## **Annual Program Assessment Report**

Academic Year Assessed: 2019-2020

College: College of Agriculture

Department: Plant Science and Plant Pathology (PSPP)

Submitted by: Matthew Lavin. Reviewed by Ryan Thum, Andreas Fischer, Mike Giroux, Alan Dyer,

Jennifer Britton, and Bill Hoch

Program Assessed: Plant Biology

#### Indicate all majors, minors, certificates and/or options that are included in this assessment:

Majors/Minors/Certificate	Options
Plant Science	Plant Biology

#### Annual Assessment Process (CHECK OFF LIST)

- 1. Data are collected as defined by Assessment Plan
  - YES<u>X</u> NO\_\_\_\_
- 2. Two faculty members using scoring rubrics to ensure inter-rater reliability score population or unbiased samples of collected assignments.

YES<u>X</u> NO\_\_\_\_

3. Highlight areas where the acceptable performance threshold not surpassed.

YES\_\_\_\_\_ NO\_\_\_\_ NA\_X\_\_

- 4. The scores presented to a program faculty meeting for assessment.
- 5. YES\_X\_\_\_ NO\_\_\_\_
- 6. The faculty reviewed the assessment results, and responds accordingly (Check all appropriate lines) Gather additional data to verify or refute the result\_\_\_\_\_

Identify potential curriculum changes to try to address the problem\_\_\_\_\_

Change the acceptable performance threshold, reassess\_\_\_\_\_

Choose a different assignment to assess the outcome\_\_\_\_\_

Faculty may reconsider thresholds\_\_\_\_

Evaluate the rubric to assure outcomes meet student skill level\_\_\_\_

Use Bloom's Taxonomy to consider stronger learning outcomes\_\_\_\_\_

Choose a different assignment to assess the outcome\_

OTHER<u>X</u> (If none of the above are appropriate, describe briefly the results of faculty review. You will have the opportunity to provide more detail within the report)

7. Does your report demonstrate changes made because of previous assessment results (closing the loop)? YES\_\_\_\_ NO\_X\_

**1. Assessment Plan, Schedule and Data Source.** A multi-year assessment schedule showing when all program learning outcomes will be assessed, and by what criteria. Data sources can be items such as randomly selected student essays or projects, specifically designed exam questions, student

Assessment reports are to be submitted annually by program/s. The report deadline is <u>September</u> 15<sup>th</sup>.

presentations or performances, or a final paper. Course evaluations and course surveys are not sources of data.

ASSESSMENT PLANNING CHART. PROGRAM: PLANT BIOLOGY								
LEARNING OUTCOME	2018 2019	2019 2020	2020 2021	2021 2022	Assessment Targets			
<b>Learning Outcome 1</b> : Demonstrate knowledge of fundamental principles spanning the breadth of biology.	BIO220		BIOO 220		Essay Question			
<b>Learning Outcome 2</b> : Demonstrate effective communication in the scientific method, experimental design, or critical assessment of the scientific literature.		BIOB 420			Specifically designed exam questions			
<b>Learning Outcome 3</b> : Attain the technical and/or analytical skills required for employment or post-graduate education in biology or biology-related careers, including professional careers and science education.	BIOB 420			BIOB 420	Specifically designed exam questions			

#### 2. What Was Done

#### a) Was the completed assessment consistent with the plan provided? YES\_X\_ NO\_\_\_\_

Assessment committee members for this academic year were Matthew Lavin, Andreas Fischer, and Ryan Thum. This committee assessed the performance of students in two courses, Botany BIOO 220 and Evolution BIOB 420 (sections 001 and 002). These are two of the required biology courses in the Plant Biology degree option. Fisher instructs BIOO 220. Lavin and Thum co-instruct BIOB 420.

To assess the Plant Biology degree program, committee members Lavin and Fisher met during October 2018 to identify data to collect from students in Botany BIOO 220. Committee members Lavin and Thum met January 2019 and 2020 to identify data to collect from students in Evolution BIOB 420.

The Plant Biology degree option caters to diverse students, including those interested in plant ecology and evolution, bee keeping, pre-biomedical and pre-veterinarian school, medicinal and herbal botany, and wildlife management, for example. Because of this, we generalized the learning outcomes following those of the Department of Biology at Boston University (<u>https://www.bu.edu/biology/</u>). The above table reports three learning outcomes that cover the diversity of general biology undergraduate students.

**b) Rubric that demonstrates evaluation of data.** This rubric pertains to learning outcome 1, as assessed in BIOO 220 during 2018-2019 and learning outcome 2, as assessed in BIOB 420 during 2019-2020.

Indicators	Beginning	Developing	Competent
Student applies information, ideas, or concepts	Identifies the fundamental issues and applies information or methods	Focuses on the fundamental issues and makes logical interpretation of data	Understands complexity of fundamental issues and applies creativity in addressing the issues
Student demonstrates ability to evaluate or synthesize information, ideas, or concepts	Identifies connections between seemingly disparate facts or ideas	Identifies alternative perspectives or methods	Connects facts or ideas in a coherent order

#### 3. What Data Were Collected

#### a) Methods of data collection.

**Assessment of learning outcome 1**. For BIOO 220 Botany, an essay question was included in the final exam. Students enrolled = 34. Students answering the essay question = 27. This question asked, "Please explain how green plants (e.g., bryophytes, ferns, gymnosperms, and angiosperms) differ from animals in terms of alternation of generations and the production of gametes. The answers to this question potentially demonstrate a student's ability apply information, ideas, and concepts related to plant diversity and a student's ability to evaluate and synthesize information, ideas, and concepts. Specifically, demonstrating an ability to apply information and synthesize knowledge derives from an essay question that allows a student to expound on what are the underlying similarities of diverse groups of plant and how do diverse plant groups differ collectively from animals by other than the ability to photosynthesize. Answers to the essay question reside in the document entitled "BIOO 220 Botany evaluation essay Fall 2018.pdf" (PDF page 47).

**Assessment of learning outcome 2**. For BIOB 420 Evolution, we designed questions that demonstrate whether students could apply information, ideas, or concepts related to study design and critical assessment of scientific literature. We also designed the questions to demonstrate whether students could evaluate or synthesis information, ideas, and concepts related to study design and critical assessment of scientific literature. Question on daily formative assessments preceded related question on monthly exams. Students enrolled = 230, almost all of whom answered all questions. Of the 230 students enrolled in Spring Semester2020 BIOB 420 Evolution, 149 students enrolled in section 01 and 81 students in section 02.

The following three examples questions (a1-a3) represent the kind of questions designed to assess whether students were learning how evolutionary biologist design historical studies dealing with origins of populations, sources of infections, and how traits evolve. These examples reflect the general trends of the class of 230 students enrolled in BIOB 420 Evolution. The study of evolutionary history is particularly vulnerable to misinterpretation by the public (or the scientifically untrained mind). Specifically, evolutionary studies commonly produced phylogenetic trees. Inevitably, phylogenies of human population samples are open to misrepresentation. The Evolution course thus not only addresses study

design but also the biases the public have when exposed to the results of well-designed historical evolutionary studies, particularly when humans are the subject of study.

A standard design of evolutionary studies involves population genetic samples that serve reference points. Such samples often resolve in a phylogenetic analysis as early branching or old lineages. Such population genetic samples could include suspected source areas of migration events (in wildlife management studies), sources of infection (in phylogenetic epidemiological studies), or as references to determine how traits evolve from older ancestral forms into more recent derived forms (where ancestral and derived refer to character states, not individuals, populations, or species).

*a1. Identifying source versus founder populations.* Populations samples resolved as early branching (older) lineages in a phylogeny often represent samples intentionally included in order to test a "place of origins" hypothesis. For human population samples, African samples are consistently resolved as the earliest branching oldest lineages, which supports the hypothesis that modern humans population ultimately originated in Africa. However, a mental bias of people not exposed to science often includes the ideas that modern African populations are "primitive" or ancestral relative to perhaps "superior" non-African populations. These biases become apparent when the same study design applies to questions involving non-human samples (e.g., populations of North American wolves and species of Ponderosa pine trees).



The above human population phylogeny is a consensus of all human population phylogenies derived from various study designs that include differences in population or genetic methods of sampling. African populations resolve as early branching lineages with older average age estimates and non-African populations consistently resolve as more recently evolved lineages and with younger average age estimates. What does this imply?

This question first asked to the class on 4 March 2020 (BIOB 420 Quiz Mar 4.pdf - p. 34) as part of an in-class formative assessment had the following responses:

 24.5% of the class incorrectly responded, "Modern African human populations are ancestral to all modern non-African populations."

- 2.5% of the class incorrectly responded, "African human populations are primitive compared to more advanced non-African populations."
- <u>52% of the class correctly responded</u>, "Africa is the ancestral area from which all non-African
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Essentially the same question asked again on 4 May 2020 (BIOB 420 Exam 4 May 4.pdf - p. 10) as part of the final exam revealed an improvement in understanding study design of evolutionary historical studies:

- 8.8% of the class incorrectly responded, "Modern day African populations are ancestral to modern day European populations."
- 0.4% of the class incorrectly responded, "African populations are primitive."
- 0.4% of the class incorrectly responded, "African populations are unperfected compared to European populations."
- <u>90.3% of the class correctly responded</u>, "The continent of Africa served as the source area from which modern non-African human populations ultimately migrated."

