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Recent advancement of application of big data technologies for precision medicine initiative

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The big data story is certainly a boon to business. But big data can also play a key role in helping enhance the personal lives of a wide swath of this planet's humanity. In essence, big data has the capability to help many people around the world work toward alleviating inequality. It can do so in several ways Internet-based health portals made available to wider populations can help reduce the cost of maintaining electronic health records and establish unique ID numbers for citizens. The data captured at these portals can also help significantly reduce the cost of drug discovery as improved analytics help determine which drugs work well and which aren't as effective for certain conditions. Big data analytics may even allow for uploading the genomics of large populations that can be stored for researching new generations of drug therapies. Improving healthcare in developing nations helps mitigate illnesses that can sap the productivity necessary to advance societies   will help remote area of India through the collaborative workshop .personalized medicine" is an innovative approach to disease prevention and treatment that takes into account differences in people's genes, environments and lifestyles. Changing paradigms in treating diseases and revolutionizing health we will focus how big data, Privacy of law will helpful for precision Medicine.

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Precision cancer medicine: Spatiotemporal genomes heterogeneity opens new therapeutic horizons

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Background: Metastasis is the cause of death for millions of cancer patients annually worldwide. Spatiotemporal identification of resistant sub clones using breakthrough technological genome systems and methods can predict and prevent therapeutic resistance and metastatic relapse before it clinically occurs on the basis of genotype-phenotype map.

Architecture of genome and nonlinear transcription: Clinical studies coupled with mathematical and experimental models, indicate that in some patients pre-existed large structural genome changes [copy number alterations (CNAs), chromosomal rearrangements] predict metastasis and death. But in most patients dynamic emergence of somatic mutations leading to intratumor heterogeneity results in metastasis as a late event or development of secondary resistance and metastatic relapse. Based on the dynamics of genomic clone's evolution following Darwinian's principles, innovative methods and next-generation sequencing (NGS) systems have been developed.

Moreover, in the post-ENCODE era breakthrough approaches are being developed for understanding and disrupting transcriptional deregulated bio circuits with future nonlinear drugs.

This lecture presents how using primary tumor multiregional NGS analysis, single-cell genome-NGS, circulating genomes sequencing as well as CRISPR-Cas system we could understand non coding genome functionality and comprehensive interpatient heterogeneity (IPH). This spatiotemporal IPH can not only predict therapeutic resistance and metastasis but also shape the discovery of novel both linear and nonlinear transcription drugs.

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