Venue: GIZA
22nd August 2007
1030-1145 hr

Symposium 3C: Importance of information technology in infectious diseases

S3C-1. Microarray gene expression analysis

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Technological developments in two areas are set to change the way we diagnose, treat and manage human diseases. First, the complete sequence of the human genome and many organisms, including a number of pathogens, are now available. Second, technological developments such as microarray approaches based on DNA, RNA and protein detection have opened up new fields in genomics and proteomics. Together, these have advanced our understanding of the pathogenicity of some organisms and contributed to our understanding of the genetic basis of human diseases. We describe how we and others have used microarray gene expression analysis to classify pathological subtypes of cancer, to identify prognostic markers or signatures, to identify predictive markers of treatment outcome and to design personalised therapy for cancer.

S3C-2. Bioinformatics analysis in the diagnosis and management of human genetic diseases – challenges and opportunities

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The Human Genome Project has generated an unprecedented wealth of biological data, which requires scientific analysis, systematic management and appropriate interpretation for the maximum benefit of society. This has led to a multidisciplinary field of computer science, mathematics, biochemistry, biophysics and biology called as bioinformatics. Although, anyone, from clinicians to molecular biologists, with access to the World Wide Web can freely discover the composition of biological molecules, but, this doesn't imply that handling and analysis of raw genomics data can easily be carried out by all. Bioinformaticians use customized and integrated software programs for organizing, storing, predicting, retrieving genomics and proteomics data to answer complicated problems of medicine and science. Bioinformatics analysis includes analysis of gene variation, prediction of gene, protein structure and function, prediction and detection of gene regulation networks, simulation environments for homology modeling, complex modeling of gene regulatory dynamics and networks, and presentation and analysis of molecular pathways in order to understand gene-disease interactions. Basic bioinformatics tools are already accessed in certain clinical situations to aid in diagnosis and treatment plans. For example, PubMed is accessed freely for biomedical journals cited in Medline, and OMIM, a search tool for human genes and genetic disorders, is used by clinicians to obtain information on genetic disorders in the clinic or hospital setting. Bioinformatics analysis will help to identify disease related genes and will serve to identify susceptibility genes and illuminate the pathogenic pathways involved in illness, and will therefore provide an opportunity for development of targeted therapy. Integrative bioinformatics analysis of genomic, pathological, and clinical data in

clinical trials will reveal potential drug toxicity reactions by use of simple genetic tests. This paper describes main bioinformatics and discusses how they are being used to interpret biological data and to further management and understanding of genetic diseases.