

1 Supporting Information

2 Appendix 1: Implementation of the Crofton Method

3 The algorithm for fitting the Crofton Method (Crofton 1971) proceeds as follows.

4 First, obtain a dataset with n hosts where each host has some parasite intensity 0

5 to p_{max} . Starting with the full dataset, guess a vector of pre-mortality parameters

6 (N_p, μ_p, k_p) and given these parameters calculate the predicted number of hosts

7 with $0, 1, 2, \dots, p_{max}$. Compare the expected number of hosts with $0, 1, 2, \dots, p_{max}$

8 parasites to the observed number hosts with $0, 1, 2, \dots, p_{max}$ parasites and calculate

9 the χ^2 -squared statistic associated with your observed and predicted vectors.

10 In reality, one often has to bin the parasite intensity data because all parasite

11 intensities are not represented in the dataset. Continue to guess (N_p, μ_p, k_p)

12 vectors until a set of parameters is found that minimizes the χ^2 -squared statistic.

13 Second, choose a truncation value (t_1) such that $t_1 < p_{max}$. Truncate the

14 data such that $\text{data}_{\text{truncated}} \leq t$ and repeat the above iterative procedure to

15 calculate another set of parameters $(N_{p2}, \mu_{p2}, k_{p2})$ that minimizes the χ^2 -squared

16 statistic on the truncated data. Choose a new truncated value $t_2 < t_1$ and repeat

17 the first two steps. Continue to truncated the dataset until it only contains hosts

18 with 0, 1, and 2 parasites (or 3 bins). As the method attempts to estimate three

19 parameters, at least 3 classes are needed if all 3 parameters are to be identifiable

20 (Royce & Rossignol 1990).

21 We provide an implementation and unit tests of the Crofton Method

22 Supplementary Information 3. Figure 7 visually shows the results of these unit

23 tests.

24 **Appendix 2: Additional Figure**

25 See Figures 1 - 6.

26 **Appendix 3: Code and unit tests for estimating parasite-** 27 **induced host mortality**

28 Python code, unit tests, and a help file for the Crofton Method, the Ad-
29 jei Method and the Likelihood Method can be found in `pihm_methods.py`,
30 `test_pihm_methods.py`, and `help_file.txt`, respectively.

31 **References**

- 32 1.
33 Crofton, H. D. (1971). A quantitative approach to parasitism. *Parasitology*, 62,
34 179–193.
- 35 2.
36 Royce, L. A. & Rossignol, P. (1990). Epidemiology of honey bee parasites.
37 *Parasitology Today*, 6, 348–353.

