

OOB error rate vs. mtry

x-axis: factor that multiplies default mtry [$\sqrt{\text{number variables}}$]

Mtry factors used: {0, 0.05, 0.1, 0.17, 0.25, 0.33, 0.5, 0.75, 0.8, 1, 1.15, 1.33, 1.5, 2, 3, 4, 5, 6, 8, 10, 13}

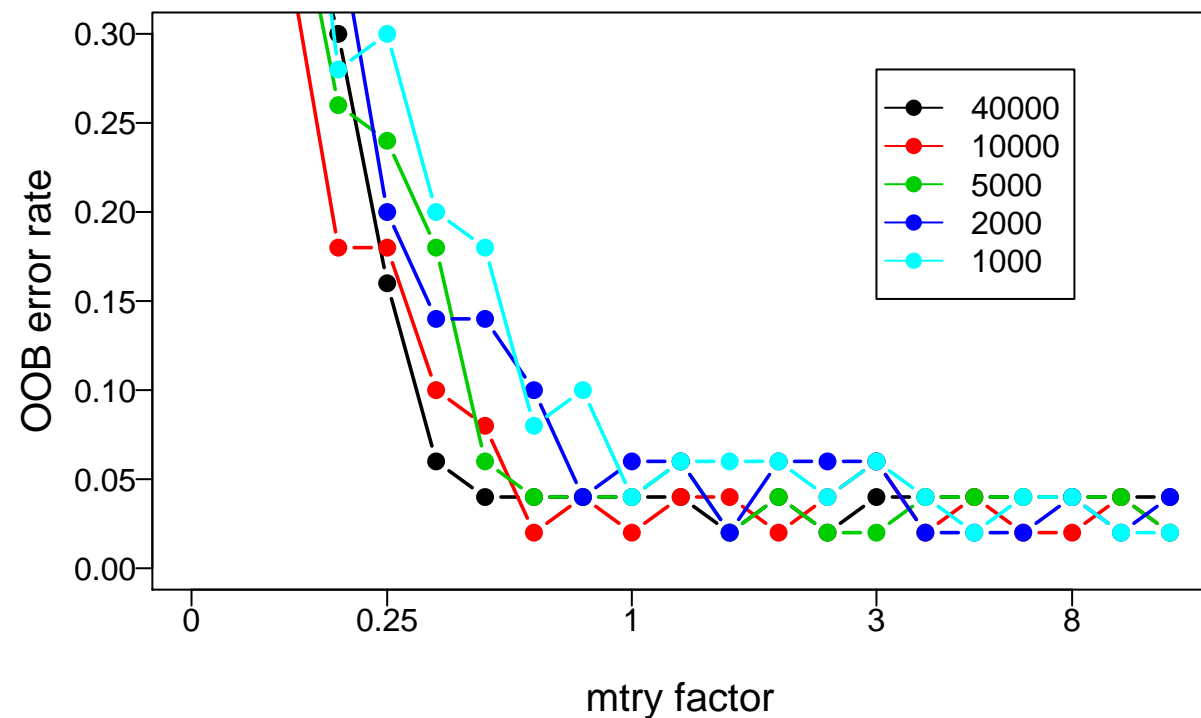
(mtry factors of 0 means mtry = 1)

I: Simulated data sets:

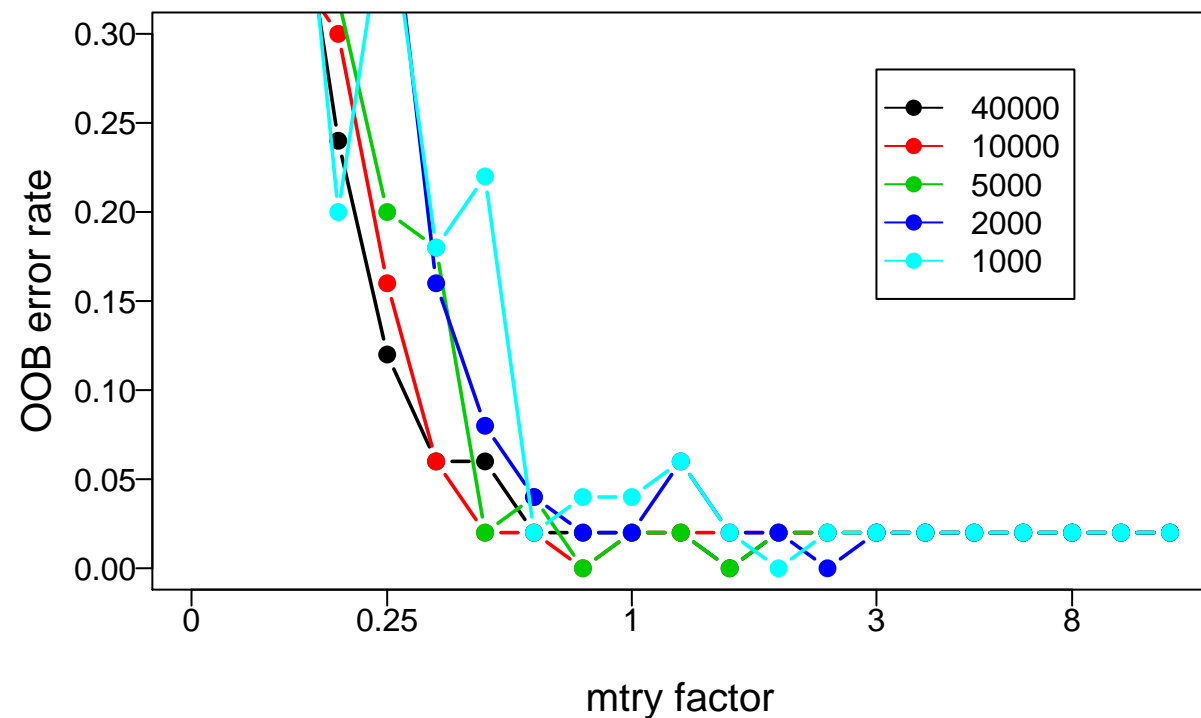
signal + 4000 noise random variables

(shown first with nodesize = 1, then nodesize = 5)

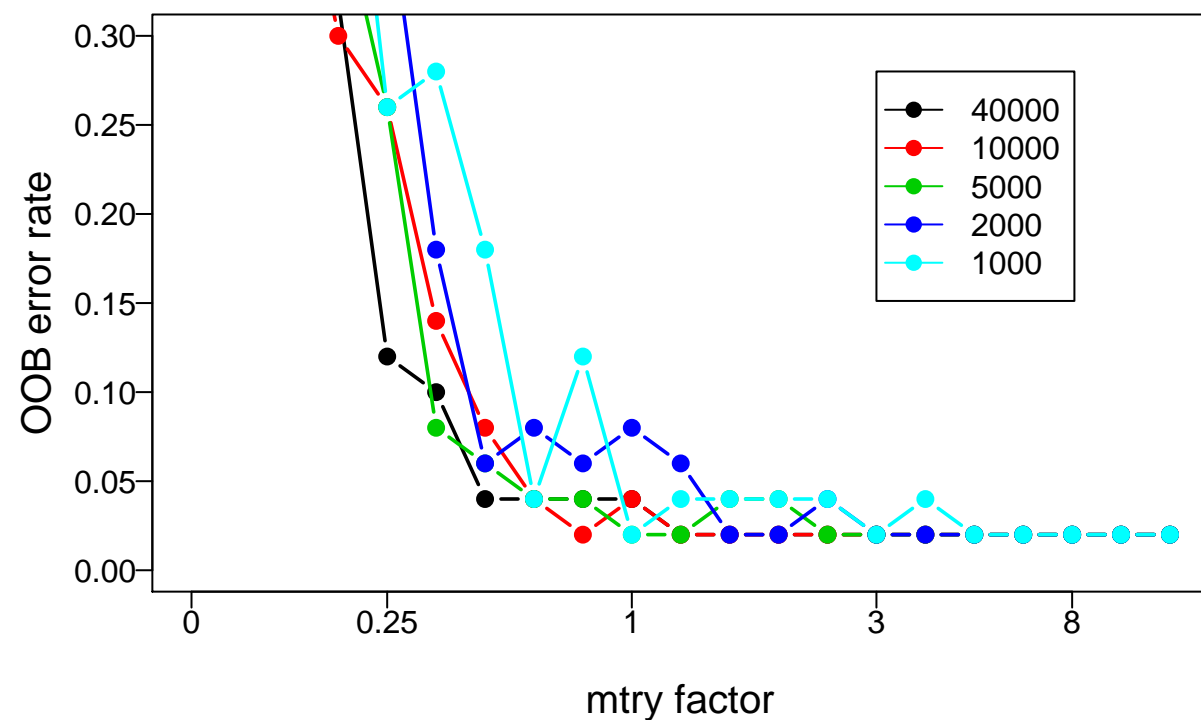
2 classes; 1 dimensions; 5 genes/dimen.; nodesize = 1



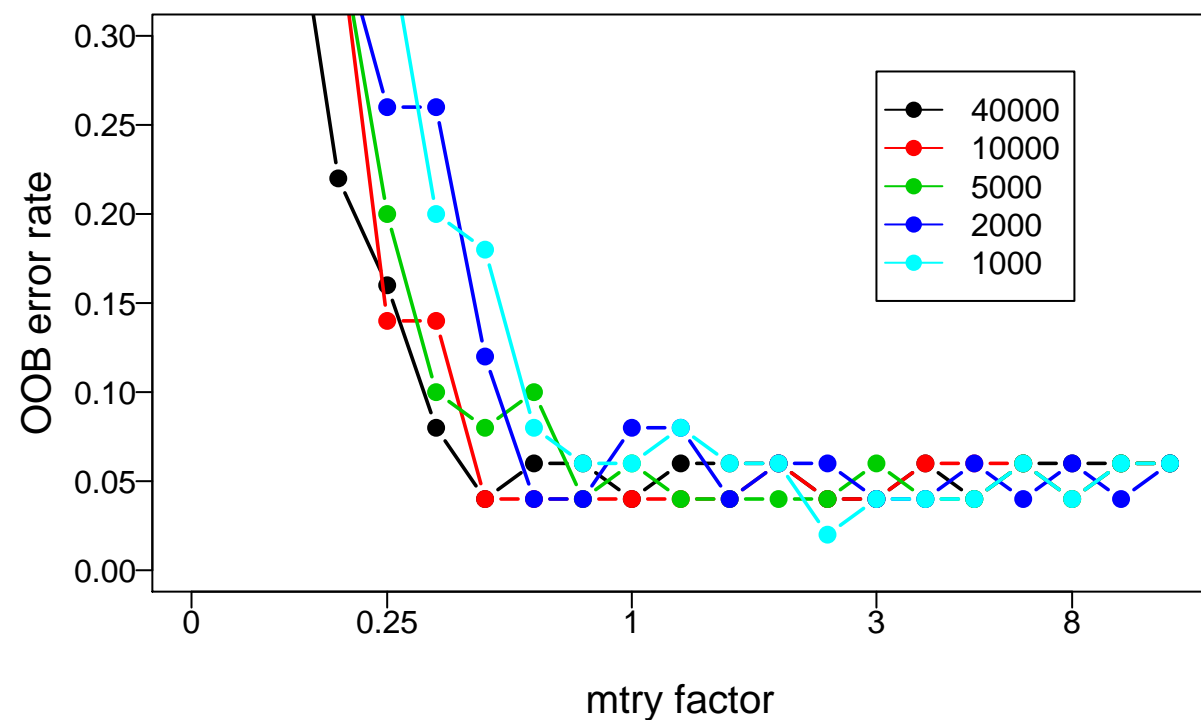
2 classes; 1 dimensions; 5 genes/dimen.; nodesize = 1



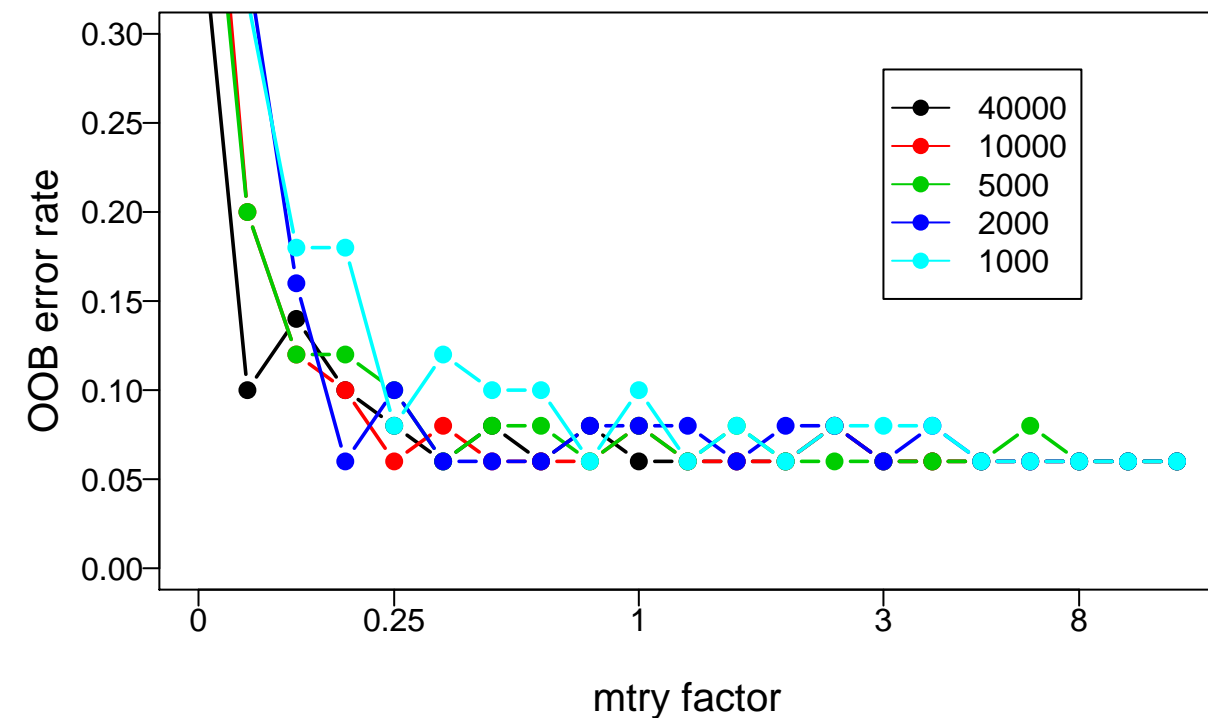
2 classes; 1 dimensions; 5 genes/dimen.; nodesize = 1



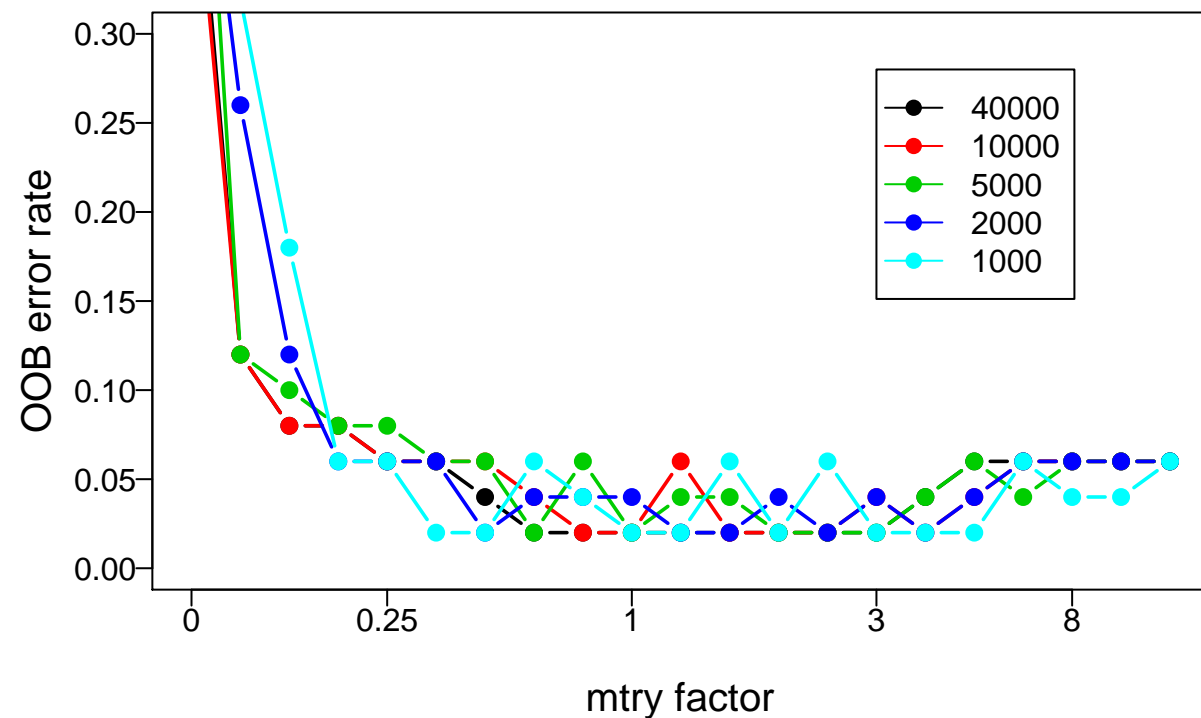
2 classes; 1 dimensions; 5 genes/dimen.; nodesize = 1



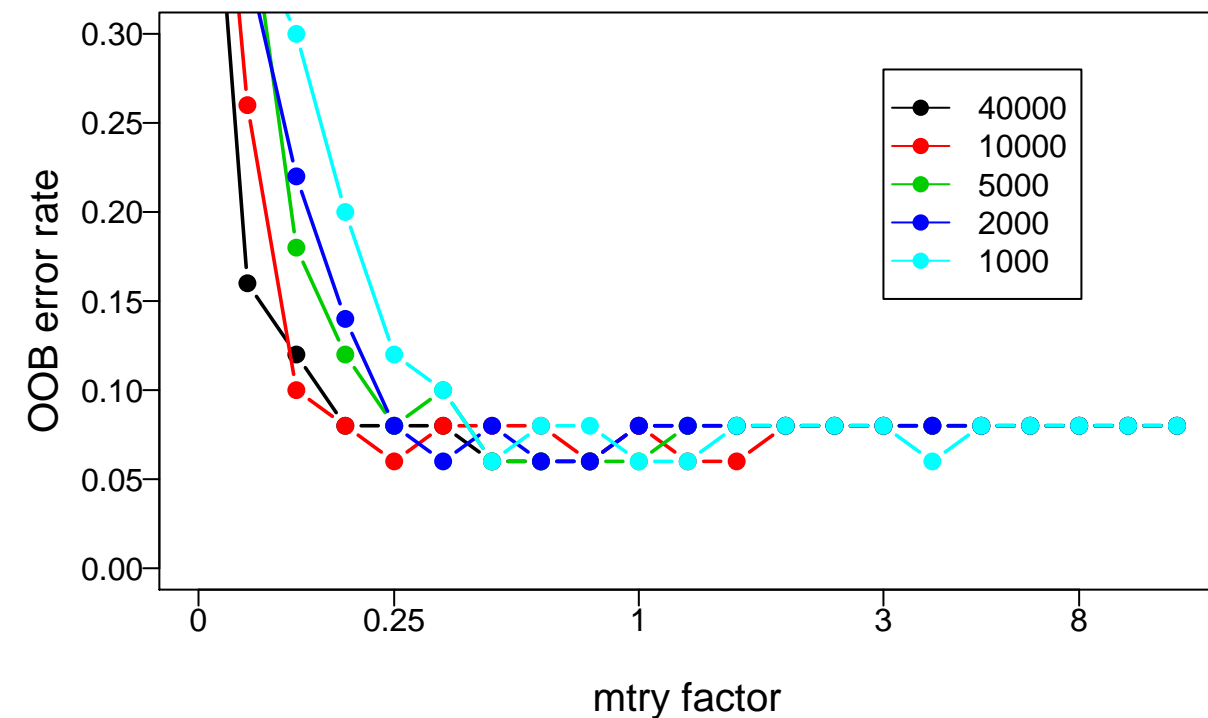
2 classes; 1 dimensions; 20 genes/dimen.; nodesize = 1



