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## A new model of ageing and mortality

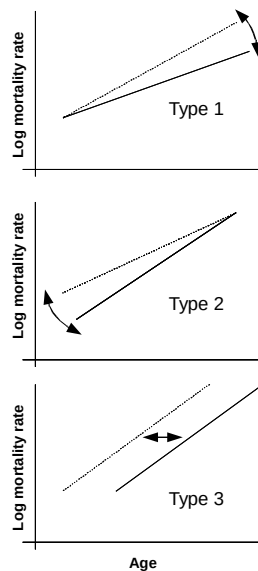
Dr Eugene Milne  
Institute for Ageing and Health  
Newcastle University  
England



  
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## Derivation and design

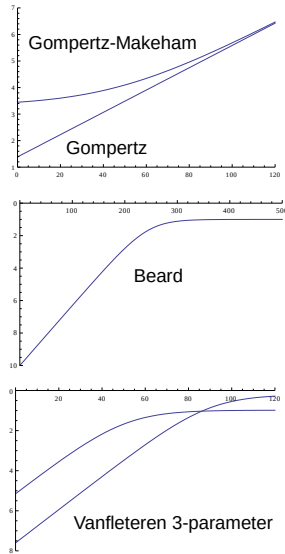
- Intended to be a model of individual risk, rather than a model of population risk
- Assumes inter-individual heterogeneity as a cause of certain population patterns



There appear to be three basic types of 'difference' in semi-logarithmic mortality curves. These differences may be seen between strains or populations of a species, in the same strain under different conditions, or in the 'same' population over time.

Type 1 and 2 differences involve changed gradient, which is widely held to indicate and altered ageing rate. Others argue that any fall in mortality may represent slower ageing.

Standard models of ageing generally exhibit type 1 and type 3 changes with changes in single parameters. However, type 2 changes necessitate adjustment in more than one parameter in order to 'fix' the apparent pivot point in later life.



Actuarial modifications (such as Makeham or Beard) to basic models (such as Gompertz) adjust for non-linearity of early to mid-life patterns, or for mortality deceleration to a plateau in late life.

Makeham has been interpreted by many as an additive component of individual risk, though this may be an ecological fallacy.

Early and late life deviations from a regular pattern may be manifestations of heterogeneity rather than expressions of modal individual risk.

## A comprehensive theory of ageing:

- Should explain why most species deteriorate with chronological age.
- Should explain exponential rises in mortality.
- Should explain [type 2] changes in mortality curves
- Should account for loss of exponentiality, plateaux, and deceleration at older ages.

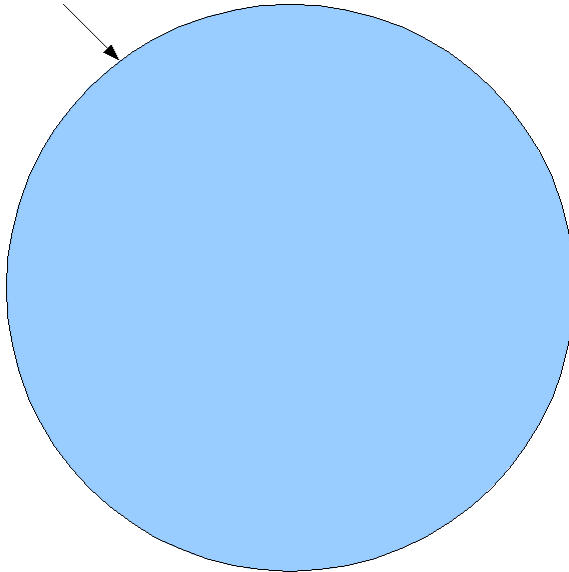
(paraphrased from Gavrilov & Gavrilova 2006)

# BASIC PRINCIPLES

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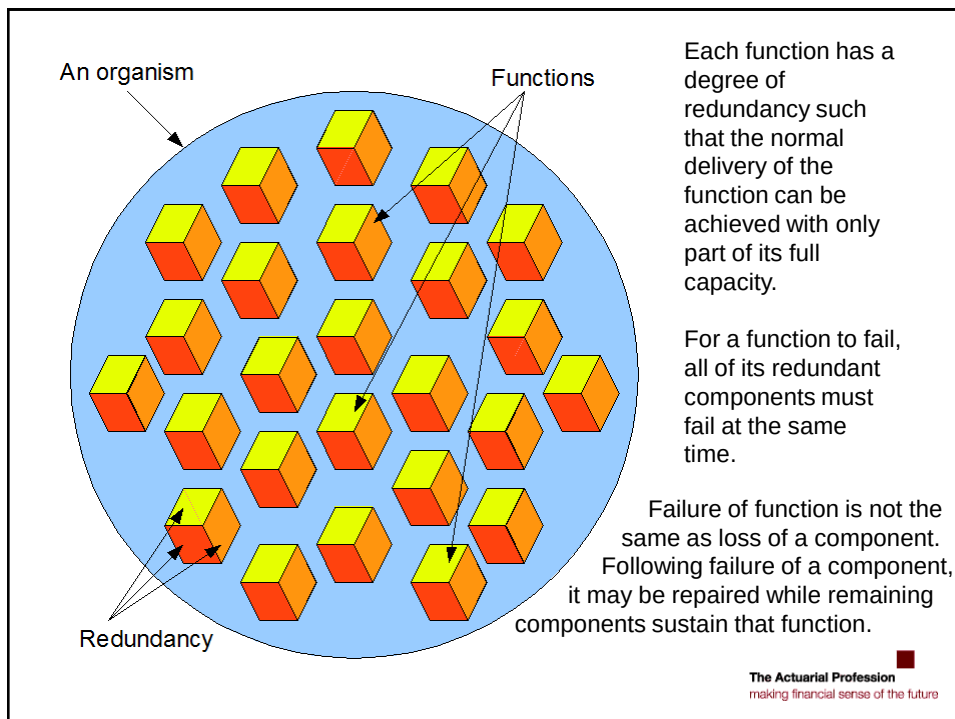
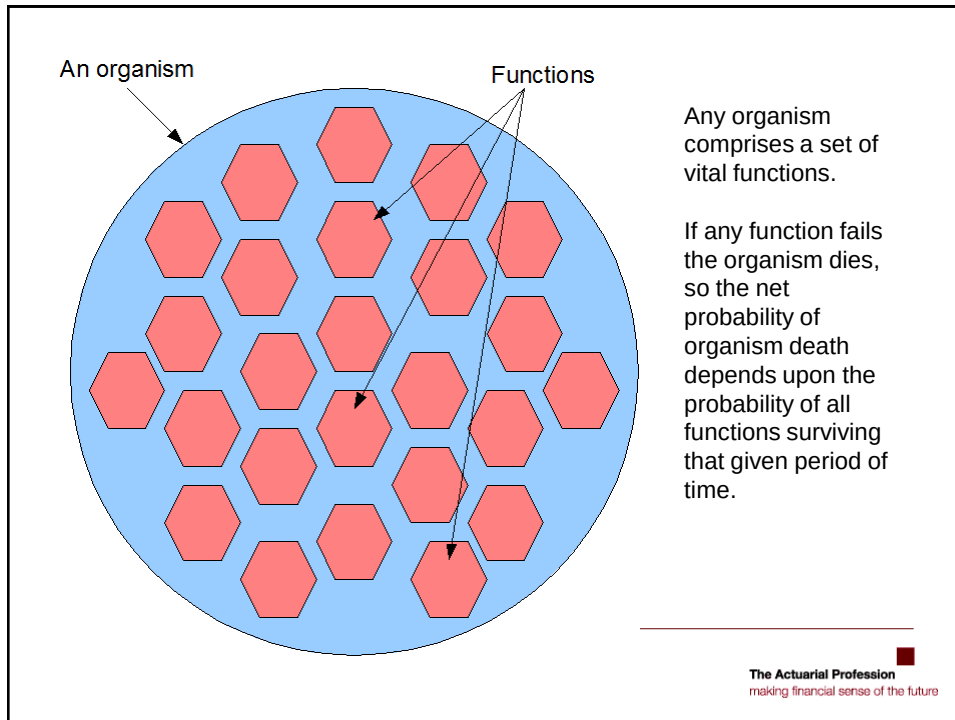
An organism

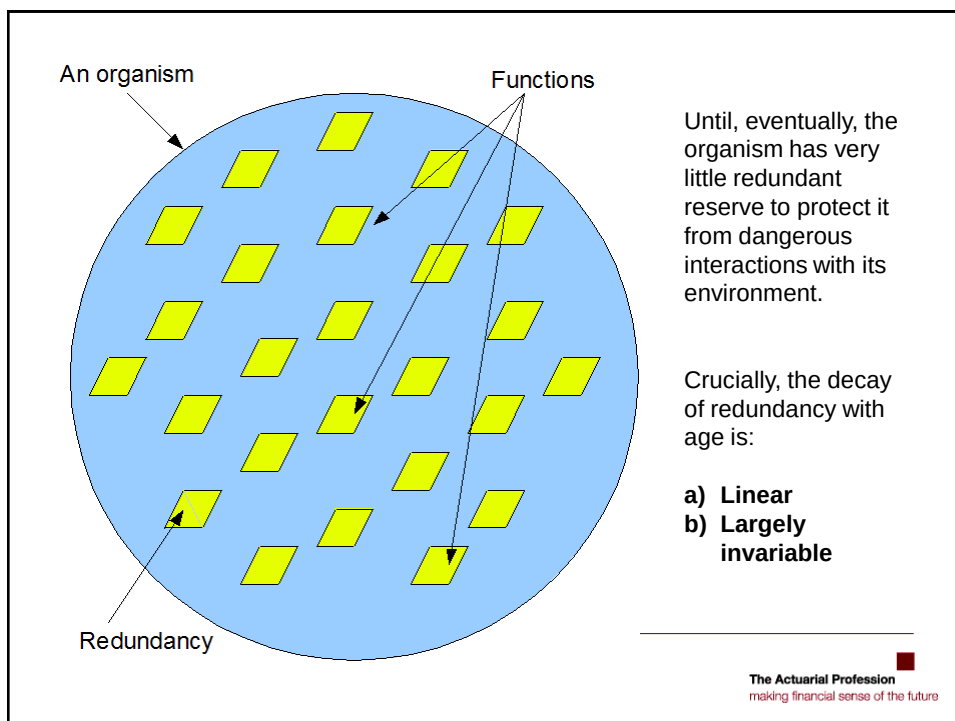
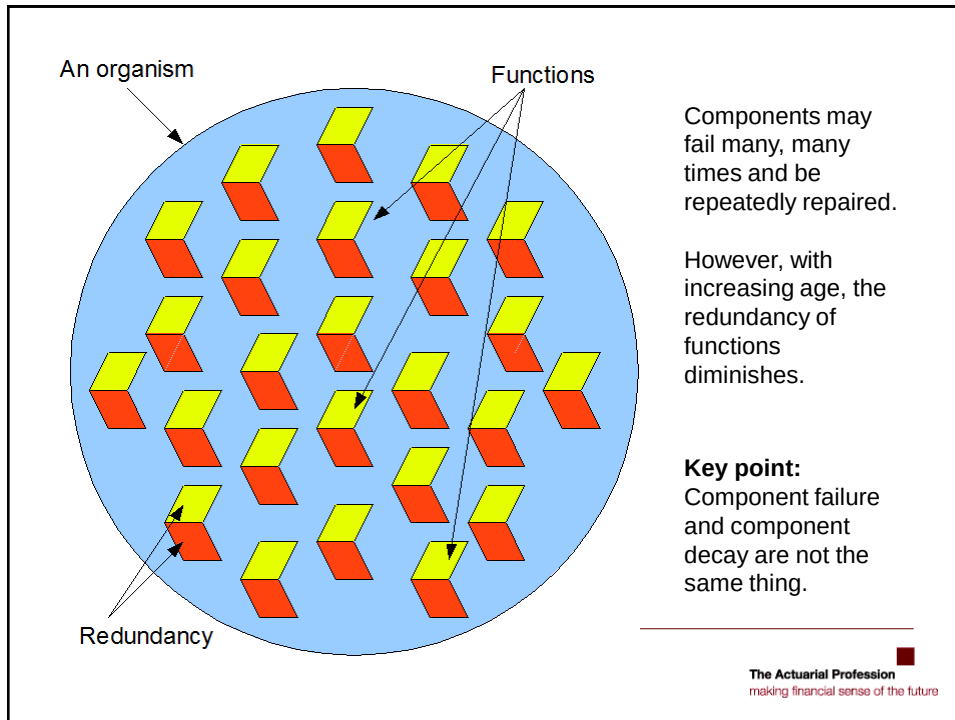