The increase from about 52% to 90% of the class was the general trend for this sort of "place of origins" question, which formed course content throughout the semester.

a2. Using control samples to identify infection routes. Populations samples resolved as early branching (older) lineages in a phylogeny often represent control samples. If one person allegedly infected another with HIV1, control samples allow this hypothesis to be properly tested.

HIV1 nucleotide substitution distances	Janice.S1	Donald.S3	Janice.S2	Donald.S7	Local.S30
JaniceTrahan.S1	0				
DonaldMcClelland.S3	0.0072	0			
JaniceTrahan.S2	0.0078	0.0081	0		
DonaldMcClelland.S7	0.0116	0.0128	0.0119	0	
LouisianaLocal.S30	0.0387	0.0362	0.0373	0.0325	0

Questions related to this aspect of study design and critical assessment of scientific literature required students to infer a phylogeny from a genetic distance matrix (above) and understand the design of that matrix. Such questions first asked to the class on 22 April 2020 (BIOB 420 Quiz Apr 22.pdf - p. 38) were part of an in-class formative assessment. Included was the following: RNA virus evolve rapidly with respect to nucleotide substitutions. When RNA viral genetic evidence is sampled years after the alleged criminal event, the genetic evidence has evolved. What constitutes a genetic "match" between victim samples and the alleged source samples if the genetic evidence evolves quickly over time?

- <u>45% of the class correctly responded</u>, "Monophyly of the victim and the alleged source samples."
- 17% of the class incorrectly responded, "Victim samples are more closely related to samples from a local control than to samples from the alleged source."
- 26% of the class incorrectly responded, "Alleged source samples are more closely related to samples from a local control than to samples from the victim."
- 12% of the class incorrectly responded, "A genetic match cannot be made."

A similar question asked again on 4 May 2020 (BIOB 420 Exam 4 May 4.pdf - p. 10): Phylogenetic evidence revealed that Janice Trahan was infected by HIV from a blood sample taken from Donald McClelland. The evidence included:

- 6% of the class responded partly correct with, "The combined viral samples from Trahan and McClelland formed a monophyletic group with respect to Louisiana local control samples."
- 3% of the class responded partly correct with, "Trahan HIV strains averaged younger in age than those sampled from McClelland."
- 3% of the class responded partly correct with, "Trahan HIV strains were not monophyletic with respect to McClelland HIV strains and were thus not genetically differentiated from McClelland strains."
- 88% of the class correctly responded, "All these."

The increase from about 45% to 88% of the class was generally the trend to this sort of "control sample" question that was a focus of course content more towards the end of the semester.

*a3. Using reference samples to determine the direction of character state evolution.* Populations samples resolved as early branching (older) lineages in a phylogeny often represent reference samples that permit the inference of character state evolution. Study design includes specifying an outgoup (e.g., other mammals is data set below) and ingroup (the other samples in data set below). Ancestral character states occur in the outgroup, whereas character states found only in the ingroup are derived. Ancestral and derived refer to character states, not the samples (taxa).

Cetartiodactyla	Paired toes	Trochleated astragalus	B-casein 162	B-casein 166	Т4	T5	Т6	T7
Other mammals	0	0	С	Т	0	0	0	0
Camels	1	1	С	А	0	0	0	0
Ruminants	1	1	Т	G	0	0	0	0
Hippopotami	1	1	Т	С	1	1	1	1
Cetaceans	0	0	Т	С	1	1	1	1

Questions related to this aspect of study design and critical assessment of scientific literature required students to infer a phylogeny from a data matrix of character states (above) and understand the design of that matrix. Such questions first asked to the class on 29 April 2020 were part of an in-class formative assessment. Included was the following (BIOB 420 Quiz Apr 29.pdf - p. 42): Characters T4-T7 are genomic characters indicating the absence (0) or presence (1) of transposable elements. When present, each of these transposable elements is inserted at a specific position in the genome of artiodactyl and cetacean species. In the above data set, the values of m and g for each of these four characters, T4-T7, is, respectively:

- 16% of the class incorrectly responded, "2 and 1."
- <u>46% of the class correctly</u> responded, "1 and 2."
- 21% of the class incorrectly responded, "4 and 8."
- 17% of the class incorrectly responded, "8 and 4."

A similar question asked again on 4 May 2020 (BIOB 420 Exam 4 May 4.pdf - p. 10): Baboons represent the outgroup in this data set. For the locomotion (gait) character, 0 = quadrupedal, 1 = quadrupedal but planting sides of palms on ground, 2 = quadrupedal but planting knuckles on ground, and 3 = fully bipedal. Which are the derived character states in this locomotion character?

	COI	tRNALys	ATPase8	ATPase8	ATPase8	ATPase8	Loco-	Broca's		Ψretro-	CMT1A	Ψalfa-
Catarrhines	2664	4028	4410	4414	4415	4417	motion	area	Canines	cyclin	repeat	enolase
Baboons	С	А	Т	С	С	С	0	0	dimorphic	0	0	0
Orangutans	С	А	А	С	С	С	1	0	dimorphic	0	0	0
Gorillas	С	А	А	А	G	Т	2	1	dimorphic	1	0	1
Chimp	А	Т	А	А	А	Т	2	1	dimorphic	1	1	1
Humans	А	Т	А	А	А	Т	3	1	monomorphic	1	1	1

- 14% of the class incorrectly responded, "0, 1, 2, and 3."
- <u>70% of the class correctly responded</u>, "1, 2, and 3."
- 8% of the class incorrectly responded, "2 and 3."
- 8% of the class incorrectly responded, "only 3."

The increase from about 46% to 70% of the class was generally the trend to this sort of "character state evolution" question, which was a focus of course content towards the end of the semester.

#### b) Explain assessment process and data analysis.

During January 2019, Lavin and Fisher read and evaluated the essay question written by students in Botany BIOO 220 as part of their final exam. Lavin and Fisher used the above rubric to evaluate student answers to the essay question. They each read the answers separately but ultimately came to conclusions about student performance during a meeting. The committee concluded that students met the basics of learning outcome 1, "Demonstrate knowledge of fundamental principles spanning the breadth of biology." In this context, students demonstrated an ability to apply information, ideas, or concepts at a competent level. However, students rarely demonstrated an ability to synthesize information, ideas, or concepts at a competent level (e.g., how plants fundamentally differ from animals including ecologically). Regardless, they demonstrated an ability to apply fundamental knowledge to answering the question, which included a knowledge of diverse plant groups and how they collectively differ from all animal groups.

During May 2020, Lavin and Thum read and evaluated the questions from daily formative assessments and related question presented on monthly exams. Student demonstrated an ability not just to apply information, ideas, and concepts, but also the ability to evaluate or synthesize information, ideas, or concepts. They did so at a competent level because they were able to connect the underlying similarities of study designs from diverse kinds of case studies (e.g., wildlife management, epidemiology, and paleontology) that formed the course content. In summary, the majority of students demonstrated increasing knowledge of study design and critical assessment of the scientific literature.

#### 4. What Was Learned

#### a) Areas of strength

The committee of Lavin and Fisher concluded from an assessment of learning outcome 1, "Demonstrate knowledge of fundamental principles spanning the breadth of biology," that students can readily report the facts, inter-relate them, and sometimes extend and connect them to disciplines outside of botany. The committee of Lavin and Thum concluded from an assessment of learning outcome 2, "Demonstrate effective communication in the scientific method, experimental design, or critical assessment of the scientific literature" that students understand the design of evolutionary historical studies and are unlikely to misrepresent the finding compared to the public untrained in historical sciences.

#### b) Areas that need improvement

A long-term goal from our assessments is to have addition biology courses incorporating exam questions, projects, and essays that allow students to make connections among the diverse disciplines of biology from astrobiology and microbiology to the omics fields and data science, all of which now regularly use data science.

#### 6. How We Responded

## a) Communication of "What Was Learned" to the department or program faculty. Was there a forum for faculty to provide feedback and recommendations?

The long-term goal reported above requires curriculum modifications. A recent step taken in this direction involved PSPP faculty discussions that led to the new requirement that students enrolled in the Plant Biology program now take both introductory statistics courses, STAT 216 and 217. This is because STAT 217 introduces the R programming language, which is an important programming language in evolutionary biology and ecology, as well as data science. No forum yet exists for faculty to provide feedback and recommendations but all involved are on board with incorporating data science into the Plant Biology program.

## b) Based on the faculty responses were there any curricular or assessment changes for the following year? (Such as plans for measurable improvements or realignment of learning outcomes).

