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Research Document 2009/108

Document de recherche 2009/108

**Modelling Northwest Atlantic harp seal
populations: modifying an Excel model
to R**

**Modélisation des populations de
phoques du Groenland du Nord-Ouest
de l'Atlantique : modification d'un
modèle Excel en R**

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This document is available on the Internet at:

<http://www.dfo-mpo.gc.ca/csas/>

Ce document est disponible sur l'Internet à:

ISSN 1499-3848 (Printed / Imprimé)

ISSN 1919-5044 (Online / En ligne)

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Canada

Correct citation for this publication:

La présente publication doit être citée comme suit :

Hammill, M.O, Ferland-Raymond, B., Rivest, L.-P. and Stenson, G. B. 2010. Modelling Northwest harp seal populations: modifying an Excel model to R. DFO Can. Sci. Advis. Sec. Res. Doc. 2009/108. iv + 13 p.

ABSTRACT

The model currently used to describe the population dynamics of the Northwest Atlantic harp seal (*Pagophilus groenlandicus*) is a two parameter model that uses information on age specific reproductive rates, ice-related mortality of young seals, removals and estimate of pup production. Although the basic model has taken a number of forms, in recent years it has been run using Excel as a basis. However, the current framework is very slow reducing the opportunities for testing different scenarios and management approaches. In order to improve performance, the model was transferred to R which allowed a reduction in the simulation processing time. During the transfer process, the model was also modified slightly, including a change to the resampling process of pregnancy rates to include correlation among age classes within a year. The R model also builds a new removal matrix for each Monte Carlo simulation using the modeled population age structure rather than the fixed age structure used previously. The Excel and the R models produced similar population trends, but the R model consistently estimated higher populations with a slightly smaller variance. This resulted from the elimination of negative age classes and by the optimisation process that produced lower mortality rates with a smaller variance. The lower variance resulted in higher L_{20} projections in the R model predictions.

RÉSUMÉ

À l'heure actuelle, le modèle qui sert à décrire la dynamique de la population de phoques du Groenland du Nord-Ouest de l'Atlantique (*Pagophilus groenlandicus*) est un modèle de population à deux paramètres qui intègre des renseignements sur les taux de reproduction selon l'âge, la mortalité des jeunes phoques associée aux glaces, les prélèvements et les estimations de la production de jeunes phoques. Bien que le modèle de base ait été présenté sous plusieurs formes, celui utilisé au cours des dernières années a été exécuté à partir de Excel. Cependant, le cadre actuel est très lent, ce qui réduit la possibilité de tester divers scénarios et diverses approches de gestion. Afin d'améliorer le rendement, le modèle a été transféré sur R, ce qui a permis de réduire la durée de traitement des simulations. Pendant le processus de transfert, certaines modifications mineures ont été apportées au modèle, notamment au processus de rééchantillonnage des taux de gestation pour tenir compte de la corrélation entre les groupes d'âge dans l'année. Le modèle sur R établit en outre une nouvelle matrice de prélèvements pour chaque simulation de Monte-Carlo en utilisant la structure des classes d'âge modélisée plutôt que la structure des classes d'âge fixe utilisée au préalable. Les modèles exécutés sur Excel et R ont produit des tendances démographiques semblables, mais de manière constante l'estimation de la population obtenue à partir du modèle exécuté sur R est légèrement supérieure avec une variance légèrement plus faible. Cela résulte de l'élimination des groupes d'âge négatifs et du processus d'optimisation qui a donné des taux de mortalité inférieurs avec une variance plus faible. La variance plus faible a donné des prévisions L_{20} plus élevées dans le cas des prédictions du modèle exécuté sur R.

