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INJURY BIOMECHANICS RESEARCH
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Estimation of Injury Risk for Biomechanical Impact Data

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ABSTRACT

The aim of this study was to compare parametric and non-parametric methods for determining injury risk curves from biomechanical data obtained from impact experiments on human surrogates. Many of the problems and pitfalls of obtaining realistic human risk curves from impact test data are covered. Methods are given for determining risk curves from both doubly censored data and data obtained from impacts to body regions in which there are more than one mechanism of injury. A detailed set of examples is presented in which different experimental data are analyzed using the Consistent Threshold method and the logistic approach. Finally risk curves for published data are presented for the head, neck, femur, and thorax.

INTRODUCTION

One important area of research for engineers seeking to understand the impact response of the human body is the determination of the risk of injury of a body region for a given stimulus input. Toward this end, experiments have been performed in which human surrogates are subjected to impacts. These experiments include sled tests, pendulum impact tests, drop tests, or any set of tests in which a human surrogate is subjected to an impact stimulus in the range where injury can be initiated. In general, it is assumed that there is some level of stimulus below which no injury occurs (minimum value) and there is some level above which all subjects are injured (maximum value). Therefore, to estimate the minimum value for the initiation of injury and the risk throughout its entire range of severity, impact experiments should be defined to encompass a range of impact severities that includes these extreme values. The question then becomes: What techniques or analytical procedures can be used to extract a risk curve from the biomechanical impact tests that have been run?

Biomechanical impact experiments are invariably contaminated with potential inaccuracies such as modeling specification errors, random noise, oversimplifications, and lack of access to the complete physical phenomenon. One area of concern is the censoring aspect of data. Often,

biomechanical impact data are censored, that is, the minimum level of stimulus needed to cause the specimen to fail, its threshold, has not been determined by the test. In particular, if the level of stimulus used by the experimenter to run the test does not produce failure of the specimen, then the observation is considered *right censored* since the failure threshold stimulus value is above the stimulus value used by the experimenter. If the level of stimulus induces an injury, then the failure threshold stimulus value is at or below the level of the stimulus used by the experimenter and the observation is *left censored*. Thus, data obtained from impact experiments will in general be *doubly censored* , i.e., both *left* and *right censored*.

A common approach to estimate a distribution from censored data is to assume a form for the injury risk distribution. The parameters that control the final shape of the assumed distribution are fit using some kind of optimization technique such as maximum likelihood or least squares. Examples of injury risk distributions using the parametric approach are: Weibull, Normal and Log-normal distributions (Hertz, 1993, Kent et al., 2001, Mertz et al., 1997, Ran et al., 1984).

Logistic regression (Hosmer et al., 1989) is one of the most widely accepted parametric procedures for developing injury risk curves using experimental biomechanical data. Logistic regression, which has been used to develop various injury criteria models (Eppinger et al., 1999), gives evidence of the advantages of using parametric approaches: well-defined procedures and methods of data manipulation, error analysis, and goodness of fit determination. However, many of the advantages and desired properties of parametric approaches are lost if the form of the risk distribution is not appropriate.

Human impact injury causation is complex. In general, for each body region there is more than one mechanism of impact injury and more than one aspect or anatomical structure that can be injured. For example, consider the chest. There is more than one way to injure the heart and there is more than one anatomical structure in the chest, such as ribs and lungs. Each of the different injury mechanisms associated with each of the anatomical structures could have a different form of its own unique risk curve; one risk curve could be Normal and another could be Log-normal. The resulting combination could be bimodal so that it can be represented by neither the Normal nor the Log-normal model. Therefore, unless a process has been employed to demonstrate a given form for the distribution, it is reasonable to assume that the risk distribution for the biomechanical impact data is unknown and there is no biological basis to justify the assumptions of the parametric approach.

We will show that the most reliable approach to estimate the injury risk function when the distribution is not known is a non-parametric method appropriate for censored data: the Consistent Threshold (CT) method (Kaplan et. al., 1958, Nusholtz et al., 1999, Turnbull, 1974). This paper will illustrate how to implement the CT method for estimating the risk function of *doubly censored* biomechanical data. Finally, we will present the CT risk function estimate on thoracic injury data (Kuppa et al., 1998), on lower extremity injury data (Kuppa, 2001, Morgan, 1990), on neck injury data (Mertz et al., 1982, Prasad et al., 1984), and on head injury data (Eppinger et al., 1999).

NOTATION AND TERMINOLOGY

Notations and symbols introduced in this section will be consistently used throughout the paper. *Right censored* observations can be called losses; since right censored observations are lost to the experimenter before the significant threshold is determined. All the *left censored* injury observations represent death or seriously injured observations, so for this reason they are also called “deaths”. A data set that includes both *Right censored* and *left censored* observations is called *doubly censored*.

The following notation will be used:

- T: a random variable denoting the loading stimulus threshold value (e.g., Axial Femur Force, Thoracic Peak Acceleration, HIC value, etc.)
- $t_1, t_2, ..., t_n$: a sequence of loading stimulus threshold values used by the experimenter.
- $d_1, d_2, ..., d_n$: the number of deaths (serious injuries) at each loading stimulus value. There were d_k deaths (serious injuries) at loading stimulus value t_k.
- $l_1, l_2, ..., l_n$: the number of losses at each loading stimulus value. There were l_k losses at loading stimulus value t_k.
- $R(t) = Prob\{T \le t\}$ is the cumulative injury probability (risk function) at the loading stimulus value $T=t$.
- $\tilde{R}_k$ is the CT Risk function estimate at t_k.

A function R is monotonically increasing if for every x and y such that $x < y$ then $R(x) \le R(y)$.

CONSISTENT THRESHOLD METHOD

The CT method is a non-parametric maximum likelihood method that provides an estimate of the distribution function of *doubly censored* data. The maximum likelihood property makes it an appealing method among all the other non-parametric methods used to handle doubly censored data. In its general form the CT method can be used to handle data sets that include *doubly censored*, *right censored*, *left censored*, and accurate observations. An accurate observation is an injury datum for which it is known at which stimulus value the injury occurred. A proof of the CT method, in the more general form, is presented in (Kaplan et. al., 1958). A simplified version of the CT method in which all the data are *doubly censored* is presented in (Turnbull, 1974, Nusholtz et al., 1999).

Biomechanical impact response injury data are almost always doubly censored with no accurate observations. Thus, to estimate the injury risk curve the simplified version of the CT method can be used. In what follows, is a simple algorithm to compute the CT estimate of the risk function for *doubly censored* data:

- [Step 1] Compute $R'_k = d_k / (l_k + d_k)$ for k=1,..., n, that is, compute R'_k at every stimulus value used. If only one test has been run at each stimulus value (the most common condition for biomechanical data), then R' resolves in a sequence of ones (where an injury occurred) and zeroes (where no injury occurred).
- [Step 2] If $R'_1 \le R'_2 \le ... \le R'_n$ then the CT has been found and $R'_k = \tilde{R}_k$ for k=1,...,n.
- [Step 3] If $R'_1 \le R'_2 \le ... \le R'_n$ does not hold then for the first k for which $R'_k > R'_{k+1}$ replace l_k with $l_k + l_{k+1}$ and replace d_k with $d_k + d_{k+1}$. Re-compute R'_k and remove R'_{k+1}. Renumber. There will now be n-1 of the R'_k.
- [Step 4] Repeat until an ordered set, the CT, has been found.

