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| Course Code | BIO541 | | |
| Course Name | Data sciences in Genomics | | |
| Credits | 4 | | |
| Course Offered to | UG/PG | | |
| Course Description | The field of Genomics is expanding its horizon with help of high throughput technologies. Scientist are trying to answer fundamental questions related to health, society and human survival outside earth using genomics. With such increase of applications, it constantly needs computational experts for systematic analysis of data and acheiving meaning full insights. Infact the computational experts have now started taking lead in genomic projects. Hence this course is meant to guide students for data analysis approach and steps involved in computational genomics and make them familiar with latest development in genomics. | | |
| Pre-requisites | | | |
| Pre-requisite (Mandatory) | Pre-requisite (Desirable) | Pre-requiste (Other) | |
| None | | None | |
| Post Conditions | | | |
| CO1 | CO2 | CO3 | CO4 |
| students can understand source and properties of different kinds of genomic data | students can use tools for regular processing different kinds of genomics data | Students can undersand the statistical approach used by tools for processing genomics data | Students can perform few complex post processing of data to make meaningful clinical and biological inference |
| Weekly Lecture Plan | | | |
| Week Number | Lecture Topic | Cos met | Assignments/Lab/Tutorials |
| Week 1 | Introduction to molecular cell biology, central dogma, measurements using microarray and ngs technologies; | CO1 | Assignment: (i) Paper reading on cellular functions and biological processes and writing in own words |
| Week 2-3 | Introduction to Genetics/Genomics; Applications to clinical diagnostics; | CO1,CO2 | |
| Week 4 | NGS concepts and applications; DNA alignment algorithms and assessment; Data QC and Filtering | CO1, CO2 | Assignment2 : R and Bioconductor; R packages for annotations, short reads handling, microarray analysis and visualizations; |
| Week 5 | Applications of NGS in single cell study, bias, drop-out and noise in single cell data | | |
| Week 6-7 | Unsupervised (Clustering and Biclustering) and supervised (Classification) , statistical approach in Normalization and Differential gene expression (microarray, bulk RNA-seq and single cell RNA-seq) | CO2, CO3, CO4 | |
| Week 8 | Network inference methods, WGCNA, visualisation | CO3, CO4 | |
| Week 9-10 | introduction to epigenome and analysis of epigenome ngs data, handling bias and noise, application of epigenome | CO2, CO3 | Assignment3: Processing ChIP-seq and RNA-seq datasets to make clinical inference |
| Week 11 | Denovo assembly; Assembly assessment; Assembly refinement; Variant calling (SNPs, MNPs, small InDels) | CO2, CO3 | |
| Week 12-13 | Variant annotations and interpretation, statistical method for effect prediction and QTL; Visualization of genomic data, population Genomics | CO3, CO4 | Assignment 4: QTL analysis |
| | Project presentations | | |
| Assessment Plan | | | |
| Type of Evaluation | % Contribution in Grade | | |
| Mid-sem | 20 | | |
| End-sem | 20 | | |
| Assignments | 20 | | |
| Project | 40 | | |
| Resource Material | | | |
| Type | Title | | |
| Textbook | B. Pierce, Genetics: A conceptual approach, | | |
| Textbook | https://en.wikibooks.org/wiki/Next_Generation_Sequencing_(NGS) | | |
| Textbook | Xinkun Wang, Next-Generation Sequencing Data Analysis, | | |
| Publication | Ryuichiro Nakato Katsuhiko Shirahige, Brief Bioinform (2017) 18 (2): 279-290 ,Recent advances in ChIP-seq analysis: from quality management to whole-genome annotation | | |
| Publication | Ryuichiro Nakato and Katsuhiko Shirahige, Recent advances in ChIP-seq analysis: from quality management to whole-genome annotation, Brief Bioinform. 2017 Mar; 18(2): 279–290. | | |
| Publication | Juliana Costa-Silva, Douglas Domingues, Fabricio Martins Lopes , RNA-Seq differential expression analysis: An extended review and a software tool PLOS one. | | |
| Publication | Robert Ekblom and Jochen B W Wolf, A field guide to whole-genome sequencing, assembly and annotation, Evol Appl. 2014 Nov; 7(9): 1026–1042. | | |