

Midterm Election Simulation Project

Group 2

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For each of $nrep$ replications:

- We first generate N_contam the size of the contaminating group using a bin(N, q). q is our assumption for the percentage of the contaminating group out of the entire sample which has a sample size N . $N - N_contam$ is the size of the sample that is not contaminated. Note that when $q = 0$, there is no contamination in the sample.
- Second, we generate the number of people in the contaminating group who prefer candidate 1 (N_true_1), candidate 2 (N_true_2) and candidate 3 (N_true_3) respectively using a multinomial (N_contam, p_1, p_2, p_3) since the proportion of people in this group favors candidate 1, candidate 2 and candidate 3 is p_1, p_2, p_3 .
- We also generate the number of people in the not contaminated group who prefer candidate 1 (N_contam_1), candidate 2 (N_contam_2) and candidate 3 (N_contam_3) respectively using a multinomial ($N - N_contam, r_1, r_2, r_3$) since the proportion of people in this group favors candidate 1, candidate 2 and candidate 3 is r_1, r_2, r_3 .
- Then we have the simulated number of people who prefer candidate 1 $N_1 = N_true_1 + N_contam_1$. People who prefer candidate 2 $N_2 = N_true_2 + N_contam_2$. People who prefer candidate 3 $N_3 = N_true_3 + N_contam_3$.

Continue for the same replication t :

- We first calculate $p_{1_hat} = \frac{N_1}{N}$, $p_{2_hat} = \frac{N_2}{N}$, $p_{3_hat} = \frac{N_3}{N}$.
- Then we calculate CI_m1_{ij} the $1 - \alpha$ confidence interval for $p_i - p_j$ using the following formula from method 1:

$$p_{i_hat} - p_{j_hat} \pm \sqrt{\frac{Ad_{i,j}}{N'}}$$
where $A = \chi_{M-1}^2 \left(\frac{\alpha}{M} \right)$, $M = m \frac{(m-1)}{2}$, $m = 3$, $d_{i,j} = p_{i_hat} + p_{j_hat} - (p_{i_hat} - p_{j_hat})^2$

Calculate CI_m2_{ij} the confidence interval for $p_i - p_j$ using the following formula from method 2:

$$p_{i_hat} - p_{j_hat} \pm \frac{a}{\sqrt{N}} \text{ where } 1 - 2[1 - z_a] - 4[m - 2][1 - z_{a\sqrt{2}}] = 1 - \alpha, m = 3$$

Note that if $p_1 - p_2 \in CI_m11,2$ and $p_1 - p_3 \in CI_m11,3$ and $p_2 - p_3 \in CI_m12,3$, then we say the simultaneous confidence interval consist of $CI_m1_{1,2}$, $CI_m1_{1,3}$ and $CI_m1_{2,3}$ covers the true value $p_1 - p_2$, $p_1 - p_3$ and $p_2 - p_3$ simultaneously for this replication. Same goes for method 2.

- The average confidence interval width is $avg_width_m1_t = \frac{2\sqrt{\frac{Ad_{1,2}}{N'}} + 2\sqrt{\frac{Ad_{1,3}}{N'}} + 2\sqrt{\frac{Ad_{2,3}}{N'}}}{3}$ for method 1 and $avg_width_m2_t = 2\frac{a}{\sqrt{N}}$ for method 2.
- The maximum confidence interval width is $max_width_m1_t = \max[2\sqrt{\frac{Ad_{1,2}}{N'}}, 2\sqrt{\frac{Ad_{1,3}}{N'}}, 2\sqrt{\frac{Ad_{2,3}}{N'}}]$ for method 1 and $max_width_m2_t = 2\frac{a}{\sqrt{N}}$ for method 2.

- The CI and its width is calculated $nrep$ times for $nrep$ replications.
- The estimated coverage probability is $\frac{nrep_cov_m1}{nrep}$ if among $nrep$ replications $nrep_cov_m1$ of them cover the true value simultaneously with the CI constructed with method 1. Same goes for method 2.
- The estimated average simultaneous CI width is $\frac{\sum_t avg_width_m1_t}{nrep}$ for method 1. Same goes for method 2.
- The estimated maximum simultaneous CI width is $\frac{\sum_t max_width_m1_t}{nrep}$ for method 1. Same goes for method 2.

Shiny app:

https://zxynj.shinyapps.io/Midterm_election_simulation_project_Stat_6341/

- When there is no contamination, method 1 is better than method 2 but with wider CI.
- CI width decreases as N increase.