From the algorithm above, it follows that the CT estimate is a monotonically increasing function of stimulus: it represents a count of the number of deaths divided by the number of observations, deaths and losses, for a given stimulus value (used by the experimenter). The CT method of calculating the $\tilde{R}_1, ... \tilde{R}_n$ depends on a grouping of observations which might very well appear to an investigator on purely intuitive grounds, however it yields the maximum likelihood estimates of the

risk injury probabilities for the stimulus values considered. It is interesting to emphasize that the CT estimated risk sequence $\tilde{R}_1,...\tilde{R}_n$ is the **unique** maximum likelihood estimate of the considered risk probabilities (Ayer et al., 1955). This implies that any other estimated risk sequence will assign to the actual data a smaller probability of being observed.

The following simple example will illustrate how to implement the CT method.
Example 1: Assume that a surrogate is subjected to a pendulum impact to an hypothetical anatomical structure: the "funny bone". In some of the impacts the funny bone breaks at a given stimulus. In some of the impacts the funny bone does not break. The data used for this example are reported in Table 1. More precisely, in the first column of Table 1 are reported the stimulus values used by the experimenter in the hypothetical test while in the second and third column are reported the total numbers of lost observations (l) and funny bone fractures (d) for each stimulus value used. Following the CT algorithm, described above, at the first stage the estimated risk function is given by:

$$R'_{300}=0;R'_{500}=1;R'_{600}=0;...;R'_{2000}=1; \qquad (1)$$

Thus, at the first stage, R' is increasing only up to t=500. This implies that l_{500} should be replaced with $l_{500}+l_{600}$ and d_{500} should be replaced with $d_{500}+d_{600}$ (Step 3, CT algorithm); Then R'_{500} is re-computed (R'_{500}=0.5) and R'_{600} is removed (stage 2, Table 1).

Table 1. CT Estimated Risk Function For The Data Described In Example 1.

T	l	d	Stage 1	Stage 2	Stage 3	Stage 4	Stage 5	$\tilde{R}$
300	1	0	0	0	0	0	0	0
500	0	1	1	0.5	0.5	0.5	0.5	0.5
600	1	0	0	-	-	-	-	-
700	0	1	1	1	0.5	0.5	0.5	0.5
800	1	0	0	0	-	-	-	-
900	0	1	1	1	1	1	0.67	0.67
1100	0	1	1	1	1	0.5	-	-
1300	1	0	0	0	0	-	-	-
1400	0	1	1	1	1	1	1	1
2000	0	1	1	1	1	1	1	1

The "-" sign is entered for each R' removed. "T" labels the column of threshold stimulus values, "l" the column of lost observations, "d" the column of bone fracture observations. $\tilde{R}$ is the CT estimated risk function.

At this stage the estimated risk function is:

$$R'_{300}=0;R'_{500}=0.5;R'_{700}=1;...;R'_{2000}=1; \qquad (2)$$

Thus, it is increasing only up to t=700. This implies that we have to repeat for t=700 and t=800 the same steps performed for t=500 and t=600 (stage 3, Table 1).
This procedure should be repeated for all the other stimulus values (stage 4-5, Table 1) until a **monotonically increasing** risk function has been found (last column, Table 1). The CT estimated risk function for the funny bone (Example 1) is plotted in Fig. 1.

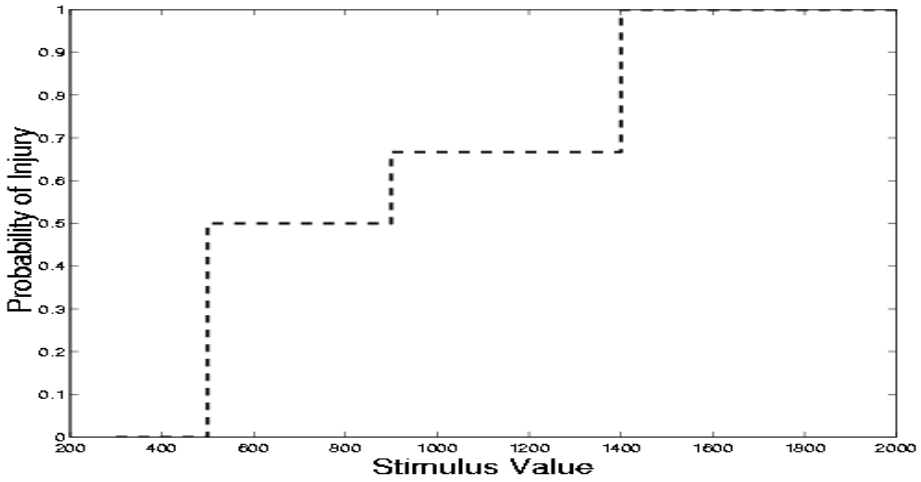

Figure 1: CT estimated risk curve for the data described in Example 1.

BIOMECHANICAL IMPACT DATA

Almost all biological systems are complex and injuries can result from multiple injury mechanisms and modes. Often these mechanisms will occur in combination with each other, so that the injury risk for the system can not be evaluated for each mechanism independently from the others. Injury criteria have been proposed for specific body regions, e.g., head, neck, thorax, and lower extremities. Each of these body regions includes anatomical structures with very different mechanical responses and risk functions under impact conditions.

For example, the thorax (the upper part of the torso, extending from the base of the neck to the bottom of the 12-th rib) contains the following anatomical structures: the heart, the lungs, the bronchi, the trachea, the great vessels, the nerves, and the esophagus which are surrounded and protected by the bony rib cage. Thoracic injuries may be subdivided into three categories: rib cage fractures, lung injuries like a pneumo- or hemothorax, and injuries of the other thoracic segments like rupture of the thoracic aorta, which is frequently a fatal injury.

It should be expected that these three injury categories will have very different injury risk functions since they have very different structures and injury mechanisms.
Thus, if the same parametric risk function model is appropriate for all three thoracic injury categories, their characteristic parameters (e.g., for a normal distribution the mean and the variance) must be different.

