

# **MORTALITY TREND RISK**

Gary G. Venter  
Columbia University  
gary.venter@gmail.com

## **Abstract:**

Mortality trend risk affects pension plans, life insurers, annuity writers and insurers of workers compensation, where the tail claims are mostly annuities. As with many risk sources, mortality risk can be broken down into process risk, parameter risk, and model risk. To have concrete examples, models are fit to US male and female mortality data. The Lee-Carter model with and without cohort effects is fit, with several distributions of residuals. Heavier-tailed distributions than Poisson turn out to be needed. The information matrix of the parameters is used to estimate parameter standard deviations and correlations.

US population mortality is higher than for typical annuity recipients, who are usually select in some way. Nonetheless trends in population mortality may be relevant for select populations as well. Moreover, mortality in the US for permanently injured workers after medical stabilization is similar to that for the population as a whole, perhaps because their better access to medical care offsets the impact of their injuries, so population mortality data may be directly applicable in that case.

The Lee-Carter model plus cohorts is found to fit the data quite well, but there are nonetheless a number of questions about the appropriateness of this model. Selection of the data to be fit can overcome some of the problems, but for female data high correlation across the parameter types was found that makes the parameter estimates unstable and not readily interpretable.

Process risk, parameter risk, and model risk are discussed using the fitted models.

Keywords: mortality risk, Lee-Carter model, cohort effects, parameter risk, model risk

## Mortality Trend Risk

The general categories of process, parameter and model risk are applicable to mortality projection. Model risk is particularly problematic, as it turns out that the better fitting models have aspects that make them questionable for projection purposes. Lee-Carter models with and without cohort effects with a few distributions of residuals are fit to the general population mortality data from the Human Mortality Database (HMD) and are compared based on penalized maximum likelihood.

The models were initially fit years of death starting with 1971. Preliminary analysis found different trends for ages of death below 55, due perhaps to reproductive health issues and the impact of HIV during some of this period. Female mortality below this age improved dramatically in the 1970s and has changed little since, whereas for males there was a sharp increase in mortality in the 1990s that has since recovered. The oldest age used is 89, as older ages had quite unusual mortality patterns before 1990 – mortality reducing with age, etc. These could be data issues. The data available during this study ends with year of death 2006. All of this resulted in using year-of-birth cohorts 1882 to 1951.

These model fits turn out to be problematic in part because the oldest cohorts have only a few observations, which makes their parameters very responsive to just a few data points, and this in turn creates distortions in other parameters. Adding the data for all years of death for cohorts 1882 and later, maintaining the age-at-death range 55-89, reduces this problem. Another problem with the fits is that in the case of female death rates the correlations among parameter estimates is high, which reduces the significance of the parameters and leads to questionable values.

Section 1 discusses the models used, section 2 looks at the fits, section 3 tries to interpret the parameters, section 4 address adding more years of death, and section 5 gets to projection risk.

### 1. Models

HMD data comes in the form of number of deaths and number of living, who are considered the exposures to death. These are in cells by year of death and age at death. Subtracting age from year gives the cohort, which is approximately the year of birth, but can be slightly different depending

on the time of year that birth and death occurred. Data is also available by actual year of birth but in most models that is considered less important, and cohort is used instead.

Here arrays are taken to have rows for year of death and columns for age at death. The years are 1971-2006, and the ages 55-89, so the arrays are 36x35, with 1260 elements. The years are indexed by  $t$  and the ages by  $d$ . The cohort is  $t - d$  and is constant along the downward-sloping diagonals of the arrays.

The starting point for recent models of mortality is the LC model from Lee and Carter (1992). It models the mortality ratio  $m$ , which is deaths divided by exposures, in log form:

$$\log m_{t,d} = a_d + b_d h_t$$

Here  $a_d$  is the base mortality for age  $d$ ,  $h_t$  is the trend level at year  $t$ , which generally goes down over time as mortality decreases, and  $b_d$  allows different ages to have trend rates that are factors times the overall trend. This is useful in the case of male mortality, for example, where mortality rates for ages 55-60 have improved at a greater rate than those for 85-89. However this is where the LC model can run into differences from actual data, as some ages might trend faster or slower for a while but not always.

A popular extension of LC is LC plus cohorts, from Renshaw-Habermann (2006) (RH):

$$\log m_{t,d} = a_d + b_d h_t + c_d u_{t-d}$$

The cohort term  $u$  allows for mortality to also vary by year of birth, independently of year of death and age. It is not always clear why it should, but allowing it to seems to substantially improve the goodness of fit of the models. The  $c$  factor allows the cohort effect to vary by age. For instance, it might wash out at older ages, or it might be stronger at older ages.

There are some identifiability problems with these models. For instance, increasing every  $b$  by a factor and reducing every  $h$  by the same factor does not change the fitted values. This is similar for  $c$  and  $u$ . Here the constraints used for this are to set  $b_{1955} = c_{1955} = 1$  and  $h_{1971} = u_{1917} = 0$ . The cohort 1917 was chosen as it is the last cohort that includes all calendar years. It is also one of the highest mortality cohorts for both males and females. The result of these constraints is that in the LC model  $a_d$  is the fitted mortality for  $t = 1971$  and  $h_t$  is the trend level for age 55. All the other parameters are relative to these. In the RH model, every  $u$  is the cohort effect at age 55, where the cohort values are relative to cohort 1917.

Fitting is done by maximum likelihood estimation (MLE). Denote the exposures in the  $t,d$  cell by  $E_{t,d}$  and the deaths by  $D_{t,d}$ . The Poisson model is that  $D_{t,d}$  is Poisson in  $m_{t,d}E_{t,d}$ , where  $m_{t,d}$  could come from either the LC or RH model. With mean  $\mu$ , the log of the Poisson probability at  $k$  is  $k\log(\mu) - \mu - \log(k!)$ . The loglikelihood is then:

$$\sum_{t,d} \{D_{t,d} \log[m_{t,d}E_{t,d}] - m_{t,d}E_{t,d} - \log[D_{t,d}!]\}$$

Two forms of the negative binomial distribution are also fit. The negative binomial has two parameters  $r$  and  $\beta$ , with mean  $r\beta$  and variance  $r\beta(1+\beta)$ . But in modeling a whole array of negative binomial variates it is customary to make the mean a parameter and model it with the covariates. In this case the mean would still be  $m_{t,d}E_{t,d}$ , as in the Poisson case.

To make the mean a parameter, set  $\mu = r\beta$ . The two forms arise by either eliminating  $r$  by setting  $r = \mu/\beta$ , or eliminating  $\beta$  by setting  $\beta = \mu/r$ . Here these are called NB1 and NB2, respectively. Both have mean  $\mu$ , but NB1 has variance  $\mu(1+\beta)$  and NB2 has variance  $\mu(1+\mu/r)$ , which are linear and quadratic in  $\mu$ , respectively. Denoting the log of the gamma function by  $\text{lgamma}$ , the log of the probability at  $k$  for the negative binomial in  $r$  and  $\beta$  is:

$$\text{lgamma}(r+k) + k\log(\beta) - \text{lgamma}(r) - \text{lgamma}(1+k) - (r+k)\log(1+\beta)$$

The loglikelihoods for NB1 and NB2 can be obtained by substituting  $\mu/\beta$  for  $r$  or  $\mu/r$  for  $\beta$ , then  $D_{t,d}$  for  $k$  and  $m_{t,d}E_{t,d}$  for  $\mu$ , and summing over the observations.

## 2. Fits

Goodness of fit of different models can be compared using penalized likelihood. The traditional comparison is to start with the negative loglikelihood, NLL, and subtract a penalty. Here the traditional criteria divided by 2 are used, as these are more directly related to the NLL, but the standard names are retained. Thus the Akaike Information Criterion, AIC, uses a penalty of 1 for each parameter. If  $N$  is the sample size (number of observed cells), the Bayesian Information Criterion (BIC) uses a penalty of  $\frac{1}{2} \log N$  for each parameter. There is some feeling among information theorists that the AIC is too lenient on extra parameters, but the BIC is too punitive. The Hannan-Quinn Information Criterion, HQIC, is intermediate. It gives a penalty of  $\log \log N$  for each para-

meter. It turns out that most of the conclusions are the same for each criterion, so initially only the BIC will be used. For  $N = 1260$ , the penalty is about 3.57 per parameter. Thus an extra parameter has to improve the NLL by that much to be justified.

LC and RH Poisson models were fit to male and female mortality. For both data sets, the RH model fit quite a bit better than LC. The RH NB1 and NB2 models were then fit. Table 1 shows the NLL for each model and the improvement in NLL required to meet the BIC requirement for the extra parameters from the model above it. After the parameter constraints there are 35 a parameters, 34 b parameters, and 35 h parameters, so the LC model has 104 parameters. In the RH model there are 34 c parameters and 69 u parameters, for cohorts 1882 – 1951, ex 1946. Thus it has 207 parameters. The negative binomial versions have yet one more parameter.