INTRODUCTION

The current model used to describe the dynamics of the Northwest Atlantic harp seal population is based on an age structured model first developed in the 1980's by Roff and Bowen (1983) and modified by Shelton et al. (1992). It is a two parameter model that uses information on age specific reproductive rates, ice-related mortality of young of the year seals (YOY) and human removals to predict population size (Hammill and Stenson 2008). The model is fitted to independent estimates of pup production by adjusting the starting population size and adult mortality. The current version of the model was built in Excel (Microsoft) using the add-in software @Risk (Palisade Corporation 2000). The model uses Monte Carlo sampling to simulate the current population size and to project it into the future. However, the model is very slow to run (several hours) which limits the number of management scenarios that can be evaluated. Reducing the amount of time taken to run the model would allow a better testing of the different model assumptions and options. The goal of the present work was to determine the impact of transferring the Excel model into R (R Development Core Team, 2009) on the estimated population projections.

MATERIALS AND METHODS

DATA

Total population of harp seals is estimated using a model that incorporates data on age specific reproductive rates and removals with independent, periodic estimates of pup production. Eight estimates of pup production are available since the 70's (1978, 1979, 1980, 1983, 1990, 1994, 1999, 2004)(Hammill and Stenson 2005). The first four were conducted using mark recapture methods while the last four were aerial surveys. The model assumes a 1:1 sex ratio and annual estimates of age-specific reproductive rates obtained from seals collected during the last quarter of pregnancy. Reproductive rate data were obtained between 1954 and 2001 (Sjare et al. 2004) and smoothed using a nonparametric regression estimator (Hammill and Stenson 2008). Seals 4 years old and younger were considered immature while seals 8 years and older were considered to be fully recruited into the population.

Five different sources of removals are incorporated into the model; 1) the Canadian commercial hunt, 2) the Greenland subsistence harvest, 3) the Arctic subsistence harvest 4) the percentage of seals killed but not reported or recovered (i.e. struck and lost) and 5) the bycatch in commercial fishing gear (Stenson 2009). Annual estimates of removals are available beginning in 1952 and are structured by age classes.

Finally, mortality of young seals due to poor ice conditions is included in the model and incorporated as a proportion of animals surviving. This factor acts on the young of the year (YOY) only and occurs prior to the start of the commercial hunt (Hammill and Stenson 2008). The level of mortality varies among years and is based upon observations of the conditions encountered (e.g. ice extent and thickness, frequency of storms, etc) and reports of dead seals.

MODEL

Modeling the dynamics of the Northwest Atlantic harp seal population actually occurs in two steps. In the first, the model is fitted to independent estimates of pup production by adjusting initial population size (α) and adult mortality rates (M). Referred to as the 'Fitting Model', multiple

population matrices are created using Monte Carlo sampling and the parameters M and α are estimated. This is done from 1960 until the last year data are available. The second part of the model is the 'Projection Model', where the population is projected into the future to examine the impacts of different management options on the population. The projection model is based on the same equations as the fitting model, α and M are assumed to be normally distributed with average (and standard error) values obtained from the fitting model.

The basic age structured model is composed of 4 different equations (based on Hammill and Stenson 2008):

$$\begin{aligned} n_{a,t} &= ((n_{a-1,t-1} * w) - c_{a-1,t-1}) e^{-\gamma M} && \text{for } a = 1, \\ n_{a,t} &= (n_{a-1,t-1} e^{-M/2} - c_{a-1,t-1}) e^{-M/2} && \text{for } 1 < a < A, \\ n_{A,t} &= (n_{A-1,t-1} e^{-M/2} - c_{A-1,t-1}) e^{-M/2} && \text{for } a = A, \\ n_{0,t} &= \sum_{a=1}^A n_{a,t} P_{a,t} && \text{for } a = 0. \end{aligned}$$

where $n_{a,t}$ = population numbers-at-age a in year t ,
 $c_{a,t}$ = the numbers caught at age a in year t ,
 $P_{a,t}$ = per capita pregnancy rate of age a parents in year t ,
 assuming a 1:1 sex ratio. P is expressed as a normally distributed variable,
 with mean and standard error taken from the reproductive data
 M = the instantaneous rate of natural mortality.
 γ = a multiplier to allow for higher mortality of first year seals. Assumed to equal
 3, for consistency with previous studies.
 w = is the proportion of pups surviving an unusual mortality event arising from
 poor ice conditions or weather prior to the start of harvesting.
 A = the 'plus' age class (i.e. older ages are lumped into this age
 class and accounted for separately, taken as age 25 in this analysis).

