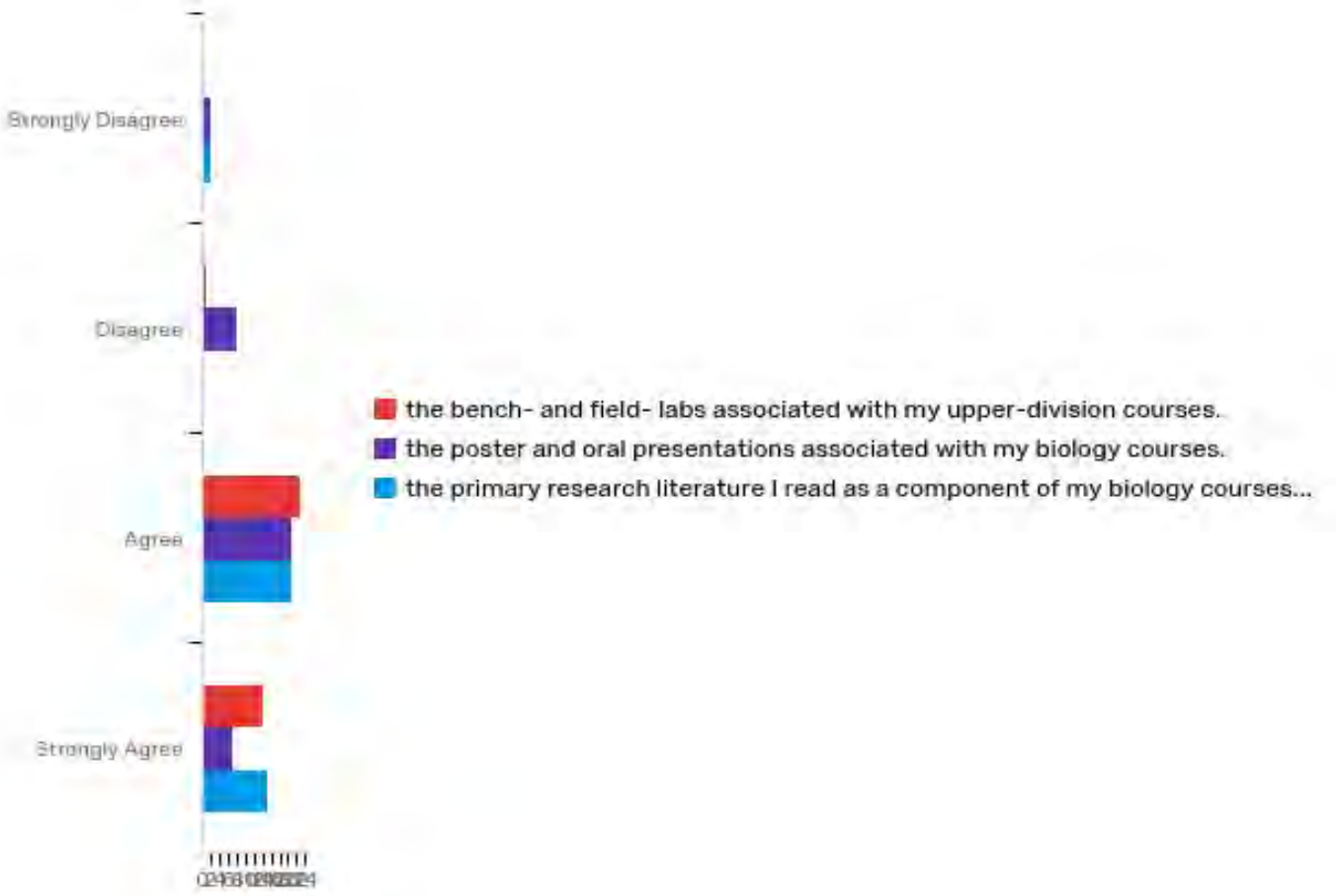
#	Question	Strongly Disagree		Disagree		Agree		Strongly Agree		Total
1	were courses I wanted to take.	0.00%	0	23.68%	9	47.37%	18	28.95%	11	38
2	were chosen from many options.	5.26%	2	50.00%	19	39.47%	15	5.26%	2	38
3	enhanced my breadth of understanding in biology.	2.63%	1	0.00%	0	55.26%	21	42.11%	16	38

Q16 - The upper- and lower-division biology courses I took



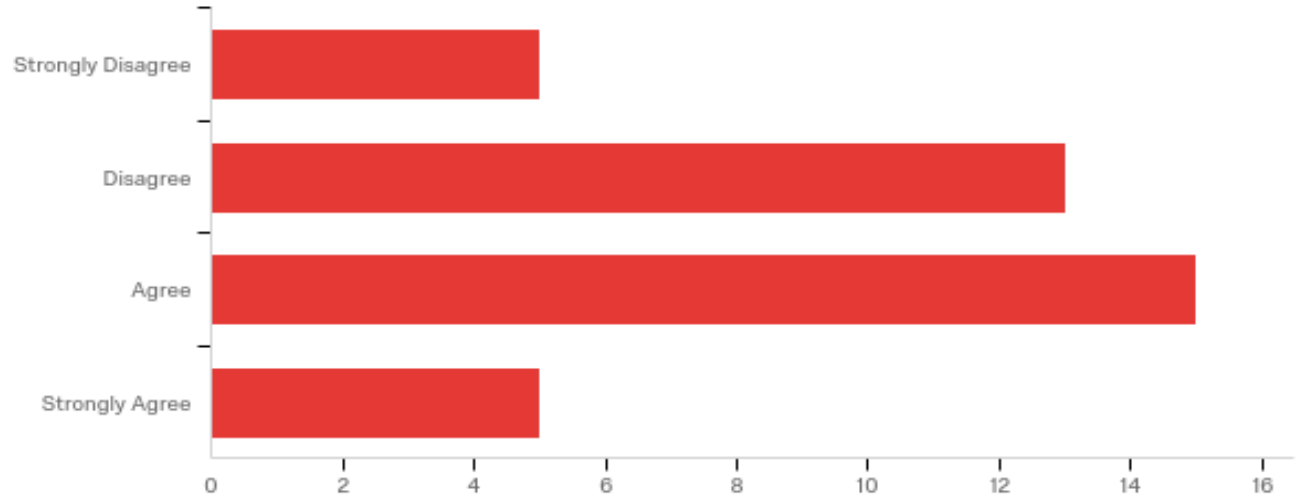
#	Question	Strongly Disagree		Disagree		Agree		Strongly Agree		Total
1	addressed underlying evolutionary themes.	0.00%	0	10.53%	4	57.89%	22	31.58%	12	38
2	incorporated the University's Mission and Values.	0.00%	0	23.68%	9	65.79%	25	10.53%	4	38
3	required too much time, work and effort.	0.00%	0	50.00%	19	34.21%	13	15.79%	6	38

Q9 - My breadth and depth of knowledge in biology was enhanced by



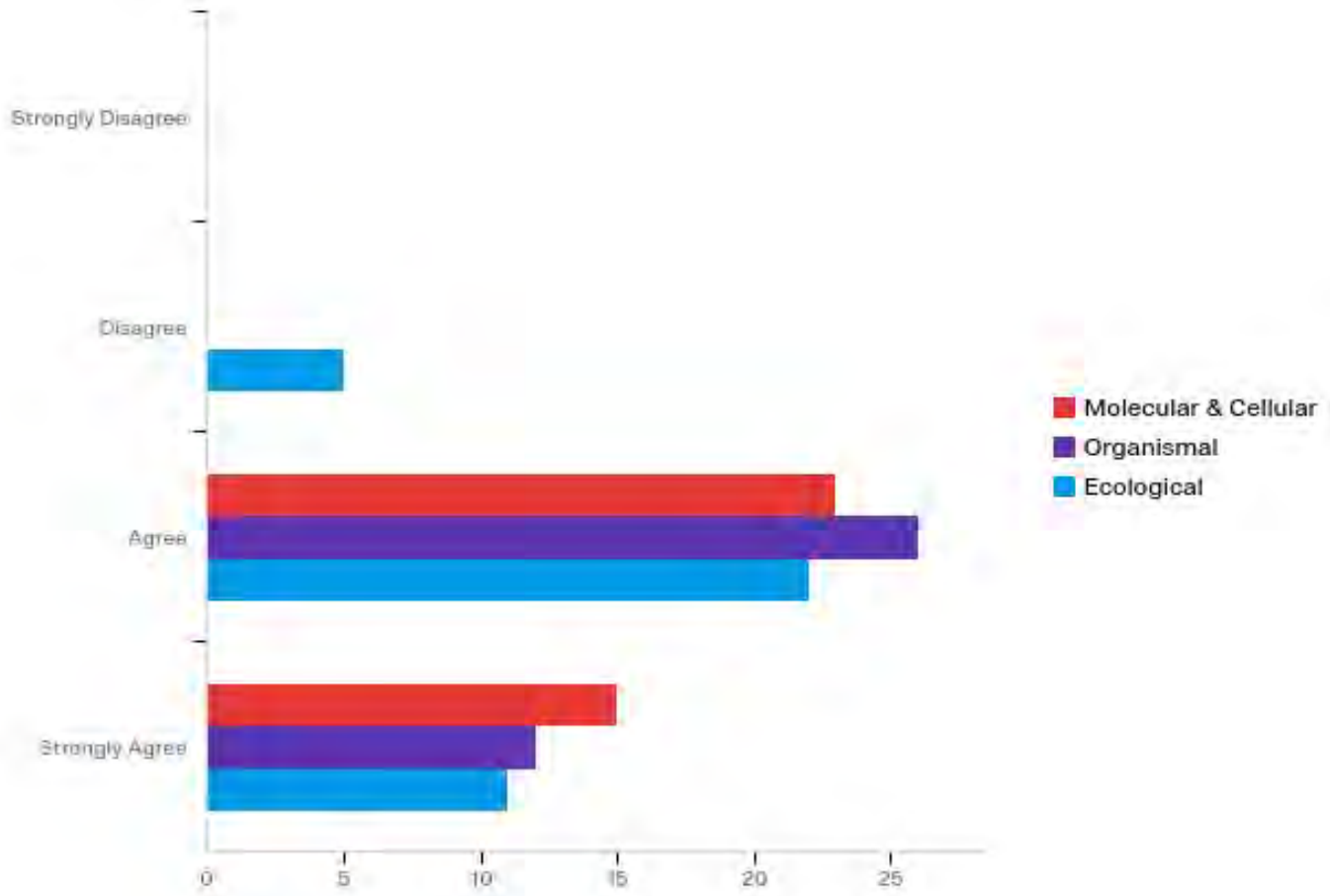
#	Question	Strongly Disagree		Disagree		Agree		Strongly Agree		Total
1	the bench- and field- labs associated with my upper-division courses.	0.00%	0	2.63%	1	60.53%	23	36.84%	14	38
2	the poster and oral presentations associated with my biology courses.	5.26%	2	21.05%	8	55.26%	21	18.42%	7	38
3	the primary research literature I read as a component of my biology courses.	5.26%	2	0.00%	0	55.26%	21	39.47%	15	38

Q17 - My biology major GPA reflects my ability and effort.



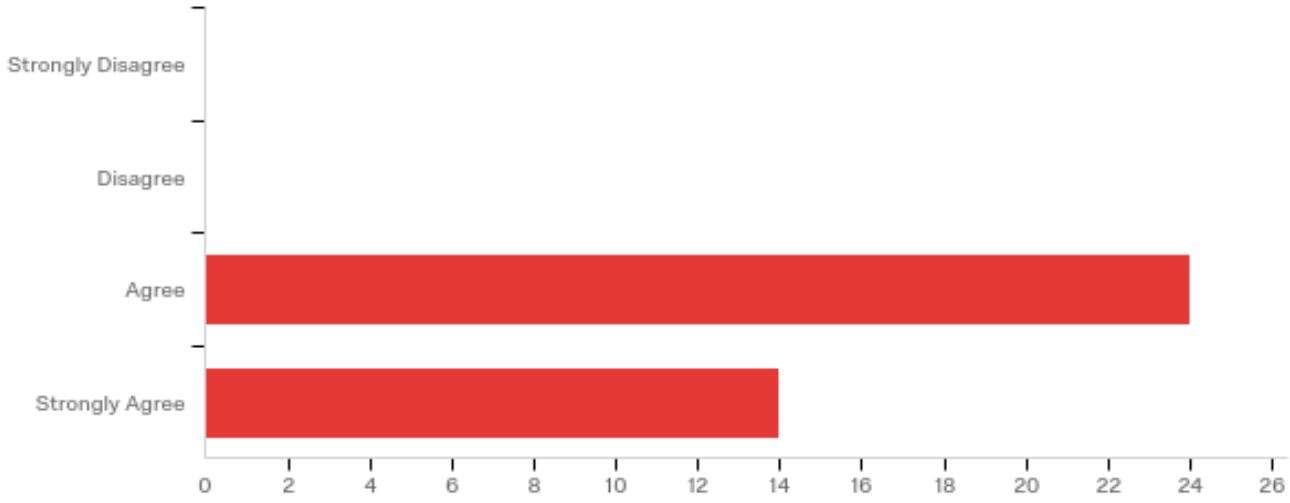
#	Answer	%	Count
1	Strongly Disagree	13.16%	5
2	Disagree	34.21%	13
3	Agree	39.47%	15
4	Strongly Agree	13.16%	5
	Total	100%	38

Q10 - I am able to describe concepts, and structure - function relationships, at the following levels:



