

Research Article

A Microsoft Excel program for bootstrap estimates of reproductive-life table parameters

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Abstract: Demographic parameters such as intrinsic rate of increase estimates are of main interest in a wide range of ecological researches. Two widely used uncertainty estimate techniques are bootstrap and jackknife methods. Bootstrap estimates are time-consuming processes that are impossible to use without a computer program. Unfortunately few programs, if any, have been developed for this task. In this study a guideline was offered to prepare a program in Microsoft Excel environment to carry out time-consuming calculations of reproductive life table data in a minute or two by repeatedly pressing a shortcut key.

Keywords: software, life-history parameters, uncertainty, resampling techniques

Introduction

Reproductive-life table users well know that variance and uncertainty estimates of stable population growth parameters like intrinsic rate of population increase is not possible via traditional variance formulae. This is because each parameter is the result of plenty of calculations bearing all individuals of a cohort over a generation (Meyer *et al.* 1986; Carey, 1993; Ebert, 1999). So there is no replication per parameter to enter in variance formula. Some solutions were offered by scientists that (Ebert, 1999) divided them into two classes of Monte Carlo estimates and resampling or recombination methods. The latter group itself is divided into two separate procedures; one Jackknife, and the other Bootstrap technique. Meyer *et al.* (1986) prefer Jackknife to Bootstrap except in circumstances that data deviate from normality. In contrast some researchers (Huang and Chi,

2013; Ebrahimi *et al.*, 2013; Yu *et al.*, 2013) recommend using Bootstrap and leaving Jackknife procedure. But this technique is more difficult to use without a program. In Jackknife method number of replications is limited and is equal to original number of individuals of cohort. Hence it is possible for a user to exclude individuals from the original set of data and recalculate the parameters based on the original program in a short interval. But this is not true for bootstrap technique, because bootstrap includes at least 500 replications (Meyer *et al.*, 1986). So we need an easier and more straightforward way to do random resampling from the original cohort for at least 500 times. In this article I focused on a guideline for writing a program in Microsoft Excel environment to resolve this problem.

Materials and Methods

Reference population

Because the main task of our article is training for writing a program for doing Bootstrap calculations, we start with a small hypothetical reproductive life table with 10 replications and

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20 ages (Table 1). In table 1 only reproduction of females was included and 0 has been inserted for no reproductive output of a female in a day and an empty cell appears after death. Let this hypothetical cohort be referred as "original or reference cohort or population".

Table 1 Reproductive table of a hypothetical cohort.

x	Replication									
	1	2	3	4	5	6	7	8	9	10
0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0	0	0	0
7	0	0	3	0	1	0	0	2	0	1
8	2	0	5	2	0	0	0	0	3	0
9	4	0	2	0	3	0	4	1	4	0
10	3	0	0	4	1	0	0		0	3
11	0	0		1	3	2	0		1	7
12	2	0		2	2	4	0		2	2
13	1			0	3	8	2		2	0
14	0			5	1	5	1		1	4
15	0			2	0	2	0		0	1
16	0			0		1	0			2
17				1		0	0			0
18				0		0				0
19				2						1
20				1						

Computer program for analysis of life history parameters in Excel

I assume that readers are familiar with Excel environment. So First let's insert the data in Excel worksheet. Open a new Excel file. For inserting data we need 11 columns (C) for replications plus age column "x". Moreover we need 22 rows (R) for age classes and number of females. So we will have an 11C × 22R table of reproduction entries in Excel. We need another table with the same dimensions for survival data *i. e.* life table. An easy way is copying the reproductive data and pasting it in a free space just beneath the previous table and replace all

data by 1 that means female has been alive at that day. Subsequent empty cells correspond to zero that may imply as mortality. A further modification also was done in order to facilitate some actions in the future. The data were transposed (rotate and columns displayed as rows). For doing the final modification choose data series, copy them, select an empty area of cells then right click on the mouse button, click on "paste special" phrase and check the box behind the "Transpose" and confirm the request by clicking on "OK". We did these actions by pasting data in another worksheet (sheet 2). Now your worksheet must seem like Fig. 1.

When a female is chosen by a random manner in bootstrap resampling, all relevant data must be picked up together. This point increases the problem. I pursued the following solution to overcome this problem. In order to choose a random sample from females 1 to 10, use RANDBETWEEN function. A dialog box like Fig. 2 will appear that asks bottom and top number among which user wishes to search and choose a random number. Let's "Bottom" and "Top" tapes to be addressed to a determined cell rather than a numerical value to give the option of manual control of the data range to user.