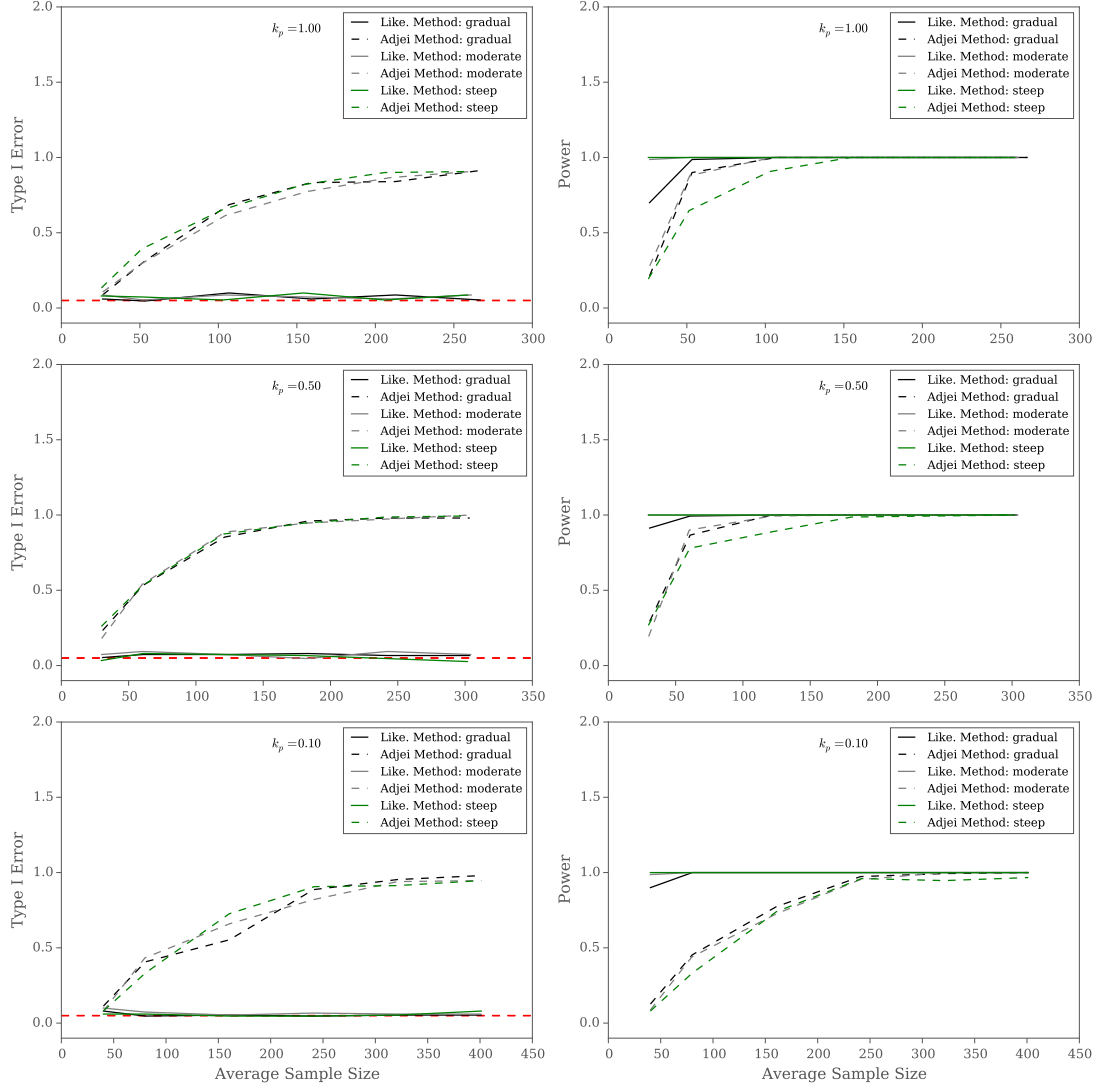


Figure 1: The type I error rate and the power of the Likelihood Method (solid line) and the Adjei Method (dashed lines) when $\mu_p = 50$ for various shapes of the host survival function and levels of aggregation k_p . The first column gives the type I error rate of each method for falsely detecting PIHM when none is present. The red line gives the the pre-set type I error rate of $\alpha = 0.05$. The second column gives the power of a given method to detect PIHM when it is actually occurring.