Model	NLL		Parameters Added	BIC Needed Improvement	BIC Improvement	
	Female	Male			Female	Male
LC Pois	13670	14868				
RH Pois	9598	10081	103	368	4072	4787
RH NB1	8798	8996	1	3.6	800	1085
RH NB2	8748	8972	0	0	50	24

Table 1 – Fit Comparisons

The LC model fits considerably worse for males, with an NLL 1198 higher than for females. The RH model fits much better for both, with an improvement in NLL of 4072 for females and 4787 for males, compared to an improvement of 368 required to justify the extra parameters according to BIC. The difference between male and females is narrowed to 483, so it is a substantial improvement for males. Adding the extra parameter for NB1 also significantly improves both fits, and NB2 is a bit better yet. The  $\beta$  parameter for NB1 is about 2.5 for females, and 3 for males, so the variance for each cell is 3.5 to 4 times the cell mean, compared to equal to the mean for Poisson. That is a substantial difference and with variances that big it is no wonder the Poisson fit is not as good. The  $r$  for NB2 is about 8600 for females and 7500 for males, which for this data translates to variances of 2 to 7 times the mean, with the higher ratios going to the larger cells.

To give a visual impression of the fits, the empirical and modeled values of  $\log m$  are graphed for a few years of death by age at death for the Poisson models. The graphs do not look much different for the negative binomial models, and in fact the parameters are not that different either. The advantage of the negative binomial models is more in the error distributions than in the fitted means.

Essentially the cells with higher variance are not penalized as much in the likelihood functions for being different from their means, so the fit gets better for the smaller cells. This is not enough to be very noticeable in the graphs, however.