For example, suppose that we are interested in a pendulum impact to an unpressurized cadaver chest and that we are interested in the injuries to the rib cage and the heart. This is a hypothetical example and the values used will not represent the actual human biomechanics values. In this hypothetical example the ribs start breaking at a low stimulus for osteoporosis individuals but they do not break for young individuals until a large stimulus/deflection occurs. However, in this testing configuration, the heart is not injured until it is pressed against the spinal cord for both old and young individuals. Once this happens, the heart is almost always injured at or near the stimulus/deflection required to push the heart against the spine. The risk of injury for an example similar to that described above is given by the resulting risk which represents the risk for the two hypothetical anatomical structures in the body region of interest. Thus, even if a normal risk function is appropriate for each of the possible injury categories of the body region of interest, the resulting risk function, associated to the whole body region, e.g. chest, could be not normal (since each injury category, e.g. rib cage and heart, has a different normal risk function).

In particular, the resulting injury risk function could present drastic changes in slope so that it could resemble a step function in some part of the stimulus interval used. To illustrate this point the following hypothetical numerical example (Example 2) was created.

Example 2: The idea of this example is to show that the risk function of a biological system with different anatomical structures and with multiple mechanisms of injury could present a non-Normal risk function even if all its possible categories of injuries have Normal risk functions. For illustrative purpose it is assumed that the biological system in the example presents only two possible mechanisms of injury both having a Normal risk function, which are denoted by R_1 and R_2 (Figure 2). To simplify the explanation and the probability formulation it is also assumed that the two mechanisms of injury are independent of each other. The overall risk function is plotted in Figure 2.

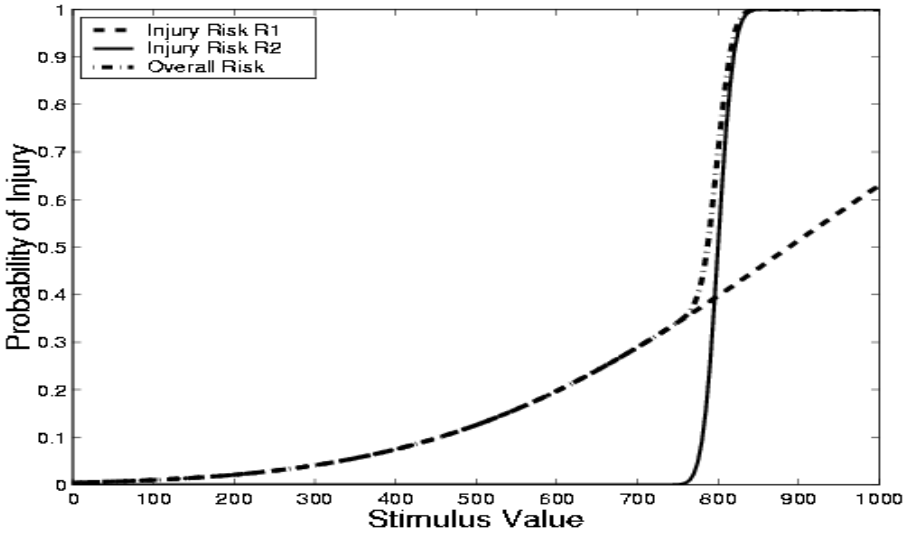

Figure 2: Risk functions for the two types of injuries considered in Example 2.

From the plot, it is evident that the risk function for the whole biological system will follow the first risk function for stimulus values lower than 800 units and the second risk function for higher stimulus values. Thus the overall risk function presents a drastic change in its slope value around 800 units. A good approximation for it is given by the overall function plotted in Figure 3.

Example 2 shows that the risk of injury of a biological system could have a shape that does not resemble the form of generally used distribution functions (normal, log-normal, weibull, sigmoidal, etc.). Therefore, unless the form of the distribution has been proven, it is not appropriate to assume it. A non-parametric approach, that is a statistical approach free of any constraint about the distribution form, provides valuable information about the risk function shape. Moreover, there does not seem to exist any theoretical or biological basis to justify the use of a continuous risk function for biomechanical impact data. In general, no prior information is available about the form and the properties of the underlying distribution of censored injury data.

Another important and well known aspect of many biomechanical impact data sets is their censored nature (Mertz et al., 1996). Censored data are data that are biased in one direction or another. The sign of the bias is known but not the magnitude. This complicates the application of conventional techniques since these methods assume data to be free from bias.

The above mentioned aspects of biomechanical data would suggest that an appropriate method for estimating the risk function should be a non-parametric method suitable for censored data. The CT method provides a non-parametric maximum likelihood estimate of the risk function specific for censored data.

A Monte Carlo simulation representing a hypothetical impact test was performed to evaluate the CT performance in estimating the overall risk function for the data presented in Example 2. In particular, 45 samples (pseudo-random numbers) of possible injury threshold values were generated from the overall Risk function (see Figigure 3). To be precise, the overall risk function is defined to be normal, with mean 888 and standard deviation 338, for stimulus values below 800 units and it has a point mass of probability 0.6 at the stimulus value of 800 units (see Figure 3).

For each injury threshold sampled from the overall risk function a second random variable, representing the test stimulus (used by the experimenter), was generated. The test stimulus was chosen to be uniformly distributed over the interval from 100 to 950 unit stimulus value.

If the sampled threshold value was below the sampled test value the observation was considered an injury, otherwise a no-injury. For this simulation a relative small sample size was used (45 samples) to resemble the limited size of available biomechanical injury data.

In Figure 3 are plotted the overall Risk function and its CT estimate. It is worthwhile to notice how well the CT method captures the smooth increase of the risk function on the interval from 100 to 800, while also estimating the size of the discontinuous/rapidly-increasing part.

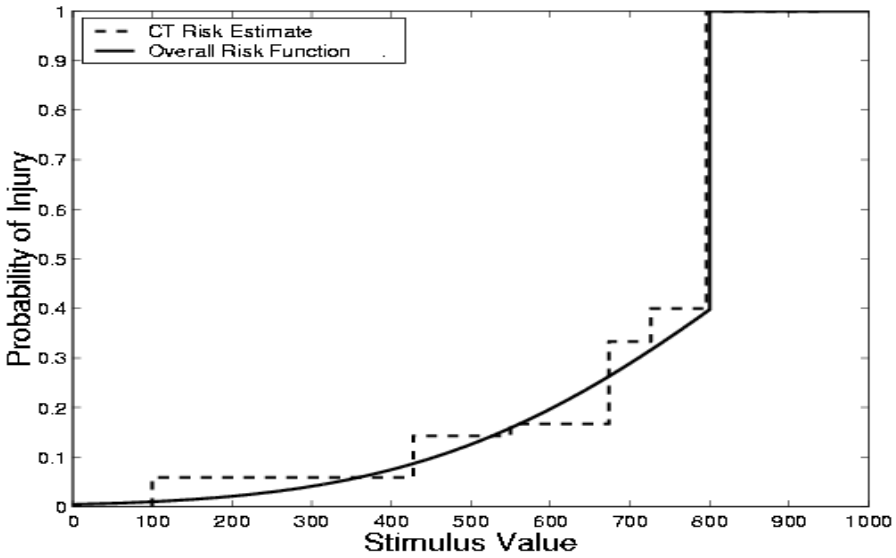

Figure 3: CT estimated risk curve for the data presented in Example 2.