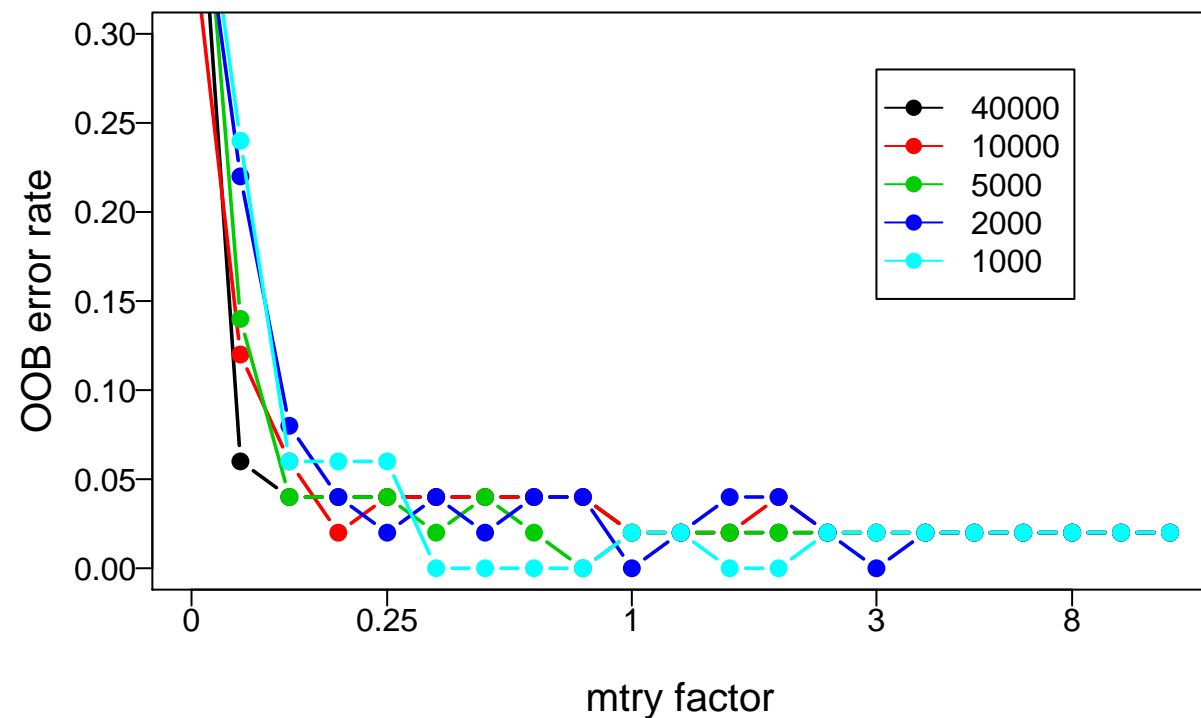
2 classes; 1 dimensions; 20 genes/dimen.; nodesize = 1



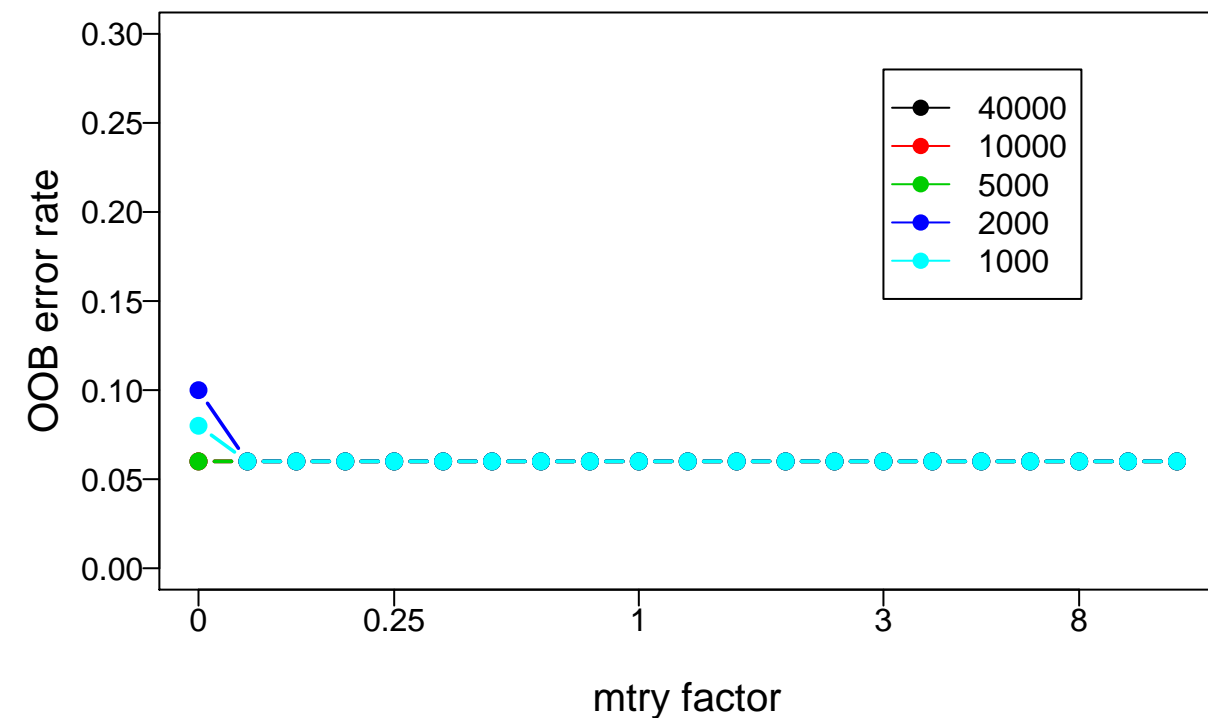
2 classes; 1 dimensions; 20 genes/dimen.; nodesize = 1



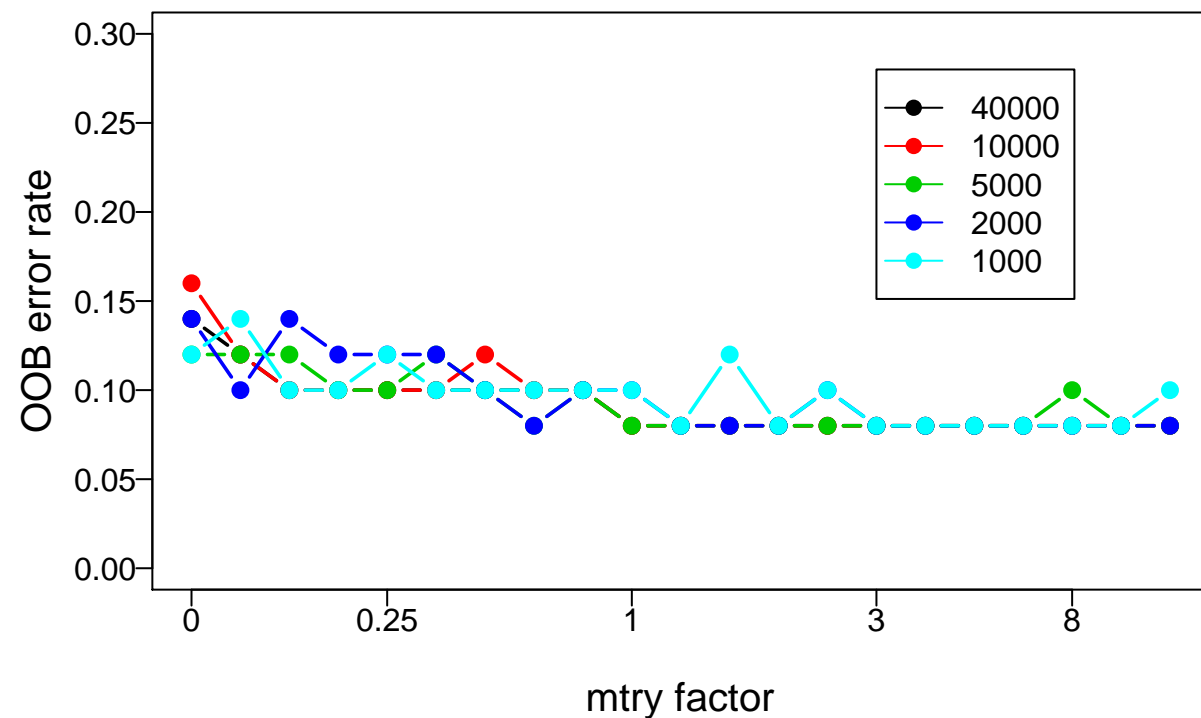
2 classes; 1 dimensions; 20 genes/dimen.; nodesize = 1



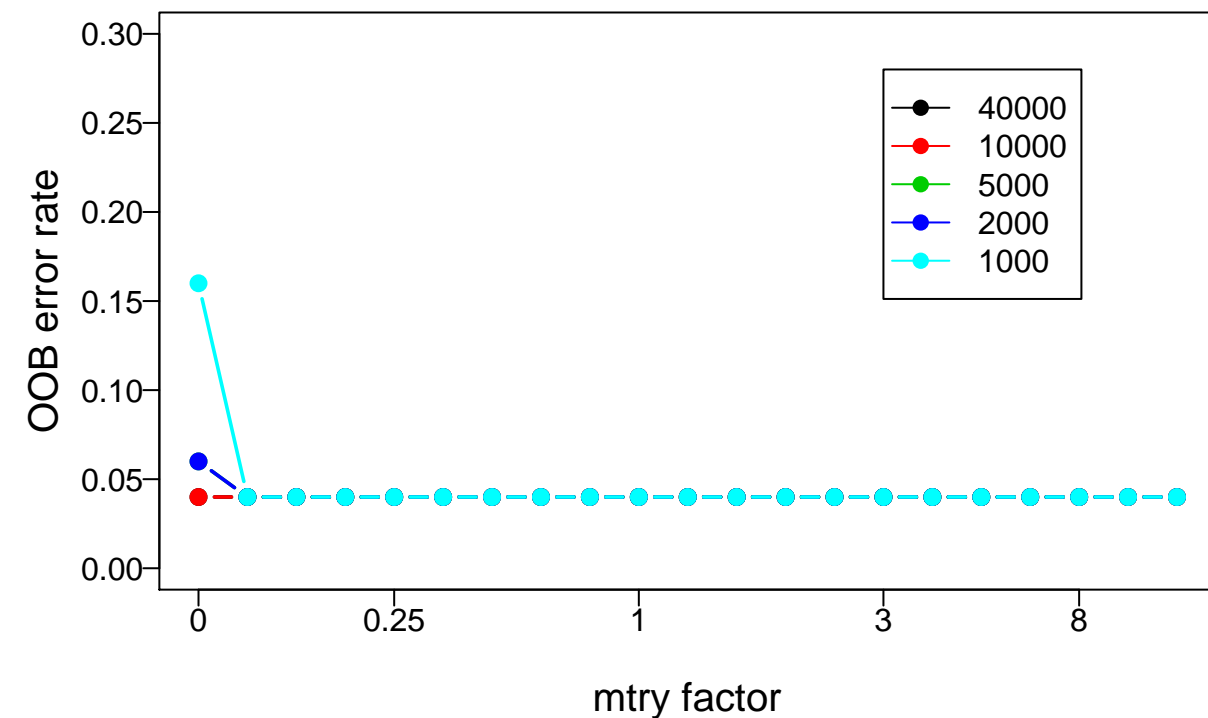
2 classes; 1 dimensions; 100 genes/dimen.; nodesize = 1



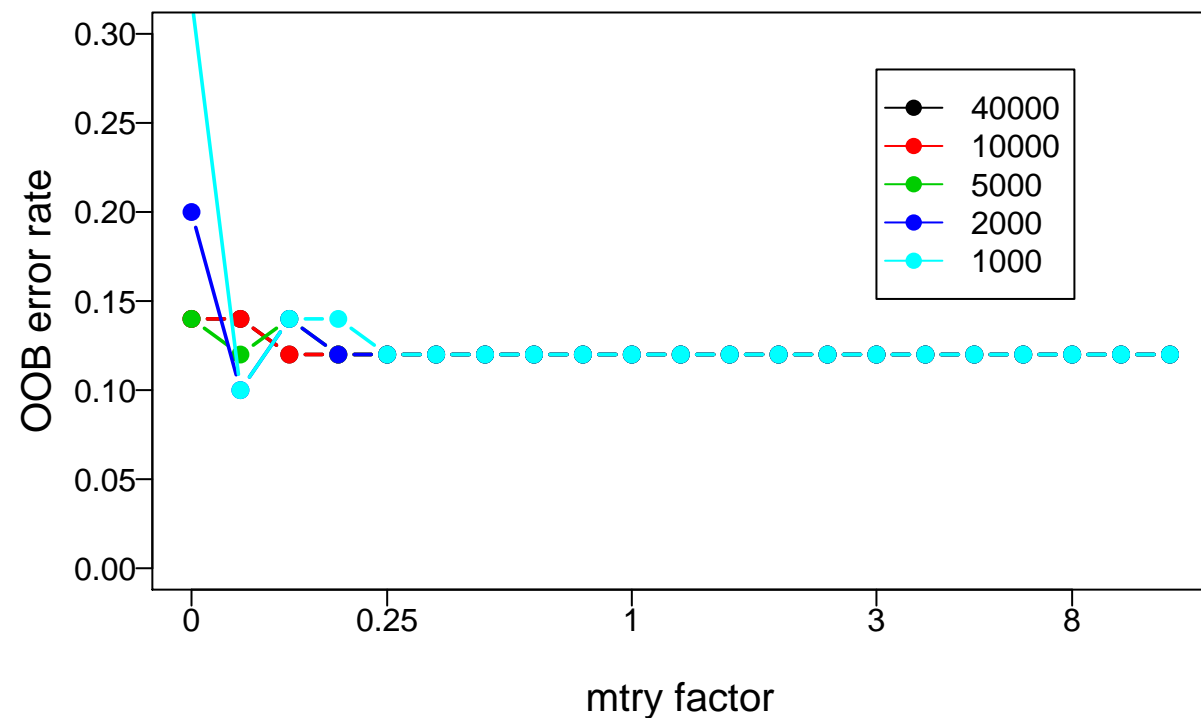
2 classes; 1 dimensions; 100 genes/dimen.; nodesize = 1



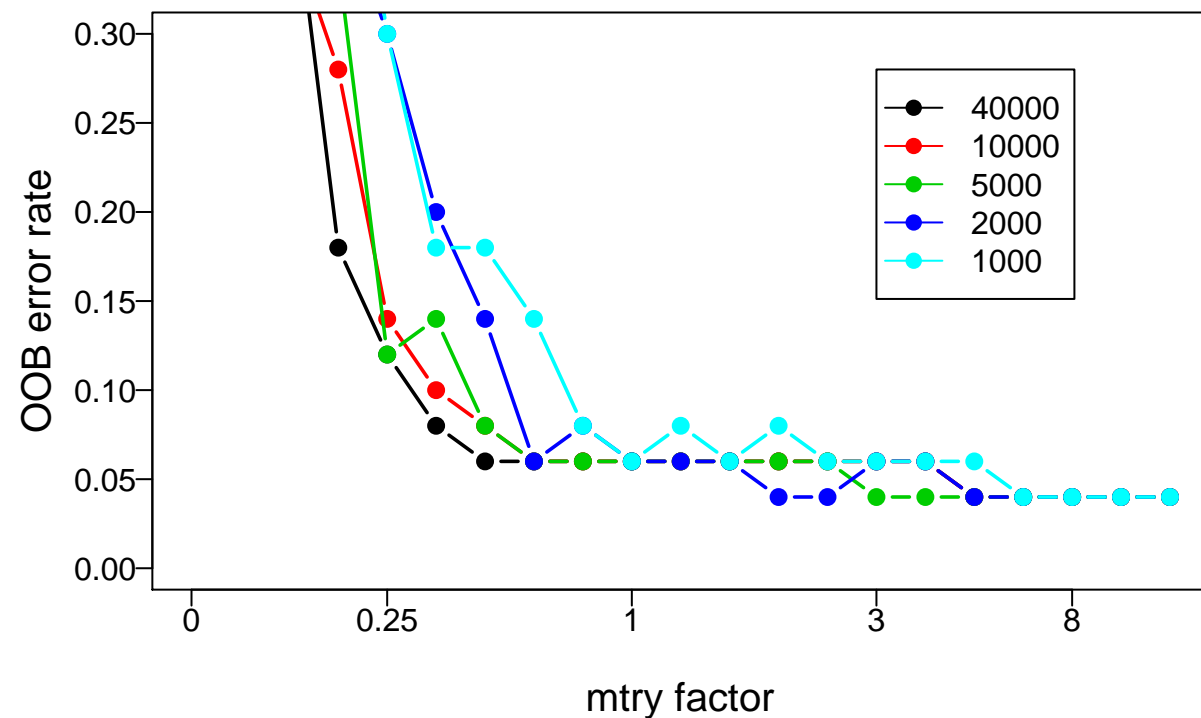
2 classes; 1 dimensions; 100 genes/dimen.; nodesize = 1



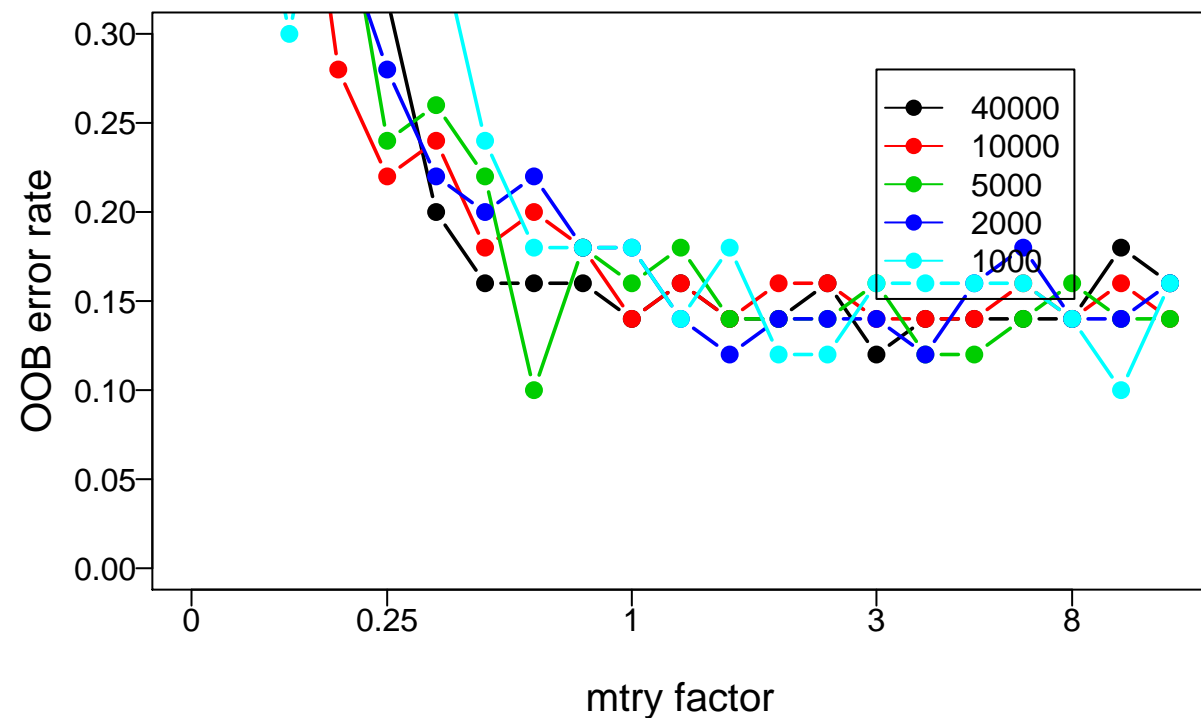
2 classes; 1 dimensions; 100 genes/dimen.; nodesize = 1