The model creates a population matrix with 26 age classes from 1960 until the current year. It is created using data on pregnancy rates, removals and ice-related mortality. Two parameters are estimated to maximise the fitting of the model to the pup production surveys; the instantaneous mortality rate (M) and the initial population factor (α). The latter parameter is used to estimate the initial population in 1960. An initial population vector (26×1) was created to which α is multiplied. This initial population vector can be interpreted as an initial population age structure and the initial population size is calculated using:

$$P = \sum_{i=1}^{26} (\alpha \cdot l_i)$$

Where P is the total population, α the initial population parameter and l_i the initial population size for the i^{th} age class.

In the model α and M are adjusted to minimize the sum of square differences between the number of pups born, as predicted by the model and the number of pups estimated from the

independent pup surveys. The model is adjusted by minimizing the weighted sum-of-square difference between the estimated pup production from the model and the observed one from the surveys by iterative methods.

We included the uncertainty in the pregnancy rates and the pup production estimates by resampling them assuming a normal distribution of known mean and standard error. For each Monte Carlo simulation, a new M and α were estimated and stored.

For the projection model, the pregnancy rate data were assumed to remain the same as in the final year of the estimation (unless specifically changed for a particular scenario). They were assumed to have a normal distribution. Ice conditions in the future are uncertain, and variable. Therefore, values are selected randomly from the vector [0, 0, 0.1, 0.2, 0.3] which gives a mean mortality rates due to poor environmental conditions of 12%.

Finally, future harp seal removals are generated by summing the projected Canadian commercial quotas, the Greenland and Arctic catches and the bycatch. Of these, only the Greenland catches are allowed to vary with a uniform distribution ranging from 70,000 to 100,000 catches per year. Bycatch and Arctic catches are assumed to be constant at 10,500 and 1,000 respectively. Canadian commercial catches are set following the different management scenarios being tested. Implementation error, to account for a TAC runover between when a closure is announced and hunting actually ends, is also incorporated into the projection model as a variable following a uniform distribution with values ranging from 1 to 1.1 and a mean of 1.05.

In every case, the age structure, taken from recent data, is taken into account in calculating the amount of mortality within the population. For example, the Canadian hunt consists of 98% of young of the year while the Greenland hunt is limited to 14% young of the year (Stenson 2009). If in one year Canada removes 200,000 animals and Greenland 100,000 seals from the population, 10% and 86% of that would be consider to be 1+ seals which would then be distributed uniformly within the 1+ age classes following the age structure of the population. Removals in the commercial and subsistence hunts are adjusted for seals that are killed but are not recovered or reported. The level of struck and lost is assumed to be the same as used in the fitting model (i.e. 95% of YOY taken in the Canadian commercial hunt and 50% of all others are assumed to been reported; Stenson 2009).

R MODEL

The basic equations and data were modified to the R language and ran to compare the outputs to the Excel model used by Hammill and Stenson (2008). However, some differences in the Fitting Model occurred due to the fundamental variations between R and Excel.

While carrying out the Monte Carlo simulations for the fitting model, pregnancy rates were resampled from a normal distribution with known mean and standard error. For every year of the simulation (from 1960 until present day), 26 new pregnancy rates were sampled. In the Excel model, all age classes were treated as being independent from one another, implying for example that 15 year old females in 1975 could have a very good breeding year while 16 year olds could, simultaneously, have a very bad one. The model was modified in R to allow the pregnancy rates to vary more naturally within a year, i.e. to create generally good and bad breeding years by adding a correlation factor between the reproductive rates of the females from each age within a year. This correlation coefficient was fixed to $r=0.85$. This implies that if the 15 year old females have a good breeding year, so do the 16 year old females. This

increases the variance in pup production which makes the model more conservative. It is also important to note that in the R model, negative pregnancy rates or pregnancy rates higher than one are not allowed which was possible in the Excel model.

