

**UCC/UGC/ECCC**

Proposal for New Course

***Please attach proposed Syllabus in*** [***approved university format***](http://www4.nau.edu/avpaa/UCCForms/syllabus.doc)***.***

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| 1. Course subject and number: | **CS 290** | 2. Units: | **3** |

 [**See upper and lower division undergraduate course definitions.**](http://www4.nau.edu/avpaa/UCCPolicy/Uplow.doc)

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| 3. College:  | **CEFNS**  | 4. Academic Unit: | **Biological Sciences** |

5**.** Student Learning Outcomes of the new course. *(*[*Resources & Examples for Developing Course Learning Outcomes*](http://www4.nau.edu/avpaa/Assessment/CourseLearningOutcomesPDF_090712.pdf)*)*

**Upon successful completion of this course, students will:**

**• Be able to implement, document and test basic software for bioinformatics applications. Students will complete bioinformatics programming assignments, and will be assessed on the accuracy and quality of their software.**

**• Be able to describe and implement core bioinformatics algorithms, including those for biological sequence alignment and phylogenetic inference. These algorithms will be taught in class, and students will implement representative algorithms in programming assignments.**

**• Have demonstrated their ability to analyze biological data employing a remote computer system. Several projects over the course of the semester will require that the students interact with a remote server via a command line to perform their analyses: a skill that is very often required in bioinformatics.**

**• Have applied currently popular bioinformatics tools, analyzed biological data using these tools, and described their results in writing. Student projects will require students to apply instructor-selected bioinformatics tools to analyze data sets. Students will present the results of their analyses in writing.**

**• Have the ability to critique bioinformatics tools based on the primary literature and application of those tools to test data sets. In an interdisciplinary group project, groups will read the primary literature on an instructor-specified bioinformatics tool, and present a description and critique of that tool to the class in an oral presentation, including discussion on the goal of the tool, previous work on addressing that goal, how the software was tested, and how the methodology was evaluated.**

6. Justification for new course, including how the course contributes to degree program outcomes, or other university requirements / student learning outcomes. *(*[*Resources, Examples & Tools for Developing Effective Program Student Learning Outcomes*](http://www4.nau.edu/avpaa/Assessment/ProgramLearningOutcomesPDF_090712.pdf)*).*

**Biology is rapidly becoming a data-intensive field, and there is high demand in industry and graduate school for students with backgrounds in both Biology and Computer Science. This course will train students in Bioinformatics, the application of the tools of Computer Science such as programming and databases to address biological questions, making NAU students competitive applicants for bioinformatics jobs and graduate programs. By integrating Computer Science and Biology students in the same classroom, it will give them an interdisciplinary experience early in their career. Group projects and class discussions will be designed to highlight the importance of interacting with people with different educational background: an essential skill in modern biology, which is becoming interdisciplinary by necessity.**

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| 7. Effective **BEGINNING** of what term and year? | **Fall 2014** |  |
|  [**See effective dates calendar**](http://www4.nau.edu/avpaa/timelines/1213Effective.xls)**.** |  |  |

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| 8.  Long course title: | **INTRODUCTION TO BIOINFORMATICS**  |
|  *(max 100 characters including spaces)* |

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| 9. Short course title: | **INTRO TO BIOINFORMATICS** |
|  *(max. 30 characters including spaces)* |

10. Catalog course description *(max. 60 words, excluding requisites):*

**Introduces computer scientists and biologists to Bioinformatics. This course will introduce essential algorithms and tools used in bioinformatics, as well as several special topics of contemporary interest. Students will work on independent programming, data analysis and writing assignments, as well as group projects that require interdisciplinary collaborations.**

11. Will this course be part of any plan (major, minor or certificate) or sub plan (emphasis)?

                                                                                                                                    Yes [ ]  No [x]

 If yes, include the appropriate plan proposal.

12. Does this course duplicate content of existing courses? Yes [x]  No [ ]

If yes, list the courses with duplicate material. If the duplication is greater than 20%, explain why NAU should establish this course.

**Proposed Cross List with BIO 290**

13. Will this course impact any other academic unit’s enrollment or plan(s)?              Yes [ ]  No [x]

       If yes, include a letter of response from each impacted academic unit.

14. Grading option:      Letter grade **[x]** Pass/Fail **[ ]**Both **[ ]**

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| 15. Co-convened with: |  | 14a. UGC approval date\*: |  |
| (For example: ESE 450 and ESE 550) [See co-convening policy](http://www4.nau.edu/avpaa/UCCPolicy/crosslist.doc). \*Must be approved by UGC before UCC submission, and both course syllabi must be presented. |

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| 16. Cross-listed with: | **BIO 290** |  |
|  (For example: ES 450 and DIS 450) [See cross listing policy](http://www4.nau.edu/avpaa/UCCPolicy/crosslist.doc).      Please submit a single cross-listed syllabus that will be used for all cross-listed courses. |
| 17. May course be repeated for additional units? |  |  Yes [ ]     No [x]  |
|  16a. If yes, maximum units allowed? |  |  |
|  16b. If yes, may course be repeated for additional units in the same term? |  | Yes [ ]     No [ ]  |

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| 18. Prerequisites: | **BIO181, BIO 181L, CS 126, CS 126L** |  |

 If prerequisites, include the rationale for the prerequisites.

