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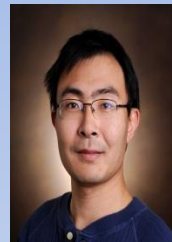


Journal of Next Generation: Sequencing & Applications

Review in 3 weeks

Publishing in 72 hours

Open Access



Yan Guo

Professor
Department of Cancer Biology

[Vanderbilt University](#)

USA



Biography

- **Yan Guo** received his PhD in computer science from University of South Carolina in 2009. Currently, he is an assistant professor at the Vanderbilt Center for Quantitative Sciences, Department of Cancer Biology department. He is also serving as the Technical Director of Bioinformatics for Vanderbilt Technologies for Advanced Genomics Analysis and Research Design (VANGARD). His research is focused on sequencing data analysis in cancer and development of bioinformatics methodology and analysis approaches for high dimensional genomic data.



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Research Interest

Research on developing bioinformatics methodologies and analytical approaches, especially in cancer research.



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Oncogenomics

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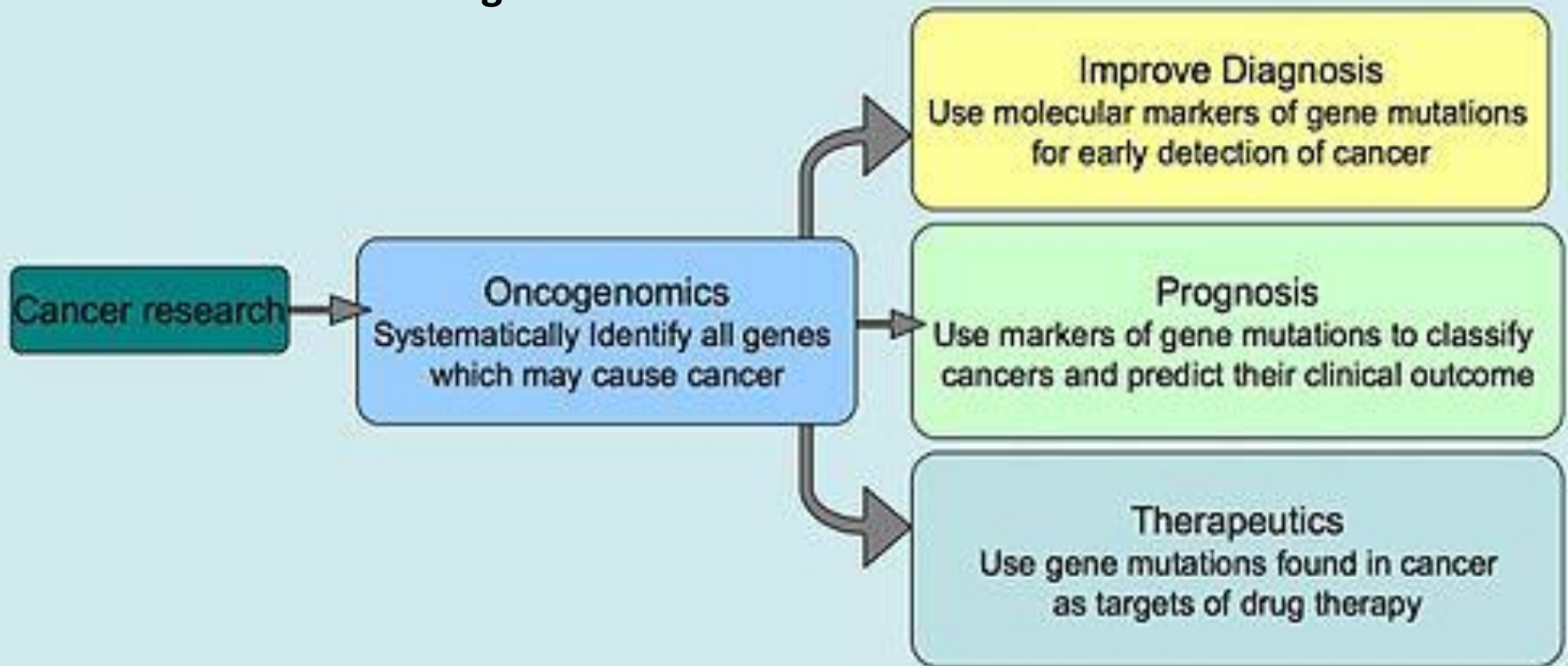


