



## Module Details

<b>Short Title:</b>	Bioinformatics for Research	APPROVED
<b>Full Title:</b>	Bioinformatics for Research	
<b>Module Code:</b>	BIOL9012	<b>NFQ Level:</b> Expert
		<b>ECTS Credits:</b> 5.0
<b>Valid From:</b>	Semester 1 - 2014/15 ( September 2014 )	
<b>Module Coordinator:</b>	Niall Smith	
<b>Module Author:</b>	SIOBHAN O SULLIVAN	
<b>Description:</b>	Students will study the theory and practical applications of bioinformatics relevant to research. Bioinformatics tools such as homology searching, sequence alignments and others will be demonstrated and assessment of learning and understanding will be based on students utilising these tools using sample data and data from their own research with particular emphasis on hands-on expertise relevant to bioinformatics.	
<b>Learning Outcomes:</b>		
<i>On successful completion of this module the learner will be able to</i>		
<ol style="list-style-type: none"> <li>1. Describe how the central dogma of molecular biology leading to -omics has evolved and its current status.</li> <li>2. Apply the theory of bioinformatics in the analysis of data structures and algorithms.</li> <li>3. Use bioinformatics tools for the analysis of varied biological data sets.</li> <li>4. Illustrate how the practice of homology searches, sequence alignments, motifs, phylogenetics, protein folding and structure predictions can be documented in reports and publications.</li> <li>5. Analyse sample gene and protein sequences using computing skills.</li> </ol>		
<b>Pre-requisite learning</b>		
<b>Module Recommendations</b>		
<i>This is prior learning (or a practical skill) that is strongly recommended before enrolment in this module. You may enrol in this module if you have not acquired the recommended learning but you will have considerable difficulty in passing (i.e. achieving the learning outcomes of) the module. While the prior learning is expressed as named CIT module(s) it also allows for learning (in another module or modules) which is equivalent to the learning specified in the named module(s).</i>		
No recommendations listed		
<b>Incompatible Modules</b>		
<i>These are modules which have learning outcomes that are too similar to the learning outcomes of this module. You may not earn additional credit for the same learning and therefore you may not enrol in this module if you have successfully completed any modules in the incompatible list.</i>		
No incompatible modules listed		
<b>Requirements</b>		
<i>This is prior learning (or a practical skill) that is mandatory before enrolment in this module is allowed. You may not enrol on this module if you have not acquired the learning specified in this section.</i>		
Students are required to have taken the modules: BIOL6024 Structural Biochemistry & GENE7002 Molecular Biology or equivalent		
<b>Co-requisites</b>		
No co-requisites listed listed		



## Module Content &amp; Assessment

## Indicative Content

- **Setting the scene**  
The central dogma of molecular biology leading to –Omics. Hierarchy of protein structure. Methods for gene sequencing (Sanger and next-generation). Gene annotation. Sequence and structure databases as archives.
- **Bioinformatics**  
Homology searches, sequence alignment, motifs, phylogenetics, protein folding and structure prediction.
- **Archives and tools for bioinformatics**  
Screening archives by name and by sequence. Aligning “by eye” the dotplot. Introduction to BLAST, FASTA, CLUSTAL , CDD and Pfam. Screening a sequence database with a single DNA sequence. Screening a sequence database with a single protein sequence. Multiple sequence alignments.
- **Interrogating sequences**  
Making functional deductions from sequence similarities. Secondary structure prediction, Predicting post-translational modification sites. Identifying protein domains. Phylogeny and phylogenetic trees. Lab: BLASTing single sequences. Creating pairwise and multiple alignments with BLAST, CLUSTAL W and the BioEdit sequence editor. Creating and editing phylogenetic trees.
- **Protein structure**  
How is structure determined? Graphics programs. Roles of side-chains. Protein stability. Superposition of structures. Root mean Square deviation. Ramachandran plots. Protein evolution and classification. Online homology modelling servers. Lab. Navigating the PDB. Downloading PDB files. Introduction to graphics programs RasMol, RasTop and SwissPDB viewer.
- **Programming/computing**  
Hands-on Linux skills, basic computing skills and databases, computer system organisation, analysis of simple data structures and algorithms, programming concepts and practice, web applications programming.
- **Systems biology**  
Genome sequencing projects and genome analysis, functional genomics, metabolome modelling, regulatory networks, interactome, enzymes and pathways.
- **NCBI as a bioinformatics resource**  
Entrez database and NCBI resources for Bioinformatics. MMD. Using Cn3D to view MMD files. Structure comparisons and annotation. Lab. Navigating Entrez. Downloading structure files from MMD. Viewing and annotating files with Cn3D.
- **Applications to –Omics**  
Genome, transcriptome and proteome resources. Use of microarrays.