Midterm election simulation project Stat 6341

Population parameters

Candidate 1 preference (p_1)
0.5

Candidate 2 preference (p_2)
0.3

Candidate 3 preference (p_3)
0.2

☐ Contamination

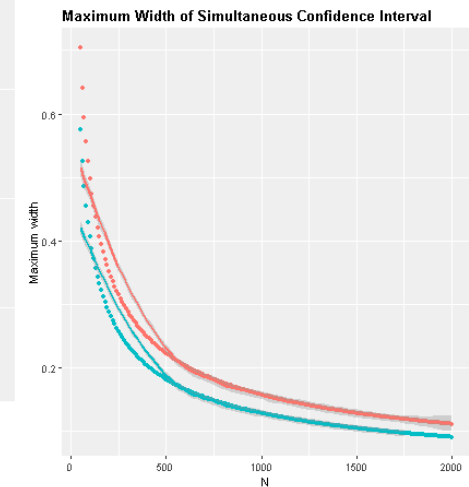
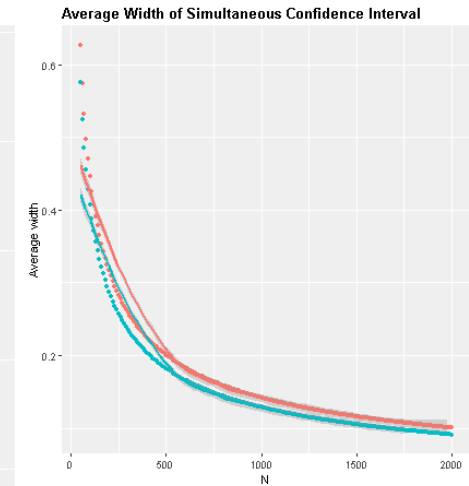
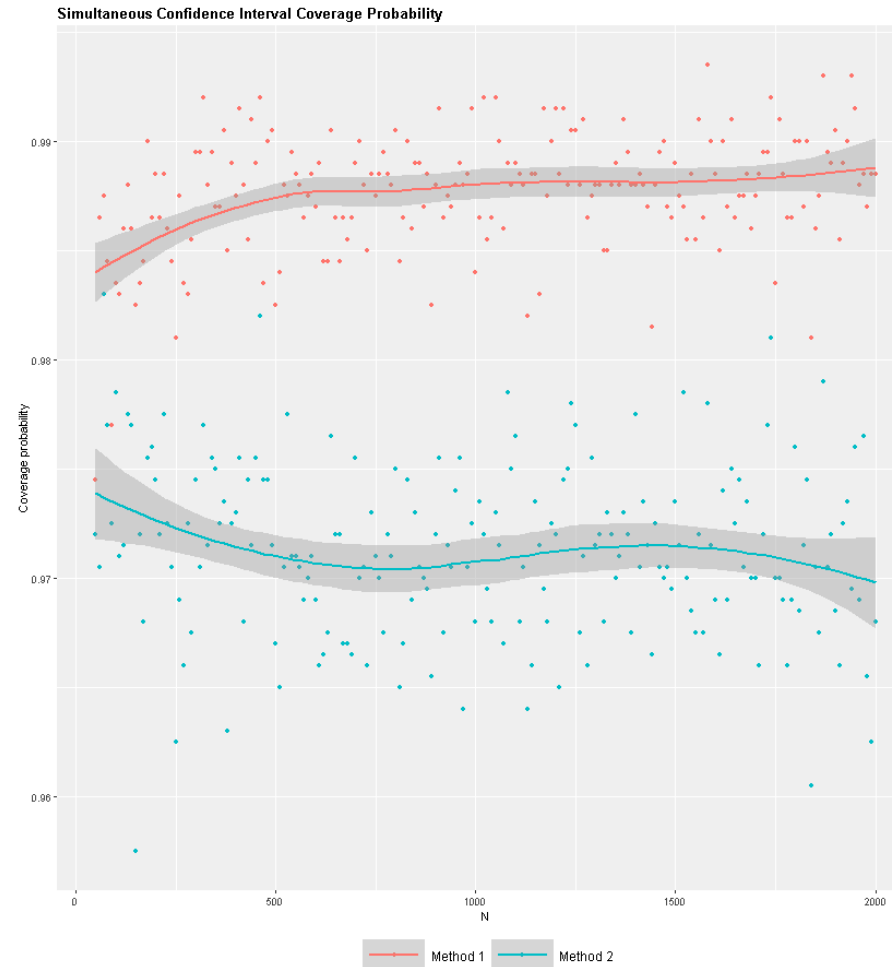
Dynamic parameters

X Axis
Sample size per replication (N)

Sample size per replication (N)
50 2,000 5,000

Number of replications (nrep)
10 2,000 10,000

Significance level (α)
0.01 0.05 0.2



- The variance of the coverage probability decreases as *nrep* increase.

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Population parameters

Candidate 1 preference (p_1)
0.5

Candidate 2 preference (p_2)
0.3

Candidate 3 preference (p_3)
0.2

☐ Contamination

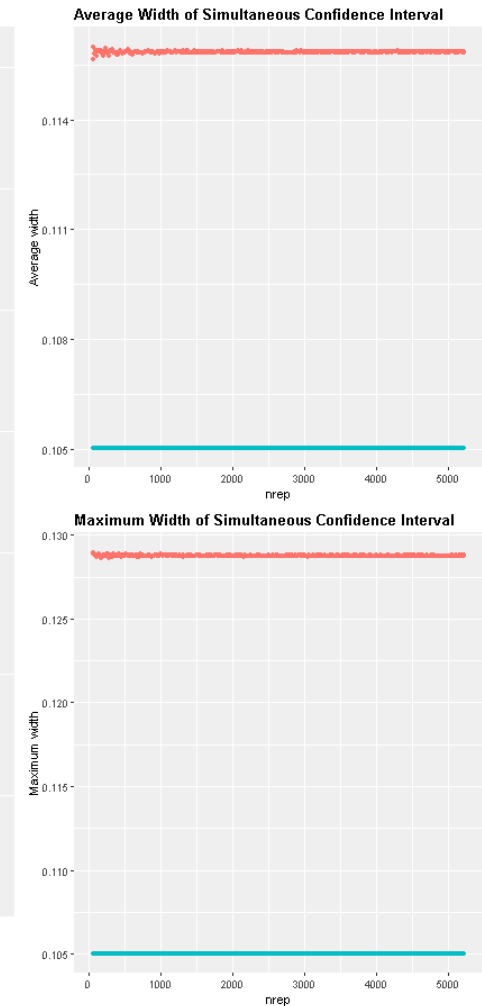
Dynamic parameters

X Axis
Number of replications (nrep)

Sample size per replication (N)
10 1,500 5,000

Number of replications (nrep)
50 5,220 10,000

Significance level (α)
0.01 0.05 0.2



- The coverage probability decreases as α increase.
- The coverage probability for Method 2 drops faster than Method 1. This could be explained by Method 2's narrower CI width and faster decreasing CI width.

