## Creative thinking

If individuals have different number of stages, e.g., some have 5 larval stages while some have 6 larval stages, but you want to show curves with L6, how can you analyze your data to show the survival curves? Or. How can you use the TWOSEX program to show the difference in stage numbers among individuals?

### Can you do this? NO!

```
"Project: Scale insect at 25°C"
"User: X. X. Yang"
"Date: 2001.4.16.-2001.6.10."
50
3.9
F,Egg,L1,L2,L3,L4,L5,L6,Pupa,Female
M,Egg,L1,L2,L3,L4,L5,L6,Pupa,Male
N,Egg,L1,L2,L3,L4,L5,L6,Unknown
L1,L6
1,M,7,2,5,6,4,5,3,12,30
2,M,7,2,4,4,4,6,0,10,44
3,N,7,-7
```

#### File A: Combine L5 and L6 to get population parameters and curves from Egg to L4

```
"Project: Scale insect at 25°C"
"User: X. X. Yang"
"Date: 2001.4.16.-2001.6.10."
50
3,8
F,Egg,L1,L2,L3,L4,L5-6,Pupa,Female
M,Egg,L1,L2,L3,L4,L5-6,Pupa,Male
N,Egg,L1,L2,L3,L4,L5-6,Pupa,Unknown
L1,L5-6
1,M,7,2,5,6,4,8,12,30
2,M,7,2,4,4,4,6,10,44
3.N.7.-7
```

#### File B: To get correct L1 to adu1t curves for L5 type insects: change all insects to N,-1 except those go through L5 and adult stage

```
"Project: Scale insect at 25C"
"User: X. X. Yang"
"Date: 2001.4.16.-2001.6.10."
50
3,8
F,Egg,L1,L2,L3,L4,L5,Pupa,Female
M,Egg,L1,L2,L3,L4,L5,Pupa,Male
N,Egg,L1,L2,L3,L4,L5,Pupa,Unknown
L1,L5
1,N,-1
2,M,7,2,4,4,4,6,10,44
3,N,-1
```

```
File C: To get correct L1 to adult curves for L6 type
 insects: change all insects to N,-1 except those go
            through L6 and adult stage
"Project: Scale insect at 25C"
"User: X. X. Yang"
 "Date: 2001.4.16.-2001.6.10."
50
3,9
F,Egg,L1,L2,L3,L4,L5,L6,Pupa,Female
M,Egg,L1,L2,L3,L4,L5,L6,Pupa,Male
N,Egg,L1,L2,L3,L4,L5,L6,Pupa,Unknown
L1,L6
1,M,7,2,5,6,4,5,3,12,30
2.N.-1
3,N,-1
```



N,-1 and keep rest N type as they are.





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## How to prepare figures

- Use file A to prepare all curves of  $s_{xj}$  (with L5+L6 combined).
- Import egg  $s_{xj}$  from file A,  $s_{xj}$  of L1-adult data of file B,  $s_{xj}$  of L1-adult data of file C,  $s_{xj}$  of L1-pupa of file D to a worksheet. Add all L1s to a new column (i.e., pooled-L1 and it should be exactly the same as L1 from file A), add all L2s to a new column (pooled-L2), etc.
- In this way, you can have  $s_{xi}$  of all stages.

### Why are all these difficulties?

Because L5 and L6 are not the last stage and some N type died in pupal stage, it is therefore not easy to prepare the curve of L6.

# You can use similar method that you used for cohort that female and male have different number of stages.