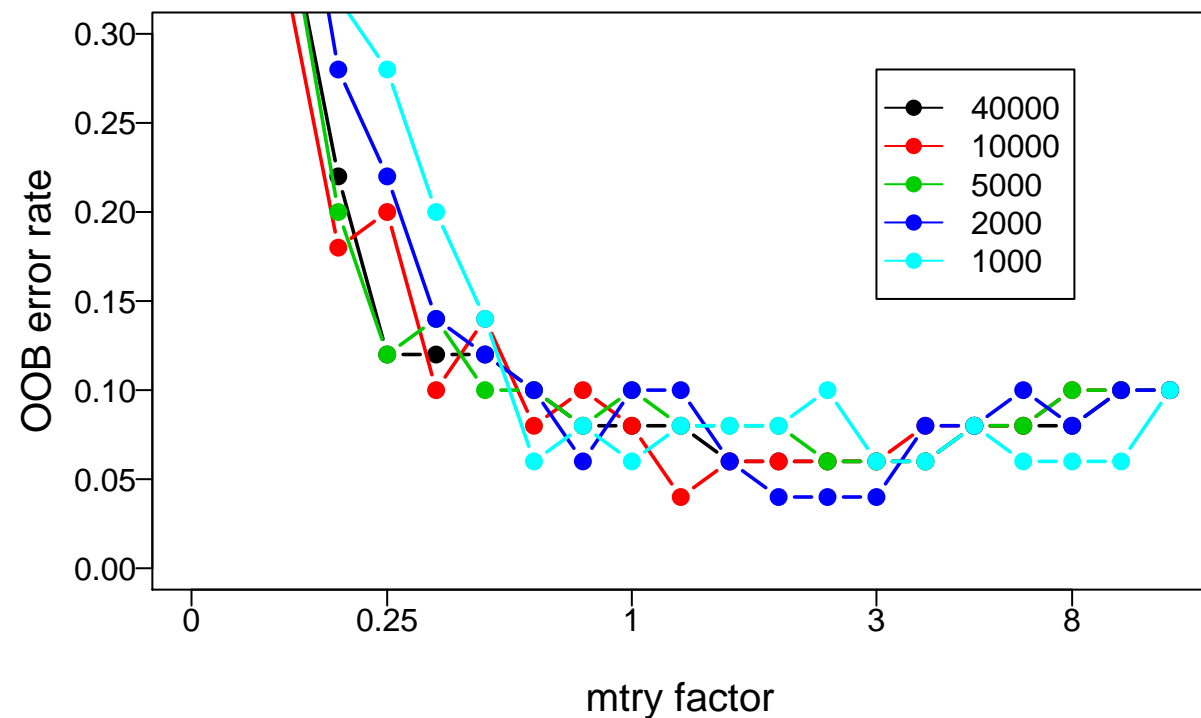
2 classes; 2 dimensions; 5 genes/dimen.; nodesize = 1



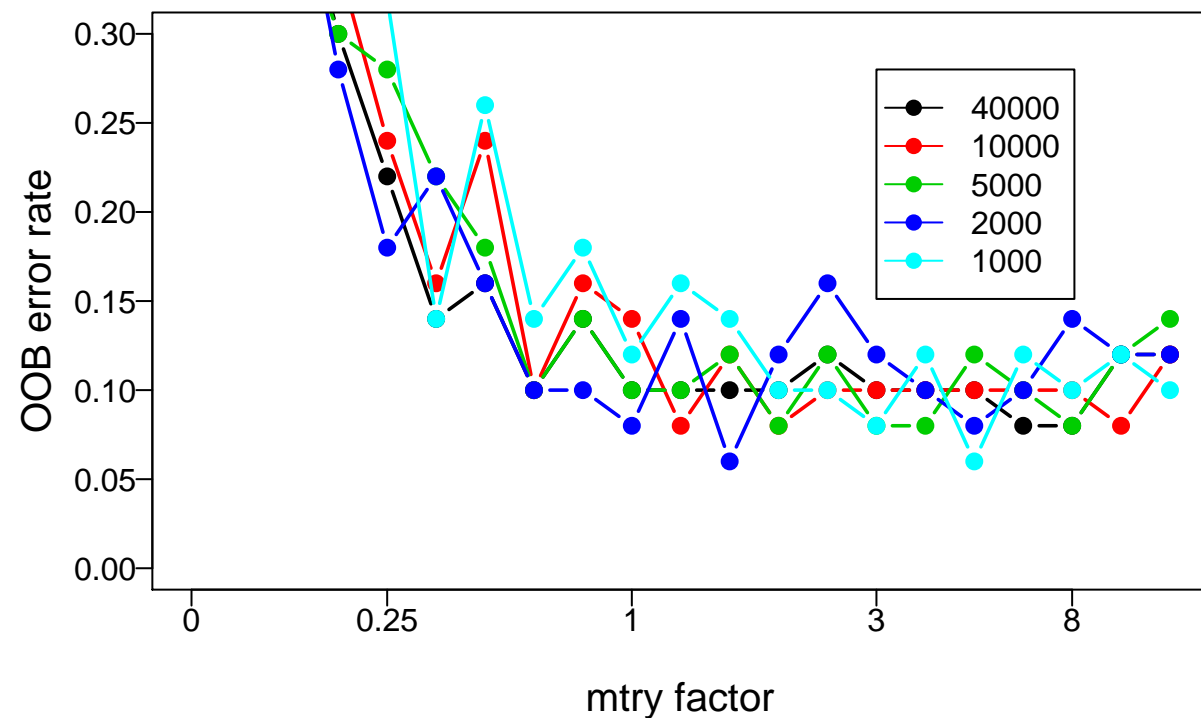
2 classes; 2 dimensions; 5 genes/dimen.; nodesize = 1



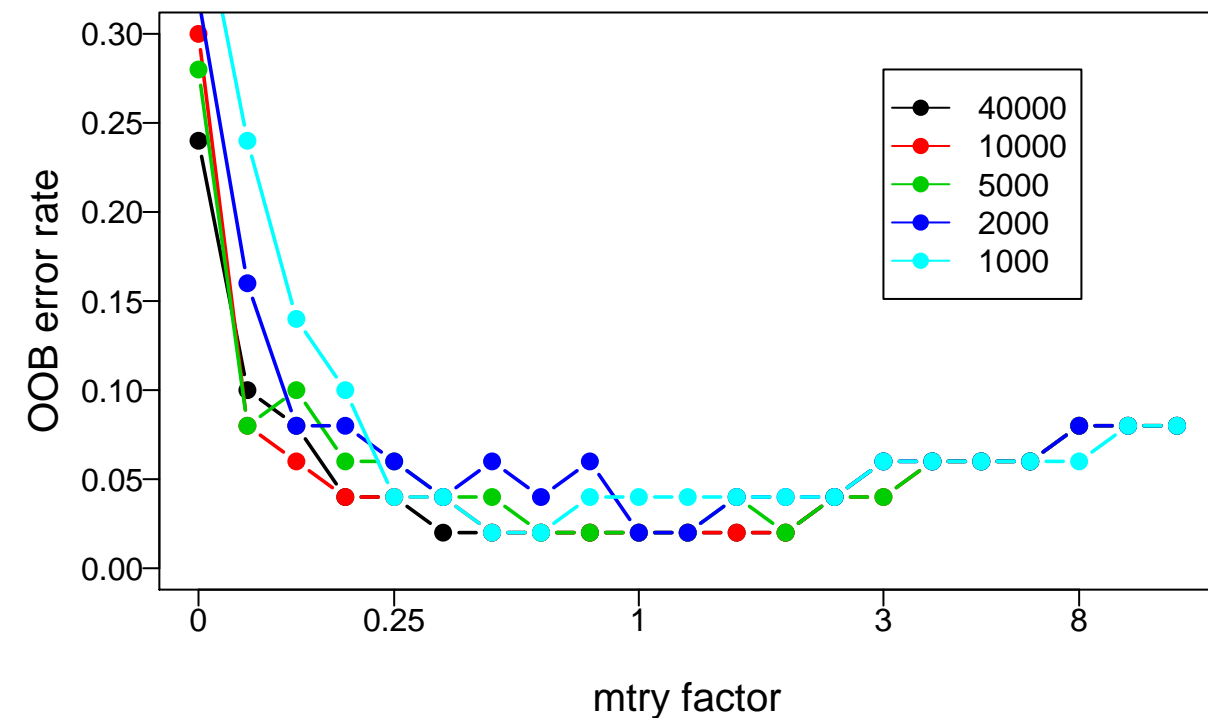
2 classes; 2 dimensions; 5 genes/dimen.; nodesize = 1



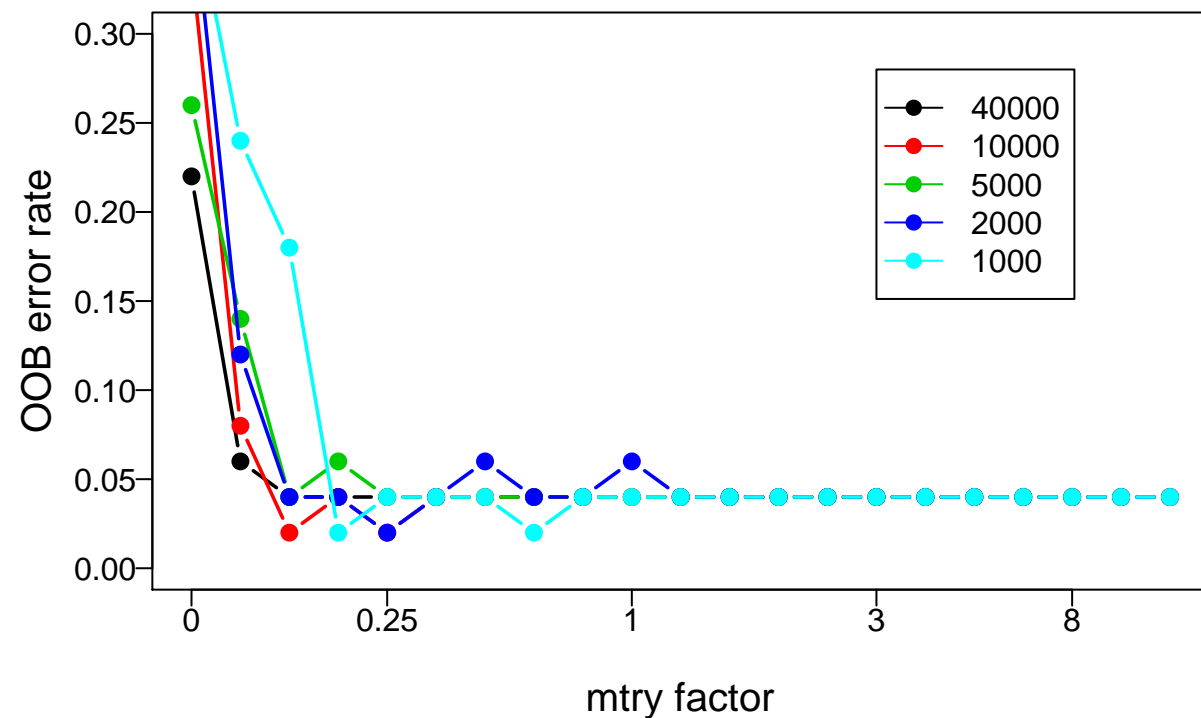
2 classes; 2 dimensions; 5 genes/dimen.; nodesize = 1



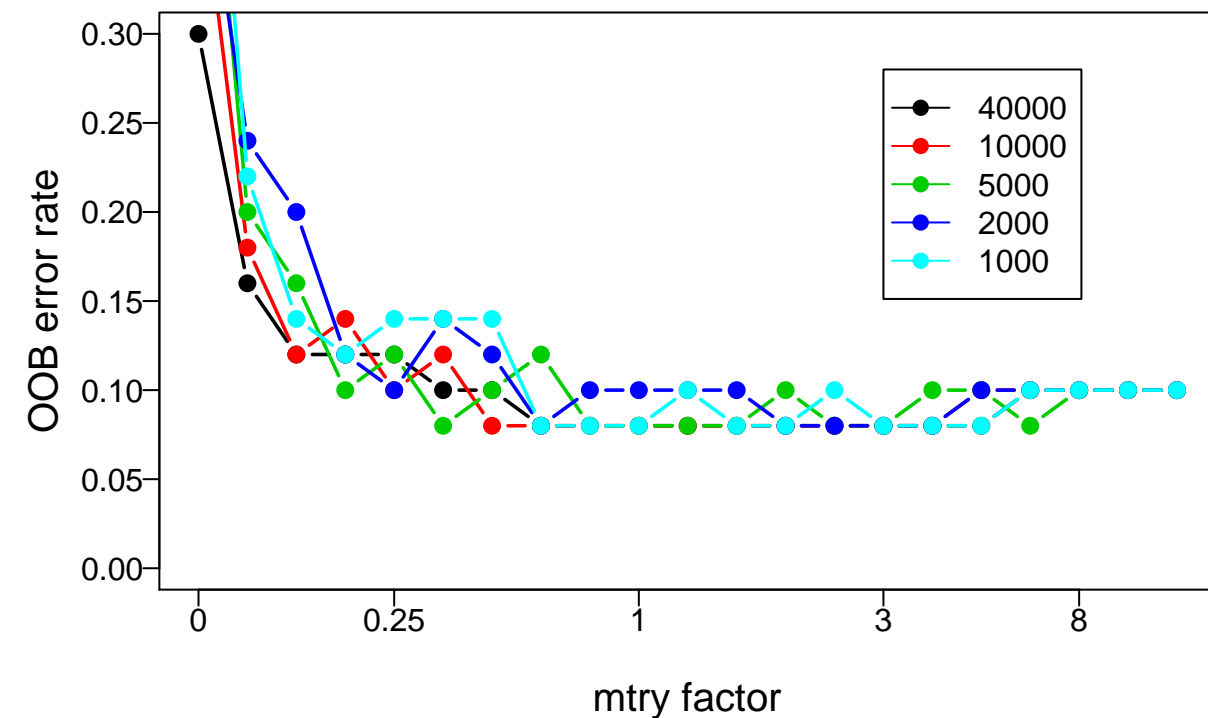
2 classes; 2 dimensions; 20 genes/dimen.; nodesize = 1



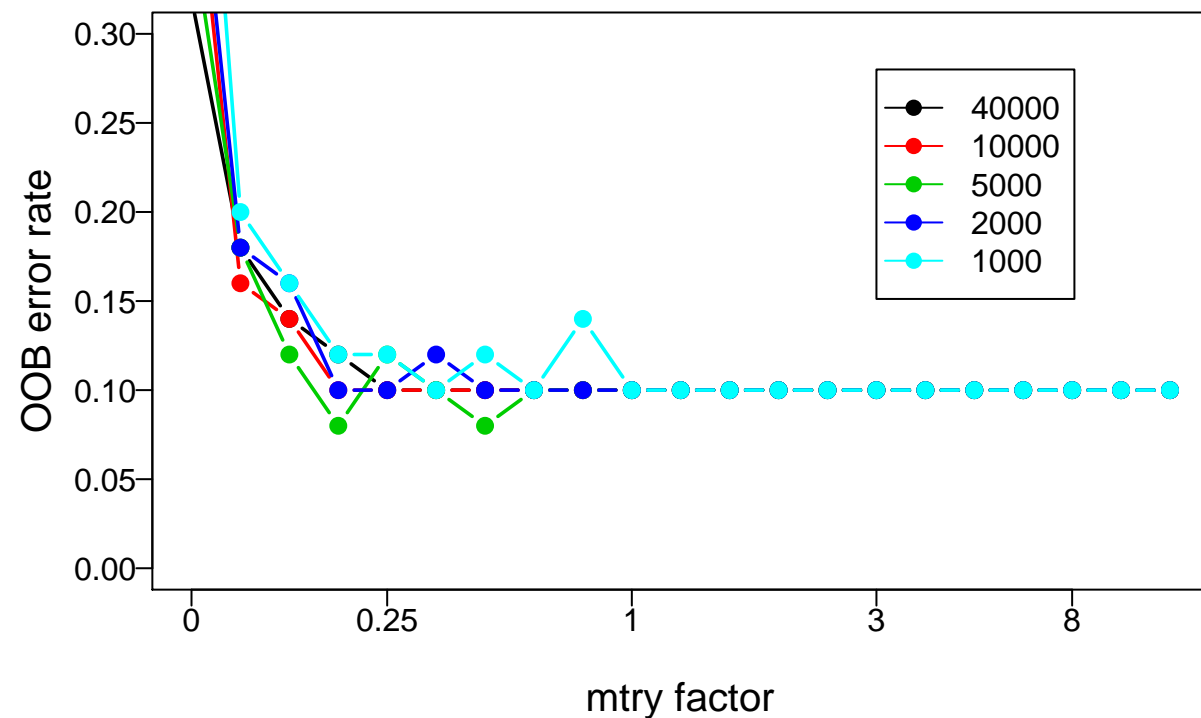
2 classes; 2 dimensions; 20 genes/dimen.; nodesize = 1



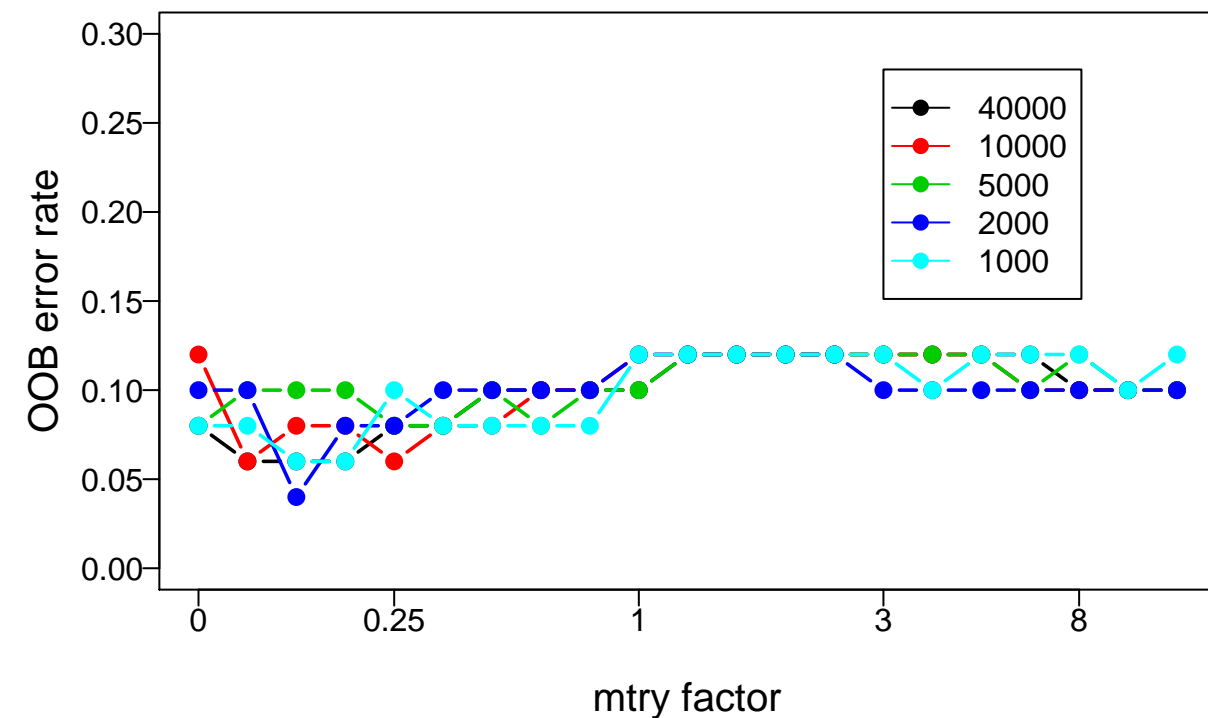
2 classes; 2 dimensions; 20 genes/dimen.; nodesize = 1