PSPP faculty have a strong genetics focus and five PSPP faculty, Drs. Michelle Flenniken, Robert Sharrock, Jamie Sherman, and Ryan Thum are involved in teaching Genetics BIOB 375. BIOB 375 is required of many biology degree programs including Plant Biology. Following discussions with these five PSPP faculty, we are considering having the Genetics course participate in the program assessment of Plant Biology. The positive side of this is that Genetics is a quantitative science and a solid knowledge of this field is required for success in many biology graduate programs. Thus, it would be straightforward to develop specifically designed exam questions or student projects on which to evaluate student performance. The downside of including Genetics is that four faculty members teach it and with varying course content. This results in not being able to integrate program and course learning outcomes consistently.

#### c) Next assessment of program and any changes.

We will assess learning outcome 3, "Attain the technical and/or analytical skills required for employment or post-graduate education in biology or biology-related careers, including professional careers and science education" in BIOB 420 Evolution during Spring Semester 2021. PSPP faculty including Drs. Matt Lavin and Ryan Thum will collect data from this class from specifically designed exam formative assessment and exam questions. We will design these to learn whether students understand methods that transform quantitative data into graphical output and whether they can look at a data set and readily infer results that apply to wildlife management, forensics, and paleontological questions.

#### 7. Closing the Loop

# Based on assessment from previous years, can you demonstrate program level changes that have led to outcome improvements?

The assessment from 2017-2018 failed in many ways (e.g., no rubric to evaluate essay questions) and we submitted our 2018-2019 assessment of the Plant Biology program too late for review. Regardless, what we are learning is that the assessment tools in Brightspace D2L provide the opportunity to evaluate regularly, via formative assessment questions, whether students understand course concepts. We will be taking more advantage of what D2L offers in forthcoming assessments.

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Question 1 Difficu	ulty: 1			

Genetic evidence sampled from RNA viruses continues to evolve between the timing of the alleged criminal event the timing of sampling. What basically constitutes a genetic "match" between victim samples and the alleged source samples if nucleotide substitutions among RNA virus populations evolve quickly over time?

Monophyly of the combined victim and the alleged source samples with respect to local control samples	223 (98.24 %)	
Victim samples are more closely related to samples from a local control than to samples from the alleged source	1 (0.44 %)	Average Grade: 2.95 / 3 (98.24 %) Standard Deviation: 13.19 % Point Biserial: 0.27 Discrimination Index: 6.56 %

Alleged source samples are more closely related to samples from a local control than to samples from the victim	2	(0.88 %)
A genetic match cannot be made	1	(0.44 %)

Question 2 Difficulty: 1

HIV1 nucleotide substitution distances	Janice.S1	Donald.S3	Janice.S2	Donald.S7	Local.S30
JaniceTrahan.S1	0				
DonaldMcClelland.S3	0.0072	0			
JaniceTrahan.S2	0.0078	0.0081	0		
DonaldMcClelland.S7	0.0116	0.0128	0.0119	0	
LouisianaLocal.S30	0.0387	0.0362	0.0373	0.0325	0

According to the above nucleotide substitution distance matrix and an average RNA virus nucleotide substitution rate of about 1 substitution per 1,000 base pairs per year, which of the following statements are true?



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Question 3 Difficulty: 1

HIV1 nucleotide substitution distances	Janice.S1	Donald.S3	Janice.S2	Donald.S7	Local.S30
JaniceTrahan.S1	0				
DonaldMcClelland.S3	0.0072	0			
JaniceTrahan.S2	0.0078	0.0081	0		
DonaldMcClelland.S7	0.0116	0.0128	0.0119	0	
LouisianaLocal.S30	0.0387	0.0362	0.0373	0.0325	0

According to the above nucleotide substitution distance matrix and an average RNA virus nucleotide substitution rate of about 1 substitution per 1,000 base pairs per year, how old is the oldest viral strain sampled from Janice Trahan?



Question 4 Difficulty: 1

HIV1 nucleotide substitution distances	Janice.S1	Donald.S3	Janice.S2	Donald.S7	Local.S30
JaniceTrahan.S1	0				
DonaldMcClelland.S3	0.0072	0			
JaniceTrahan.S2	0.0078	0.0081	0		
DonaldMcClelland.S7	0.0116	0.0128	0.0119	0	
LouisianaLocal.S30	0.0387	0.0362	0.0373	0.0325	0

According to the above nucleotide substitution distance matrix and an average RNA virus nucleotide substitution rate of about 1 substitution per 1,000 base pairs per year, viral samples from randomly sampled local infected individual always resolve as early branches in the HIV and HCV phylogeny. This is an indication that viral samples from random local infected individuals are:

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	primitive	3	(	(1.32 %)	
	ancestral	19	(	(8.37 %)	Average Grade: 2.68 / 3 (89.43 %)
	imperfect	2	(	(0.88 %)	Standard Deviation: 31.06 %
-	distantly related				Point Biserial: 0.45
	to the clade of				Discrimination Index: 31.15 %
	Trahan- McClelland samples	203	(8	39.43 %)	

## Question 5 Difficulty: 1

Phylogenetic evidence revealed that Janice Trahan was infected by HIV from a blood sample taken from Donald McClelland. The evidence included:

	The combined viral samples from Trahan and McClelland formed a monophyletic group with respect to Louisiana local control samples	-	15	(6.61 %)	
	Trahan HIV strains averaged younger in age than those sampled from McClelland	•	7	(3.08 %)	Average Grade: 2.63 / 3 (87.67 %) Standard Deviation: 29.62 % Point Biserial: 0.34 Discrimination Index: 23.77 %
	Irahan HIV strains were not monophyletic with respect to McClelland HIV strains and were thus not genetically differentiated from McClelland strains		6	(2.64 %)	
<b>⇒</b> Ouest	All these	v: 1	199 (	87.67 %)	
Quest	ion 6 Difficult	y: 1			

HIV1 nucleotide substitution distances	Mediterranean	EqGuin.S1	EqGuin.S2	Al-Fateh.S8	EqGuin.S3	Al-Fateh.S9
Mediterranean	0					
Equatorial Guinea.S1	0.092	0				
Equatorial Guinea.S2	0.103	0.042	0			
Al-Fateh.S8	0.097	0.035	0.029	0		
Equatorial Guinea.S3	0.098	0.034	0.031	0.026	0	
Al-Fateh.S9	0.106	0.039	0.032	0.024	0.013	0

According to the above nucleotide substitution distance matrix and an average RNA virus nucleotide substitution rate of about 1 substitution per 1,000 base pairs per year, what is the average age of the viral strains sampled from Libyan children patients at al-Fateh Hospital (Al-Fateh strains S8 and S9)?



#### Question 7 Difficulty: 1

HIV1 nucleotide substitution distances	Mediterranean	EqGuin.S1	EqGuin.S2	Al-Fateh.S8	EqGuin.S3	Al-Fateh.S9
Mediterranean	0					
Equatorial Guinea.S1	0.092	0				
Equatorial Guinea.S2	0.103	0.042	0			
Al-Fateh.S8	0.097	0.035	0.029	0		
Equatorial Guinea.S3	0.098	0.034	0.031	0.026	0	
Al-Fateh.S9	0.106	0.039	0.032	0.024	0.013	0

According to the above nucleotide substitution distance matrix and an average RNA virus nucleotide substitution rate of about 1 substitution per 1,000 base pairs per year, what is the average age of the the viral strains sampled from Equatorial Guinea patients (S1, S2, and S3) at al-Fateh Hospital?

	about 7 years	3	(1.32 %)		
•	about 14 years	145	(63.88 %)	Average Grade:	1.92 / 3 (63.88 %)
			<b>`</b>	Standard Deviation:	43.16 %
	about 20 years	47	(20.7 %)	Point Biserial:	0.34
	much older than			Discrimination Index:	36.89 %
	20 years	32	(14.1 %)		

Question 8 Difficulty: 1						
HIV1 nucleotide substitution distances	Mediterranean	EqGuin.S1	EqGuin.S2	Al-Fateh.S8	EqGuin.S3	Al-Fateh.S9
Mediterranean	0					
<b>Equatorial Guinea.S1</b>	0.092	0				
Equatorial Guinea.S2	0.103	0.042	0			
Al-Fateh.S8	0.097	0.035	0.029	0		
Equatorial Guinea.S3	0.098	0.034	0.031	0.026	0	
Al-Fateh.S9	0.106	0.039	0.032	0.024	0.013	0

According to the above nucleotide substitution distance matrix and an average RNA virus nucleotide substitution rate of about 1 substitution per 1,000 base pairs per year, viral strains sampled from random HIV or HCV infected people living in the Mediterranean region resolve as the earliest (most basal) branches. What is concluded from this about Mediterranean viral strains?