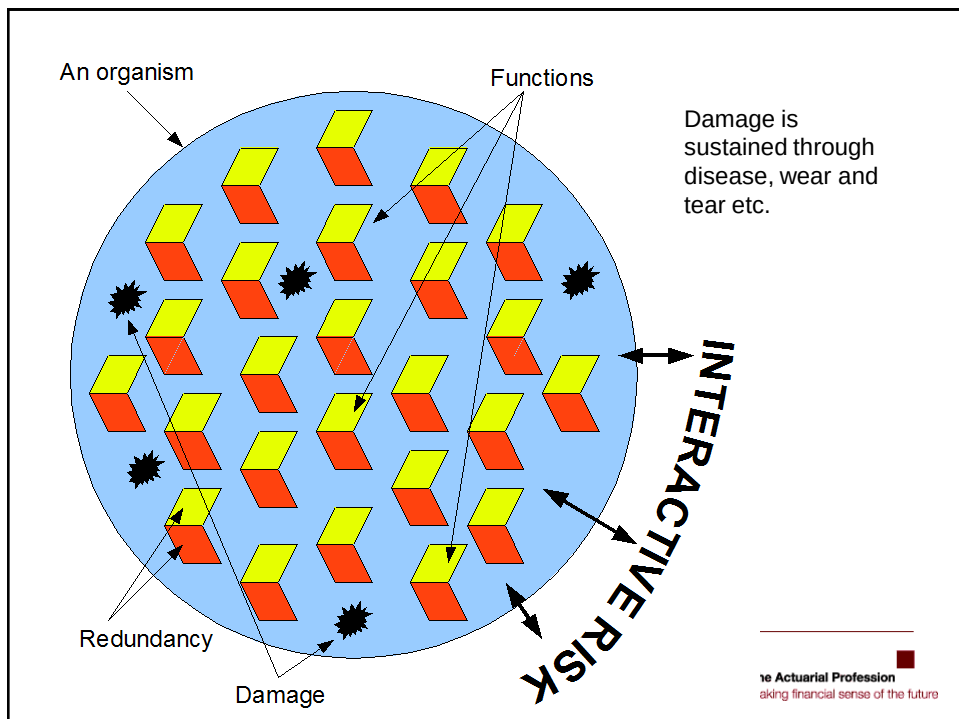
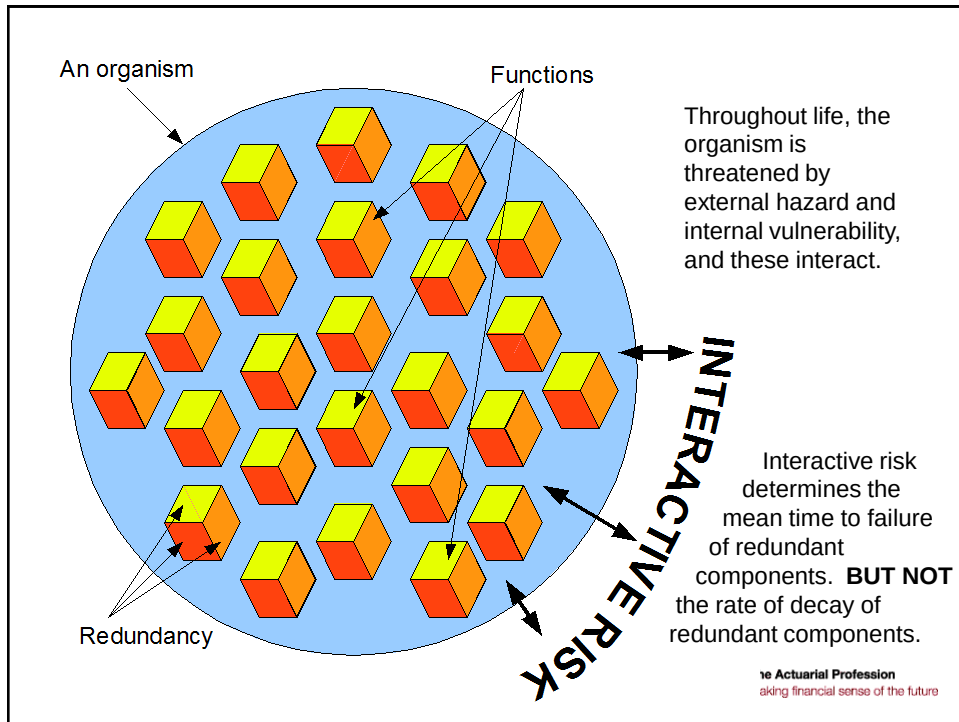
Any organism at any instant has a given probability of failing per unit time

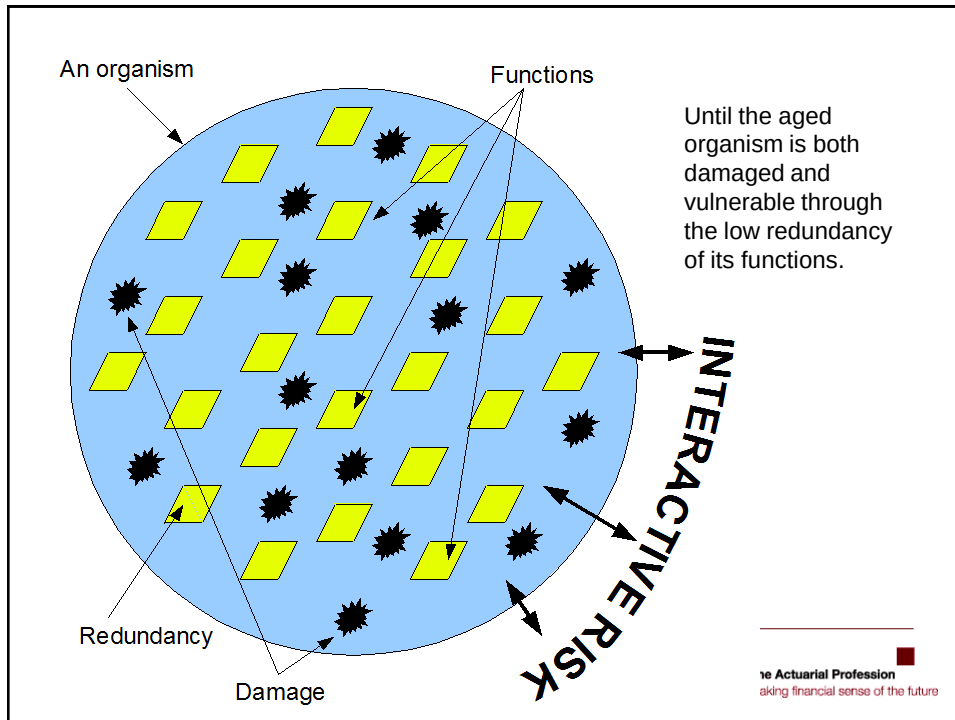
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## The nested binomial model

- Divides age-related risk into two distinct partitions:
  - Redundancy decline, which is linear and largely invariable.
  - Interactive risk, which is markedly variable and describes all other influences upon mortality risk.



## The nested binomial model

- Assumes that:
  - organisms may be regarded simply as a set of ( $n$ ) vital functions connected in series
  - each function has an initial species or strain-specific quantity ( $s$ ) of redundancy which declines linearly at a largely invariable rate ( $a$ ) throughout life
  - net risk of dying depends upon both the redundant state of the organism's functions and a level of interactive risk ( $k$ ) which varies independently of the redundant state

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Milne EMG. The natural distribution of survival. Journal of Theoretical Biology 2008;doi:10.1016/j.jtbi.2008.07.021

$$\mu_c = -\text{Ln} \left( 1 - \left( 1 - 0.5^{\frac{1}{r_c k}} \right)^{r_c} \right)^n$$

Where redundancy ( $r$ ) at the current age ( $c$ ) is described by:

$$r_c = s - \frac{c}{a}$$

$s$  = theoretical redundancy level  $r$  in arbitrary units at age 0

$a$  = time taken for decay of 1 unit of redundancy in the same units as age

$k$  = interactive risk parameter = the unit-specific half-life when  $r = 1$

$n$  = number of functions that comprise the organism

$c$  = current age

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$$\mu_c = -\text{Ln} \left( 1 - \left( 1 - 0.5 \frac{1}{r_c k} \right)^{r_c} \right)^n$$