INJURY CRITERIA AND PROBABILITY OF INJURY

Finding an appropriate model to analyze the risk function of each body region of interest is a very challenging task. As stated in the previous section, the complexity of a biological system and the possibility to have multiple injury mechanisms, imply that the underlying risk function of a biological system could present drastic changes in its risk function slope and even discontinuities. If the injury risk function is not continuous, then a parametric method like Weibull, Logistic, or Normal could have a very poor performance in estimating the risk at the extremes of the data. In other words, the estimated risk could be unreliably high (or low) at the extreme stimulus values. An

example can be given by the logistic regression estimate of serious-to-fatal thoracic injury risk reported in (Eppinger et al., 1999) from which Fig.4 is taken. This risk curve shows 20% risk of serious-to-fatal injury at zero thoracic-spine-acceleration (Figure 4). All the details about the data can be found in (Kuppa et al., 1998), a brief summary is reported in the next section.

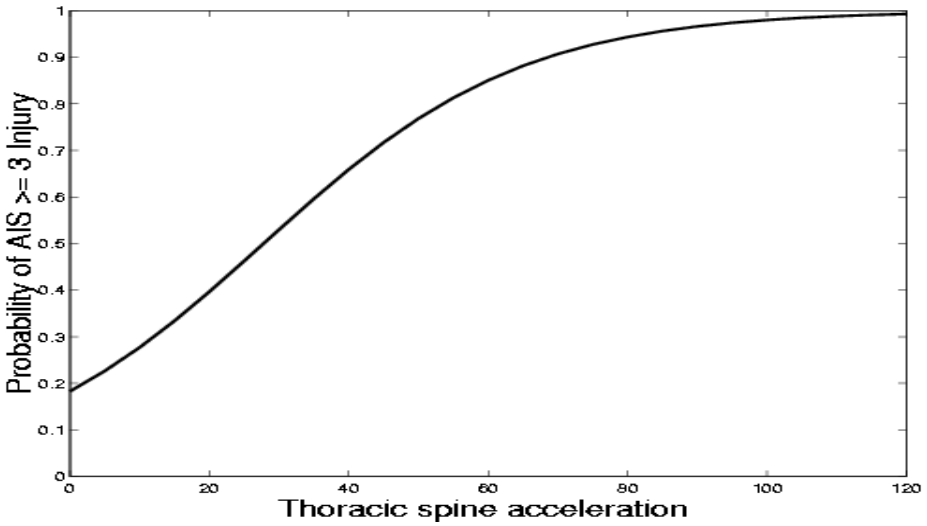

Figure 4: Logistic regression estimate for the probability of serious-to-fatal injury (*AIS*≥3) using thoracic spine acceleration (first thoracic vertebra acceleration) as risk factor. This figure has been taken from (Eppinger et al., 1999).

Logistic regression is a widely used parametric method to analyze biomechanical human surrogate injury data (Eppinger et al., 1999). Usually it is chosen because it is a maximum likelihood method and it provides established statistical measures to evaluate absolute and relative predictive capabilities of the resulting relationships (Hosmer et al., 1989). Moreover, this procedure is easily available in many statistical software packages.

Another important benefit of the logistic regression analysis is the possibility of including confounder factors in the injury prediction model. On the other hand, to include confounders in the CT method is not straightforward; It requires a pre-analysis of the data to reduce the study to univariate one (Nusholtz et al., to appear). However, as for any parametric model many of the advantages are lost when the assumed form of the distribution is not appropriate. In particular, when the assumption of a monotonic sigmoidal relationship between the probability of a serious injury (or fatality) and the stimulus values used by the experimenter (required by the logistic model), is not appropriate, the estimated risk function can be a questionable estimate even if all statistical tests indicate accepting the model as reasonable. "The formal chi-square goodness of fit test can detect major departures from a logistic response function, but it is not sensitive to small departures from a logistic response function" (Neter et al., 1998), this could make the model questionable at the extreme values. Moreover, for the development of injury criteria there is, generally, more concern on the goodness of the model at the lower values than on the overall performance of the model.

To emphasize the potential short-coming that can result from using an inappropriate parametric model, the logistic model has been implemented on the data used in Example 2 (Figure 5).

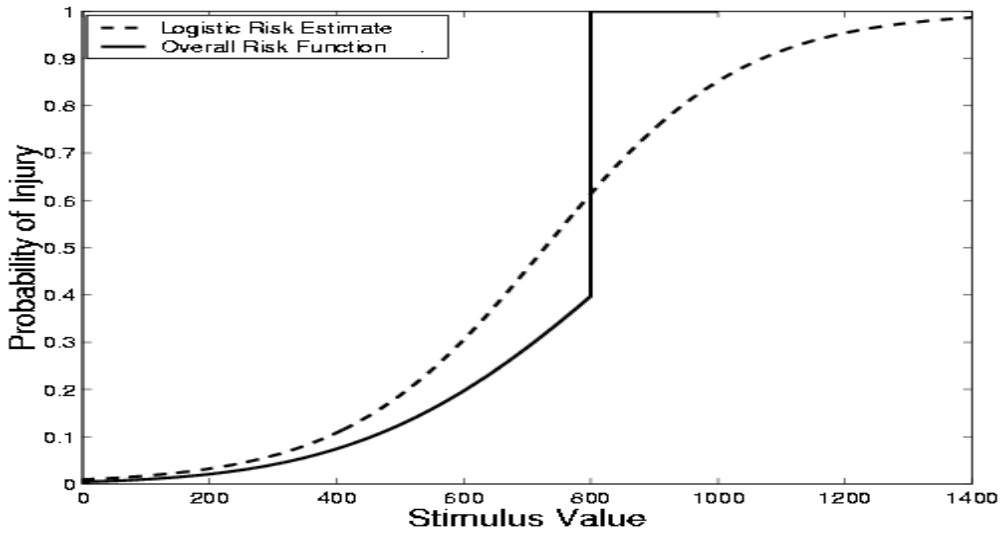

Figure 5: Logistic regression estimated risk curve for the data presented in Example 2.

All the details for the logistic model are reported in Table 2. All the statistics reported in Table 2 indicate good predictability for the model. But, the model consistently over-estimates the risk at lower stimulus values and under-estimates the risk at higher stimulus values.

Table 2. Details of The Logistic Regression Model for Example 2 Data**.** S is for Stimulus.

Logit = -4.68 + 0.006 S					
-2Log(LR)	14.97	**discord**	16.3%	**Gamma**	0.673
p-value	0.0001	**concord**	83.7%	**c**	0.837

Other parametric models used to estimate censored impact data are: Normal, Log-normal (Hertz, 1993), and two-parameter Weibull (Ran et al., 1984, Hertz, 1993). These parametric models will have the same limitations as the logistic regression model if the underlying distribution function does not have the form assumed by the model. In conclusion, the lack of prior information about the form of the underlying risk function distribution and the possible presence of discontinuities should encourage the use of non-parametric statistical models appropriate for censored data to estimate the injury risk function. Non-parametric analyses have the important task of suggesting or confirming properties of the underlying risk function (see next section) and of supplying the estimate itself in case suitable parametric assumptions are not known.

