Chapter 7-4
Matching immature and adult life tables: Bootstrap random match

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 1

Main reference

Masood Amir-Maafi, Hsin Chi, Zhen-Zhen Chen, and Yong-Yu Xu. 2022. Innovative bootstrap-match technique for life table set up. Entomologia Generalis. DOI: 10.1127/entomologia/2022/1334. 108.

 2

Matching: why and how

In general, life table is constructed by collecting data of all individuals of a cohort from birth to death. The sunn pest adults migrate to mountain arears for overwinter. The overwintered adults emerge in the next spring and fly to the invasion areas (agricultural fields) to feed and reproduce offspring. Because it is impractical to collect the life history data continuously from the birth of egg to the death of adult, it is necessary to collect the immature data (the survival and duration of each stage) and the adult data (the adult longevity and daily fecundity of females) separately. By using the bootstrap technique, you can match an immature with an adult of the same sex to construct a complete life table.

 3

Ratio'nale of matching

- If you collect the immature data for all 200 eggs from birth to the adult emergence, but only data of a limited number (e.g., 30 pairs) of all emerged adults (e.g., 85 males and 70 females), then you can use this method to include all immature data (100).
- The 30 pairs of adults give a sex ratio 1:1. It is, however, not the true sex ratio. The original proportion of female is 70:200 and the original proportion of male is 85:200. By using the bootstrap matching, the original sex ratio and more data of immature individuals can be taken into consideration.

 4

Note well!

- Because the proportion of N_f, N_m and N_n (they are better than the widely used "sex ratio") of matched population is dependent on the immature data, it is critical and necessary to collect the immature data by using a large number of eggs.
- Based on the same rationale, if there is double about these proportions in the original cohort, the data of the original cohort can be split into immature and adult data and use the bootstrap match technique.

 5

Bootstrap match

If you collected the adult life table first and the immature life table after that, e.g., the Sunn pest (*Eurygaster integriceps*), the biting midge (*Forcipomyia taiwana*), *Tessaratoma papillosa* Drury, then you can use this method to construct a complete life table.



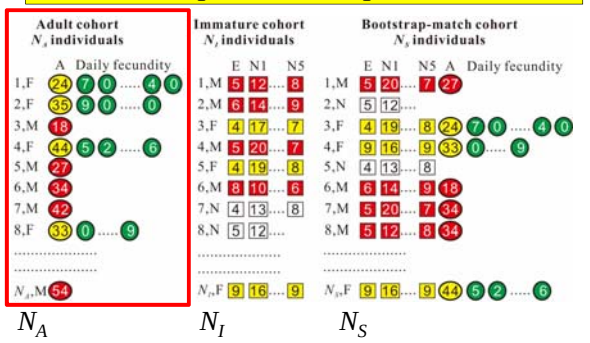
 6

Cases for bootstrap match

1) It is necessary to collect the immature and adult life table data separately due to obligatory diapause.
2) It is necessary to collect the immature and adult life table data separately due to the difficulties in mating the adults under controlled laboratory conditions.
3) A large cohort is used for collecting immature data but a much smaller cohort is used for the adult data.
4) The life table data for the immatures were collected using individually reared insects while the adult data was obtained using group-reared insects.
5) You paired only some adults (due to errors in experiment or there were no enough female or male adults).

 7

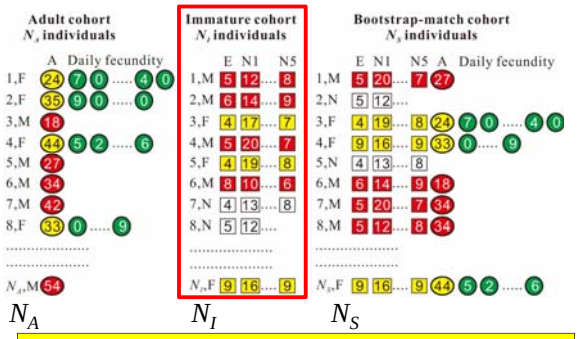
I. The concept of bootstrap random match



The adult life table data and female fecundity are collected first.

 8

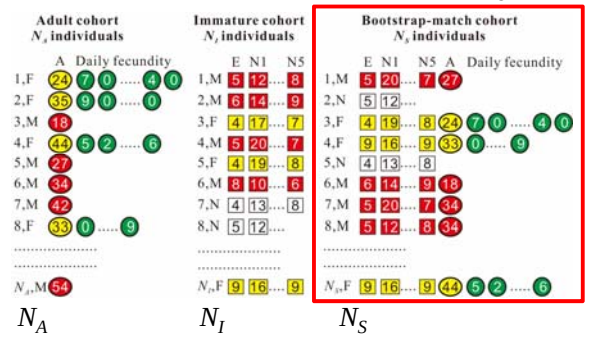
The concept of random match



The immature life table data are collected using the offspring of the adult cohort or field sampled adults.