You need to conduct this function for an arbitrary number of replications for example for $n = 10$ times. So in a free space just under the original data insert numbers 1 for bottom and 10 for top and in right hand cells, then run the "RANDBETWEEN" function. Your worksheet now resembles Fig. 3 but random numbers in cells B18 to B27 may be different. Structure of the function is displayed in formula bar, by double clicking on cell B18. Absolute cell addresses were used in both tapes of dialog box of Fig. 2 by pressing button F4 after entering the reference cells A14 and A16, so they appear as \$A\$14 and \$A\$16 in formula (Fig. 3).

Now we are going to pick up data related to the chosen females. Each female determined by a specific number of replications. In Excel there is a function as VLOOKUP (Fig. 4) that may refer to a series of reference data, choose a determined row referring to the specific

value, looking up among the data of the first left hand column and read and enter one of the data related to the mentioned row in one of the right hand cells chosen by user. For example in Fig. 4, the first blank rectangle in front of "Lookup_value" looks up for specific data in left hand column and finds it. You can insert directly a value such as 4 that tells Excel to find specific value 4 or the 4th female in reference population. But here we will address a cell with a random selection from 1 to 10, for example cell B18 in which RANDBETWEEN function has already been run. In order to have 10 random selections we run this function 10 times each time with a different address cell (B18 to B27). The second phrase "Table_array" refers to data array of reference population including also specific values or numbers of replications. In our example you may address data as cells A2 to V11. Because reference population is the same in all subsequent choices, so please use absolute address as \$A\$2:\$V\$11 in front of this phrase. The 3rd phrase "Col_index_num" refers to

column within which the mentioned datum has been inserted. For example if you insert 1, 2, 3, ... in front of this phrase, it will imply that go 1, 2, 3, ... cells right hand and select datum in final cell. Thus Excel will select a data that its coordinates obtains by putting row addressed in the first tape together column addresses in the third one by seeking data array addressed in 2nd tape of dialog box of Fig. 4. Leave the 4th box blank. Press OK for confirming actions. Now the following address will appear in the cell C18 as well as formula bar:

= VLOOKUP(\$B\$18;\$A\$2:\$V\$11;C1)

Finally we have to run this function in 10 successive rows, each time with a different address in front of the first tape. Choose all 10 rows together and drag and drop them to the right while absolute addresses were used in front of the first two tapes but the 3rd one allowed to increase one unit each time. The data of the first row (age x) were addressed at the 3rd tape.

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU			
1	x	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20							
2	1	0	0	0	0	0	0	0	1	0	0	3	7	2	0	4	1	2	0	0	1		1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1				
3	2	0	0	0	0	0	0	0	3	4	0	1	2	2	1	0							2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1					
4	3	0	0	0	0	0	0	2	0	1												3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1					
5	4	0	0	0	0	0	0	0	4	0	0	0	2	1	0	0	0					4	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1				
6	5	0	0	0	0	0	0	0	0	0	2	4	8	5	2	1	0	0				5	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
7	6	0	0	0	0	0	0	1	0	3	1	3	2	3	1	0						6	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
8	7	0	0	0	0	0	0	2	0	4	1	2	0	5	2	0	1	0	2	1		7	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
9	8	0	0	0	0	0	0	3	5	2	0											8	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1			
10	9	0	0	0	0	0	0	0	0	0												9	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
11	10	0	0	0	0	0	0	2	4	3	0	2	1	0	0	0						10	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		

Figure 1 Reproduction and life table data entered in an Excel worksheet and transposed for starting bootstrap calculations.