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Population parameters

Candidate 1 preference (p_1)
0.5

Candidate 2 preference (p_2)
0.3

Candidate 3 preference (p_3)
0.2

☐ Contamination

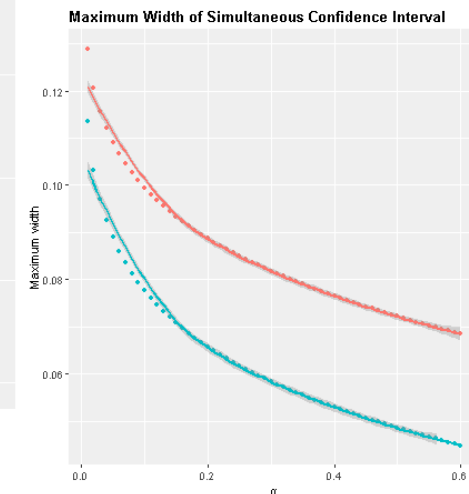
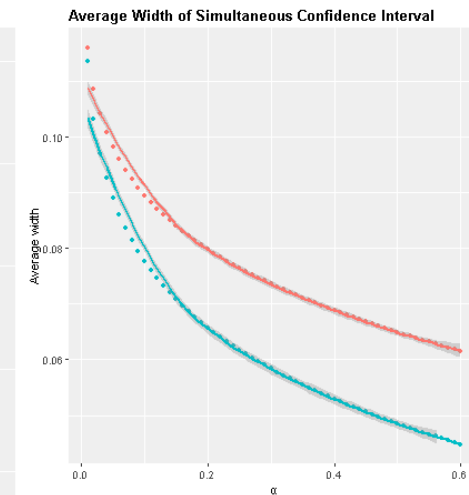
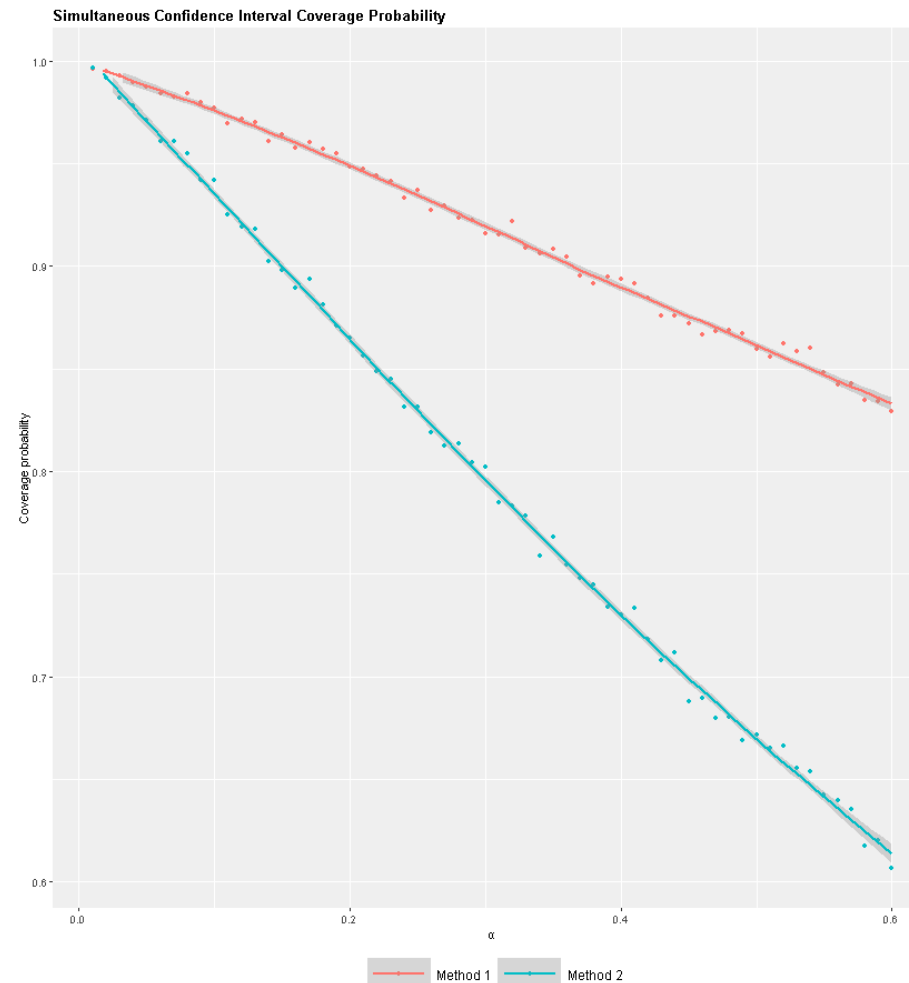
Dynamic parameters

X Axis
Significance level (α)

Sample size per replication (N)
10 2,090 5,000

Number of replications (nrep)
10 5,270 10,000

Significance level (α)
0.01 0.6



- When one candidate dominates the race, the CI width for Method 1 $\rightarrow 0$ which cause its coverage probability to perform poorly comparing to Method 1 which has a fixed CI width.
- $$d_{i,j} = p_{i_hat} + p_{j_hat} - (p_{i_hat} - p_{j_hat})^2$$

