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Degree Project in Bioinformatics

Masters Programme in Molecular Biotechnology Engineering,
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Author	Annelie Johansson	
Title (English)	Identifying gene regulatory interactions using functional genomics data	
Title (Swedish)		
Abstract	<p>Previously studies^{1,2,3} used correlation of DNase I hypersensitivity sites sequencing (DNase-seq) experiments to predict interactions between enhancers and its target promoter gene. We investigate the correlation methods Pearson's correlation and Mutual Information, using DNase-seq data for 100 cell-types in regions on chromosome one. To assess the performances, we compared our results of correlation scores to Hi-C data from Jin <i>et al.</i> 2013⁴. We showed that the performances are low when comparing it to the Hi-C data, and there is a need of improved correlation metrics. We also demonstrate that the use of Hi-C data as a gold standard is limited, because of its low resolution, and we suggest using another gold standard in further studies.</p>	
Keywords	Bioinformatics, gene regulation, promoter, enhancer, DNase-seq, Hi-C, Pearson's correlation, Mutual Information	
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