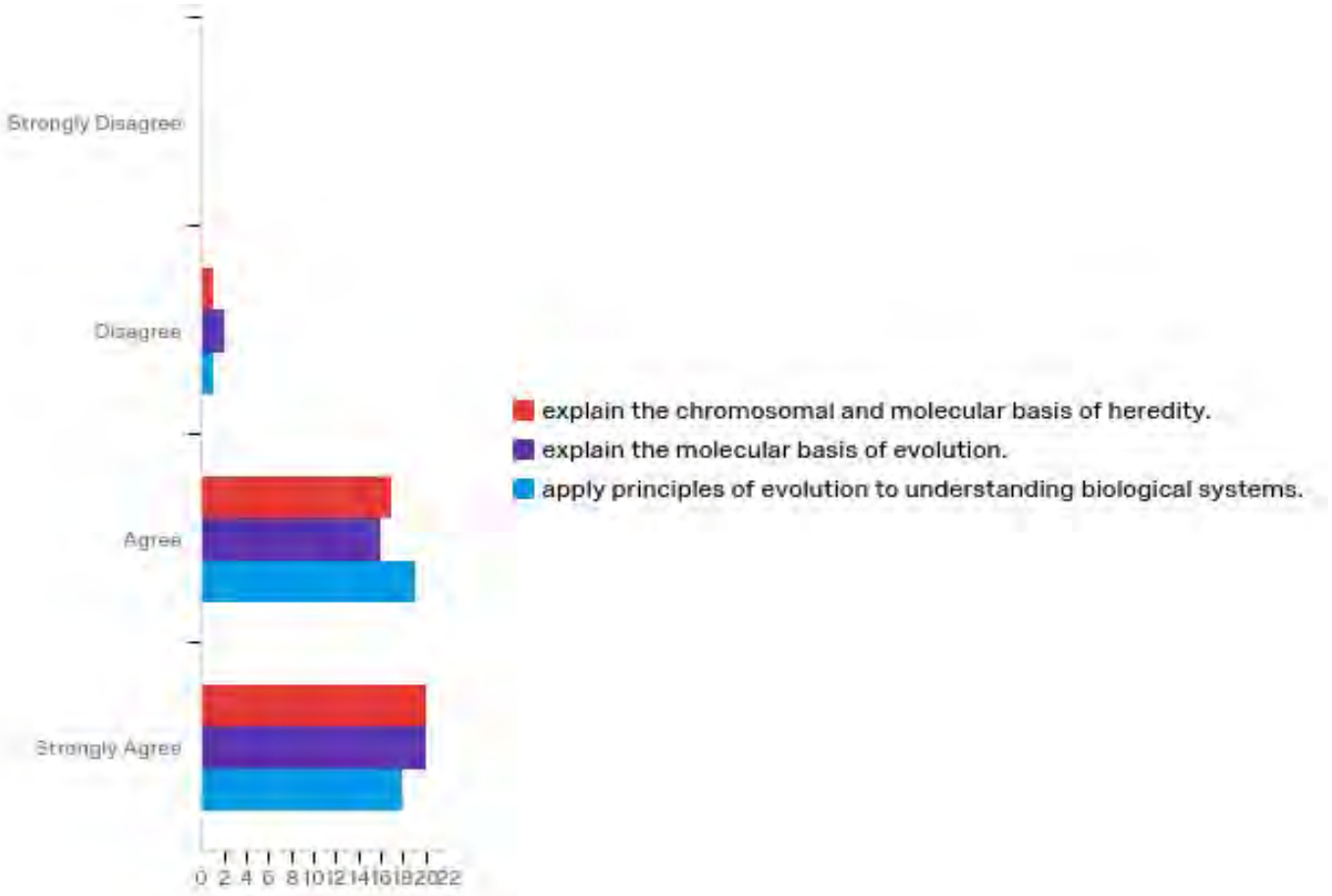
#	Question	Strongly Disagree		Disagree		Agree		Strongly Agree		Total
1	Molecular & Cellular	0.00%	0	0.00%	0	60.53%	23	39.47%	15	38
2	Organismal	0.00%	0	0.00%	0	68.42%	26	31.58%	12	38
3	Ecological	0.00%	0	13.16%	5	57.89%	22	28.95%	11	38

Q11 - I am able to integrate molecular, cellular, organismal and ecological principles to understand and describe biological systems.



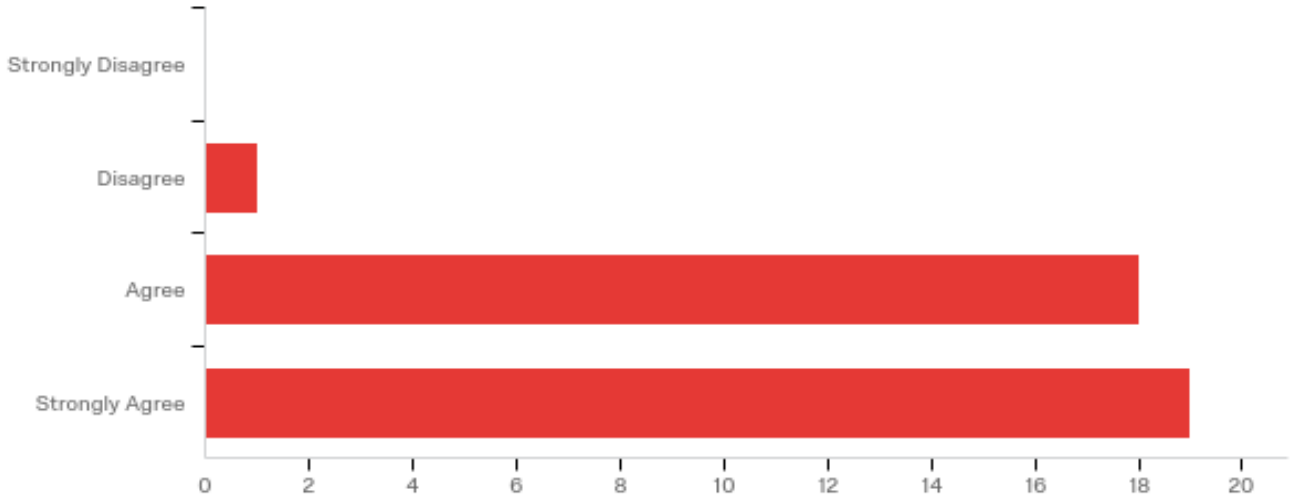
#	Answer	%	Count
1	Strongly Disagree	0.00%	0
2	Disagree	0.00%	0
3	Agree	63.16%	24
4	Strongly Agree	36.84%	14
	Total	100%	38

Q12 - I am confident in my ability to



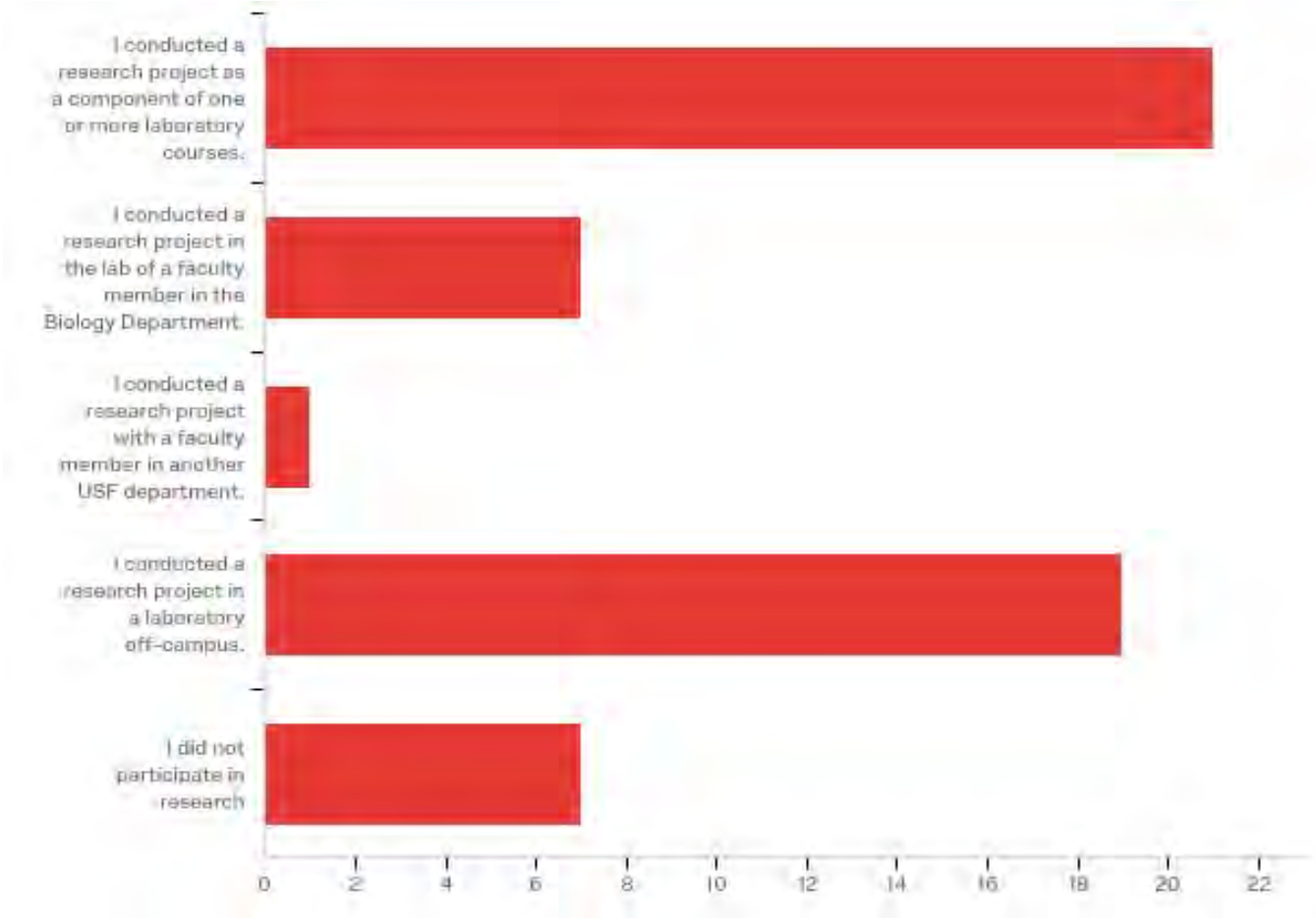
#	Question	Strongly Disagree		Disagree		Agree		Strongly Agree		Total
1	explain the chromosomal and molecular basis of heredity.	0.00%	0	2.63%	1	44.74%	17	52.63%	20	38
2	explain the molecular basis of evolution.	0.00%	0	5.26%	2	42.11%	16	52.63%	20	38
3	apply principles of evolution to understanding biological systems.	0.00%	0	2.63%	1	50.00%	19	47.37%	18	38

Q11 - I am confident in my ability to understand and critically evaluate primary research articles and other scientific publications in biology.



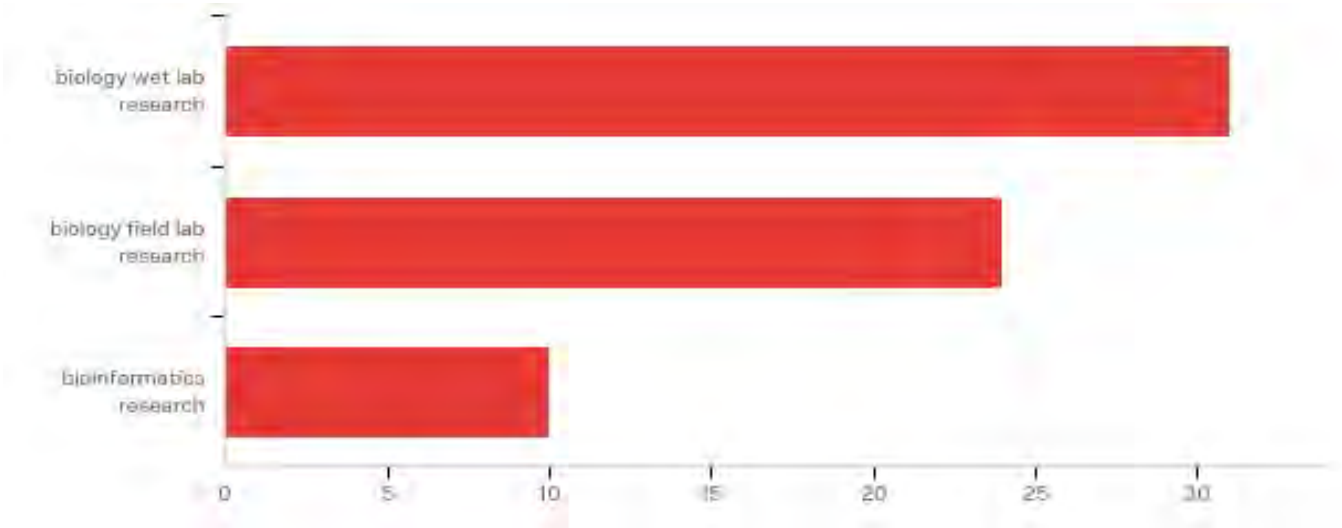
#	Answer	%	Count
1	Strongly Disagree	0.00%	0
2	Disagree	2.63%	1
3	Agree	47.37%	18
4	Strongly Agree	50.00%	19
	Total	100%	38

Q12 - During my years in college I participated in research in the following way/s:



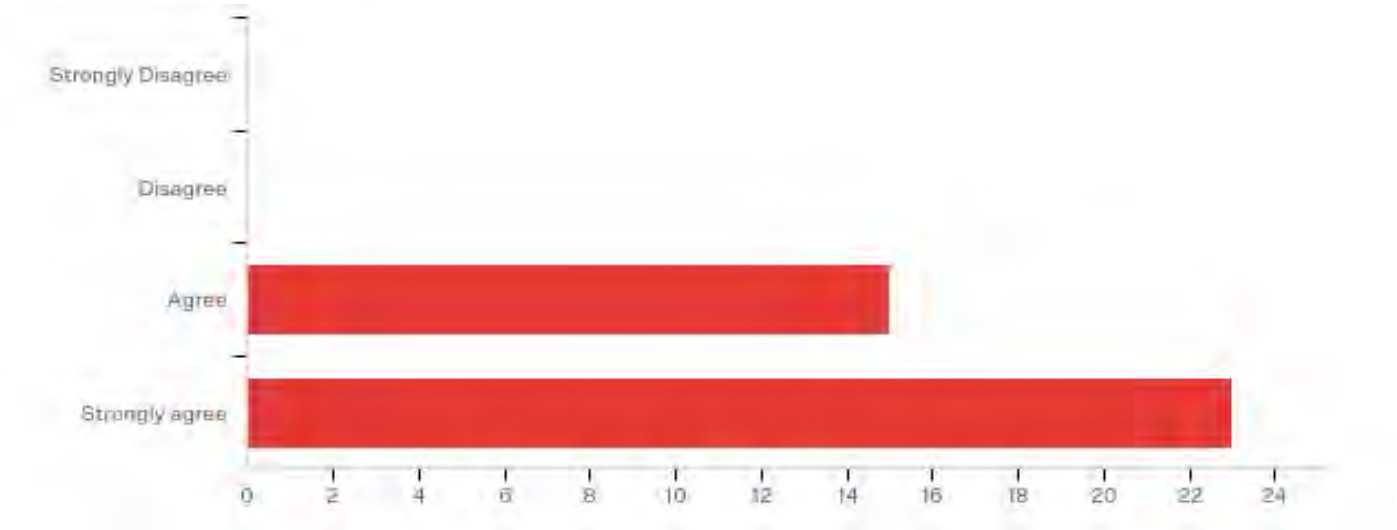
#	Answer	%	Count
1	I conducted a research project as a component of one or more laboratory courses.	55.26%	21
2	I conducted a research project in the lab of a faculty member in the Biology Department.	18.42%	7
3	I conducted a research project with a faculty member in another USF department.	2.63%	1
4	I conducted a research project in a laboratory off-campus.	50.00%	19
5	I did not participate in research	18.42%	7
	Total	100%	38

