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researchers often use vectors with special ability to insert and disrupt genes to create models of human disease. in the past several years, researchers have used the crispr/cas9 system, which uses a tool called cas9, to edit genes. this study proposes a method for using cas9 and its guide rna to create and delete entire genes. after cloning the desired cas9 and the guide rna required for a particular target gene, and expressing these in the desired cells, researchers can use the cas9/guide rna combination to both knock out (ko) and create a deletion (del) of the gene by using a design tool on the web. we demonstrate the use of this method to delete the mst1 gene in human cells and show that the proposed method functions efficiently. we further provide several possible applications of this method, such as ko in which cells are already deficient in a gene to create a cell line for the study of that gene, and heterozygous knockout (hetero-ko) in which the mutant gene is partially complemented by the wild-type allele. we also demonstrate that targeted deletion of part of the gene can be used to successfully create disease models. we study the relationship between the power of detecting peaks of enrichment and the number of available whole genome sequencing (wgs) samples using the well-studied yeast data set. based on synthetic data sets, the power of detecting enrichment, in addition to the wgs sample size and the enrichment signal strength, depends on the number of wgs samples used per condition. we show that performing similar peak calling in pooled wgs samples can improve the power of enrichment detection. our computational analysis on the yeast data set suggests that the data structure of the pooled wgs samples should match the data structure of the original wgs samples to achieve the maximum power. however, our experimental validation on the human cancer data set indicates that pooled samples can sometimes result in less accurate peak detection due to the lack of technical replicates. pmid:25330585

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this paper presents an innovative and interactive approach for controlling the operation of a vessel using a hybrid network structure. the proposed approach uses a three-layer network architecture and can control the operation of a vessel in real time. the control system’s first layer is responsible for receiving the inputs from the environment. the second layer is responsible for converting the inputs into the control parameters and sending them to the third layer, which is a real time control layer. the third layer is responsible for updating the state of the system, as well as making decisions and issuing instructions to the first layer in order to control the system. the proposed approach has been applied to a ship model to demonstrate its efficiency. pmid:27509823 this paper proposes an innovative method for developing the control system for a vessel in real time using a hybrid network structure. the proposed approach is responsible for converting the environmental inputs into the control parameters for the second layer. the second layer is responsible for converting the control parameters to the control signals for the third layer. the third layer is responsible for updating the state of the vessel and making decisions and issuing the instructions to the first layer to control the

vessel in real time. the proposed approach is applied to a ship model, demonstrating its efficiency. pmid:27509823 the development of novel high-throughput sequencing methods for chip (chromatin immunoprecipitation) has provided a very powerful tool to study gene regulation in multiple conditions at unprecedented resolution and scale. proactive quality-control and appropriate data analysis techniques are of critical importance to extract the most meaningful results from the data. over the last years, an array of r/bioconductor tools has been developed allowing researchers to process and analyze chip-seq data. this chapter provides an overview of the methods available to analyze chip-seq data based primarily on software packages from the open-source bioconductor project. protocols described in this chapter cover basic steps including data alignment, peak calling, quality control and data visualization, as well as more complex methods such as the identification of differentially bound regions and functional analyses to annotate regulatory regions. 5ec8ef588b