

Abstract Submitted
for the TSF17 Meeting of
The American Physical Society

Maximum Entropy Methods in Survival Analysis JOSCELYNE GUZMAN, SOROUR HOSSEINI, MARIAN MANCIU, Physics Department, University of Texas at El Paso — The fundamental problem of the traditional Biostatistics is to calculate the probability that an experimental result is due entirely to chance (the null hypothesis). When that probability is sufficiently low (typically, below 5 %) it can be assumed that an underlying "effect" might explain the results (the alternate hypothesis), but in general the "effect" is not quantitatively determined. For example, in Survival Analysis there are a number of algorithms that can determine whether two groups have statistically significant different survivals (time-to-event distributions). However, the difference between the median survival times of the groups, which is typically reported, is not always a good estimator of the quantitative survival differences between groups. Even more important, when the populations of the groups are very small, there is almost impossible to obtain statistically significant differences between them, regardless of how strong the underlying "effect" might be. We suggest an alternative approach, in which we calculate the most likely "effect" that explains the given experimental outcome, namely the "effect" that maximizes the entropy of the result. It will be shown (via Monte-Carlo simulations) not only that such an estimator is in a very good agreement with the average survival time difference between the two groups, but also that it remains reasonably accurate even at low sample numbers, for which traditional Biostatistical methods suggest that the null hypothesis cannot be rejected.

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Date submitted: 17 Sep 2017

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