 9

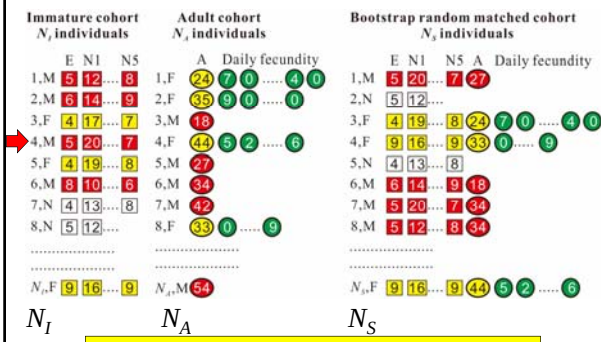
Sample size of random match (N_S)



If $N_I > N_A$, $N_S = N_I$. If $N_A > N_I$, $N_S = N_A$.

 10

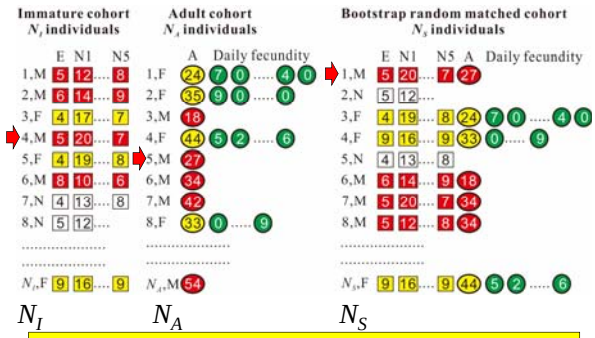
Random match begins with immature



Data of an immature individual is randomly selected.

 11

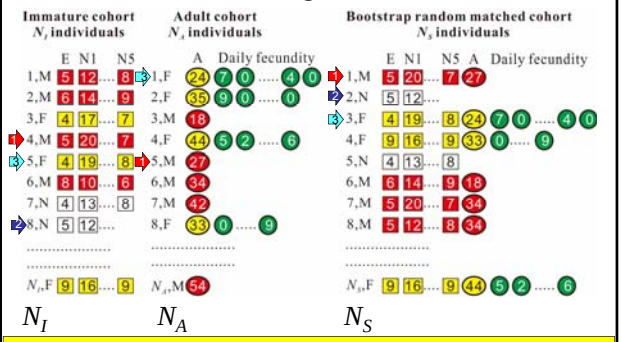
The concept of random match



Data of an adult individual of the same sex is randomly selected.

 12

Random match begins with immature



Data of an immature individual is randomly selected. If it survived to adult stage, data of an adult individual of the same sex is randomly matched.

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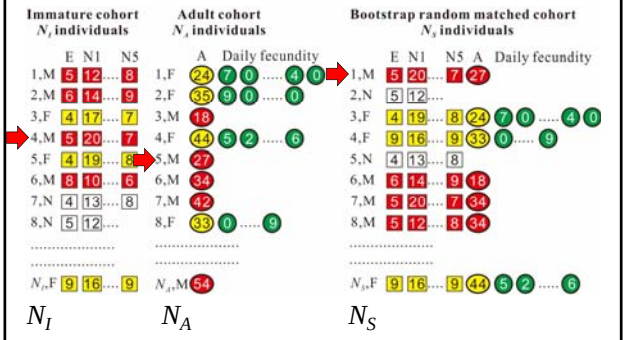
The concept of random match



If $N_I > N_A$, $N_S = N_I$. If $N_A > N_I$, $N_S = N_A$.

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In general, $N_I > N_A$ and $N_S = N_I$. Why?

- The number of females, males and n-type can be obtained from N_I. Sex ratio is evolved from the number of adults emerged from immature individuals.
- The pairing of adults is intentionally 1:1.
- The preadult survival rate is obtained from N_I.
- The immature duration plays deterministic role on first reproductive age.
- Because the adult longevity is usually longer than immature stage and collecting female fecundity of all female adults is time- and labor-consuming, a smaller cohort of adults is used to collect adult life table data.