Assessment Breakdown	%
Course Work	100.0%
End of Semester Formal Examination	0%

Coursework Breakdown				
Type	Description	Outcome addressed	% of total	Assessment Date
Short Answer Questions	Application of theory of bioinformatics in the analysis of data structures.	1,2	25.0	Week 2
Written Report	Screening archives by name and sequence. Practice use of sequencing alignment tools such as BLAST and CLUSTAL. Interrogating sequences and making functional deductions from sequence similarities and constructing phylogenetic trees.	1,3	25.0	Week 4
Written Report	Structure predictions, protein databases and practical use of graphics programs.	1,4	25.0	Week 6
Written Report	Use of computer programming and the application of programming concepts and applications in analysis of data structures and algorithms	2,5	25.0	Sem End

## Reassessment Requirement

**Coursework Only**

*This module is reassessed solely on the basis of re-submitted coursework. There is no repeat written examination.*

**The institute reserves the right to alter the nature and timings of assessment**



## Module Workload &amp; Resources

Workload		Full-time		
Type	Description	Hours	Frequency	Average Weekly Learner Workload
Lecturer-Supervised Learning (Contact)	Theory of Bioinformatics and practical applications	6.0	Every Second Week	3.00
Independent & Directed Learning (Non-contact)	Self-directed learning and data analysis	8.0	Every Second Week	4.00
Total Weekly Learner Workload				7.00
Total Weekly Contact Hours				3.00

Workload		Part-time mode		
Type	Description	Hours	Frequency	Average Weekly Learner Workload
Lecturer-Supervised Learning (Contact)	Theory of Bioinformatics and practical applications	6.0	Every Second Week	3.00
Independent & Directed Learning (Non-contact)	Self-directed learning and data analysis	8.0	Every Second Week	4.00
Part-Time Total Weekly Learner Workload				7.00
Part-Time Total Weekly Contact Hours				3.00

## Resources

## Recommended Book Resources

- **Tore Samuelsson, 2012, *Genomics and Bioinformatics*, Cambridge University Press UK [ISBN: 9781107401242]**
- **Warren J. Ewens, Gregory R. Grant (Contributor) 2010, *Statistical Methods in Bioinformatics*, 2nd Ed., Springer [ISBN: 978-1441923028]**
- **edited by Pavel Pevzner and Ron Shamir. 2011, *Bioinformatics for biologists*, 1st Ed., Cambridge University Press UK [ISBN: 978-1107011465]**
- **Jonathan Pevsner 2009, *Bioinformatics and functional genomics*, 2nd Ed., Wiley-Blackwell Hoboken, N.J. [ISBN: 978-0470085851]**

## Supplementary Book Resources

- **Richard E. Neapolitan 2009, *Probabilistic methods for bioinformatics*, Elsevier Science and Technology San Francisco/US [ISBN: 9780123704764]**
- **James D. Tisdall 2002, *Beginning Perl for bioinformatics*, O' Reilly Media Inc, USA USA [ISBN: 9780596000806]**
- **David Sankoff (Editor), Lusheng Wang (Editor), Francis Chin (Editor) 2007, *Proceedings of the 5th Asia-Pacific Bioinformatics Conference: Hong Kong 15 - 17 January 2007*, Cambridge University Press London/GB [ISBN: 9781860947834]**
- **Conrad Bessant, Ian Shadforth, Darren Oakley 2009, *Building bioinformatics solutions*, 1st Ed., Oxford University Press New York [ISBN: 978-0199230235]**