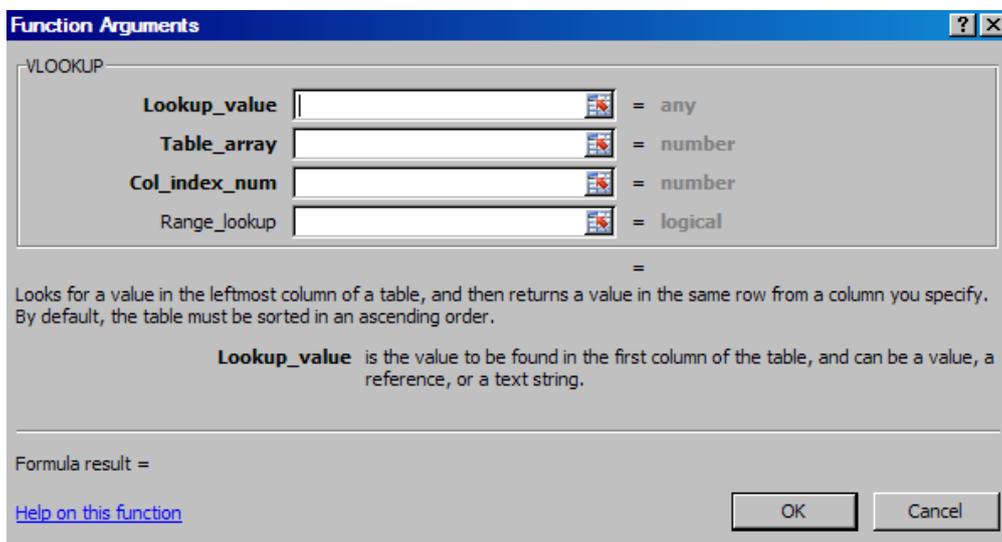


Figure 4 Dialog box of VLOOKUP function in Excel.

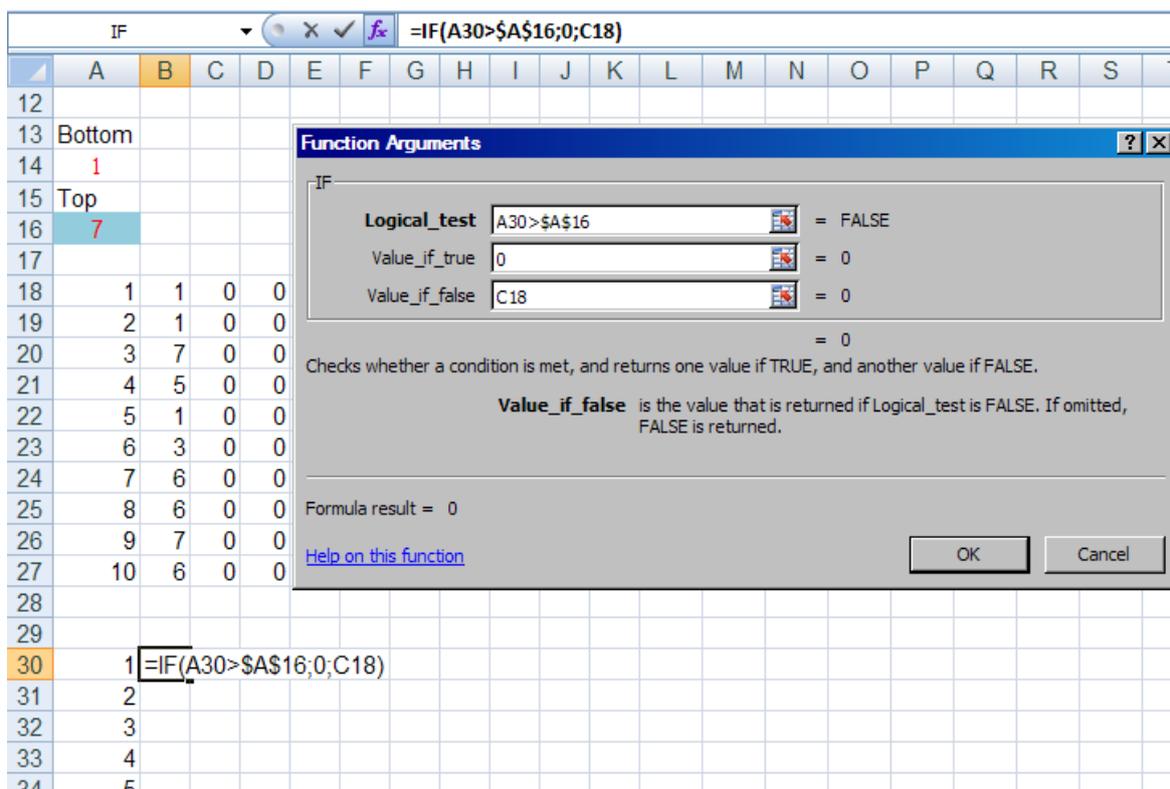


Figure 5 Dialog box of function IF in Excel.