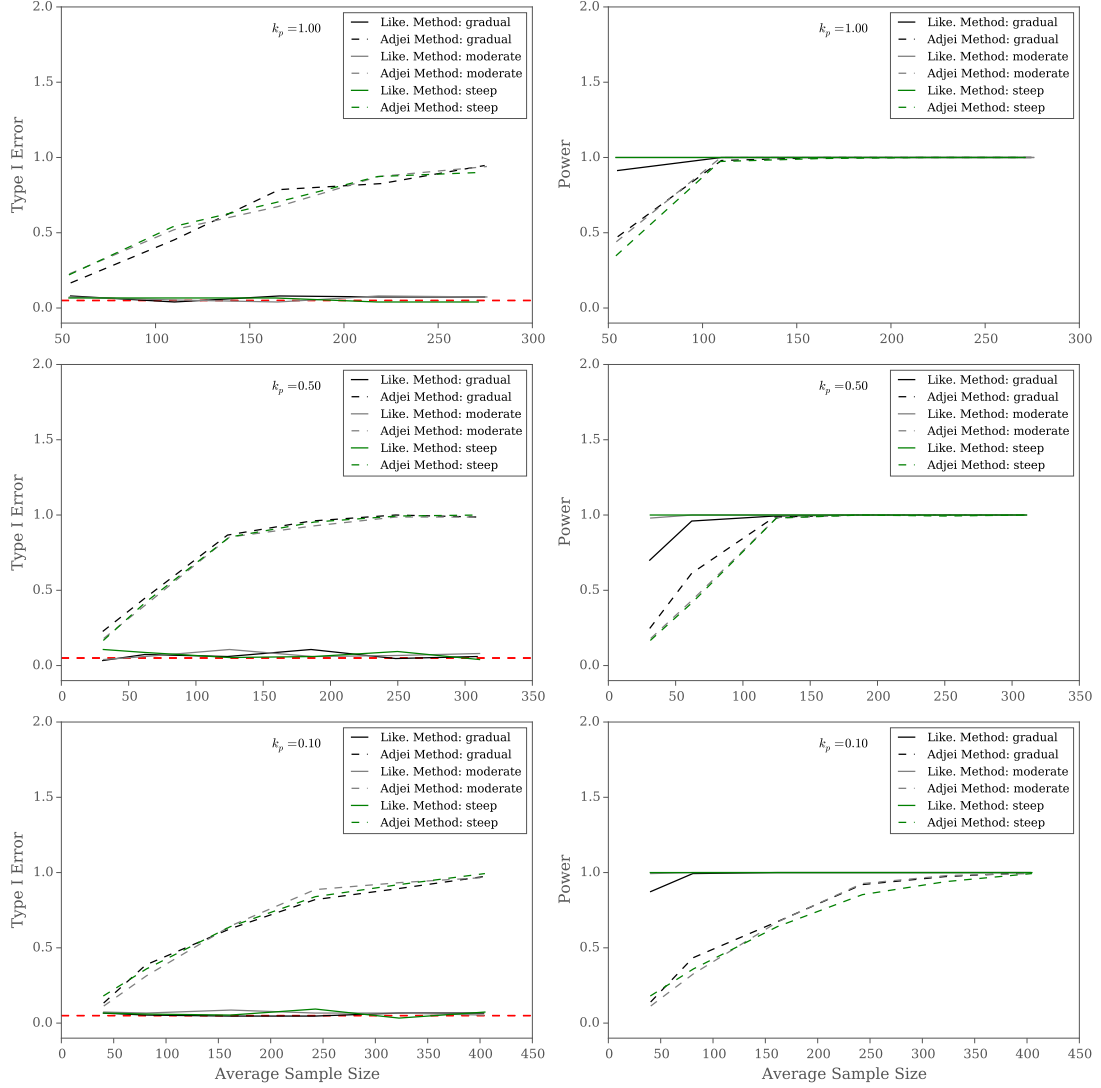


Figure 2: The type I error rate and the power of the Likelihood Method (solid line) and the Adjei Method (dashed lines) when $\mu_p = 100$ for various shapes of the host survival function and levels of aggregation k_p . The first column gives the type I error rate of each method for falsely detecting PIHM when none is present. The red line gives the the pre-set type I error rate of $\alpha = 0.05$. The second column gives the power of a given method to detect PIHM when it is actually occurring.