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Population parameters

Candidate 1 preference (p_1)
0.9

Candidate 2 preference (p_2)
0.05

Candidate 3 preference (p_3)
0.05

☐ Contamination

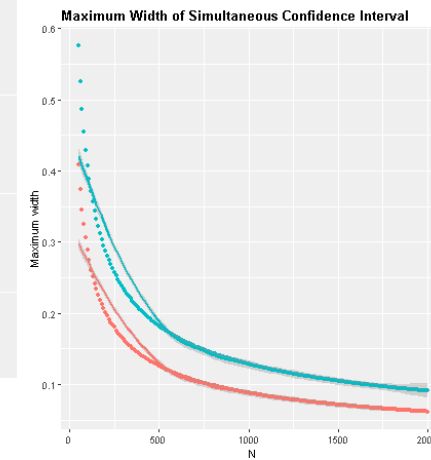
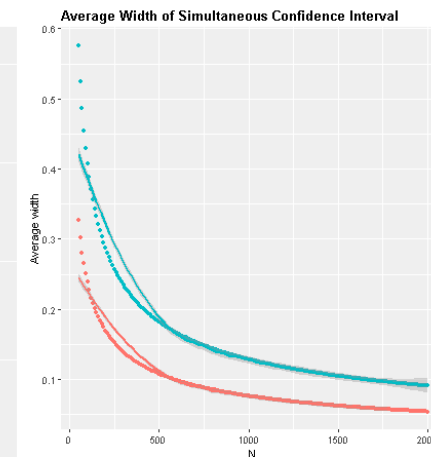
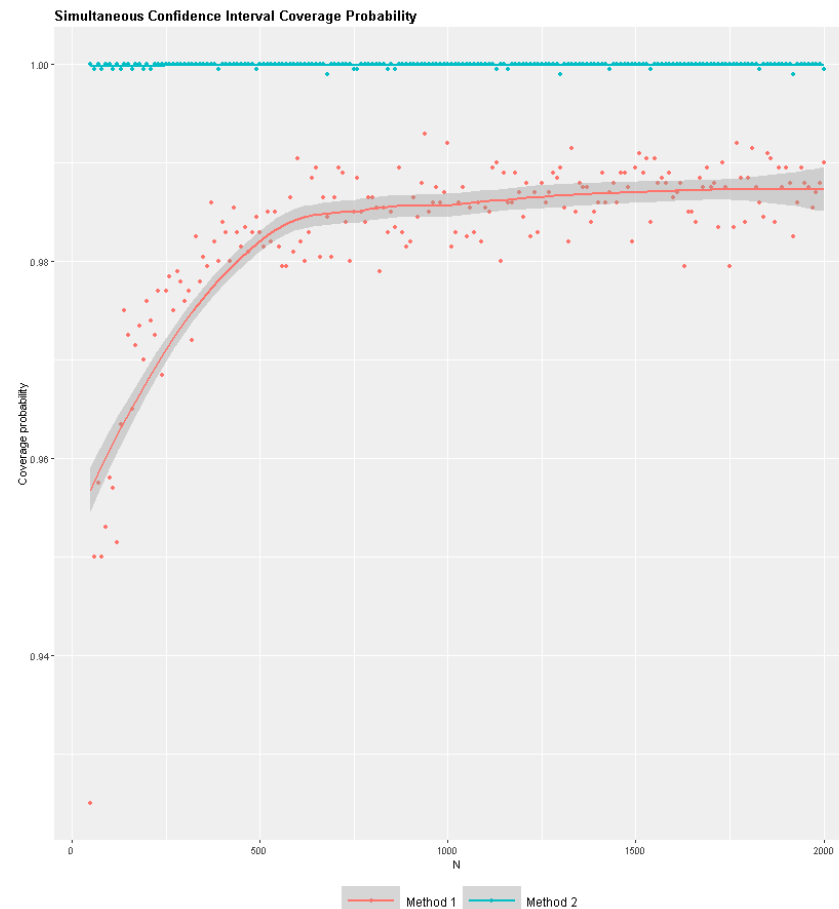
Dynamic parameters

X Axis
Sample size per replication (N)

Sample size per replication (N)
50 2,000 5,000

Number of replications (nrep)
10 2,000 10,000

Significance level (α)
0.01 0.05 0.6



- When all three candidates are very close.