	Mediterranean viral strains are ancestral	23 (10.13 %)	
	Mediterranean viral strains are primitive	1 (0.44 %)	
•	The Mediterranean region was not source of the HIV		Average Grade: 2.67 / 3 (88.99 %) Standard Deviation: 31.06 % Point Biserial: 0.45
	and HCV infection of the Libyan children patients in the al-Fateh hospital	202 (88.99%)	Discrimination Index: 31.15 %
	Mediterranean viral strains are unperfected	1 (0.44 %)	

Question 9 Difficulty: 1

Phylogenetic evidence revealed that al-Fateh Libyan children were infected with HIV and HCV that originated in patients who were immigrant laborers from equatorial Africa. The evidence included:

Combined HIV and HCV strains from all al-Fateh patients, both the Libyan children and the migrant laborers

from equatorial Africa, formed a monophyletic group with respect to the Mediterranean control samples		6 (	(2.64 %)	
HIV and HCV strains from Libyan children averaged younger in age than those sampled from migrant laborers from equatorial Africa		6 (	2.64 %)	Average Grade: 2.79 / 3 (92.95 %) Standard Deviation: 29.62 % Point Biserial: 0.34 Discrimination Index: 23.77 %
HIV and HCV strains from Libyan children were not monophyletic with respect to those sampled from migrant laborers from equatorial Africa and thus were not genetically different from migrant laborer strains		4 (	(1.76 %)	
All these		211 (9	2.95 %)	
Question 10 Difficu	lty: 1			

![](_page_16_Figure_1.jpeg)

The upper arrow indicates a set of points each representing pairs of wolf samples that genetically differ by an average Fst of about 0.40. What characterizes this set of points?

![](_page_16_Figure_3.jpeg)

![](_page_17_Figure_1.jpeg)

Genetic variation of the wolf populations samples along the north to south transect from taiga forest to Rocky Mountain coniferous forest is not explained by the isolation-by-distance model. This suggests that taiga wolves belong to a breeding population that is separate from that of coniferous forest wolves.

![](_page_17_Figure_3.jpeg)

#### Question 12 Difficulty: 1

In 1995–1996, 66 wolves from Fort St. John, British Columbia (taiga forest habitat), and Hinton, Alberta (Rocky Mountain coniferous forest habitat), were translocated to Idaho, Montana, and Wyoming to rehabilitate wolf populations in this region of the northern Rocky Mountains. What was distinctive about this 1995–1996 sample of 66 wolves?

![](_page_17_Figure_6.jpeg)

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![](_page_18_Figure_1.jpeg)

The upper set of points represents pairs of Ponderosa pine samples that genetically differ by an average Fst of about 0.90. What characterizes this set of points?

![](_page_18_Picture_3.jpeg)

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the other sample of the same pair comes from east of Holter Dam

Question 14 Difficulty: 1

![](_page_19_Figure_3.jpeg)

The lower set of points represents pairs of Ponderosa pine samples that genetically differ by an average Fst of 0 or close to it. What characterizes this set of points?

![](_page_19_Figure_5.jpeg)

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one sample of a		
pair comes from		
Holter Dam and	20	(8.81 %)
to the west and		
the other sample		
of the same pair		
comes from east		
of Holter Dam		

Question 15 Difficulty: 1

![](_page_20_Figure_3.jpeg)

Population variation of Ponderosa pine mtDNA sampled along an west-east transect across the Continental Divide in Montana is not explained by the isolation-by-distance model. This finding suggests that all Ponderosa pine samples from west and east of the Continental Divide all belong to the same breeding population.

![](_page_20_Figure_5.jpeg)

West slope Ponderosa pine is a tall statured and economically important timber tree. East slope Ponderosa pine is a shorter statured tree that is managed more for wildlife habitat than for timber production. Genetic analyses of these forms of Ponderosa pine in Montana demonstrate that:

Tall stature is simply a function of Montana Ponderosa pine growing in wetter habitats west of the Divide	2	(0.88 %)
Short stature is only a function of of Montana Ponderosa	2	(0.88 %)

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![](_page_21_Figure_1.jpeg)

Question 17 Difficulty: 1

![](_page_21_Figure_3.jpeg)

For population variation in Ponderosa pine cpDNA across the Continental Divide in Montana:

![](_page_21_Figure_5.jpeg)

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	geographically limited zone of contact			Average Grade: Standard Deviation: Point Biserial:	1.68 / 3 (55.95 %) 49.75 % 0.24
	The isolation- by-distance model does not explain cpDNA variation across the state of Montana, from the Blackfoot Range in the west to Lame Deer in the east		4 (1.76%)	Discrimination Index:	39.34 %
•	All these		127 (55.95 %)		

Question 18 Difficulty: 1

sample/cpDNA data	n	West	East
Blackfoot Range (B)	20	20	0
Rogers Pass (C)	20	15	5
Holter Dam (D)	20	10	10
Monarch (E)	20	3	17
Lewistown (F)	20	1	19

The frequency of the East cpDNA haplotype, q, at the Rogers Pass sample site is equal to:

![](_page_22_Figure_5.jpeg)

cnDNA sample	a nairs	Km	n	West	Fast	n	a	Ht(2ng)	Hs(2ng)	Ect
Rogers-Holter	e pans	30	40	25	15	0.625	0 375	0.469	0.438	0.067
Rogers-Mona	rch	115	40	18	22	0.450	0.550	0.495	0.315	0.364
Rogers-Lewist	own	220	40	16	24	0.400	0.600	0.480	0.235	
For the Rogers Pass and Lewistown sample sites, Fst is equal to about:       6       (2.64 %)         0.067       6       (2.64 %)         1.000       4       (1.76 %)         0.000       1       (0.44 %)         Point Biserial: 0.47       Discrimination Index: 16.39 %										
➡ 0.510	■ 0.510 Discrimination Index: 16.39 %									
Question 20 Difficulty: 1										
Haploid genomes like have small effective population sizes	Haploid genomes like those of mitochondria and chloroplasts are expected to: have small effective population sizes 5 (2.2 %)									
diversity within a breeding population	_					3 (	(1.32 %)	Average G Standard Devia	irade: 2.63 / 3 ation: 32.96 %	(87.67 %)
show differences between two genetically isolated populations	-					20 (	C 8.81 %)	Point Bis	serial: 0.11 ndex: 4.92 %	
have or show all these						199 (8	7.67 %)			
Question 21 Difficul	ty: 1									
When analyzing species relationships among humans and apes, the ingroup, with reference to monkeys and other primates, the outgroup, character states such as small cranium capacity, long canine teeth, and a quadrupedal gait represent:										
shared derived character states						56 (2	4.67 %)			

•	shared ancestral character states		124 (54.63 %)	Average Grade: 1.64 / 3 (54.63 %)
				Standard Deviation: 49.90 %

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unique ancestral character states	 /	Point Biserial: 0.22
	24 (10.57%)	Discrimination Index: 24.59 %
unique derived		
character states	23 (10.13 %)	

#### Question 22 Difficulty: 1

Catarrhines	COI 2664	tRNALys 4028	ATPase8 4410	ATPase8 4414	ATPase8 4415	ATPase8 4417	Loco- motion	Broca's area	Canines	Ψretro- cyclin	CMT1A repeat	Ψalfa- enolase
Baboons	С	А	Т	С	С	С	0	0	long	0	0	0
Orangutans	С	А	Α	С	С	С	1	0	long	0	0	0
Gorillas	С	А	Α	Α	G	Т	2	1	long	1	0	1
Chimps	Α	т	Α	Α	А	т	2	1	long	1	1	1
Humans	Α	т	Α	Α	Α	т	3	1	short	1	1	1

The Old World monkey group, baboons, represents the outgroup. The values of m and g, respectively, for the character ATPase8 site 4415 and its three states (C, G, and A), are:

![](_page_24_Figure_5.jpeg)

#### Question 23 Difficulty: 1

Cetartiodactyla	Paired toes	Trochleated astragalus	B-casein 162	B-casein 166	т4	Т5	т6	T7
Other mammals	0	0	С	Т	0	0	0	0
Camels	1	1	С	Α	0	0	0	0
Ruminants	1	1	Т	G	0	0	0	0
Hippopotami	1	1	Т	С	1	1	1	1
Cetaceans	0	0	Т	С	1	1	1	1

Characters T4–T7 are genomic characters indicating the absence (0) or presence (1) of transposable elements. When present, each of these transposable elements is inserted at a specific position in the genome of artiodactyl and cetacean species. In the above data set, the values of m and g for each of these four characters, T4–T7, is, respectively:

![](_page_24_Figure_9.jpeg)

![](_page_25_Figure_1.jpeg)

What is the value of s for each of the genomic characters, Tr4-Tr7, for hypothesis 2:

![](_page_25_Figure_3.jpeg)

Question 25 Difficulty: 1

![](_page_25_Figure_5.jpeg)

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![](_page_26_Figure_1.jpeg)

In this study of cetaceans and artiodactyls, paired toes (cloven hooves) represent a shared derived character state found in the samples Hippos, Ruminants, and Camels. Using parsimony analysis to minimally evolve this derived character, the value of s for hypothesis 1 and 2 is, respectively:

![](_page_26_Figure_3.jpeg)

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![](_page_27_Figure_1.jpeg)

The RI for hypothesis 1 is 0.50. The RI for hypothesis 2 = 1.00. With this information, which of these two hypotheses best explains the evolution of all shared derived characters, where "best explains" means minimally evolving all derived character states.

