McGill

New Course Proposal Form

(07/2004)

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1. Will this new course affect a current program? Yes ☒ No ☐
   If "yes", has a Program Revision Form been submitted concurrently? Yes ☒ No ☐

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2. Teaching Department:

   | School of Computer Science |

4. Campus
   (Downtown, Macdonald, Off Campus, Distance Ed, Other – specify)

   | Downtown |

5. Effective Term of Implementation
   (Ex. Sept. 2004 = 200409)

   Term:

   | 200709 |

3. Administering Faculty/Unit:

   | Faculty of Science / Computer Science |

6. Responsible Instructor

   | Mathieu Blanchette |

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7. Course Title (Limit 30 Characters) - required for all courses:

   | Comp. Biol. Methods & Research |

8. Course Number(s)
   Indicate course number & the number of terms spanned:
   (tick all that apply)

   Subject/course number: | COMP 561 |

   Course(s) Span:

   ☒ 1 term

   ☐ 2 consecutive terms (D1, D2)

   ☐ 2 non-consecutive terms (N1, N2)

   ☐ 3 consecutive terms (J1, J2, J3)

9. Course Title to Appear in the Calendar (optional)
   (Limit 59 characters):
   Note: This can ONLY be an expansion of word(s) abbreviated in the 30 character course title above.

   | Computational Biology Methods and Research |

10. Credit Weight
    (or CEU's for non-credit CE courses):

    | 4 |

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11. Rationale for new course

   Our department currently lacks an introductory computational biology course suitable for graduate students. This effectively reduces the access to more advanced bioinformatics courses to the few graduate students who enter the program with a pre-existing background in the area. This also makes it difficult for graduate students who lack this background to be introduced to the area. The proposed course will provide a solid core for any graduate student interested in computational biology. Every graduate student studying in the area will be expected to take COMP 561 or have taken its equivalent. This will allow advanced graduate courses (COMP 563, COMP 564, COMP 680) to focus on more advanced material, thus reducing duplication. The proposed course will share its lectures with "COMP 462 – Computational Biology Methods" but will require additional work (see list below), making it suitable for a graduate, 4-credit course. The material covered in COMP 462 is appropriate for an entry-level graduate course, but graduate students cannot take it for credits because it is at the 400-level. COMP 561 will also be open to undergraduate students interested in pushing further their study of bioinformatics, allowing them to undertake a significant research project.

   Please see continuation in Appendix.

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12. Course Description
    (as it will appear in the Calendar [maximum 50 words]):
    (N.B. Faculty of Medicine must append complete course outline)

   This course consists of the lectures of COMP462 but will be assessed at the 500 level.

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13. Supplementary information to appear in the Calendar in addition to the course description.
    Such as: equivalent course(s), contact hours, enrolment limitations, language of instruction etc.
    Please enter the information as it should appear in the calendar notes.

   Additional work will consist of assignments and of a substantial final project that will require to put in practice the concepts covered in the course.

14. Schedule Types(s):
    (Enter all that apply – see course guidelines for a complete list.)
    (i.e. Lecture, Labs, Tutorial)

	Hours per Week		Hours per Week		Hours per Week
Lecture	3				

Total Hours per Week: 3

Total Number of Weeks: 13

15. Projected Enrolment:

15

16. Required text and/or preliminary reading list sent to library?

☐ Yes   x No

17. Prerequisite(s) (Courses or Tests)
    Specify course number(s) or name(s) of test(s):

COMP 360, MATH 323

If the student does not have a prerequisite
should web registration be blocked?
☐ Yes   ☑No

If "Yes" complete A and B:

A. Indicate minimum grade or test score(s) the student
must attain in prerequisite course(s) or test(s):

B. Can the prerequisite course(s) or test(s) be taken in the
same term as this course?
☐ Yes   ☐ No

18. Corequisite(s) Course Number(s):
    Specify course number(s) and title(s):

If the student does not register for the corequisite
in the same term should web registration be blocked?
☐ Yes   ☐No

19. Restriction(s):

Not open to students who have taken COMP 562. Not open to
students who are taking or have taken COMP 462.

20. Consultation Reports Attached
    ☐ Yes   ☑ N/A

21. Additional Course Charges (must be approved by the Fee
    Policy Committee)

Description of Fee
(e.g. screening fee)   Amount

22. Requires Teaching, Physical, or Financial Resources
    Not Currently Available (attach explanation)
    ☐Yes ☑No

To be completed by the Faculty	*To be completed by ARR*	*For Continuing Education Use*
Slot Course: ☐ Yes ☐ No	CIP Code	CE Admin. Unit :
		CE Non-Grant Courses:
Thesis Component: ☐ Yes ☐ No		Flat Rate: CdnFlat Rate: ☐ Yes ☐ N/A

23. Approvals:

Routing Sequence	Departmental Meeting	Departmental Chair	Other Faculty	Curric/Academic Committee	Faculty	SCTP
Name		Sue Whitesides				
Signature						
Date		March 20, 2007				

Departmental Contact Person (name/phone/email)	Marisa Lento/ ext.00895/ marisa@cs.mcgill.ca (for Judy Kenigsberg)

Course rational (cont.)

Currently, the most closely related course offered at McGill is BINF 621 (Bioinformatics: Molecular Biology), but this course focuses on the biological (rather than computational) aspects of bioinformatics, and only students enrolled in the Bioinformatics Graduate Option can get credits for taking it. Finally, we note that having two courses sharing the same lectures is common practice in several departments (e.g. MATH 423 – MATH 533) and seems to be an effective and flexible teaching strategy.

Additional material (compared to COMP 462):

Students taking COMP 561 will be expected to do additional reading in order to write more advanced assignments. Advanced topics covered only in COMP 561 will include:

-   Word statistics (Karlin-Altschul statistics)
-   Advanced phylogenetics methods
-   Multiple sequence alignment
-   Simple statistical analysis of micro-array data.
-   Advanced algorithms for peptide identification by mass spectrometry
-   RNA secondary structure prediction

The class project will require a deep understanding of several of the topics listed above.