In addition to the CT method, other non-parametric methods which are considered in the literature to estimate biomechanical impact data include: Median Rank, Modified Median Rank (Mertz et al., 1982) and Certainty Grouping method (Mertz et al., 1996).

Median Rank method is not appropriate for censored data. For this reason Mertz and Weber (Mertz et al., 1982) proposed a modified version of the Median Rank approach. The major limitation of the Modified Median Rank approach is that "the accuracy of the method is dependent on having knowledge of the form of the cumulative distribution function" (Mertz et al., 1996). Thus, with the Modified Median Rank approach we are back to the problem of needing to know the form of the underlying distribution.

The Certainty Grouping method is a partition scheme which is used to divide the test sequence into two groups for each considered level of stimulus: the certainty group and the

uncertainty group. The certainty group is the set of all the specimens for which it is known with certainty whether or not the specimen has failed or not at the considered level of stimulus. All the other specimens are considered uncertain (for the considered stimulus level) and they are not included in the estimation of the risk for the considered stimulus level. Thus, the information contained in the items that are considered uncertain are not used in the estimation. In particular, at the lower stimulus values, the majority of the uncertain data are deaths and at the upper end, the majority of the uncertain data are losses. This implies that the risk estimates are too low at the lower stimulus values and too high at the higher stimulus values. This limitation makes the use of the Certainty Grouping method questionable for the development of a reliable injury criterion; An approach that will give too low an estimate of risk in the lower stimulus range will suggest too liberal injury criteria.

The best approach to estimate the risk of injury for biomechanical impact data would be a maximum likelihood and non-parametric method that considers the censoring aspect of the data: the CT method.

CONSISTENT THRESHOLD ESTIMATE OF INJURY RISK CURVES

In this section, the CT risk curve estimate for the following biomechanical impact data will be presented: head injury data (Mertz et al., 1996), neck injury data (Mertz et al., 1982, Prasad et al., 1984), thoracic injury data (Kuppa et al., 1998), and lower extremity injury data (Morgan, 1990). It is not our intention to go into biomechanical details or judgments on the sampled specimens behind the data. The method for estimating probability of injury is to assign each human surrogate that showed no sign of injury a zero, otherwise a one.

Head Injury Risk Analysis

In 1985, Prasad and Mertz (Mertz et al., 1985) presented and analyzed the available biomechanical data for frontal bone impacts to the heads of Post Mortem Human Surrogates (PMHS) where values for the head injury criterion (HIC) were given. These data have been used for the CT and Log-normal method estimate presented in Fig. 6. The Log-normal risk curve estimate presented in Fig. 6 has been performed by Hertz (Hertz, 1993) and is reported in (Eppinger et al., 1999).

In 1996, the Prasad and Mertz data were expanded by Mertz, Prasad and Nusholtz by including non-fracture HIC values for a number of cadavers which had skull fractures at higher impact severities and by including the cadaver test results of Ono and Tarriere reported in (Mertz et al., 1996). This expanded data set (Mertz et al., 1996) was used for the CT estimate HIC risk function presented in Fig. 7. No attempt has been made to filter the data.

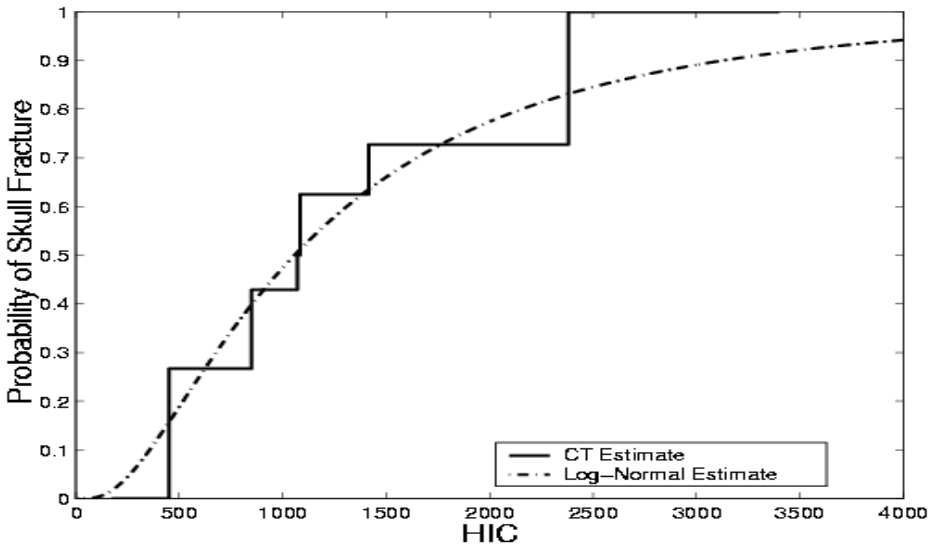

Figure 6: CT and Log-normal estimate (Hertz, 1993, Eppinger et al., 1999) for the probability of skull fracture using the data set presented by Prasad and Mertz (Mertz et al., 1985).

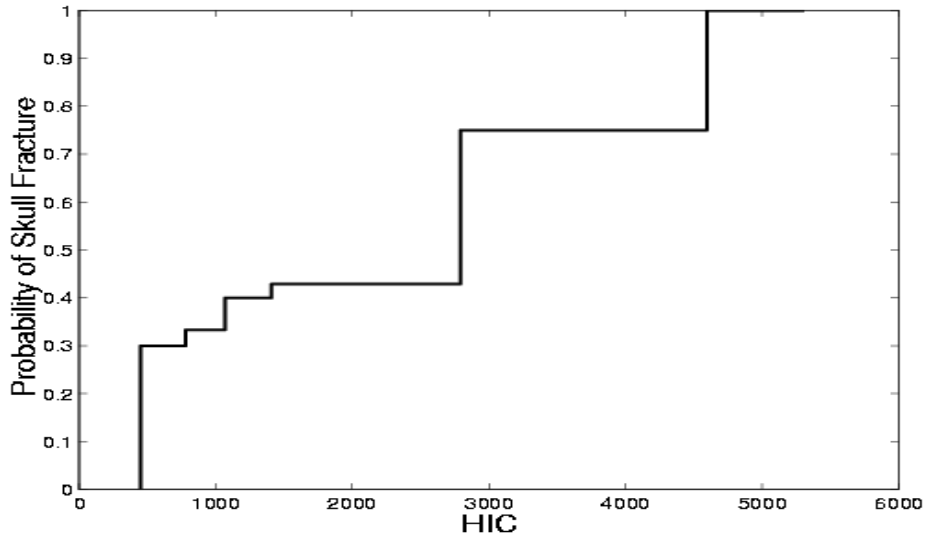

Figure 7: CT estimate for the probability of skull fracture using the expanded data set presented in (Mertz et al., 1996).

