

If female and male have different stages,
how can you analyze your data?

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Creative thinking

If the male and female have different number of stages, for example, females go through 3 stages (egg, nymph and adult), while males go through 4 stages (egg, nymph, pupa, and adult), how can you analyze your data to show the different survival curves? Or. How can you use the TWOSEX program to show the difference in the male and female stage numbers?

You should NOT write the data file as:

"Project: Scale insect at 25°C"

"User: X. X. Yang"

"Date: 2001.4.16.-2001.6.10."

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3,3

F,Egg,Nymph,Female

M,Egg,Nymph,Pupa,Male

N,Egg,Nymph,Unknow

Egg,Nymph

1,M,6,12,5,6

2,**F,7,13,6**,4,12,9,5,8,0,-1

3,N,5,7,-3 (died as pupa)

4,N,5,-2 (sex unknown)

5,N,-2 (died as egg)

6,

There are **3 stages for female** and **4 stages for male**. The TWOSEX cannot analyze this kind of data.

File no. 1 (female)

- Assuming you begin life table with 100 eggs.
- Prepare a data file No. 1 (3 types, 3 stages, with 100 individuals) for female individuals to get survival curves (s_{xj}) of nymph and adult stage of female individuals.
- All other individuals can be assigned as N_{j-1} .
- You can get all detailed life table files. But you cannot use the population parameters.

File no. 1

"Project: Scale insect at 25°C"

"User: X. X. Yang"

"Date: 2001.4.16.-2001.6.10."

50

3,3

F,Egg,Nymph,Female

M,Egg,Nymph,Male

N,Egg,Nymph,Unknow

Egg,Nymph

1,N,-1

2,**F,7,13,6**,4,12,9,5,8,0,-1

3,N,-1

4,N,-1

5,N,-1

6,

Assuming there are **3**
stages for male.

File no. 2 (male)

- Prepare a data file No. 2 (3 types 4 stages, with 100 individuals) for male individuals to get survival curves (s_{xj}) of nymph, pupa, and adult stages of male individuals. Individuals died in pupal stage should be entered as is, e.g., N,4,5,-6 (died in pupal stage).
- All females and those died in nymphal stage should be written as N,-1.
- You will not get population parameters (because there is no female). You cannot run bootstrap.

File no. 2

"Project: Scale insect at 25°C"

"User: X. X. Yang"

"Date: 2001.4.16.-2001.6.10."

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3,4

F,Egg,Nymph,Pupa,Female

M,Egg,Nymph,Pupa,Male

N,Egg,Nymph,Pupa,Unknow

Egg,Nymph

1,M,6,12,5,6

2,**N**,-1

3,N,5,7,-3 (died as pupa)

4,N,-1 (sex unknown)

5,N,-1 (died as egg)

6,

Assuming there are 4 stages for both females and males.

File no. 3 (individuals died as nymphs)

- Prepare a data file No. 3 (with 100 individuals) to get **the s_{xj} curve of individuals died in nymphal stage.**
- All males, females, and those died in egg stage are written as N_{j-1} .
- You cannot calculate population parameters. You cannot run bootstrap.

File no. 3

"Project: Scale insect at 25°C"

"User: X. X. Yang"

"Date: 2001.4.16.-2001.6.10."

50

3,3

F,Egg,Nymph,Female

M,Egg,Nymph,Male

N,Egg,Nymph,Unknow

Egg,Nymph

1,N,-1

2,N,-1

3,N,-1

4,N,5,-2 (sex unknown)

5,N,-1

6,

Assuming all individuals
have **3 stages.**

File no. 4

(Egg curve and population parameters)

- Prepare a data file No. 4 (3 types, 3 stages with 100 eggs) for **survival curve s_{xj} of egg stage and population parameters.**
- Combine nymph and pupa of male individuals as nymph. The nymph and pupa of N type should be combined too.
- You can get correct population parameters. You can also run bootstraps.

File no. 4

"Project: Scale insect at 25°C"

"User: X. X. Yang"

"Date: 2001.4.16.-2001.6.10."

50

3,3

F,Egg,Nymph,Female

M,Egg,Nymph,Pupa,Male

N,Egg,Nymph,Unknow

Egg,Nymph

1,M,6,17,6

2,**F,7,13,6**,4,12,9,5,8,0,-1

3,N,5,-10 (died as pupa)

4,N,5,-2 (sex unknown)

5,N,-2 (died as egg)

6,

Assuming all individuals
have 3 stages.

Combine all curves

- You can import all graphic data of these files to show the survival curves (s_{xj}) females (nymph and adult, file no. 1), males (nymph, pupa, and adult, file no. 2), individuals died in nymphal stage (sex unknown, file no. 3) and egg (file no. 4).
- Important: You have to use the same number of individuals in all files.



