



## Detection of Genomic Signals by Resequencing

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Several problems of genomic analysis involve detection of local genomic signals. For data generated by paired end reads, the variability of read depth at different positions on the genome suggests models involving non-homogeneous Poisson processes, perhaps modified to account for excess variability. We discuss a number of general models and consider in detail a model for detection of insertions and deletions on a genome wide scale. Statistics are suggested that use (i) variations in insert length, (ii) hanging reads, or (iii) read depth. Genome wide significance thresholds are determined. The marginal power is computed and used to determine and compare the usefulness of the different statistics under various conditions.

**Keywords:** paired ends; indels; Poisson; genomewide