	Hypothesis 1		6	(2.99 %)	
•	Hypothesis 2		195 (	(97.01 %)	
	Hypothesis 1 and Hypothesis 2 are equally parsimonious		0	(0 %)	Average Grade: 2.91 / 3 (97.01 %) Standard Deviation: 17.06 %
	In a parsimony analysis, the value of RI does not provide enough information to choose between the two competing hypotheses		0	(0 %)	Point Biserial: 0.18 Discrimination Index: 5.56 %
_		w. 1			

![](_page_27_Figure_4.jpeg)

Adult	Body	Beak	Beak	P9	P1	Tail	Neck
males	mass	width	length	feathers	feathers	plumes	Plumes
	(g)	(mm)	(mm)	(mm)	(mm)	(mm)	(mm)
Gunnison1	2135	16.0	14.2	215.5	150.0	345.0	150.0
Gunnison2	2145	16.1	14.3	216.5	152.0	350.0	146.0
Greater1	3179	21.0	16.4	231.0	168.0	310.0	110.0
Greater2	3195	22.0	16.7	230.0	167.0	302.0	100.0
Greater3	3201	23.0	16.7	229.0	166.0	300.0	101.0
mean	2771.0	19.6	15.7	224.4	160.6	321.4	121.4
std. dev.	576.1	3.3	1.3	7.7	8.8	24.2	24.6

The standardized measurement of body mass for the Greater3 sage grouse sample is:

![](_page_28_Figure_3.jpeg)

Question 29 Difficulty: 1

Adult	Body	Beak	Beak	P9	P1	Tail	Neck
males	mass	width	length	feathers	feathers	plumes	plumes
Gunnison1	-1.10	-1.09	-1.13	-1.15	-1.20	0.98	1.16
Gunnison2	-1.09	-1.06	-1.05	-1.02	-0.98	1.18	1.00
Greater1	0.71	0.41	0.57	0.86	0.84	-0.47	-0.46
Greater2	0.74	0.71	0.80	0.73	0.73	-0.80	-0.87
Greater3	0.75	1.01	0.80	0.60	0.61	-0.88	-0.83

The units of measurement in the above standardized data:

•	are numbers of standard deviations above or below the mean	22	22 (97.8%)	
	vary from length and width in mm to mass in grams		2 (0.88%)	Average Grade: 2.93 / 3 (97.8 %)
	have been converted to numbers of millimeters (mm) above or below the mean		3 (1.32 %)	Standard Deviation: 14.71 % Point Biserial: 0.17 Discrimination Index: 6.56 %
	are designed to give each character a mean of 1 and a standard deviation of 0		0 (0 %)	

### Question 30 Difficulty: 1

Adult	Body	Beak	Beak	P9	P1	Tail	Neck
males	mass	width	length	feathers	feathers	plumes	plumes
Gunnison1	-1.10	-1.09	-1.13	-1.15	-1.20	0.98	1.16
Gunnison2	-1.09	-1.06	-1.05	-1.02	-0.98	1.18	1.00
Greater1	0.71	0.41	0.57	0.86	0.84	-0.47	-0.46
Greater2	0.74	0.71	0.80	0.73	0.73	-0.80	-0.87
Greater3	0.75	1.01	0.80	0.60	0.61	-0.88	-0.83

The Euclidean Distance (D) for the sample pair Greater2 and Greater3 is:

![](_page_29_Figure_5.jpeg)

Point Biserial: 0.16

$D=SQRT[(0.74 + 0.75)^{2}+ (0.71 + 1.01)^{2}+(0.80 + 0.80)^{2}+(0.73 + 0.60)^{2}+ (0.73 + 0.61)^{2}+(-0.80 + -0.88)^{2}+(-0.87 + -0.83)^{2}]$	3 (1.32 %)	Discrimination Index: 9.84 %
$D=(0.74 - 0.75)^{2}+(0.71)$ $- 1.01)^{2}+(0.80 - 0.80)^{2}+(0.73 - 0.60)^{2}+ (0.73 - 0.61)^{2}+(-0.80)^{2}+(-0.87 - 0.83)^{2}+(-0.87 - 0.83)^{2}$	9 (3.96 %)	)

#### Question 31 Difficulty: 1

When two separate breeding population have been separated for a significant evolutionary time, they will fix different alleles at some genetic loci such that a combined sample of 100 individuals, half from each breeding population, would show at some genetic loci 50 AA, 0 Aa, and 50 aa. This would be the case for sage grouse from the Gunnison Colorado area and sage grouse from the north in Wyoming. What is the Chi Square value for such a genetic sample comprising 50 AA, 0 Aa, and 50 aa?

![](_page_30_Figure_5.jpeg)

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Question 32 Difficulty: 1
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Fst distance matrix	Gunnison1	Gunnison2	Greater1	Greater2	Greater3
Gunnison1	0				
Gunnison2	0.002	0			
Greater1	0.586	0.511	0		
Greater2	0.665	0.649	0.003	0	
Greater3	0.609	0.537	0.004	0.002	0

All analyses of the Gunnison and Greater sage grouse samples consistently revealed that these two main groups of populations (Gunnison and Greater):

can be ranked at the species level according to the biological 13 (5.73 %)

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	species concept			
	can be ranked at the species level according to the morphological species concept	14	(6.17 %)	Average Grade: 1.74 / 2 (86.78 %) Standard Deviation: 33.94 % Point Biserial: 0.30
	can be ranked at the species level according to the phylogenetic species concept	3	(1.32 %)	Discrimination Index: 22.95 %
⇒	All these	197 (	(86.78 %)	

#### Question 33 Difficulty: 1

Lawrence 1	COI	tRNALys	ATPase8	ATPase8	ATPase8	ATPase8	Loco-	Broca's		Ψretro-	CMT1A	Walfa-
Catarrhines	2664	4028	4410	4414	4415	4417	motion	area	Canines	cyclin	repeat	enolase
Baboons	С	А	Т	С	С	С	0	0	long	0	0	0
Orangutans	С	А	Α	С	С	С	1	0	long	0	0	0
Gorillas	С	А	Α	Α	G	Т	2	1	long	1	0	1
Chimps	Α	т	Α	Α	Α	т	2	1	long	1	1	1
Humans	A	Т	Α	Α	Α	Т	3	1	short	1	1	1

Baboons represent the outgroup in this data set. For the locomotion (gait) character, 0 = quadrupedal, 1 = quadrupedal but planting sides of palms on ground, 2 = quadrupedal but planting knuckles on ground, and 3 = fully bipedal. Which are the derived character states in this locomotion character?

![](_page_31_Figure_5.jpeg)

#### Question 34 Difficulty: 1

This is a general question taken from all the information presented during this last half of the Evolution course. All modern human phylogenies derived from all kinds of data consistently resolve modern African population samples as early branching (e.g., the basal-most branches) and modern European population samples as recently evolved. This indicates that:

Modern day African populations are ancestral to modern day European populations	20 (8.81%)
---	------------

	African populations are primitive	1 (0.44 %)	
	African populations are unperfected compared to European populations	1 (0.44 %)	Average Grade: 2.71 / 3 (90.31 %) Standard Deviation: 29.65 % Point Biserial: 0.36 Discrimination Index: 24.59 %
•	The continent of Africa served as the source area from which modern non- African human populations ultimately migrated	205 (90.31 %)	

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(Number of First Attempts: 78) What do the statistics on this page mean?

### Question 1 Difficulty: 1

Now

Apply

![](_page_34_Figure_1.jpeg)

African human population samples represent all of the early branching lineages in every phylogenetic study of human genetic diversity. This indicates that:

	African human populations are ancestral to all non-African populations		19 (24.68 %)	
	African human populations are primitive compared to more advanced non-African populations	•	2 (2.6 %)	Average Grade: 0.51 / 1 (51.28 %) Standard Deviation: 50.31 % Point Biserial: 0.66
⇒	Africa is the ancestral area from which all non-African populations ultimately dispersed		40 (51.95 %)	Discrimination Index: 80.95 %
	All the above		16 (20.78 %)	
Quest	ion 2 Difficult	ty: 1		

A single population genetic sample from northern Spain includes 50 Basque individuals and 50 non-Basque individuals. Which of the following genotypes is in Hardy Weinberg equilibrium?

➡ 100 aa	0 AA, 0 Aa, 0	13 (16.88 %)	
33	AA, 34 Aa,	34 (44.16 %)	Average Grade: 0.17 / 1 (16.67 %)
33	aa		Standard Deviation: 37.51 %
40	AA, 20 Aa,	23 (29.87 %)	Point Biserial: 0.42
40	aa		Discrimination Index: 38.10 %
50 50	AA, 0 Aa, aa	7 (9.09%)	

#### Question 3 Difficulty: 1

A population genetic sample from northern Spain including 50 Basque individuals and 50 non-Basque individuals is found to be in Hardy Weinberg equilibrium. This suggests:

The sample comes from one
breeding population		17 (22.08 %)	
A high rate of gene flow among Basque and non-Basque populations	_	4 (5.19%)	Average Grade: 0.54 / 1 (53.85 %) Standard Deviation: 50.17 % Point Biserial: 0.68
Basque and non-Basque population do not genetically differ		14 (18.18%)	Discrimination Index: 76.19 %
All the above		42 (54.55 %)	

Evolution CL - BIOB\_420\_001002\_202030\_CL

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	Now	Apply (Number	of First Attempts: 199) <sub>What do t</sub>	he statistics on this page mean?
Question 1 Diffic	ulty: 1			

HIV1 nucleotide substitution distances	Janice.S1	Donald.S3	Janice.S2	Donald.S7	Local.S30
JaniceTrahan.S1	0				
DonaldMcClelland.S3	0.0072	0			
JaniceTrahan.S2	0.0078	0.0081	0		
DonaldMcClelland.S7	0.0116	0.0128	0.0119	0	
LouisianaLocal.S30	0.0387	0.0362	0.0373	0.0325	0

According to the above nucleotide substitution distance matrix and an average RNA virus nucleotide substitution rate of about 1 substitution per 1,000 base pairs per year, how old is the oldest viral strain sampled from Janice Trahan?

