



Theodor Brinkmann Graduate School



	Applied bioinformatics	
Coordinator(s)	Heiko Schoof	
Instructor(s)	Heiko Schoof, Florian Boecker, Lena Altrogge	
Course Description	<p>We will analyse a Next Generation Sequencing dataset measuring genome-wide gene expression using the Cufflinks package. Aim: Introduce to the reproducible application of current bioinformatics methods to high-throughput data analysis</p> <p>We will:</p> <ul style="list-style-type: none"> <li>- not hide the ugly details</li> <li>- use state-of-the-art algorithms</li> <li>- work on single data sets using methods that scale to dozens of data sets</li> <li>- focus on technical skills</li> <li>- use high performance computing infrastructure</li> <li>- not introduce programming new algorithms</li> <li>- not discuss algorithms or introduce various methods</li> </ul>	
Course Outline	<ul style="list-style-type: none"> <li>-introduction to Unix and computing</li> <li>-QC, trim and filter (trimmomatic), map to reference (tophat2)</li> <li>-view mapping (IGV), assemble transcripts (cufflinks)</li> <li>-expression counts, differential expression (cuffmerge, cuffdiff)</li> <li>-expression plots and analyses (R, cummerbund, DEseq, GStat, Mapman)</li> <li>-interpretation and documentation</li> <li>-exam</li> </ul>	
Requirements	Basic skills in R, background in molecular biology	
Credit Points 3	Teaching Methods	
	Lectures	20%
	Practical computer work	80%
Grading	Test on 30.6.	
References	Trapnell C et al., Nature Protocols (2012) 7(3)	
Organization and time	6.6.-30.6., Mon-Thu 14-17 Computer pool, Nussallee 17 (Wednesdays 2.003, Nussallee 1)	
Language	English	
Remarks	Register by email to <a href="mailto:cropbio@uni-bonn.de">cropbio@uni-bonn.de</a>	