Q13 - I am familiar with a range of techniques / methods employed in



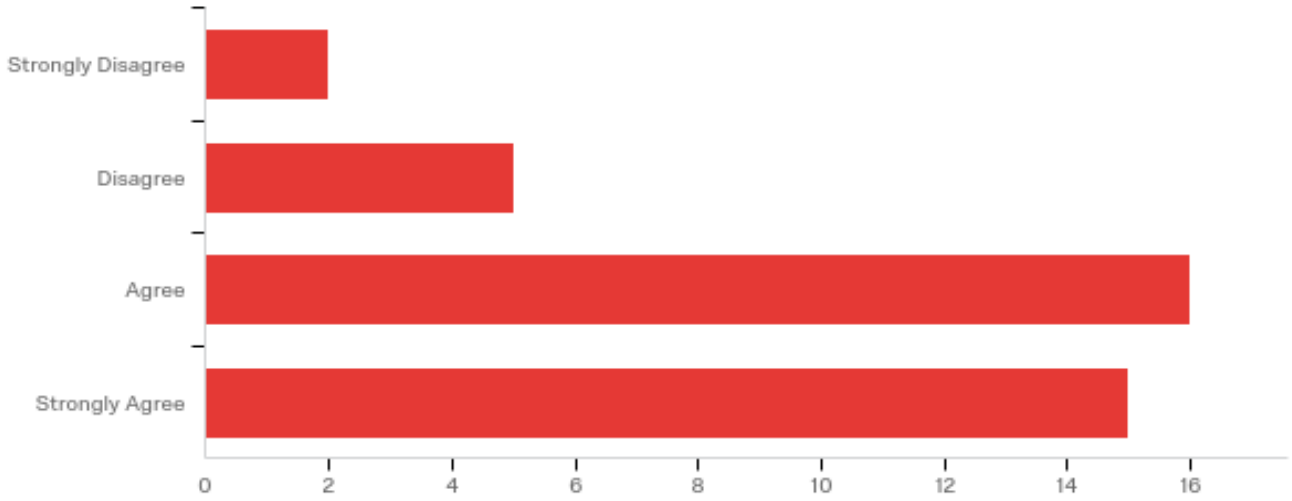
#	Answer	%	Count
1	biology wet lab research	86.11%	31
2	biology field lab research	66.67%	24
3	bioinformatics research	27.78%	10
	Total	100%	36

Q14 - I am able to apply the scientific process to answer biological questions: observe, formulate an hypothesis, and test that hypothesis through a set of experiments.



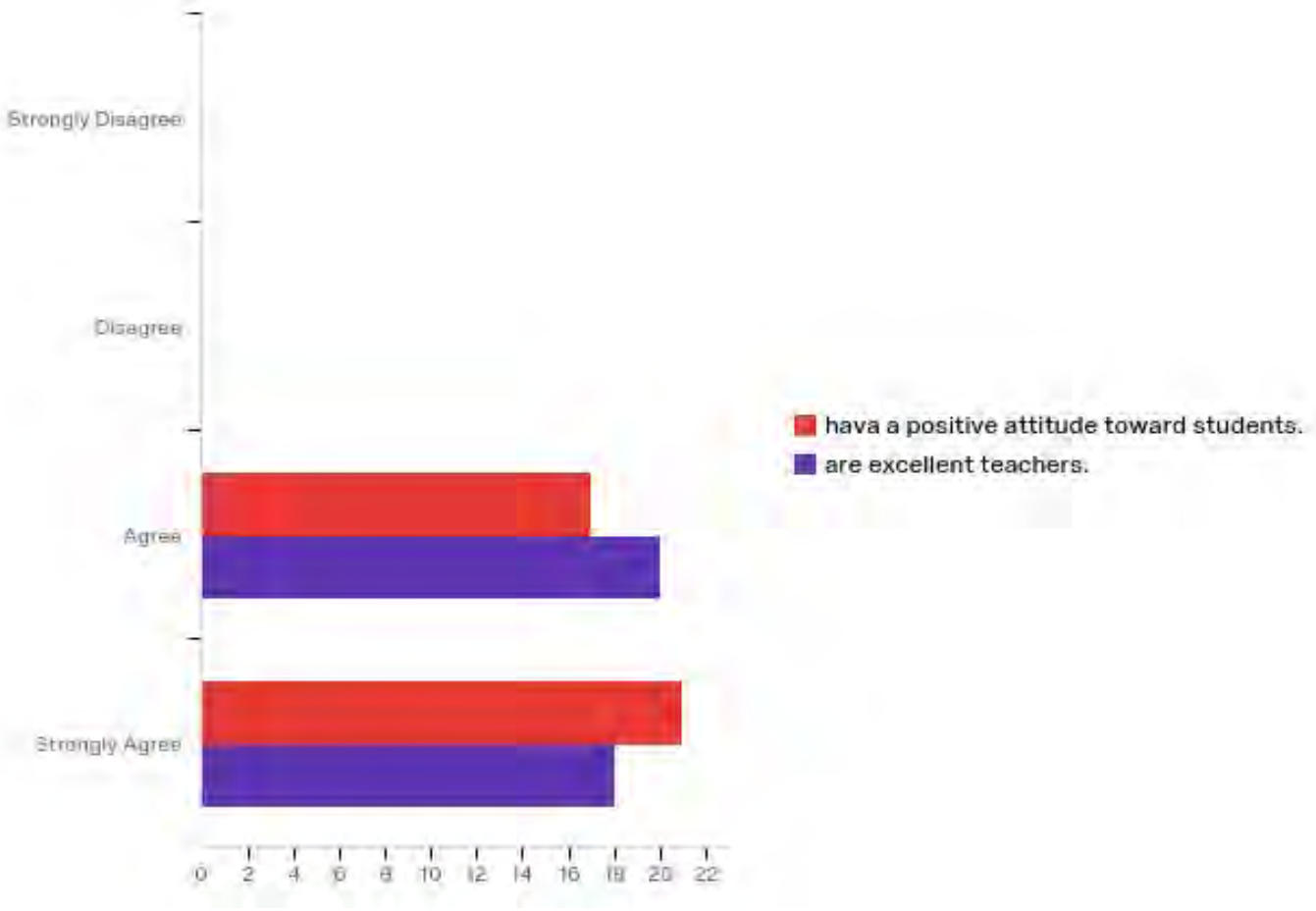
#	Answer	%	Count
1	Strongly Disagree	0.00%	0
2	Disagree	0.00%	0
3	Agree	39.47%	15
4	Strongly agree	60.53%	23
	Total	100%	38

Q20 - My academic adviser was consistently available, informed, and helpful.



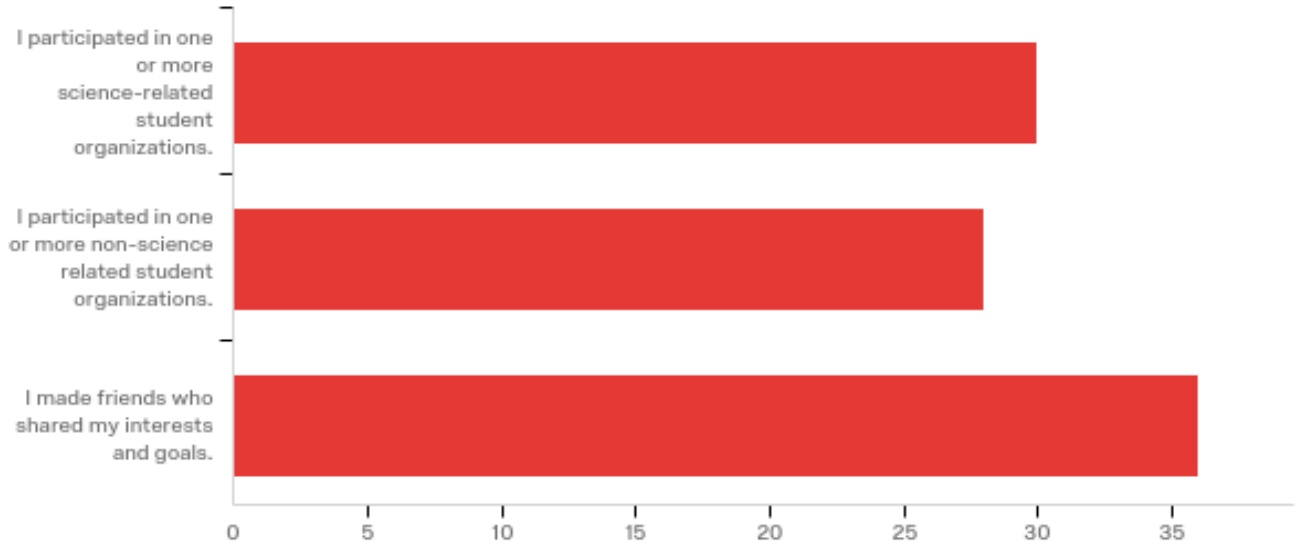
#	Answer	%	Count
1	Strongly Disagree	5.26%	2
2	Disagree	13.16%	5
3	Agree	42.11%	16
4	Strongly Agree	39.47%	15
	Total	100%	38

Q21 - The professors in the Department of Biology



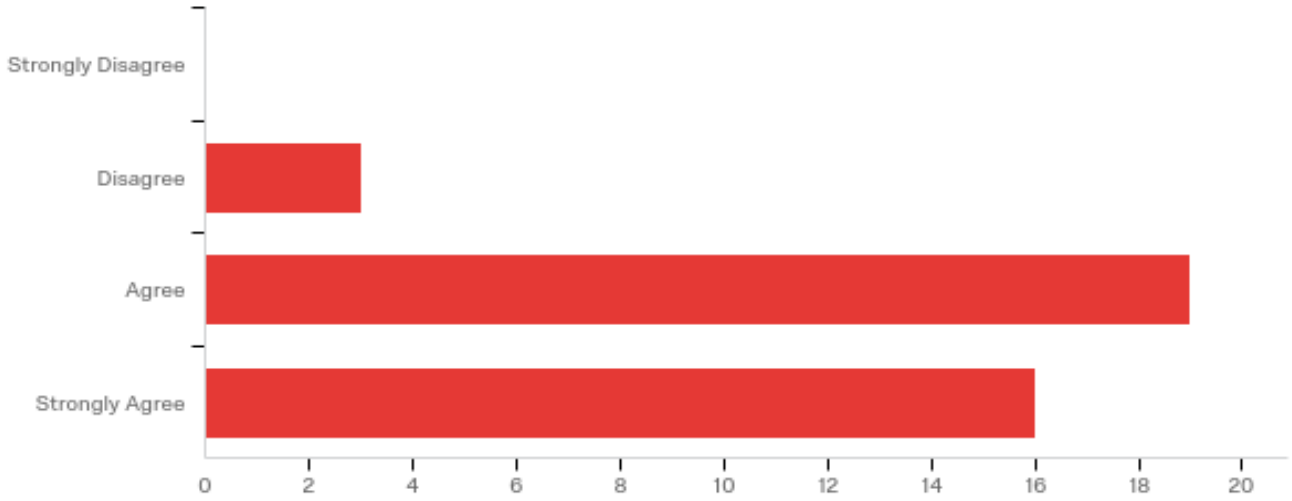
#	Question	Strongly Disagree		Disagree		Agree		Strongly Agree		Total
1	hava a positive attitude toward students.	0.00%	0	0.00%	0	44.74%	17	55.26%	21	38
2	are excellent teachers.	0.00%	0	0.00%	0	52.63%	20	47.37%	18	38

Q19 - As a biology major at USF,



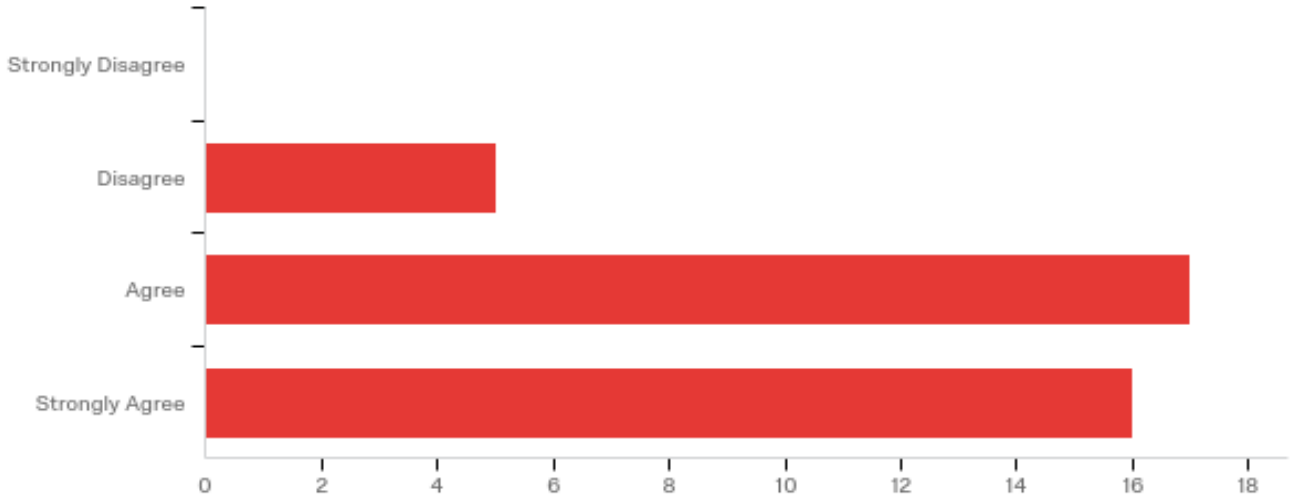
#	Answer	%	Count
1	I participated in one or more science-related student organizations.	83.33%	30
2	I participated in one or more non-science related student organizations.	77.78%	28
3	I made friends who shared my interests and goals.	100.00%	36
	Total	100%	36

Q22 - I am aware of a variety of careers and professions in the biological sciences.