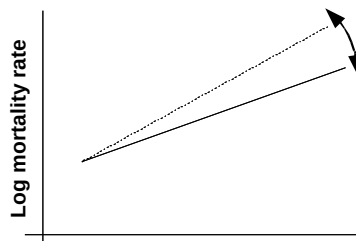
Interactive risk (parameter  $k$ )

$$r_c = s - \frac{c}{a}$$

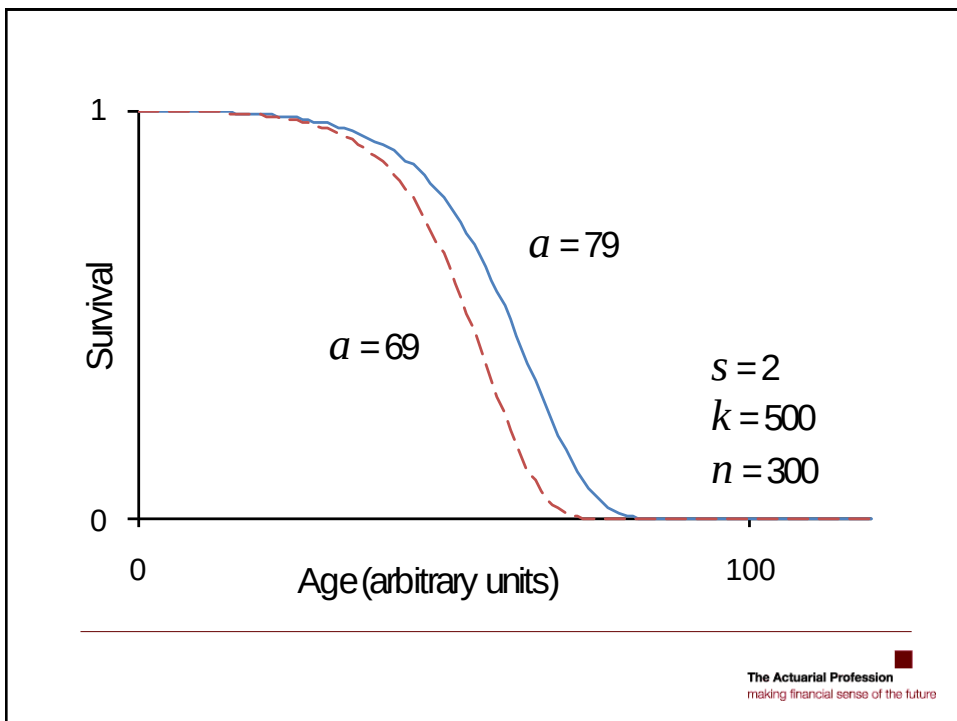
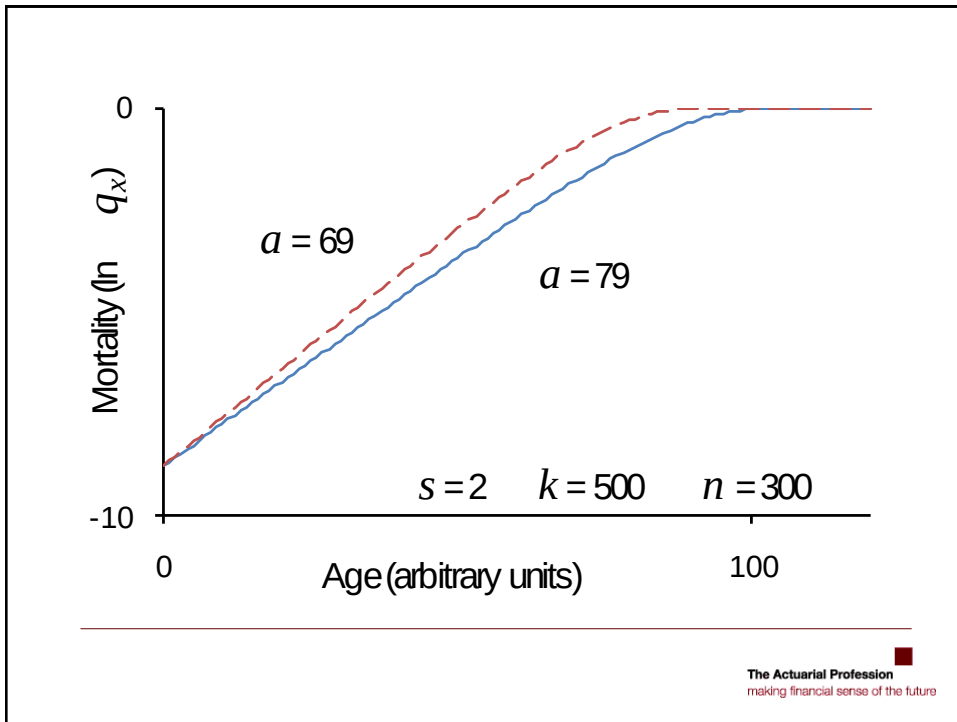
Determinant of the rate of redundancy decline (parameter  $a$ )

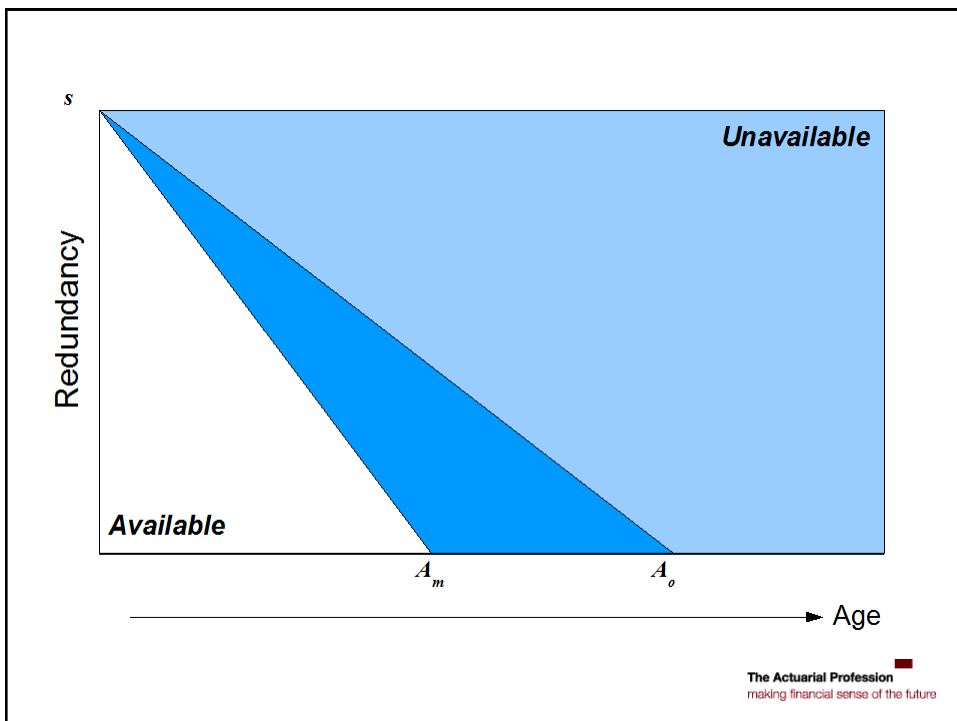
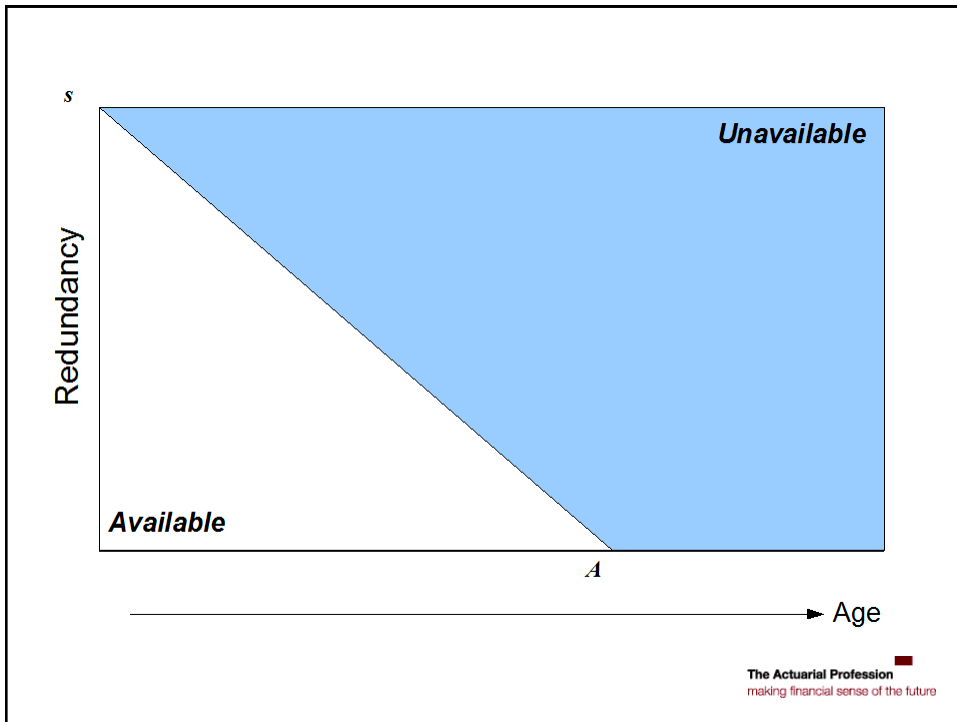
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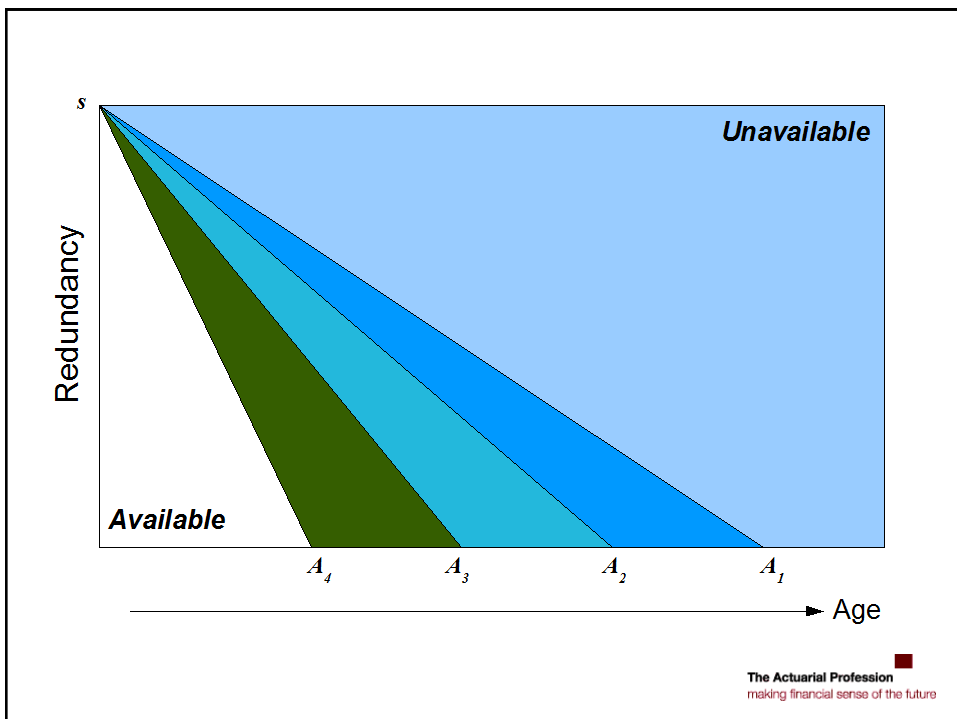
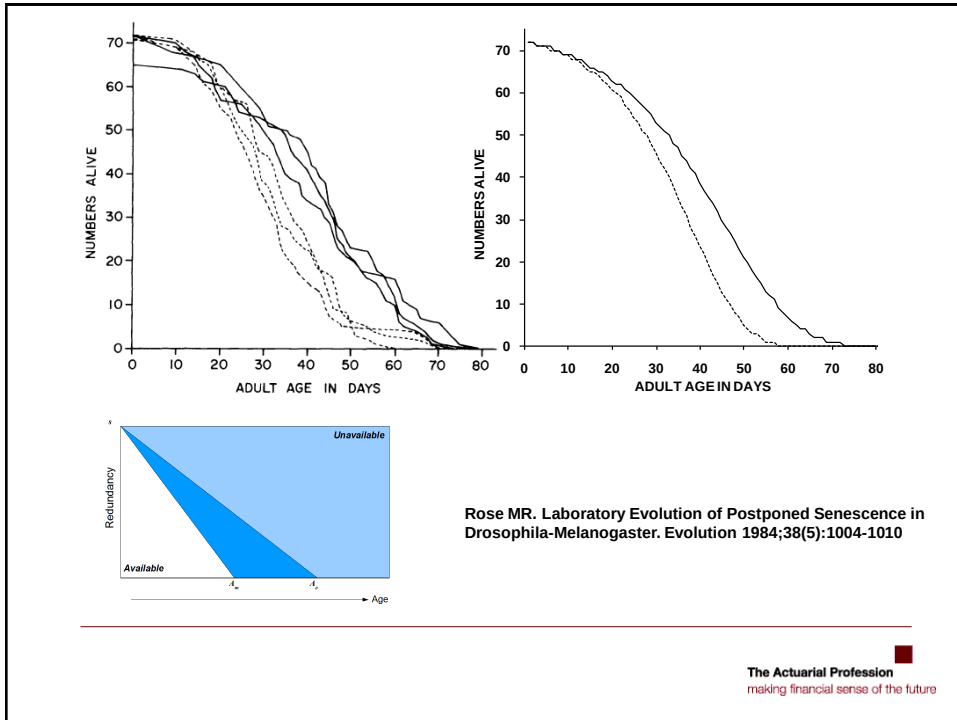
## PARAMETER $a$ – type 1 change