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Population parameters

Candidate 1 preference (p_1)
0.34

Candidate 2 preference (p_2)
0.33

Candidate 3 preference (p_3)
0.33

☐ Contamination

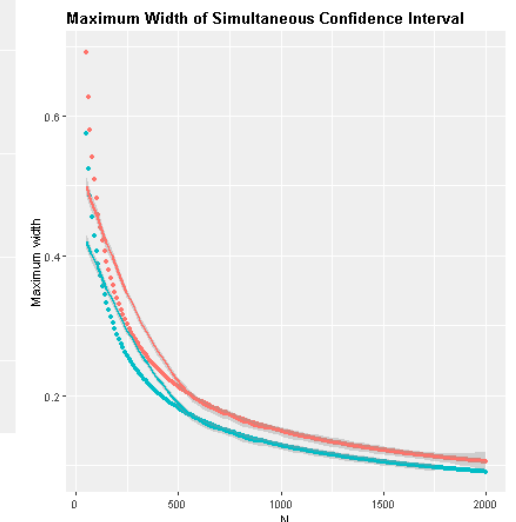
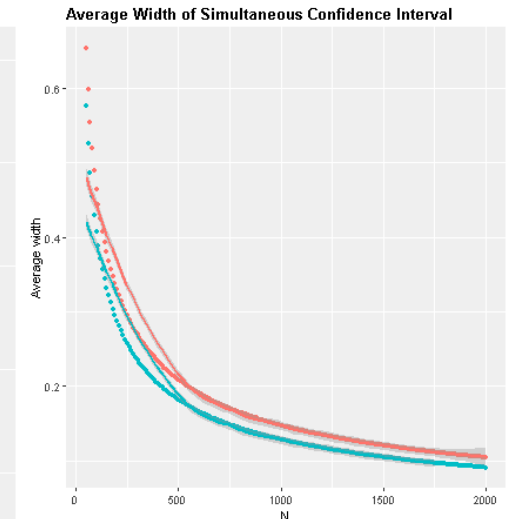
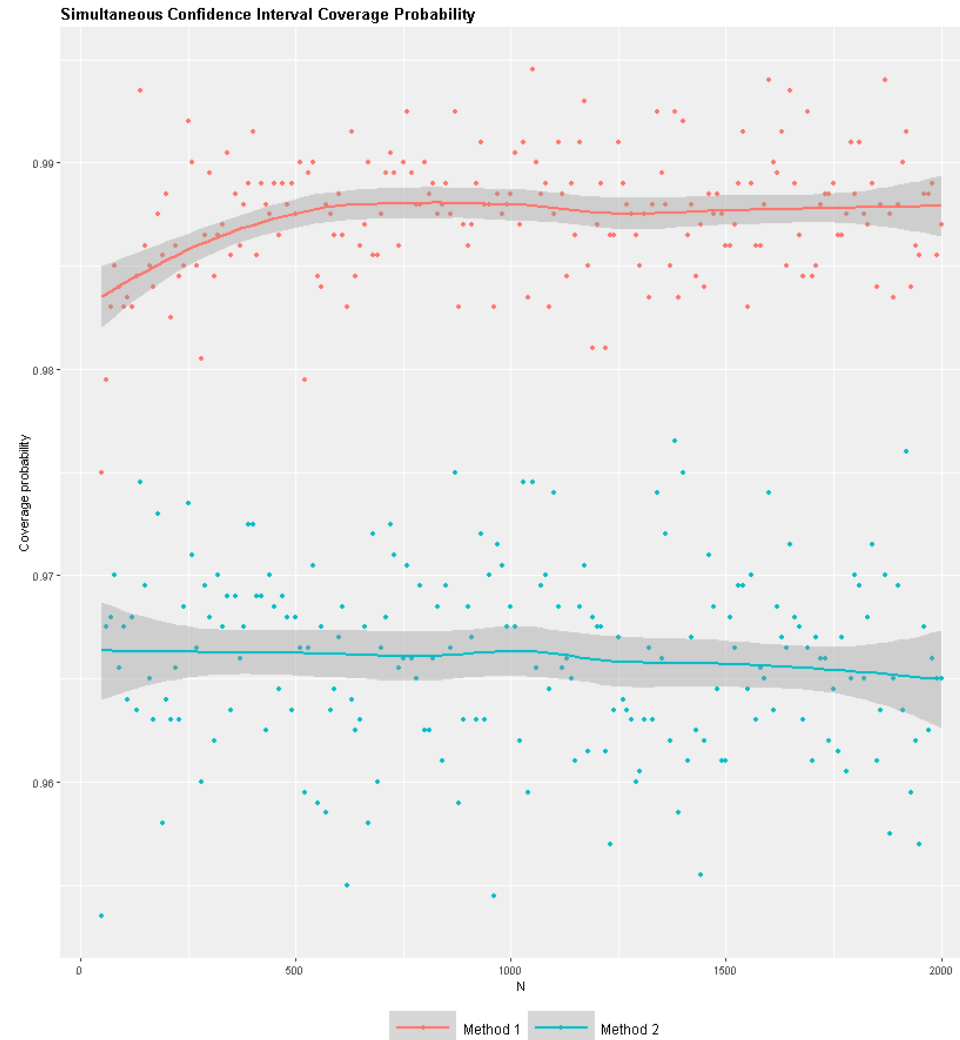
Dynamic parameters

X Axis
Sample size per replication (N)

Sample size per replication (N)
50 2,000 5,000

Number of replications (nrep)
10 2,000 10,000

Significance level (α)
0.01 0.05 0.6



- When there is contamination, the CI width was wide enough at the beginning to achieve 90%+ coverage probability.

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Population parameters

Candidate 1 preference (p_1)
0.5

Candidate 2 preference (p_2)
0.3

Candidate 3 preference (p_3)
0.2

☒ Contamination

Candidate 1 preference for contamination population (r_1)
0.34

Candidate 2 preference for contamination population (r_2)
0.33

Candidate 3 preference for contamination population (r_3)
0.33

Dynamic parameters

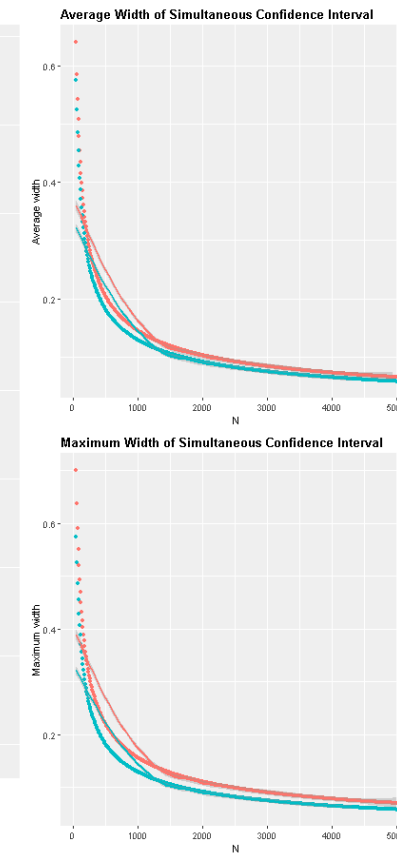
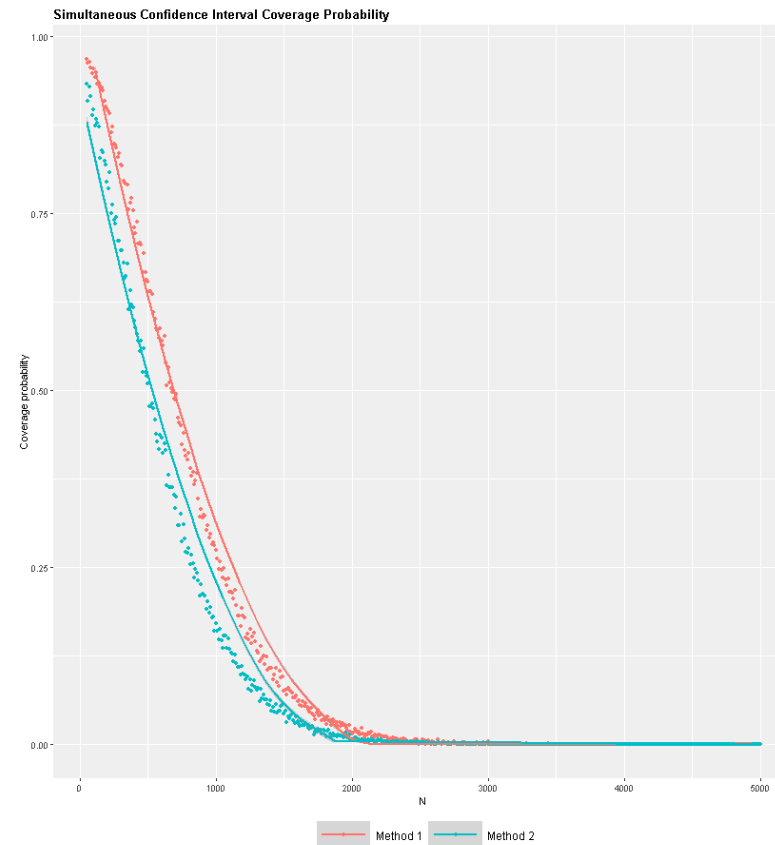
X Axis
Sample size per replication (N)