Calculations of life history parameters

Hereafter we will be concerned with parameter estimations of reproductive-life tables. Our calculations will proceed through

the third table. The row 41 was assigned for pivotal age (x + 0.5) by adding value 0.5 to cell values in row 1 and choosing caption of x + 0.5 at cell A41 (Fig. 6). The second

function is B_x that represents total reproduction of cohort at age x summed over an age class for all 10 replications. Whenever a datum is excluded or an individual dies, 0 will be contributed in the summation. The third row is assigned to N_x or number of females alive at age x . These values are obtained by summing up survival data over each age for all replications. These sets of data (pivotal age, B_x and N_x) constitute the raw data for subsequent calculations. The first function is age-specific survival rate (l_x). Mind that l_x may be obtained by dividing each N_x to N_0 . Value of N_0 in our program appears in cell B43 (Fig. 6). So formula = B43/\$B\$43 should be inserted in cell B44 and dragged to right and dropped in cell V44. According to Carey (1993) L_x rather than l_x is used in calculations because it is assumed that all events occur at pivotal age rather than at its onset. So we need to calculate L_x values as average of the two successive l_x values in a distinct row. Therefore you may insert = (B44 + C44)/2 in cell B45 and drag it to right as long as previous row and then drop. As mentioned earlier, B_x represents overall number of eggs laid by all females at age x and because this number of eggs are deposited by N_x females, it seems adequate to divide B_x values by N_x 's, but two further problems need to resolve. First problem arises when individuals with shorter life spans are selected by chance. This will lead to values of 0 in denominator of higher age classes because N_x is zero. A conditional IF function is needed again for overcoming the problem. In this function it is asked if the data in N_x row (row 43) is 0; if true then 0 is inserted, otherwise the value of the fraction B_x/N_x will be inserted. For the first cell the function will be as = IF(B43 = 0; 0; B42/B43) and for subsequent ones only drag and drop is used. The second correction is averaging two successive values for the same reason already mentioned for L_x . The divisions and further averaging has been done in rows 46 and 47 respectively. In order to calculate m_x values we need be aware of age-specific sex ratios

S_x . Often sexing the progeny at birth is impossible. So a common sex ratio of 0.5 is a logical value for many bisexual organisms that may apply for all ages. If significant deviations from 0.5, however, is present we may use the observed sex ratios instead of 0.5. Let cell B14 be assigned for common sex ratio. Hence in row 48 run = B47*\$B\$14 for m_0 and drag and drop it for completing the row.

Prior to solving Euler-Lotka equation we need two calculation rows, one for $L_x m_x$ and the other for $(x + 0.5) L_x m_x$. These values are obtained easily by multiplication, so further explanation is avoided. Sum of the recent columns as well as values of $\ln R_0$, T_c and r_c are displayed in cells B52 to B56 (Fig. 6). Because r_c is near to r_m , it is a good starting point for solving Euler-Lotka equation.

There are several methods like interpolation (Birch, 1948), Newton-Raphson algorithm (Carey, 1993; Ebert, 1999), projection (Ebert, 1999) and trial and error (Ebert, 1999) for estimating r_m . I followed Newton-Raphson algorithm owing to its high accuracy. This algorithm consists of a series of iterative calculations of Euler-Lotka equation by trying an initial value of r_i , solving the equation and calculating the first derivative of the equation, a value of r_{i+2} nearer than r_i to r_m is reached using eq. 1 below:

$$r_{i+1} = r_i - f(r)/f'(r) \quad (\text{eq. 1})$$

This action is repeated again by trying the new value. The $f(r) = 0$ is the same Euler-Lotka equation rearranged by subtracting from both sides by unity to obtain a function leading to 0 per r_m value (eq. 2):

$$f(r) = \sum e^{-r m^x} l_x m_x - 1 = 0 \quad (\text{eq. 2})$$

and $f'(r)$ is its first derivative (Carey, 1993; Ebert, 1999). The nearer r_i to r_m , the fewer iteration. This is why we start by r_c . Often four or five iterations are adequate, but we continue for 10 iterations to insure rare events. We use a couple of rows for calculations of each round of iterations; the first one for Euler-Lotka