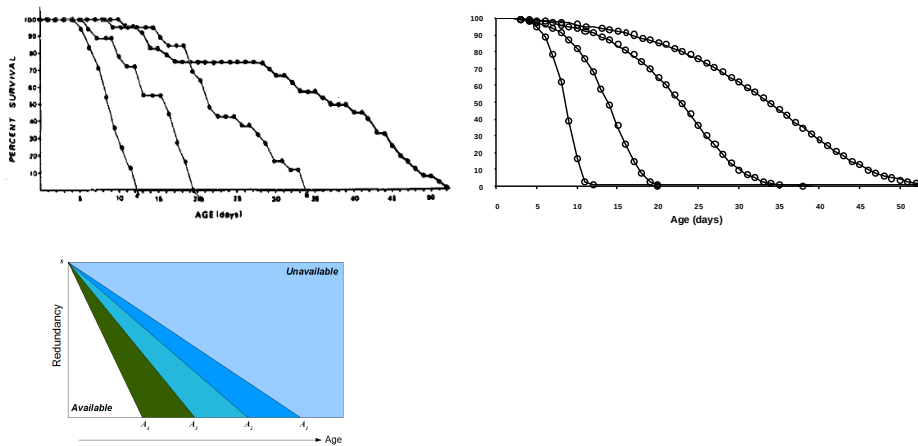
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Klass MR. Aging in the nematode *Caenorhabditis elegans*: major biological and environmental factors influencing life span. *Mech Ageing Dev* 1977;6(6):413-29



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## Parameter $\alpha$

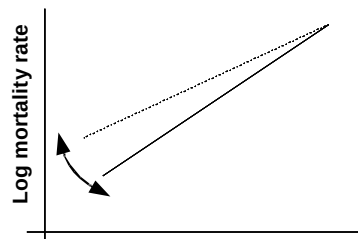
- Describes the rate of redundancy decline
- Is largely invariable
- BUT**
- Varies with temperature (also with dietary restriction, oxygen tension – not illustrated)
- Is the element of the model that changes with evolved longevity

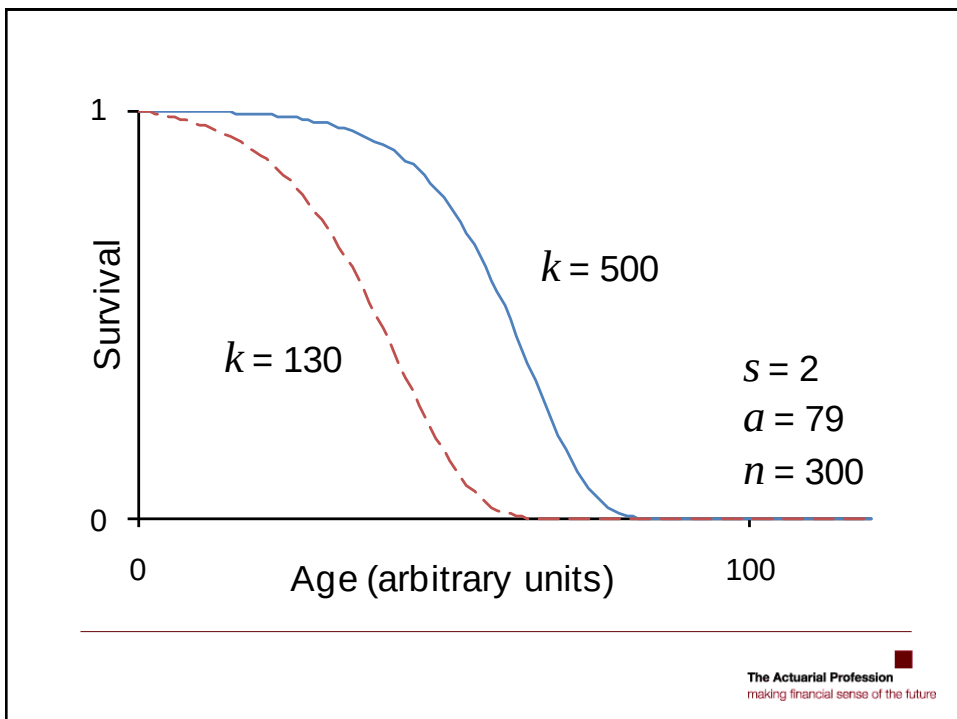
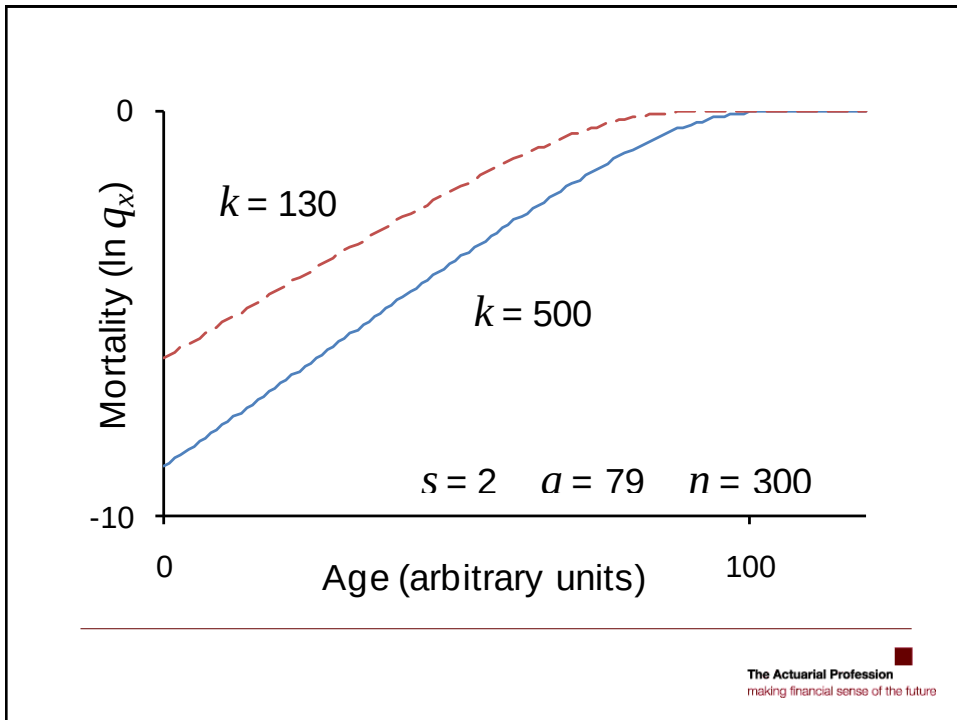
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## Parameter $a$

- Has similarities to “senescence” (Finch) or “ageing” (Hayflick)
- Determines the structure and scale of the mortality curve