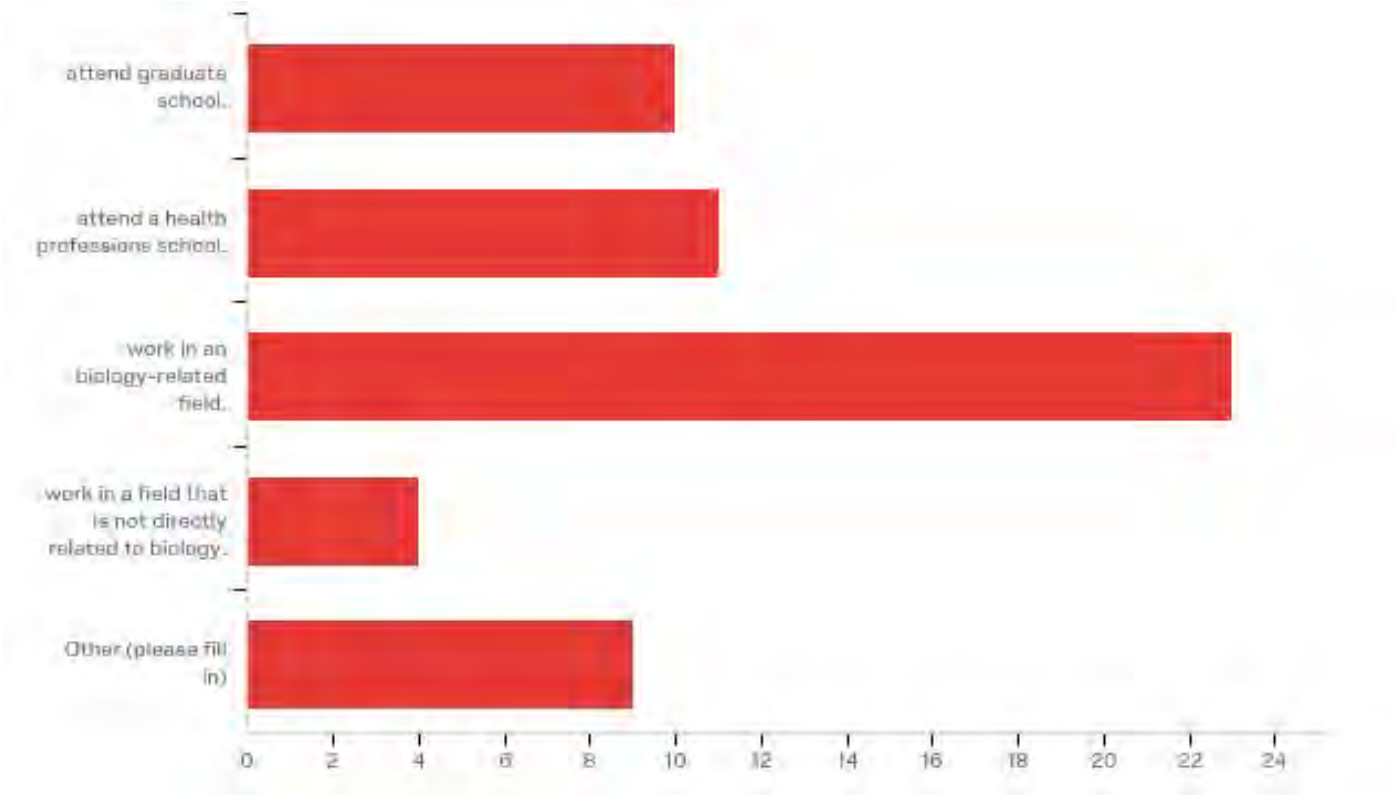
#	Answer	%	Count
1	Strongly Disagree	0.00%	0
2	Disagree	7.89%	3
3	Agree	50.00%	19
4	Strongly Agree	42.11%	16
	Total	100%	38

Q23 - My degree in biology has prepared me for the next step in my life.



#	Answer	%	Count
1	Strongly Disagree	0.00%	0
2	Disagree	13.16%	5
3	Agree	44.74%	17
4	Strongly Agree	42.11%	16
	Total	100%	38

Q25 - In the coming year, I plan to



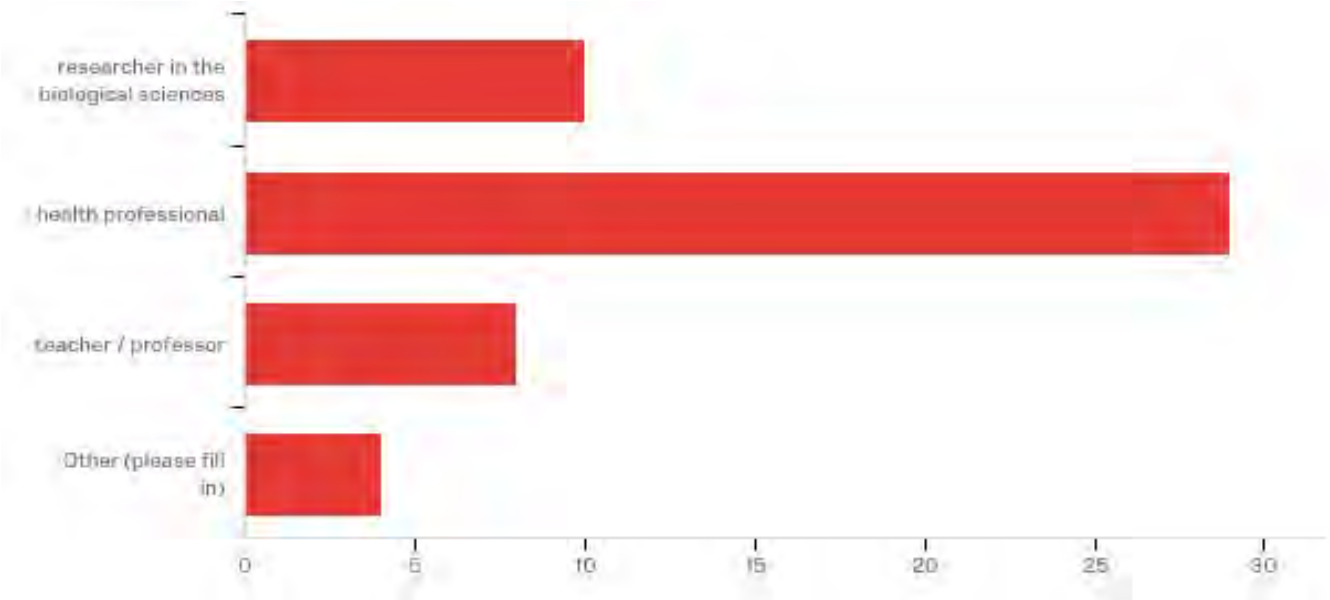
#	Answer	%	Count
1	attend graduate school.	26.32%	10
2	attend a health professions school.	28.95%	11
3	work in an biology-related field.	60.53%	23
4	work in a field that is not directly related to biology.	10.53%	4
5	Other (please fill in)	23.68%	9
	Total	100%	38

Other (please fill in)

Other (please fill in)
Apply to a health profession school
MCAT
Apply for pharmacy school

Taking a year off
I will be taking a year off
figure my life out
Then hopefully attend a grad program
gap year

Q26 - My long range plan is to become a



#	Answer	%	Count
1	researcher in the biological sciences	26.32%	10
2	health professional	76.32%	29
3	teacher / professor	21.05%	8
4	Other (please fill in)	10.53%	4
	Total	100%	38

Other (please fill in)

Other (please fill in)
I don't know
Certified Lab Scientist
Unsure
do life stuff

Q27 - We welcome your comments related to your experience in biology at USF. **Please do not refer to specific faculty or staff members**

We welcome your comments related to your experience in biology at USF. **Pl...
They are top notch
It was interesting while I was here. Though at times I begged to be considered as a special circumstance and allowed to move forward through the curriculum and was rejected time and time again by many of the professors and staff, I still was able to take enough courses to graduate with 180 credits.
The strength of this program lies in the faculty -- thank you, all!
It would have been nice to have more options to upper division courses to take in the spring. The limitation to spring/fall classes was a disadvantage and one thing I disliked about USF. I felt my opportunity to learned was restricted.
The biology department is great but could really hold more of their classes in CSI
The class registration process could be organized better (it would be nice to not have 3+ classes be canceled after registration has closed).
I am very grateful to have been able to major in Biology as it has cultivated skills I feel are important lifelong. I don't know how plausible this would be, but for upper division courses that are not offered every year, it would be nice to know of a time estimate of when they would be offered as a freshman entering biology to better plan out the future semesters.
I am so happy and grateful to be taught by amazing professors! I absolutely loved my upper division courses! Bio is LIFE (pun intended)!! :)
Cell Physiology and Genetics are hard and important classes, but to have them be as difficult and rigorous as they are makes us as students weight them more important than other classes and therefore don't do well in those classes. They are designed to prepare us for upper division classes, but they are mostly used to filter out students and it's clearly obvious. Upper division classes are totally different and care more about actually learning the material. Genetics and cell Phys have become classes where people just memorize everything to get by and forget it later. That is not the point of biology!!! Some teachers are really nice and helpful and others can be standoffish. For the most part I am happy with my degree and major choice but the upper division classes that are most sought after need to be offered more often!
I wish some classes had a little bigger class size because I took some classes I wasn't really interested in since the ones I wanted to take filled up. Maybe having a survey for which classes students are interested in taking the next semester would be really helpful!
I wished that our department helped more for future careers such as the business department does.
My time at USF and with the Biology Department has been amazing. ALL of my Professors have been such a great, supportive and hardworking network. I have loved each and every one of them. Yes, we may lack resources but we are in a city filled with so many scientific opportunities (UCSF, Genentech, Cal Academy of Science, etc.) and USF provides us with so many emails for opportunities to be involved. My only issue is that for my upper division classes, the ones I performed bad on were the ones I didn't want in the first place, I just had no other choice so I had to take them. I wish there were more classes variety because it sucked being stuck in a class I wasn't even interested. So more classes or a higher capacity of students per class would be great. Other than that, I thank USF for the supportive and excellent faculty I have been blessed with!!!!!!!
I wish some classes had bigger class sizes just because some classes I wanted to take were filled up and I also couldn't take it the next year. I ended up taking classes I didn't want to take.

Committee to Prepare Proposal for Curriculum Change
A. Justification statement for the categories listed (e.g., examples from other universities)
B. Criteria for placing classes in categories

Proposal: Upper-division **Electives** (20 units)
At least one lecture-lab course from category 1: Organismal Diversity
At least one lecture-lab course from category 2: Ecology / Population Biology
At least one lecture-lab course from category 3: Cell / Molecular Biology
Two more courses from any category (1, 2, 3), or "other UD electives" list

Placement of each course into a particular category is up for discussion. Ultimately, each course would be placed in only one category.

Category 1	**Category 2**	**Category 3**
Organismal Diversity	**Ecology / Population Biology**	**Cell / Molecular Biology**
Field Botany	Molecular Ecology*	Endocrinology
Invertebrate Zoology	Conservation Biology	Medical Microbiology**
Herpetology	California Wildlife***	Developmental Biology
General Microbiology*	Marine Biology	Immunology
Biology of Insects	Oceanography	Techniques in LM & EM
General Parasitology	Bioinformatics	Techniques in Cell Biology***
Mycology	Biology of the Galapagos	Molecular Genetics & Biotechnology
Ornithology		

*move to Cell / Molecular?
**continue to offer? move to "other" list?
***continue to offer? resurrect this course?

Other UD Electives	
BIOL 319	Ecology
BIOL 330	Female Biology
BIOL 340	Animal Toxicology
BIOL 345	Virology
BIOL 350	Comparative Animal Physiology
BIOL 368	Neurobiology
BIOL 370	Biology of Cancer
BIOL 405	Molecular Medicine
BIOL 420	Molecular Biology
BIOL 470	Environmental Animal Physiology
BIOL xxx	Animal Behavior
BIOL xxx	Human Physiology (Lecture only)
BIOL 320-321	Comparative Animal Physiology (formerly human physiology)
BIOL 365-366	Comparative Anatomy (formerly human anatomy)
BIOL 362-363	Histology

BIOL 352/353—Comparative Anatomy/Lab
Fall 2017

Lecture: MWF 1:00-1:50

Lab: M 2:00-4:50, Harney 346

Instructor: Scott Nunes
314-B Harney
1-415-422-5645
nunes@usfca.edu

Office Hours:

- Wednesday 9:30-10:30 (Harney 314-B)
- Friday 1:00-2:15 (Open lab, Harney 349)
- Other times by appointment

Course Content: Comparative Anatomy examines the form and function of the vertebrate body from a comparative perspective. The course explores the evolutionary history of vertebrates, their characteristic anatomical and physiological features, and how those features allow individuals to survive in their ecological niches. Lectures examine prominent anatomical features and their functions. Labs provide a hands-on opportunity to learn using skeletons, models, and dissection of preserved specimens, and allow students to gain insight into vertebrate body plans and develop dissection skills.

Textbooks:

- Kardong, K. V. 2015. Vertebrates: Comparative Anatomy, Function, and Evolution, 7th Edition. McGraw Hill. ISBN: 978-0-07-802302-5.
- Fischbeck, D. W. and Sebastiani, A. M. 2015. Comparative Anatomy: Manual of Vertebrate Dissection, 3rd Edition. Morton. ISBN: 978-1-61731-042-5.

Lecture Exercises: There will be various in-class exercises during lecture periods throughout the semester. These exercises CANNOT be made up if they are missed because of absence from class. However, students can be excused from an exercise if they provide a doctor's note or other written documentation to excuse the absence.

Lab Exercises: Labs sessions will include exercises that are designed to explore topics related to anatomy and reinforce material covered in lecture. Exercises are designed to be completed during the lab period. In some cases, missed lab exercises can be made up during open lab time on Fridays.

Additional Exercises: There will be three exercises to be completed outside of lecture and lab sessions.

- Zoo Exercise: Students will go to the zoo on their own to observe and compare the anatomy of different animals. One comparison will be between two species in the same vertebrate class that occupy different ecological niches, and the other comparison will be between two species from different vertebrate classes that occupy roughly the same niche. Students will prepare a written report evaluating how differences or similarities in anatomy relate to adaptation of the different animals to their niches.
- Dissection Video: Working in small groups, students will prepare a short video demonstrating laboratory safety and dissection techniques.
- Video Comparing Skeletal Systems: Working in small groups, students will prepare a video comparing the skeletons between two of the species that were studied in lab. The video should evaluate how the anatomical and functional differences of the skeletons adapt the different animals to their specific ways of life.

Lecture Quizzes: There will be a 50 point quiz on lecture material every 1-2 weeks. Quizzes will consist of fill-in-the blank, matching, true or false, multiple choice, or short answer questions. Most quizzes will be given in lab at the beginning of the lab session. One will be given in lecture at the beginning of the period, and one will be given during the final exam period.

Lab Exams: Assessment of work in the lab will include three practical lab exams, which will primarily ask you to identify structures labeled on dissected specimens, skeletons, models, or diagrams.

Practical Exam #1: Monday, October 2nd

Lancelet and hagfish
Tissues
Skull
Axial skeleton
Appendicular skeleton

Practical Exam #2: Monday, November 6th

Muscles

Practical Exam #3: Wednesday, December 4th

Cardiovascular system
Visceral systems
Nervous system
Sensory systems

Grades: Your final grade will be the same for both lecture and lab, and will be based on the grading scale below.