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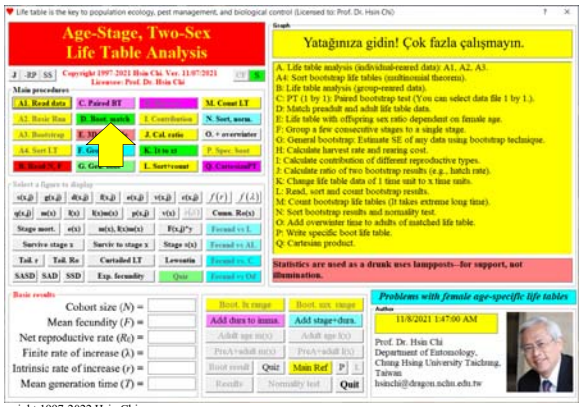
Part A: Match life tables



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Data format

Immature life table

```
"Sunn pest. 2020-02-28"
"Masood Amir-Maafi"
"Immature"
280
3,7
F,Egg,N1,N2,N3,N4,N5,Female
M,Egg,N1,N2,N3,N4,N5,Male
N,Egg,N1,N2,N3,N4,N5,Unknown
N1,N5
1,F,7,2,8,10,6,7
2,N,7,2,8,-1
3,M,7,2,7,6,9,10
4,N,7,2,8,4,-7
5,M,7,2,8,4,10,9
6,N,7,2,9,4,9,-3
7,F,7,2,8,7,6,12
8,F,7,2,8,4,9,9
```

Adult life table

```
"Sunn pest. 2020-02-28"
"Masood Amir-Maafi"
"Adult"
135
3,7
F,Egg,N1,N2,N3,N4,N5,Female
M,Egg,N1,N2,N3,N4,N5,Male
N,Egg,N1,N2,N3,N4,N5,Unknown
N1,N5
1,F,43,0,0,0,0,0,0,0,0,0,14,0,0,13,0,0,14,0,0,
0,0,0,0,0,0,0,14,-1
2,F,16,0,0,0,0,0,0,0,0,0,0,0,0,0,14,-1
3,F,26,0,0,0,0,0,0,0,0,14,0,0,0,14,0,0,14,0,1
4,0,0,12,0,0,0,14,-1
4,M,19
5,M,29
6,M,39
```

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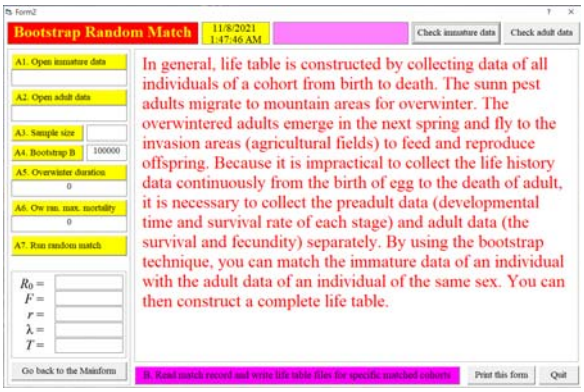
Random match



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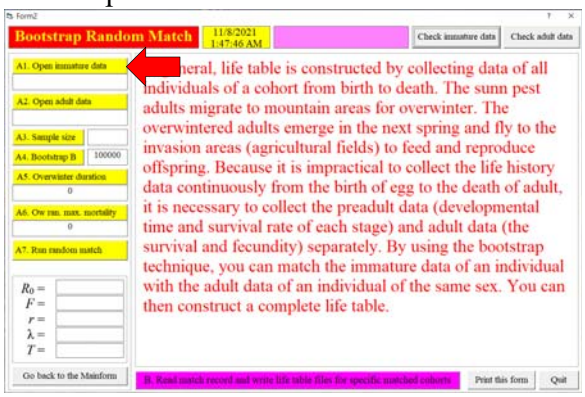
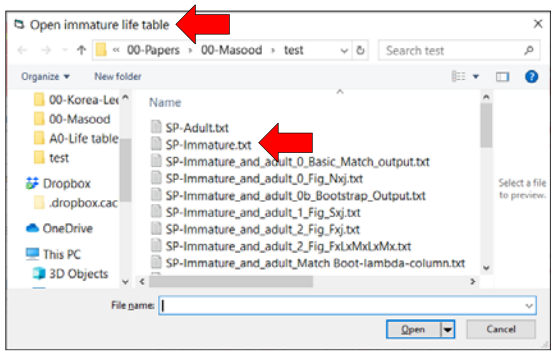
Open immature life table data file