The building of the population matrix uses the removal data from Stenson (2008), who provides a fixed age structure matrix from specific periods to spread the mortality from the general 1+ age class across 26 year classes for all years. Using a fixed harvest age structure could result in negative estimates of the number of individuals for some age classes during some years. In reality, however, the true population age structure and age structure of the harvest are not well known and, at best, the raw data are only divided between the young of the year and the 1+ age class for some components of the catch. The R model was modified to assume that the 1+ catches were proportional to the age structure of the population, i.e. dividing the 1+ mortality using a new age structure matrix created at time $t-1$. Raw data are directly entered in R as animals aged 0 years and 1+ years.

The major difference in the fitting model between R and Excel versions arises from the optimisation technique. The optimisation in Excel uses @Risk Optimizer from Palisade Corporation which is based on the Excel Solver. This algorithm uses generalized reduced gradient technique (GRG2) derived from Lasdon and Waren (1978) which uses a robust implementation of the BFGS quasi-Newton algorithm. On the other hand, different optimisation techniques are available in R such as Nelder-Mead or BFGS. Nelder-Mead uses function values to find the minimum of our function (Nelder and Mead, 1965) while BFGS uses gradients to build up a picture of the surface to be optimized (Broyden, 1970; Fletcher, 1970; Goldfarb, 1970; Shanno, 1970). The BFGS technique can also be constrained in R. Both techniques were tested and showed similar results. However, the Nelder-Mead method was approximately twice as fast to compute, was more consistent and robust to different starting values, and therefore was preferred.

Some modifications were also incorporated into the projection component of the R model. To estimate future population changes, the parameter α was no longer defined as the initial population size vector from 1960. Instead the R model selects an age structure from the last year of the fitted model and selects a value from M . M can be selected in one of two ways. In the first method, an age vector from the last year of the fitted model is chosen randomly, and a value for M is selected randomly assuming a Normal distribution with mean and standard error from the fitting model runs. Alternatively, the model selects randomly paired values for the age structure vector and M . Data on pregnancy rates, seal removals, ice conditions and implementation error are then extrapolated to complete the projection as outlined for the Excel model.

SIMULATIONS

The two models were used to project future population trends using the five scenarios examined by Hammill and Stenson (2008) (Table 1). For every catch scenario, Monte Carlo simulations were using the estimated values of α and M , assuming they follow a Normal distribution, annual pregnancy rates, an ice-related mortality factor (Uniform distribution with a mean of 12%) and removal data as described above. The simulations were carried out using 10,000 model runs and population vectors obtained were kept. Their mean, standard error and 20th percentile are then calculated to evaluate the population trend.

Table 1: Different management scenarios for the North-West Atlantic harp seal hunt.

Plan	2009	2010	2011
A	270,000	270,000	270,000
B	300,000	250,000	170,000
C	200,000	200,000	200,000
D	300,000	300,000	300,000
E	250,000	250,000	250,000

RESULTS AND DISCUSSION

FITTING MODEL

Using the R optimisation algorithm gave consistently different parameters estimation results from the Excel model. The mean for α between R and Excel were similar (0.248 ± 0.007 and 0.247 ± 0.008 respectively, mean \pm SD) but still marginally different (Wilcoxon test: $W = 5.1 \times 10^7$, $p = 0.03$, Figure 1a). The difference in the mean is minimal and the statistical difference shown by the Wilcoxon test is likely to be due to the large sample size ($n = 10,000$). This indicates that the R model predicts a slightly higher initial population size, although the difference may not be biologically significant.