Oncogenomics (Cancer Genomics)

- **Oncogenomics** is a relatively new sub-field of genomics that applies high throughput technologies to characterize genes associated with cancer.
- Cancer is a genetic disease caused by accumulation of mutations to DNA leading to unrestrained cell proliferation and neoplasm formation.
- The goal of oncogenomics is to identify new oncogenes or tumor suppressor genes that may provide new insights into cancer diagnosis, predicting clinical outcome of cancers, and new targets for cancer therapies.
- The success of targeted cancer therapies such as Gleevec, Herceptin, and Avastin raised the hope for oncogenomics to elucidate new targets for cancer treatment.

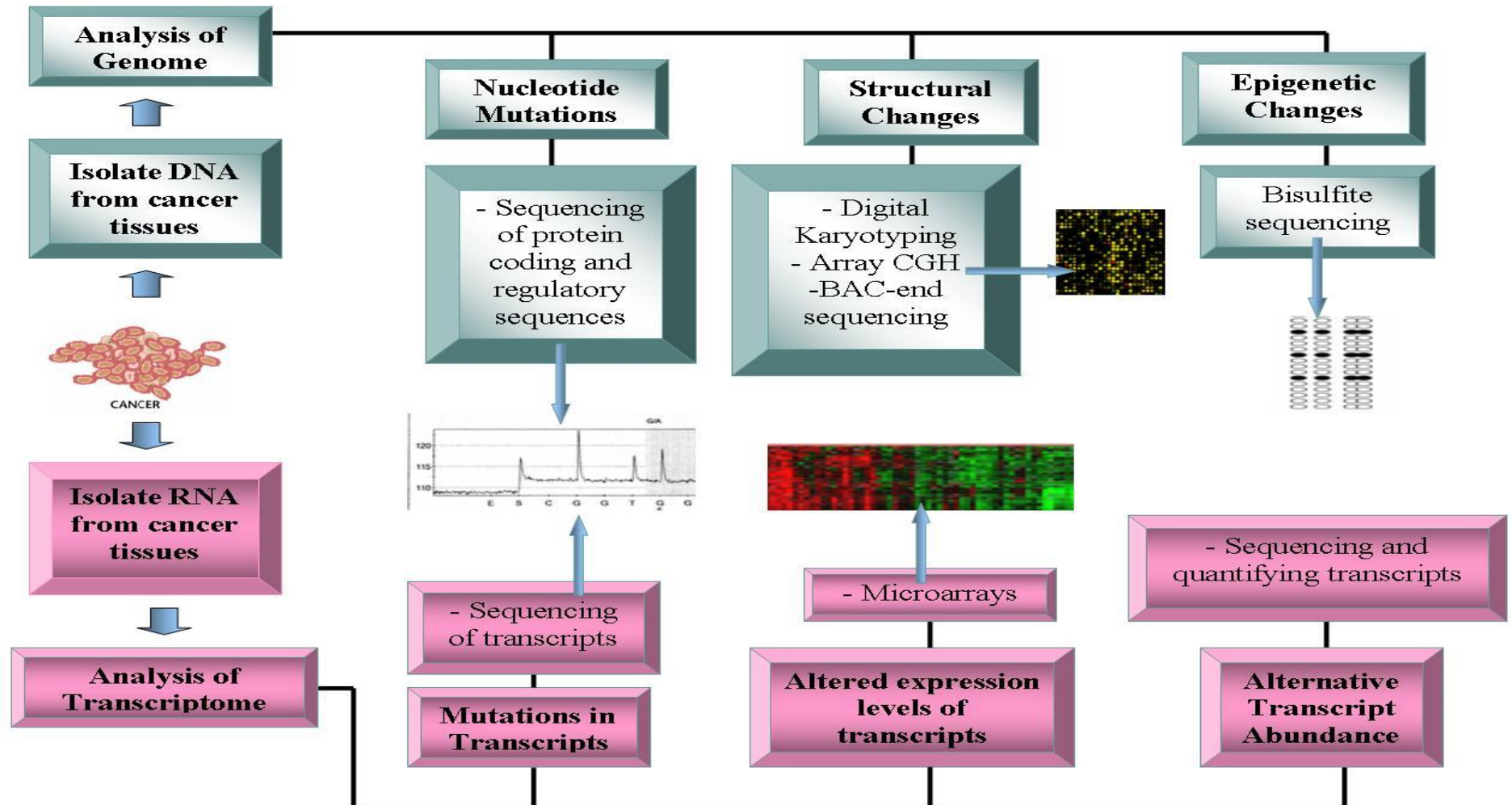


Overall Goals of Oncogenomics





Current Technology being used in Oncogenomics





Databases for Cancer Research

- Cancer Genome Project is an initiative to map out all the somatic intragenic mutations in cancer.
- COSMIC is a resource
- Oncomine has compiled data from cancer transcriptome profiles.
- IntOGen integrates multidimensional human oncogenomic data classified by tissue type using the ICD-O terms.
- International Cancer Genome Consortium is so far the biggest project to collect human cancer genome data. The data is accessible through the ICGC website.



Advances from Oncogenomics

- Mutational analysis of entire gene families has been a powerful approach to oncogenomics which has been informative. Genes of the same family have similar functions, as predicted by similar coding sequences and protein domains, have been systematically sequenced in cancerous genomes to identify particular pathways which may be associated with cancer progression.
