From Diagnostics to Risk Assessment, Causality and Therapeutic intervention

Andrew Lynn School of Computational and Integrative Sciences Jawaharlal Nehru University

Current Diagnostics are threshold classifiers or images that require visual interpretation





Machine Learning can be used to identify new multivariate diagnostics and automate visual interpretation





Machine Learning can be used to identify new multivariate diagnostics and automate visual interpretation



Science 23 Feb 2018: Vol. 359, Issue 6378, pp. 926-930 DOI: 10.1126/science.aar3247





SEEK and you may find cancer earlier

Many cancers can be cured by surgery and/or systemic therapies when detected before they have metastasized. This clinical reality, coupled with the growing appreciation that cancer's rapid genetic evolution limits its response to drugs, have fueled interest in methodologies for earlier detection of the disease. Cohen *et al.* developed a noninvasive blood test, called CancerSEEK that can detect eight common human cancer types (see the Perspective by Kalinich and Haber). The test assesses eight circulating protein biomarkers and tumor-specific mutations in circulating DNA. In a study of 1000 patients previously diagnosed with cancer and 850 healthy control individuals, CancerSEEK detected cancer with a sensitivity of 69 to 98% (depending on cancer type) and 99% specificity.

Machine Learning can be used to identify new multivariate diagnostics and automate visual interpretation







Genetic testing is used for risk prediction



Genetic testing is used for risk prediction



Novel diagnostics and risk predictors can be identified from modern DNA/RNA sequencing methods



Epigenetic changes like CpG island hypomethylation or hypermethylation can be used as potential biomarkers in risk stratification and therapeutic response generation for various diseases like colorectal cancer, glioblastoma, breast cancer, asthma, neurodegenerative diseases etc.

Detection of relative abundance of transcript copies with tissue-specific effects is done commonly for cancer diagnosis and can also be used for detecting differentially expressed variants. The impact of genomic variations can be understood from protein structure, dynamics and network analysis





A similar impact can be studied with environmental factors using both data mining with feature extraction and network analysis



A similar impact can be studied with environmental factors using both data mining with feature extraction and network analysis





9.4: GIS integrated Malarial hotspots

Integrated multiparameter data model for prediction of malaria hotspots

- 1. Socio-economic aspects
 - Population, child population, literacy, and workforce participation
- 2. Epidemiology
 - Annual parasitic index (API) and slides collected and examined)
- 3. Geographical features
 - Settlement, forest cover, water bodies, rainfall, relative humidity, and temperature
 - Malaria Journal, 2014



Integrated multiparameter data model for prediction of malaria hotspots

- 1. Socio-economic aspects
 - Population, child population, literacy, and workforce participation
- 2. Epidemiology
 - Annual parasitic index (API) and slides collected and examined)
- 3. Geographical features
 - Settlement, forest cover, water bodies, rainfall, relative humidity, and temperature
 - Malaria Journal, 2014