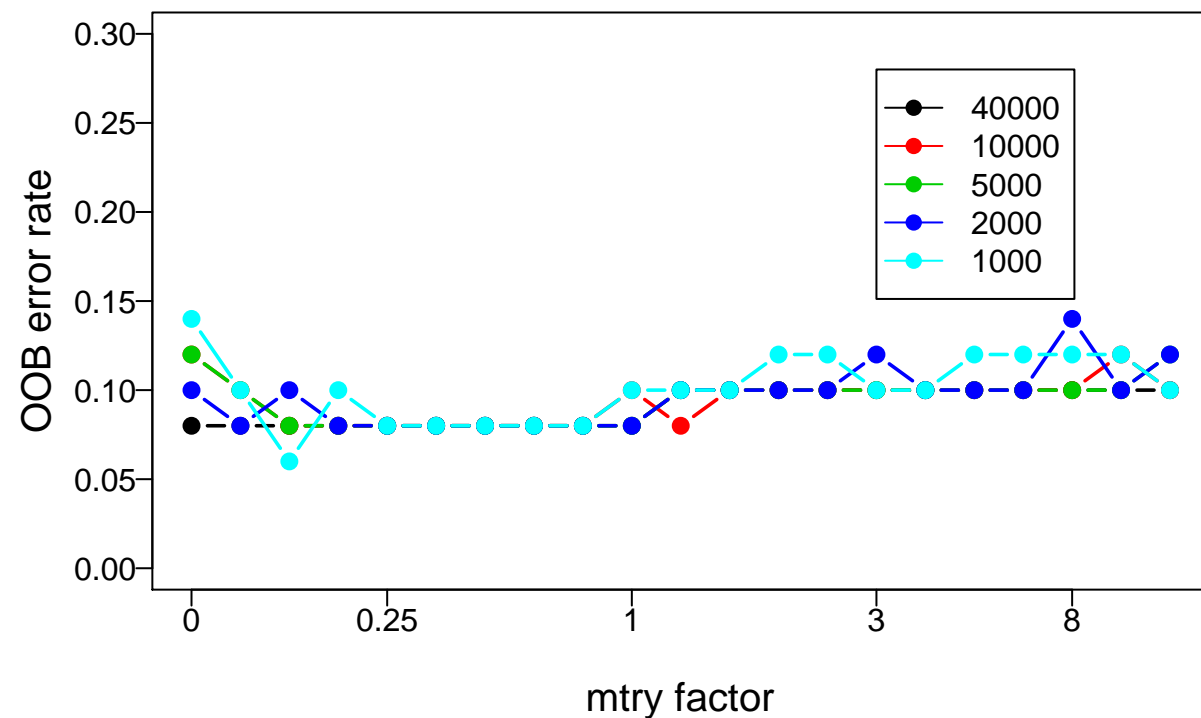
2 classes; 2 dimensions; 20 genes/dimen.; nodesize = 1



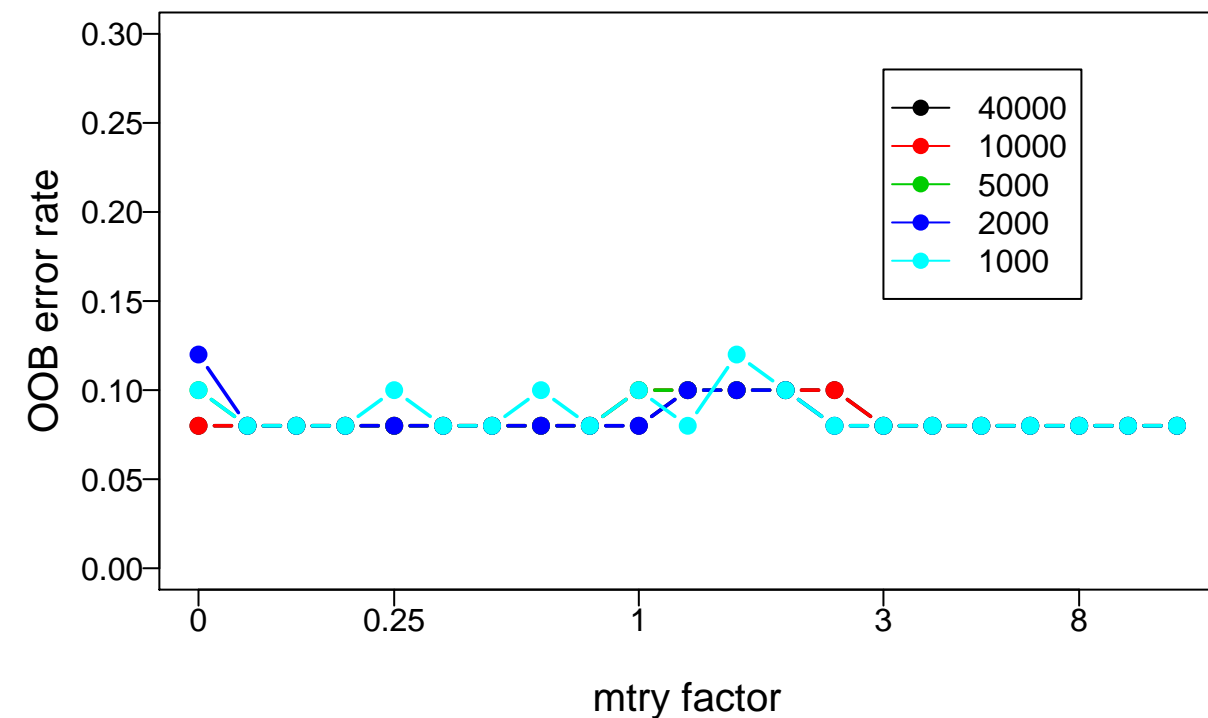
2 classes; 2 dimensions; 100 genes/dimen.; nodesize = 1



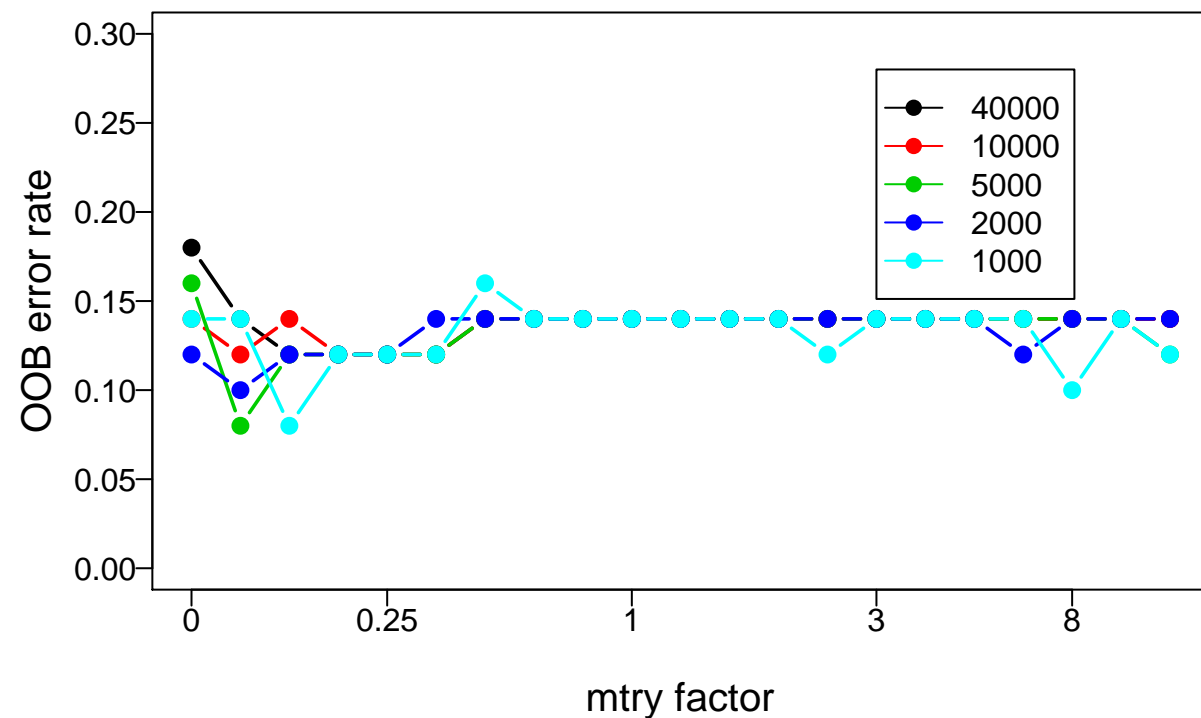
2 classes; 2 dimensions; 100 genes/dimen.; nodesize = 1



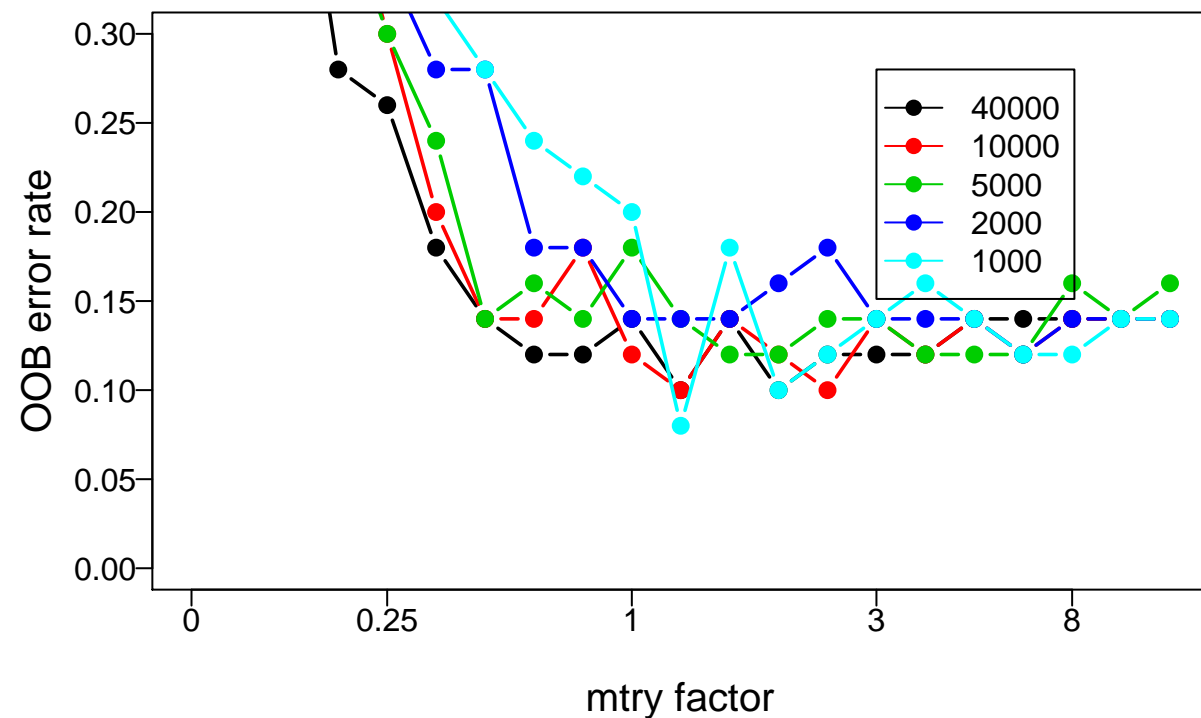
2 classes; 2 dimensions; 100 genes/dimen.; nodesize = 1



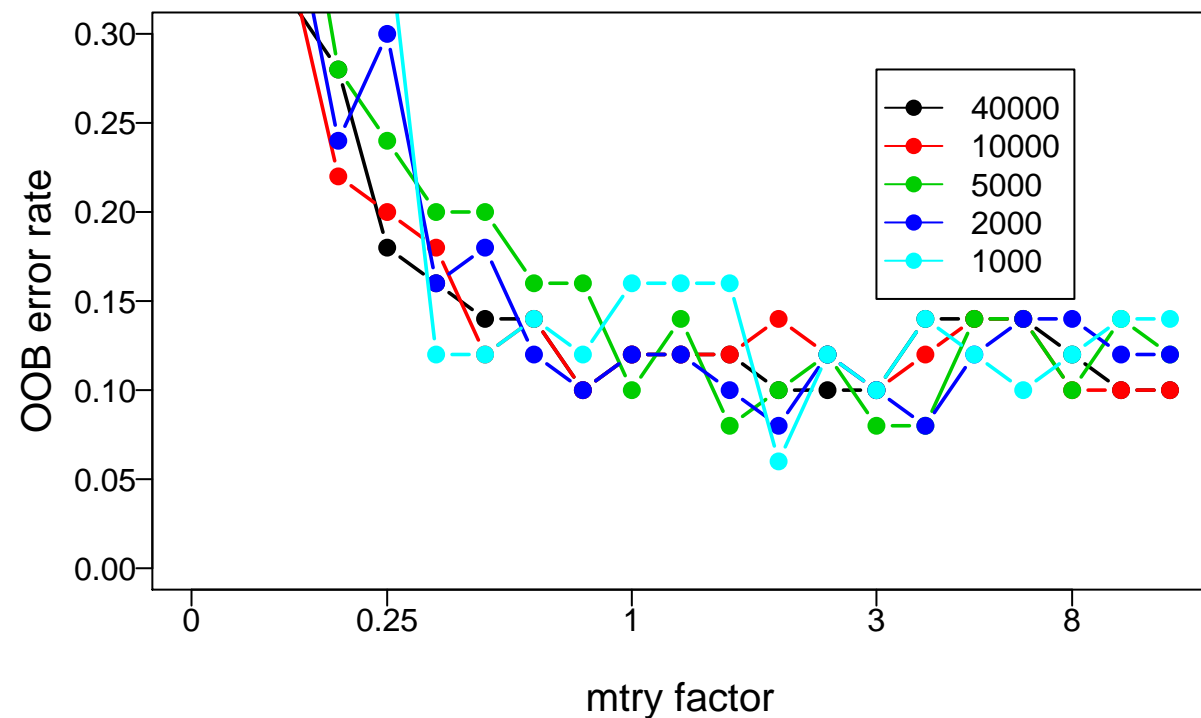
2 classes; 2 dimensions; 100 genes/dimen.; nodesize = 1



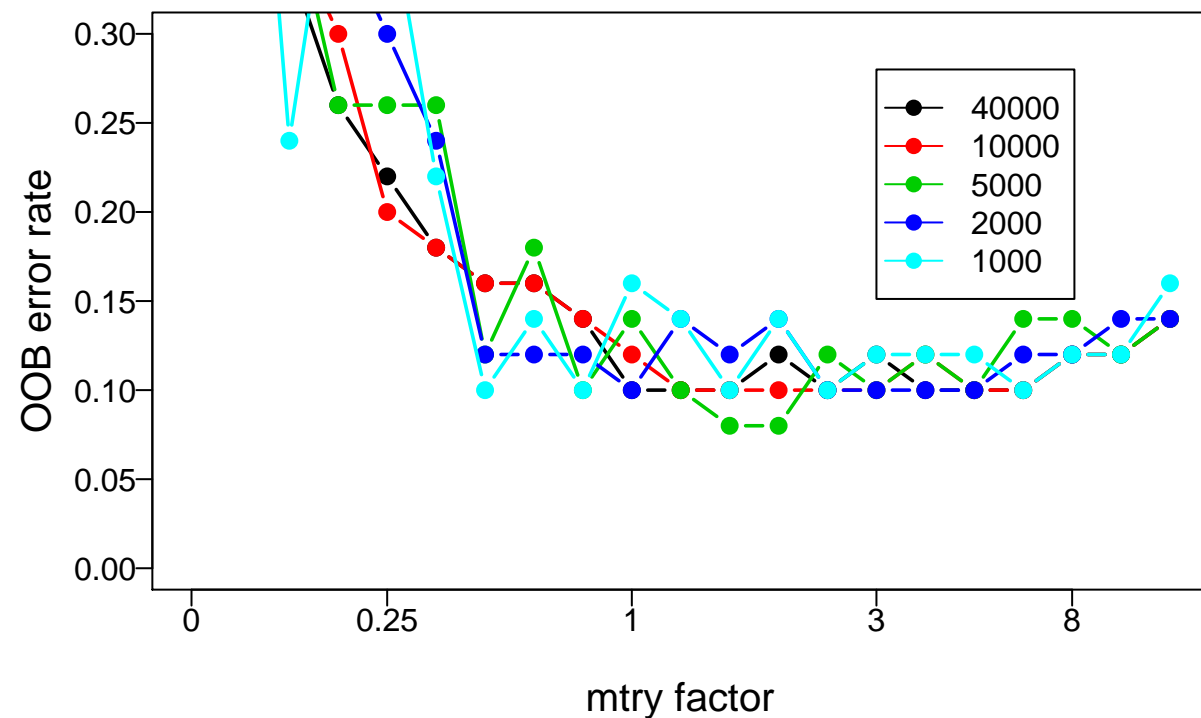
2 classes; 3 dimensions; 5 genes/dimen.; nodesize = 1



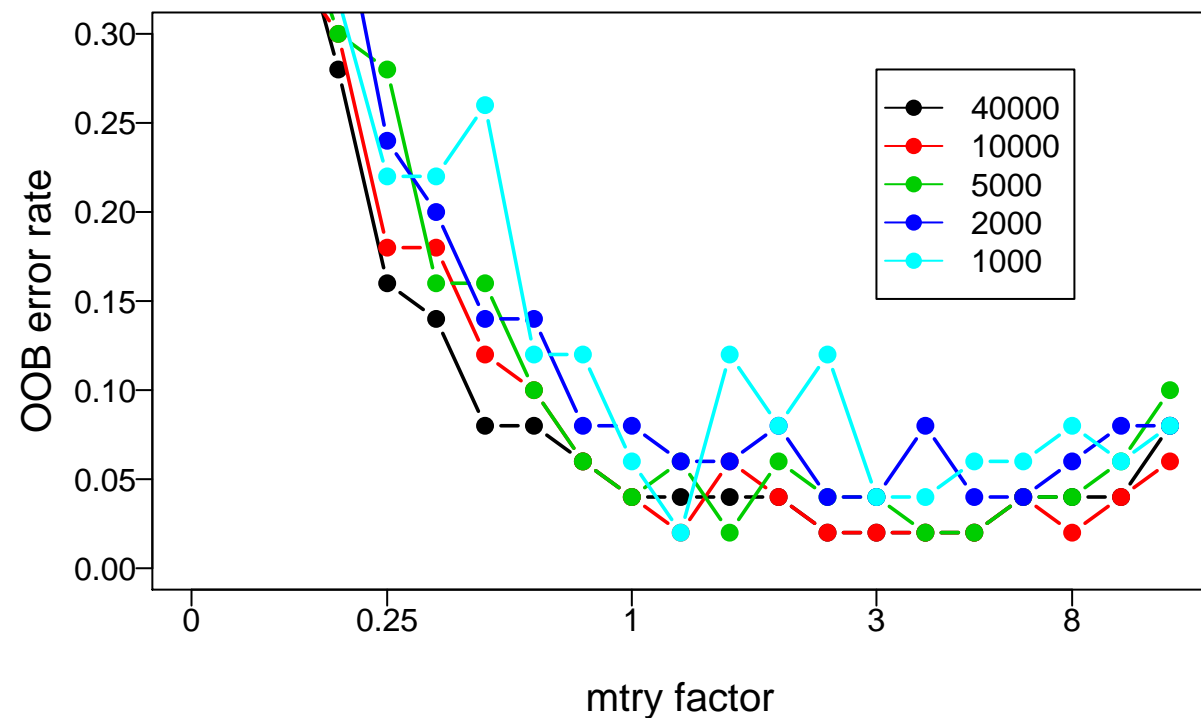
2 classes; 3 dimensions; 5 genes/dimen.; nodesize = 1



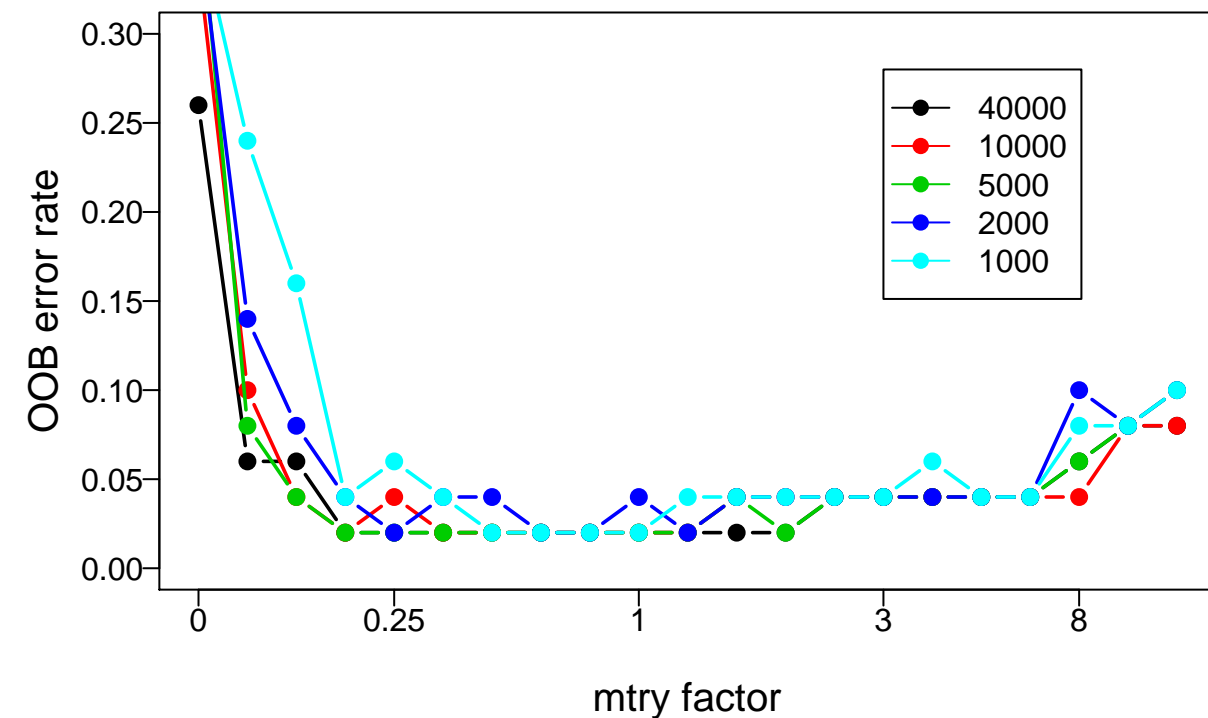
2 classes; 3 dimensions; 5 genes/dimen.; nodesize = 1