Sample size per replication (N)
50 5,000

Number of replications (nrep)
10 10,000

Significance level (α)
0.01 0.05 0.6

Contamination percentage (q)
0 0.3 1



- When there is contamination, the coverage probability drops as contamination proportion increases.

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Population parameters

Candidate 1 preference (p_1)

Candidate 2 preference (p_2)

Candidate 3 preference (p_3)

☒ Contamination

Candidate 1 preference for contamination population (r_1)

Candidate 2 preference for contamination population (r_2)

Candidate 3 preference for contamination population (r_3)

Dynamic parameters

X Axis

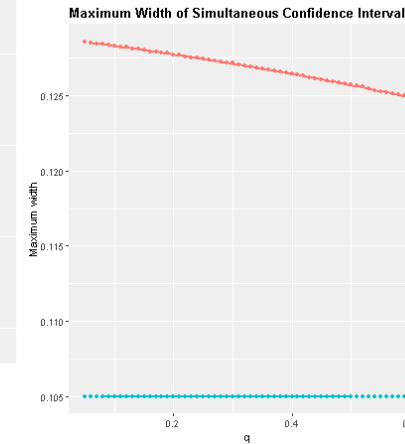
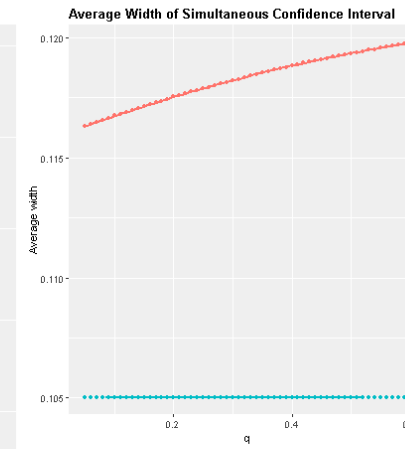
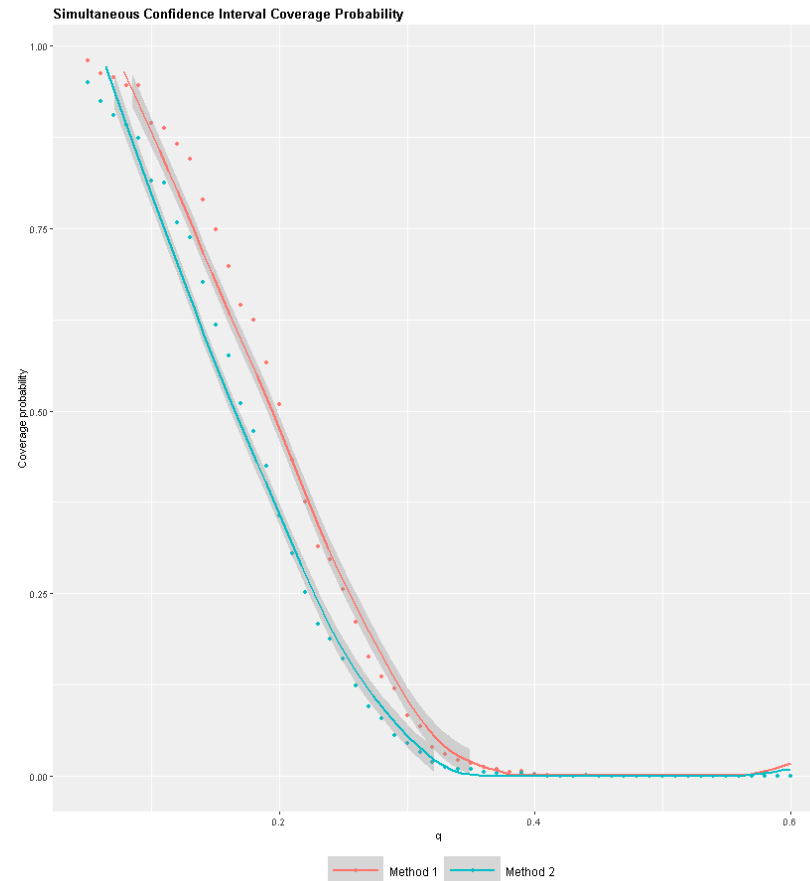
Contamination percentage (q)

Sample size per replication (N)

Number of replications ($nrep$)

Significance level (α)

Contamination percentage (q)



- When single domination is contaminated with close preference, the CI width for method 1 is smaller than Method 2 as expected.
- As the sample gets more contaminated, the CI center shifts towards the contaminating group's preference probability (close preference) which has a larger CI.