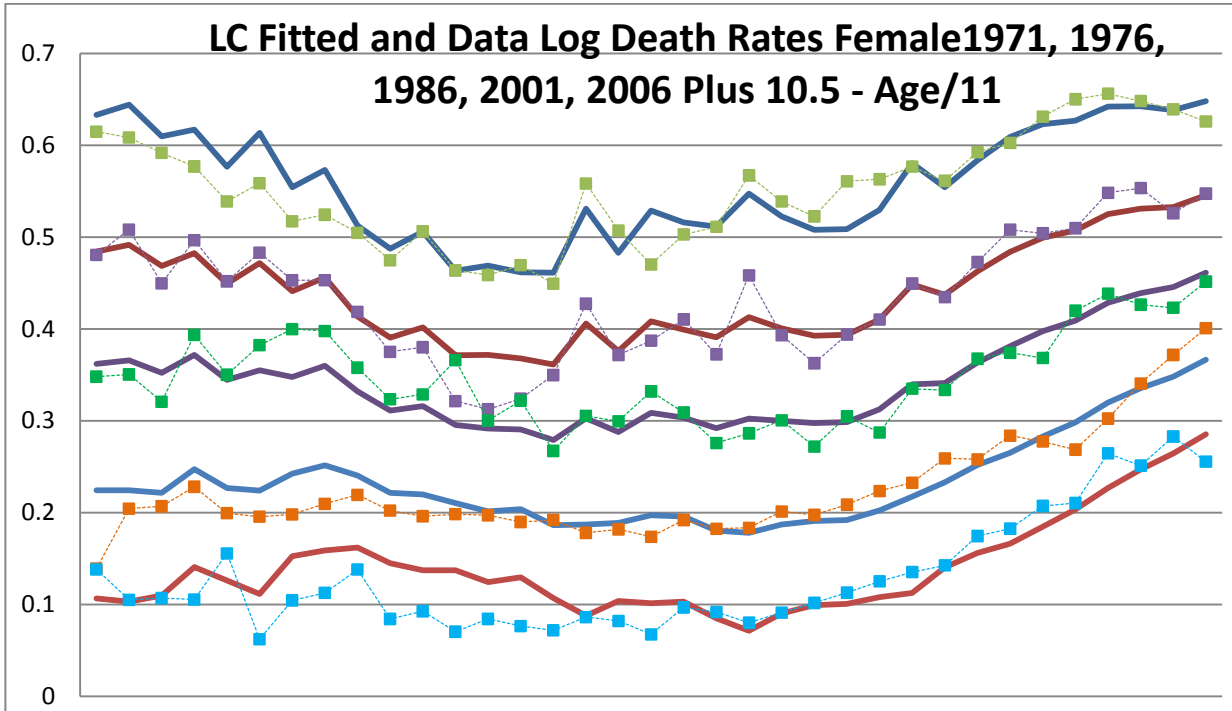


Figure 1 – LC Female

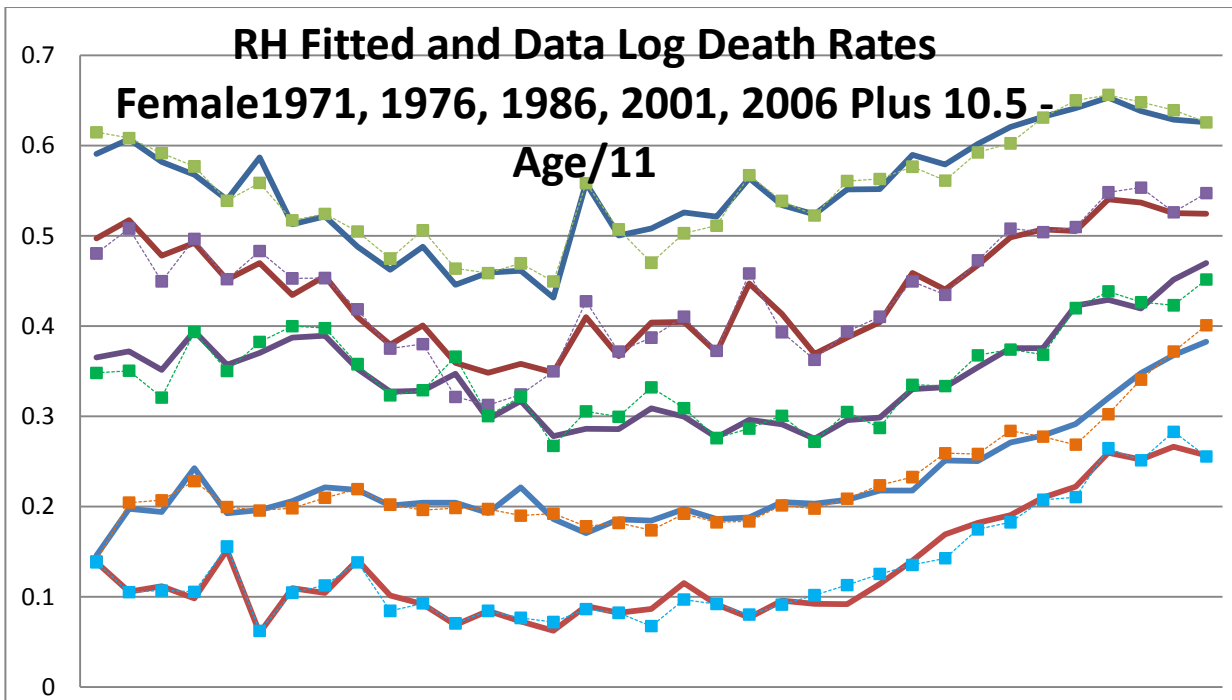


Figure 2 – RH Female

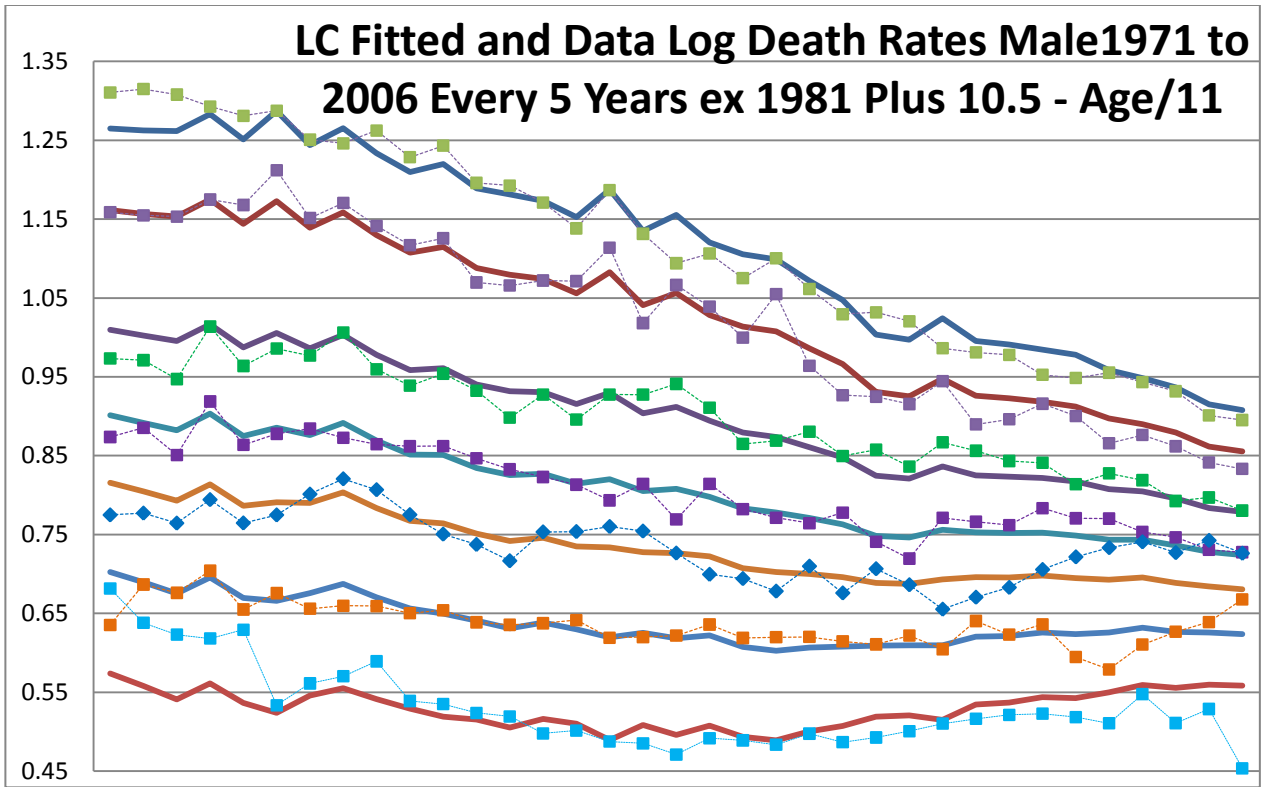


Figure 3 – LC Male

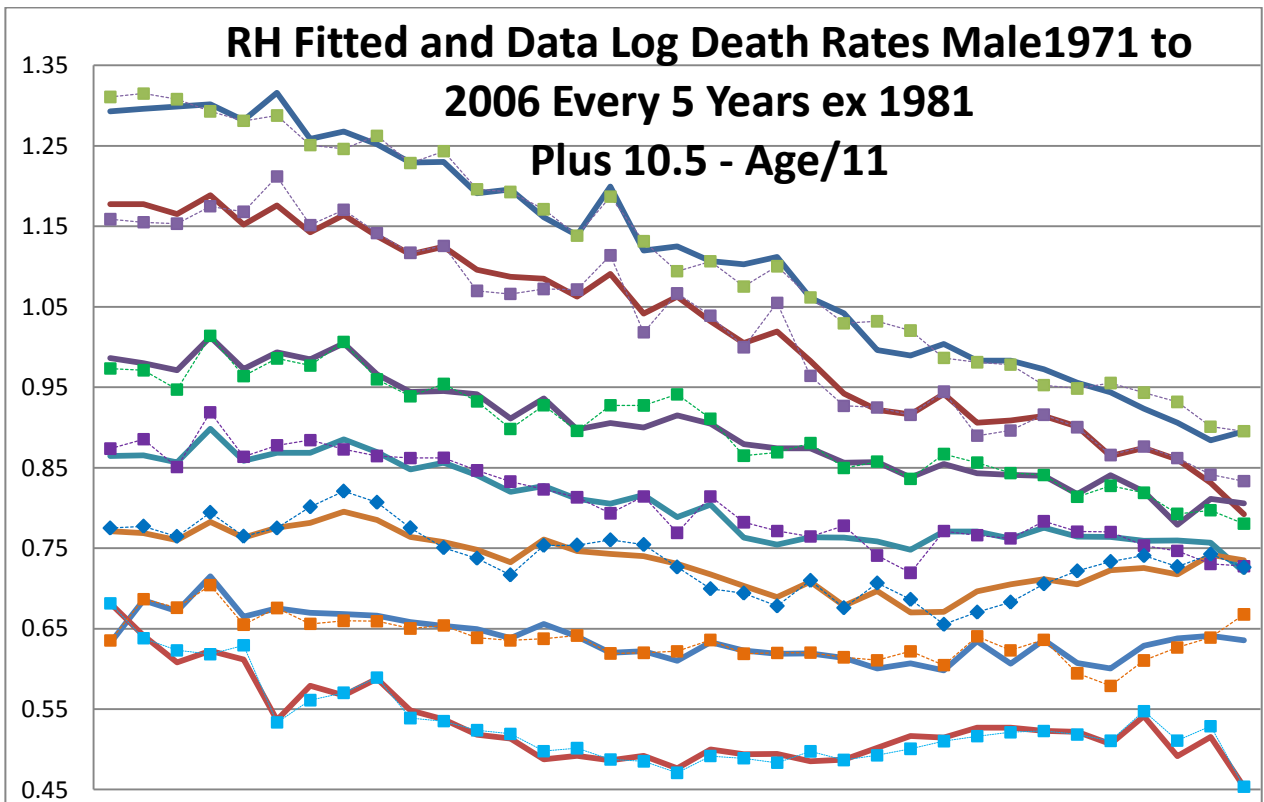


Figure 4 – RH Male

Figures 1 and 2 show the female data and fits. The  $\log m$  values have been rotated by a linear function of age at death in order to make them more horizontal, which facilitates comparison. Figures 3 and 4 are similar for males, but more years are able to be shown as the trends were greater for males, which separates the curves a bit. The more recent years are at the bottom of the graph, as that is where the mortality is the lowest. The dotted lines are the data and the solid lines are the model.

For males, the downward trend from year to year is less at the older ages. The LC model is able to handle this aspect by having lower  $b$  factors for the older ages. When the LC model misses, it seems to be mostly for the youngest and oldest age groups. By adding in cohort parameters, the RH model can account for many of these effects. However some of this is suspicious, as some of the cohorts have few observations in the data. Hence the modeled mortality at age 55 is higher in 2006 than in 2001, which follows the data, but that in itself does not establish 1951 as a high-mortality cohort.

For females the shape of the graph is somewhat different than for males, and there is not so much diminishing trend at older ages. The LC model does not have enough flexibility to capture the changes in shape, and some of the years have long strings of significant errors of the same sign. The RH cohort-effects are able to adjust for a lot of this, but again this is sometimes because of cohorts with only a few observations, such as age 55 for 2001 and 2006.

The RH model provides clearly better fits both by graphical tests and penalized MLE. Although the fits are worse for males, the difference narrows considerably for the better-fitting models. The negative binomial versions are much better than the Poisson, with the NB2 a bit better fitting than the NB1. There are some plausibility problems with the RH model, however.

### **3. Interpreting the Parameters**

The best-fitting NB2 parameterizations are used in this section, but first, does the fact that NB2 fits better than NB1 have any implications? NB2 is the form that comes from mixing a Poisson by a gamma distribution. This arises in experience rating, for instance, where each policy is Poisson distributed, but there is a gamma distribution of Poisson means across the population. Taking a policy at random, its distribution of claims is conditionally independent given its Poisson mean, but un-



conditionally correlated due to the common Poisson mean. This is thus a way of modeling non-independent claims, or contagion.

It is tempting then to argue that the population as a whole is a mixture of groups with different mortality, due to different lifestyles, access to medical care, etc., and that is the source of the contagion observed. However that is a different kind of mixture. The population as a whole consists of all the groups taken together, not one drawn at random. The sum of independent Poisson distributions is itself Poisson, so the mixture argument does not explain contagion at the level of the entire population. Moreover, the number of deaths is the sum of Bernoulli processes and would be binomial, not Poisson, if there were not already some source of contagion to begin with.

There are factors affecting mortality rates for the population as a whole, such as weather, flu outbreaks, etc., that make deaths not independent. This seems the principal source of contagion at the population level. The NB1 model makes the variance about 4 times the mean for each cell in the data, whereas for the NB2 model it ranges from about 2 to 7 times the mean, with the factor larger for the larger cells. The fact that NB2 fits better suggests that the contagion events hit the larger cells harder. That is, the ages with the greatest number of deaths also have the greatest increases in deaths when adverse conditions arise.

Starting with the  $a_d$  parameters, which represent the base log mortality rate by age, before application of trends and cohort effects, Figure 5 graphs  $a_d$  for males and females.

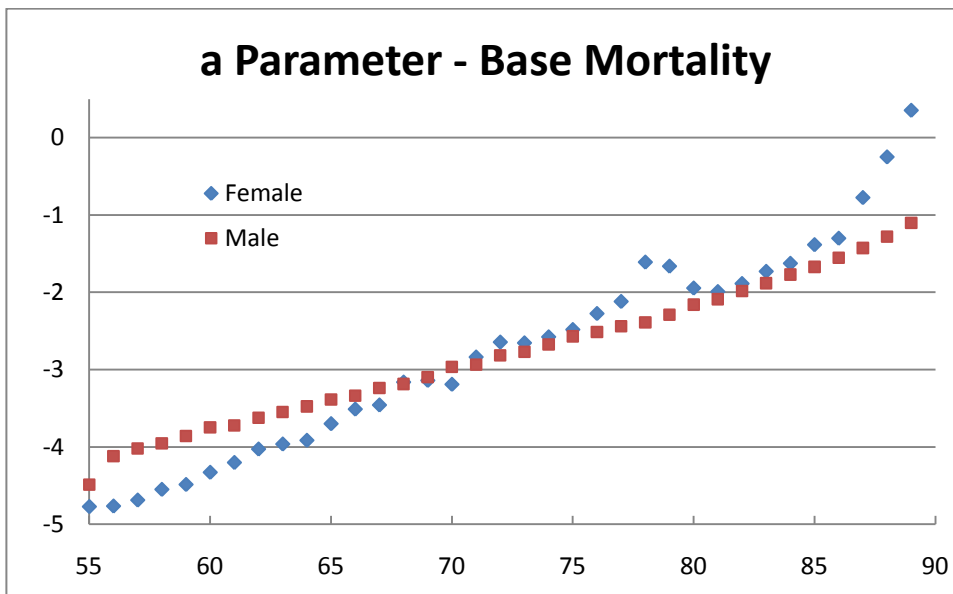


Figure 5 –  $a_d$  Parameters

Male mortality is higher than female at all ages, but that does not show with these parameters. The calendar-year parameters and cohort parameters interact with these so in themselves they are not that meaningful.