雌雄蟲齡期不一樣

我的實驗對象是"木瓜秀粉介殼蟲"

它的雌雄蟲齡期不一樣，我不知道要如何打記事本

雌蟲(egg,N1,N2,N3,adult)

雄蟲(egg,N1,N2,N3,pupa,adult)

我看了老師那天來屏東上課的ppt，試著去理解，

但是才要跑時，就出現"check data of individual no.0 or 1"

我試了好久，一直解不開

老師麻煩您教我一下，

謝謝您了



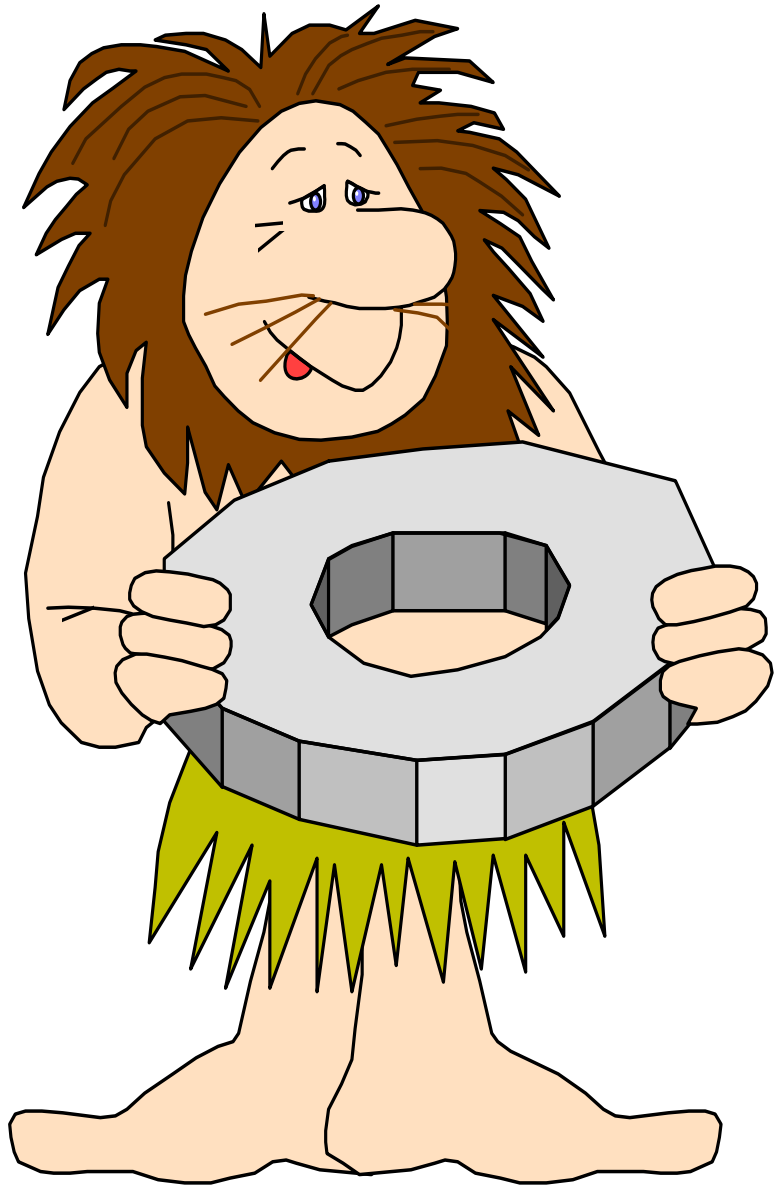
Possible solution

- 生命表檔案A: 型態與齡期設為3,5. 並先將雄蟲的N3與pupa合併為N3, 這樣可以得到正確的族群介量、egg, N1, N2的發育期、雌蟲的繁殖率、成蟲期、正確的egg, N1, N2的線條、也可以做 $l_x, m_x, l_x m_x$ 的圖。
- 生命表檔案B: 型態與齡期設為3,5. 並先假設雄蟲與N-type都在N1死亡, 可以得到雌蟲N3與雌成蟲的survival rate線條、雌蟲N3的發育期。
- 生命表檔案C: 型態與齡期設為3,6. 並先假設雌蟲與N-type都在N1死亡, 可以得到雄蟲N3、pupa與雄成蟲的發育期與survival rate線條。



Solution

- 生命表檔案D: 型態與齡期設為3,6. 並先假設雌蟲與雄蟲都在N1死亡，可以得到死在N3與pupa期的survival rate線條、N-type的N3發育期。(N-type不會活過pupa期，因此沒有pupa發育期)
- 將A的Egg, N1, N2 的survival rate, B的N3與雌成蟲的survival rate, C2的雄蟲N3、pupa與雄成蟲的survival rate, D的N3與pupa期的survival rate線條合併作圖。這是很好的圖。
- 可以用類似方法得到詳細變化曲線。用3D life table可以得到全部的曲線。



Teşekkür ederim!

سپاسگزارم

謝謝!

Děkuji

Danke!

¡Muchas gracias!

Thank you!

ご清聴ありがとうございます
ます!