**BIO 181/181L, CS 126/126L. Students need introductory Biology and Computer Science so we can avoid spending too much time introducing these topics in the beginning of the semester. This is particularly important for this class as students are coming from different disciplines, so spending time on introductory programming in the first couple of weeks of the semester, for example, would be a waste of time for Computer Science students in the class. Similarly, introductory biology will be a waste of time for the biology students in the class.**

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| 19. Co requisites: |  |  |

 If co requisites, include the rationale for the co requisites.

20. Does this course include combined lecture and lab components?                   Yes [ ]  No [x]

 If yes, include the units specific to each component in the course description above.

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| 21. Names of the current faculty qualified to teach this course: | **Greg Caporaso, Jason Sahl, Steven Beckstrom-Sternberg** |

**Answer 22-23 for UCC/ECCC only:**

22. Is this course being proposed for Liberal Studies designation?             Yes [ ]  No [x]

       If yes, include a [Liberal Studies proposal](http://www2.nau.edu/~d-ugstdy/_source/docs/LS_Proposal_form.doc) and syllabus with this proposal.

23. Is this course being proposed for Diversity designation?Yes [ ]    No [x]

       If yes, include a [Diversity proposal](http://www4.nau.edu/avpaa/EthDiv/Divform2010.doc) and syllabus with this proposal.

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| **FLAGSTAFF MOUNTAIN CAMPUS** |  |
| **Scott Galland**  | **04/17/2013** |
| Reviewed by Curriculum Process Associate | Date |
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| **Approvals**: |  |
| **Signature.jpg** | **04/16/2013** |
| Department Chair/Unit Head (if appropriate) | Date |
|  |  |
| Chair of college curriculum committee | Date |
|  |  |
| Dean of college | Date |
|  |  |
| **For Committee use only:** |  |
|  |  |
| UCC/UGC Approval | Date |

Approved as submitted: Yes [ ]  No [ ]

Approved as modified: Yes [ ]  No [ ]

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| **EXTENDED CAMPUSES** |  |
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| Reviewed by Curriculum Process Associate | Date |
|  |  |
| **Approvals:**  |  |
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| Academic Unit Head | Date |
|  |
| Division Curriculum Committee (Yuma, Yavapai, or Personalized Learning) | Date |
|  |
| Division Administrator in Extended Campuses (Yuma, Yavapai, or Personalized Learning) | Date |
|  |
| Faculty Chair of Extended Campuses Curriculum Committee (Yuma, Yavapai, or Personalized Learning) | Date |
|  |
| Chief Academic Officer; Extended Campuses (or Designee) | Date |
|  |  |

Approved as submitted: Yes [ ]  No [ ]

Approved as modified: Yes [ ]  No [ ]

**BIO/CS 290: Introduction to Bioinformatics (Spring 2013)**

• Professor: Greg Caporaso (gregcaporaso@gmail.com)

• Office hours: M 3:15-4:15, W 1:00-2:00; Engineering (building 69) room 265

• TA: John Chase (chase.johnh@gmail.com)

• Office hours: TBD; TBD

• M/W 2-3:15 (3 credit hours) in Engineering (building 69), Room 314

• Course website: http://bit.ly/W3qaxT

• Course schedule: http://bit.ly/W3D5zj [The schedule is dynamic - check it regularly!]

**Course Prerequisites:** CS 126/126L and Bio 181/181L, or instructor consent.

**Course Description**

Introduces computer scientists and biologists to Bioinformatics. This course will introduce important tools and algorithms used in bioinformatics and several topics in detail with the aim of teaching students how to use and evaluate bioinformatics tools, and develop their own bioinformatics pipelines to address biological questions.

Topics covered will include biological sequence alignment, phylogeny reconstruction, sequence clustering, working with “Next Generation” (i.e., 454 and Illumina) DNA sequencing data, cloud computing, microbial ecology, and genome assembly. Students will learn to use tools including BLAST, muscle, uclust, PyCogent, and QIIME.

**Student Learning Expectations/Outcomes for this Course**

After taking this course, students should be comfortable with developing, documenting and testing basic python software and working on remote Linux systems in a cloud-computing environment. Students will have experience with software tools that are used in real-world bioinformatics, and will understand how to initiate, perform, carry out and present a bioinformatics experiment, and evaluate new bioinformatics tools.