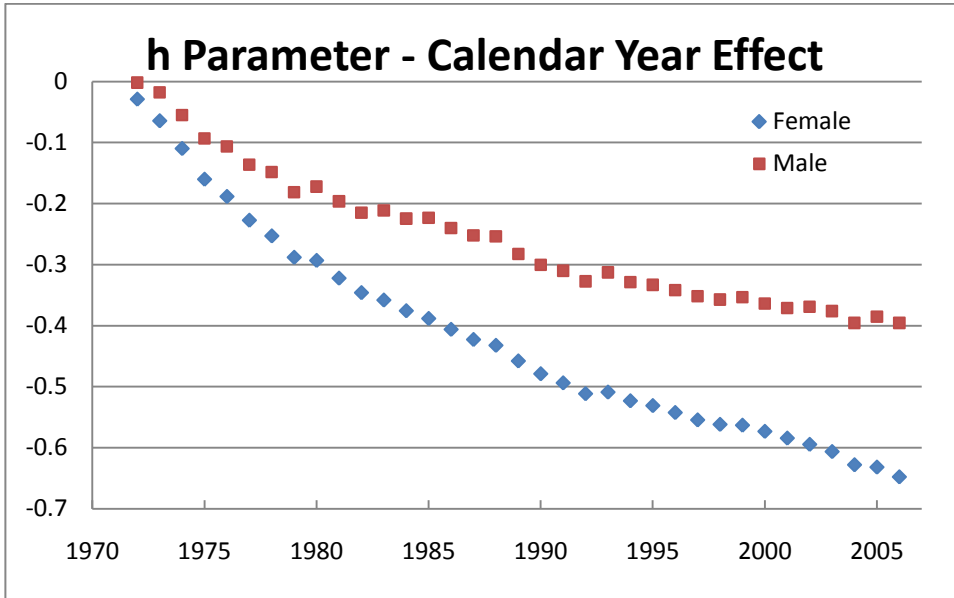


Figure 6 –  $h_t$  Parameters

Figure 6 shows the calendar-year trends as reflected in the  $h_t$  parameters. These were forced to be zero at year 1971. The female levels are trending faster, even though at the younger ages in the range the male rates are dropping faster. This is a distortion of the calendar-year parameters due to interaction with other parameters.

The  $b_d$  parameters, which modify the overall trend to produce an age-specific trend, are shown in Figure 7. The surprise here is the accentuation of the trend effect for male octogenarians, whose trend has actually been less than for other ages. In the model the cohort effects offset this effect to match the data. The last cohort that affects ages 87, 88, and 89 is 1899, and cohorts prior to 1900 do not get into this dataset at ages less than 72, leaving room for the parameters to adjust themselves to produce the best possible fit at older ages without affecting younger ages. This raises questions, however, about the applicability of the parameters beyond this data range.

The cohort parameters  $u_{t-d}$  are graphed in Figure 8. This includes the 1917 cohort that is forced to zero. The sharply lower mortality for females in the earlier decades is not realistic. It produces an increasing trend across cohorts which partially offsets the trend across calendar years.

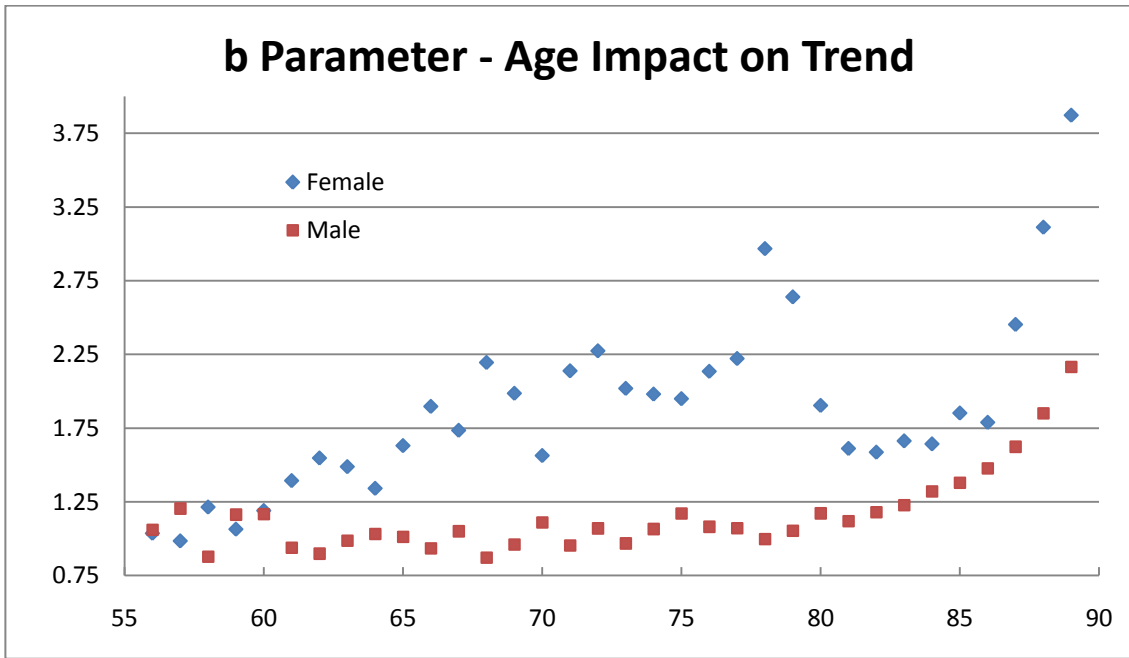


Figure 7 – Trend Age Modifiers  $b_d$

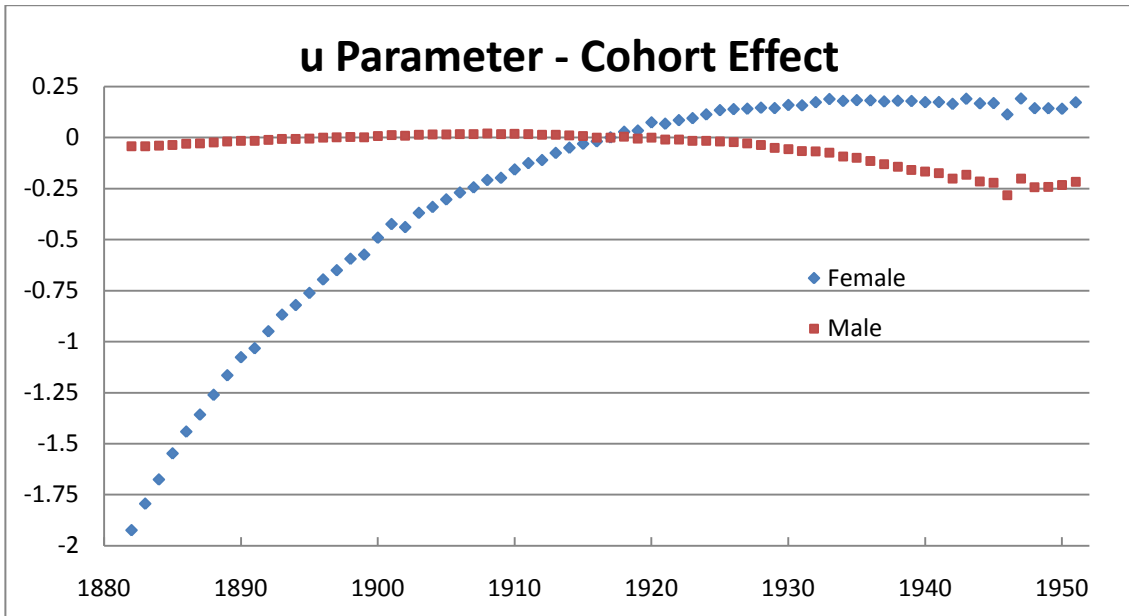


Figure 8 – Cohort Parameters  $u_{t-d}$

Although it is much milder, an increase in mortality is seen in the first 30 or so cohorts for males. A possible explanation is that they reflect a selection effect. It was more unusual for men and women born in the 1880s to reach higher ages, so those that did were a select group more likely to live even longer. The cohort parameters are intended to represent a mortality differential for the

cohort that would apply at all ages, but because not all ages are in the data, the most it could represent is a conditional differential, conditional on having lived long enough to get into the data in the first place. Such an effect would be further enhanced by the fact that the oldest cohorts only appear in the oldest ages in this data.