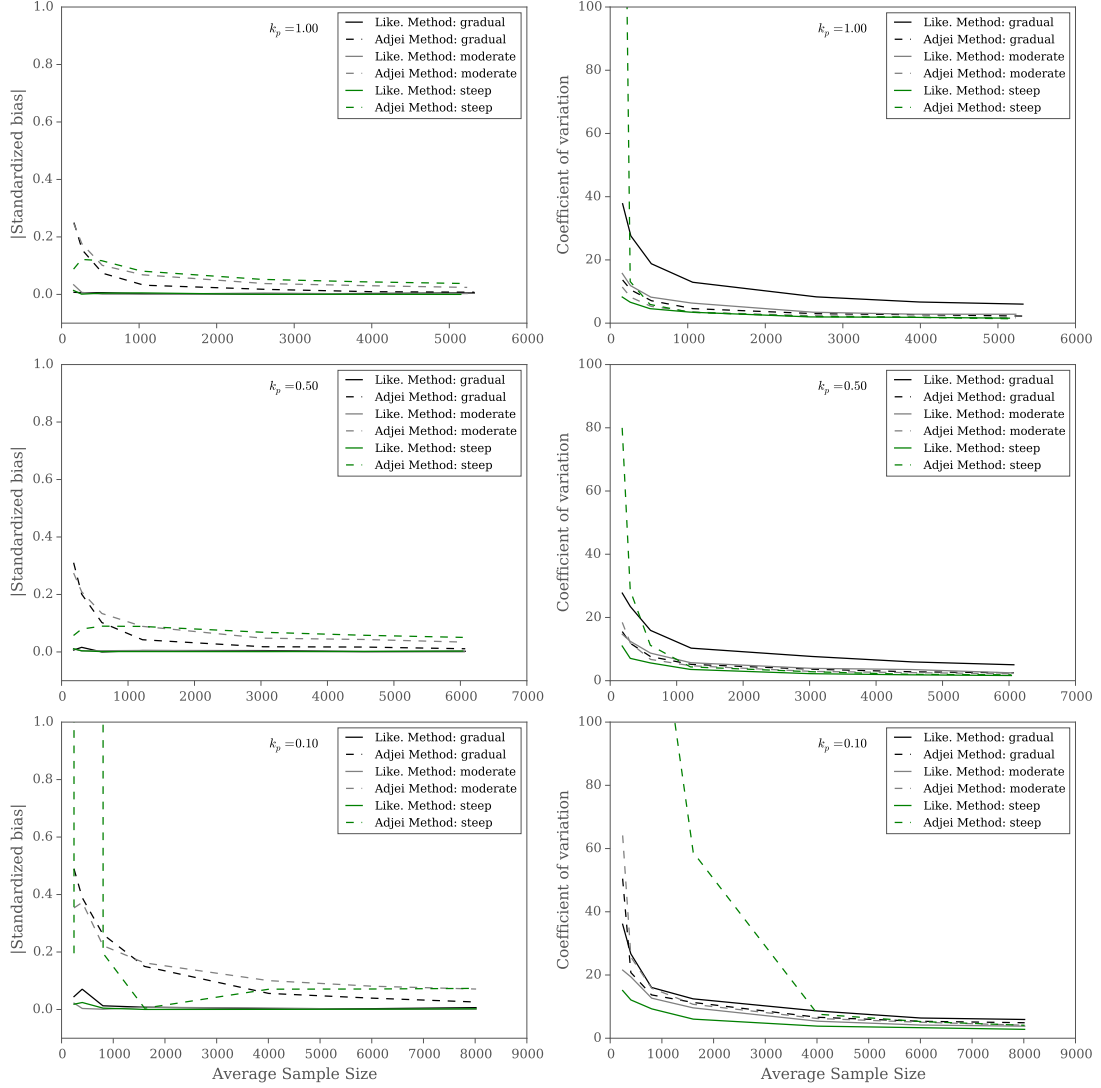


Figure 3: The bias and the precision of the Likelihood Method (solid line) and the Adjei Method (dashed lines) when $\mu_p = 50$ for various shapes of the host survival function and levels of aggregation k_p when estimating LD_{50} . The first column gives the bias of each method's LD_{50} estimate over 150 simulations. The second column gives the precision of each method's LD_{50} estimate over 150 simulations.