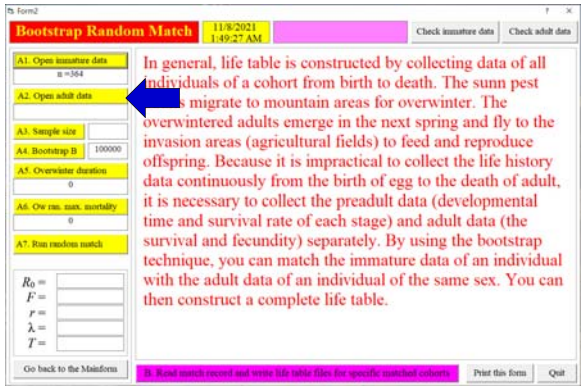
 19

Open immature life table data file



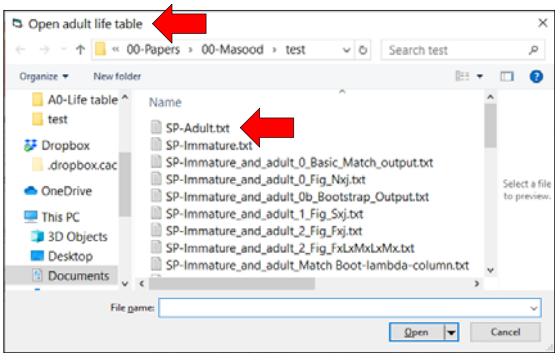
 20

Open adult life table data file



 21

Open adult life table data file



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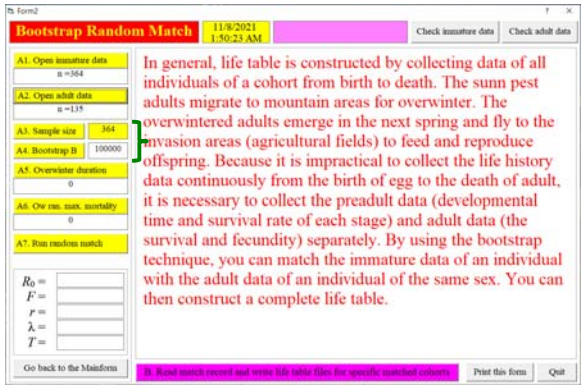
Sample size and bootstrap number



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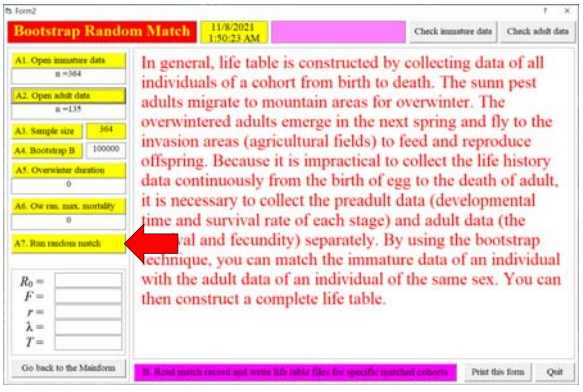
Run bootstrap random match



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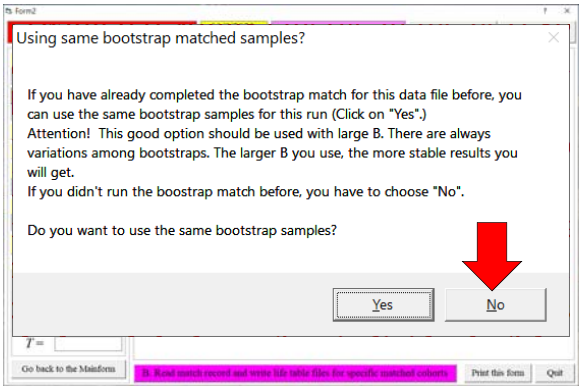
Using the same bootstrap match record?



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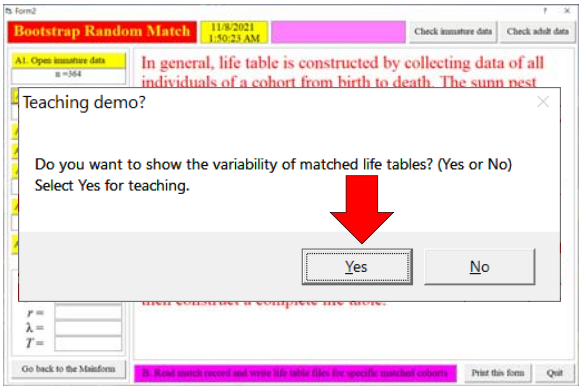
Show the variability of random match to audiences



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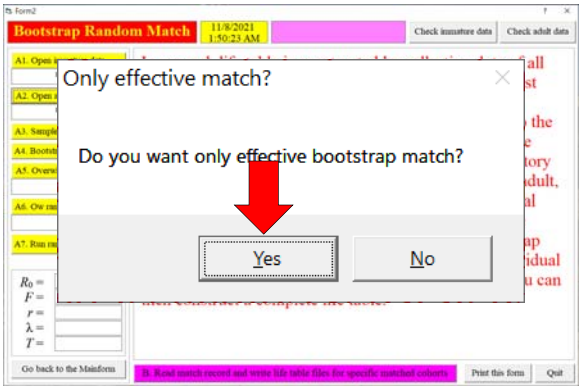
Effective bootstrap match only?