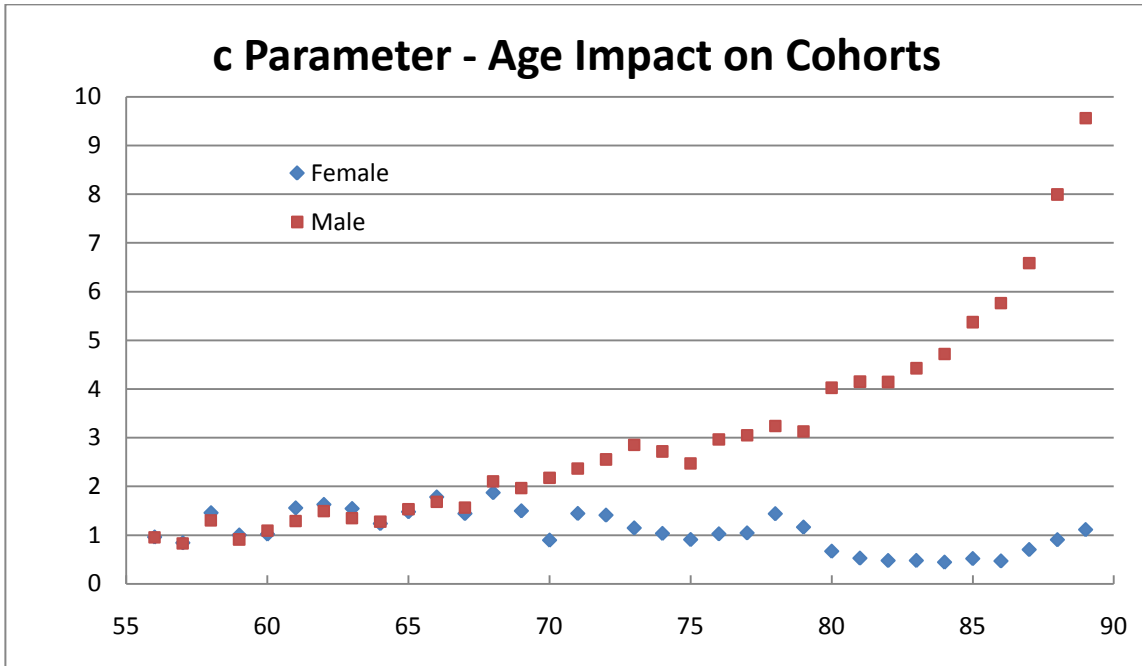


Figure 9 – Cohort Effect by Age Parameters  $c_d$

Finally the  $c_d$  parameters, which are by-age modifiers to the cohort effects, are in Figure 9. These are forced to unity at age 55, and stay near there for a year or two before moving to the vicinity of 2 for ages in the late 60s. From there the female parameters get generally lower for the older ages, indicating a reduced impact of the cohort effects at later ages. This partially offsets the much greater trend in cohorts for females. For the males the parameter accelerates in the 80s, ending near 10. This appears to be part of the fine-tuning of the fit for higher ages made possible by the cohort parameters with few supporting observations.

The observed slower trend in mortality at older ages for males is modeled in this RH parameterization by an underlying higher trend at older ages (b parameters), offset by a starting group of cohorts who had lower mortality rates to begin with (u parameters), the effects of which increased sharply at older ages (c parameters). The LC plus cohorts model for female mortality is an even stranger combination of offsetting effects.

## 4. Fixing the Fits

One of the problems with the fits above is the sparsity of data in many cohorts. Another is the high correlation among parameters in the female model, which is discussed later. For the recent cohorts the only way to add data is to wait. For the older cohorts, however, there is data available. Extending the data to include all calendar years of death for cohorts 1882 – 1915 with death ages 55-89 is possible, and this increases the number of observations to 35 for each such cohort. This would be expected to give better estimates for those cohort parameters  $u_{t-d}$ , but also for the  $c_d$  parameters that modify the cohort parameters for age effects, and indirectly on all the other parameters, which may have less flexibility to fit to random fluctuations in the data. The original data will be referred to as the partial data and the expanded set as the full data.

The per-parameter penalty  $\log(N)/2$  for BIC goes up to 3.763, with 1855 observations, from 3.569 for the 1260 observations in the partial data. The full data need calendar year parameters  $h_t$  starting with 1937 (assuming zero at 1936) instead of from 1972, so the models have 33 more parameters. There are no additional a, b, c or u parameters. Thus the LC model now has 137 parameters and the RH negative binomial models have 242 parameters. The full sequence of models above was fit but now the NB1 fit better for males. To resolve this, more distributions were fit for the RH model. The NB3 is intermediate between the NB1 and NB2, the Poisson-inverse Gaussian (PiG) is similar to the negative binomial, but is more skewed, and the Sichel is a three-parameter generalization of the PiG which can be more or less skewed than the PiG but not less skewed than the NB. These distributions are discussed further in Appendix 1. The results are:

Model	NLL		Parameters Added	BIC Needed Improvement	BIC Improvement	
	Female	Male			Female	Male
LC Pois	21,726	24,047				
RH Pois	15,452	16,630	103	388	6274	7417
RH NB1	13,176	13,567	1	3.8	2276	3063
RH NB2	13,172	13,576	0	0	4	-9
RH NB3	13,163	13,568	0	0	9	-1
RH PiG	13,172	13,567	0	0	-0.4	0.015
RH Sichel	13,172	13,565	1	3.8	0	2.2

Table 2 – Triangle Fit Comparisons

Again the RH model provides a tremendous improvement in the fit, as does moving from Poisson to negative binomial. The NB3 is the best fit for females, but the NB1 is the best NB for males.

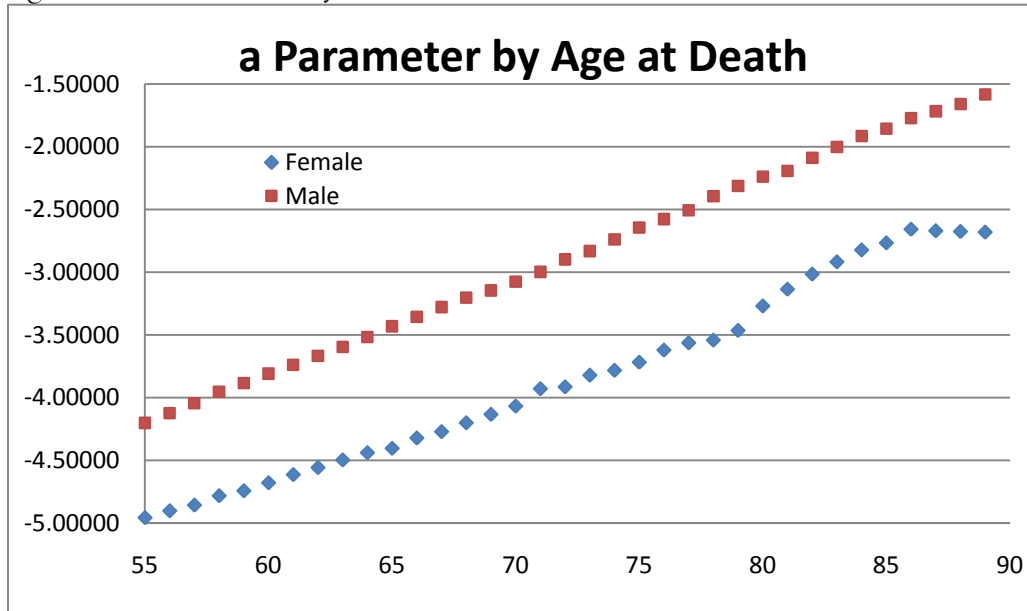
The difference between the NB models is that VM, the variance/mean ratio, is fixed at  $1+\beta$  for the NB1, is  $1+\mu/r$  for the NB2, and is  $1+(\mu/r)^{1/2}$  for the NB3. For females the cell means range from 6000 to 44,000. With the fitted parameters this gives VM of 5.1 for NB1, 2.4 to 11.1 for NB2, and 3.4 to 7.4 for NB3, which gives the best fit. For males the NB1 VM is 6.1. Another version of the NB discussed in Appendix 2 fits slightly better with a range for VM of 5.3 to 6.7, but uses an additional parameter which does not give enough better fit to justify it.

The improvements shown for the last three models are from the better of NB1 and NB2. The PiG and Sichel models also have 1, 2, and 3 versions like the NB. For females, the 2 version of the PiG was found to be slightly worse than the NB2, indicating that the additional skewness was not helpful. The corresponding Sichel has the NB2 as a limiting case, but otherwise has higher skewness than the NB2 with the same mean and variance. The fact that it did not give any improvement over the NB2 suggests that if anything, less skewed distributions may fit better for females.

For males the PiG, version 1, was very slightly better than the NB1. The Sichel fit even better with an intermediate skewness. However the improvement in NLL is problematic. At 2.2 it is less than the 3.8 required by the BIC, but better than 1, which the AIC requires, or 2.0, which the HQIC calls for. There is a good deal of literature suggesting that BIC is too stringent in rejecting parameters. Burnham and Anderson (2004) make a strong push for AIC and the small sample AIC, based on the idea that the sample is not generated from the model being fit, but rather the model is a fairly compact representation of a more complex process. For a sample size of  $N$  and  $p$  parameters, the small sample AIC penalizes the NLL by  $Np/(N-p-1)$ . With  $N = 1855$ , the additional penalty for the 243<sup>rd</sup> parameter over the 242<sup>nd</sup> is 1.32. Thus the AIC, HQIC, and small sample AIC all support the additional parameter for the Sichel distribution in this case. Thus it will be taken as the best fitting model.

The parameters shown below are from the best fitting Sichel model for males and NB3 model for females. It appears that the full data helps with the male model but does not solve the problems with correlation in the female model.

Figure 10 – Base Mortality – a Parameter



The a parameters look quite reasonable for males but strange for females, especially the decline for the oldest ages.

