

Course title: Gene Expression Analysis and Transcriptomics				
Course code: BBP 163		No. of credits: 2	L-T-P: 30-0-0	Learning hours: 30
Pre-requisite course code and title (if any): None				
Department: Department of Biotechnology				
Course coordinator(s): Prof. Ramakrishnan Sitaraman			Course instructor(s): Prof. Ramakrishnan Sitaraman	
Contact details: rkraman@terisas.ac.in				
Course type: Core			Course offered in: Semester 3	
<p>Course description: An understanding of the range of methods available to interrogate gene expression on a large scale as well as the correct usage and interpretation of high-throughput data is indispensable for the modern biologist. Together with its complementary course on proteomics and protein engineering, Accordingly, this course provides an overview of methods available to analyse gene transcription and complements the course titled “proteomics and protein engineering.” Starting with due emphasis to the biological complexity that high-throughput methods aim to interrogate in the first module, the course moves progressively from a description of the different techniques available and their comparative analysis to an overview of the approaches to and problems in analysis, integration and biological inference. The concluding module introduces two fast-moving areas of research – meta-omics and single-cell omics – and surveys their potential to provide insights into the heterogeneity of cellular communities.</p>				
<p>Course objectives:</p> <ol style="list-style-type: none"> 1. To present an integrative view of cellular processes at progressively complex levels. 2. To enable synthesis of isolated information in order to analyze biological phenomena in a contextually relevant manner. 3. To delineate the overarching role of evolutionary considerations at multiple levels of complexity. 				
Course contents				
S.No	Topic	L	T	P
Module 1	The biological problem	9		
1	Regulation of gene expression in prokaryotes and eukaryotes, similarities and differences in gene regulation across the domains of life, historical impact of genetic approaches on the study of gene expression.	3		
2	Levels of regulation – transcriptional to post-translational, phenotypic plasticity and epigenetics; the impact of DNA rearrangements on gene expression.	4		
3	Evolutionary considerations in gene regulation and their role in speciation	2		
Module 2	Tools and techniques for gene expression analysis	9		
1	Low to medium throughput methods (blotting and PCR).	1	0	0
2	High throughput platforms/methods – Microarrays, RNA-seq, Nanostring, Nanopore, PacBio, pyrosequencing, flow cytometry and phenotyping of single cells	6	0	0
3	Quality control, comparison of methods – their scope and limitations	2	0	0
Module 3	Analysis, inference and integration	10		
1	Multiple hypothesis testing and the false discovery rate	2	0	0
2	Normalization, correlation and clustering to determine differential gene expression, guilt-by-association and regulatory networks	8	0	0
Module 4	Prospects and perspectives	2		
	Meta-omics and single-cell omics,	2		

	Total	30	0	0
Evaluation criteria				
1. Minor test 1	30%			
2. Minor test 2	30%			
3. Major test (end semester)	40%			
Learning outcomes:				
1. Detailed knowledge of gene regulatory mechanisms in across the three major kingdoms and the evolution of regulatory systems. (Minor test 1).				
2. Understanding the methods available to analyse gene expression, their scope and limitations (Minor test 2-Major test).				
3. Ability to understand the conceptual bases of analytical approaches to derive biological information (Minor test 2-Major test).				
Pedagogical Approach:				
Lectures, tutorials supported by critical appraisal of original research articles, reviews, books and book chapters, hands-on-training and demonstration of online resources				
Skill Set:				
1. Design and critical analysis of experimental approaches to analyse gene transcription.				
2. Interpretation of data from high-throughput approaches.				
3. Formulation of testable hypotheses based on gene expression data.				
Employability:				
1. Academic and industrial research.				
2. Intellectual property firms.				
3. Life science teaching at school and undergraduate levels.				
4. Management and/or supervision of laboratory research in academic/industrial settings.				
Materials:				
Required texts				
1. Campbell, A. M. & Heyer, L. J. Discovering genomics, proteomics, and bioinformatics. (CSHL Press : Pearson/Benjamin Cummings, 2007).				
2. Conesa, A. <i>et al.</i> A survey of best practices for RNA-seq data analysis. <i>Genome Biol.</i> 17 , 13 (2016).				
3. DeRisi, J. L., Iyer, V. R. & Brown, P. O. Exploring the metabolic and genetic control of gene expression on a genomic scale. <i>Science</i> 278 , 680–686 (1997).				
4. Hughes, T. R. <i>et al.</i> Widespread aneuploidy revealed by DNA microarray expression profiling. <i>Nat. Genet.</i> 25 , 333–337 (2000).				
5. Kirienko, N. V. & Fay, D. S. Transcriptome profiling of the <i>C. elegans</i> Rb ortholog reveals diverse developmental roles. <i>Dev. Biol.</i> 305 , 674–684 (2007).				
6. Wittkopp, P.J. Evolution of Gene Expression. <i>in</i> The Princeton Guide to Evolution (<i>eds.</i> Losos, J. B. <i>et al.</i>) 413–419 (Princeton University Press, 2013). doi:10.1515/9781400848065-058.				
7. Lovén, J. <i>et al.</i> Revisiting global gene expression analysis. <i>Cell</i> 151 , 476–482 (2012).				
8. Noble, W. S. How does multiple testing correction work? <i>Nat. Biotechnol.</i> 27 , 1135–1137 (2009).				
9. Shoemaker, D. D. <i>et al.</i> Experimental annotation of the human genome using microarray technology. <i>Nature</i> 409 , 922–927 (2001).				
10. Wang, B., Kumar, V., Olson, A. & Ware, D. Reviving the Transcriptome Studies: An Insight Into the Emergence of Single-Molecule Transcriptome Sequencing. <i>Front. Genet.</i> 10 , 384 (2019).				
11. Karahalil, B. Overview of Systems Biology and Omics Technologies. <i>Curr. Med. Chem.</i> 23 , 4221–4230 (2016).				
12. Martins, R. P. The conceptual structure of evolutionary biology: A framework from phenotypic plasticity. <i>Eur. J. Ecol.</i> 4 , 111–123 (2018).				
13. Stein, C. M., Weiskirchen, R., Damm, F. & Strzelecka, P. M. Single-cell omics: Overview, analysis, and application in biomedical science. <i>J. Cell. Biochem.</i> 122 , 1571–1578 (2021).				

Case studies**Suggested readings**

1. Ptashne, M. A Genetic Switch, Phage Lambda Revisited. (CSHL Press, 2004, 3rd ed.)

Journals**Other readings****Additional information (if any):****Student responsibilities:**

1. Class attendance (online/offline).
2. Study/self-study of course materials as specified by the instructor.
3. Ensuring functionality of essential IT hardware & software at their preferred location(s).

Course reviewers:

1. Prof. Vijaya Satchidanandam, Department of Microbiology and Cell Biology, Indian Institute of Science, Bengaluru (superannuated) and Adjunct Professor, St. John's Medical College, Sarjapur Road, Bengaluru – 560034
2. Dr. S. Ramachandran, Chief Scientist, Professor of the AcSIR in the Faculty of Biological Sciences, Room 130, CSIR-Institute of Genomics and Integrative Biology, Mathura Road, Near Sukhdev Vihar Bus Depot, New Delhi – 110025