The estimate of mortality rate was lower in the R simulations than in the Excel (0.0510 ± 0.003 and 0.0544 ± 0.004 respectively, $W = 2.5 \times 10^7$, $p < 0.001$, Figure 1b). This mortality rate predicts a seal lifespan of 19.6 years in R and 18.4 years in Excel and as a result, will cause the population to decline at a slower rate in the R model. We also observed a difference in the variance of each parameter. Ansari-Bradley tests of dispersion showed that the variance of both parameters is smaller in R than in Excel (α : $AB = 5.2 \times 10^7$, $p < 0.001$, M : $AB = 5.1 \times 10^7$, $p < 0.001$). This has the general tendency of reducing the global variance of the model. Finally, Excel seems to generally find a smaller minimum sum of squares for the function (Figure 1c). We could not explain this characteristic of the Excel model, but the modification in the randomisation of the pregnancy rates and the recalculation of the removal table had the effect of increasing the minimum obtained by the objective function in R. We are confident that R is giving a true minimum as six optimization techniques available in R were all tested with similar value results.

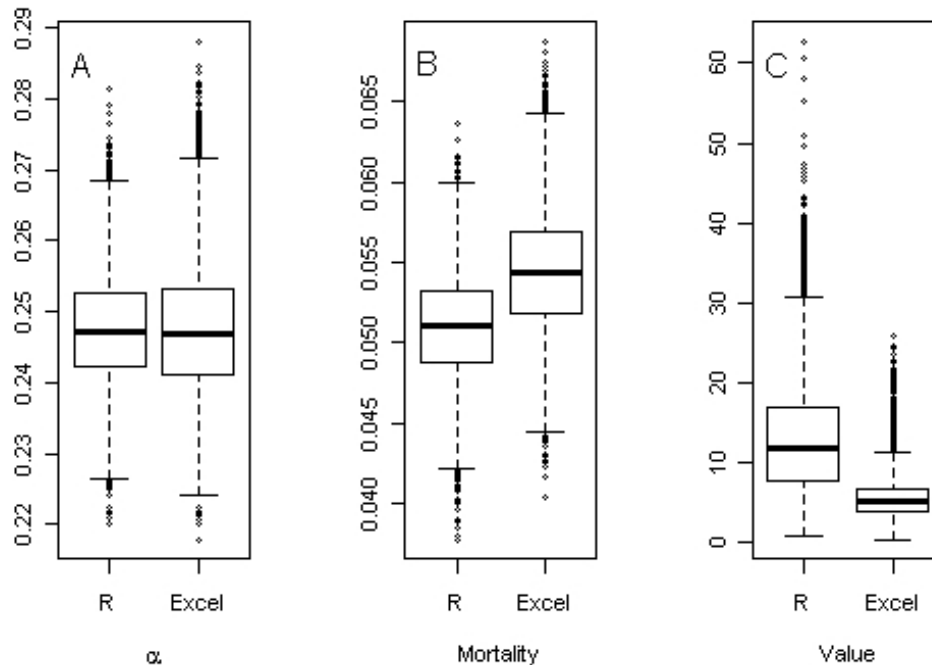


Figure 1: Comparison of the parameters generated by R and Excel from 10,000 Monte Carlo simulations.

We compared the fitting model of R and Excel using data from Hammill and Stenson (2008) produced with Excel and new simulations produced with R. Both programs showed similar patterns in their predicted harp seal population and pup production, but the R model seemed to provide a slightly better fit to the pup production survey estimates (Figure 2). The major difference between the two models came from the consistently higher population numbers estimated by R in most recent years. This can be explained by the lower mortality rate in R simulations, although the fact that in the Excel model it was possible to have negative numbers of animals at age could be a contributing factor. We also observed a difference in the variance of the two models. The variance total population appeared to increase at a faster rate in the Excel model in the total population (Figure 2a). The smaller variance in R can be explained primarily by the smaller variance in the parameter estimates.

PROJECTION

The modifications applied to R in the fitting model were also applied for the projection model. In the R version of the projection model, the pregnancy rates are correlated within years and the 1+ mortality is distributed between age classes using the year $t-1$ age structure vector. Excel and R projections showed very similar patterns in their predicted population size (Figure 3). The R consistently predicted higher population estimates which are a residual of the higher population estimates estimated by the fitting model in 2008 (Figure 2a).