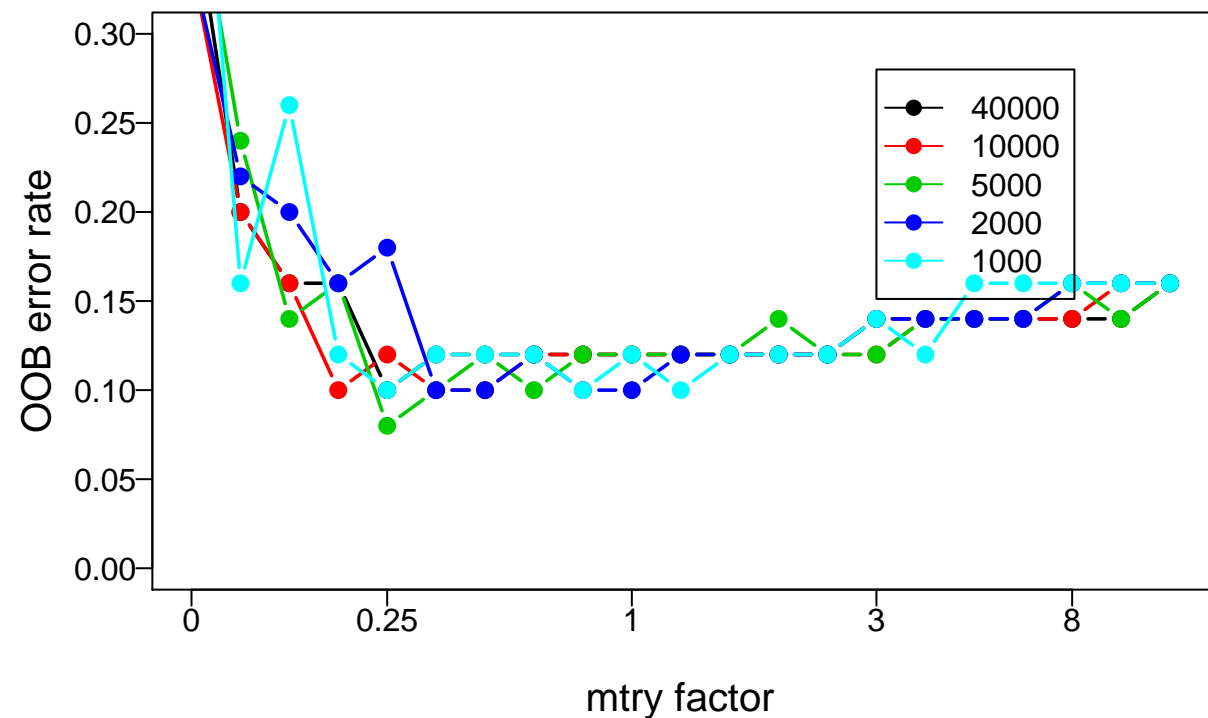
2 classes; 3 dimensions; 5 genes/dimen.; nodesize = 1



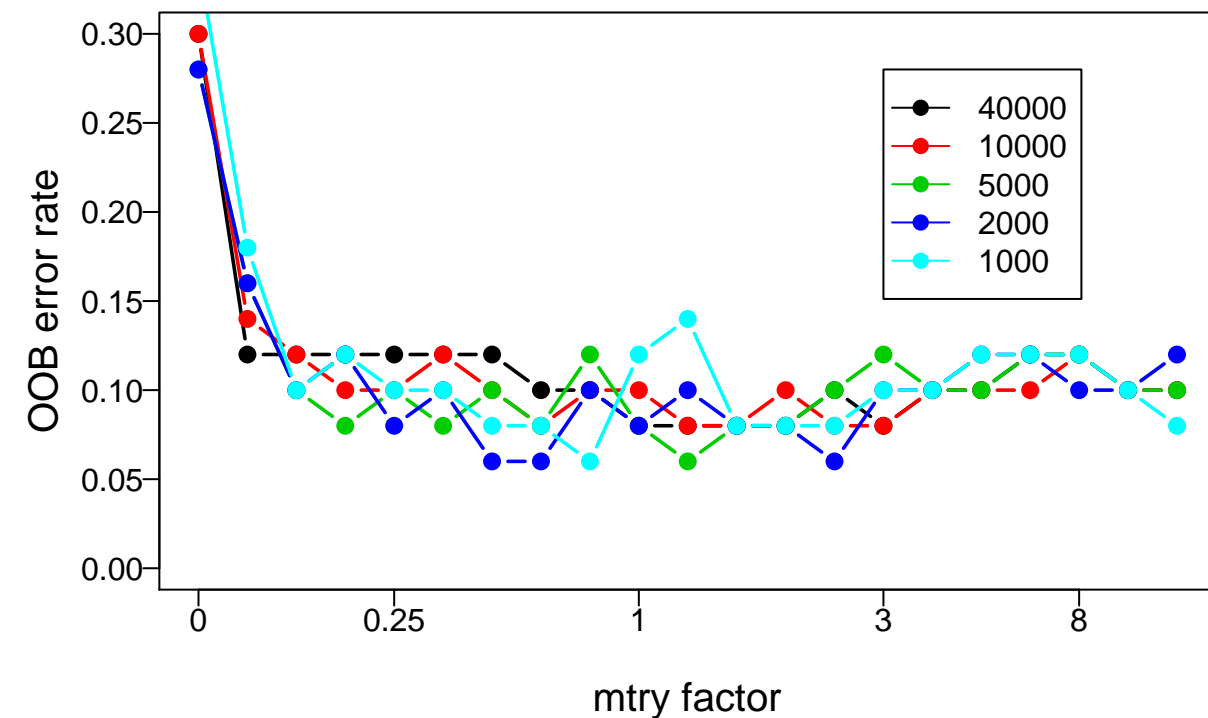
2 classes; 3 dimensions; 20 genes/dimen.; nodesize = 1



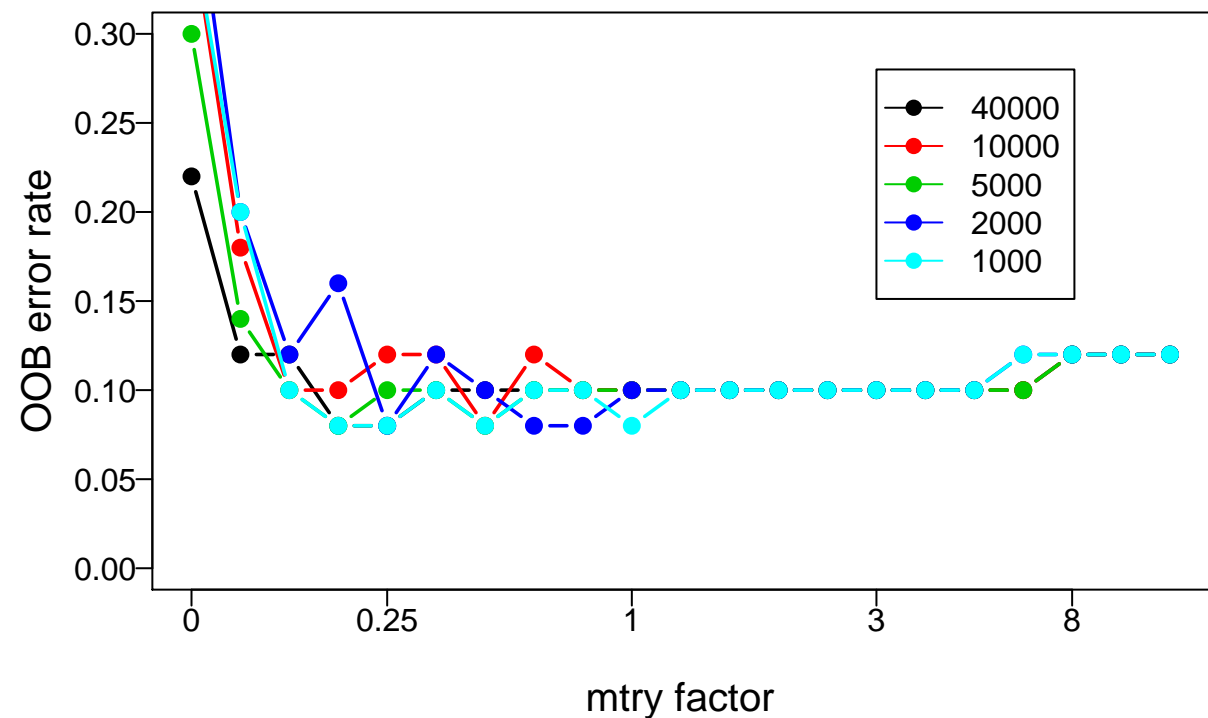
2 classes; 3 dimensions; 20 genes/dimen.; nodesize = 1



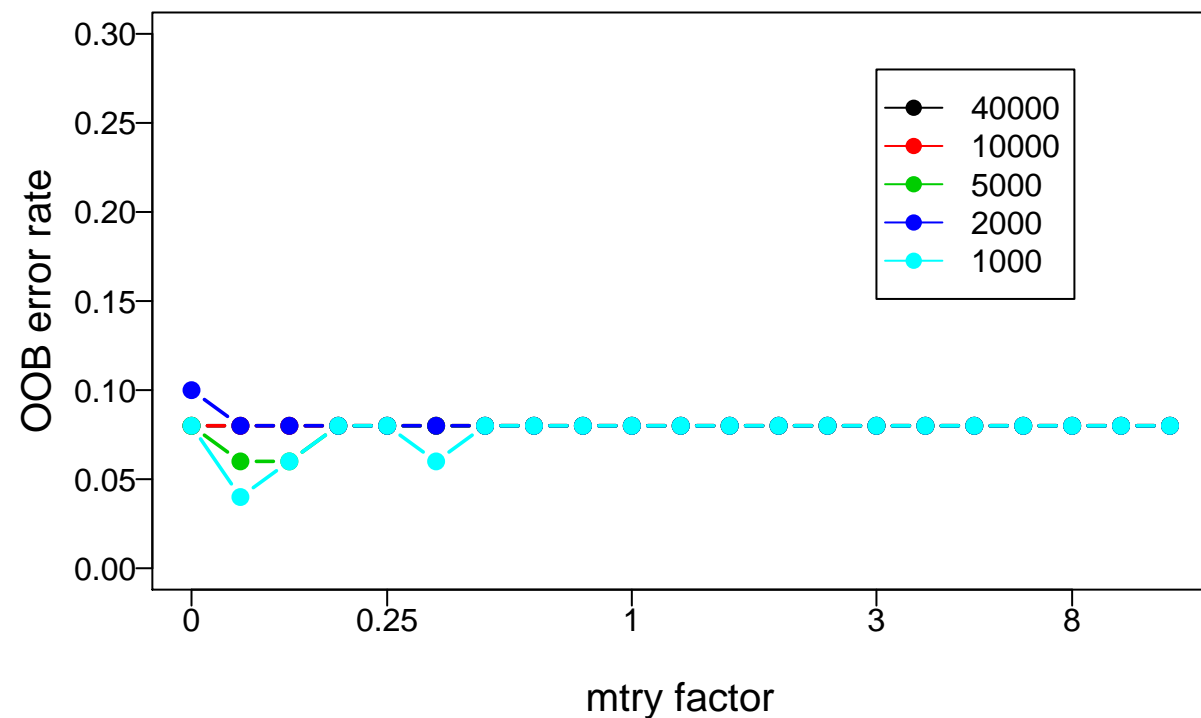
2 classes; 3 dimensions; 20 genes/dimen.; nodesize = 1



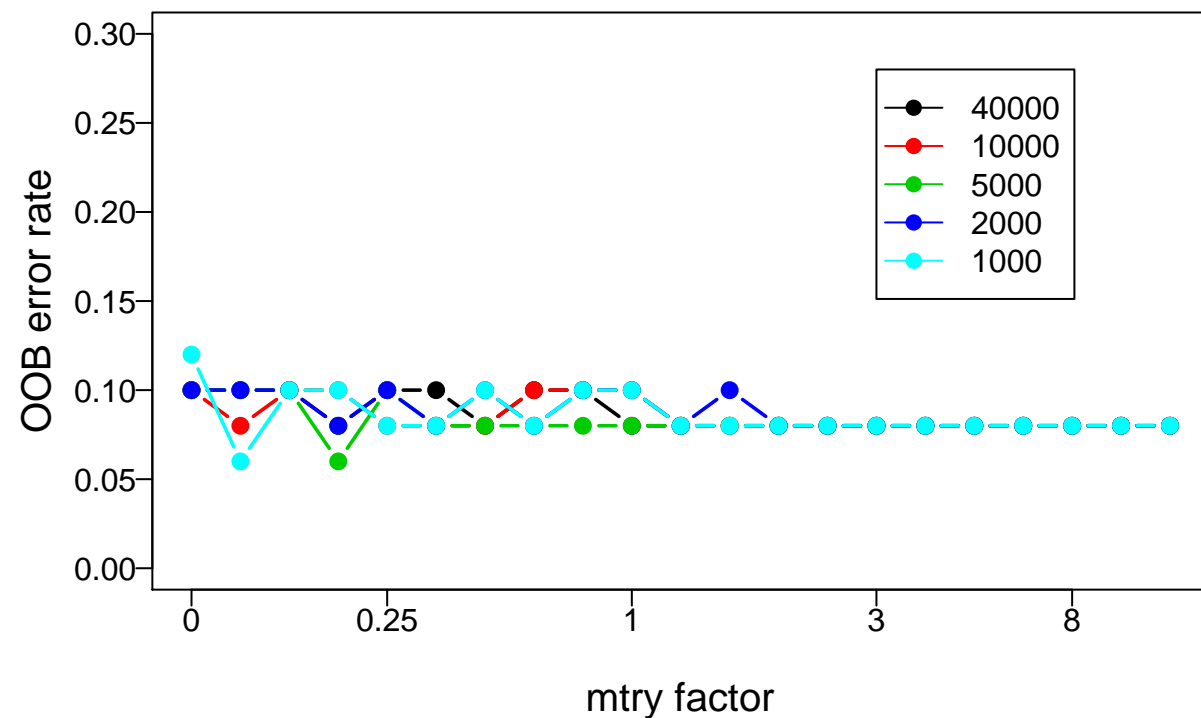
2 classes; 3 dimensions; 20 genes/dimen.; nodesize = 1



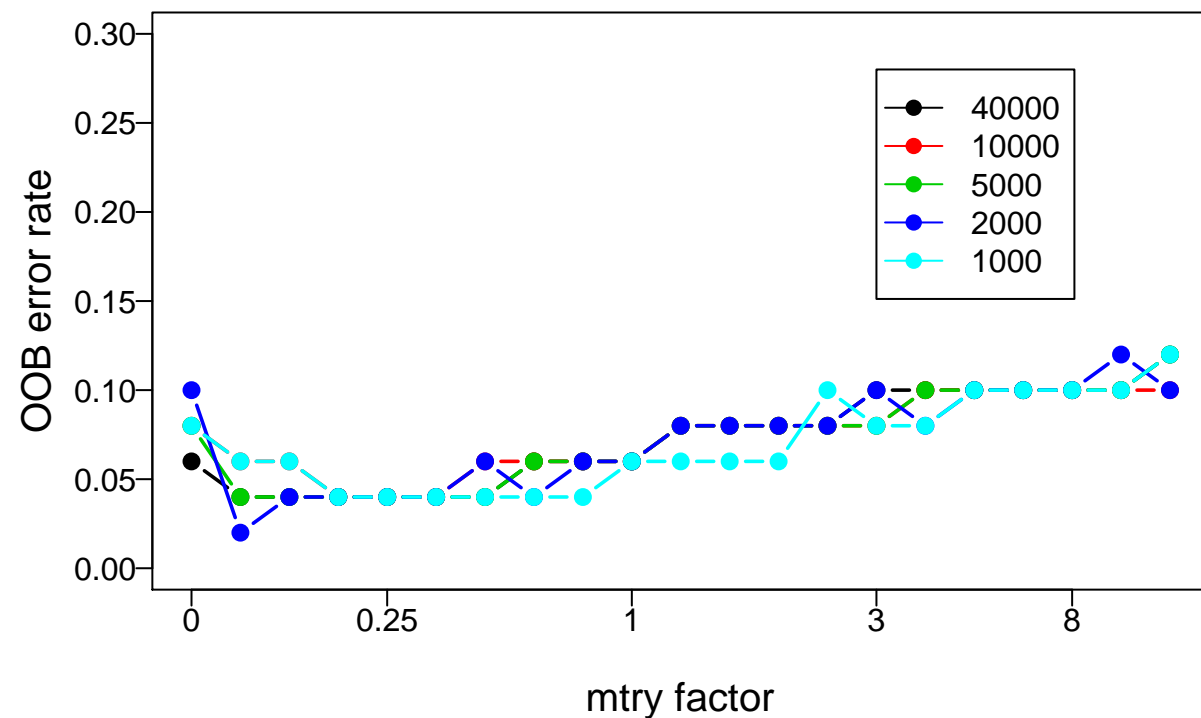
2 classes; 3 dimensions; 100 genes/dimen.; nodesize = 1



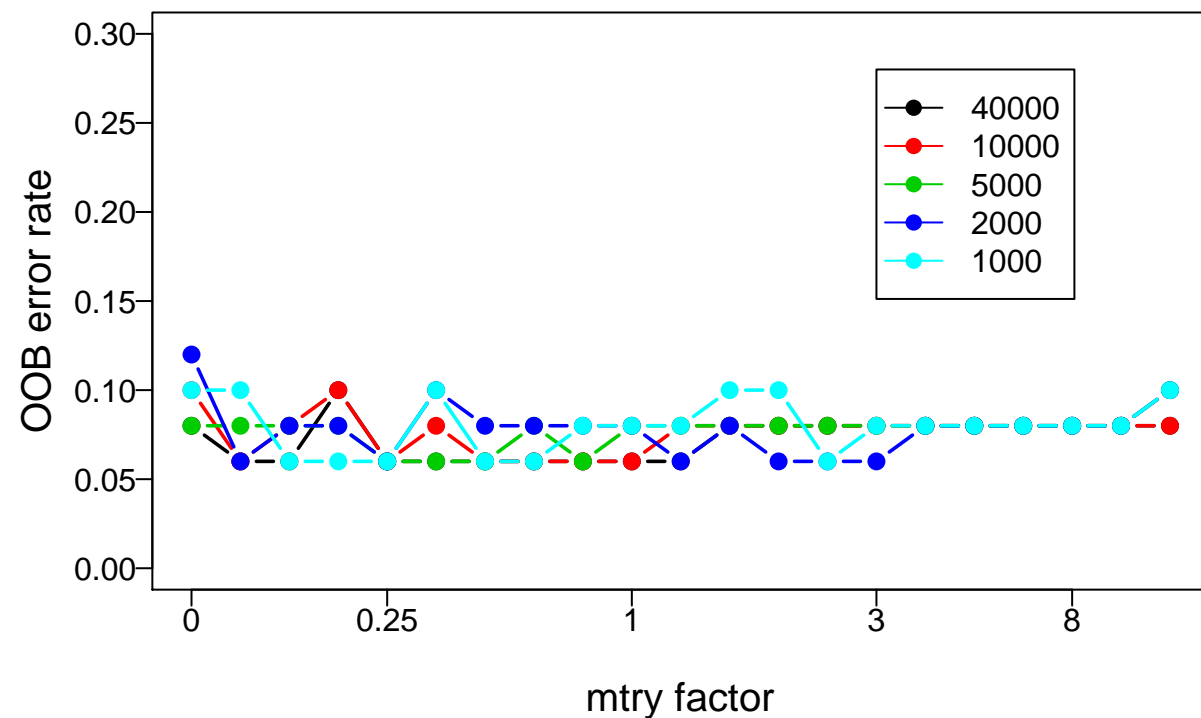
2 classes; 3 dimensions; 100 genes/dimen.; nodesize = 1