72 years old	32 (16.08%)	
about 79 years old	57 (28.64 %)	Average Grade: 0.08 / 0.2 (39.7 %)

 $https://ecat.montana.edu/...,3\% 3A\% 5B\% 27 grid\% 27,\% 27 pagesize\% 27,\% 27 htpleditor\% 27,\% 27 htpg\% 27\% 5D\% 7D\&d2l\_stateGroups=&d2l\_stateGroups=&dd2l\_stateGroups=&dd2l\_stateGroups=&dd2l\_stateGroups=&dd2l\_sta$ 

Standard Deviation: 49.05 %

➡ about 4 years old	 79	(39.7 %)	Point Biserial: 0.71
			Discrimination Index: 85.19 %
about 18 years old	31 (1	5.58 %)	

Question 2 Difficulty: 1

HIV1 nucleotide substitution distances	Janice.S1	Donald.S3	Janice.S2	Donald.S7	Local.S30
JaniceTrahan.S1	0				
DonaldMcClelland.S3	0.0072	0			
JaniceTrahan.S2	0.0078	0.0081	0		
DonaldMcClelland.S7	0.0116	0.0128	0.0119	0	
LouisianaLocal.S30	0.0387	0.0362	0.0373	0.0325	0

According to the above nucleotide substitution distance matrix and an average RNA virus nucleotide substitution rate of about 1 substitution per 1,000 base pairs per year, how old is the oldest viral strain sampled from Donald McClelland?



#### Question 3 Difficulty: 1

HIV1 nucleotide	Janice.S1	Donald.S3	Janice.S2	Donald.S7	Local.S30
substitution distances					
JaniceTrahan.S1	0				
DonaldMcClelland.S3	0.0072	0			
JaniceTrahan.S2	0.0078	0.0081	0		
DonaldMcClelland.S7	0.0116	0.0128	0.0119	0	
LouisianaLocal.S30	0.0387	0.0362	0.0373	0.0325	0

According to the above nucleotide substitution distance matrix and an average RNA virus nucleotide substitution rate of about 1

substitution per 1,000 base pairs per year, how old is the viral strain sampled the Louisiana control individual?

	about 72 years old	38 (19.1%)	
	about 36 years old	56 (28.14 %)	Average Grade: 0.07 / 0.2 (35.68 %) Standard Deviation: 48.03 %
•	about 18 years old	71 (35.68 %)	Point Biserial: 0.63 Discrimination Index: 70.37 %
	about 4 years old	34 (17.09 %)	

#### Question 4 Difficulty: 1

Phylogenetic evidence revealed that Janice Trahan was infected by HIV from a blood sample take from Donald McClelland. The evidence included:

	HIV strains from Trahan and McClelland formed a monophyletic group with respect to Louisiana local control samples	_		27 (13.57 %)	
	Trahan HIV strains averaged younger in age than those sampled from McClelland	_		23 (11.56 %)	Average Grade: 0.13 / 0.2 (66.83 %) Standard Deviation: 47.20 % Point Biserial: 0.39 Discrimination Index: 48.15 %
	Trahan HIV strains were not monophyletic with respect to McClelland HIV strains and were thus not genetically differentiated	-		16 (8.04%)	
•	All these			133 (66.83 %)	
Quest	ion 5 Difficul	lty: 1			

View Statistics - Quiz Apr 22 - Evolution CL - Montana State University

RNA virus evolve rapidly with respect to nucleotide substitutions. When RNA viral genetic evidence is sampled years after the alleged criminal event, the genetic evidence has evolved. What constitutes a genetic "match" between victim samples and the alleged source samples if the genetic evidence evolves quickly over time?

Monophyly of the victim and the alleged source samples	89 (44.72 %)	
Victim samples are more closely related to samples from a local control than to samples	34 (17.09 %)	Average Grade: 0.09 / 0.2 (44.72%)
from the		Standard Deviation: 49.85 %
anegeu source		Point Riserial: 0.65
Alleged source samples are more closely		Discrimination Index: 79.63 %
samples from a local control than to samples from the victim	51 (25.63 %)	
A genetic match cannot be made	25 (12.56 %)	

Evolution ( 

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	Now					
Has End Date						
	Now	Apply	(Number of	First Attempts	s: 185) What do t	the statistics on this page mean?
Question 1 Difficul	ty: 1					
Cetartiodacty	Paired	Trochlea	ted B-case	in B-caseii	<sup>1</sup> T4 T5	T6 T7

Characters T4-T7 are genomic characters indicating the absence (0) or presence (1) of transposable elements. When present,
each of these transposable elements is inserted at a specific position in the genome of artiodactyl and cetacean species. In the
above data set, the values of m and g for each of these four characters, T4–T7, is, respectively:

astragalus

0

1

1

1

0

toes

0

1

1

1

0

**Other mammals** 

Camels

**Ruminants** 

Cetaceans

Hippopotami

162

С

С

Т

Т

Т

0

0

0

1

1

0

0

0

1

1

0

0

0

1

1

0

0

0

1

1

166

Т

Α

G

С

С

2 and 1	29 (15.68 %)	
📫 1 and 2		Average Grade: 0.09 / 0.2 (45.95 %)
	85 (45.95 %)	Standard Deviation: 49.97 %



The value of s for each of the genomic characters, Tr4-Tr7, for hypothesis 1 and 2 is, respectively:



Question 3 Difficulty: 1



The value of ri for each of the genomic characters, Tr4-Tr7, for hypothesis 1 and 2 is, respectively:



The trochleated astragalus is a hinged ankle bone that acts as a pulley in both a forward and backward direction (imagine an elbow joint that could flex in both forward and backward directions). Among mammals, this is a shared derived character state found in all artiodactyls (here Hippos, Ruminants, and Camels). Using parsimony analysis to minimally evolve this derived character, the value of s for hypothesis 1 and 2 is, respectively:

```
View Statistics - Quiz Apr 29 - Evolution CL - Montana State University
```

paired toes

Hypothesis 1: Whales are not Artiodacytla

trochleated astragalus

beta-casein 162(T)

beta-casein 166(C)



The RI for hypothesis 1 is 0.55. The RI for hypothesis 2 = 0.82. With this information, which of these two hypotheses best explains the evolution of all shared derived characters, where "best explains" means minimally evolving all the shared derived characters.

beta-casein 162(T)

beta-casein 166(G)

paired toes

trochleated astragalus

beta-casein 166(A)

Tr 6 Tr 7

Hypothesis 2:

Whales are Artiodacytla

Hypothesis 1		29 (15.68 %)	
Hypothesis 2		84 (45.41 %)	
Hypothesis 1 and Hypothesis 1 are			
equally parsimonious		37 (20%)	Average Grade: 0.09 / 0.2 (45.4 %)
			Standard Deviation: 49.92 %
In a parsimony			Point Biserial: 0.65
value of RI does not provide			Discrimination Index: 76.00 %
information to		35 (18.92 %)	
choose between			
competing			
hypotheses			
	Hypothesis 1 Hypothesis 2 Hypothesis 1 and Hypothesis 1 are equally parsimonious In a parsimony analysis, the value of RI does not provide enough information to choose between the two competing hypotheses	Hypothesis 1 Hypothesis 2 Hypothesis 1 and Hypothesis 1 and Hypothesis 1 are equally parsimonious In a parsimony analysis, the value of RI does not provide enough information to choose between the two competing hypotheses	Hypothesis 129 (15.68 %)Hypothesis 284 (45.41 %)Hypothesis 1 and Hypothesis 1 are equally parsimonious37 (20 %)In a parsimony analysis, the value of RI does not provide enough information to choose between the two competing hypotheses35 (18.92 %)

#### For <u>10 extra credit points</u>, please answer the following essay question:

Please explain how green plants (e.g., bryophytes, ferns, gymnosperms, and angiosperms) differ from animals in terms of alternation of generations and the production of gametes. Keep your answer brief, but as complete as possible (half a page of text at most; directly in the box below).

2 alternating generations: Granetophytes and sporophytes. (haplaidely and sporophytes) In animals, diploid organisms produce haplaid gametes, which form a new diploid generation. Lower plants have gametophytes as the dominant generation. (n) Gametes' go inder pertitization and initiate sporophyte (2n) Generation. Dispersed spores can germinate and this user generations alternate. Gametophytes of higher plants are much reduced and they nutritionally depend on spanophytes.