- Drug therapies have already been developed to inhibit PIK3CA. Another example is the BRAF gene was identified in 2004, which was one of the first genes ever to be implicated in melanomas.
- BRAF encodes a serine/threonine kinase which is involved in the RAS-RAF-MAPK growth signaling pathway, and they found that mutations in BRAF causing constitutive phosphorylation and activity were found in 59% of melanomas. Before BRAF, there was very little understanding of the genetic mechanism of the development of melanomas, and therefore, prognosis for patients was poor.

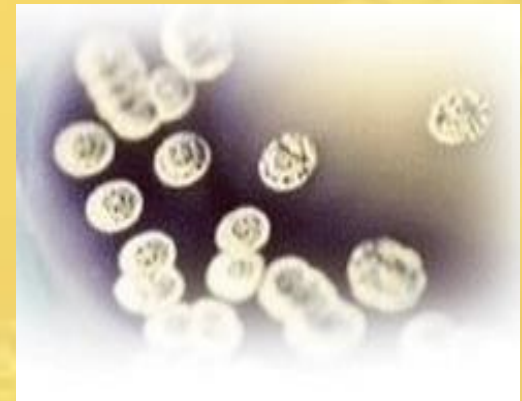


Potential Diagnostic Applications

- Currently anticancer drugs have been manufactured to target mtDNA and have shown positive results in killing tumor cells. There has also been research done in using mitochondrial mutations as biomarkers for cancer cell therapy.
- It is easier to target mutation within the mitochondrial DNA as opposed to nuclear DNA because the mitochondrial genome is much smaller and therefore easier to screen for specific mutations. It is also thought that the mtDNA content alterations found in blood samples might be able to serve as a screening marker for predicting future cancer susceptibility as well as tracking malignant tumor progression.
- with these potential helpful characteristics of mtDNA, it is also not under the control of the cell cycle and it is important for maintaining ATP generation and mitochondrial homeostasis. These characteristics make targeting mtDNA a practical therapeutic strategy.

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