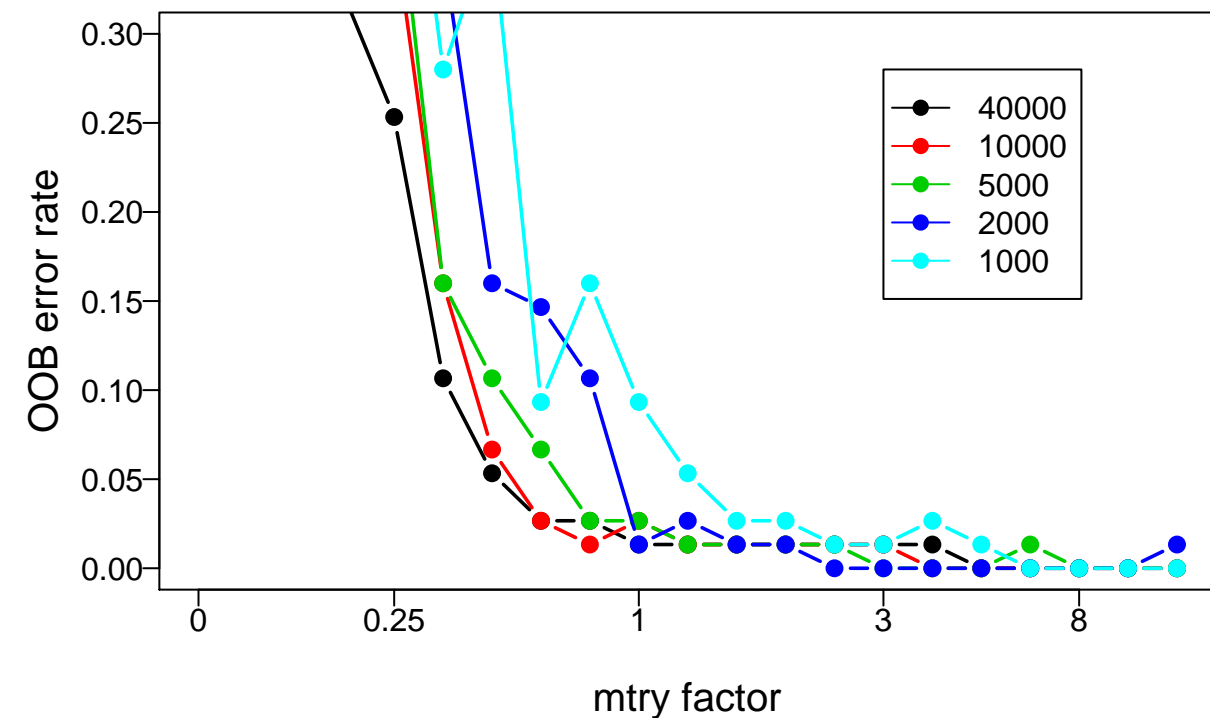
2 classes; 3 dimensions; 100 genes/dimen.; nodesize = 1



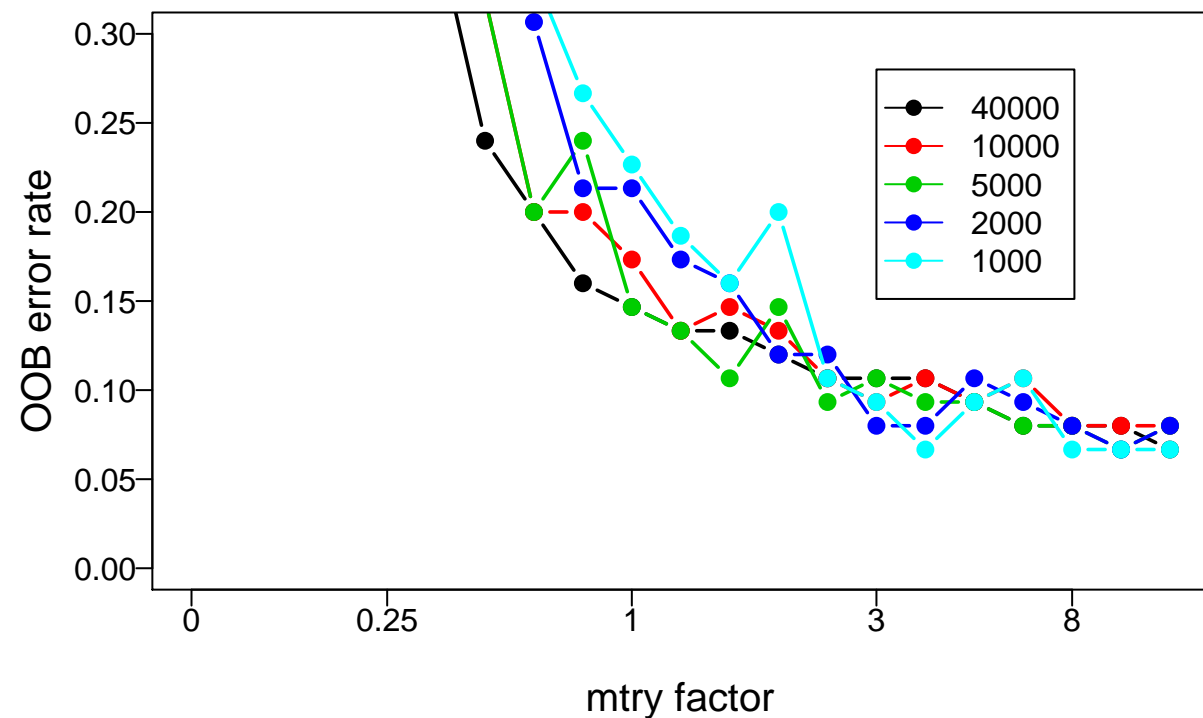
2 classes; 3 dimensions; 100 genes/dimen.; nodesize = 1



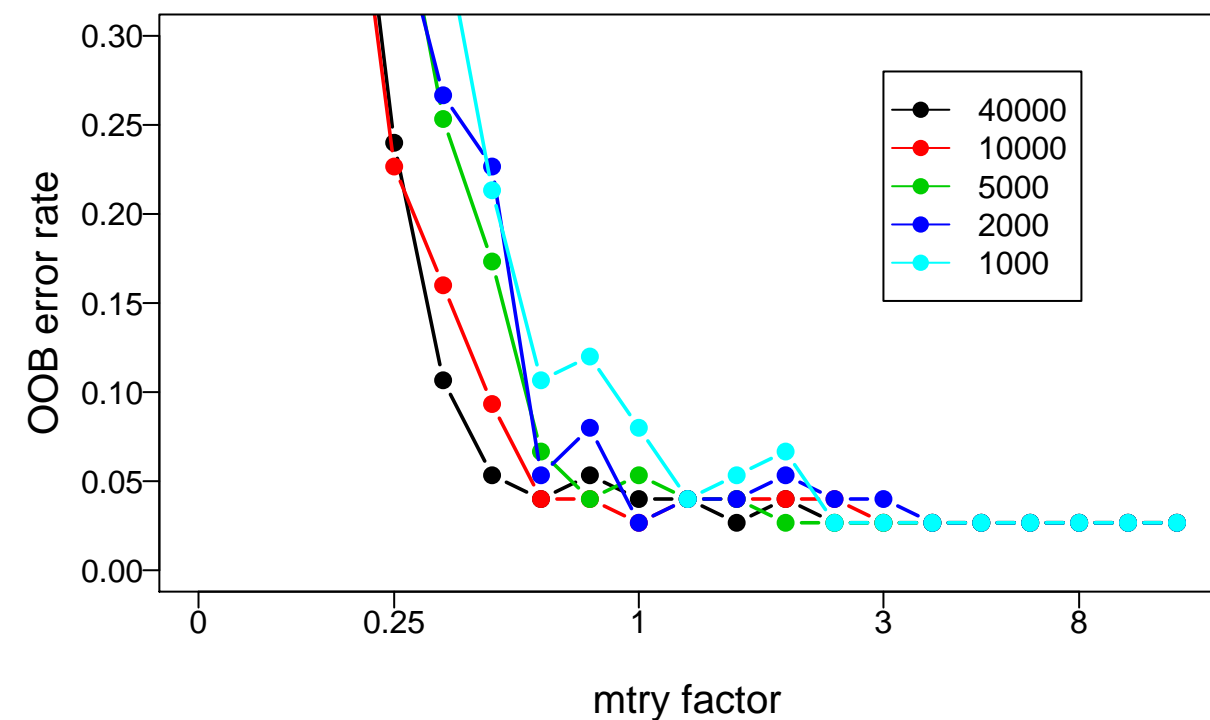
3 classes; 1 dimensions; 5 genes/dimen.; nodesize = 1



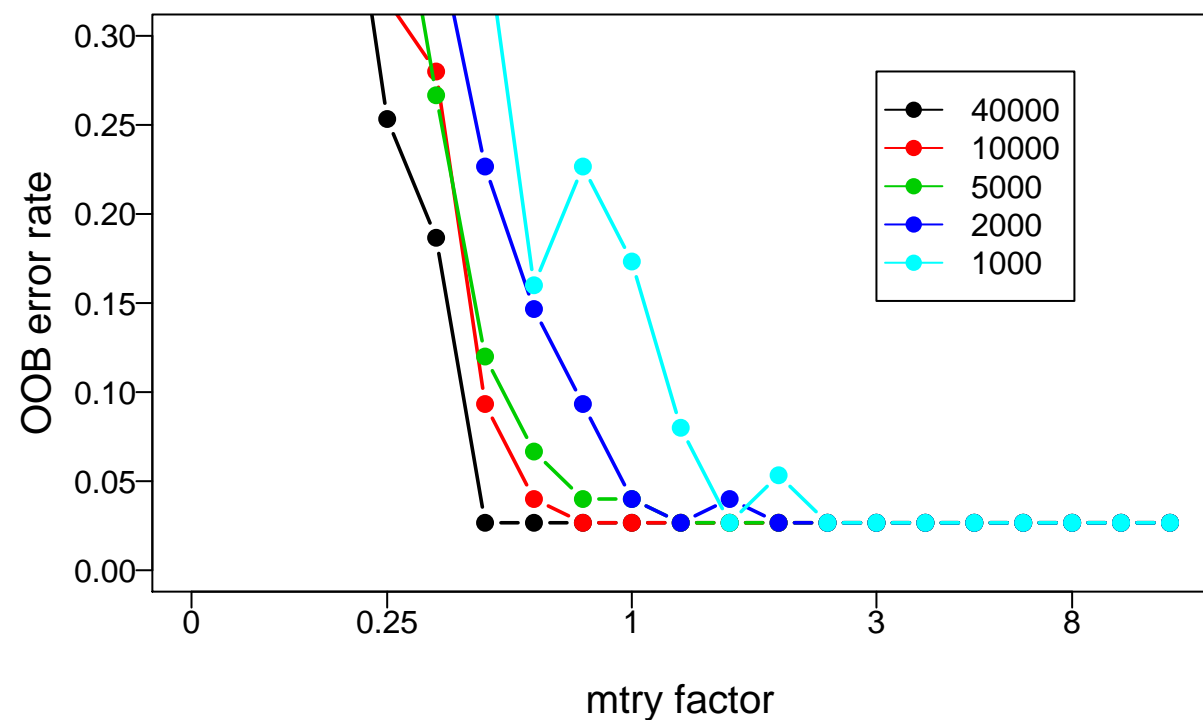
3 classes; 1 dimensions; 5 genes/dimen.; nodesize = 1



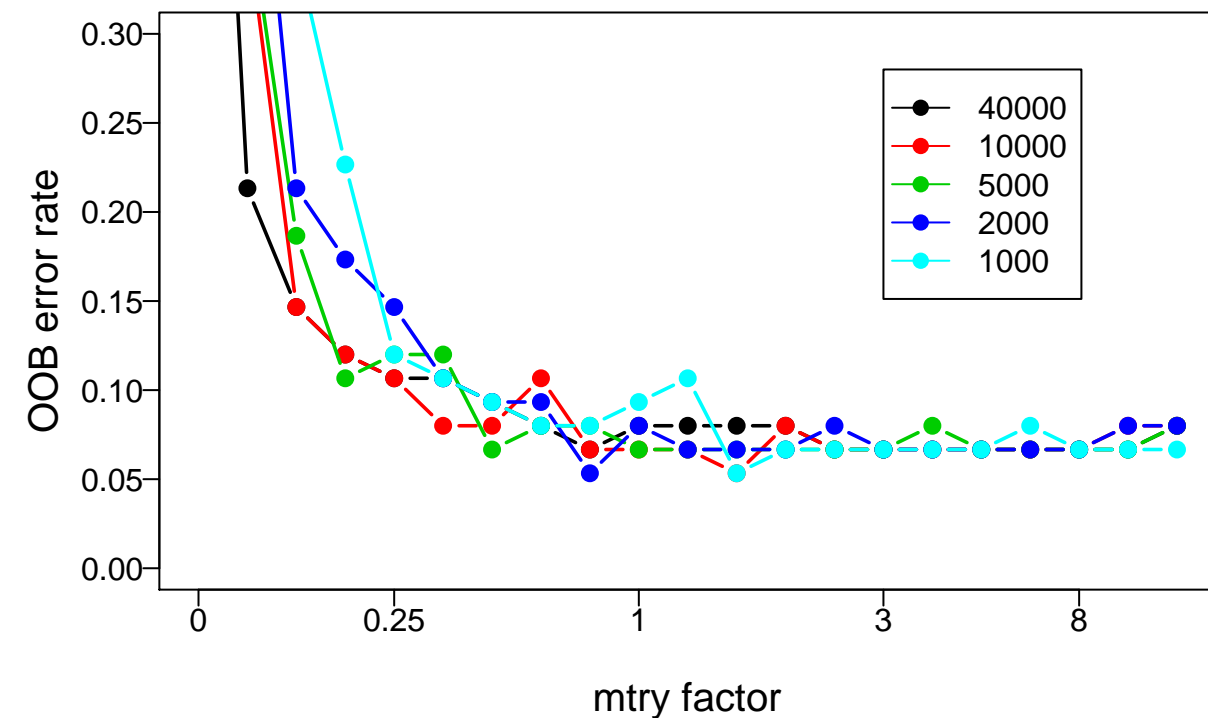
3 classes; 1 dimensions; 5 genes/dimen.; nodesize = 1



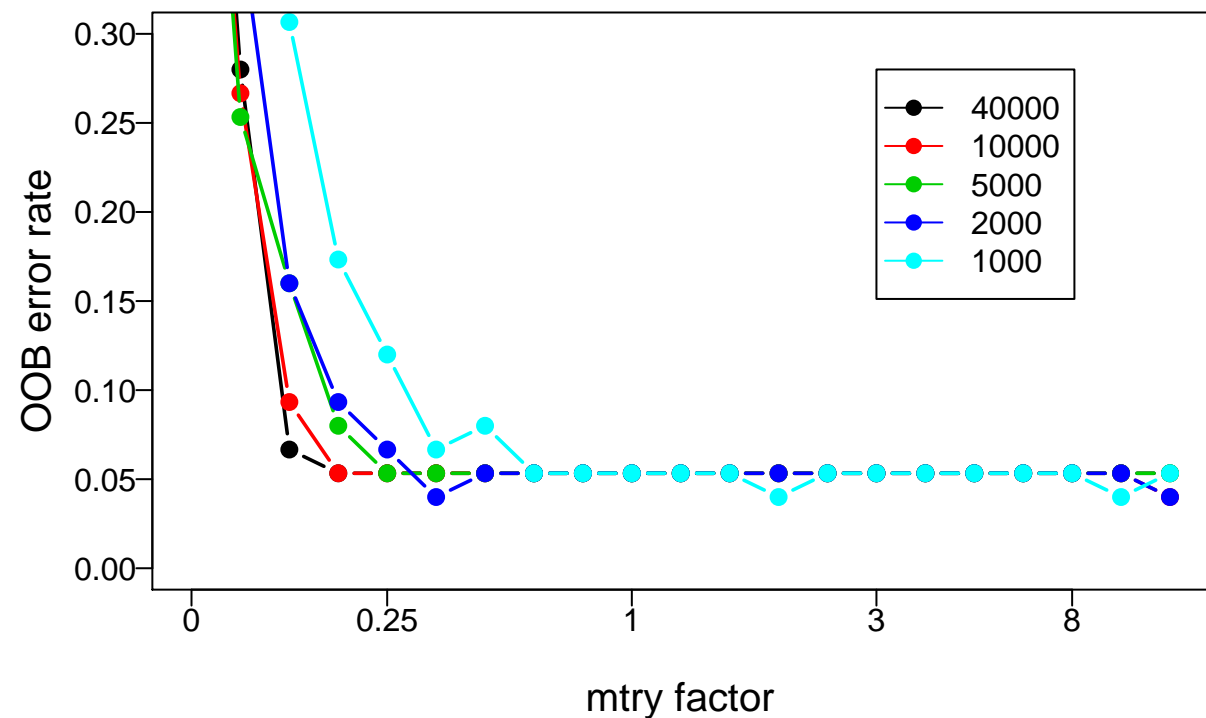
3 classes; 1 dimensions; 5 genes/dimen.; nodesize = 1



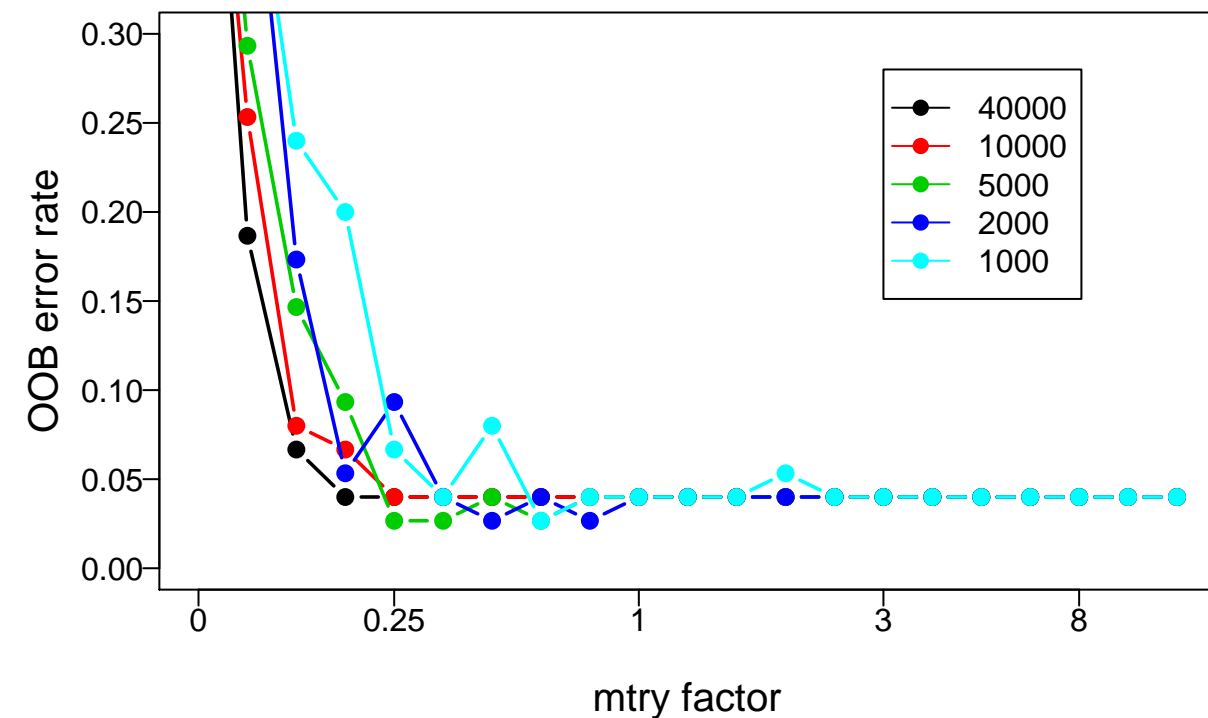
3 classes; 1 dimensions; 20 genes/dimen.; nodesize = 1