+10

#### BIOO 220 Botany evaluation essay Fall 2018.pdf.

Name (last, first): Bear Class, Angela

### 3|+|0 = 4|

### BIOO 220 / General Botany: Final Exam, 12/13/2018, 4:00 to 5:50 pm. There is an extra credit question on page 1; the regular (multiple-choice) exam is on pages 2-9.

#### For <u>10 extra credit points</u>, please answer the following essay question:

Please explain how green plants (e.g., bryophytes, ferns, gymnosperms, and angiosperms) differ from animals in terms of alternation of generations and the production of gametes. Keep your answer brief, but as complete as possible (half a page of text at most; directly in the box below).

gran plants rich as bigophytes and terms law alternation of generation they have z forms during development at gane top hytes in form of spores. Animals on the other hand do not, they starl with haploid cells (egg & spern) that through firtilization form gametes that are dipland. Angiaspenns do not have alternation at servertion but deverly seeds

#### For <u>10 extra credit points</u>, please answer the following essay question:

Please explain how green plants (e.g., bryophytes, ferns, gymnosperms, and angiosperms) differ from animals in terms of alternation of generations and the production of gametes. Keep your answer brief, but as complete as possible (half a page of text at most; directly in the box below).

Green plants use different methods of reproduction when than animals which leads to a specific alternation of generations.

#### For <u>10 extra credit points</u>, please answer the following essay question:

Please explain how green plants (e.g., bryophytes, ferns, gymnosperms, and angiosperms) differ from animals in terms of alternation of generations and the production of gametes. Keep your answer brief, but as complete as possible (half a page of text at most; directly in the box below).

ADIMALS DO NOT HAVE AN ALTERNATION OF GENERATIONS. ANIMARS GO THROUGH SEXUAR ADAMOUTION IN ONE STOP. PLANTS HAVE TWO STEPS. IN ONE CHEVERATION, IS PRODUCED, AND IN THE NEXT LIENGRATION. SPOLOPHYNE 4 GAMENDRHATE IS PRODUCED.

#### For <u>10 extra credit points</u>, please answer the following essay question:

Please explain how green plants (e.g., bryophytes, ferns, gymnosperms, and angiosperms) differ from animals in terms of alternation of generations and the production of gametes. Keep your answer brief, but as complete as possible (half a page of text at most; directly in the box below).

Green plants feature a heteromorphic alternation of generations, where every othegeneration consists of asexually reproducing sporophytes or sexually reproducing game tophytes. In contrast, animals sexually reproduce regardless of generation. The gametophyte generations of green plants produce gametes through archegonium and anerithium which serve as the plants' sex organs, where male gametes are produced via a microsporangium and female gametes are produced via a megasporangium, producing microspores (male) and megaspores (female) respectively, where the sperm of the plants are transferred where the sperm of the plants are transferred animals generally produce their gametes internally, then transfer them directly via sexual intercourse

#### For <u>10 extra credit points</u>, please answer the following essay question:

Please explain how green plants (e.g., bryophytes, ferns, gymnosperms, and angiosperms) differ from animals in terms of alternation of generations and the production of gametes. Keep your answer brief, but as complete as possible (half a page of text at most; directly in the box below).

Green plants switch in between a haploid and a diploid generation. This is because the first step of development is a haploid gamete fusing with another to fertilize a diploid sporophyte. The plant lives two lives in both states. While animals need two gametes to fertilize to produce a living diploid offspring. Plants can live separetly in a haploid phase while animals ramat.

#### For <u>10 extra credit points</u>, please answer the following essay question:

Please explain how green plants (e.g., bryophytes, ferns, gymnosperms, and angiosperms) differ from animals in terms of alternation of generations and the production of gametes. Keep your answer brief, but as complete as possible (half a page of text at most; directly in the box below).

Nonvascular green plants have a dominant gametophyte that supports a completely dependent sporophyte. This is much different from animals whose gametes are only present until fertilization, and then grew into a mature adult which will make it's own gametes. The production of gametes differs in green plants and animals. Animals produce gametes through meiosis, in which a cell will have half of the genetic information of the parent. This gamete must be introduced to a gamete of the opposite sex through sexual reproduction, resulting in the formation of a zygote. When two compatible gemetes of plants meet, fertilization may take much longer than in animals. A seed encloses an embryo(En) which may not grow for many years.

27 + 10 = 3

#### For <u>10 extra credit points</u>, please answer the following essay question:

aren plants differ from animals as they are able to fix CO2. This in twin, allows plants to produce. Their own food from photosynthesis, a process involving light reactions, whereas animals cannot.

#### For <u>10 extra credit points</u>, please answer the following essay question:

In animals, reproduction or curs when a male and female gamete (IN) from different organisms merge and produce a zygot & D. with this method, every zygote has a new combination of genes. In green plants, reproduction can be done sexually like animals or asexually where a 2N sporophyte with identical DNA os the parent plant can be produced.

#### For <u>10 extra credit points</u>, please answer the following essay question:

Green plants alternate making haploid and diploid gametes by generation. Where as animals produce haploid gametes only.

#### For <u>10 extra credit points</u>, please answer the following essay question:

green plants produce large gometophytes, which are The primary producers of small seeds. These seeds Then produce the next gometophyte generation. In Animals, the gametophyte (egg + sporm) are small secondary structures.

Name (last, first):

# t): Tenkins, William (02402228) 28+10=38

### **BIOO 220** / General Botany: Final Exam, 12/13/2018, 4:00 to 5:50 pm. There is an extra credit question on page 1; the regular (multiple-choice) exam is on pages 2-9.

#### For <u>10 extra credit points</u>, please answer the following essay question:

Animals produce gametes Hey lombin, Sixvally 10 Zydote which eventually Develops Into Speares. When plants Create game the offs prin Allernation of general fince or Edward other other genetic (Sexually almerations menny the dametes are fishing During denetic Informat (sund Sexual damete. prosing 0 dadep Connected / Dependen Sexcally while plants In Sum, alternate give glways loduce

Name (last, first):

### BIOO 220 / General Botany: Final Exam, 12/13/2018, 4:00 to 5:50 pm. There is an extra credit question on page 1; the regular (multiple-choice) exam is on pages 2-9.

JUZA THOMAS R' 36+10=4

#### For <u>10 extra credit points</u>, please answer the following essay question:

Please explain how green plants (e.g., bryophytes, ferns, gymnosperms, and angiosperms) differ from animals in terms of alternation of generations and the production of gametes. Keep your answer brief, but as complete as possible (half a page of text at most; directly in the box below).

Animals - single diploid individual grows by mitosis from a zygote, within that ind. meioss produces haploid gametes (speam or egg cells) -Directly produce haploid gametes. -Directly produce haploid cells. But, they ne not gametes, produces haploid cells. But, they ne not gametes, produces haploid cells. But, they ne not gametes, produces haploid cells. But, they not gametes, produces them is a sporophyte. Each divides by Produces them is a sporophyte. Each divides, mitosis to film new, seperate haploid individuals, mitosis to film new, seperate haploid individuals. Asexval us sexual ret. depends on both haploid sides & diploids. Asexval us sexual ret. depends on both haploid ses well-developed thum in literworks muses. & hornworts sporophyte is less well-developed thum of plother - alternative haploid dividuals from the construction on the plot of the produce - haploritic - only a haploid multicelluke stage returns. haplantic - only a haplaid multicellubu

Name (last, first): KENYON, WOODROW

### 25 + 10 = 35

### BIOO 220 / General Botany: Final Exam, 12/13/2018, 4:00 to 5:50 pm. There is an extra credit question on page 1; the regular (multiple-choice) exam is on pages 2-9.

#### For <u>10 extra credit points</u>, please answer the following essay question:

Please explain how green plants (e.g., bryophytes, ferns, gymnosperms, and angiosperms) differ from animals in terms of alternation of generations and the production of gametes. Keep your answer brief, but as complete as possible (half a page of text at most; directly in the box below).



Name (last, first):

28 + 10 = 38

#### BIOO 220 / General Botany: Final Exam, 12/13/2018, 4:00 to 5:50 pm. There is an extra credit question on page 1; the regular (multiple-choice) exam is on pages 2-9.

#### For 10 extra credit points, please answer the following essay question:

Liand, Men

Please explain how green plants (e.g., bryophytes, ferns, gymnosperms, and angiosperms) differ from animals in terms of alternation of generations and the production of gametes. Keep your answer brief, but as complete as possible (half a page of text at most; directly in the box below).

O plants has different way to creat a new generations, when they are Proparyotic. they just copy the gene and divide to two cells, such as green algae, after that, they use spore to creat new generation, such as Bryophytes and vascular plants. also, they do have seed for new generations such as gymnosperAnimals are different, they use egg or embryo in temale body to get a new generation. @ plants can't be pretect, both male and temale an same plants, but most. animals can't be bisen

- 3 different way to creat new generations, plants creat generations by bees, winds animal most by sex @ plant's normally has more gametes and generations than animals

#### For <u>10 extra credit points</u>, please answer the following essay question:

Please explain how green plants (e.g., bryophytes, ferns, gymnosperms, and angiosperms) differ from animals in terms of <u>alternation of generations</u> and the <u>production of gametes</u>. Keep your answer brief, but as complete as possible (half a page of text at most; directly in the box below).