The management plan adopted by Canada for Atlantic seals requires that there is an 80% likelihood that the population is above the precautionary reference level (Hammill and Stenson 2007). This lower 20th percentile of the population estimated is referred to as the L_{20} . The estimates of L_{20} varied between the two models, with the Excel simulations resulting in lower estimates of L_{20} than those obtained from the R model (Figure 4). This may result from a number of differences. The first is that 2009 population size obtained from the R model is higher. The second factor is that the R model has higher precision (i.e. less variance) in the fitting model. The third factor is that, in the fitting model, the initial population size and M are

very highly correlated ($r=0.996$). However, for the projection model, Hammill and Stenson (2005, 2008) relaxed this assumption to 0.98, which artificially increased the variance around the projections and causes L20 to decline at a much higher rate.

This is an important difference as it changes the actual biological conclusion aimed at selecting the best management plan. This was done because simulations to examine the performance of the management plan in the face of failure of different assumptions have not been examined. Therefore, the correlation between α and M was relaxed to 0.98, which results in some artificial increase in the variance to account for some of the uncertainty surrounding the impacts of harvest decisions on the population within the context of the management plan.

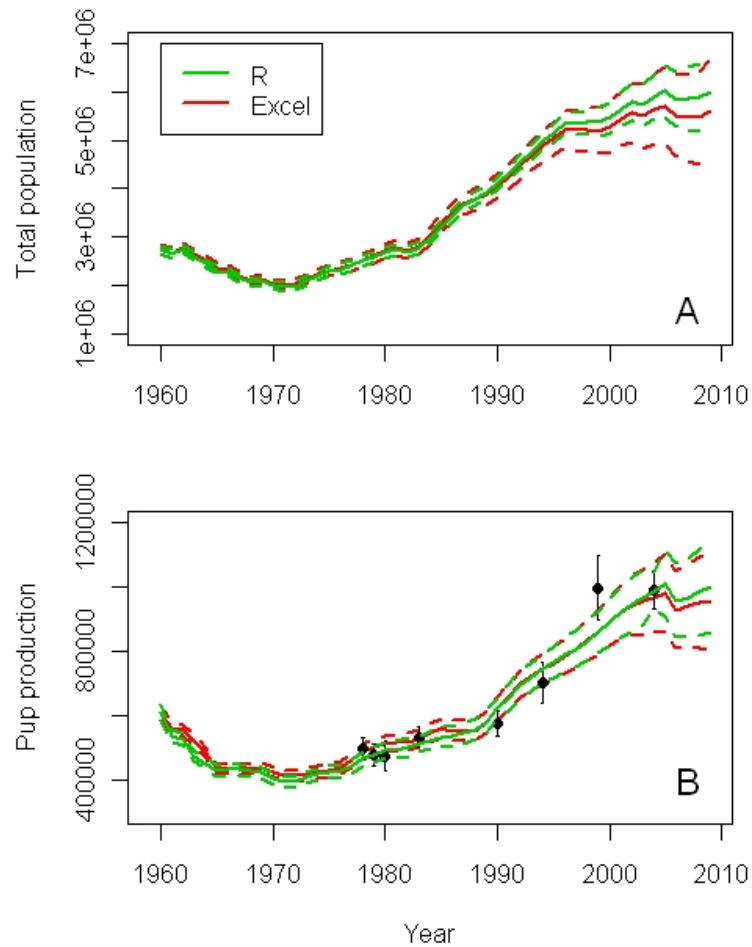


Figure 2: Harp seal total population (a) and pup production (b) estimated from 10,000 Monte Carlo simulations. The solid line is the mean and the dash lines represent the standard deviation.