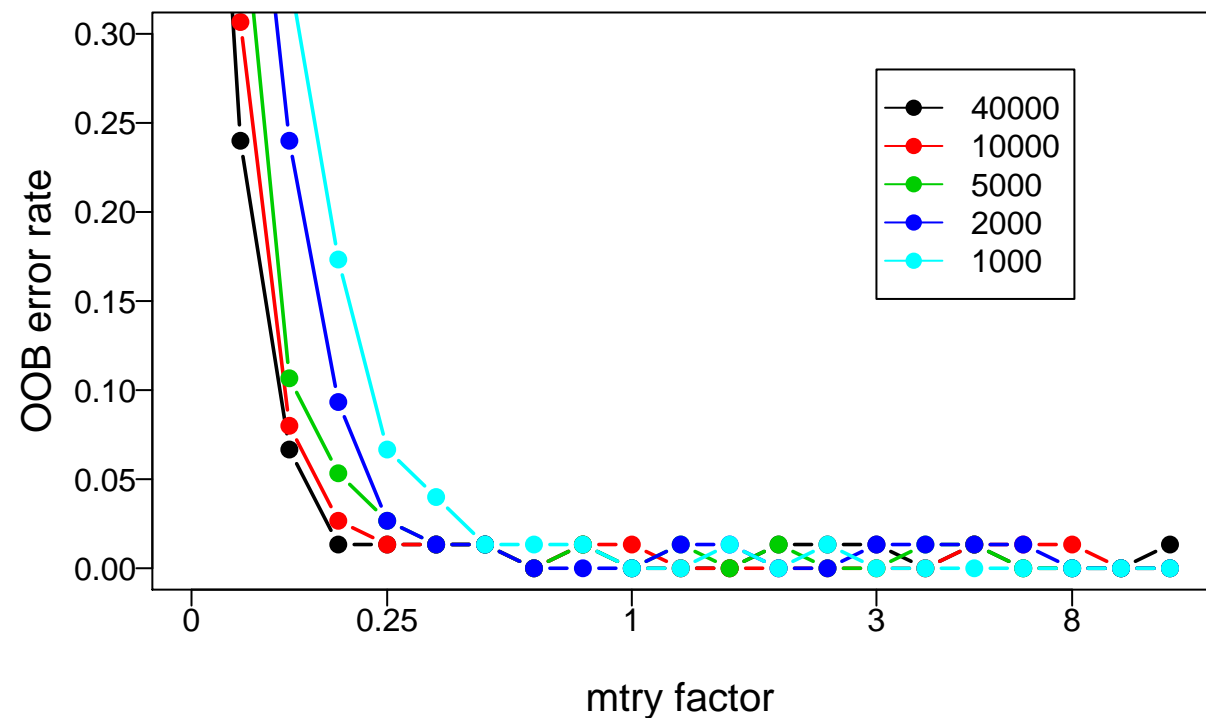
3 classes; 1 dimensions; 20 genes/dimen.; nodesize = 1



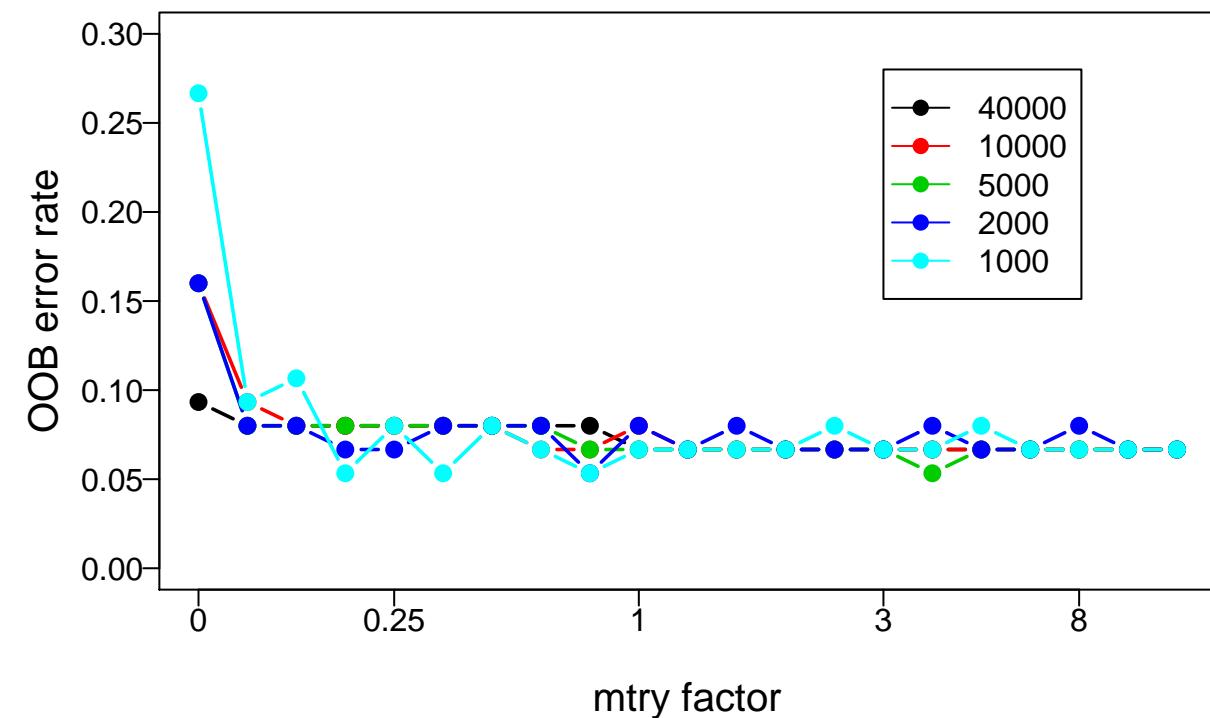
3 classes; 1 dimensions; 20 genes/dimen.; nodesize = 1



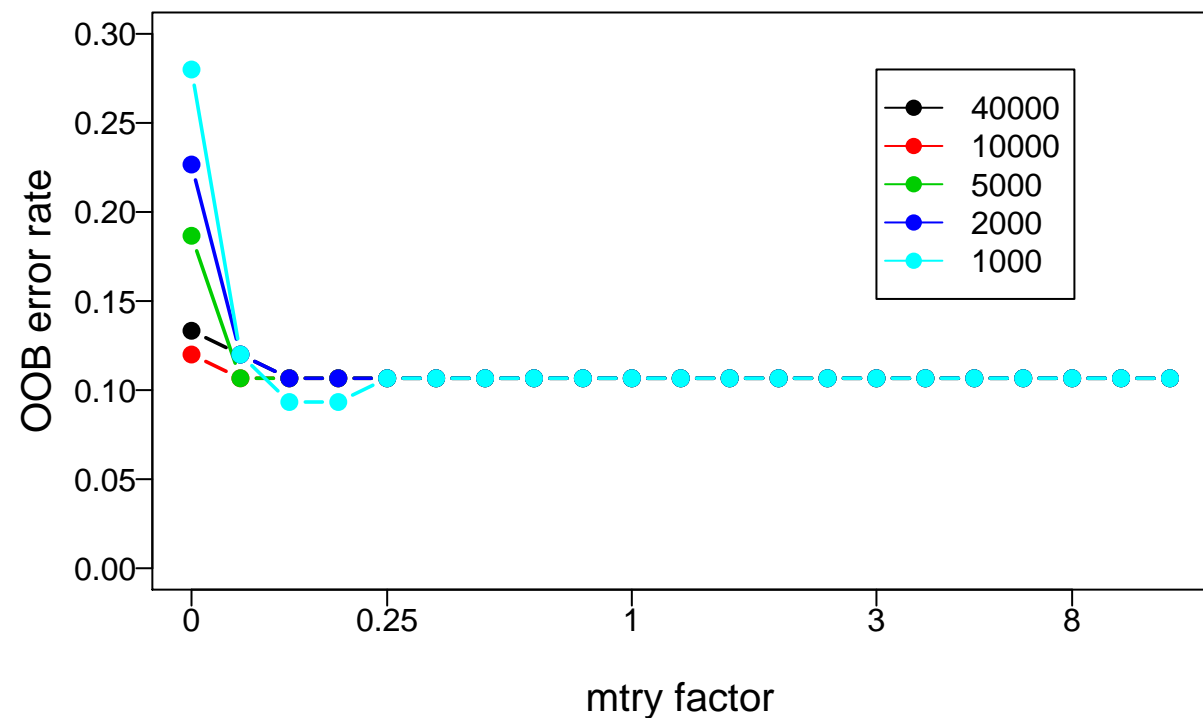
3 classes; 1 dimensions; 20 genes/dimen.; nodesize = 1



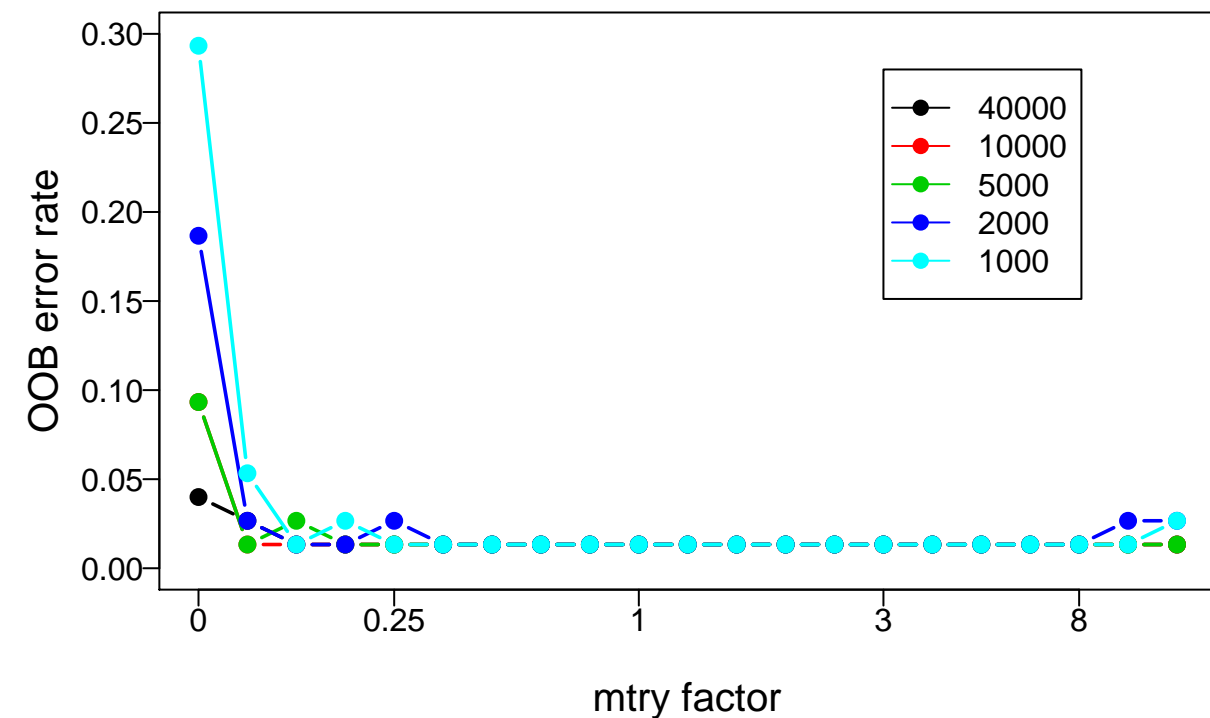
3 classes; 1 dimensions; 100 genes/dimen.; nodesize = 1



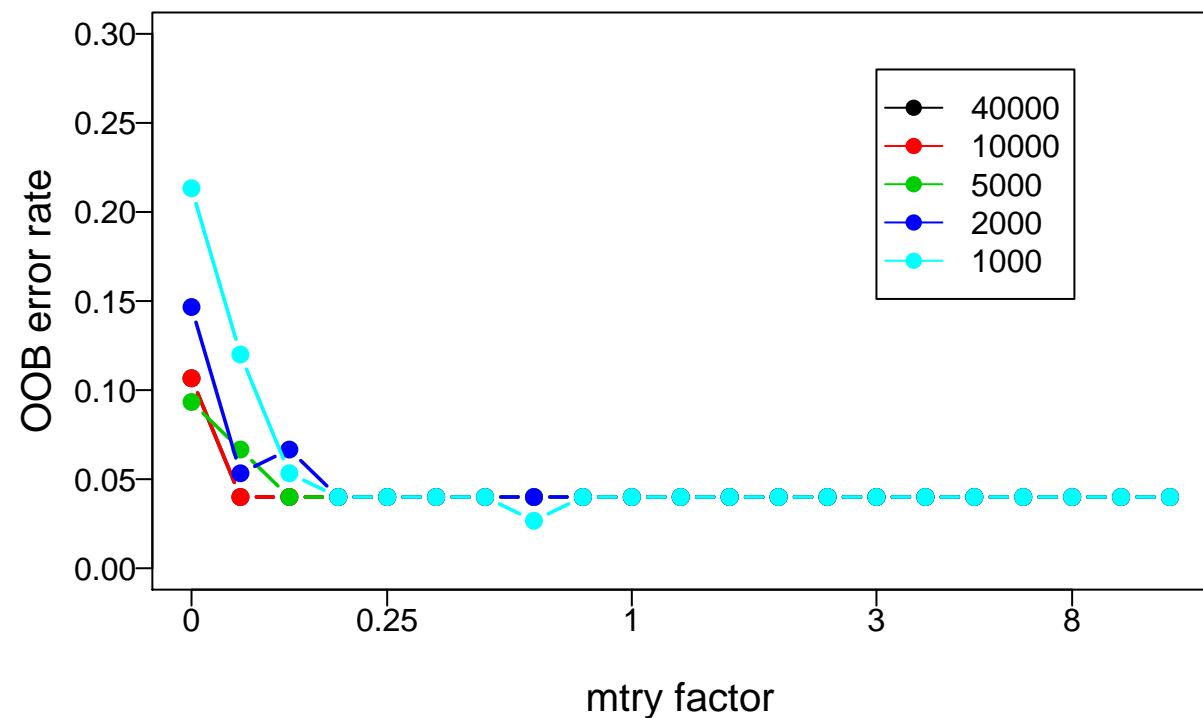
3 classes; 1 dimensions; 100 genes/dimen.; nodesize = 1



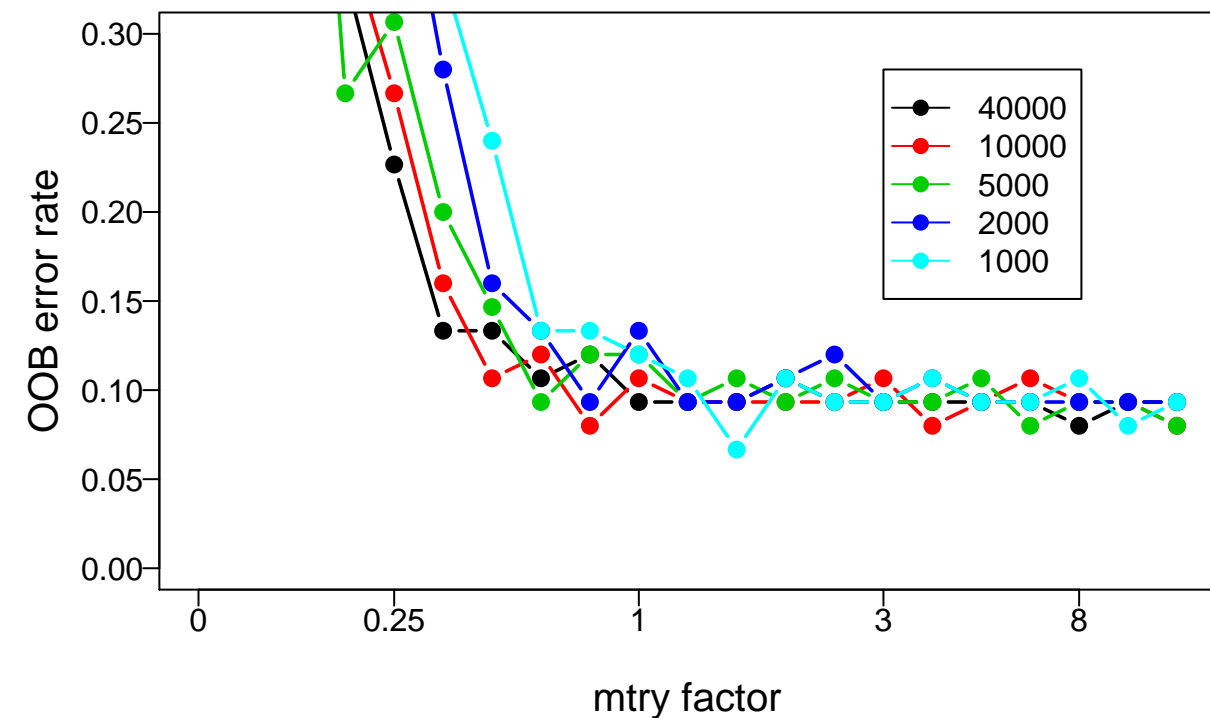
3 classes; 1 dimensions; 100 genes/dimen.; nodesize = 1



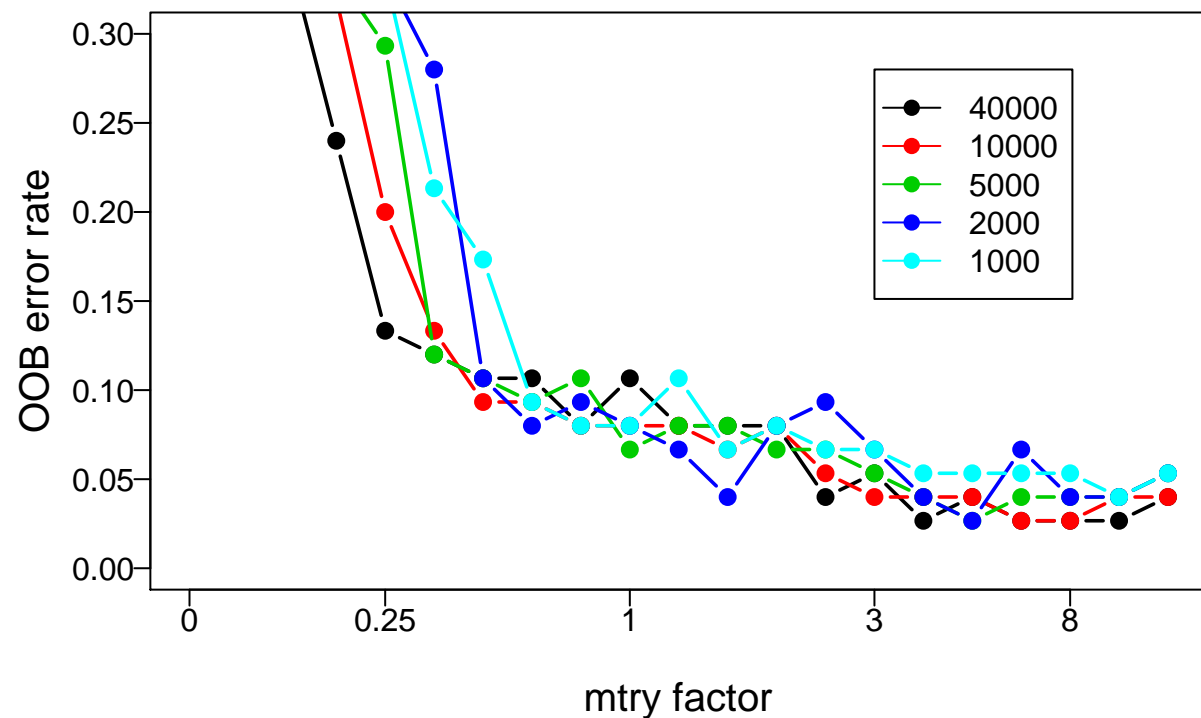
3 classes; 1 dimensions; 100 genes/dimen.; nodesize = 1