Animals atternation of generation begins with 2n, when Melosis occurs, a n gamete is made then fertilization occurs to create the 2n generation again. However im plants, a gametophyte - will grow from a seed or spore, get fertilized, then have the sporophyte an generation.

#### For <u>10 extra credit points</u>, please answer the following essay question:

Please explain how green plants (e.g., bryophytes, ferns, gymnosperms, and angiosperms) differ from animals in terms of alternation of generations and the production of gametes. Keep your answer brief, but as complete as possible (half a page of text at most; directly in the box below).

There is a lot more variation within the plant kingdom specifically in regard to alternation of generations and the production of gametes compared to the animal kingdom. The plant genome has more flexibility to mutation such as with polyploidy and the formation of the Modern wheat Species. If a mutation occurs that alters the number of chromosomes in an animal embryo, the embryo is not likely to develop further. In plants, the process of gamete production, as well as fertilization, can occur internally or externally, differing by species. Whereas in amimals, both processes most frequently occur internally. Plant species can also occur with both male and female reproductive parts on the Seame plant or flowen which is rare for animals. Alternation of generations and the production of gametes is more diverse and flexible for plants than for animals.

27 + 10 = 37

#### For <u>10 extra credit points</u>, please answer the following essay question:

Please explain how green plants (e.g., bryophytes, ferns, gymnosperms, and angiosperms) differ from animals in terms of alternation of generations and the production of gametes. Keep your answer brief, but as complete as possible (half a page of text at most; directly in the box below).

Animal emblyo development consists of a mother's egg being fertilized with the father's sperm. This ten becomes a Zygote until a pleanta is formed and attached, ten it becomes a single embryo, until 9 or so months go by and it turns birthed ababy. The bally is reliant on the mother for guite a bit after it is born. The motor, at the fuster, can podue another generation after 9 months and after the 1st bally generation is born. In green plante a semale eggs is fertilized by male sperm/ar polens and a zygote is formed, it gres through the embryo, gibbolar, torpedo, and vent phase until it is considered a microphyle while the mother is considered a unicrospore. The embryo is to their curd is not reliant on the mother with it is fully developed. There is an alternation of generations where it takes two rounds of gamate further of generations where it takes two rounds of gamate further with a repodutive fruit is produced.

#### For <u>10 extra credit points</u>, please answer the following essay question:



Name (last, first): Packinson, Kevin

### BIOO 220 / General Botany: Final Exam, 12/13/2018, 4:00 to 5:50 pm. There is an extra credit question on page 1; the regular (multiple-choice) exam is on pages 2-9.

28 + 10 = 38

#### For <u>10 extra credit points</u>, please answer the following essay question:

Green plants produce generates that either go on to become sporophytes or quickly join to form a sugote. In any case, nowever, the spores undergo multiplication to tog multicellular the before fertilization occurs. This can be seen in the sporophytes and in muticellular female gametophytes. Haplow animal cells This differs from animals. Komen always join before dividing and becoming multicellular, whether in eggs or in placental pregnanties in mammais. Animais do not have multicellular services sporophytes. You could also argue that animal zygotes are formed in more protected ways than plants as a whole - the joining of two haploid cells occurs within the parent and then go on to develop. I might be forgetting some fish fertilization though.

+ 10

### BIOO 220 / General Botany: Final Exam, 12/13/2018, 4:00 to 5:50 pm. There is an extra credit question on page 1; the regular (multiple-choice) exam is on pages 2-9.

#### For <u>10 extra credit points</u>, please answer the following essay question:

Green plants differ from animals in terms of alternation of generations in that they alternate heteromorphic generations. In animals a single individual is grown from a diploid zygote through mitoris. Plants can alternate from a haploid/diploid and can reproduce meiotically or mitotically. Plants create game to phytes and sporophytes in the thousands. Meiosis produces haploid cells.

Name (last, first): Paulin Seam

#### For <u>10 extra credit points</u>, please answer the following essay question:

Please explain how green plants (e.g., bryophytes, ferns, gymnosperms, and angiosperms) differ from animals in terms of alternation of generations and the production of gametes. Keep your answer brief, but as complete as possible (half a page of text at most; directly in the box below).

Basic animal reproduction is simply 2 parents meet and both give a set of chromosonus + produce offspring directly. - green plants nowever may alternate guirations, union is when tw IN from each parent is in is it's aim being + fren it will individual Meet tw other IN individual of Some specifies to produce a 2N individual

### 28 + 0 = 28

### BIOO 220 / General Botany: Final Exam, 12/13/2018, 4:00 to 5:50 pm. There is an extra credit question on page 1; the regular (multiple-choice) exam is on pages 2-9.

#### For <u>10 extra credit points</u>, please answer the following essay question:



JOSEL Ularin, Name (last, first):

## 33+10=43

### **BIOO 220** / General Botany: Final Exam, 12/13/2018, 4:00 to 5:50 pm. There is an extra credit question on page 1; the regular (multiple-choice) exam is on pages 2-9.

#### For <u>10 extra credit points</u>, please answer the following essay question:

Please explain how green plants (e.g., bryophytes, ferns, gymnosperms, and angiosperms) differ from animals in terms of alternation of generations and the production of gametes. Keep your answer brief, but as complete as possible (half a page of text at most; directly in the box below).

(QIII animal cells are diploid (2n) except for reproductive cells which are haploid (in). When the reproductive culls marge they create a duploid zygote. Means of producing gametes is more variable in plants; both male & female chromosomes may be on one plant or in the case of bryophytes, the dominant form of the plant is the gametophyte

#### For <u>10 extra credit points</u>, please answer the following essay question:

Please explain how green plants (e.g., bryophytes, ferns, gymnosperms, and angiosperms) differ from animals in terms of alternation of generations and the production of gametes. Keep your answer brief, but as complete as possible (half a page of text at most; directly in the box below).

PLANTS DISPUTY AN ALTERNATION OF GENERATIONS IN WHICH (DEPENDING ON THE PLANT) A DECENT PIECE OF THEIR LIFE CYCLE IS SPENT IN BOTH THE HAPLOID FORM AND THE DIPLOID FORM. IN CONTRAST, ANIMAS ONLY PRODUCE HAPLOID SEX CEUS THAT JOIN TOGETHER IN OR OUTDIDE OF THE ANIMAL. THESE HAPCOID MEIOTIC CELLS DO NOT REPRODUCE AND GROW TO FORM MY FORM OF SECT SUFFICIENT ORGANISH/STRUCTURE; THEY AREAS AREAS AREAS AREAS PEQUIFE FEFTILIZATION WITH ANOTHER MEIOTIC CELL TO PRODUCE & ZYGOTE AND THEN BEGIN TO DIVIDE MITOTICITURY. PLANTS ARE INCREDIBLE IN THAT THEY CAN FUNCTION, GROW, AND THRIVE IN BOTH MAPLOID AND DIPLOID GENERATIONS.

-10

#### For <u>10 extra credit points</u>, please answer the following essay question:

Please explain how green plants (e.g., bryophytes, ferns, gymnosperms, and angiosperms) differ from animals in terms of alternation of generations and the production of gametes. Keep your answer brief, but as complete as possible (half a page of text at most; directly in the box below).

The main difference between green plants and animals in terms of reproduction is that plants produce a little clone of themselves that gets to have sex. The little clone, or gametophyte, produces gametes, pollen & eggs, and then participates in the act of fertilization. This gives rise to a sporophyte which then grows and eventually divides micotically to produce a new gametophyte. Animals, in contrast, do not produce alternating generations of sporophytes and gametophytes, rather they produce gametes directly and participate in fertilization to reproduce.
# BIOO 220 / General Botany: Final Exam, 12/13/2018, 4:00 to 5:50 pm. There is an extra credit question on page 1; the regular (multiple-choice) exam is on pages 2-9.

37 + 10 = 42

### For 10 extra credit points, please answer the following essay question:

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Significancy LOS revice than an inecs, having the ability to racs produce air forme Being mesneds of conception ( wave and fenere gunets) alland tenet Creation of her nervors of the species. conferen to entired, mere the new one ference must be in the same crese provinity, green franks' perote conception allows for the same crese seekings open a conge area. Since Chinals can any have a han the Of other of the prover a long perior of time, green plants covered hours a much more ethechistel method of procreation.

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Name (last, first): Witter, Cole

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Green plants differ from animals in terms of alternation of generations because of the haploid and diploid cells present in green plants. The production of gametes allows micosis to occur which is -a critical difference from animal cells.

+10

Name (last, first): Wright Lucas

# 3|+|0=4|

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They start by fortillizing those eggs then To drie off and give rise to one nucleans. then that nucleans goes through the 5 stages of an embryo.

+10