1. Record Nr. UNINA9910298966703321 Autore Xu Ying <1960-> Titolo Cancer Bioinformatics / / by Ying Xu, Juan Cui, David Puett New York, NY:,: Springer New York:,: Imprint: Springer,, 2014 Pubbl/distr/stampa **ISBN** 1-4939-1381-6 Edizione [1st ed. 2014.] Descrizione fisica 1 online resource (386 p.) 004 Disciplina 570 570285 610 Soggetti **Bioinformatics** Cancer - Research Systems biology Medicine Computational Biology/Bioinformatics Cancer Research Systems Biology Biomedicine, general Lingua di pubblicazione Inglese **Formato** Materiale a stampa Livello bibliografico Monografia Note generali Description based upon print version of record. Nota di bibliografia Includes bibliographical references at the end of each chapters and index. Nota di contenuto Basic cancer biology -- Omic data, information derivable and computational needs -- Cancer classification and molecular signature identification -- Understanding cancer at the genomic level --Elucidation of cancer divers through comparative omic analyses --Hyaluronic acid: A key facilitator of cancer evolution -- Multiple routes

for survival: Understanding how cancer evades apoptosis -- Cancer

responses -- Understanding cancer invasion and metastasis -- Cancer after metastasis: The second transformation -- Searching for cancer biomarkers in human body fluids -- In silico investigation of cancer using publicly available data -- Understanding cancer as an evolving

development in competitive and hostile environments -- Cell proliferation from regulated to deregulated state via epigenomic

complex system: our perspective.

## Sommario/riassunto

This book provides a framework for computational researchers studying the basics of cancer through comparative analyses of omic data. It discusses how key cancer pathways can be analyzed and discovered to derive new insights into the disease and identifies diagnostic and prognostic markers for cancer. Chapters explain the basic cancer biology and how cancer develops, including the many potential survival routes. The examination of gene-expression patterns uncovers commonalities across multiple cancers and specific characteristics of individual cancer types. The authors also treat cancer as an evolving complex system, explore future case studies, and summarize the essential online data sources. Cancer Bioinformatics is designed for practitioners and researchers working in cancer research and bioinformatics. It is also suitable as a secondary textbook for advanced-level students studying computer science, biostatistics or biomedicine.