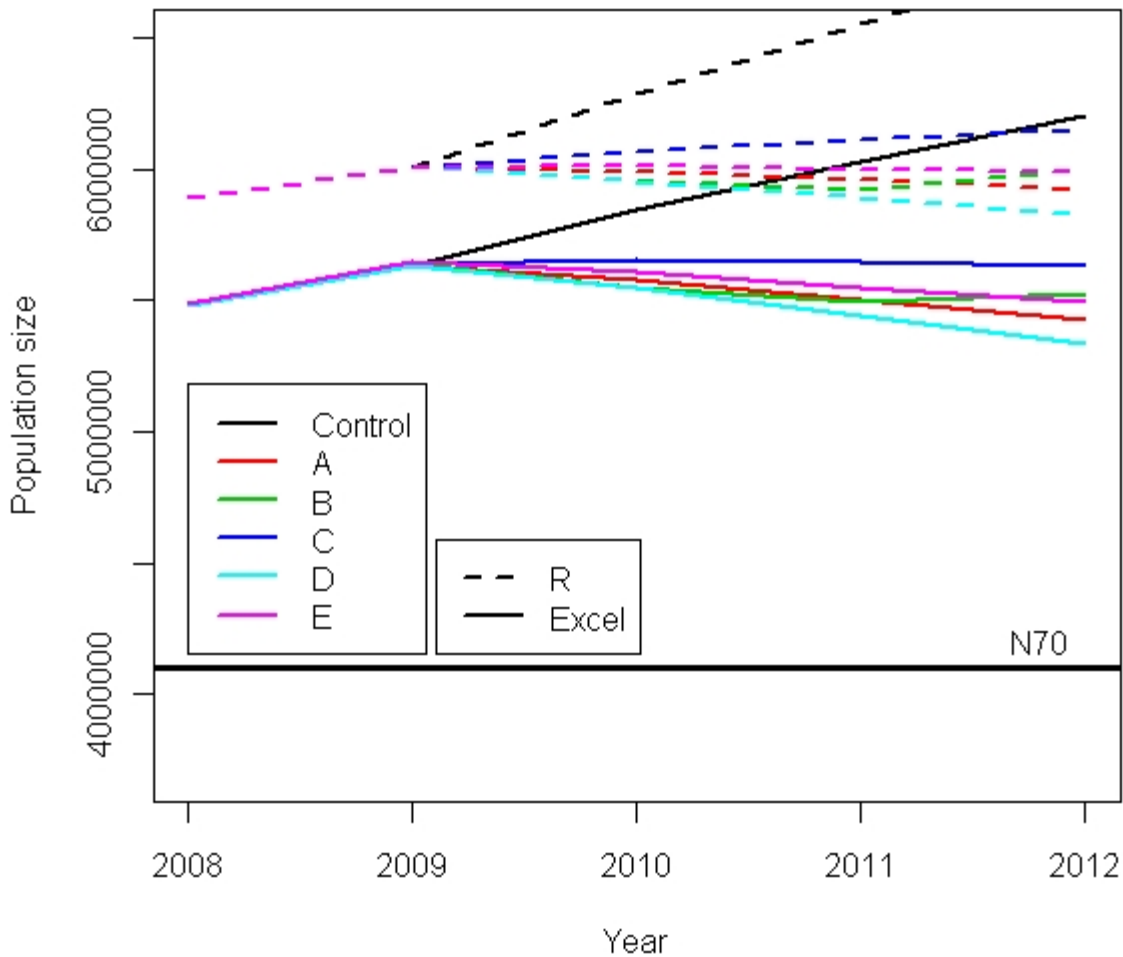


Figure 3: Mean harp seal population size projected up to 2012 following 5 different management plans (showed in table 1). R means come from 10,000 Monte Carlo simulations while Excel's come from 1,000 simulations. The horizontal line represents the N_{70} limit.

CONCLUSION

The main goal of transferring the model from Excel to R was to facilitate and accelerate its usage. This was successfully done as running time passed from days in Excel to hours in R. The general accuracy of the model was kept as both models gave similar population and pup production patterns. However, R gave higher estimates with a slightly smaller variance. This was explained by the smaller estimate of instantaneous mortality rate in R and the smaller variance in R parameter estimates. R was also giving consistently higher L_{20} values which can be mostly explained by the fact the R is not forcing a correlation factor between the parameters.