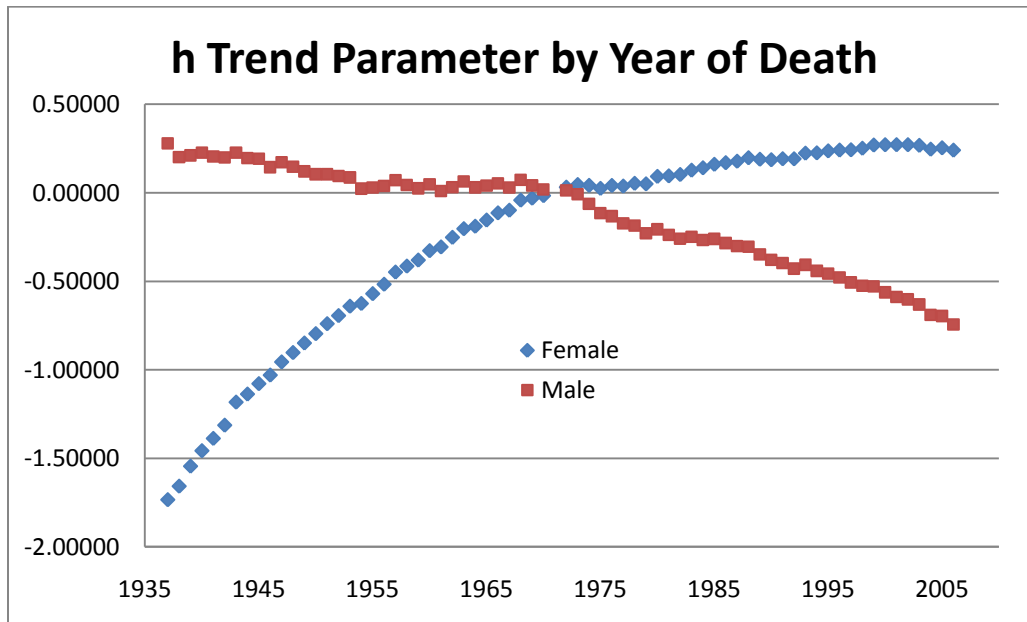


Figure 11 – Calendar Year h Parameters

The calendar-year h parameters also appear reasonable for males but trend upward for females. In this parameterization for females, the downward trend over time ends up as a cohort trend, partially offset with an opposing calendar-year trend.

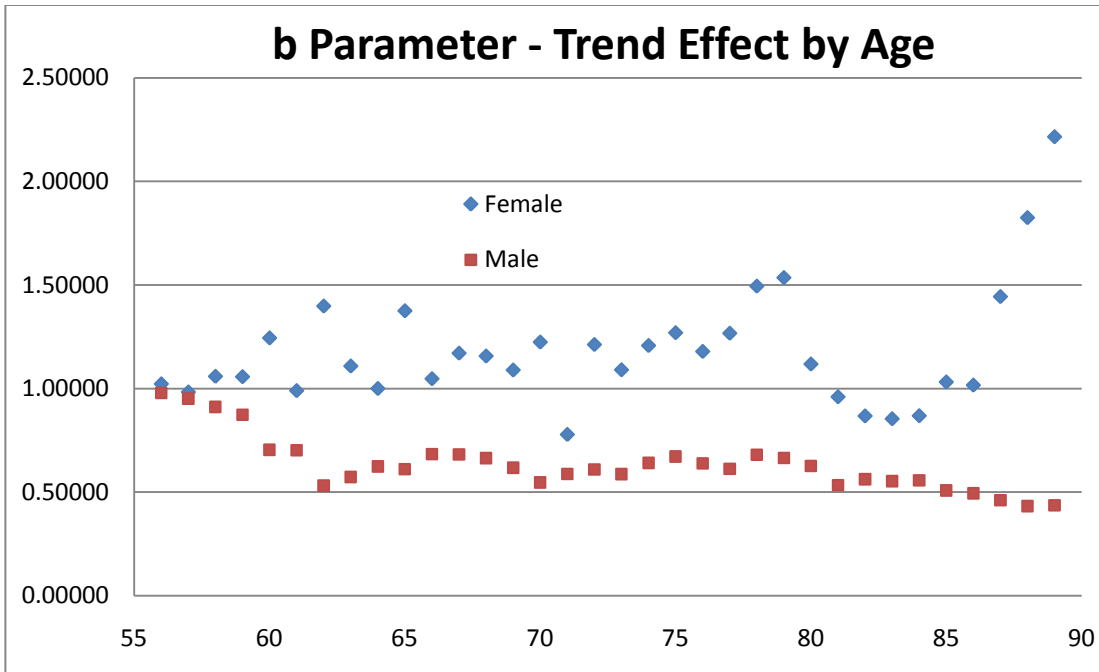


Figure 12 – Trend Effect by Age at Death – b Parameters

For the b parameters in Figure 12, the sharp upward movement at the oldest ages for females probably has something to do with the lower base mortality at the corresponding points.

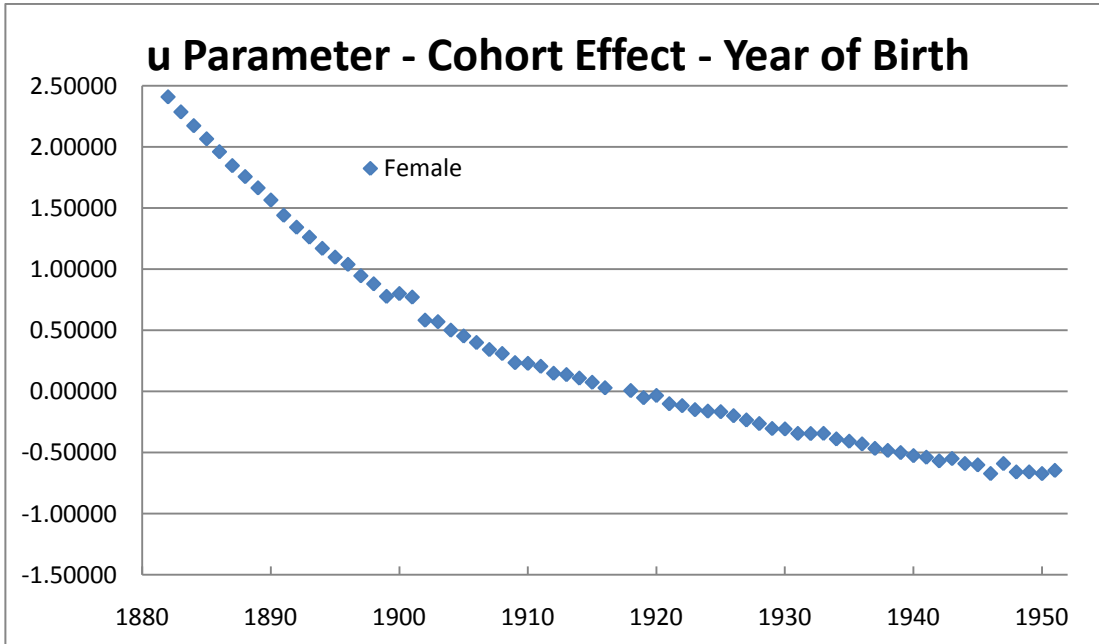


Figure 13 – Female Cohort Effect u

The female cohort trend is in Figure 13, which shows a sharp downward trend in mortality in the direction of later years. This overwhelms the upward trend by calendar year to produce an



overall downward trend in mortality, which matches the data, but is not intuitive as an explanation of the data.

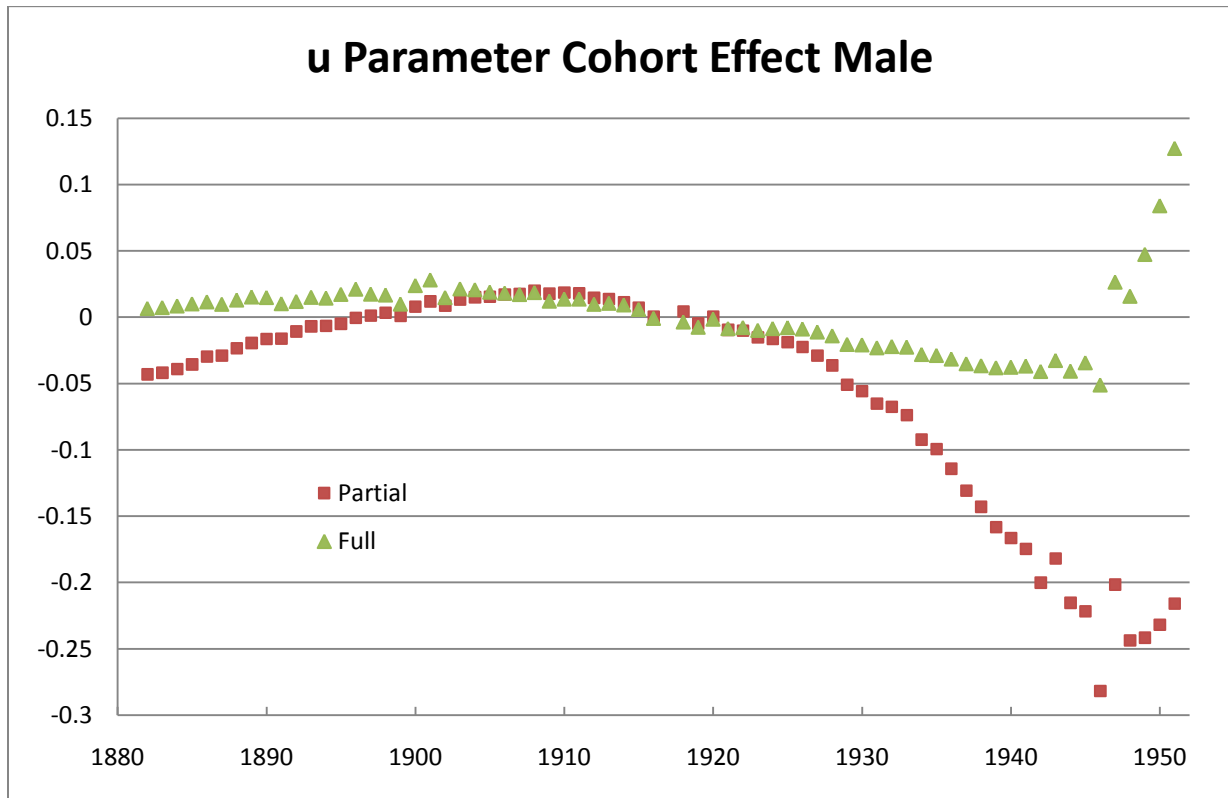


Figure 14 – Male Cohort Effects for Partial and Full Cohorts

The male cohort parameters are on a completely different scale so are graphed separately in Figure 14. The full and partial cohort parameters are graphed together. On this scale the effect of conditioning on attaining various ages is clearer in the partial cohorts, where the conditioning is on progressively older ages, peaking in about 1910. There is a similar but much smaller effect in the full cohorts, perhaps due to a changing significance on the fact of attaining age 55. In both cases there is an increase in the mortality in the most recent cohorts, but these are based on very few data points so may not hold up. Also for the male model, the  $c$  parameter, set to 1 at age 55, stays that low only for a few ages then goes to much higher values at older ages, as shown in Figure 15. Thus the higher cohort parameters for the latest cohorts are getting relatively low  $c$  parameters applied, and are not likely to remain so low when more data comes in, with higher  $c$  parameters.