## PARAMETER $k$ – *type 2 change*







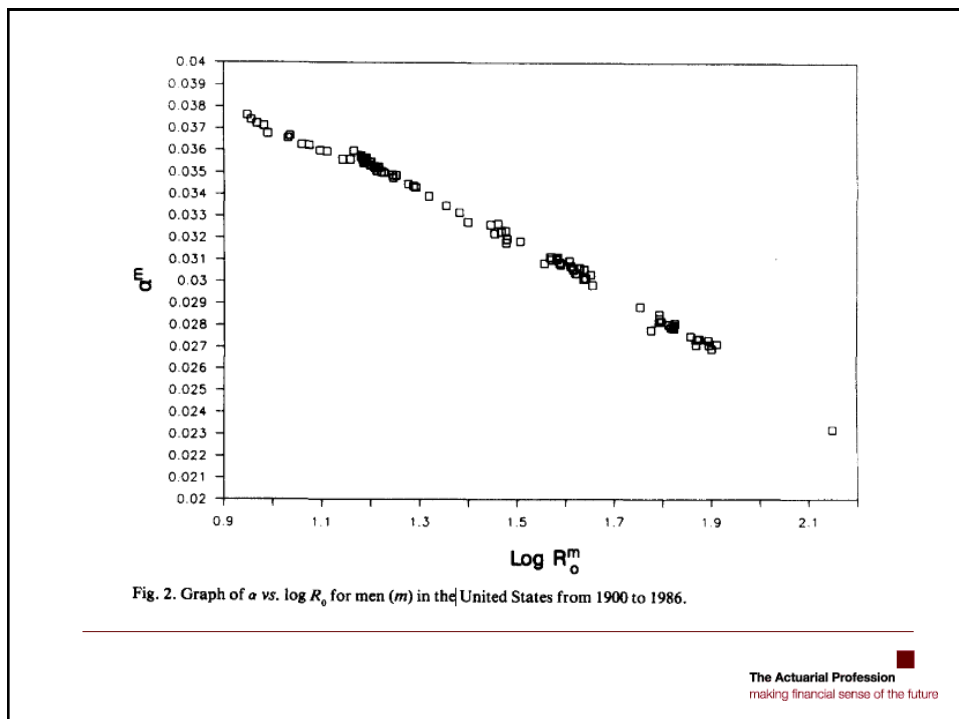
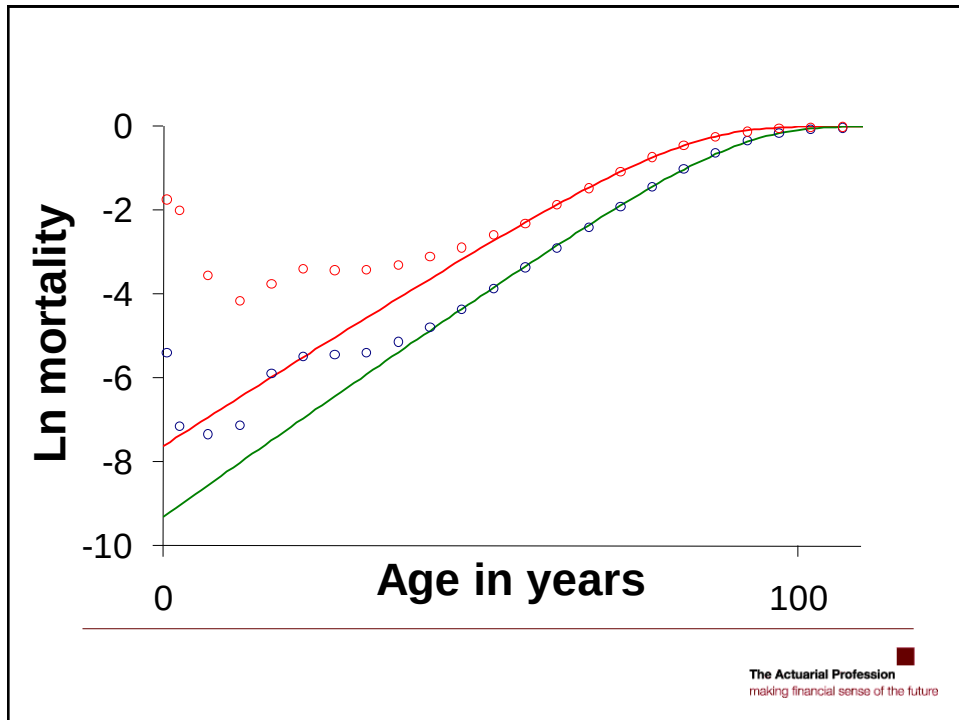
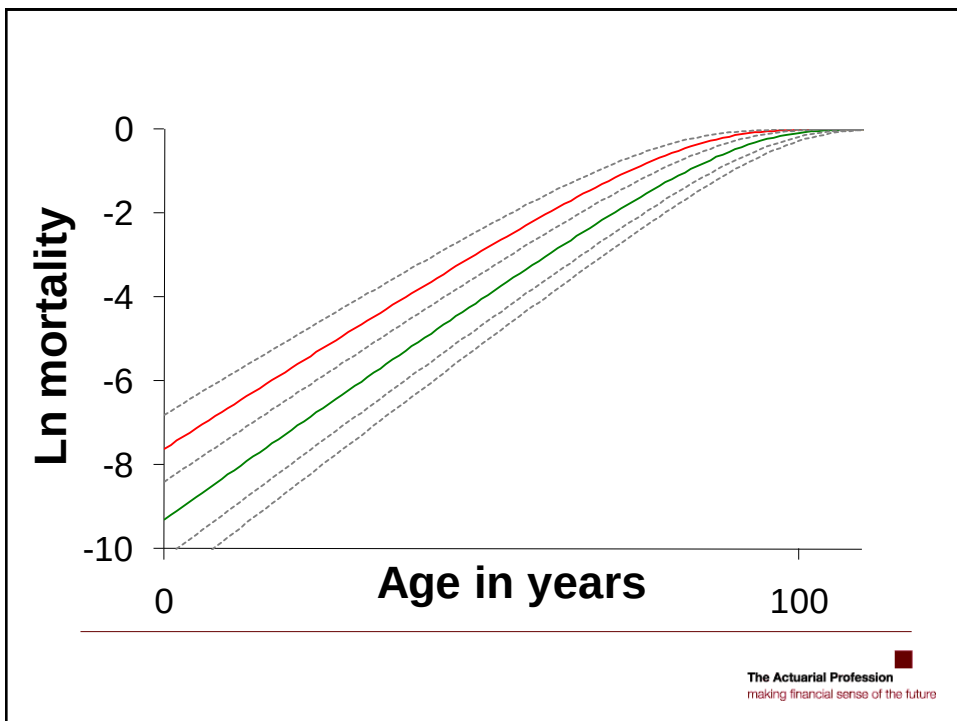
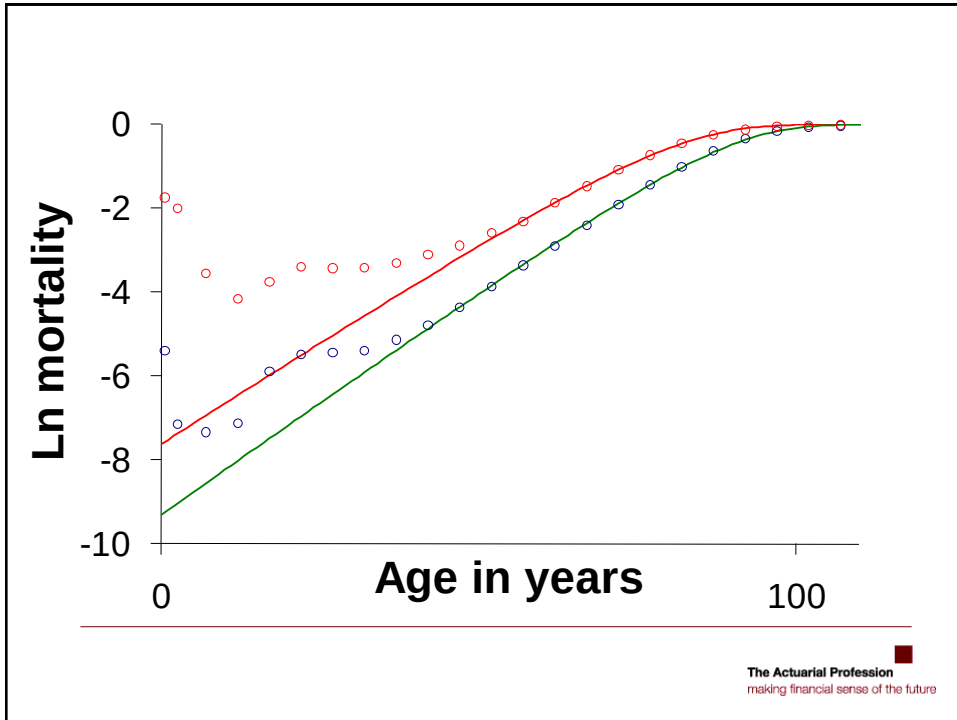
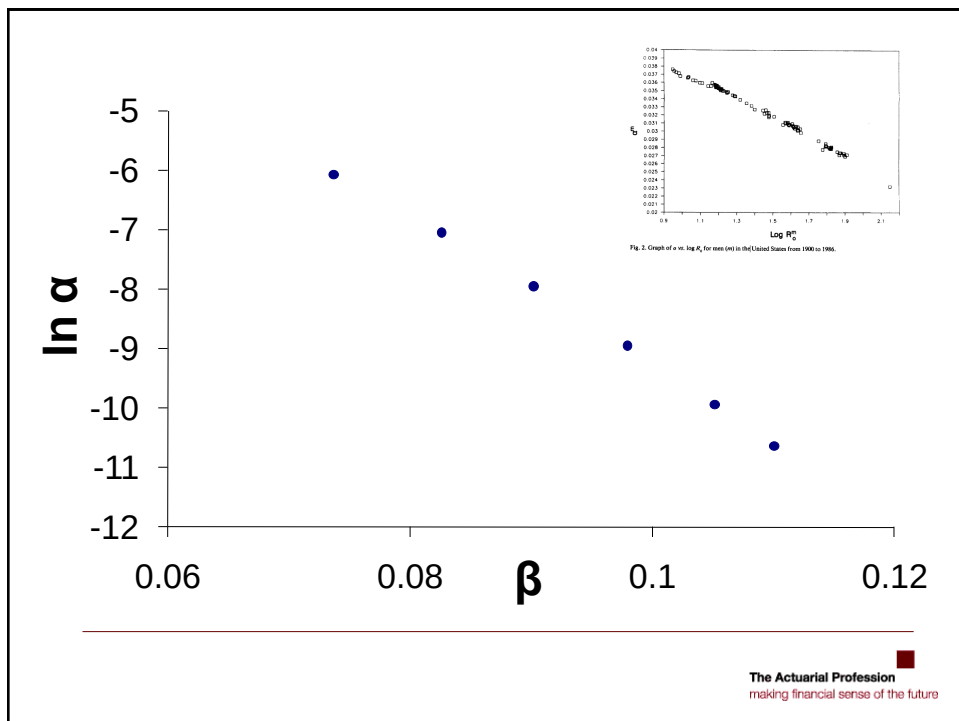
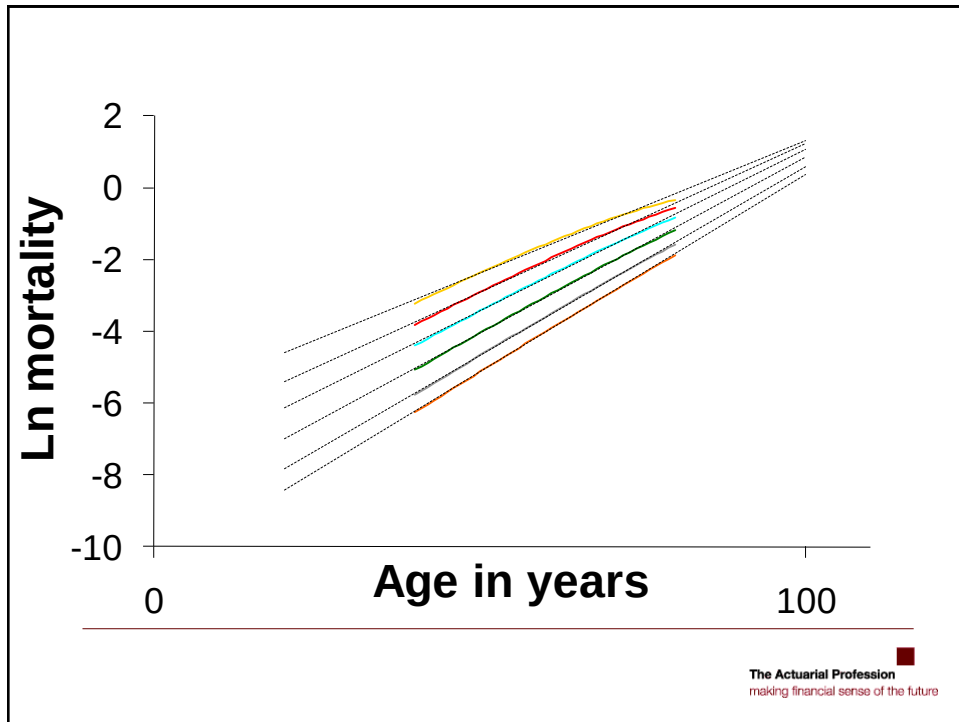
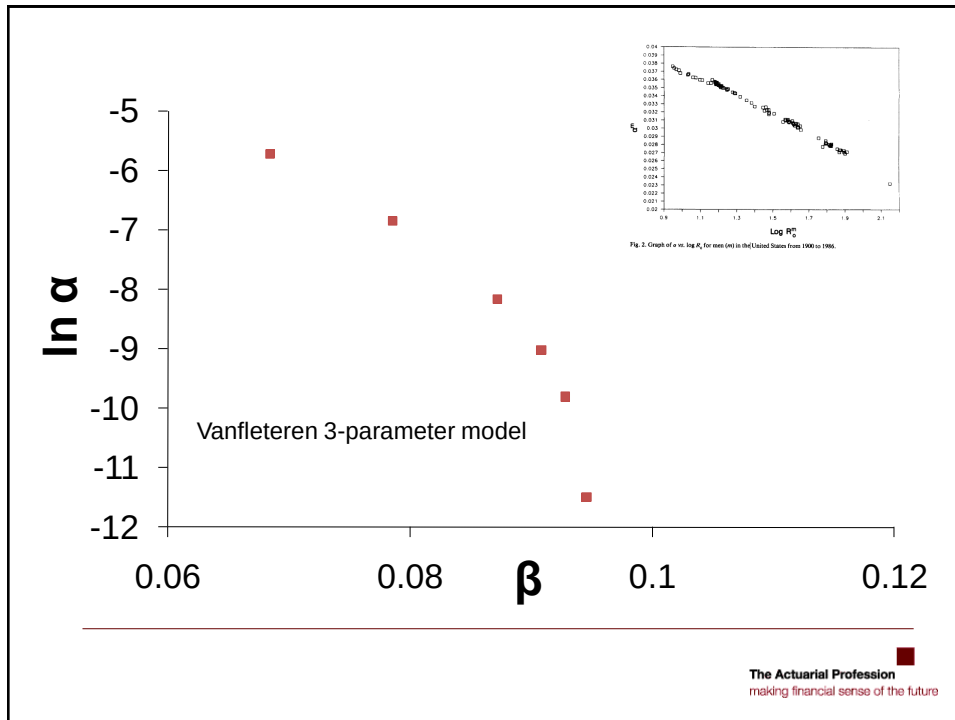