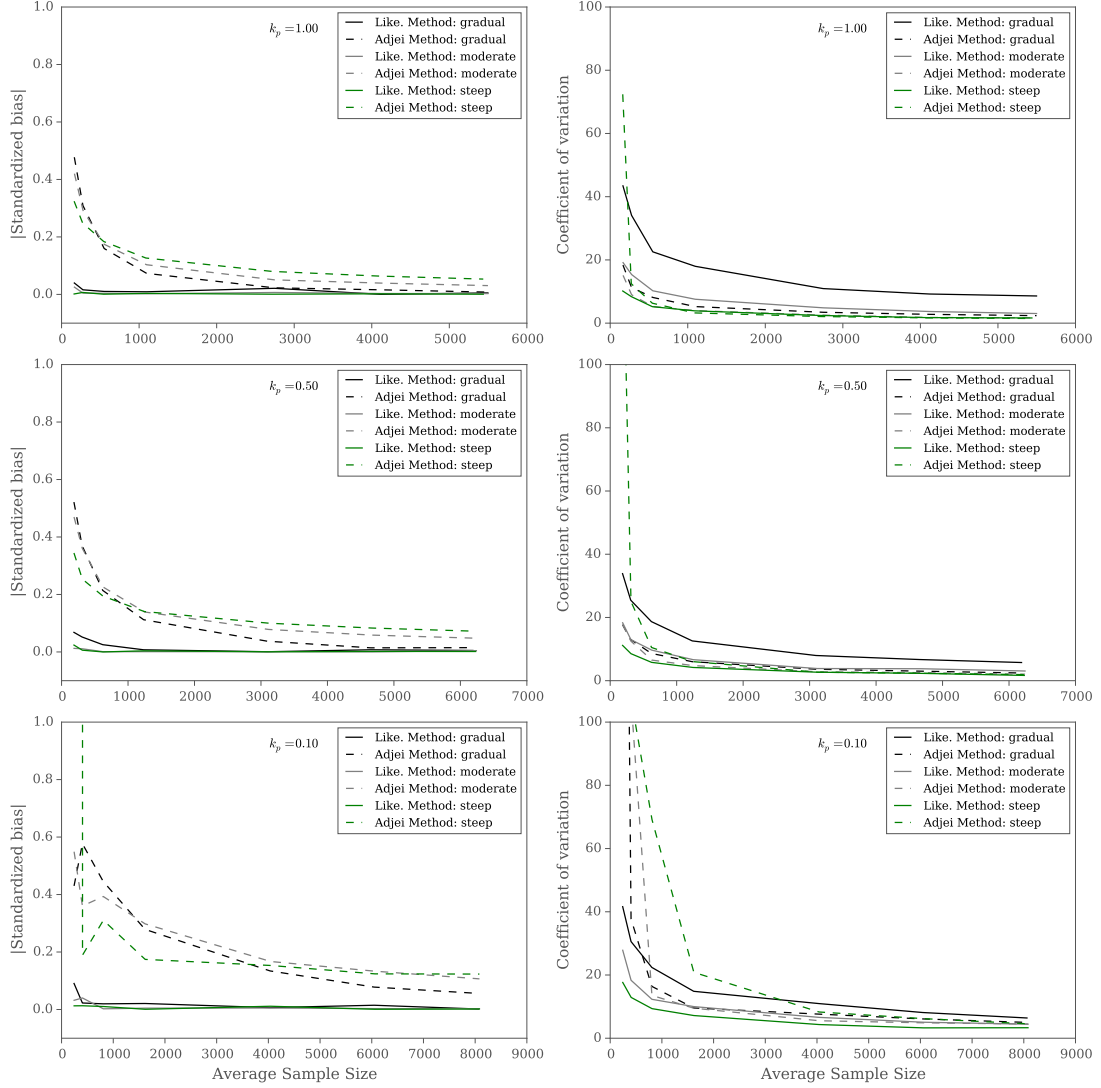


Figure 4: The bias and the precision of the Likelihood Method (solid line) and the Adjei Method (dashed lines) when $\mu_p = 100$ for various shapes of the host survival function and levels of aggregation k_p when estimating LD_{50} . The first column gives the bias of each method's LD_{50} estimate over 150 simulations. The second column gives the precision of each method's LD_{50} estimate over 150 simulations.