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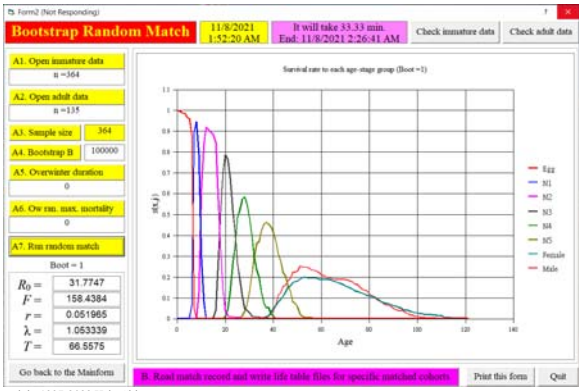
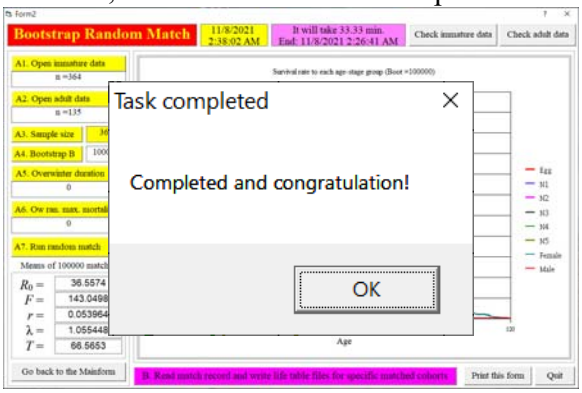
First random match result



 28

100,000 random matches completed!



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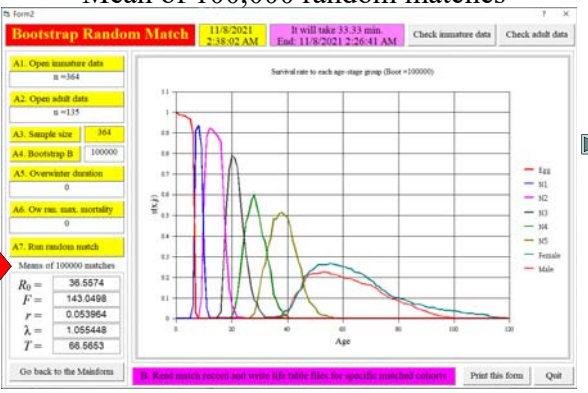
Mean of 100,000 random matches



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Sort bootstrap-match life tables

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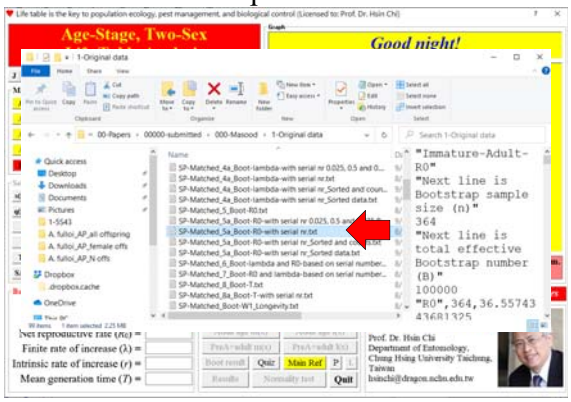
Sort bootstrap-match life tables



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File with/without serial number

…..-Matched_5_Boot-R0.txt

```
"R0"
"Next line is Bootstrap sample size (n)"
280
"Next line…Bootstrap number (B)"
100000
"R0",280,34.7432612499998
36.9964285714286
34.4428571428571
38.9107142857143
32.5964285714286
41.9107142857143
38.6821428571429
```

…..-Matched_5a_Boot-R0-with serial nr.txt

```
"R0"
"Next line is Bootstrap sample size (n)"
280
"Next line…Bootstrap number (B)"
100000
"R0",280,34.7432612499998
"Boot no.","Boot(R0)"
1,36.9964285714286
2,34.4428571428571
3,38.9107142857143
4,32.5964285714286
5,41.9107142857143
6,38.6821428571429
```