equation and the second one for its derivative (Fig. 7). As a result 20 rows (58-77) are assigned for these calculations. Because all pairs of these rows are similar in structure and differ only in reference cell for initial number of r_i , so let's be concerned only with calculations of the first iteration. In column B (cells B58 to B77) we just insert row captions (Fig. 7), and calculations begin from column C. Our task is to make an input of an initial r_i value (r_c in this case) in eq. 2 and get an output as r_{i+1} . Exponential phrase in eq. 2 will repeat in all cells of row 58 from C58 to W58 by absolute addressing to cell B56 (r_c value) and changing the other components by age. Remember that $x + 0.5$ and L_x will be used instead x and l_x respectively. Exponential function in Excel is EXP, hence formula in cell C58 will appear as = EXP(-\$B\$56*B41)*B49 that commands to Excel to pick up minus value in cell B56 multiply it by value in cell B41, give exponent of the result, then multiply the exponent value by value in cell B49. Drag and drop this cell content to the right up to cell W58. In cell X58 sum up all these values. Herewith you run \sum in eq. 2. You can subtract unity in a separate cell but it preferably should be combined with the next

step that will be defined soon. Let derivative calculations be done in row 59. Only multiply contents of previous row by negative value of $x + 0.5$ or contents of corresponding cells in row 41. Sum of the recent row is also required, that we obtained it in column Y, to avoid confusion. Now we are going to calculate new $r_{i + 1}$ in cell A59 using eq. 1. The obtained value is displayed by r_1 which is calculated in cell A59. In this cell formula = B56-((X58-1)/(Y59)) has been used where B56 is the value of r_c , X58 is the value of Euler-Lotka equation solved for r_c and Y59 is the value of first derivative. Now r_1 in cell A59 is a better estimate than r_c for r_m and in turn it is the starting point of the second iteration. In the second set of calculations, reference cell for r_i value will be A59 and the remaining steps are the same. Please look at green right column in Fig. 7. Right hand of Euler-Lotka equation became unity at fourth iteration. Difference between r_3 and r_{10} is actually zero. The difference of the two final r_i 's has been shown in blue in the left bottom cell A80. As a result r_m -value is $0.184 d^{-1}$ in a random sample taken from the original population. Calculation of birth rate (row 82) is similar to Euler-Lotka equation so we avoid further explanation.

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X
39	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
40																								
41	x+.5	0.5	1.5	2.5	3.5	4.5	5.5	6.5	7.5	8.5	9.5	10.5	11.5	12.5	13.5	14.5	15.5	16.5	17.5	18.5	19.5	20.5		
42	Bx	0	0	0	0	0	0	0	3	2	14	9	16	12	18	18	5	3	1	0	3	1		
43	Nx	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	5	5	3	2	1		
44	lx	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.71	0.71	0.43	0.29	0.14		
45	Lx	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0.86	0.71	0.57	0.36	0.21	0.07		
46	Mx	0	0	0	0	0	0	0.4	0.3	2	1.29	2.29	1.71	2.57	2.57	0.71	0.6	0.2	0	1.5	1			
47		0	0	0	0	0	0	0.2	0.4	1.1	1.6	1.79	2	2.14	2.57	1.64	0.66	0.4	0.1	0.75	1.25	0.5		
48	m _x	0	0	0	0	0	0	0.1	0.2	0.6	0.8	0.89	1	1.07	1.29	0.82	0.33	0.2	0.05	0.38	0.63	0.25		
49	L _x m _x	0	0	0	0	0	0	0.1	0.2	0.6	0.8	0.89	1	1.07	1.29	0.82	0.28	0.14	0.03	0.13	0.13	0.02		
50	xL _x m _x	0	0	0	0	0	0	0.7	1.3	4.9	7.8	9.38	11.5	13.4	17.4	11.9	4.37	2.36	0.5	2.48	2.61	0.37		
51																								
52	ΣL _x m _x	7.48878																						
53	ΣxL _x m _x	90.9099																						
54	ln R ₀	2.01341																						
55	T _c	12.1395																						
56	r _c	0.16586																						
57																								

Figure 6 Fecundity life table of a random sample of seven individuals taken from a reference population presented in table 1 excluding last three replications.

and Select" option under submenu "Editing" and click on the first option "Find". Dialog box like Fig. 9 will appear. Leave "Find what" box blank. Select the second option "Replace". Click on button "Options >>". Now the dialog box must appear as Fig. 10.