Because of their similarities, R and Excel models share similar weaknesses. As pointed out by Hammill and Stenson (2008), there is a strong correlation between α and M , which is similar to the correlation observed between the slope and the intercept of a linear regression. Indeed, our model contains two parameters, where the first one, α , is a coefficient of initial population size that can be view as an intercept, while, M , the mortality rate is the slope. A higher mortality rate implies a slower growth of the population while a smaller one implies a faster growth. The

correlation between these two parameters makes it harder for the optimisation technique to find the minimum. Optimisation techniques usually use Hessian matrices to solve the problem. However, when two parameters are correlated, the matrix almost become singular which makes its inversion harder and unstable mathematically.

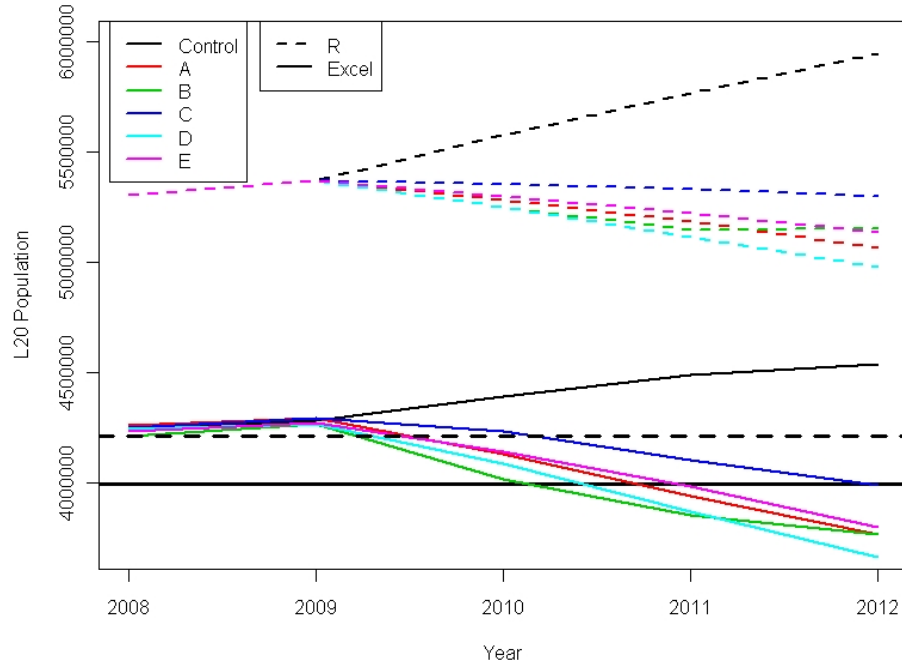


Figure 4: 20th percentile obtained from the projection of the harp seal population in Excel (1,000 simulations) and R (10,000 simulations) for different management plans presented in table 1. The horizontal lines represent the N_{70} associated with Excel (below) and R (above).

A major weakness of any model is the absence of real knowledge on the natural population age structure. The initial vector used in the model was built using extrapolated mortality rates and not on real data. Knowing that two major model parts are based on age structure (pup production calculated from pregnancy rates and 1+ removals), a biased initial vector could potentially falsify the model. However, this is thought to be less of a problem as time since 1960 increases and because we are looking mostly at pup production and total population and less at the specific age classes distribution. Starting the model earlier (eg 1950), would further reduce the impact of the initial population vector, on our views of the population in later years.

It is important to note that no variance was entered in the Monte Carlo simulations in total removals in the fitting part of the model. This implies that we consider the numbers used to be exact which is unlikely the case. Since 1960, some data have been missing and extrapolated (Stenson 2008) and it is also likely that some are badly reported or recorded. Some of the error and variance associated with the Struck and Loss correction are already incorporated into M as during the fitting model, but adding uncertainty to the removal table would increase the overall variance of the estimates. Similarly, no variance was included in the projection part of the model for the total Arctic catches and the fishery bycatch of harp seals. However, considering the small numbers of seal involved in each (around 1,000 and 10,500 kills respectively, compared to the approximately 400,000 to 600,000 animals removed from other harvests, this represents a maximum of 2.6% of the total removal), and that there are reports that current catches may in fact be lower (Stenson 2008) it is unlikely to have an impact on the final projection numbers.

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