94 – 100% = A	80 – 81.9% = B-	67 – 69.9% = D+
90 – 93.9% = A-	77 – 79.9% = C+	62 – 66.9% = D
87 – 89.9% = B+	72 – 76.9% = C	60 – 61.9% = D-
82 – 86.9% = B	70 – 71.9% = C-	< 60% = F

Breakdown of Credit:

Lecture Quizzes (10 x 50 points each)	40%
Lecture Exercises	5%
Lab Exercises	10%
Additional Exercises	10%
Lab Practical (3 x 175 points each)	35%

Extra Credit: Extra credit will NOT be available during or at the end of the semester to make up for missed quizzes or exercises or low exam scores, so set priorities to do well on these during the semester.

On-Line Notes: Some course materials will be available on Canvas. These materials will not be handed out in class.

- Lecture notes (note: lecture attendance is mandatory even though notes are online).
- Lab handouts.
- Powerpoint files with figures for lab.

Electronic Devices: Computers and tablets can be used during regular lecture and lab periods; however, other electronic devices should be turned off. During quizzes and exams, electronic devices are not permitted. Computers and tablets must be closed and other devices must be put away. If they are not, you will receive a zero on the quiz or exam.

Attendance: Attendance is MANDATORY in lecture and lab. Note: You will not be allowed to make up a missed lecture quiz, lab exercise, or lab exam without a doctor's note or other verification of a valid excuse.

Tardiness: You are expected to be in class on time. If you come to class after announcements have been made, you are still responsible for the information in the announcements. If you are talking while announcements are made, you are still responsible for the information in the announcements.

Students with Disabilities: Students with disabilities who need reasonable accommodations for this course should contact Disability Related Services (415) 422-2613 within the first two weeks of the course. Students with learning disabilities may contact Learning Disabilities Services (415) 422-6876.

Academic Honesty: Plagiarism of lab reports or written assignments or cheating on exams will not be tolerated. Any plagiarism or cheating will result in a score of zero for the assignment or exam, a report to the Academic Integrity Committee, and a permanent record of the incident in your academic file. No second chances.

1. You cannot copy from another student or consult your notes or electronic devices during exams.
2. You cannot turn in work completed by another person as your own.
3. You cannot use the words or ideas of another person without citing your source.
4. You cannot use work completed in another course to satisfy requirements for this course.

Learning Outcomes in Lecture:

Outcome #1—Biological Literacy

Students will be able to demonstrate a basic vocabulary of anatomical terms and an understanding of the basic adaptive functions across vertebrate taxa of structures in the integumentary, skeletal, muscular, nervous, sensory, cardiovascular, respiratory, digestive, urinary, endocrine, and reproductive systems.

Outcome #2—Synthesis and Communication of Information

Students will be able to synthesize information relevant to anatomical topics and comparison of anatomy across vertebrate taxa and prepare written and oral evaluations of the information.

Outcome #3—Humanistic Applications and Social Responsibility

Students will be able to discuss challenges faced by people with physical disabilities.

Assessment of Learning Outcomes in Lecture:

Outcome #1—Biological Literacy

Students will take quizzes that assess general their knowledge and understanding and complete in-class exercises.

Outcome #2—Synthesis and Communication of Information

Students will prepare written and video evaluations of anatomical topics.

Outcome #3—Humanistic Applications and Social Responsibility

Students will write a short paper reflecting on their experience simulating having a sensory disability.

Learning Outcomes in Lab:

Outcome #1—Biological Literacy

Students will be able to demonstrate a basic knowledge of the location and function of prominent structures in the skeletal, muscular, nervous, sensory, cardiovascular, digestive, respiratory, urinary, and reproductive systems across vertebrate taxa.

Outcome #2—Proficiency in Laboratory Procedures

Students will be able to discuss and follow lab safety guidelines and perform dissections of preserved specimens (dogfish, frog, snake, turtle, pigeon, cat, sheep heart, sheep brain, sheep eye) using manuals and diagrams to locate and identify structures.

Outcome #3—Scientific Investigation

Students will be able to make and record scientific observations.

Assessment of Learning Outcomes in Lab:

Outcome #1—Biological Literacy

Students will take three practical exams in which they are asked to identify various structures. Students will prepare a video in which they explain and compare the function of different structures across vertebrate taxa.

Outcome #2—Proficiency in Laboratory Procedures

Students will prepare a video outlining lab safety and dissection technique.

Outcome #3—Scientific Investigation

Students will observe animals at the zoo, record their observations, and prepare a written report comparing the animals they observed.

Tentative Lecture and Lab Schedule

	Date	Day	Lecture	Text	Lab
1	23 Aug	W	Introduction Chordate evolution and phylogeny	Ch 2	No Lab
2	25 Aug	F	Vertebrate evolution and phylogeny	Ch 3	
3	28 Aug	M	Vertebrate evolution and phylogeny	Ch 3	1a. Orientations 1b. Lancelet anatomy 1c. Hagfish dissection
4	30 Aug	W	Tissues	Ch 5	
5	1 Sep	F	Integument **Quiz 1 (Lectures 1-3)**	Ch 6	
	4 Sep	**M**	**Labor Day**		**Labor Day—No Lab**
6	6 Sep	W	Integument	Ch 6	
7	8 Sep	F	Cartilage and bone		
8	11 Sep	M	Skeleton: skull	Ch 7	2a. Tissues 2b. Skeleton: Skull **Quiz 2 (lectures 4-6)**
9	13 Sep	W	Skeleton: skull	Ch 7	
10	15 Sep	F	Skeleton: axial skeleton	Ch 8	
11	18 Sep	M	Skeleton: axial skeleton	Ch 8	3. Skeleton: Axial skeleton **Quiz 3 (lectures 7-9)**
12	20 Sep	W	Skeleton: appendicular skeleton	Ch 9	
13	22 Sep	F	Modes of locomotion	Ch 9	
14	25 Sep	M	Modes of locomotion	Ch 9	4. Skeleton: Appendicular skeleton **Quiz 4 (lectures 10-12)**
15	27 Sep	W	Articulations		
16	29 Sep	F	Muscle function	Ch 10	
17	2 Oct	M	Muscle function	Ch 10	Practical 1: Lancelet, hagfish, tissues, skeleton
18	4 Oct	W	Muscles: head and trunk		
19	6 Oct	F	Muscles: limbs		
20	9 Oct	M	Cardiovascular system	Ch 12	5. Muscles: Head and trunk muscles **Quiz 5 (lectures 13-17)**
21	11 Oct	W	Cardiovascular system	Ch 12	
22	13 Oct	F	Zoo exercise		
	16 Oct	**M**	**Fall Break**		**Fall Break—No Lab**
23	18 Oct	W	Cardiovascular system	Ch 12	
24	20 Oct	F	Respiratory system **Skeleton video due** **Zoo exercise due**	Ch 11	

25	23 Oct	M	Respiratory system	Ch 11	6. Muscles: Forelimb muscles **Quiz 6 (lecutres 18-21, 23)**
26	25 Oct	W	Digestive system	Ch 13	
27	27 Oct	F	Digestive system	Ch 13	
28	30 Oct	M	Dentition	Ch 13	7. Muscles: Hindlimb muscles **Quiz 7 (lectures 24-27)**
29	1 Nov	W	Urinary system	Ch 14	
30	3 Nov	F	Urinary system	Ch 14	
31	6 Nov	M	Reproductive system	Ch 14	Practical 2: Muscles
32	8 Nov	W	Reproductive system	Ch 14	
33	10 Nov	F	Development	Ch 5	
34	13 Nov	M	Nervous system	Ch 16	8. Cardiovascular system **Quiz 8 (lectures 28-32)**
35	15 Nov	W	Nervous system	Ch 16	
36	17 Nov	F	Nervous system	Ch 16	
37	20 Nov	M	Sensory systems	Ch 17	9. Visceral systems **Dissection video due**
38	22 Nov	W	Open Lab		
	24 Nov	**F**	**Thanksgiving Break**		
39	27 Nov	M	Sensory systems	Ch 17	10a. Nervous system 10b. Sensory systems **Quiz 9 (lectures 33-36)**
40	29 Nov	W	Sensory systems	Ch 17	
41	1 Dec	F	Sensory disabilities: Beep ball		
42	4 Dec	M	Endocrine system	Ch 15	Practical 3: Cardiovascular, visceral, nervous, sensory systems
43	6 Dec	W	Endocrine system	Ch 15	
	13 Dec	W	10:00-12:00, Final **(Quiz 10, lectures 37, 39-40, 42-43)** **Visceral systems video due**		

September 8th, Friday: Census date, last day to drop without "W" on transcript

November 3rd, Friday: Last day to drop

COMPARATIVE ANIMAL PHYSIOLOGY
BIOLOGY 350/351
FALL 2017
UNIVERSITY OF SAN FRANCISCO

INSTRUCTOR: Leslie A. King
OFFICE HOURS: Mondays and Thursdays 1:00-2:30PM, or by appointment
OFFICE: HRN 314A
PHONE: 415-422-5704
EMAIL: kingle@usfca.edu
TWITTER: @kinglebiol (check out #physioUSF)

COURSE DESCRIPTION:
Comparative Animal Physiology is an upper-division lecture/lab course focusing on the physiological systems of animals at the molecular, cellular, and organ levels. In addition to examining the mechanisms by which animals function, we will explore physiology from ecological and evolutionary perspectives, discussing how representative invertebrate and vertebrate animals are adapted to meet the physiological challenges of different environments.

Lectures will present key concepts and experimental results in order to study the wide variety of physiological adaptations present in different animal taxa. There will also be in-class paper discussions and activities, and an end-of-semester "teach your classmates" activity.

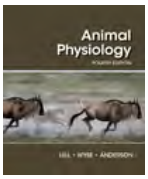
An integral part of this course is the laboratory component (Biology 351). Laboratory sessions will consist of experiments, case studies, and other activities that reinforce and expand upon the information presented in the lecture component (Biology 350). Biology 351 is discussed in further detail later in this syllabus.

Course policies for both Biology 3501 and 351 are found at the end of this syllabus.

BIOLOGY 350

MEETING TIME: MWF 10:30-11:20AM
Location: TBA

TEXTBOOK:



Hill, R., Wyse, G., and Anderson M. *Animal Physiology, 4rd Edition.* Sinauer Associates, Inc. Publishers, 2016. ISBN 978-1-60535-471-2
The text is also available in electronic format.

Course Prerequisites:

Completion of Genetics with a C or higher, and all prior prerequisites, including Organic Chemistry II or Fundamentals of Organic Chemistry.

The material learned in prerequisite courses will form the foundation for your understanding of physiology. If you would like to review prerequisite material that is most relevant to this course, please consult the chapters below. Note that these are not required reading, but if you find that you need to review some topics from previous courses, these chapters will be helpful. I am also available to answer any questions you have on this material and I will provide an optional review quiz on Canvas (not worth points) to help you test your knowledge.

- Molecules and cells in animal physiology: Chapter 2
- Transport of Solutes and Water: Chapter 5
- Aerobic and anaerobic metabolism: Chapter 8: pp189-200
- Membrane Potential: Chapter 12: pp312-318

Course Corequisite: Biology 351 (Comparative Animal Physiology Lab)

Course Learning Outcomes:

Upon completion of this course, you should be able to:

- Discuss thermal relations that animals maintain with their environments; describe poikilothermy and endothermy and their advantages and limitations
- Compare and contrast the functioning of the nervous, muscular, respiratory, circulatory, digestive, and excretory systems in different animal taxa
- Compare and contrast the physiological challenges of living in aquatic and terrestrial environments
- Discuss the mechanisms by which aquatic and terrestrial invertebrates and vertebrates are physiologically adapted to their environment
- Understand the role of natural selection in the evolution of physiological adaptations to the environment;
- Understand the role that phenotypic plasticity plays in allowing many organisms to respond to chronic changes in their environment
- Read and evaluate articles from the primary literature discussing current physiological research

Assessment of Learning Outcomes and course grades:

You will receive the same grade for both Biology 350 and 351. The laboratory component is an integral part of the course and therefore your scores on lab assignments are factored into your total course grade. Assessment of your attainment of the course learning outcomes in lecture and lab will be as follows:

Exam 1	100
Exam 2	100
Final exam	150
Paper discussions (2)	40
Group teaching session	100
	+160 points (lab)
	650 total points

At the end of the course your point total out of 650 will be converted to a percentage. This percentage will be used to assign your letter grade as follows:

A	93-100%	C-	70-72%
A-	90-92%	D+	67-69%
B+	87-89%	D	63-66%
B	83-86%	D-	60-62%
B-	80-82%	F	Below 60%
C	73-76%		

EXAMS:

There will be two midterm exams and a final exam given in the course. Midterm exams will be held during class time on the following dates:

Exam 1: Monday October 2 (covers material through 9/25)
Exam 2: Monday November 6 (covers material 9/27-11/1)

Exams will be made up of multiple choice, short answer, and essay questions. I will discuss exam format more as the first exam approaches. For the multiple choice portion of each exam, I will provide you with a Scantron form on which to record your answer choices. A review sheet for each exam will be posted to Canvas.

Exams must be taken at the scheduled time. You will be allowed to make up missed exams only in cases of medical issues and other emergencies. If you have an emergency, please do your best to notify me by phone or email no later than the beginning of the exam. If this is not possible, you must contact me within 24 hours after missing the exam in order to be considered for a make-up exam, regardless of the reason for missing the exam. If you miss an exam and have a legitimate excuse as described, you must take the make-up exam within one week or you will receive a grade of zero for that exam. I reserve the right to give a make-up exam that is different in format from the regular exam.

The final exam will consist of two parts. The first part will be worth 100 points and will cover the material from class November 3 – December 6: water and salt physiology, kidneys and excretion, and the material covered in the teaching sessions; the second part will be cumulative (i.e. will cover material from the entire semester) and will be worth 50 points. The final exam is scheduled for **Monday December 11, 10AM-12PM**. Do not make travel plans or schedule other appointments during this time. No early or late final exams will be given.

Absolutely no electronic devices of any kind may be used or be within sight during exams. Anyone found using electronic devices during an exam will receive a zero on that exam.

PAPER DISCUSSIONS

During the semester you will read and discuss two papers from the primary literature covering physiological research. One of these discussions will occur in lecture, and the other will occur in lab. For each paper, you will be assessed by answering questions ("pre-discussion questions") on the paper prior to the discussion period (10 points) and by actively participating in the class discussion (10 points). Journal articles and pre-discussion questions will be posted no later than one week in advance of the paper discussion. Failure to attend and participate in class

discussions will result in forfeiture of the participation points. Answers to pre-discussion questions must be submitted to Canvas prior to the beginning of class on the day of the discussion. The format for class discussions will be explained in class.

GROUP TEACHING SESSIONS: TEACH YOUR CLASSMATES!