Midterm election simulation project Stat 6341

Population parameters

Candidate 1 preference (p_1)
0.9

Candidate 2 preference (p_2)
0.05

Candidate 3 preference (p_3)
0.05

☒ Contamination

Candidate 1 preference for contamination population (r_1)
0.34

Candidate 2 preference for contamination population (r_2)
0.33

Candidate 3 preference for contamination population (r_3)
0.33

Dynamic parameters

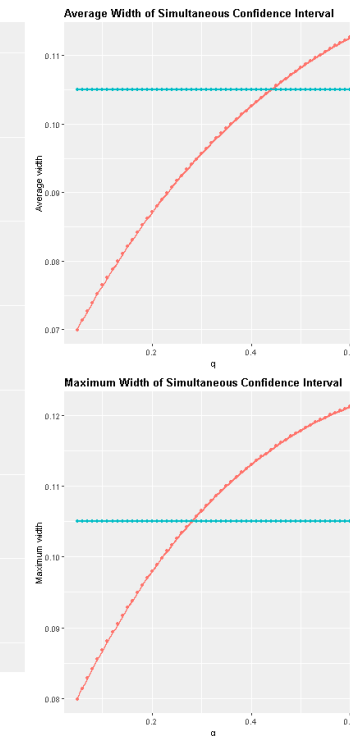
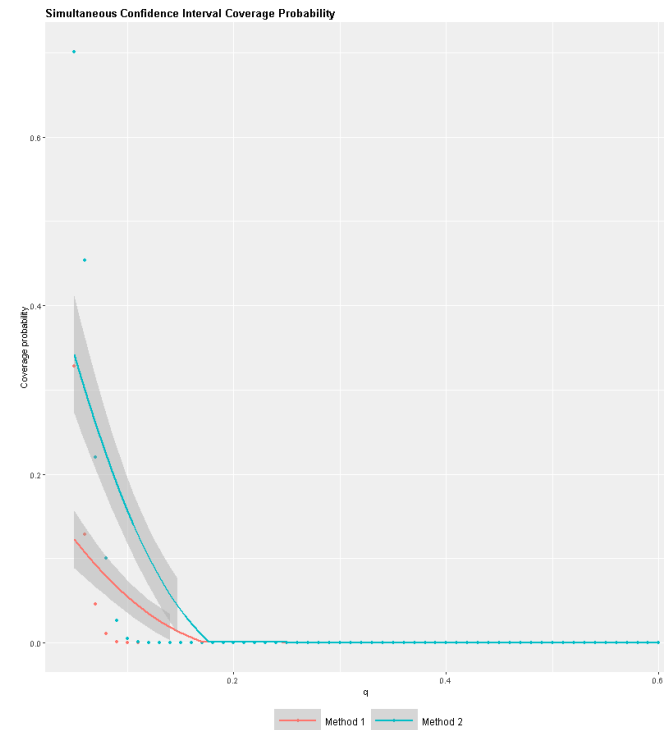
X Axis
Contamination percentage (q)

Sample size per replication (N)
10 1,500 5,000

Number of replications ($nrep$)
10 2,000 10,000

Significance level (α)
0.01 0.05 0.5

Contamination percentage (q)
0 0.05 0.6 1



- When close preference is contaminated with single domination, as the sample gets more contaminated the CI center shifts towards the contaminating group's preference probability (single domination) which has a smaller CI.
- Even the overall trend of maximum CI width is decreasing, it actually goes up a little bit as the mixed p_1, p_2, p_3 becomes a little bit different.

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Population parameters

Candidate 1 preference (p_1)
0.34

Candidate 2 preference (p_2)
0.33

Candidate 3 preference (p_3)
0.33

☒ Contamination

Candidate 1 preference for contamination population (r_1)
0.9

Candidate 2 preference for contamination population (r_2)
0.05

Candidate 3 preference for contamination population (r_3)
0.05

Dynamic parameters

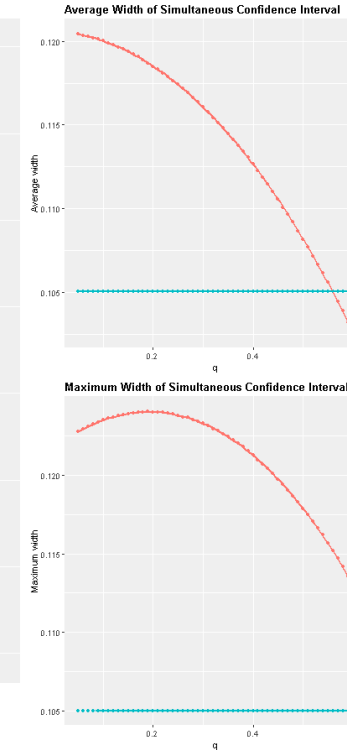
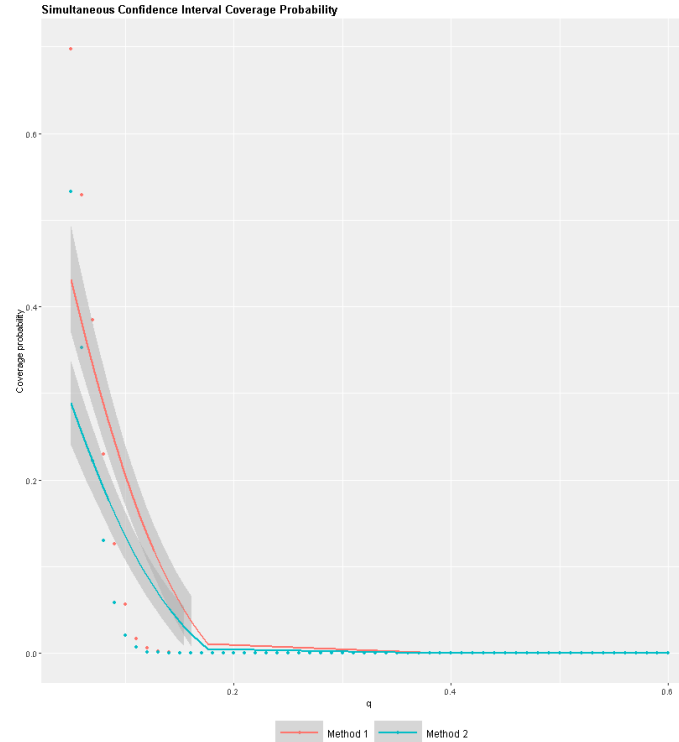
X Axis
Contamination percentage (q)

Sample size per replication (N)
10 1,500 5,000

Number of replications ($nrep$)
10 2,000 10,000

Significance level (α)
0.01 0.05 0.6

Contamination percentage (q)
0 0.05 0.9 1



- Compare p_1, p_2, p_3 mixed with r_1, r_2, r_3 and p_1, p_2, p_3 mixed with r_1, r_3, r_2 .
- Coverage probability becomes 0 at $q = 0.25$ and average CI width has a small ascent right after mixing.