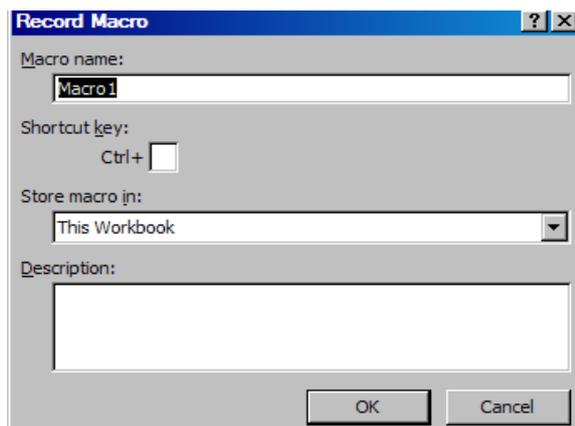


Figure 8 Dialog box of "Record Macro".

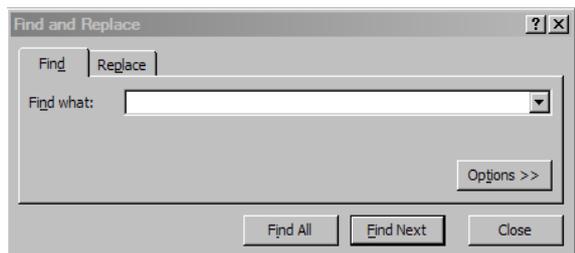


Figure 9 Dialog box of Find and Replace.

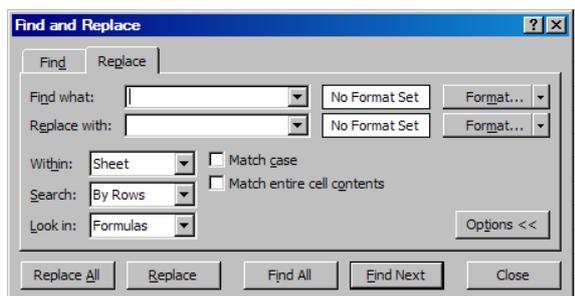


Figure 10 Second sheet of dialog box "Find".

Change the phrase "By Rows" to "By Columns" in front of "Search" option. Click on "Find Next" button and exit. You can now observe that cursor has been moved one cell downward. Now right click and choose paste

special option put checkmark behind value and confirm action by "OK". All data in row 85 now is copied in lower row. Stop recording Macro in menu "Developer". Before using shortcut key for successive trials don't forget to change calculation options once again to automatic position by following similar orders as mentioned earlier. Now keep and hold button Ctrl in key board and press sequentially button "b" to take new random samples and copying and pasting them in successive rows. In a span of time as short as 3 min you can run 1000 trials.

As a final step you need to calculate mean and standard error of 1000 trials for all eight parameters. I also presented minimum and maximum amounts of each parameter by conducting MIN and MAX functions. Remember that variance of the 1000 trials is variance of the mean and then standard deviation of mean or those of the trials is the same SE (Fig. 11).

B1088		=MIN(B86:B1085)									
	A	B	C	D	E	F	G	H	I	J	K
1073	Trial988	9.043	6.12	0.1699	1.185	0.228	0.058	10.656	4.0785		
1074	Trial989	8.464	7.86	0.1867	1.205	0.237	0.05	11.042	3.7118		
1075	Trial990	11.19	10.2	0.1876	1.206	0.236	0.048	12.384	3.694		
1076	Trial991	8.536	7.59	0.1677	1.183	0.21	0.042	12.085	4.1327		
1077	Trial992	9.179	5.65	0.1538	1.166	0.215	0.062	11.264	4.5081		
1078	Trial993	8.012	6.57	0.1745	1.191	0.228	0.053	10.788	3.9723		
1079	Trial994	7.5	6.19	0.1657	1.18	0.216	0.05	11.001	4.1838		
1080	Trial995	10.44	7.3	0.1718	1.187	0.227	0.056	11.576	4.0351		
1081	Trial996	9.349	7.56	0.1785	1.195	0.23	0.051	11.334	3.8838		
1082	Trial997	8.75	7.82	0.1753	1.192	0.22	0.045	11.734	3.9551		
1083	Trial998	6.85	5.28	0.1553	1.168	0.212	0.056	10.716	4.4624		
1084	Trial999	8.375	5.1	0.148	1.16	0.207	0.059	11.009	4.6819		
1085	Trial1000	8.602	6.7	0.1642	1.178	0.213	0.048	11.582	4.2219		
1086											
1087		GRR	R0	rm	λ	b	d	T	DT		
1088	Min	3.3571	2.82	0.1021	1.108	0.151	0.04	9.9011	3.5523		
1089	Max	11.89	10.4	0.1951	1.215	0.246	0.068	12.639	6.7856		
1090	Mean	8.981	7.18	0.1712	1.187	0.222	0.051	11.401	4.0728		
1091	S ² x	1.572	1.66	0.0002	2E-04	1E-04	2E-05	0.2133	0.1086		
1092	SE	1.254	1.29	0.0127	0.015	0.012	0.004	0.4618	0.3296		
1093											