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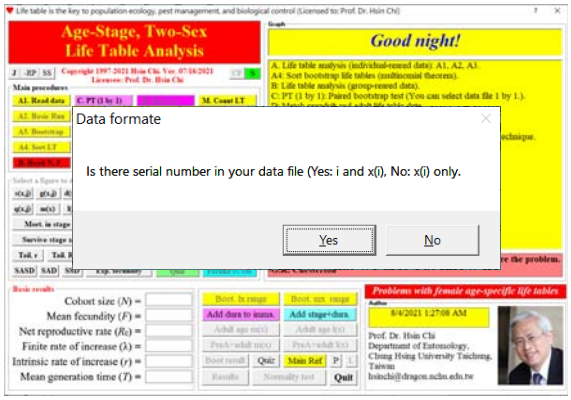
With/without serial number



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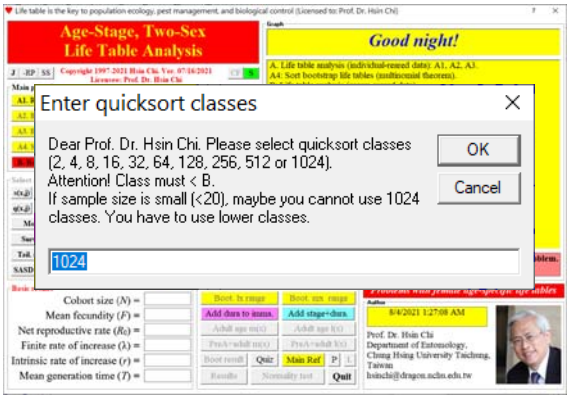
Quick sort classes



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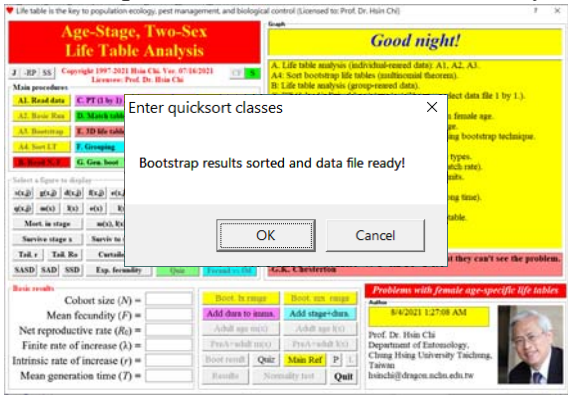
Bootstrap results sorted and data file ready.



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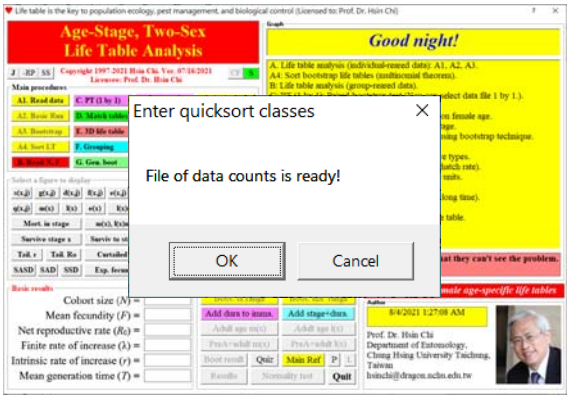
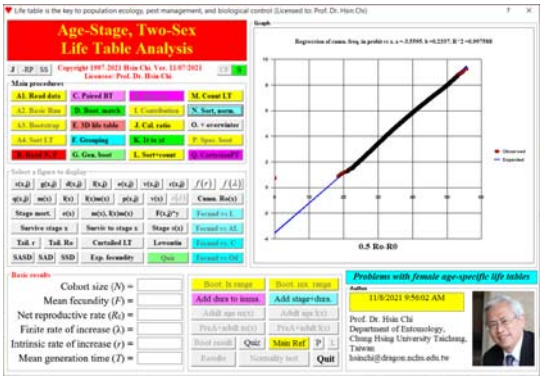
File of data counts ready.



Cumulative frequency of R_0 in probit

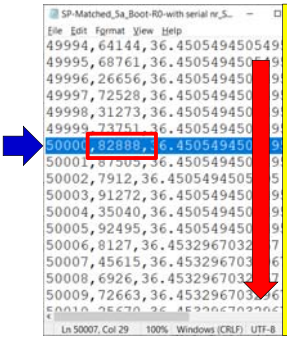


In the following file you can find the 0.025, 0.5 and 0.975 samples …..-Matched_5a_Boot-R0-with serial nr 0.025, 0.5 and 0.975 R0.txt

File:… with serial nr 0.025, 0.5 and 0.975 lambda.txt
"The 0.025 percentile life table of lambda is 41969"
"The 0.5 percentile life table of lambda is 62359"
"The 0.975 percentile life table of lambda is 14617"

