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J Biom Biostat 2016, 7:4(Suppl)
http://dx.doi.org/10.4172/2155-6180.C1.003

5th International Conference on
Biometrics & Biostatistics
October 20-21, 2016 Houston, USA

On modeling of lifetime data using one parameter continuous distributions

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The time to the occurrence of event of interest is known as lifetime or survival time or failure time in reliability analysis. The event may be failure of a piece of equipment, death of a person, development (or remission) of symptoms of disease, health code violation (or compliance). The modeling and statistical analysis of lifetime data are crucial for statisticians and research workers in almost all applied sciences including biomedical sciences, engineering, insurance and finance, amongst others. Two important one parameter lifetime distributions that have been popular in Statistics literature for modeling lifetime data are exponential and Lindley distributions. Shanker *et al.* (2015) has done extensive study on these two distributions for modeling lifetime data from medical sciences and engineering and observed that there are many cases where these two distributions are not suitable from theoretical and applied point of view. Recently the author (2015, 2016) has introduced four one parameter lifetime distributions namely Akash, Aradhana, Shanker, and Sujatha to model lifetime data. In this paper, the comparative study of Akash, Aradhana, Shanker, Sujatha, Lindley and exponential distributions have been made to model lifetime data. The relationships of these distributions, their distributional properties and estimation of parameter have been discussed. The theoretical justifications and applications of these distributions for modeling lifetime data have been discussed and explained through several examples from biomedical science and engineering.

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Monovar: Single-nucleotide variant detection in single cells

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Sequence data produced by recently developed single-cell sequencing (SCS) technologies have the power to resolve cancer genome at a single-cell level and can characterize the genomic alterations that might differ from one cell to another. Unresolved issues in cancer research pertaining to the admixture signal reflected by bulk-tissue sequencing data produced by the next-generation sequencing (NGS) methods can be potentially addressed through the proper analysis of single-cell sequencing data. The inherent errors associated with SCS data such as amplification errors and non-uniform coverage make the bioinformatics analysis of such data challenging. The existing SNV calling methods developed for NGS data tend to produce large number of false-positive calls when applied on SCS data. Here, we present Monovar, a novel statistical method for discovering and genotyping SNVs from SCS data. Monovar accounts for the various native errors present in the SCS data to distinguish between true variants and sequencing artifacts. The proposed multi-sample SNV calling method leverages data from multiple single cells to combat against non-uniform coverage distribution across single cells. The underlying probabilistic model for SNV calling accounts for allelic drop-out, deamination and other amplification errors associated with the SCS data. A candidate site is called as a SNV based on the posterior probability of the site being a SNV, calculated using Bayes' rule along with population genetic prior. The genotyping method also leverages data from other single cells to quantify the posterior probability of genotype calculated via a dynamic programming algorithm. We validated the sensitivity and specificity of Monovar using data from normal female fibroblast skin cells, for which, it achieved better performance compared to GATK and samtools, two state-of-the-art SNV calling methods for NGS data. We also applied Monovar on SCS data from triple-negative breast cancer cells. For two different cell lines of this dataset, Monovar dramatically outperformed GATK in terms of precision without affecting the detection efficiency. Finally, Monovar performed better than GATK on three public datasets as well proving it to be a versatile method applicable to SCS data generated using different technologies. A manuscript describing Monovar is currently in press at *Nature Methods*.

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