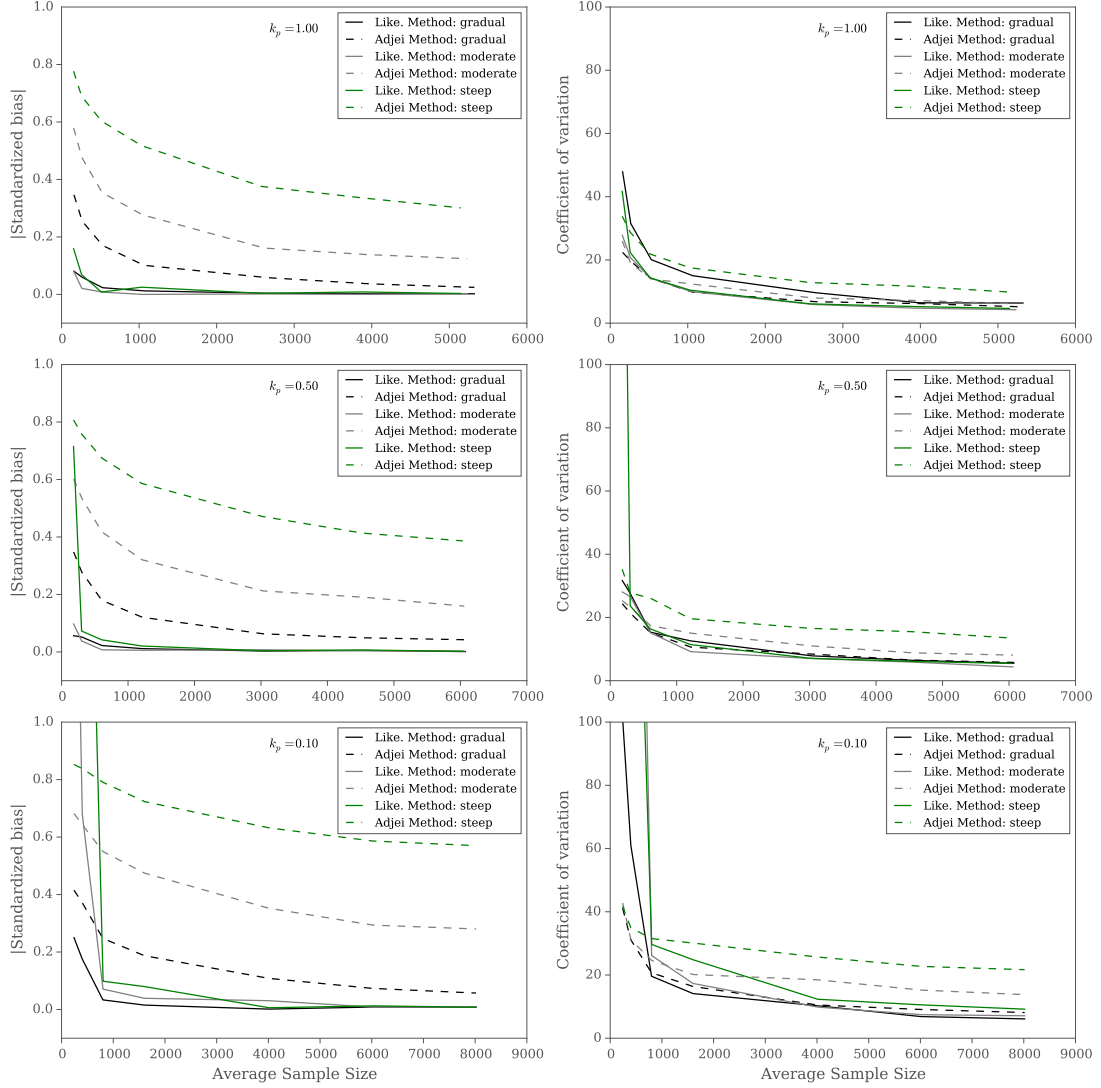


Figure 5: The bias and the precision of the Likelihood Method (solid line) and the Adjei Method (dashed lines) when $\mu_p = 50$ for various shapes of the host survival function and levels of aggregation k_p when estimating the a parameter of the host survival function. The first column gives the bias of each method's a estimate over 150 simulations. The second column gives the precision of each method's a estimate over 150 simulations.