Fig. 2. Graph of  $\alpha$  vs.  $\log R_0$  for men (m) in the United States from 1900 to 1986.



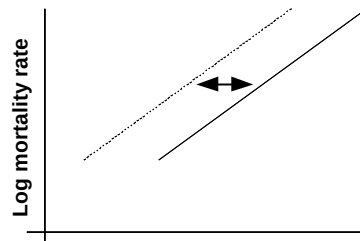




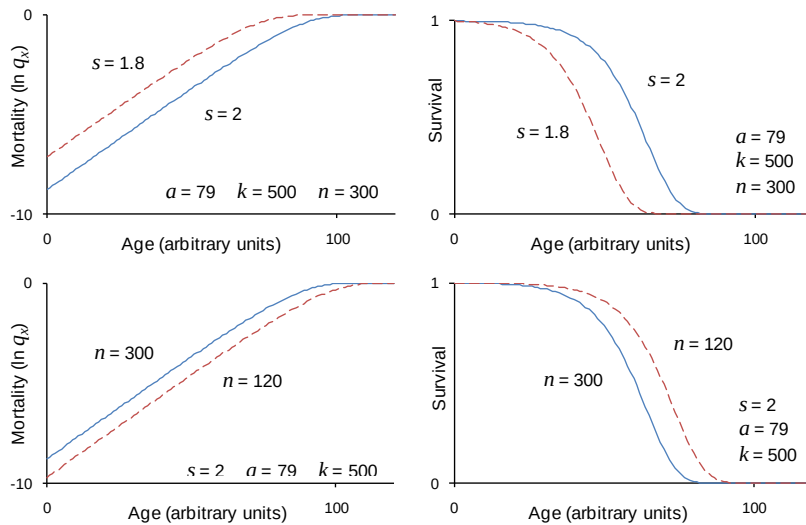
## Parameter $k$

- Describes interactive risk - the aggregate of all other variable, individual and environmental risks including cumulative and (non-senescent) genetic risks.
- The derivation of parameter  $k$  is that it is the half-life of "1 unit" of redundancy, therefore:
  - Low parameter  $k$  = high risk
- Is the element that is changed when organisms age in different environments, and with different external risk exposures.

## PARAMETER $s$ & $n$ – type 3 change



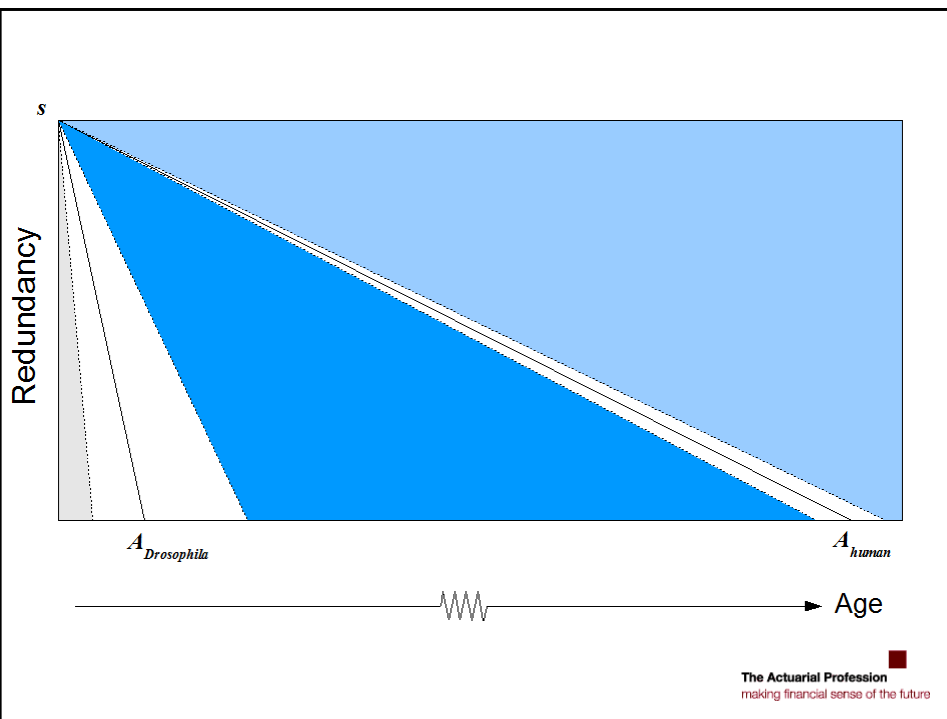
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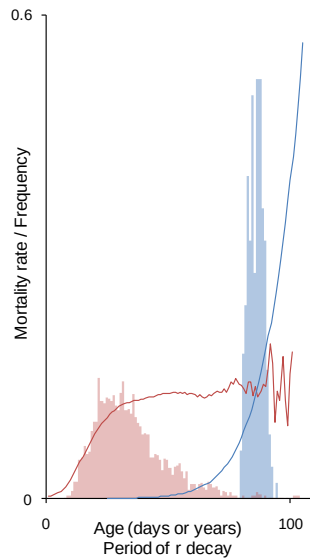
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# PARAMETER $\alpha$ HETEROGENEITY

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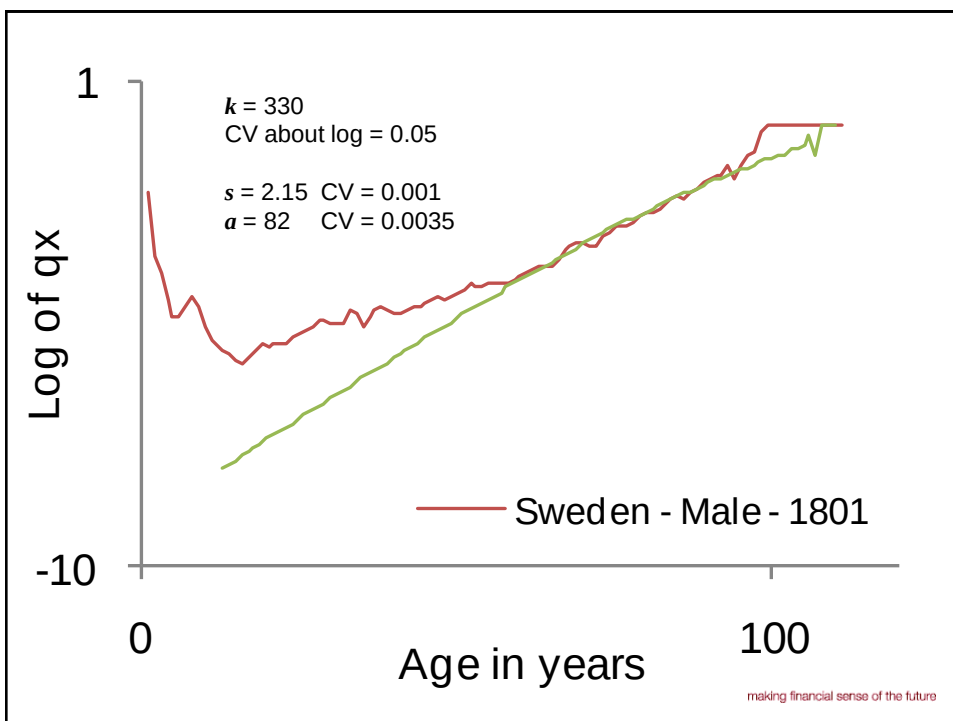
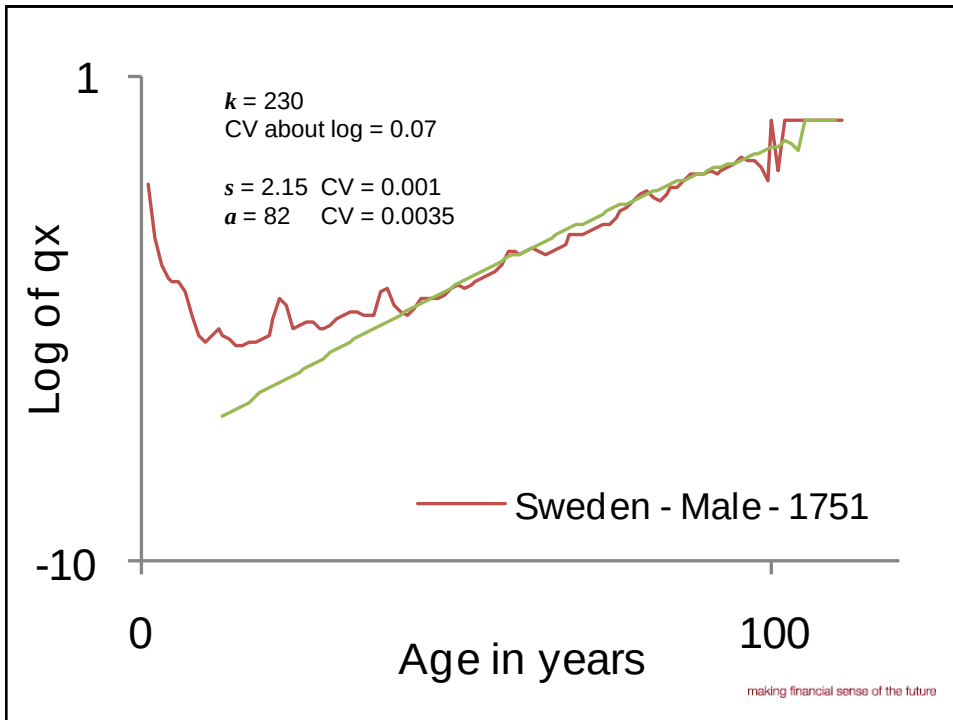
### Parameter $\alpha$

When parameter  $\alpha$  distribution is wide, skewed and its period is short, plateaux of mortality appear.