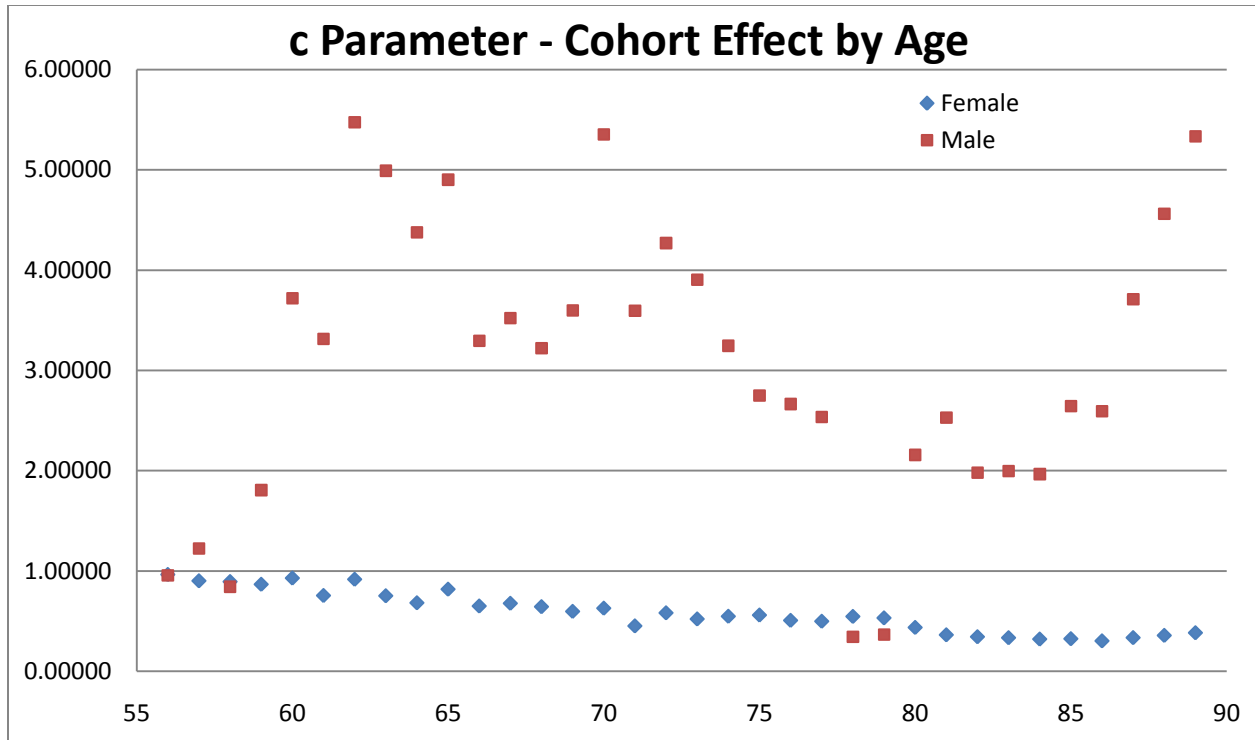


Figure 15 – Age Impact on Cohorts – c Parameter

An idea of the statistical significance of the parameters can be gained by estimating the parameter covariance matrix as the inverse of the Fisher information matrix from the MLE estimation. Recall that this is the matrix of all 2<sup>nd</sup> partial derivatives of the NLL. This yields parameter standard deviations and so t-statistics for each parameter and also covariances, and so correlations, among parameters.

For the male triangle parameters, virtually all the parameters had t-statistics with absolute values above 2. The few exceptions are parameters very close to zero, usually near points that were forced to be zero. With 242 parameters there are over 25,000 correlations, so they are not printed here. However the average of the absolute value of the correlations by type of parameter (excluding parameters with themselves) are shown in Table 3 for males and Table 4 for females.

	<b>a</b>	<b>h</b>	<b>b</b>	<b>u</b>	<b>c</b>
<b>a</b>	52.7%	31.9%	36.1%	43.7%	25.3%
<b>h</b>	31.9%	35.6%	22.3%	45.9%	37.3%
<b>b</b>	36.1%	22.3%	42.7%	27.3%	22.0%
<b>u</b>	43.7%	45.9%	27.3%	79.0%	67.3%
<b>C</b>	25.3%	25.3%	22.0%	67.3%	67.4%

Table 3 – Average Absolute Value of Correlations by Parameter Types – Males

	<b>a</b>	<b>h</b>	<b>b</b>	<b>u</b>	<b>c</b>
<b>a</b>	98.9%	98.2%	9.4%	97.6%	34.1%
<b>h</b>	98.2%	98.9%	8.4%	98.4%	31.6%
<b>b</b>	9.4%	8.4%	40.9%	8.5%	30.5%
<b>u</b>	97.6%	98.4%	8.5%	97.9%	31.3%
<b>c</b>	34.1%	34.1%	30.5%	31.3%	56.5%

Table 4 – Average Absolute Value of Correlations by Parameter Types – Females

The extremely high correlations among the a, h, and u parameters in the female model makes the individual parameters highly questionable. There could be many local maxima of the likelihood function, and there is no guarantee that the parameters found are a global maximum. Even if they are, the correlations make the parameter values unstable.

This shows up in the t-statistics as well, which are near 1 in absolute value for all the h and u parameters in the female model.

Moving to the full cohorts then appears to improve the male model, which has reasonable parameters and correlations among parameters, as well as significant t-statistics. For the female model the high correlations (which though not shown are similar for the partial cohorts) make the fit problematic.

Usually when there are high correlations, the solution is to leave out some variables. But the greatly improved fit of the RH model over the LC model appears to rule out omitting the cohort parameters. Parameter reduction through smoothing would still leave quite problematic parameter values as well. One option may be to keep the cohort parameters but not the calendar-year parameters, making the trend a purely cohort matter. It does not seem likely that this would give a good fit, but it might be worth trying.

Another option would be to set the base mortality parameters as the average or some weighted average of the mortality rates for each age in the full data. This was actually Lee and Carter’s initial recommendation. This would give the other parameters less opportunity for mischief. A similar approach could be to use a parameterized curve, like Makeham or splines, for the base mortality. Yet another possibility might be to multiply the cohort and calendar-year parameters, and then apply a single age parameter to the product. This type of model is used extensively in casualty loss reserving, but has had mixed results (informally communicated) in mortality studies.

## 5. Projection Risk

Projection risk can be calculated for a particular dataset of annuitants, which is not what is available here, but some general observations on how to carry out such a calculation are presented.

To begin, the calendar-year trend levels have to be projected. Standard time-series methodologies produce ever-widening ranges as the trend continues. However here there is another wrinkle, as the points being trended are estimated parameters, and so are observed with error. An area of regression studies is errors-in-variables models, which has a number of potential methods. If the variances of the  $h$  parameters have been estimated and they are relatively constant, then a simple reasonable simulation of a future level could assume that same variance, and do a simulation of the actual future level from the already-simulated contaminated future level from the trend intervals.

A number of mortality modelers have used AR1 models for the annual difference in levels, usually with a negative autocorrelation, to project the trend. Most of these do not take into account the errors-in-measurement issue. For an independent series measured with a constant error variance, differencing induces an autocorrelation of -50%, arising from the same error having opposite signs in consecutive observations. Some mortality projection studies have used the Kalman filter, which recognizes measurement errors, to project the levels, but if that is based on a random walk it can have too much autocorrelation. An alternative to both is the area of state-space models, which provide generalizations of time-series and Kalman filter models.

If projections are needed for cohorts not in the study, then trending cohorts also has to be considered. Even the use of the recent cohort parameters should take into account their potential measurement errors, perhaps with a state-space model.

Parameter uncertainty can be implemented by simulating the parameters from the covariance matrix based on the Fisher information matrix from the estimation. The information matrix gives an estimate of the covariance matrix of the parameters. Asymptotically the parameters have a multivariate normal distribution with this covariance matrix, so they can be simulated using the normal copula, Cholesky decomposition, etc.