An excellent way to solidify your understanding of a subject is to explain the material to others. This semester, you will work in a group of 3-4 people to teach one of the following topics to the rest of the class:

Group 1: Diving by Marine Mammals: Cardiovascular and Metabolic Responses (text chapter 26)
Group 2: The Lives of Mammals in Frigid Places: Brown Fat, Hibernation (text chapter 11 and text chapter 10 pp274-277)
Group 3: Physiological Adaptations of Mammals of Deserts and Dry Savannas (chapter 30 and chapter 28 pp773-776)

These topics, as indicated in parentheses, are covered in the textbook and it is fine for this particular assignment to use the text as your sole resource. This assignment will be discussed in great detail in class, but here are a few of the specifics:

1. These teaching sessions will occur over three class periods
    - Wednesday November 30: Group 1
    - Friday December 2: Group 2
    - Monday December 5: Group 3
    - Wednesday December 7: Group 4

2. Each group should plan on teaching for 40-45 minutes. Your group will choose the reading assignment for the class for your session.

3. The format in which your group chooses to teach the class is flexible. For example, you may:
    - provide the class with discussion questions/topics prior to the class session, and then lead a class discussion
    - present powerpoint (or similar) on the material
    - make a video to show to the class (if this is chosen, you must do this in conjunction with some sort of in-class interaction)
    - use a combination of the above

    ...other formats are possible too!

4. I realize that two main challenges of group assignments are finding times to meet and communicating with one another. Once groups are chosen, I will set up groups within our Canvas site to make it easier for you to share materials with each other. You are not required to use Canvas to collaborate and communicate, but I will set it up for you in case you find it useful. (You will eventually be submitting your group materials to this area in Canvas.)

I have scheduled two check-ins/meeting times with groups prior to the teaching sessions. These will occur on the dates/weeks specified below.

Check-in #1:
Date: Tuesday October 3 (in lab). Please bring your textbook; you will have the entire time to meet in your groups.

Prior to this checkpoint: skim the chapter/pages assigned to your group to get an idea of the topics covered; you do not need to fully comprehend all the material but you should have some ideas of what parts of the chapter could be taught in your group's class session. I will talk more about this in class.

Purposes of this check-in:

- To decide whether you want to cover all or part of material in the chapter and decide upon the reading assignment (taken from the text) for the class.
- To brainstorm ways to teach/discuss the material
- To divide group duties/subtopics among group members

I will be circulating between groups during your discussions to help you with the above.

What's due from check-in #1?

Prior to leaving class, each group must submit, in writing, the following information:

- A brief description of how each group member will contribute to the teaching session and of how your group will teach the material (it is fine to change this, but you must update me with any major changes made to group members' duties).
- The reading assignment for your teaching session. I will post this to Canvas.

I will provide a worksheet during the check-in to help you organize the above.
The above assignment is worth 15 points toward your group grade.

Check-in #2:

Date: Week of November 6; meeting time TBA for each group; location: my office.
Each will sign up for a meeting time. Meeting time slots will be 30 minutes. Failure of a group to schedule a session with me will result in a point deduction from the assignment. If it is not possible for all group members to make the same time slot in my office, we will schedule a time for an online chat in Canvas.

Purposes of this check-in:

- To check in about progress on your teaching session
- To discuss materials you plan to post for class, e.g. notes outlines, handouts, discussion questions.

The check-ins are the only formal times I've scheduled to meet with groups, but I am available all semester in office hours and by appointment to meet with groups and individual group members; I am happy to help!

Other components of teaching session:

Class materials:

Each group is required to provide the class with materials that accompany their session. These may be handouts, note outlines, or other. These materials must be submitted to your group's Canvas prior to Monday November 20 at 6PM. I will then post these to Canvas for the class to download prior to your teaching session.

Final exam question submission:

Each person is required to write and submit a final exam multiple choice question on their group's teaching topic. Your question must be submitted to Canvas prior to Wednesday, December 6, 11PM. The question must be original, i.e. you may not simply find one on the internet and use it.

Assessment of teaching session:
The teaching session assignment is worth 100 points total, divided as follows.

Group component of assignment: 70 points
Checkpoint 1: 15 points
Checkpoint 2: no points, but points will be deducted for failure to meet with me
Materials for teaching session: 20 points
Teaching session: 35 points

Individual component of assignment: 30 points
Participation in teaching session: 20 points
Submission of multiple choice question for final exam: 10 points

We will discuss the above in more detail in class and grading rubrics will be provided.

BIOLOGY 350 TENTATIVE LECTURE SCHEDULE

Date	Day	Topic	Reading
8/23	W	Course Introduction; Introduction to physiology	Chapter 1; course syllabus
8/25	F	Introduction to physiology/energy metabolism	Ch. 7: 165-172; table 7.3; 175-184
8/28	M	Energy Metabolism	Same as above
8/30	W	Energy Metabolism; Thermal Relations	Ch. 10: 233-238; 242-274
9/1	F	Thermal Relations; Assign groups for teaching sessions	Ch. 10: 233-238; 242-274
9/4	**M**	**NO CLASS – LABOR DAY**	
9/6	W	Thermal Relations	Ch. 10: 233-238; 242-274
9/8	F	Thermal Relations	Ch. 10: 233-238; 242-274
9/11	M	Thermal Relations/Feeding and Digestion	Ch. 6
9/13	W	Paper discussion; pre-discussion questions due to Canvas prior to class	Assigned paper posted to Canvas: *Whole body endothermy in a mesopelagic fish, the opah,* L. guttatus
9/15	F	Feeding and Digestion	Ch. 6
9/18	M	Feeding and Digestion; Neurons, Synapses, and Sensory Processes	Ch. 13: 305-354; 360 (synaptic plasticity)-365; 369-372
9/20	W	Neurons, Synapses, and Sensory Processes; NS Organization	Ch. 14: 391 (photoreception)-398; ch. 15
9/22	F	Nervous System Organization and Muscles	Ch. 15 and Ch. 20
9/25	M	Muscles and Movement	Ch. 20
9/27	W	Oxygen and Carbon Dioxide Physiology	Ch. 22
9/29	F	Oxygen and Carbon Dioxide Physiology	Ch. 22

10/2	**M**	**EXAM 1**	
10/4	W	External Respiration: Physiology of Breathing	Ch. 23: 599-618; 622-633
10/6	F	External Respiration: Physiology of Breathing	Ch. 23: 599-618; 622-633
10/9	M	Respiratory Pigments and Gas Transport in Body Fluids	Ch. 24: 635-663
10/11	W	Class discussion of lab results from 10/10; Respiratory Pigments and Gas Transport in Body Fluids	Ch. 24: 635-663
10/13	F	Respiratory Pigments and Gas Transport in Body Fluids	Ch. 24: 635-663
10/16	**M**	**NO CLASS – FALL BREAK**	
10/18	W	Circulation	Ch. 25: 667-676; 679-699
10/20	F	Circulation	Same as above
10/23	M	Circulation	Same as above
10/25	W	Circulation	Same as above
10/27	F	Endocrine and Reproductive Physiology	
10/30	M	Endocrine and Reproductive Physiology	
11/1	W	Discuss results from lab Oct 31; Endocrine and Reproductive Physiology	
11/3	F	Introduction to Water and Salt Physiology	Ch. 27
11/6	**M**	**EXAM 2**	
11/8	W	Intro to Water and Salt Physiology; Water and Salt Physiology in Freshwater Animals	Ch. 28: 741-748
11/10	F	Water and Salt Physiology in Freshwater Animals	Ch. 28: 741-748
11/13	M	Water and Salt Physiology in Marine and Euryhaline Animals	Ch. 28: 749-762
11/15	W	Water and Salt Physiology in Marine and Euryhaline Animals	Ch. 28: 749-762
11/17	F	Kidneys and Excretion	Ch. 29
11/20	M	Kidneys and Excretion; **materials for teaching session due to Canvas prior to 6PM**	Ch. 29
11/22	W	Kidneys and Excretion	
11/24	**F**	**NO CLASS – THANKSGIVING BREAK**	
11/27	M	Kidneys and Excretion and Nitrogenous wastes; teaching session last minute prep	Ch. 29
11/29	W	Group teaching session: group 1	Group Materials posted on Canvas
12/1	F	Group teaching session: group 2	Group Materials posted on Canvas

12/4	M	Group teaching session: group 3	Group Materials posted on Canvas
12/6	W	Discuss results from lab Dec 5; teaching session recap	
12/11	**M**	**FINAL EXAM: 10:00AM – 12:00PM**	

BIOLOGY 351

Biology 351 is the laboratory component of the comparative animal physiology course. In the laboratory, you will collect and evaluate physiological data from select organisms to gain an appreciation of and understanding of the variety of mechanisms utilized by animals to function in their environments. Laboratory experiments will reinforce and enhance your knowledge of the material presented in lecture.

MEETING TIME: T 1:00PM – 3:50PM, HRN 346

TEXTBOOK: All lab exercises will be posted to Canvas by one week prior to lab.

COURSE PREREQUISITES:
Completion of Genetics with a C or higher, and all prior prerequisites, including Organic Chemistry II or Fundamentals of Organic Chemistry.

COREQUISITE: Biology 350 (Comparative Animal Physiology Lecture)

COURSE LEARNING OUTCOMES:
Upon completion of this course, you should:

- be able to perform laboratory skills related to physiological measurement, including but not limited to: measuring electrical activity of neurons; measuring blood pressure; measuring hematocrit; measuring human lung volumes and capacities; performing sensory tests; and obtaining a 3-lead electrocardiogram
- construct clear figures and tables to illustrate physiological data
- describe and evaluate experiments, including via basic statistical tests
- evaluate and discuss physiological case studies

LAB WORK:

Statistics lab assignment	20 points
Three lab results summaries	60 points
Three case studies	20 points
CAS field trip quiz	20 points
	+490 points (lecture)
	650 total points

As mentioned earlier, your point total out of 650 points will be converted to a percentage, and you will receive the same letter grade for lecture and lab (see grading scale earlier in this syllabus).

STATISTICS LAB ASSIGNMENT:
You will be using basic statistical tests to analyze the data in several of your lab results summaries (explained below). The first lab of the semester will include an introduction to (or review of) the purpose of these tests and also to how to perform them in Excel. You are not required to perform the analyses in Excel if you have another program you prefer, but this is the program we'll be using in the first lab. The assignment from the statistics lab will involve completing statistical tests on data sets I provide. We will be working on them together in lab, and more information will be provided then.

This lab exercise requires the use of laptops. Please bring a laptop to class. If you do not have a laptop, you may borrow one from Gleeson Library: https://www.usfca.edu/library/borrowing. Please come see me if you have any questions or concerns about this.

Lab results summaries:

You will be writing three lab summaries this semester. Each summary is worth 20 points. See the lab schedule for due dates. While requirements for each summary will differ slightly, the general purposes of results summaries are to present the data in graphical form, to analyze it, and to discuss it.

General sections of summaries:

Title: The title should consist of a descriptive phrase that represents the content of the report. Note that this should not read like a newspaper headline. Do not use the title of the laboratory exercise as the title of your report.

Results and Discussion: (past/ present tense as appropriate) Report your results in a concise and organized manner. Present your data as tables and graphs (graphs are listed as figures). Figures and tables are numbered in the order in which they are referred to in this section. Each table must have a descriptive title above it; each figure must have a descriptive title placed directly below it. Your figures should be understandable without having to refer to the narrative of the summary. In the narrative, explain and interpret the results, referring to each figure in parentheses at the end of the appropriate sentence (Figure 1.) If the experiment did not work, suggest reasons why it may have failed and what could be done to remedy the problem. Are there factors that could have altered your expected results that could be controlled in future repeats of this experiment? End this section with a concluding sentence or two.

More information will be given for each lab results summary assignment as it approaches.

Field trip to California Academy of Sciences (CAS)

Many of the exhibits at CAS are perfect for reviewing the comparative physiology we cover in this course, so on Saturday November 18 we will take a field trip there. (Due to time constraints, we cannot go during regular class time). This field trip replaces a lab session.

Some notes about our CAS visit:

- I will provide tickets to the CAS for all of you; you do not need to purchase your own ticket.
- The CAS is accessible by MUNI (44 bus drops off in front), but it is also a short walk from USF.
- You should plan on spending about 2.5-3 hours there to complete the assignment; we will meet at CAS in front at 9:30AM.
- The assignment I give is nothing you will turn in, but completion of the assignment will be essential in successfully completing a Canvas quiz you will take after our visit. The Canvas quiz will be available until Wednesday November 23, 11PM.
- If you have a conflict with the November 18 date, you may visit the CAS on your own, but soon enough so that you can complete the Canvas quiz. Please speak with me if you have a conflict with attending the field trip on Nov 18 (9:30AM-12:00PM).

Additional information about the Canvas quiz:

- You must take the quiz in one sitting: you may not attempt to take it multiple times, nor may you save it to finish at another time.
- Once you have taken the quiz and submitted it, you may not go back. The quiz will be timed—as mentioned, you will have one hour to take it.
- Notes, the paper, and your classmates may be used as resources during the quiz; however, if you rely solely on looking up answers as you go along, there will not be enough time to complete the quiz. The format will be multiple choice and short answer.
- Complete the quiz early so that you can notify me about any problems encountered.
- Remember, the USF Computer labs are available to take the quizzes too!

BIOLOGY 351 TENTATIVE LAB SCHEDULE

Session	Date	Lab exercise	Assignment from this lab
1	Aug 29	Group work and discussion: • Statistics Review Activities • Membrane Transport, Fluid Compartments, and Cell Biology Case Studies • Introduction to physiological recording equipment (iWorx)	Statistics and graphing assignment submitted to Canvas prior to lab Sep 6
2	Sep 5	Effects of temperature on metabolic rate in poikilotherms; investigating allometric relationships between body size and metabolic rate; calculating the respiratory exchange ratio (RER)	Results summary 1, submitted to Canvas prior to lab time Sep 12
3	Sep 12	Mammalian Digestive Enzymes; Earthworm and Crayfish gut pharmacology	Material covered on exam 1
4	Sep 19	The Earthworm Action Potential; Measurement of Human Medial Nerve Conduction Velocity; Special Senses activities	Results summary 2, submitted to Canvas prior to lab time Sep 26
5	Sep 26	Cockroach Leg Mechanoreceptors; Human Muscle Twitch Physiology: Summation and Tetanus	Material covered on exam 1
6	Oct 3	Check-in #1 for teaching sessions	
7	Oct 10	Effects of Hypoxia and normoxia on ventilation in decapod crustaceans; Assessing human ventilation via spirometry	Material covered on exam 2; Respiratory case study submitted to Canvas prior to lab Oct 24 (two

			weeks); be prepared to present results in class tomorrow (Oct 11)
	Oct 17	No LAB – FALL BREAK	
8	Oct 24	Cardiovascular Physiology: ECG and peripheral circulation	Cardiovascular case study, submitted to Canvas prior to lab Oct 31
9	Oct 31	Blood glucose regulation and endocrine case studies	Results summary 3, submitted to Canvas prior to beginning of lab, Nov 7
10	Nov 7	Paper discussion #2: pre-discussion questions due prior to lab	
11	Nov 14	Extrarenal salt excretion via teleost gill MRCs (mitochondria-rich cells)	Material covered on final exam
	Nov 21	NO LAB – CAS Field trip on Sat Nov 18	
12	Nov 28	Active transport in insect Malpighian tubules	Material covered on final exam
13	Dec 5	Renal physiology: renal response to salt and water loading	Renal physiology case study

GENERAL INFORMATION AND POLICIES FOR BIOLOGY 350 AND 351:

CANVAS:

Canvas is the online Learning Management System to which USF subscribes. All you need to log in to Canvas is your MyUSF Username and password. An online student guide to Canvas may be found at: https://community.canvaslms.com/docs/DOC-4121. This is a very helpful guide and explains how to do all of the things you will need to do in Canvas. If you are having technical difficulties with Canvas, send an email to: **itshelp@usfca.edu**. On our Canvas site I will post outlines of lecture notes, exam review questions, journal articles, and other material as the semester progresses. In addition, you will be submitting all class assignments to Canvas.

