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Targeted analytic methods for deep sequencing

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Abstract

While genome-wide association studies (GWAS) have been marginally successful at identifing high risk SNPs for cancer, further deep sequencing efforts are needed. This presentation discusses novel analytic approaches for optimizing search strategy and reducing false positive findings. Validation techniques also will be discussed in the context of independent multicentric approaches.

Biography

Jimmy Efird is an Associate Member of the Leo Jenkins Cancer at Brody School of Medicine. Additionally, he holds a joint appointment as Associate Professor in the Department of Public Health and as Epidemiologist/Chief Statistician (Director, Shared Resources) in the Center for Health Disparities. Dr. Efird received his Ph.D. from Stanford University (Epidemiology with a concentration in Biostatistics). His expertise includes statistical methods for assessing gene-environment interaction, clinical trial design, computing power and sample size for correlated samples, and multiplicity adjustment for confidence intervals. He has over 100 publications in scientific journals and technical proceedings. Additionally, Dr. Efird serves as a Senior Consultant for The NCRR-funded RCMI Translational Research Network Data and Technology Coordinating Center.