Neck Injury Risk Analysis

The biomechanical test database for establishing regulatory airbag neck loading (NHTSA, 2000) consists primarily of a series of tests conducted to study airbag interactions with the out-of-position three-year-old occupant by Mertz et al. (Mertz et al., 1982) and Prasad and Daniel (Prasad et al., 1984). They reported sets of matched tests conducted on piglets and an Anthropomorphic Test Device (ATD or dummy) representing a three-year-old child.

The piglets were chosen to represent the size, weight, and state of tissue development of a three-year-old child. Details of the experimental procedures, testing, and results can be found in (Mertz et al., 1982) and (Prasad et al., 1984). These results are used to estimate neck injury criteria for the three-year-old and then scaled to determine neck injury criteria for the other size occupants

(Mertz et al., 1997). Analyses of these data suggest that peak tension is the best predictor of out-of-position neck injuries (Nusholtz et al., to appear). For this reason the risk of serious-to-fatal neck injury (AIS ≥3) is presented as function of peak tension alone in Figure 8.

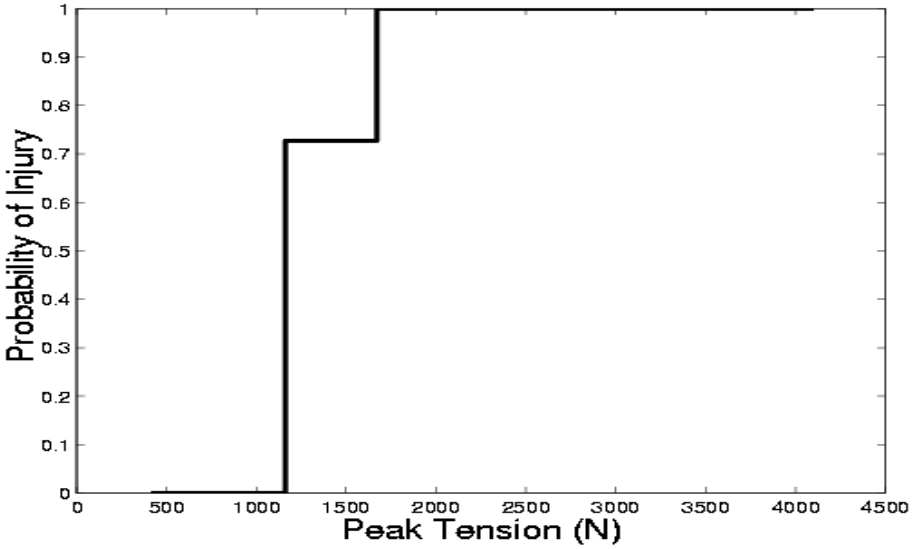

Figure 8: CT estimate for the probability of serious-to-fatal neck injury.

Thoracic Injury Risk Analysis

Currently recommended thoracic performance criteria and tolerance limits are based on results from the analysis of a series of seventy-one PMHS frontal impact tests. Details of the experimental procedures and testing results can be found in (Kuppa et al., 1998). These tests have been used to evaluate the thoracic risk curves presented in Figure 9 and Figure 10. Precisely, in Figure 9 is presented the CT estimated relationship between the thoracic spine acceleration (first thoracic vertebra acceleration) and the risk of serious-to-fatal thoracic injury (AIS ≥3). In the same figure is also plotted the logistic regression estimated risk function presented in (Eppinger et al., 1999).

In Figure 10 are plotted the CT estimated risk curve of serious-to-fatal thoracic injury as a function of maximum normalized deflection and the logistic regression estimated risk function presented in (Eppinger et al., 1999).

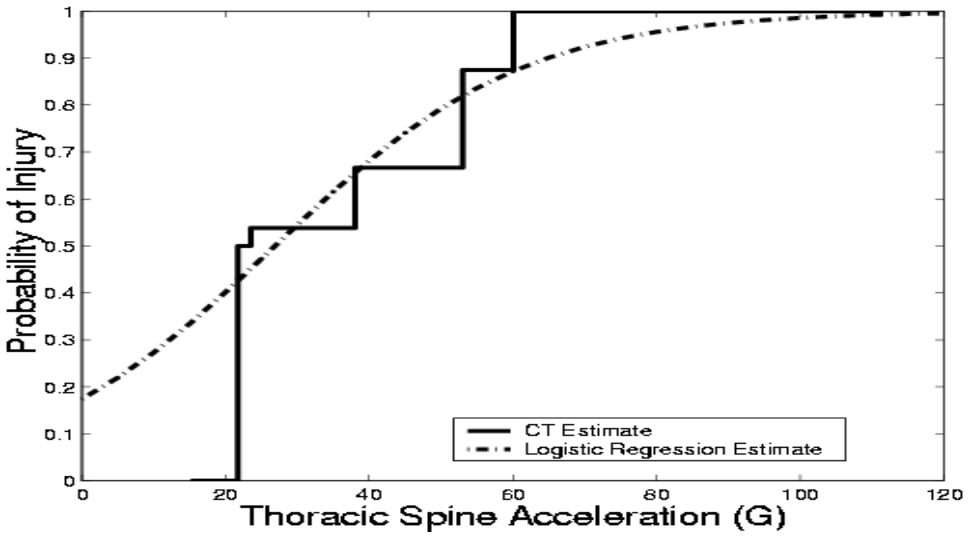

Figure 9: CT and logistic regression estimate for the probability of serious-to-fatal thoracic injury.

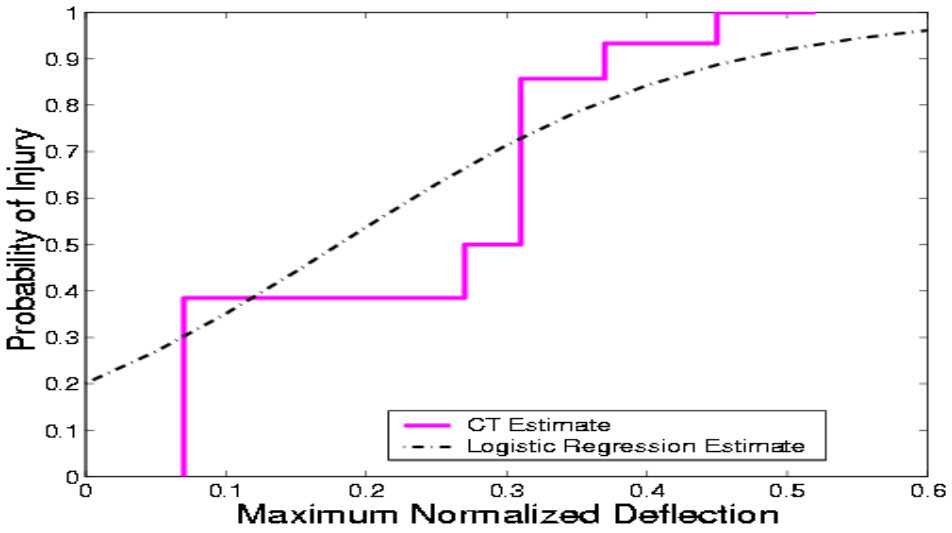

Figure 10: CT and logistic regression estimate for the probability of serious-to-fatal thoracic injury.