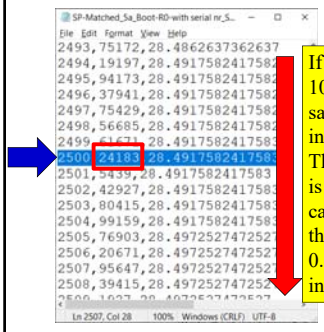
File: … with serial nr 0.025, 0.5 and 0.975 R0.txt
"The 0.025 percentile life table of R0 is 24183"
"The 0.5 percentile life table of R0 is 82888"
"The 0.975 percentile life table of R0 is 87958"

In the sorted file, you can also find 0.5 percentile
(It is the bootstrap sample of mean R_0)



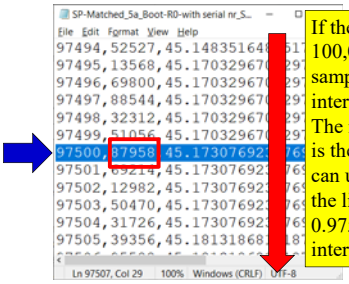
This file contains the sorted R_0. The last column is the sorted R_0 in ascending order. The second column is the original bootstrap matched sample. The first column is the sorted sequence number. If the total bootstrap match is 100,000, the 50000th of the sorted sample gives the mean of R_0 (36.45 offspring). The respective original sequence is the 82888th match. Thus you can use the 82888th sample to get the life table representing the mean of R_0.

Use sorted file to find 0.025 percentile
(It is the bootstrap sample of 0.025 CI of R_0)



If the total bootstrap match is 100,000, the 2500th of the sorted sample gives the 0.025 confidence interval of R_0 (28.49 offspring). The respective original sequence is the 24183th match. Thus you can use the 24183th sample to get the life table representing the 0.025 percentile of confidence interval of R_0.

Use sorted file to find 0.975 percentile
(It is the bootstrap sample of 0.975 CI of R_0)



If the total bootstrap match is 100,000, the 97500th of the sorted sample gives the 0.975 confidence interval of R_0 (45.17 offspring). The respective original sequence is the 87958th match. Thus you can use the 87958th sample to get the life table representing the 0.975 percentile of confidence interval of R_0.

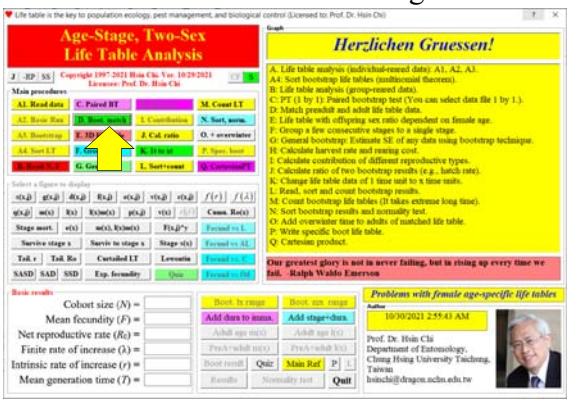
Find a sample give both 0.5th percentile of R_0 and λ

- In regular life table study, the original population parameters is calculated from the original cohort. The 0.025th and 0.975th percentiles of both R_0 and λ can be obtained from the same original cohort.
- However, for matched life tables, there is no "original cohort". The 100,000 bootstrap matches may generate different 0.5th percentile life table files for R_0 and λ.
- Because different life tables can give the same R_0, you can try to find the bootstrap-matched sample that gives both the 0.5th R_0 and 0.5th λ (it may be impossible).

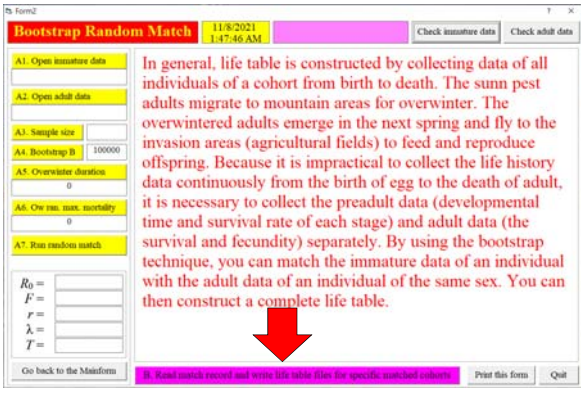
Note well!

- You can generate life table files for different bootstrap matched cohorts (samples), e.g., 69446, 21120 and 69126.
- If you want to generate more than one life table data files, please write down the bootstrap sample numbers in ascending order, e.g., 21120, 69126, and 69444. Then you can save your time.
- If you make mistake, just re-run the procedure.