ATTENDANCE

Attendance in lecture is expected. Repeated absences from lecture will result in a lowering of your overall course grade.

Attendance in lab is required. If you need to be absent due to an emergency or illness, please email me prior to lab. If this is not possible, you must email me within 24 hours of your absence for it to be excused. In some cases I may request a physician's note. There are no make-up labs.

If you are absent from lab due to illness or other emergency, you still must submit any lab assignments due that day on time according to the dates in this syllabus.

If you miss lab and I do not hear from you within 24 hours after your absence, it will not count as excused even if you were ill or had an emergency.

Please come to the lab on time and prepared to proceed with the experiment of the day. Being prepared includes having the exercise for the day available (either hard copy or electronic).

Late assignments

Failure to submit any assignment on time will result in the following penalties:
Turned in same day as due date, but after specified time: -10% of assignment point total
Turned in one day late: -50% of assignment point total
Turned in more than one day late: no credit
A weekend counts as two days.

Email

Email is a convenient way for me to communicate with the class outside of class time. Please check your email regularly so you do not miss any important updates and announcements about the course. The emails I send will go to your Dons email account; please check this account or have your Dons email forwarded to the email address you check most regularly.

Academic Honesty

From the USF website: "In order to uphold a culture of fairness and integrity, USF students are required to adhere to the university's honor code....As a Jesuit institution committed to *cura personalis* — the care and education of the whole person — USF has an obligation to embody and foster the values of honesty and integrity. USF upholds the standards of honesty and integrity from all members of the academic community."

The details of the honor code may be found at: http://www.usfca.edu/academic-integrity/

Cheating and plagiarism will not be tolerated. Any plagiarism or cheating will result in a grade of F on the assignment or exam, possibly an F in the course, and a report will be submitted to the Dean resulting in a permanent record of the incident in your academic file. If you observe someone else cheating, you also have the responsibility to bring this situation to my attention.

Student Disability Services

Pursuant to the Americans with Disabilities Act and Section 504 the Rehabilitation Act, students with disabilities who will need reasonable accommodations for this course should contact Student Disability Services (415) 422-2613 within the first two weeks of this course.

Electronic devices

Cell phone sounds are disruptive to the class, so please turn these devices off or place into the silent mode during class. Please do not text during class.

	PLO1	PLO2	PLO3	PLO4	PLO5
Program Learning Outcomes X Courses	Demonstrate both in-depth and broad knowledge of the concepts that comprise the biological sciences.	Apply the scientific process, including designing and conducting experiments and testing hypotheses.	Perform laboratory, field, and analytical techniques.	Discuss and critically review scientific papers and prepare oral and written reports in a standard scientific format.	Demonstrate an awareness of the significance ethics plays in the biological sciences.
Courses or Program Requirement					
BIOL 105-General Biology I	I	I	I		I
BIOL 106-General Biology II	I		I		I
BIOL 212-Cell Physiology	I			I	I
BIOL 310/311-Genetics/Lab	A	I	I	I	I
BIOL 390-Biology Seminar					
BIOL 414-Evolution	A	(A)	(A)	A	A
BIOL 319-Ecology	I	I		I	
BIOL 320/321-Human Physiology/Lab	A	A		A	I
BIOL 324/325-Molecular Ecology	A	A	A	A	I
BIOL 326/327-Field Botany/Lab	A	I	A	A	
BIOL 328/329-Invertebrate Zoology/Lab	A	A	A	A	I
BIOL 330-Female Biology					
BIOL 331/332-Herpetology/Lab					
BIOL 333/334-Endocrinology/Lab					
BIOL 340-Animal Toxicology	A			A	
BIOL 341/342-Medical Microbiology/Lab	A	I	A	I	I
BIOL 345-Virology	A	A		A	
BIOL 346/347-General Microbiology/Lab	A	A	A	A	
BIOL 350-Comparative Animal Physiology	A			A	I
BIOl 355/356-Developmental Biology/Lab	A	A	A	A	A
BIOL 362/363-Histology/Lab	A		A		
BIOL 365/366-Human Anatomy/Lab	A		A		A
BIOL 368-Neurobiology	A	A		A	A
BIOL 379/380-Conservation Biology/Lab					
BIOL 383/384-Biology of Insects/Lab					
BIOL 385/386-Parasitology/Lab	A		A		A
BIOL 387/388-Hematology/Lab	A		A		
BIOL 392/393-Oceanography/Lab	A		A	A	
BIOL 395/396-Biology of Fishes/Lab	A	A		A	I
BIOL 405-Molecular Medicine	A	A		A	A
BIOL 420-Molecular Biology	A			A	
BIOL 443/444-Immunology/Lab	A	A	A	A	I
BIOL 458/459-Advanced Microscopy/Lab					
BIOL 485/486-Molcular Genetics and Biotechnology/Lab	A	A	A		A
Key:					
I = Introductory					
A = Advanced					
CLO = Course Learning Outcome					
(A) or (I) = variable depending on faculty teaching the course					

	PLO1	PLO2	PLO3	PLO4	PLO5
Program Learning Outcomes X Courses	Demonstrate both in-depth and broad knowledge of the concepts that comprise the biological sciences.	Apply the scientific process, including designing and conducting experiments and testing hypotheses.	Perform laboratory, field, and analytical techniques.	Discuss and critically review scientific papers and prepare oral and written reports in a standard scientific format.	Demonstrate an awareness of the significance ethics plays in the biological sciences.
Courses or Program Requirement					
BIOL 105-General Biology I	I	I	I		I
CLO (& Assignment): Demonstrate a basic understanding of biochemistry, cell biology, genetics, evolution, and ecology (lecture exams, lab exercises, lab reports)	X				X
CLO (& Assignment): Perform laboratory procedures to explore the content and principles of biology (lab exercises, lab reports)	X	X	X		
CLO (& Assignment): Carry out laboratory work in a socially responsible manner, which includes treating live organisms humanely, respecting animals used for dissection, observing laboratory safety procedures, adhering to waste disposal regulations, and refraining from cheating or plagiarizing in any way (lab exercises, lab reports)					X
BIOL 106-General Biology II	I		I		I
CLO (& Assignment): Demonstrate a basic understanding of the phylogenies, life histories, physical characteristics, physiology, and ecological importance of living organisms (lecture exams, lab exercises, lab practicals)	X				
CLO (& Assignment): Perform laboratory or field procedures to explore the content and principles of biology (lab exercises, lab practicals)			X		
CLO (& Assignment): Carry out laboratory work in a socially responsible manner, which includes treating live organisms humanely, respecting animals used for dissection, observing laboratory safety procedures, adhering to wast disposal regulations, and refraining from cheating or plagiarizing in any way (lab exercises, lab practicals)					X
BIOL 212-Cell Physiology	I			I	I
CLO (& Assignment): Describe the subcellular structure of prokaryotic and eukaryotic cells. (lectures, quizzes, exams)	x				
CLO (& Assignment): Understand the roles that biological macromolecules such as proteins, nucleic acids, lipids, and carbohydrates play within the cell. (lectures, quizzes, exams)	x				
CLO (& Assignment): Understand the molecular mechanism, regulation, and control of cellular processes such as intracellular transport, cell communication, and the cell division cycle. (lectures, quizzes, exams)	x				
CLO (& Assignment): Be able to find, read, and understand scientific review articles and primary scientific papers. (scientific paper assignments, scientific literature summary report)				x	
CLO (& Assignment): Understand how defects in DNA, proteins, and cells can cause a variety of human diseases. (lectures, quizzes, exams)					x
BIOL 310/311-Genetics/Lab	A	I	I	I	I
CLO (& Assignment): Analyze the biochemistry underlying genetics (lecture exams)	x				
CLO (& Assignment): Investigate the chromosome theory of heredity (lecture exams, lab exercises, lab reports)	x	x	x	x	
CLO (& Assignment): Apply the concepts of genic interactions and gene-protein-phenotype relationships to solve genetic problems. (lecture exams, lab exercises, lab reports)	x	x	x	x	
CLO (& Assignment): Recognize the impact of recent advancements in the area of molecular genetics, genomics and bioinformatics. (lecture exams, ethics paper/presentation)	x	x	x	x	
CLO (& Assignment): Examine population genetics, evolutionary genetics, and quantitative genetics. (lecture exams, lab exercises)	x		x		
CLO (& Assignment): Research the significance of ethics in the field of genetics. (ethics paper/presentation)	x			x	x
BIOL 390-Biology Seminar	A			A	A
BIOL 414-Evolution	A	A		A	A
JS - CLO (& Assignment): Evaluate the forces that drive evolutionary change within populations	X	X		X	
JS - CLO (& Assignment): Evaluate phylogenetic relationships among organisms	X	X	X	X	
JS - CLO (& Assignment): Assess the relevance of evolutionary theory in modern issues such as infectious disease, animal behavior, & education	X			X	X
JS - CLO (& Assignment):Evaluate the role evolution plays in all areas of research and study in the biological sciences	X		X	X	X
DK - CLO: Recall the notions of evolution before Darwin and discuss how the theory of natural selection was formulated. (Lectures, exams, class activities and discussions.)	X				
DK - CLO: Define evolution and describe the various processes that bring about evolutionary change. (Lectures, exams, class activities and discussions.)	X				
DK - CLO: Recognize the bodies of evidence in support of evolutionary biology, and recognize the errors in most arguments and misconceptions often described by opponents of evolutionary biology. (Lectures, exams, class activities and discussions.)	X				
DK - CLO: Recognize the relevance of evolutionary theory in many modern issues, including but not limited to infectious disease, environmental change, human behavior, genetic engineering, general education and religion.	X			X	X
DK - CLO: Demonstrate the ability to read, understand, and critically review scientific papers.				X	

JP - CLO 1 Understand the historical progression of evolutionary thought;		x		x	x
JP - CLO 2 Understand the patterns of evolution preserved in fossils, phenotypes, and genomes;	x			x	
JP - CLO 3 Understand and evaluate the forces that drive evolutionary change within populations (selection, genetic drift, gene flow);	x	x		x	
JP - CLO 4 Assess the role of mutation in evolution and understand the principles of molecular evolutionary change;	x			x	
JP - CLO 5 Recognize and evaluate the evidence from fossils, organisms, and molecules in support of evolution	x			x	
JP - CLO 6 Evaluate the phylogenetic relationships among organisms based on the concept of descent with modification and the various approaches to inferring phylogenies	x	x		x	
JP - CLO 7 Recognize the relevance of evolutionary biology to other fields of biology and medicine				x	x
JP - CLO 8 Understand the arguments and misconceptions touted in opposition to evolution					x
BIOL 319-Ecology	I	I		I	
BIOL 320/321-Human Physiology/Lab	A	A	A	A	I
CLO: describe the importance of homeostasis to proper physiological function	X				
CLO: describe the mechanisms involved in the functioning of the nervous, endocrine, muscular, cardiovascular, respiratory, digestive, urinary and reproductive systems.	X				
CLO: read and evaluate articles from the primary literature discussing physiological topics				X	
CLO: apply your knowledge of human physiology to evaluating news about health- or physiology-related issues in the popular press					X
CLO: perform laboratory skills related to physiological topics, including but not limited to: measuring blood pressure, hematocrit, heart rate, and lung volumes and capacities; performing basic vision and hearing tests; obtaining a 3-lead electrocardiogram; and measuring electrical activity of neurons	X	X	X		
CLO: construct figures and tables to illustrate physiological data, describe and evaluate experiments, including via basic statistical tests		X		A	
CLO: evaluate and discuss patient case studies	X			X	
BIOL 324/325-Molecular Ecology	A	A	A	A	I
CLO 1. Critically read, assess, and discuss research articles on molecular ecology from the primarily literature.				x	
CLO 2. Differentiate among different classes of molecular markers and know their applications	x			x	x
CLO 3. Apply population genetic, phylogenetic, and evolutionary principles to the interpretation of molecular marker data	x				
CLO 4. Write an NSF-style pre-proposal on a molecular ecology topic	x	x		x	
CLO 5. Extract DNA from animals and plants.			x		
CLO 6. Amplify DNA markers using polymerase-chain reaction (PCR)			x		
CLO 7. Build alignments of DNA sequence data.			x		
CLO 8. Analyze DNA sequence data (population genetic and phylogenetic analyses).		x			
CLO 9. Conduct basic molecular ecology analyses in the statistical programming language R		x			
BIOL 326/327-Field Botany/Lab	A	I	A	A	
CLO 1. Identify native Californian plants to the level of family			x		
CLO 2. Recognize locally important plants to genera and selected plants to species			x		
CLO 3. Develop and keep a scientific field journal and digital photograph collections of plants seen in the field			x		
CLO 4 1. Understand the significance of the California flora within an evolutionary and global context	x			x	
CLO 5. Know key morphological and ecological characteristics that define the major plant families of the California flora			x		
CLO 6. Fundamental ecological concepts that help explain the abundance and distribution of plants with emphasis on case studies of Californian plants.		x		x	
BIOL 328/329-Invertebrate Zoology/Lab	A	A	A	A	I
CLO (& Assignment): Develop critical ability to identify the major and minor invertebrate phyla in the laboratory and field	x				
CLO (& Assignment): Interpret evolutionary relationships among phyla through the construction & interpretation of phylogenetic trees	x	x		x	
CLO (& Assignment): Gain skills in field colleciton techniques, maintaining field notebooks, and electron/confocal miscrocopy techniques			x		x
CLO (& Assignment): Evaluate the evolutionary innovations & ecological interactions that have shaped life history and community structure	x	x		x	
BIOL 330-Female Biology	A			A	A
BIOL 331/332-Herpetology/Lab	A	A	A	A	I
BIOL 333/334-Endocrinology/Lab	A	A	A	A	A

