

<b>Course title:</b> Gene Expression Analysis and Transcriptomics			
<b>Course code:</b> BBP 163	<b>No. of credits:</b> 2	<b>L-T-P:</b> 30-0-0	<b>Learning hours:</b> 30
<b>Pre-requisite course code and title (if any):</b> None			
<b>Department:</b> Department of Biotechnology			
<b>Course coordinator(s) :</b> Prof. Ramakrishnan Sitaraman		<b>Course instructor(s):</b> Prof. Ramakrishnan Sitaraman	
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<b>Course type:</b> Core		<b>Course offered in:</b> Semester 3	
<p><b>Course description:</b> 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><b>Course objectives:</b></p> <ol style="list-style-type: none"> <li>1. To present an integrative view of cellular processes at progressively complex levels.</li> <li>2. To enable synthesis of isolated information in order to analyze biological phenomena in a contextually relevant manner.</li> <li>3. To delineate the overarching role of evolutionary considerations at multiple levels of complexity.</li> </ol>			