Figure 11 Summary statistics of the 1000 bootstrap estimates of eight life history parameters of table 1.

3. Analysis of real data

In order to examine our program, we analyzed two series of data. 1) Hypothetical population mentioned earlier. 2) Data available by Moshtaghi *et al.* (2016) collected in laboratory on an artificial diet of grapevine moth *Lobesia botrana* (Lep., Tortricidae).

An extended version of the program including 200 age classes and 100 replications is available that was used for these estimations.

Results and Discussion

The above program was used to estimate two series of life history data:

1) Hypothetical data mentioned earlier in this article: Table 2 shows the results of Jackknife and bootstrap estimates as well as estimates of original population without recombination. No distinct trend is seen in SE estimated in the two methods. It seems that estimates of both

methods are broadly logical and similar to each other and the original population.

2) Moshtaghi *et al.* (2016) used both Jackknife and bootstrap method using our program for estimating the same parameters of three cohorts of grapevine moth *Lobesia botrana* in three sets of temperatures. The results are presented in Table 3. The results are even closer in the two methods by these series of data compared with the hypothetical data presented in table 2.

Table 2 Jackknife, bootstrap and original estimates of hypothetical data available in Table 1.

Entries		GRR	R ₀	r _m	λ	b	d	T	DT
No recombined		8.73	6.0921	0.166	1.181	0.1834874	0.017	10.857	4.16
Jackknife	Min	2.69	0.025	0.074	1.072	0.1143161	-9E-04	7.4916	2.92
	Max	17.3	11.213	0.215	1.238	0.2300839	0.047	14.404	6.34
	Mean	9.18	6.0864	0.168	1.182	0.1840587	0.0166	10.901	4.11
	SE	1.42	1.1919	0.015	0.017	0.0110379	0.0052	0.6157	0.36
Bootstrap	Min	3.82	2.548	0.094	1.098	0.1574092	0.0426	8.6218	3.52
	Max	12.6	9.6629	0.197	1.217	0.2587049	0.0705	12.442	7.4
	Mean	8.41	6.0678	0.165	1.179	0.2192626	0.0545	10.820	4.25
	SE	1.31	1.1574	0.016	0.019	0.0164046	0.0047	0.5557	0.47

Table 3 Comparison of jackknife and bootstrap estimates of life table parameters of the grapevine moth *Lobesia botrana* reared on an artificial diet. Data contributed by Moshtaghi *et al.* (2016).