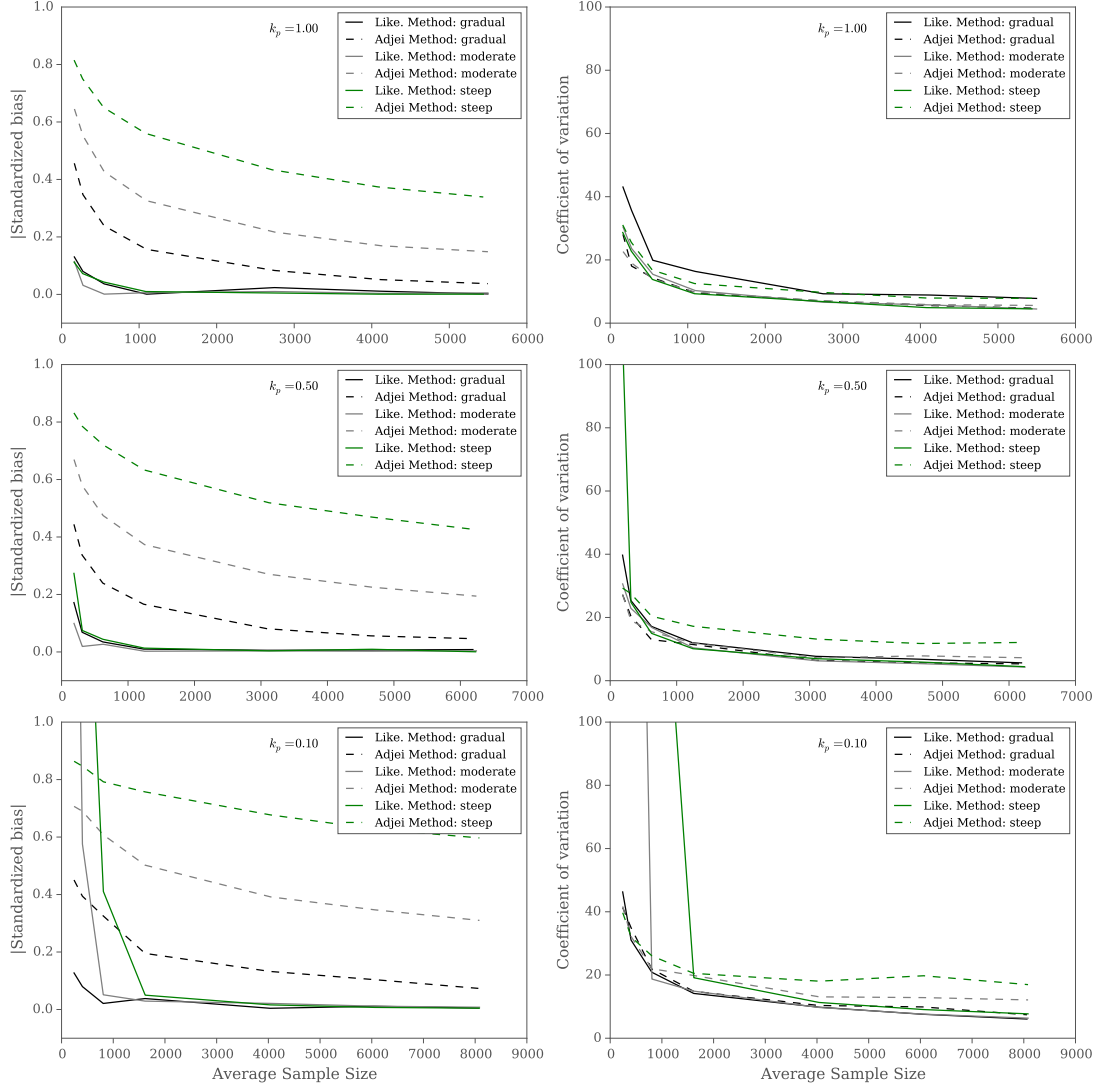


Figure 6: The bias and the precision of the Likelihood Method (solid line) and the Adjei Method (dashed lines) when $\mu_p = 100$ for various shapes of the host survival function and levels of aggregation k_p when estimating the a parameter of the host survival function. The first column gives the bias of each method's a estimate over 150 simulations. The second column gives the precision of each method's a estimate over 150 simulations.

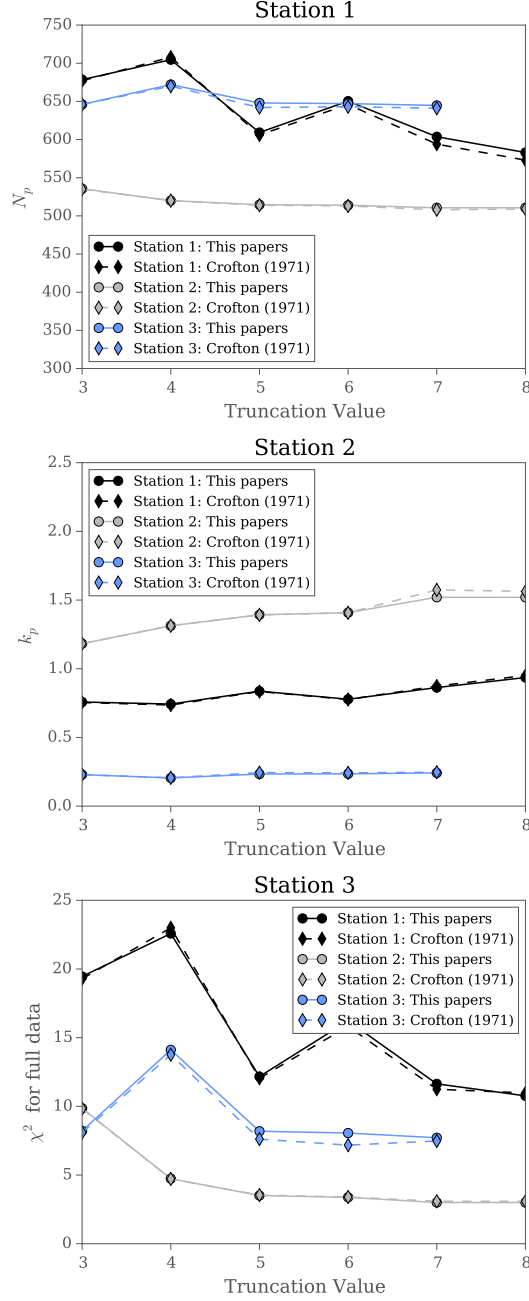


Figure 7: A comparison of this papers implementation of the Crofton Method with the results given in Crofton (1971). Three of the 6 stations fit by Crofton (1971) are shown here and all three show that the two implementations give very similar results.