Lower Extremity Risk Analysis

Figure 11 shows the CT estimated probability of sustaining an AIS ≥2 femur injury. The CT estimate is based on the data published by Morgan et al. (Morgan, 1990).

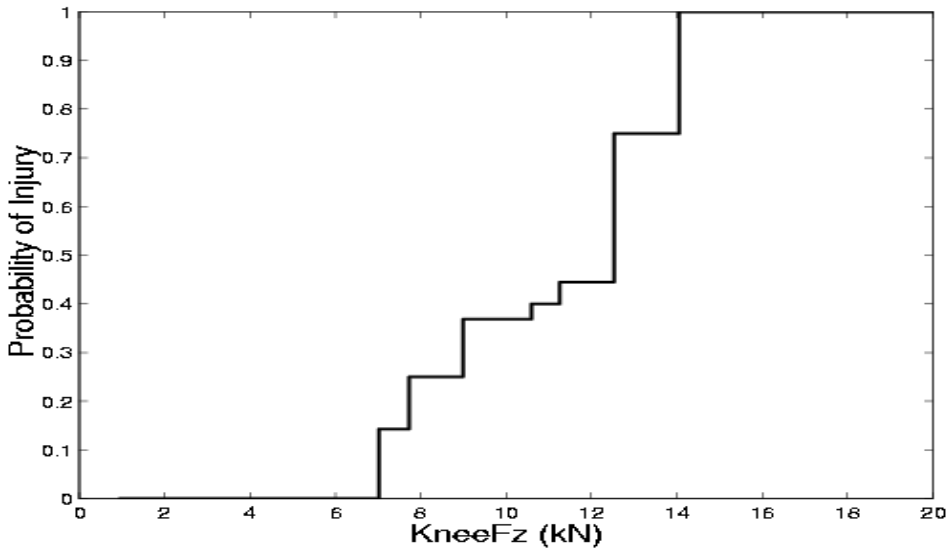

Figure 11: CT estimate for the probability of AIS ≥2 femur injury.

CONCLUSIONS

Biomechanical injury data is conditioned on the way the system is loaded and how the experiment is performed. The complexity of a biological system and the presence of multiple different injury modes and mechanisms make possible the presence of discontinuities/ drastic slope changes in the risk function. In addition, biomechanical impact data is almost always censored and there is no basis that suggests an underlying distribution: all these characteristics should encourage the use of non-parametric models specific for censored data. A non-parametric estimate (appropriate for censored data and with the maximum likelihood property) has the flexibility to be closer than the parametric estimate to the actual distribution at the extreme values of the stimulus, since it is not constrained by a prior specified risk form.

In addition, a non-parametric analysis also can be performed to suggest or confirm properties of the underlying distribution; A non-parametric analysis may help to choose or to support a specific parametric model and it can supply the estimate itself in case suitable parametric assumptions are not known.

Among all the non-parametric methods for censored impact data, the only one that has the appealing statistical property of being a maximum likelihood estimate is the CT method.

APPENDIX

Basic CT Method

Let $S(t)$ be the survival function at $T=t$, that is $S(t)=Prob\{T>t\}=1-R(t)$. Let $S_1, S_2, ..., S_n$ denote the probability of survival at the loading stimulus threshold values $t_1, t_2, ..., t_n$. Then the a priori probability of the specified outcome satisfies:

$$P= \prod_{k=1}^{n} S_k^{l_k}(1-S_k)^{d_k} \tag{3}$$

with the constraint that the probabilities of survival are decreasing with the increasing stimulus threshold values:

$$1 \geq S_1 \geq S_2 \geq ... \geq S_n \geq 0 \tag{4}$$

What is wanted is a set of numbers $\tilde{S}_1, \tilde{S}_2, ..., \tilde{S}_n$ so that:

$$\prod_{k=1}^{n} \tilde{S}_k^{\,l_k}(1-\tilde{S}_k)^{d_k} = max \prod_{k=1}^{n} S_k^{\,l_k}(1-S_k)^{d_k} \tag{5}$$

That there is such a set of numbers follows from the fact that the product in (3) is a continuous function of the variables $S_1, S_2, ..., S_n$ on the compact set defined by equation 4.
Define the intuitive estimate:

$$S_k^{+} = \frac{l_k}{l_k + d_k} \tag{6}$$

for k=1,2,...,n.
THEOREM (Ayer et al., 1955): We have that $\tilde{S}_1 \geq S_1^{+}$ and $\tilde{S}_n \leq S_n^{+}$. Furthermore if $\tilde{S}_k > \tilde{S}_{k+1}$ for some k then:

$$S_k^{+} \geq \tilde{S}_k > \tilde{S}_{k+1} \geq S_{k+1}^{+} \tag{7}$$

PROOF: First we show that $S_k^{+} \geq \tilde{S}_k$.. Observe that the function $S^x(1-S)^y$ increases for $0 \leq S < x/(x+y)$ and decreases for $x/(x+y) < S \leq 1$. Suppose that $S_k^{+} < \tilde{S}_k$. Select $S'_k = max\{S_k^{+}, \tilde{S}_{k+1}\}$. Then we have:

$$\tilde{S}_1 \geq \tilde{S}_2 \geq ... \geq \tilde{S}_{k-1} > S'_k \geq \tilde{S}_{k+1} \geq ... \geq \tilde{S}_n \tag{8}$$

but, that says that:

$$S'^{\,l_k}_k(1-S'_k)^{d_k} > \tilde{S}_k^{\,l_k}(1-\tilde{S}_k)^{d_k} \tag{9}$$

contrary to equation 5. Therefore $S_k^{+} \geq \tilde{S}_k$.. Similarly $\tilde{S}_{k+1} \geq S_{k+1}^{+}$. The proof of the first statement of the theorem is similar.

Step Functions

The non-parametric CT estimates will be in the form of step functions. The value of $S(t)$ in the interval $[t_k, t_{k+1}]$ is assumed to be the estimate $\tilde{S}_k$, for the CT. If the step function is a good estimate it will "capture" the underlying distribution; the curve of the distribution will fall somewhere in the convex hull of the step function. The widths of the steps will then be a measure of the error of the estimator. If a smooth curve is desired, the set of points $(t_1, S_1), (t_2, S_2), ..., (t_n, S_n)$, can be fit in a least square sense with some continuous curve. The step function might well be enough, however, if the data have significant noise or experimental

error. If this is the case, then there is no point in distinguishing between HIC values that are close compared to the noise, such as a continuous function would do.