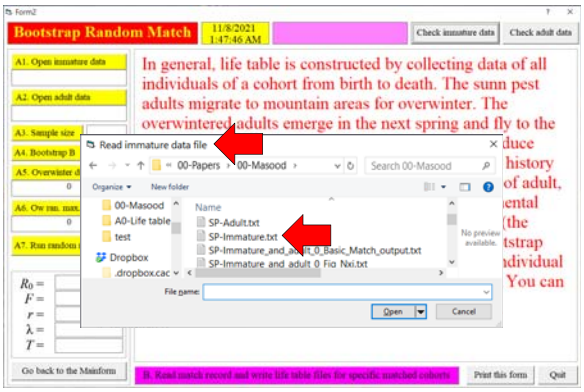
Run "E. Match tables" again



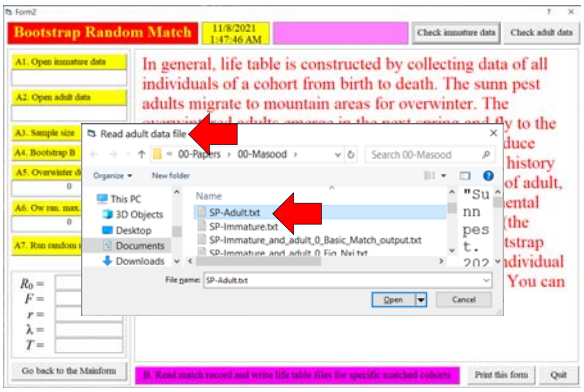
Click "Read match record and write spec. life table"



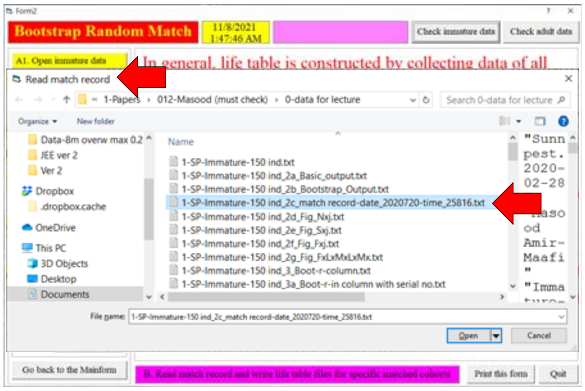
Read immature life table file



Read adult life table file



Read match record



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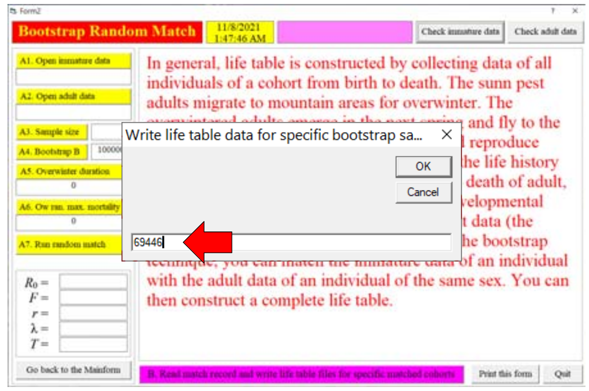
Enter the sample for 0.5 percentile R_0 life table



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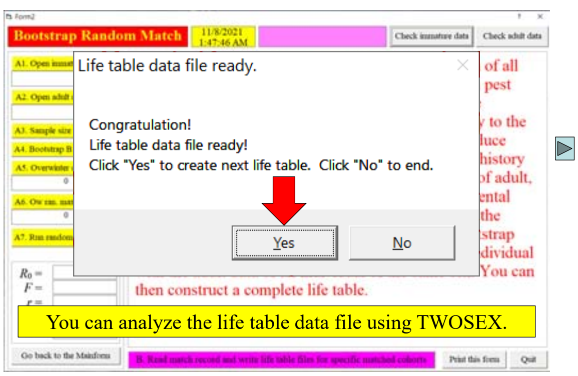
Life table data file of mean R_0 is ready!



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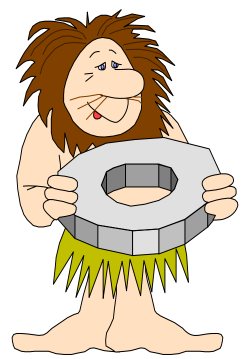

Teşekkür ederim!
سپاسگزارم
謝謝!
˝Å¼É˘ß
Děkuji
Danke!
¡Muchas gracias!
Thank you!
ご清聴ありがとうございます!

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