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	Cancers; 1.18 Conclusion; References 2 Cancer Stem Cells - Finding and Capping the Roots of Cancer2.1 Introduction - Stem Cells and Cancer Stem Cells; 2.1.1 What are Stem Cells?; 2.1.2 Concept of Cancer Stem Cells (CSCs); 2.2 Hematopoietic Stem Cells as a Paradigm; 2.2.1 Leukemia as a Paradigmatic Disease for Cancer Research; 2.2.2 CFUs; 2.2.3 LTC-ICs; 2.2.4 In Vivo Repopulation; 2.2.5 Importance of the Bone Marrow Niche; 2.2.6 Leukemic Stem Cells; 2.2.6.1 Leukemic Stem Cells in the Bone Marrow Niche; 2.2.7 CML as a Paradigmatic Entity; 2.3 Current Technical Approach to the Isolation and Characterization of Cancer Stem Cells 2.3.1 Tools for the Detection of Cancer Stem Cells2.3.2 Phenotype of Cancer Stem Cells; 2.4 Cancer Stem Cells in Solid Tumors; 2.4.1 Breast Cancer; 2.4.2 Prostate Cancer; 2.4.3 Colon Cancer; 2.4.4 Other Cancers; 2.5 Open Questions of the Cancer Stem Cell Hypothesis; 2.6 Clinical Relevance of Cancer Stem Cells; 2.6.1 Diagnostic Relevance of Cancer Stem Cells; 2.6.2 Therapeutic Relevance - New Drugs Directed Against Cancer Stem Cells; 2.7 Outlook; References; 3 Multiple Testing Methods; 3.1 Introduction; 3.1.1 A Brief More Focused Introduction; 3.1.2 Historic Development of the Field 3.2 Statistical Background3.2.1 Tests; 3.2.2 Test Statistics and p-Values; 3.2.3 Resampling Based Testing; 3.3 Type I Error Rates; 3.4 Introduction to Multiple Testing Procedures; 3.4.1 Adjusted p-values; 3.4.2 Categories of Multiple Testing Procedures; 3.4.3 Estimation of the Proportion of False Nulls; 3.5 Multiple Testing Procedures; 3.5.1 Procedures Controlling the FWER; 3.5.2 Procedures Controlling the FDR; 3.5.3 Procedures Controlling the FDX Figure; 3.6 Type I Error Rates Control Under Dependence; 3.6.1 FWER Control; 3.6.2 FDR and FDX Control 3.7 Multiple Testing Procedures Applied to Gene Discovery in DNA Microarray Cancer Studies
Sommario/riassunto	A collection of highly valuable statistical and computational approaches designed for developing powerful methods to analyze large-scale high-throughput data derived from studies of complex diseases. Such diseases include cancer and cardiovascular disease, and constitute the major health challenges in industrialized countries. They are characterized by the systems properties of gene networks and their interrelations, instead of individual genes, whose malfunctioning manifests in pathological phenotypes, thus making the analysis of the resulting large data sets particularly challenging. This is