Extended Consistent Threshold Method

The CT that we have defined can be extended so that it can be applied to data that have no censoring, data that contain right censoring, and data that are mixed with both right and left censoring and actual values. Most biomechanical impact response injury data is doubly censored and the method that we have presented thus far can be used, but, for completeness, the extended method will now be given. What follows can be found in more detail in (Turnbull, 1974, Kaplan et al., 1958).

The Product Limit

The product limit (PL) is the standard method for non-parametric estimation of the survival function when the data contain losses but it is not doubly censored. First the range of the data is partitioned by a sequence of stimulus threshold values, $t_1, t_2, ..., t_n$ where each t_k is the stimulus threshold value of at least one death or as least one loss, where, for now, we assume that deaths are not censored. We have then that:

$$Prob\{T>t_k|T>t_{k-1}\}=1-\frac{d_k}{Y_k} \tag{10}$$

where,

$$Y_k = \sum_{i=k}^{n} d_i + \sum_{i=k-1}^{n} l_i \tag{11}$$

Therefore, we have the estimate:

$$S_0^{+}=1 \tag{12}$$

$$S_k^{+}= \prod_{i=1}^{k} (1-\frac{d_i}{Y_i}) \tag{13}$$

As one can see from these formulae, the PL estimate at t_k is formed by computing the probability of a threshold value falling in the interval $(t_k,t_k]$ given that it is larger than t_{k-1} and taking the product with the PL estimate for S_{k-1}.

Computing the Extended Consistent Threshold Method

For the PL method, death stimulus values are assumed known exactly. Suppose now that only some deaths are known exactly. The others are left censored. Denote by d_k^0 deaths at stimulus values t_k which are known exactly and denote by d_k those deaths that are censored.

Suppose also that we know the values of $S_1, S_2, ..., S_n$ .Consider a censored death at t_k . We know only that the threshold stimulus value lies at or below t_k, but since we know the distribution, we also know that

$$Prob\{t_{j-1}<T<t_j|T\le t_k\}=\frac{S_{j-1}-S_j}{1-S_k} \tag{14}$$

Set

$$\alpha_{k,j}=\frac{S_{j-1}-S_j}{1-S_k} \tag{15}$$

What we intend to do, instead of counting a censored death in any one interval, is to count it partially according to the above probability formula in every interval. Our new derived count will be considered not censored and we will thus be able to use the PL method. Define:

$$\delta'_j=d_j^0+\sum_{i=j}^{n} d_i\alpha_{ij} \tag{16}$$

$$Y'_j=\sum_{i=j}^{n} d'_i+\sum_{i=j-1}^{n} l_i \tag{17}$$

$$\hat{S}_0=1 \tag{18}$$

$$\hat{S}_j=(1-\frac{\delta'_j}{Y'_j})\hat{S}_{j-1} \tag{19}$$

These equations will provide us with a new estimate of the distribution, but we would like this new estimate to be the same as the one that we already have. This property of a distribution was defined by (Efron, 1967), and is called self-consistent. To find a self-consistent distribution we need substitute $\hat{S}_k$ for every S_k in the above equations and solve with the additional condition that $1=\hat{S}_0\geq\hat{S}_1\geq...\geq\hat{S}_n\geq 0$. Turnbull suggests simple iteration, beginning with an initial guess of the PL estimate, ignoring left-censored deaths. It does seem to converge quickly.

The Extended CT is a Maximum Likelihood Estimate

The procedure defined in the last subsection is the unique maximum likelihood estimate of $S_1, S_2, ..., S_n$.

Outline of Proof: The logarithm of the likelihood function is:

$$L=\sum_{j=1}^{n}[d_j^0 ln(S_{j-1}-S_j)+l_j lnS_j+d_j ln(1-S_j)]$$

with the condition that $1\geq S_0\geq S_1\geq...\geq S_n\geq 0$. This can be found by simple differentiation but taking the constraint value when necessary. The matrix of second derivatives is negative definite. Hence all solutions yield maxima. But L is continuous and if it were to have two maxima, there would be a minimum between them. There are no minima and so *L* has a unique maximum.

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DISCUSSION

PAPER: **Estimation of Injury Risk From Biomechanical Impact Data**

PRESENTER: ***Guy Nusholtz, Daimler/Chrysler***

QUESTION: Thanks, Guy. Does this technique provide for a method of estimating standard errors and error balance confident to this kind of a curve?

ANSWER: The answer would be no, and the reason for it is: If you don't know what the underlying risk is, or the underlying distribution, then you can't estimate standard bounds or range. I can do–What some non-parametric methods do they assume that it's basically a normal distribution, and then I could go ahead and make the estimations. So if I follow it strictly on the grounds that I don't know what the underlying distribution is, I can't do it. However if I assume that I know, then I can get some level of risk. So, I sort of make both assumptions simultaneously: I don't know it and I do know it.

Q: I think those parametric models they're looking at in all those cases, if you included confidence bounds, they would incorporate your curve within those bounds, particularly at the higher and lower ends where the confidence bounds get very large for those parametric models.

A: We've done some of that. It's not always true although most of the time it probably is.

Q: *Jim Funk, Biodynamic Research Corporation*
I was wondering if there's a corresponding type of non-parametric method for uncensored data. So, you have biomechanical data where peak force is an accurate predictor of injury and then maybe you have some non-injury tests, too. Maybe you have right censored and uncensored. Is there–but you still might have the problem of not knowing the underlying distribution. So, you may want to use a non-parametric method. Is there–Are you familiar with one for non-censored data?

A: Yes.

Q: What is it?

A: In the original paper, I had the generalized form of this which is a modification from–and I forgot the other authors–which can be used for both doubly censored, right censored only, left censored only, some exact data and some censored data. So, it does exist. It's very similar to the CT with slight modifications. However, the algorithm for calculation is much more complicated and it–and it requires the use of an inter-ration program where you estimate what the intervals are and then you keep going until you basically check almost all the intervals to find out which one has, produces the maximum number of intervals; but, it does exist.

Q: *Paul Masiello, JAYCOR*
Two questions. First, does your method lend itself to multi-varied analysis, like if you want to use more than one risk factor; for example, age and something else. Age plus two or three other variables?

A: First question is yes. Go on.

Q: Okay. The second question is: Is there a way to express your result as an analytic function? It seems like you're giving the answer as just some numeric step distribution, and aren't people more interested in having a function they use to express the probability?

A: Okay. Now, let me go through both of those. The first answer is yes. It can take care of the confounding factors; and you can ask, actually, not only produce just a one-dimensional space, but you could produce multi-dimensional space. However, as I tried to explain, it's much more difficult. When you do it when a non-parametric, it requires you to think a lot more which you may not want to do.
The second part is with regard to having, to continuing the parametric curve. If you want–If you have to do that, for whatever reason, then first check it against the non-parametric to find out which one appears to fit that best, and then switch to your parametric.