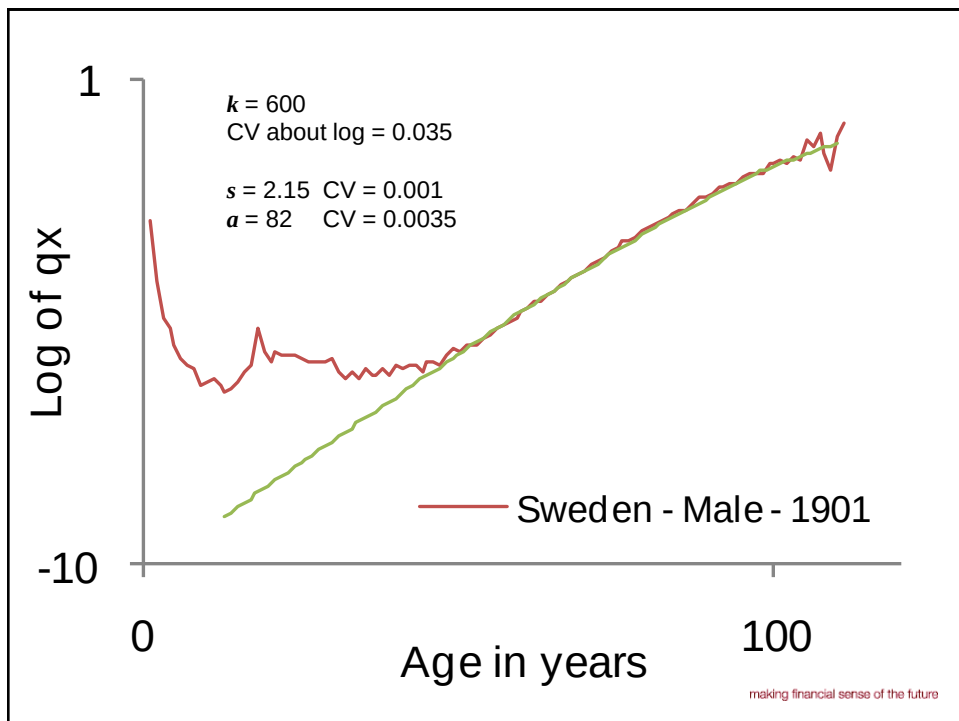
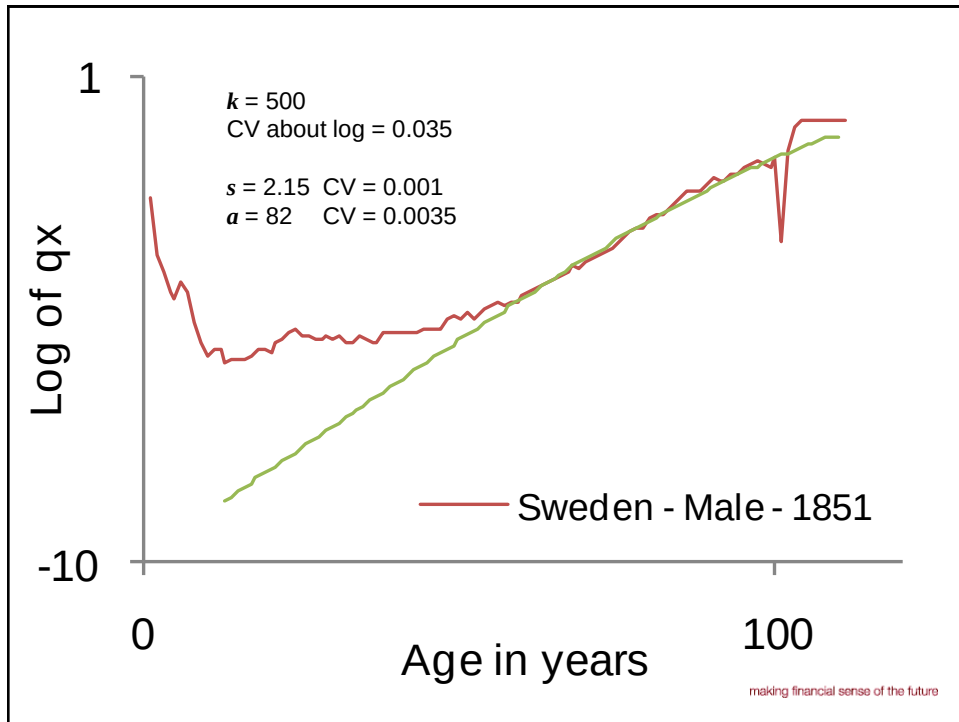
Conversely, when the distribution is relatively narrow and the period is long, the mortality curve is dominated by an exponential rise.

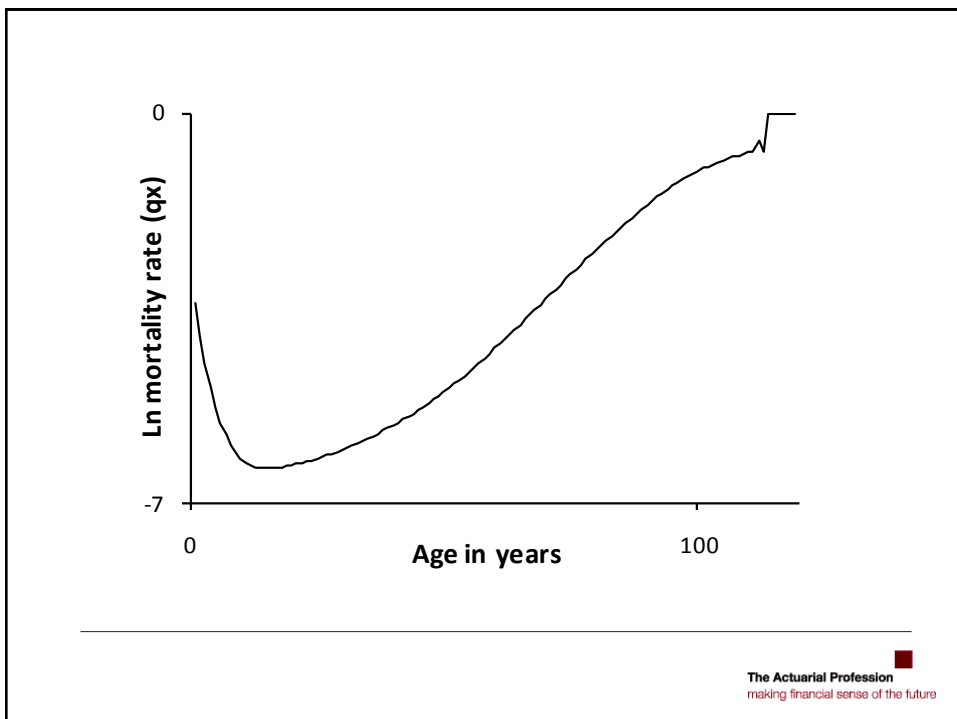
Thus, loss of exponentiality, plateaux and deceleration of mortality can be accounted for by heterogeneity in parameter  $\alpha$ .