Population parameters	Variance Estimation Technique (Mean ± SE) ^{a,b}								
	Original			Jackknife			Bootstrap		
	20 ± 1 °C	25 ± 1 °C	30 ± 1 °C	20 ± 1 °C	25 ± 1 °C	30 ± 1 °C	20 ± 1 °C	25 ± 1 °C	30 ± 1 °C
Gross reproductive rate (GRR) (offspring)	24.47	55.47	12.40	24.44 ± 0.64b	55.47 ± 2.26a	12.40 ± 0.73c	24.50 ± 0.63b	55.54 ± 2.19a	12.38 ± 0.69c
Net reproductive rate (R ₀) (offspring)	7.87	22.99	4.09	7.87 ± 1.51b	22.98 ± 3.37a	4.09 ± 0.77b	7.83 ± 1.47b	23.00 ± 3.35a	4.06 ± 0.77c
Intrinsic rate of increase (r _m) (day ⁻¹)	0.0183	0.0719	0.0386	0.0184 ± 0.0017c	0.0723 ± 0.0036a	0.0391 ± 0.0052b	0.0180 ± 0.0017c	0.0717 ± 0.0034a	0.0379 ± 0.0054b
Finite rate of increase (λ) (day ⁻¹)	1.0184	1.0746	1.0394	1.0186 ± 0.0017c	1.0749 ± 0.0036a	1.0399 ± 0.0054b	1.0182 ± 0.0018c	1.0744 ± 0.0037a	1.0386 ± 0.0056b
Mean generation time (T) (day)	113.02	43.55	36.50	113.02 ± 0.20a	43.55 ± 0.12b	36.49 ± 0.27c	113.03 ± 0.19a	43.55 ± 0.11b	36.51 ± 0.25c
Doubling time (DT) (day)	37.96	9.63	17.94	37.29 ± 3.61a	9.57 ± 0.45b	17.39 ± 2.46b	38.81 ± 4.13a	9.68 ± 0.48c	18.74 ± 3.23b
Instantaneous birth (b)	0.0385	0.1159	0.0894	0.0384 ± 0.0023c	0.1164 ± 0.0055a	0.0886 ± 0.0055b	0.0386 ± 0.0024c	0.1162 ± 0.0055a	0.0896 ± 0.0059b
Intrinsic death rate (d)	0.0202	0.044	0.0508	0.0200 ± 0.0035b	0.0442 ± 0.0076a	0.0495 ± 0.0083a	0.0206 ± 0.0036c	0.0444 ± 0.0077b	0.0517 ± 0.0089a

a) Sample size of grapevine moth is n = 120 for original and jackknife estimation and n = 1000 for bootstrap estimation.

b) Means followed by different letters within a row, separately for jackknife and bootstrap

method, were significantly different at P < 0.05 (Tukey HSD test).

In this article we focused on sampling from a reference cohort many times to provide a bootstrap estimate of 1000 replications. This is a

difficult task because it needs extraordinarily great calculations. Donovan and Welden (2002) offered a guideline for random bootstrap samplings from a reference population to examine central limit theorem in statistical context. Their program largely was used in preparing the present program, but we tackled with one more complicated problem. They did sampling among a determined number of identities that each represented an attribute of a live organism. For example a sample consisted of a population of stem length of a plant species. So each time they took a random sample from a population with determined values of stem length. In our program however there was no determined measure of a variable for an individual to choose as random. Rather there are individuals with a series of conjunct data all of which must be chosen simultaneously to constitute age specific survival and reproduction data of an individual. The same series of data must be taken from many individuals of the cohort to construct a random cohort. Therefore we had to apply a common random number of individuals for all series of data belonging to different age classes of an individual. An expanded version of program including 100 replications and 200 age classes was used for the more realistic situations of Moshtaghi *et al.* (2016) data. We believe that such dimensions meet requirements of majority of entomological studies. This program also can be extended to cover age-stage two sex life table data (Chi and Liu, 1985), but is deliberately prepared for traditional female-cohort life table analyses, to provide needs of users whose data are in female-cohort framework and hence have to ignore two-sex-MSChart (Chi, 2013).

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برنامه‌ی رایانه‌ای برای تخمین پارامترهای جدول زندگی تولیدمثلی در محیط مایکروسافت اکسل

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چکیده: پارامترهای دموگرافیک نظیر نرخ ذاتی افزایش جمعیت در بسیاری از پژوهش‌های اکولوژیک از توجه زیادی برخوردارند. دو روش پر استفاده در تخمین عدم قطعیت این پارامترها روش‌های بوتسترپ و جکنایف هستند. برآوردهای بوتسترپ وقت‌گیر می‌باشند که بدون یک برنامه رایانه‌ای قابل محاسبه نیستند. متأسفانه برنامه‌های رایانه‌ای چندان برای این منظور توسعه نیافته‌اند. در این بررسی، راهنمایی برای تهیه‌ی یک برنامه‌ی رایانه‌ای در محیط مایکروسافت اکسل ارائه شده که محاسبات وقت‌گیر جدول‌های زندگی تولیدمثلی را با فشار دادن مکرر یک دگمه‌ی میانبر ظرف یکی دو دقیقه عملی می‌سازد.

واژگان کلیدی: نرم‌افزار، پارامترهای جدول زندگی، عدم قطعیت، روش‌های نمونه‌گیری مجدد