CLO: Describe the mechanisms of hormone action in cells including the role of hormone receptors, intracellular signaling cascades and cellular effects. (lectures, quizzes, exams, case studies, grant proposal)	x	x		x	
CLO: Use learned methodology to design experiments with appropriate controls (lecture, quizzes, exams, grant proposal, original research paper, lab reports)	x	x	x		x
CLO: Explain the synthesis of hormones, their physiological targets and their specific actions. (lectures, quizzes, exams, case studies)	x	x		x	
CLO: Explain the physiological effects of hormones on human health and disease. (lectures, quizzes, exams, case studies, grant proposal)	x	x		x	x
CLO: Describe the impact and importance of endocrinology on basic scientific as well as medical research. (exams, case studies, grant proposal, original research paper)	x	x		x	x
CLO: Read and summarize primary scientific research articles. (journal club, case studies, grant proposal, original research paper, lab reports)	x			x	x
CLO: Carry out scientific procedures in an ethical manner, including humane treatment of live organisms, adherence to laboratory safety procedures, and proper disposal of laboratory waste. (lab reports, original research paper, lab notebook)	x	x	x		x
CLO: Accurately observe, record, analyze, and report data collected in the laboratory. (lab reports, original research paper, lab notebook)	x	x	x		
CLO: Carry out original scientific research, write up and interpret their results. (original research paper)	x	x	x	x	
BIOL 340-Animal Toxicology	A			A	
CLO: Demonstrate (on exams and weekly online quizzes) an understanding of mechanisms of absorption, distribution, biotransformation, and excretion of toxicants.	X				
CLO: Demonstrate (on exams and weekly online quizzes) an understanding of mechanisms of mutagenesis, carcinogenesis, embryotoxicity	X				
CLO: Demonstrate (on exams and weekly online quizzes) an understanding of mechanisms of damage to selected organs and systems, and the environment.	X				
CLO: Demonstrate (written assignment) the ability to critically assess an experimental toxicology research paper				X	
BIOL 341/342-Medical Microbiology/Lab	A	I	A	I	I
Define the science of microbiology, give examples of pathogenic microbes, and describe some of the general methods used in the study of microorganisms.	X		X		
Describe the different types of immune responses, their importance in control of foreign agents, and involvement in pathological conditions.	X				
Analyze medical case studies, ask relevant questions, and present a differential diagnosis.		X		X	X
BIOL 345-Virology	A	A		A	
CLO (& Assignment): Describe, diagram and label a typical enveloped virus and a typical non-enveloped virus as well as a typical replication cycle (lecture exams).	X				
CLO (& Assignment): Suggest an experiment or set of experiments to identify and/or characterize an unknown virus (lecture exams).	X				
CLO (& Assignment): Explain how the pattern of gene expression for a particular virus is determined by the structure of its genome and how the genome is replicated (lecture exams).	X				
CLO (& Assignment): Explain the scientific basis for therapeutic interventions against virus diseases (lecture exams).	X				
CLO (& Assignment): Discuss the molecular basis for virus-induced immunodeficiency and transformation by viruses (lecture exams).	X				
CLO (& Assignment): Compare and contrast cells, viruses, viroids and prions (lecture exams).	X				
CLO (& Assignment): Cemonstrate the ability to understand and evaluate both popular and scientific virology literature, and describe the techniques used to study viruses (Presentation-Discussion Primary Literature Assignment)				X	
BIOL 346/347-General Microbiology/Lab	A	A	A	A	
CLO (& Assigment) Define the science of microbiology and describe methods used in the study of microorganisms.	X				
CLO (& Assigment) Describe the interactions and impact of microorganisms with humans and in the environment.	X				
CLO (& Assigment)Discuss the principles of evolution as they apply to microbiology and give specific examples of evolutionary processes that may be observed in the microbial world.	X				
CLO (& Assigment)Gain proficiency with basic microbiology lab techniques such as bright field microscopy, preparation of bacterial smears, Gram staining, aseptic technique, isolation streaks, DNA isolations, restriction digests, and gel electrophoresis.			X		
CLO (& Assigment)Develop analytical skills including collecting, analyzing, and presenting data and drawing appropriate conclusions based on the results.		X	X	X	
BIOL 350-Comparative Animal Physiology	A			A	I
CLO: • Discuss thermal relations that animals maintain with their environments; describe poikilothermy and endothermy and their benefits and limitations	X				
CLO: • Compare and contrast the functioning of the nervous, respiratory, circulatory, and excretory systems in different animal taxa	X				
CLO: • Explain the physiological challenges of living in aquatic and terrestrial environments	X				
CLO: • Discuss the mechanisms by which aquatic and terrestrial invertebrates and vertebrates are physiologically adapted to their environment	X				
CLO: • Read and evaluate articles from the primary literature discussing physiological topics				X	X
BIOl 355/356-Developmental Biology/Lab	A	A	A	A	A
CLO (& Assignment): Evaluate the experimental basis of our current understanding of animal development through study of model systems	x	x		x	x
CLO (& Assignment): Gain skills in molecular laboratory techniques used in the molecular study of development		x	x		x
CLO (& Assignment): Critically evaluate experimental evidence to describe mechanisms of embryonic and post-embryonic development in animals	x	x	x	x	x

CLO (& Assignment): Evaluate the evolutionary conservation of developmental mechanisms throughout animals	x			x	
BIOL 362/363-Histology/Lab	A		A		
CLO: 1. Demonstrate (on exams) an understanding of the relationship between biological structure and function, from the subcellular to the organ level.	X				
CLO: Reconstruct the three-dimensional microanatomy of tissues based on the study of two- dimensional tissue sections.			X		
CLO: Use histological study resources that are available on the internet..					
CLO: Develop proficiency in the setup and use of the compound microscope.			X		
CLO: Understand the procedures used to make histological sections.			X		
CLO: Demonstrate (on a laboratory practical exam and weekly quizzes) the ability to recognize the microscopic appearance of cells and tissues of the major organ systems.	X				
BIOL 365/366-Human Anatomy/Lab	A		A		A
CLO (& Assignment): Demonstrate knowledge of the names, locations, and functions of structures in the human body (lecture exams, lab practicals)	X				
CLO (& Assignment): Demonstrate proficiency in dissecting preserved specimens (dissections, production of dissection video)			X		
CLO (& Assignment): Demonstrate understanding of ethical considerations when dealing with cadavers (short papers)					X
BIOL 368-Neurobiology	A	A		A	A
CLO (& Assignment): Demonstrate knowledge of the organization of the mammalian nervous system, including both sensory and motor systems. Demonstrate knowledge of chemical neurotransmission, electrical properties of neurons, and neuroplasticity (lecture exams)	X	X			X
CLO (& Assignment): Critically evaluate and present current peer-reviewed research articles in the field of neuroscience (term paper and journal club presentation)		X		X	X
BIOL 379/380-Conservation Biology/Lab	A	A	A	A	I
BIOL 383/384-Biology of Insects/Lab	A	A	A	A	
BIOL 385/386-Parasitology/Lab	A		A		A
Lecture CLO: Demonstrate an understanding of (in exams and weekly online quizzes) taxonomy, geographic distribution, hosts, life cycle stages, pathological effects, control measures, and immune interactions of the parasites infecting humans.	X				X
Lab CLO: Demonstrate the ability set up and use a compound light microscope.			X		
Lab CLO: Describe (on sketches) the detailed structure of parasites and their vectors	X				
Lab CLO: Identify (in laboratory practical exams and weekly pre-lab quizzes) unknown parasites based upon microscopic appearance.	X				
BIOL 387/388-Hematology/Lab	A		A		
BIOL 392/393-Oceanography/Lab	A		A	A	
CLO: Understand the complex interactions between land, sea and air relative to processes that are involved in regulating life in the biosphere, and more specifically for supporting life in the oceans. (Lectures, exams, class discussions, field trip reports.)	x				
CLO: Demonstrate scholarly appreciation of the physical, chemical and biological aspects of the world oceans in the context of knowing how the oceans are integrated into Earth's biosphere. (Lectures, exams, class discussions, field trip reports.)	x				
CLO: Recognize the factors of global climate change that affect marine populations and the implications for marine conservation and management. (Lectures, exams, class discussions, field trip reports.)	x			x	x
CLO: Become proficient in collecting, analyzing and managing data, interpreting results and identifying trends in data sets. (Lectures, exams, class activities, field trip and data reports.)	x		x		
CLO: Improve the ability to review and critically appraise writings on marine issues in the popular press and in scientific journals to develop an informed scholarly personal position in relation to current issues in marine science. (Lectures, exams, class discussions, field trip reports.)	x			x	x
BIOL 395/396-Biology of Fishes/Lab	A	A		A	I
BIOL 405-Molecular Medicine	A	A		A	A
CLO. Understand how drugs function and how new drugs are discovered and deve	X	X			
CLO Understand the many obstacles a new drug must overcome to be approved by the FDA as an effective and safe medication. Understand the purpose of the FDA and the				X	X
CLO Explain both specific and general genetic factors underlying efficacy and toxic	X			X	
CLO Assess the value of phenotyping and genotyping in guiding drug therapy of in	X			X	
CLO Provide examples of genetic polymorphisms that affect the metabolism and response of specific groups of drugs used to treat various types of diseases	X			X	
BIOL 420-Molecular Biology	A			A	
CLO (& Assignment): Describe and diagram gene structure and expression in prokaryotes and eukaryotes as well as the differences and similarities in prokaryotic and eukaryotic gene structure and expression (lecture exams).	X				
CLO (& Assignment): Provide examples of how intracellular signals may lead to changes in gene expression and demonstrate an understanding of how information is stored and expressed in cells (lecture exams).	X				
CLO (& Assignment): Diagram and describe DNA replication (lecture exams).	X				
CLO (& Assignment): Appreciate how knowledge of biology at the molecular level is key to understanding health and disease (lecture exams).	X				

CLO (& Assignment): Describe a number of experimental approaches used in molecular biology, genomics and Proteomics and demonstrate the ability to interpret and evaluate data arising from molecular biological experiments (lecture exams, Presentation-Discussion Primary Literature Assignment)	X				
CLO (& Assignment): Suggest an experiment, or set of experiments, to address a molecular problem or point of inquiry (lecture exams, in-class problem solving)	X				
CLO (& Assignment): Demonstrate the ability to understand and evaluate primary scientific literature and formally present molecular concepts in a coherent, concise and logical fashion (Presentation-Discussion Primary Literature Assignment)	X			X	
BIOL 443/444-Immunology/Lab	A	A	A	A	I
CLO (& Assignment): Diagram and label the cells and molecules involved in innate and adaptive immune responses in infection and cancer, as well as the tissues in which lymphocytes develop, reside and function (lecture exams).	X				
CLO (& Assignment): Explain the process of hematopoiesis; lymphocyte development in particular (lecture exams).	X				
CLO (& Assignment): Diagram and label each of the five classes of antibodies, and state the ways in which antibodies assist in the disposal of antigens (lecture exams).	X				
CLO (& Assignment): Describe how knowledge of cellular and molecular immunology is key to understanding aspects of health and disease, and to the development of immune adjuvant therapies (lecture exams).	X				
CLO (& Assignment): Provide examples of B cell, T cell, and macrophage functions that involve processes such as intracellular trafficking, exocytosis, endocytosis, phagocytosis, cell motility, intracellular signaling, gene structure and gene expression, the cell cycle, and the interactions between cells and their environments (lecture exams).	X				
CLO (& Assignment): Appreciate the complexities of cell function yet recognize the molecular themes that are common in all living systems (lecture exams).	X				
CLO (& Assignment): Understand and evaluate scientific immunological literature (lecture exams, case presentations, primary research article presentations).	X			X	
CLO (& Assignment): Explain the theory of antibody – antigen interactions and how such interactions have allowed for the development of immunological assays, interpret these assays and, given a particular biological problem or point of inquiry, suggest one or a series of experiments to address it, along with proper controls (laboratory practice and laboratory exams).	X	X	X		
BIOL 458/459-Advanced Microscopy/Lab					
BIOL 485/486-Molcular Genetics and Biotechnology/Lab	A	A	A		A
CLO (& Assignment): Demonstrate a keen understanding of the structure, function and biochemistry of DNA (lecture and laboratory exams).	X				
CLO (& Assignment): Distinguish and diagram DNA-based structures: nucleoside, nucleotide, nucleic acids (lecture and laboratory exams).	X				
CLO (& Assignment): Be able to independently carry out techniques in DNA manipulation, cloning, and analysis (observation of laboratory practice).	X	X			
CLO (& Assignment): Be able to describe a range of methods used in the manipulation, propagation, analysis and storage of DNA, RNA and protein samples (laboratory practice; lecture and laboratory exams).	X	X	X		
CLO (& Assignment): Perform calculations and design graphs, applying statistical methods(lecture and laboratory exams).	X		X		
CLO (& Assignment): Gain an appreciation of the importance of accurate documentation in the laboratory (electronic lab notebook).			X		
CLO (& Assignment): Understand that our knowledge of molecular biology is key to understanding physiological health and disease, and to the development of therapies (lecture exams).	X				
CLO (& Assignment): Demonstrate an understanding of the biotechnology industry and the ethical implications of emerging technologies (lecture exams).	X				X
Key:					
I = Introductory					
A = Advanced					
CLO = Course Learning Outcome					

	PLO1	PLO2	PLO3	PLO4	PLO5
Institutional Learning Outcomes X Program Learning Outcomes	Demonstrate both in-depth and broad knowledge of the concepts that comprise the biological sciences.	Apply the scientific process, including designing and conducting experiments and testing hypotheses.	Perform laboratory, field, and analytical techniques.	Discuss and critically review scientific papers and prepare oral and written reports in a standard scientific format.	Demonstrate an awareness of the significance ethics plays in the biological sciences.
Institutional Learning Outcomes					
1. Students reflect on and analyze their attitudes, beliefs, values, and assumptions about diverse communities and cultures and contribute to the common good.					
2. Students explain and apply disciplinary concepts, practices, and ethics of their chosen academic discipline in diverse communities.	x	x		x	x
3. Students construct, interpret, analyze, and evaluate information and ideas derived from a multitude of sources.	x	x		x	x
4. Students communicate effectively in written and oral forms to interact within their personal and professional communities.				x	x
5. Students use technology to access and communicate information in their personal and professional lives.		x	x	x	
6. Students use multiple methods of inquiry and research processes to answer questions and solve problems.		x	x	x	x
7. Students describe, analyze, and evaluate global interconnectedness in social, economic, environmental and political systems that shape diverse groups within the San Francisco Bay Area and the world.					