Upon successful completion of this course, students will:

* Be able to implement, document and test basic software for bioinformatics applications. Students will complete bioinformatics programming assignments, and will be assessed on the accuracy and quality of their software.
* Be able to describe and implement core bioinformatics algorithms, including those for biological sequence alignment and phylogenetic inference. These algorithms will be taught in class, and students will implement representative algorithms in programming assignments.
* Have demonstrated their ability to analyze biological data employing a remote computer system. Several projects over the course of the semester will require that the students interact with a remote server via a command line to perform their analyses: a skill that is very often required in bioinformatics.
* Have applied currently popular bioinformatics tools, analyzed biological data using these tools, and described their results in writing. Student projects will require students to apply instructor-selected bioinformatics tools to analyze data sets. Students will present the results of their analyses in writing.
* Have the ability to critique bioinformatics tools based on the primary literature and application of those tools to test data sets. In an interdisciplinary group project, groups will read the primary literature on an instructor-specified bioinformatics tool, and present a description and critique of that tool to the class in an oral presentation, including discussion on the goal of the tool, previous work on addressing that goal, how the software was tested, and how the methodology was evaluated.

**Course Structure/Approach**

This course will be focused on lectures, projects, student presentations, short surprise quizzes, a midterm exam, and a final project. Regular in-class time will be scheduled for hands-on work, such as interacting with the IPython interpreter to accomplish computational tasks, identifying the source of erroneous sequence reads from “next-generation” DNA sequencers, and reconstructing phylogeny from sequence data. Homework assignments and reading should be completed by the due date provided on the course schedule.

There will be regular quizzes throughout the semester. These will be unannounced in order to ensure that you are keeping up on the material. These will cover material that was recently presented, and should not be difficult if you are attending class and doing the readings. Quizzing on the homework and reading assignments due the same day is fair game.

This course covers a lot of diverse material, and office hours are your chance to directly interact with the instructor and TA to ensure that you understand the concepts being covered in class. Coming to office hours is also a great way to boost your class participation score.

Some course projects will be focused on using the PyCogent and QIIME bioinformatics software packages. These are widely used open-source bioinformatics packages. Contributions that you make to these software packages, in the form of new documentation or new features, can be applied as extra credit in the course. If you’re interested in making a contribution, talk with me ahead of time and we will discuss whether it is a contribution worthy of extra credit, and if so how much it will be worth. Additionally, submitting bug reports or contributing to the QIIME forum (in the form of correctly answering questions) will count toward increasing your participation grade. If you submit bug reports or respond on the forum, forward that information to me by email.

**Required Materials**

A computer: You will need access to a computer for this course. If you have a laptop, get in the habit of bringing it to class. Mac computers are ideal for Bioinformatics. A good computing environment that includes most or all of the tools we will use in this course is the QIIME Virtual Machine, available for VirtualBox or EC2. See http://qiime.org/install/virtual\_box.html or http://qiime.org/install/vm\_ec2.html for more details.

**Course Schedule:** http://bit.ly/W3D5zj

A tentative course schedule is provided at the link above. The schedule will change over the course of the semester as we identify certain areas that we want to spend additional time on. For that reason the outline is provided in a dynamic format. The spreadsheet at the above link will always be the definitive source for the outline, reading assignments, and

homework assignments. **Check this link regularly!**

**Assessment of Student Learning Outcomes**

You will be assessed primarily thorough graded material (see *Grading System*). A small portion of your assessment will be based on participation. This allows me to determine if you understand the material well enough to ask questions and engage in discussion in class and in office hours. I will strive to return all graded materials within seven days. Under some circumstances I may need a little more time. Check with me at any time during the semester on your current participation score.

**Grading System**

• 10% Participation

• 10% Group presentation

• 20% Surprise quizzes (around 10-20 minutes), lowest quiz score will be dropped.

• 20% Homework assignments

• 20% Midterm exam

• 20% Final project

**Grading Scale:** A: 90-100; B: 80-90; C: 70-80; D: 60-70; F: 0-59

**Course Policy**

• If you have a legitimate reason why you cannot make one of the quiz times or why you won’t be able to complete an assignment by the due date, talk with me early on and something can be arranged. Students who do not show up for quizzes without making prior arrangements will get a zero.

• Students are not graded on attendance, but there will be **no make-ups of quizzes** (unless an institutional excuse form is provided *in advance*) so it is highly recommended that you don’t miss classes. If you have to miss a lecture and there is a quiz that day, it will count as your dropped quiz score.

• Plagiarism and cheating will not be tolerated. Any students found guilty of either will receive a failing grade in the class. We will discuss what counts as plagiarism of software on the first day of the course.

• No computers, cell phones, headphones, books or papers may be used during quizzes or exams. If a student is observed looking at or touching any of these items during a quiz it will be considered cheating – this includes checking to see who just texted you! To be safe, I recommend turning off cell phones during quizzes.

• Computers may be used for course-related work during the class such note taking or working along with programming examples that are being done on the overhead. You may not however use computers for noncourse-related work such as checking e-mail or Facebook. If I notice you doing this I will document it and count it against your participation grade in the course.

• I expect you to check your university e-mail at least once per day. If you miss important information because you didn’t check email, that is your fault.

**University Policies**

The Safe Environment, Students with Disabilities, Institutional Review Board, Academic Integrity, Academic Contact Hour, Classroom Management and Professional Ethics and Code of Conduct policies are available at http://www4.nau.edu/avpaa/policy1.html. Students are responsible for reviewing and understanding these policies.