Once a routine is in place to simulate parameters and to trend the  $h$  and  $u$  parameters, the number of deaths can be simulated from the negative binomial or Sichel distribution. If a routine to do this is not available, probably simulating from a transformed gamma with the same first three mo-

ments would not be too far off.

Model risk is a more difficult issue. The RH-Sichel model appears fairly reasonable for the male data, but the cohort parameters for the last several cohorts are questionable, being based on few observations. Parameter uncertainty should be large for such parameters. Perhaps using the models but including more parameter uncertainty for model risk would give usable results.

## 5. Summary and Future Directions

The RH model fits much better than LC, which is what most studies have found. Basically the shape of the mortality curve has been changing more than LC can accommodate. Also the negative binomial fits better than the Poisson, which has been seen before and is also likely to be a standard result. The best form for the NB is not consistent, however, and may differ for different datasets, depending on how contagion actually applies. For males the Sichel distribution is better still.

Model risk is an issue, since the RH model can fit well at the ends of the age range using cohort parameters based on few observations. Using full cohorts can reduce this risk. However the RH parameters can be highly correlated, as in the female model, suggesting that some other model should be found, possibly by reducing the number of parameters.

Projections of mortality risk under current methodologies are thus likely to be unreliable. But better-fitting models are not likely to solve this problem as the bigger issue is parameter stability.

## References

- [1] Burnham, K.P. and D.R. Anderson 2004 "Multimodel Inference: Understanding AIC and BIC in Model Selection," *Sociological Methods Research*, 33: 261-304.
- [2] Hannan, E. and B. Quinn 1979 "The determination of the order of an autoregression," *Journal of the Royal Statistical Society B*(41), 190-195.
- [3] Lee, R.D., and Carter, L.R. 1992 "Modeling and forecasting U.S. mortality," *Journal of the American Statistical Association*, 87: 659-675.
- [4] Renshaw, A.E., and Haberman, S. 2006 "A cohort-based extension to the Lee-Carter model for mortality reduction factors," *Insurance: Mathematics and Economics*, 38: 556-570.
- [5] Rigby, R.A. D.M. Stasinopoulos, and C. Akantziliotou. 2008. "A framework for modelling overdispersed count data, including the Poisson-shifted generalized inverse Gaussian distribution," *Computational Statistics and Data Analysis* 53: 381-393.

## Appendix 1 – Count Distributions

The negative binomial distribution has two parameters  $r$  and  $\beta$ , with mean  $r\beta$  and variance  $r\beta(1+\beta)$ . In the full data there are 1855 cells, and when the negative binomial is used, each cell has a value of  $r$  and  $\beta$ . The mean  $\mu = r\beta$  is the value given by the RH model, but how  $r$  and  $\beta$  vary across cells depends on how the model is set up. In the NB1, it is assumed that every cell has the same value of  $\beta$ , so the ratio of variance to mean is  $1+\beta$  for every cell. In the NB2 every cell is assumed to have the same value of  $r$ , with  $\beta$  set to  $\mu/r$ , which gives variance to mean ratio  $1+\mu/r$ , which is higher for the cells with higher means. However there are many other ways the parameters can vary across cells. For instance, suppose there is a constant  $q$  for all cells, with  $r$  and  $\beta$  given by  $r = q\mu^{1/2}$  and  $\beta = \mu^{1/2}/q$ . Then the mean is still  $r\beta = \mu$ , and the variance to mean ratio for a cell is  $1 + \mu^{1/2}/q$ . This is what is called the NB3 in the text. Its variance/mean ratio is still higher for the larger cells, but not by as much as in the NB2.

This can be generalized to the NB $p$  distribution, which adds a parameter  $p$  to control the variance/mean ratio. It sets  $r = q\mu^{1-p}$  and  $\beta = \mu^p/q$ . The mean is again  $r\beta = \mu$ , but now the variance to mean ratio for a cell is  $1 + \mu^p/q$ . The value of  $p$  can be found by MLE. For males the resulting value of  $p$  is 0.2, but the NLL is not enough better to justify the additional parameter by any of the information criteria. For females the  $p$  is 0.53, but again this did not improve the NLL enough to justify the extra parameter. It might be argued that the NB3 already has an extra parameter of  $p = 1/2$ , but this is a bit ambiguous as the parameter is not free to be fit. In this case the NB3 fits the female data by enough better to justify an additional parameter.

When fitting a single NB distribution to a data set, all of these forms are the same. The difference comes when fitting a number of distributions to a number of cells where a common relationship of variance and mean is desired. The NB $p$  forms discussed here by no means exhaust the possible such relationships. In general if the variance/mean ratio desired is  $1+G(\mu)$ , just set  $r = \mu/G(\mu)$  and  $\beta = G(\mu)$ . For instance,  $G(\mu) = q \log(\mu)$  might work in some cases, possibly even for the male data in this paper.

The Poisson – inverse Gaussian distribution can be derived analogously to the NB as a Poisson

mixture, but now the Poisson parameter is mixed by the inverse Gaussian instead of the gamma. Again it has 1, 2, 3, and p versions, etc. The inverse Gaussian is 50% more skewed than the gamma with the same mean and variance, and the PiG inherits this greater skewness, although not by the same ratio. The third central moment divided by the mean is the 3<sup>rd</sup> moment analogue of variance/mean for count distributions. For the negative binomial this is  $1+3\beta+2\beta^2$ , while for the PiG it is  $1+3\beta+3\beta^2$ . For  $\beta=5$ , which is fairly typical in the fits here, that gives 66 for the NB and 91 for the PiG, both of which would have variance/mean = 6.

The Sichel distribution is a generalization of the PiG and is a Poisson mixed by a generalized inverse Gaussian. It can be more or less skewed than the PiG but not less than the NB, which is a limiting case. It uses the modified Bessel function of the second kind (sometimes called the third kind),  $K_\nu(t) = \frac{1}{2} \int_0^\infty x^{\nu-1} \exp\left[-\frac{1}{2}t(x+x^{-1})\right] dx$ .

The Sichel distribution with parameters  $r$ ,  $\beta$ , and  $\nu$  can be most readily expressed with two auxiliary parameters  $c$  and  $s$ , with  $c = K_\nu(r)/K_{\nu+1}(r)$  and  $s^2 = 1+2\beta c$ . The probability function at  $j$  is:

$$p_j = \frac{(r\beta c)^j K_{j+\nu}(rs)}{s^{\nu+j} j! K_\nu(r)}$$

This is a reformulation of the version given in Rigby et al.(2008). Their parameters can be mapped from these by taking  $\alpha = rs$ ,  $\sigma = 1/r$ ,  $\mu = r\beta$ , and  $c = 1/c$ .

The PiG is just the case  $\nu = -1/2$ , for which  $c = 1$ . The mean is  $r\beta$  and the variance is  $\mu(1+h)$  with  $h = 2\beta c(\nu+1) + \mu(c^2 - 1)$ . For the PiG, this simplifies to  $h = \beta$ . The ratio of the third central moment to the mean is  $\mu_3/\mu = 1 + 2\mu(\beta c - h) + 3h + 2\beta ch(\nu+2)$ .

The  $\nu$  parameter can be very different than  $-1/2$ , and for the male data here was estimated as 2155. The  $\beta$  parameter was close to 6, and  $r$  was set at  $\mu/\beta$ . The resulting third moments were usually intermediate to those of the PiG and NB.

## Appendix 2 – Fitting Notes

With several distributions to be fit, routines were sought that did not use derivatives of the NLL or could use numerical derivatives. The R package subplex uses an efficient form of the simplex

algorithm, and was found useful in getting rapid improvement in the NLL from initial guesses. However it seemed to have difficulty in final convergence, often ending up in a region where the NLL was changing very slowly but was not near a minimum. Running sublex 2 or 3 times with default settings usually helped a good deal.

From there the `optim` routine in the `Stats` package was found to be useful in proceeding more towards a minimum. The `optim` option used most often was BFGS with `gr=NULL`, which takes fast approximate numerical derivatives of the NLL to find the best direction for improvement. Usually it would start off with only small improvements, but usually ended up finding a region where more rapid improvement was possible, then slowing down again near to convergence. Relative and absolute convergence criteria of  $1e-17$  and  $1e-12$  were used, which may be beyond machine precision. However the routine would converge, although usually not to a true minimum.

The next step was to define a gradient function of the parameters using numerical derivatives from the `numDeriv` package. This is a slower but more accurate gradient, and using BFGS with it always improved the fit. The problem is that the convergence is defined by the NLL not changing much, which does not always end up with all derivatives very close to zero. Since the 2<sup>nd</sup> derivatives at the minimum are needed for the information matrix, it seemed a good idea to make the derivatives reasonably close to zero. For this the routine `dfsane` from the `BB` package was found helpful. In perhaps 50 iterations it could find points close to the `optim` parameters but with a reduction of 2 or 3 orders of magnitude in the largest (absolute) derivatives. It usually produced only very small changes in the NLL from what `optim` had yielded, however.

For the Bessel functions, the base R package function does not work with high values of the index (say  $\nu > 1500$ ). There is a Bessel package available for Windows in R-Forge. It has a function `besselK.nuAsym` that does work for large values of the index, but not for small values. It needs an additional package `Rmpfr`, which is available on CRAN.

There are recursive formulas for the PiG and Sichel probabilities, but these are awkward at best for probabilities for tens of thousands of events.

(Yilu Zhang and Lina Ma helped research the R methodology for fitting distributions used here.)