

## How to calculate age-specific hatch rate and SE of overall hatch rate

1. Analyze your life table data file (total-eggs.txt) of daily **total eggs** of each female and complete the bootstrap.
2. Analyze your life table data file (hatched-eggs.txt) of daily **hatched eggs** of each female. Run the bootstrap using the same bootstrap samples (open no. 11 in folder of total eggs).
3. You can show the  $m_x$  curves of total eggs and hatched eggs in the same figure. The age-specific hatch rate ( $h_x$ ) can be calculated as:

$$h_x = \frac{m_{x,hatched-eggs}}{m_{x,total-eggs}}$$

Because you cannot calculate  $h_x$  for  $m_{x,total-egg} = 0$ , you should only show the curve  $h_x$  for  $m_{x,total-egg} > 0$ .

4. Note well! If you don't use the same bootstrap samples, you will get a fecundity of 100 eggs for bootstrap sample  $x$  from the total eggs and 110 eggs for bootstrap sample  $x$  from the hatched eggs. Then you will get a hatch rate  $>1$ . It is wrong.

## Calculation of SE of overall hatch rate

5. In SigmaPlot, import xxx\_Effective Boots-W\_Fecundity-in column.txt (total eggs) to column 1.
6. In SigmaPlot, import xxx\_Effective Boots-W\_Fecundity-in column.txt (hatched eggs) to column 2.
7. In SigmaPlot, run Analysis User-defined: Col(3)=col(2)/col(1). Col(3) is the hatch rate.
8. Create histogram from col(3).
9. Single click on histogram and fit it to regression (Gaussian 3 parameters). The  $b$  value is the SD of the normal curve. It is the SE of overall hatch rate of all bootstrap samples.

If there are only few female produced offspring, you may encounter problems in step 2. Then you can try following reversed way:

1. Analyze your life table data file of daily **hatched eggs** of each female and complete the bootstrap first.
2. Analyze your life table data file of daily **total eggs** of each female. Run the bootstrap using the same bootstrap samples (open no. 11 in folder of hatched eggs).
3. If you don't use the same bootstrap samples, you will get a fecundity of 100 eggs for bootstrap sample  $x$  from the total eggs and 110 eggs for bootstrap sample  $x$  from the hatched eggs. Then you will get hatch rate  $>1$ . It is wrong.
4. In SigmaPlot, import xxx\_Effective Boots-W\_Fecundity-in column.txt (total eggs) to column 1.
5. In SigmaPlot, import xxx\_Effective Boots-W\_Fecundity-in column.txt (hatched eggs) to column 2.
6. In SigmaPlot, run Analysis User-defined: Col(3)=col(2)/col(1). Col(3) is the hatch rate.
7. Create histogram from Col(3).
8. Single click on histogram and fit it to regression (Gaussian 3 parameters). The  $b$  value is the SD of the normal curve. It is the SE of hatch rate.
9. This method can find the SE of hatch rate. However, there will be problem because only female produced offspring.

### How to compare overall hatch rates of different treatments:

Because this calculation involves two files (total eggs and hatched eggs), TWOSEX program cannot prepare the bootstrap hatch rate for you. You have to prepare the file for paired bootstrap test as follows:

1. Calculate the hatch rate for each treatment (assuming you have 4 treatments: A, B, C, and D. The bootstrap number is 100,000.) as above.
2. Follow the “how to prepare data file for paired test” as next step.
3. Write the file headers (a~d):
  - a. **“Project: .....”**
  - b. **“User: .....”**
  - c. **“Hatch rate”**
  - d. **4**
  - e. **“A”, 2700, 0.8889**  
(You can find total eggs 2700 in total eggs\_output\_basic.txt. In Notepad, use find “ftotal” you can find the total eggs. Then find the total hatched eggs 2400 in the file hatched eggs\_output\_basic.txt using “ftotal”. Then use 2400/2700 to find the original hatch rate 0.8889)
4. Copy the 100,000 bootstrap hatch rate from SigmaPlot column (Col(3)), paste them below the line **“A”, 2700, 0.8889**.
5. Write “-1” at the bottom of the file.
6. Then write following line for treatment B.  
**“B”, 2454, 0.7644**
7. Repeat Step 3e to Step 5 for B.
8. Then write following line for treatment C.  
**“C”, 598, 0.6782**
9. Repeat Step 3e to Step 5 for C.
10. Then write following line for treatment D.  
**“D”, 2226, 0.3452**
11. Repeat Step 3e to Step 5 for D.
12. Run TWOSEX paired test.