## PARAMETER $k$ HETEROGENEITY

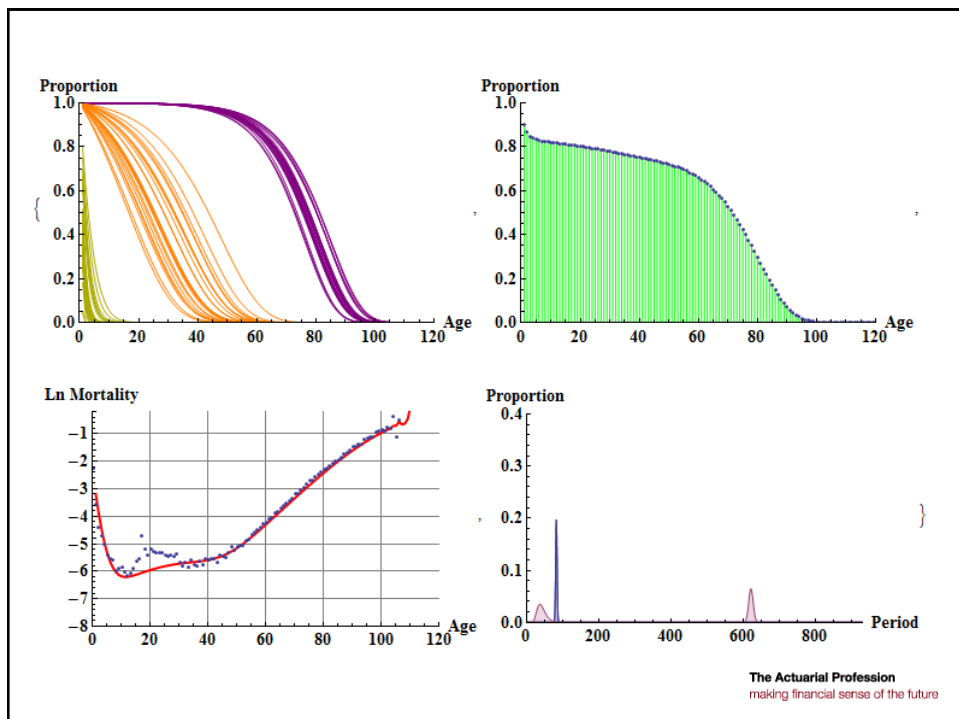


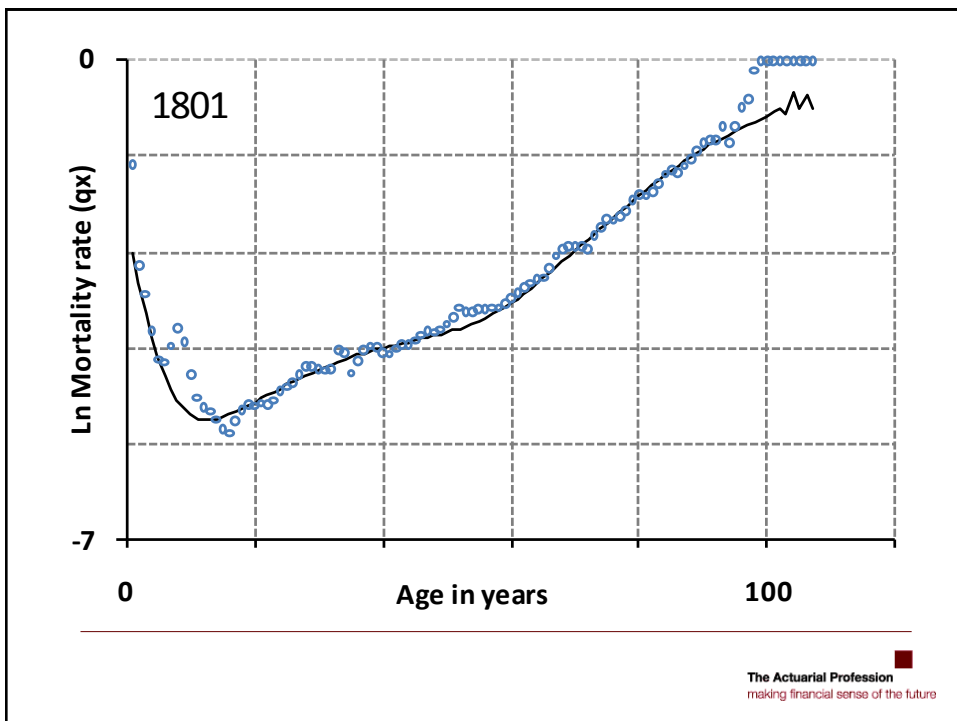
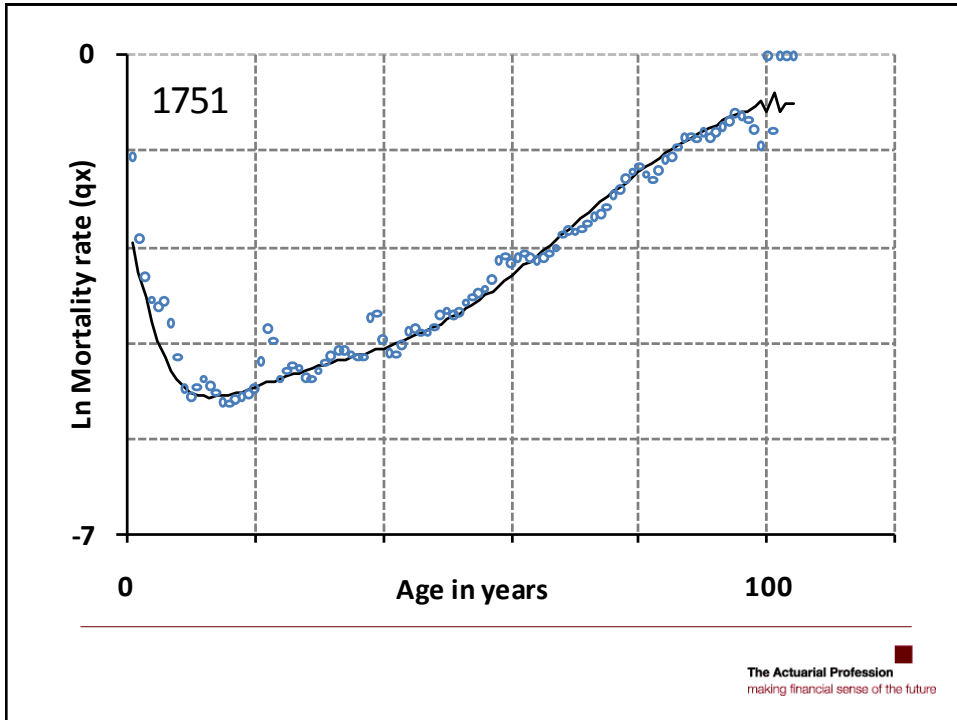


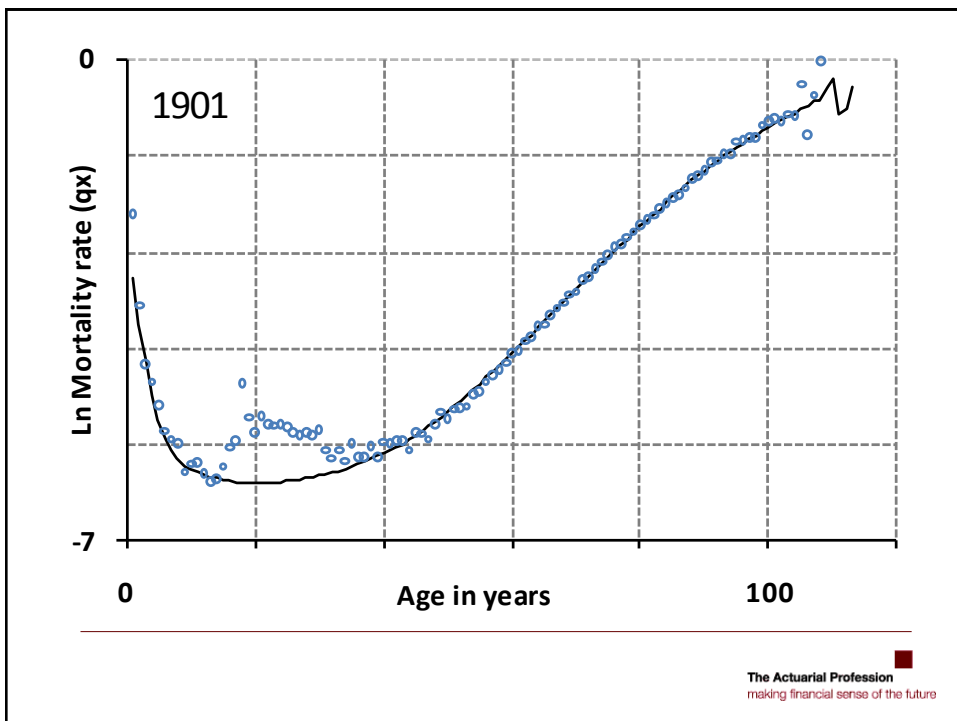
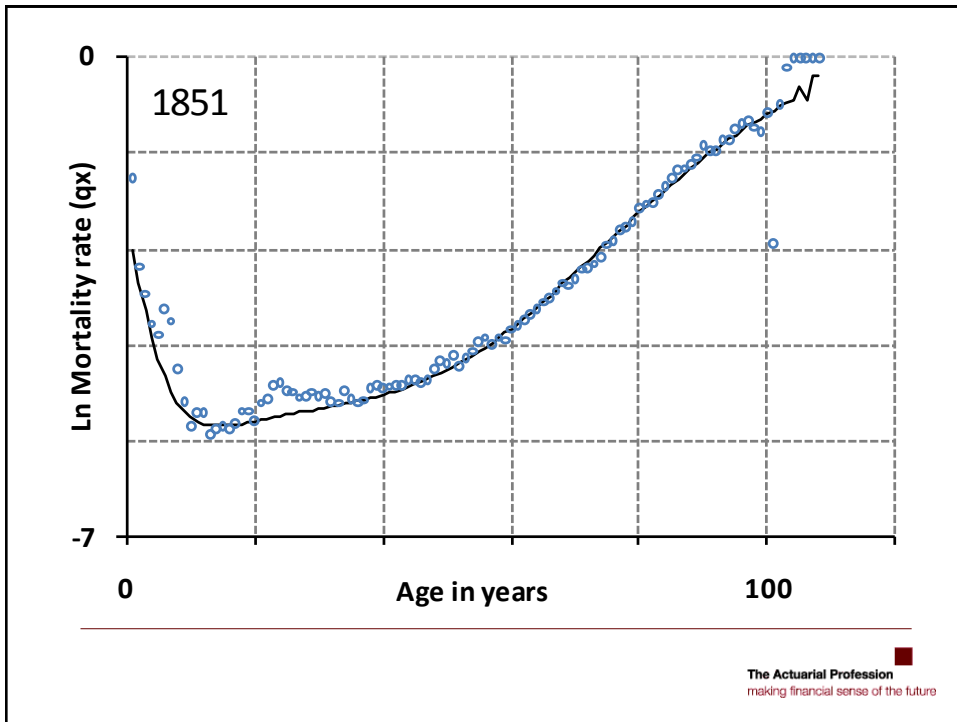




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|-----------------------------------------------------------------------------------------------------------------|--|-----------------------------------------------------------------|--|
| Number of subgroups <input type="text" value="25"/><br>Number of functions (n) <input type="text" value="300"/> |  |                                                                 |  |
| <b>Sub-population 1</b>                                                                                         |  |                                                                 |  |
| Sample size <input type="text" value="75000"/>                                                                  |  | Sample size <input type="text" value="80000"/>                  |  |
| Initial redundancy (s) <input type="text" value="2.15"/>                                                        |  | Initial redundancy (s) <input type="text" value="2.15"/>        |  |
| Std Dev of initial redundancy <input type="text" value="1.01"/>                                                 |  | Std Dev of initial redundancy <input type="text" value="1.01"/> |  |
| Period of redundancy decay (ba) <input type="text" value="82"/>                                                 |  | Period of redundancy decay (ba) <input type="text" value="82"/> |  |
| Std Dev of decay period <input type="text" value="1.025"/>                                                      |  | Std Dev of decay period <input type="text" value="1.025"/>      |  |
| Interactive risk (k) <input type="text" value="620"/>                                                           |  | Interactive risk (k) <input type="text" value="40"/>            |  |
| Std Dev of interactive risk <input type="text" value="1.01"/>                                                   |  | Std Dev of interactive risk <input type="text" value="1.35"/>   |  |
| Scale <input type="text" value="120"/>                                                                          |  | Sub-population 3                                                |  |
| Zoom <input type="text" value="360"/>                                                                           |  | Sample size <input type="text" value="170000"/>                 |  |
| Re-randomize using current values <input type="button" value="Recalculate"/>                                    |  | Initial redundancy (s) <input type="text" value="2.15"/>        |  |
| Reset to human values <input type="button" value="Human"/>                                                      |  | Std Dev of initial redundancy <input type="text" value="1.01"/> |  |
| Reset to mouse values <input type="button" value="Mouse"/>                                                      |  | Period of redundancy decay (ba) <input type="text" value="82"/> |  |
| Reset to Medfly values <input type="button" value="Medfly"/>                                                    |  | Std Dev of decay period <input type="text" value="1.025"/>      |  |
| Reset to Drosophila values <input type="button" value="Drosophila"/>                                            |  | Interactive risk (k) <input type="text" value="5"/>             |  |
| Reset to C.elegans values <input type="button" value="C.elegans"/>                                              |  | Std Dev of interactive risk <input type="text" value="1.35"/>   |  |







## Summary – Basic Principles

- The NBM:
  - allows modelling of mortality and survival curves, late-life mortality deceleration, S-M correlation, mortality plateaux and slowing of mortality .
  - partitions mortality risk into two main elements: redundancy decay and interactive risk.
  - No single parameter represents 'ageing' although parameter  $a$  is closest to the definition commonly used by gerontologists (e.g. Hayflick)

## Human mortality

- Once a fixed human value for parameter  $a$  is assumed, variation in historical mortality can be modelled relatively simply by variation exclusively in parameter  $k$ .
- So what does parameter  $a$  / redundancy actually represent?

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Health***



## Questions?

- Thanks to:
- Stephen Singleton
- Oliver Milne
- Tom Kirkwood
- Daryl Shanley

**Funding and support:**

NHS North East  
Newcastle University  
Human Mortality Database

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