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*Functional Data Analysis of Copy Number Alterations in Bladder Cancer Tumors.*

Genomic structural changes known as copy number alterations (CNAs) have a role in tumor progression. CNAs are changes in the chromosome where regions are either amplified or deleted. It is thought that bladder cancer subgroups have varying CN profiles that are similar within groups but differ across groups. We analyze array comparative genomic hybridization (aCGH) data from 93 bladder cancer patients whose profiles are in muscle invasive and non-muscle invasive subgroups. We are treating these CN profiles as functions across the entire chromosome, and using functional data analysis tools for inference. We use Bayesian, wavelet-based, functional response regression to characterize the CN profiles of muscle invasive and non-muscle invasive patients. We develop simulated aCGH profiles in order to test these methods. We find that our wavelet bases method using a fixed effects model for functional regression confirms the results of prior research about CN amplifications at 1q23.3, 1q21.2, and 11q13.2. Further, we find on chromosome 11 of our dataset that RRM1, RIN1, FG19, and ANO1, genes which are known to be associated with bladder cancer, are altered due to the effects of muscle invasiveness within a tumor. (Received September 06, 2016)