SRM UNIVERSITY
FACULTY OF ENGINEERING & TECHNOLOGY
DEPARTMENT OF BIOINFORMATICS

BI0510- MICROARRAY BIOINFORMATICS

LECTURE PLAN

Class & Sem: M.Tech & II sem **Staff Name:Mrs. S.Shobana**
Subject code: BI0 510 **Subject: MicroarrayBioinformatics**

Lecture Hour	Contents	Learning Outcome
1.	INSTRUCTIONAL OBJECTIVES DNA MicroArray: The Technical Foundations Why are MicroArray Important? What is a DNAMicroArray	o Introduction to the student about microarray technology and its uses. o It gives a brief description about the making and using of microarrays. o Also the different databases used for creating probes are taught.
2.	Microarray- Introduction	
3.	types of Microarray	
4.	Making microarrays	
5.	Spotted arrays	
6.	Insitu synthesized oligonucleotide arrays	
7.	Steps involved in use of microarray	
8.	Sample preparation and labeling, Hybridisation	
9.	Washing, image aquisition	
10.	Filtering of low complexity sequences	o In the method “insitu synthesized oligonucleotides” certain rules have to be followed for preparing probes which has been discussed in this unit. o Also feature extraction methods are discussed o DNA Microarray and its statistical analysis o Analysis of RNA data o Statistical computing and Statistical Genetics
11.	cross-hybridization prediction	
12.	Prediction of melting temperature	
13.	Secondary structure prediction of probe	
14.	Feature extraction steps	
15.	Identifying positions of features	
16.	Types of segmentation & Background pixel identification	
17.	Data cleaning and transformation within array normalization-	o Normalization techniques to correct systemic and spatial effects o Quantify non systemic variability
18.	Loess regression	
19.	Correcting Spatial effects	
20.	between array normalization steps	
21.	measuring and quantifying microarray variability	
22.	Calibration experiments and pilot studies	

23.	Method for measuring variability	
24.	Analysis of differentially expressed genes	
25.	fundamental concepts and hypothesis rules	
26.	Classic parametric tests- paired and unpaired.	
27.	Non parametric tests- bootstrap analysis	o Differentially expressed genes can be obtained from the numerical data and can be done using clustering algorithms. o Classification of tissues and genes using different algorithms and its validation. o Also microarray data is a high dimensional data- thus dimension reduction is discussed
28.	Multiplicity of testing- bonferroni adjustment and ANOVA	
29.	Similarity analysis of relationships between genes using correlation coefficient, rank coefficient and Euclidean distance	
30.	Hierarchial clustering & Linkage methods for clustering	
31.	Machine learning methods of clustering	
32.	classification of tissues and samples- methods	
33.	Validation and cross validation	
34.	Dimensionality reduction- PCA &Individual gene selection	
35.	Pairwise gene selection,Voting algorithms, genetic algorithms	
36.	UNIT V-EXPERIMENTAL DESIGN Blocking	
37.	randomization & blinding-	o The basic experimental design for a microarray experiment o The ways and means to store large microarray data is discussed.
38.	choice of technology using experimental designs	
39.	Power analysis and confidence	
40.	data standards- LIMS	
41.	storage and sharing- MIAME, MAGE, Ontologies	
42.	Future direction of microarray approach,	
43.	Pharmacogenomics,	
44.	Toxicogenomics	
45.	Data mining	

REFERENCES

1. Arun Jogota , *Microarray Data Analysis and Visualization*, The Bay Press, 2001.
2. Ernst Wit and John McClure, *Statistics for Microarrays Design, Analysis and Inference,* John Wiley & Sons, 2004.
3. Steen Knudsen, *Guide to analysis of DNA Microarray data*, John Wiley & Sons, 2004.
4. Dov Stekel , *Microarray Bioinformatics*, Cambridge University Press, 2003.
5. S. Draghic, Chapman, Data Analysis tools for DNA Microarray, Hall/ CRC Press, 2002.

E Mail ID: shobanas@ktr.srmuniv.ac.in

Contact No: 9841988577