

**Applied Bioinformatics GPLS716  
Spring 2010 course**

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**Course description:** The explosive growth of data derived from genomic and post-genomic projects has revolutionized biology and medicine. As a result, a solid foundation in computational biology and bioinformatics is now essential for all practitioners of biological and biomedical research. This course emphasizes both the theory and application of fundamental computer-based approaches to sequence analysis, datamining, integration and interpretation of data related to genes and their function. Using a hands-on problem-based learning approach, students will acquire familiarity with computational tools useful for analysis of the structure, function, and evolution of nucleic acids and proteins.

Topics to be covered in this 2-credit course include analysis packages, unix, computer programming, alignment and motif discovery, ontologies & metadata, genome annotation, human genome, transcriptomics, phylogeny, comparative genomics, metagenomics, proteomics, homology modeling, protein-protein interactions. A 1-credit Perl programming option is also available.

This course is intended for all graduate students in the biological sciences, both beginners and those at an advanced level. Each weekly class meeting will include a lecture, a demonstration/exercise, and a take-home problem. Completion of all assigned problems will be critical to achieving the learning objectives and attendance at each class meeting will be expected. The course will utilize a fully networked classroom in the HSHSL with each student at his or her own workstation.

**Prerequisites:** Advanced undergraduate or graduate-level courses in genetics, biochemistry, and molecular biology. Familiarity with fundamentals of genetics, biochemistry, cell and molecular biology will be assumed. Some familiarity with statistics or mathematical analysis would be helpful.

**Class meetings:** Tuesdays 9:45-11:55 am, Health Sciences Library, Lower level computer classroom, Greene St. and Lombard St, University of Maryland-Baltimore

**Grading:** Students will be graded primarily on their performance on weekly take home exercises (80 %) and class attendance and participation (20 %).

**Readings:** Weekly required readings will be posted on the course website. Students are expected to familiarize themselves with topics before lectures.

**Course website:** TBA

**Useful textbooks and reference books (not required):**

**Essential Bioinformatics**, Jin Xiong, Cambridge University Press, 2006

**Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins**, Edited by: Andreas D. Baxevanis, B.F. Francis Ouellette, Wiley-Interscience 1st edition: 1998; 2nd edition: 2001; 3rd edition: 2005

**Bioinformatics: Sequence and Genome Analysis**, David W. Mount, Cold Spring Harbor Laboratory Press; 2001 (first edition); 2004 (second edition).

**Bioinformatics, Biocomputing and Perl**, Michael Moorehouse and Paul Barry, Wiley & Sons; 2004

**Setting up LAMP**, Eric Rosebrick, Eric Filson, Sybex Press 2004

**Bioinformatics and functional genomics**, Jonathan Pevsner, Wiley & Sons; 2003

**Sequence Analysis in a Nutshell**, Darryl Leon, Scott Markel, Lorrie LeJeune, O'Reilly Media, Inc., 2003

**Introduction to Bioinformatics: A Theoretical and Practical Approach**, Edited by: Stephen A. Krawetz and David Womble, Humana Press; 2003

**A Primer of Genome Science**, Greg Gibson and Spencer V Muse, Sinauer Associates; 2002

**Beginning Perl for Bioinformatics**, James Tisdall, O'Reilly Media, Inc., 2001

**Introduction to Bioinformatics**, Teresa K. Attwood & David J. Parry-Smith, Prentice Hall; 1999

**Of URFS and ORFS: A Primer on How to Analyze Derived Amino Acid Sequences**, Russell F. Doolittle, University Science Books; 1986

#### Class schedule

	Date	Topic	Instructor	Contact
1	1-26	Course overview and analysis packages	C. Stine/ S.DasSarma	<a href="mailto:ostin001@umaryland.edu">ostin001@umaryland.edu</a> <a href="mailto:dassarma@umbi.umd.edu">dassarma@umbi.umd.edu</a>
2	2-2	Unix	S. DasSarma	
3	2-9	Programming	J. Orvis	<a href="mailto:jorvis@gmail.com">jorvis@gmail.com</a>
4	2-16	Perl	J. Orvis	
5	2-23	Alignment and motif discovery	I. Erill	<a href="mailto:erill@umbc.edu">erill@umbc.edu</a>
6	3-2	Ontologies & metadata	M. Giglio	<a href="mailto:mgiglio@som.umaryland.edu">mgiglio@som.umaryland.edu</a>
7	3-9	Genome annotation	M. Giglio	
8	3-23	Human genome	J. Wortman	<a href="mailto:jwortman@som.umaryland.edu">jwortman@som.umaryland.edu</a>
9	3-30	Transcriptomics	S. Dorsey	<a href="mailto:sdorsey@son.umaryland.edu">sdorsey@son.umaryland.edu</a>
10	4-6	Phylogeny	K. Omland	<a href="mailto:omland@umbc.edu">omland@umbc.edu</a>
11	4-13	Comparative genomics	J. Carneiro da Silva	<a href="mailto:jcsilva@som.umaryland.edu">jcsilva@som.umaryland.edu</a>
12	4-20	Metagenomics	C. Fraser-Liggett	<a href="mailto:cmfraser@som.umaryland.edu">cmfraser@som.umaryland.edu</a>
13	4-27	Proteomics	A. Yang	<a href="mailto:austinjiang@gmail.com">austinjiang@gmail.com</a>
14	5-4	Homology modeling	J. Coker	<a href="mailto:coker@umbi.umd.edu">coker@umbi.umd.edu</a>
15	5-11	Protein-protein interactions	M. Kann	<a href="mailto:mkann@umbc.edu">mkann@umbc.edu</a>