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Population parameters

Candidate 1 preference (p_1)
0.5

Candidate 2 preference (p_2)
0.3

Candidate 3 preference (p_3)
0.2

☒ Contamination

Candidate 1 preference for contamination population (r_1)
0.2

Candidate 2 preference for contamination population (r_2)
0.7

Candidate 3 preference for contamination population (r_3)
0.1

Dynamic parameters

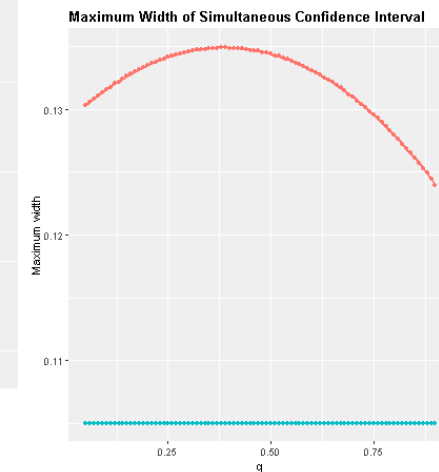
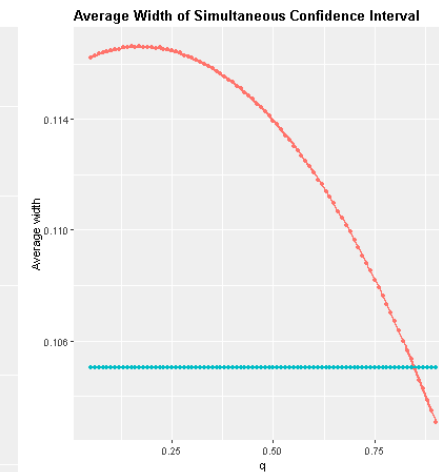
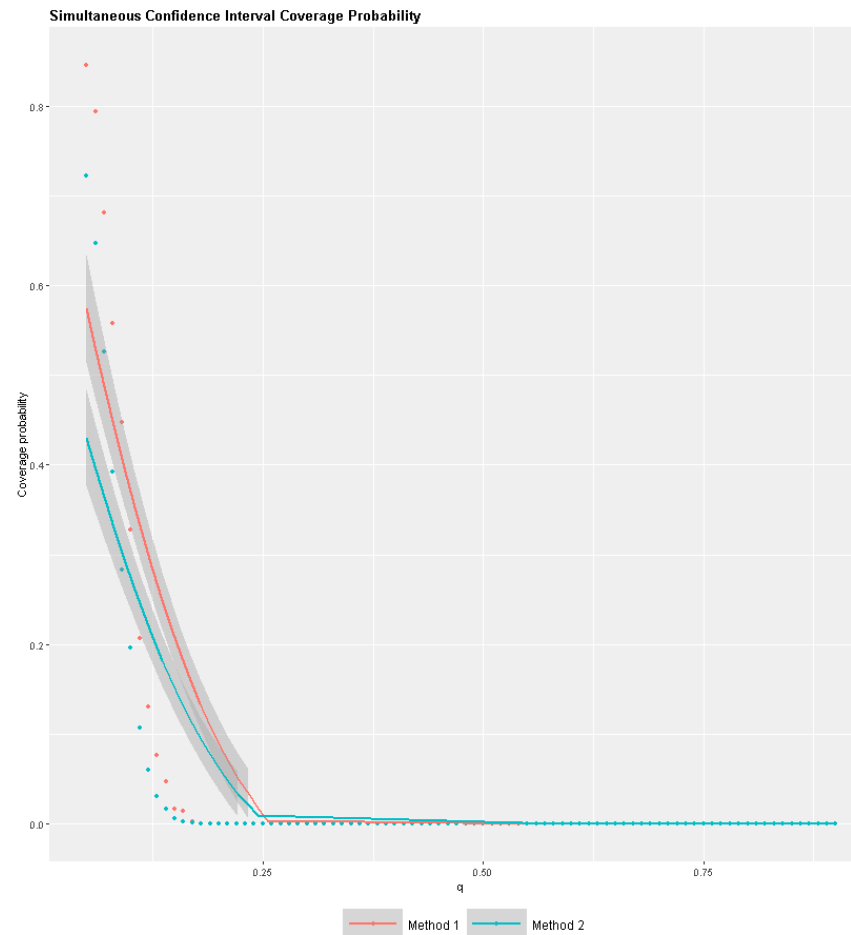
X Axis
Contamination percentage (q)

Sample size per replication (N)
10 1,500 5,000

Number of replications ($nrep$)
10 2,000 10,000

Significance level (α)
0.01 0.05 0.6

Start



- Compare p_1, p_2, p_3 mixed with r_1, r_2, r_3 and p_1, p_2, p_3 mixed with r_1, r_3, r_2 .
- Coverage probability becomes 0 at $q = 0.35$.

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Population parameters

Candidate 1 preference (p_1)
0.5

Candidate 2 preference (p_2)
0.3

Candidate 3 preference (p_3)
0.2

☒ Contamination

Candidate 1 preference for contamination population (r_1)
0.7

Candidate 2 preference for contamination population (r_2)
0.2

Candidate 3 preference for contamination population (r_3)
0.1

Dynamic parameters

X Axis
Contamination percentage (q)

Sample size per replication (N)
10 1,500 5,000

Number of replications ($nrep$)
10 2,000 10,000

Significance level (α)
0.01 0.05 0.6