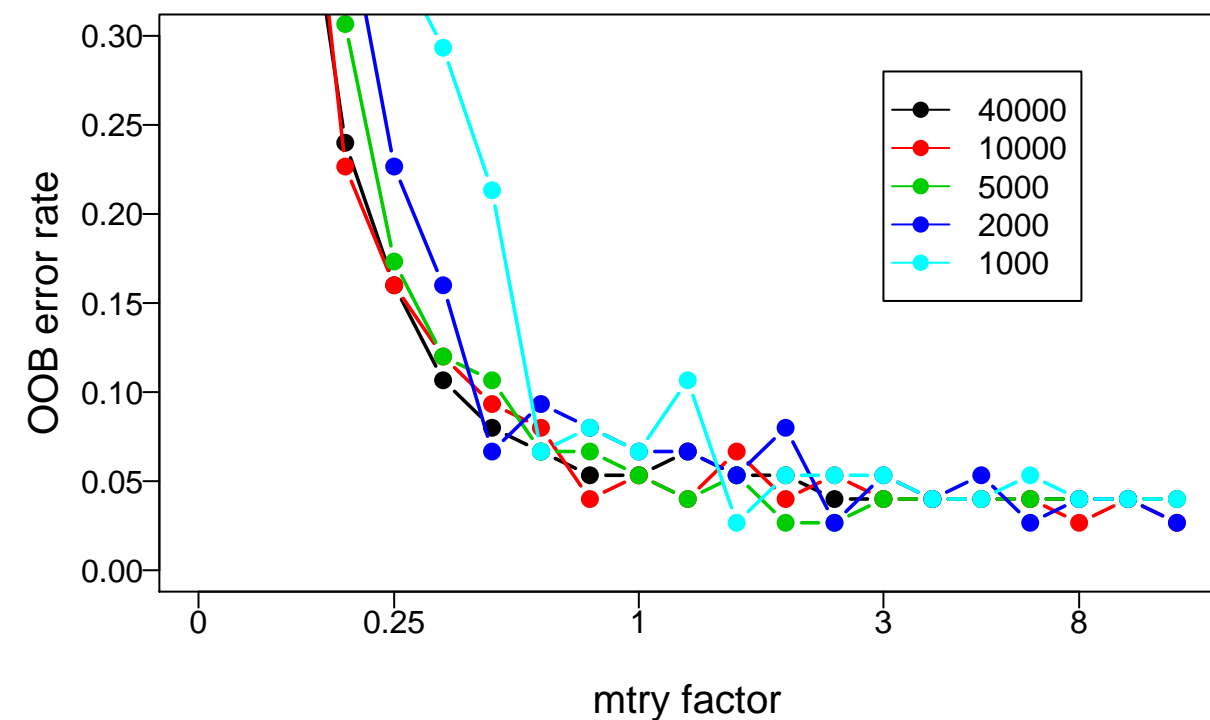
3 classes; 2 dimensions; 5 genes/dimen.; nodesize = 1



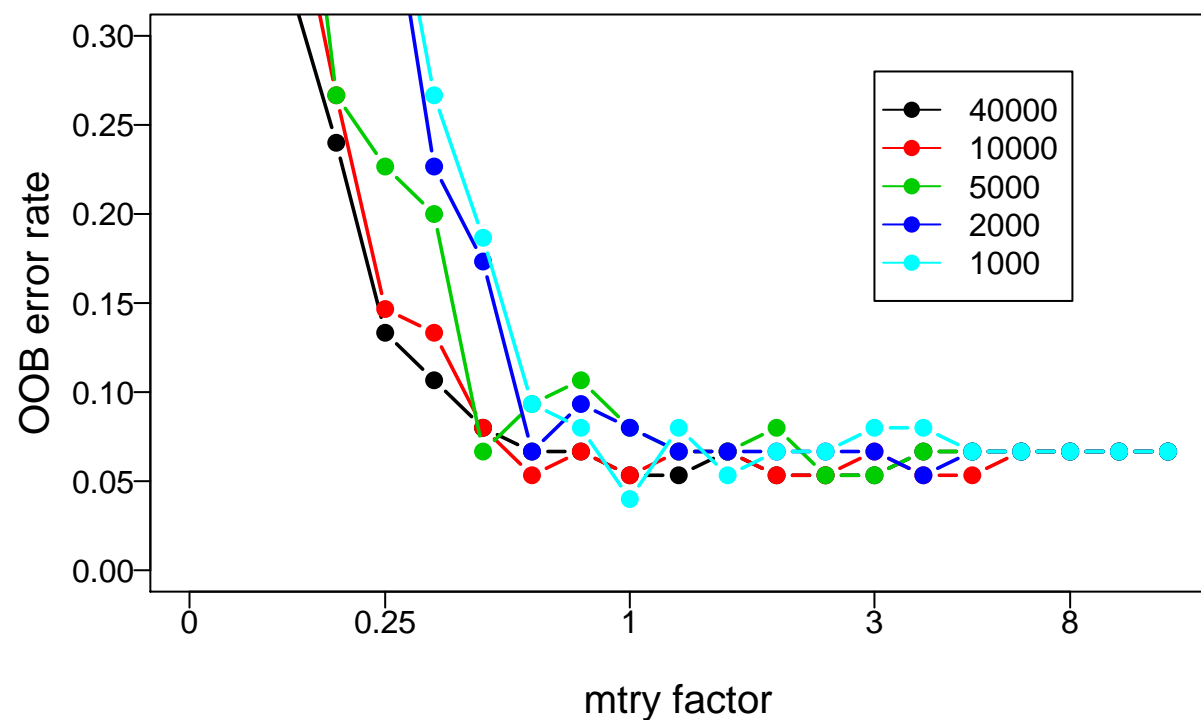
3 classes; 2 dimensions; 5 genes/dimen.; nodesize = 1



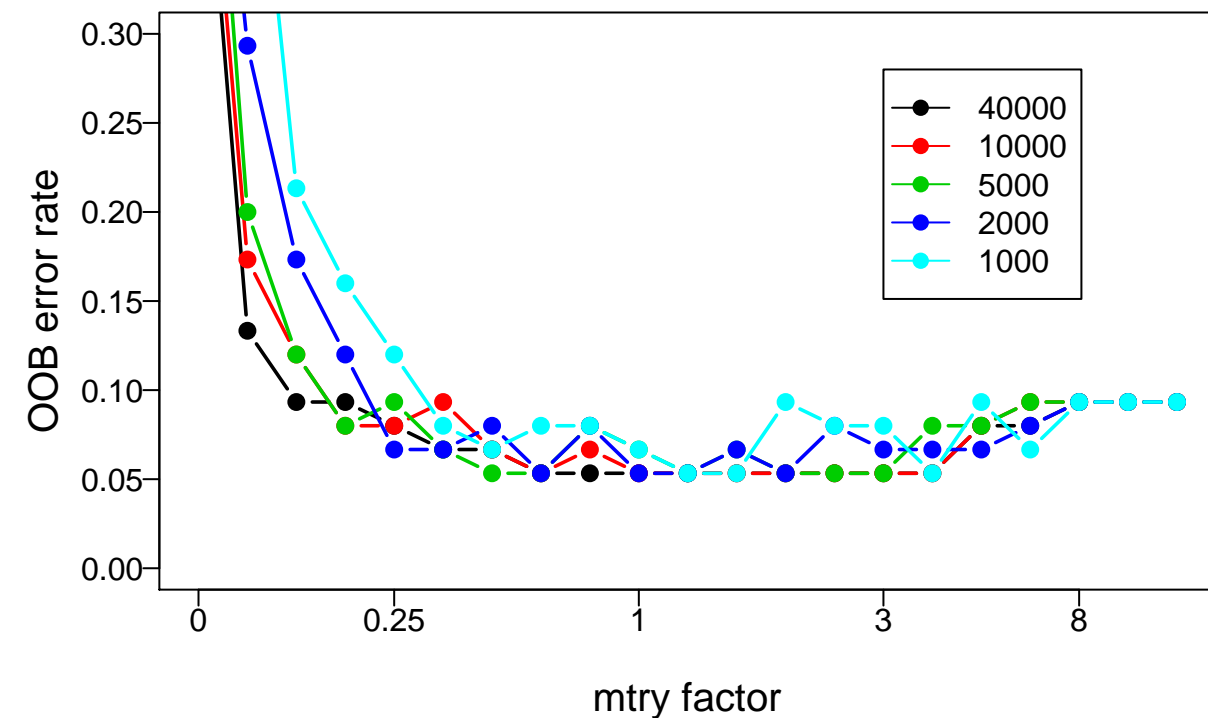
3 classes; 2 dimensions; 5 genes/dimen.; nodesize = 1



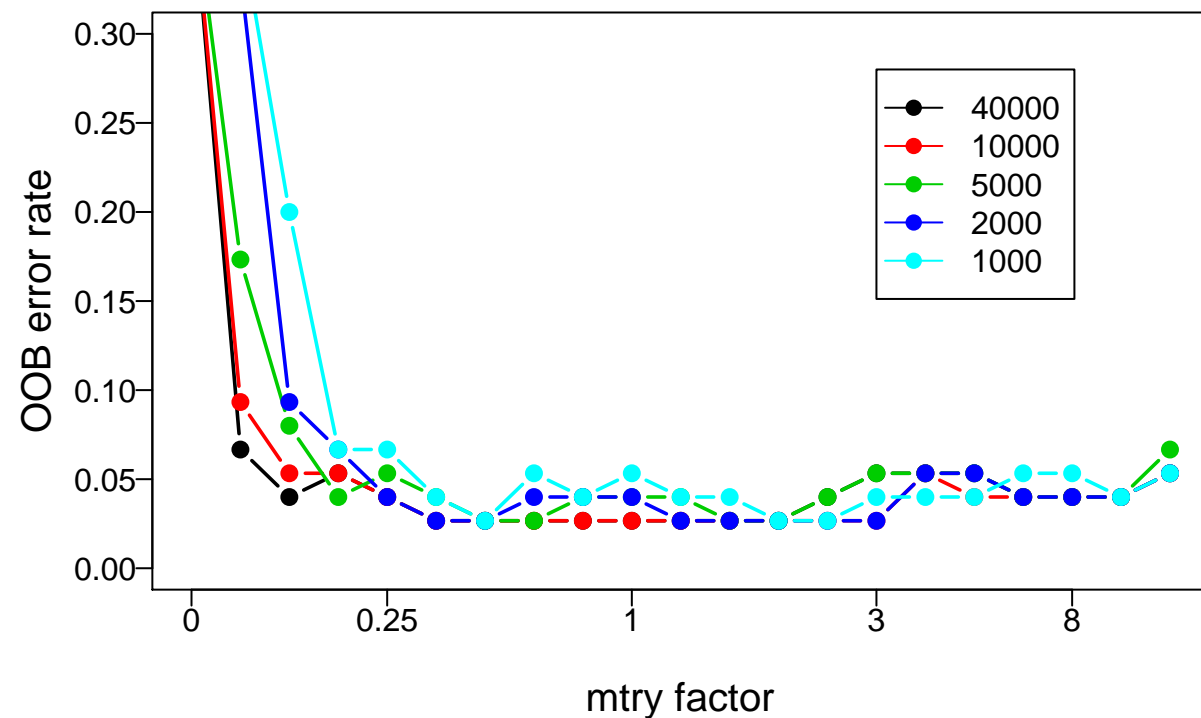
3 classes; 2 dimensions; 5 genes/dimen.; nodesize = 1



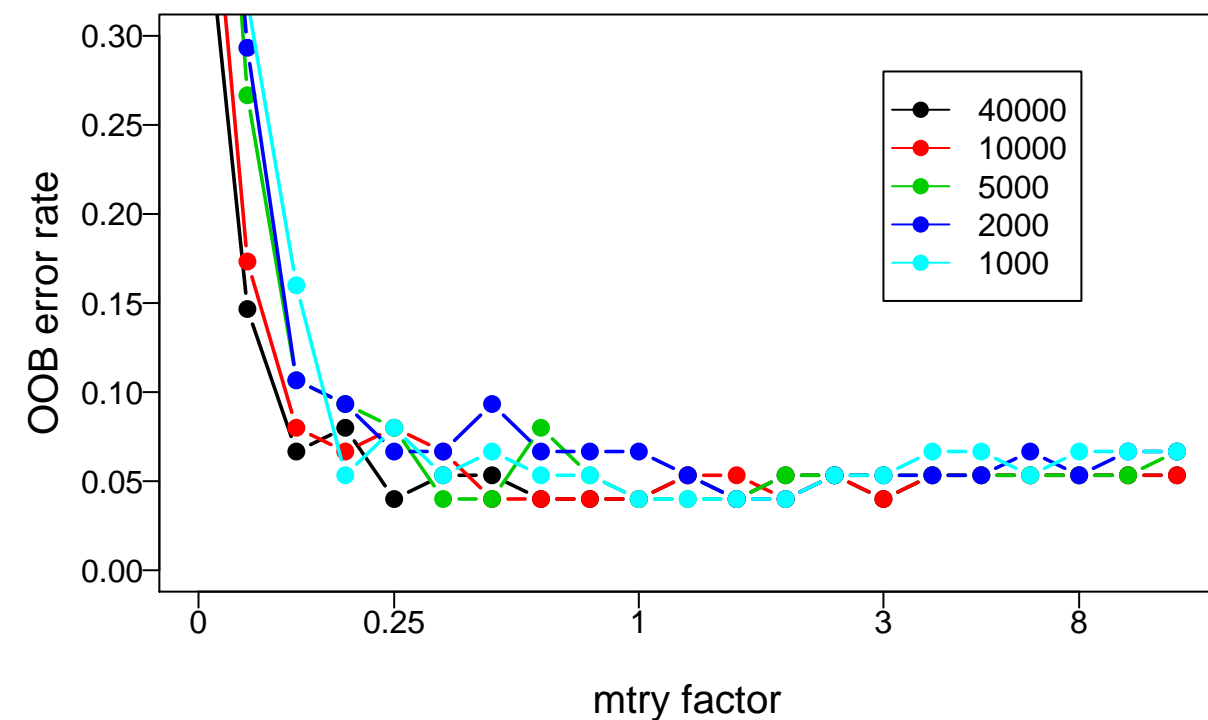
3 classes; 2 dimensions; 20 genes/dimen.; nodesize = 1



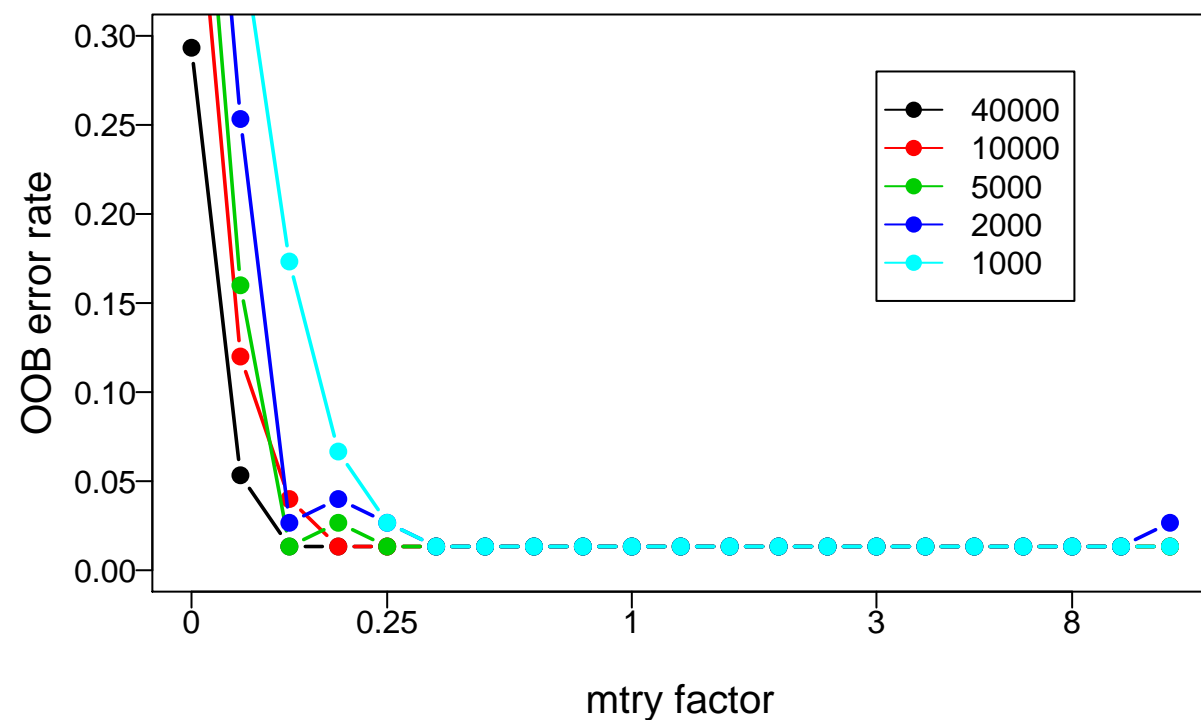
3 classes; 2 dimensions; 20 genes/dimen.; nodesize = 1



3 classes; 2 dimensions; 20 genes/dimen.; nodesize = 1



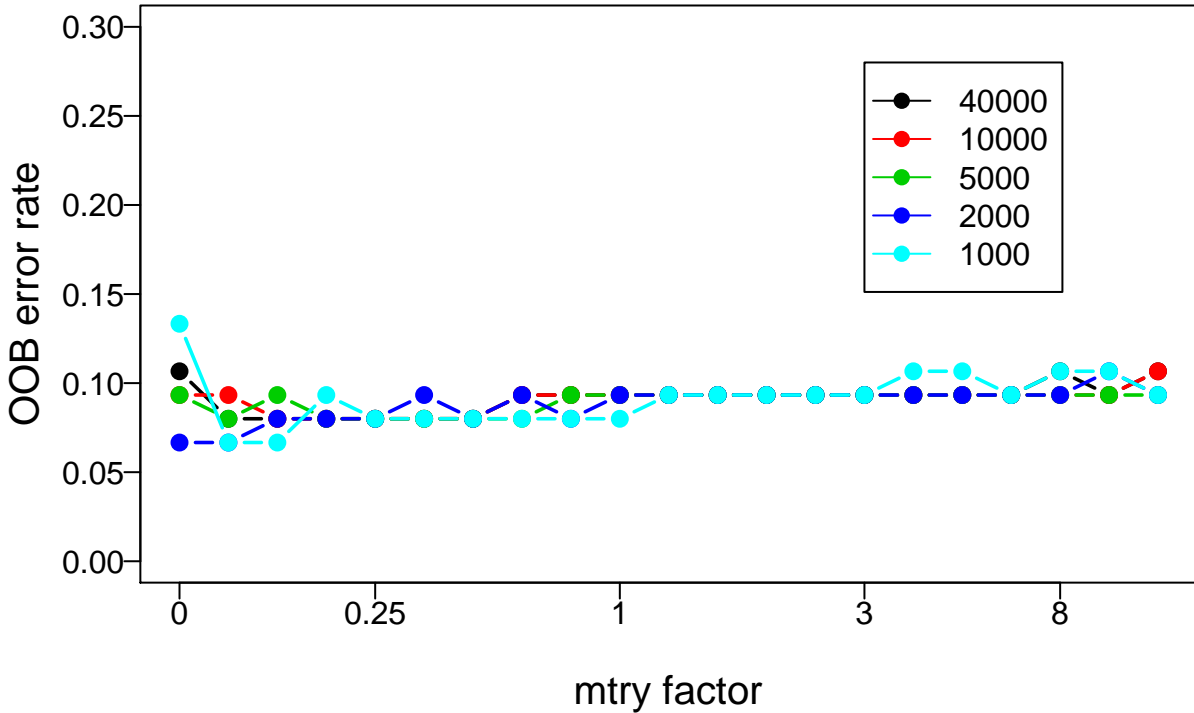
3 classes; 2 dimensions; 20 genes/dimen.; nodesize = 1



Line plot showing the number of iterations (Y-axis) versus the mtry factor (X-axis) for different sample sizes (40000, 10000, 5000, 2000, 1000). The X-axis is labeled 'mtry factor' and has major ticks at 0, 0.25, 1, 3, and 8. The Y-axis is labeled 'iterations' and has major ticks at 0, 1000, 2000, 3000, 4000, 5000, 6000, 7000, 8000, 9000, and 10000. The legend indicates the following series:

- 40000 (Black line)
- 10000 (Red line)
- 5000 (Green line)
- 2000 (Blue line)
- 1000 (Cyan line)

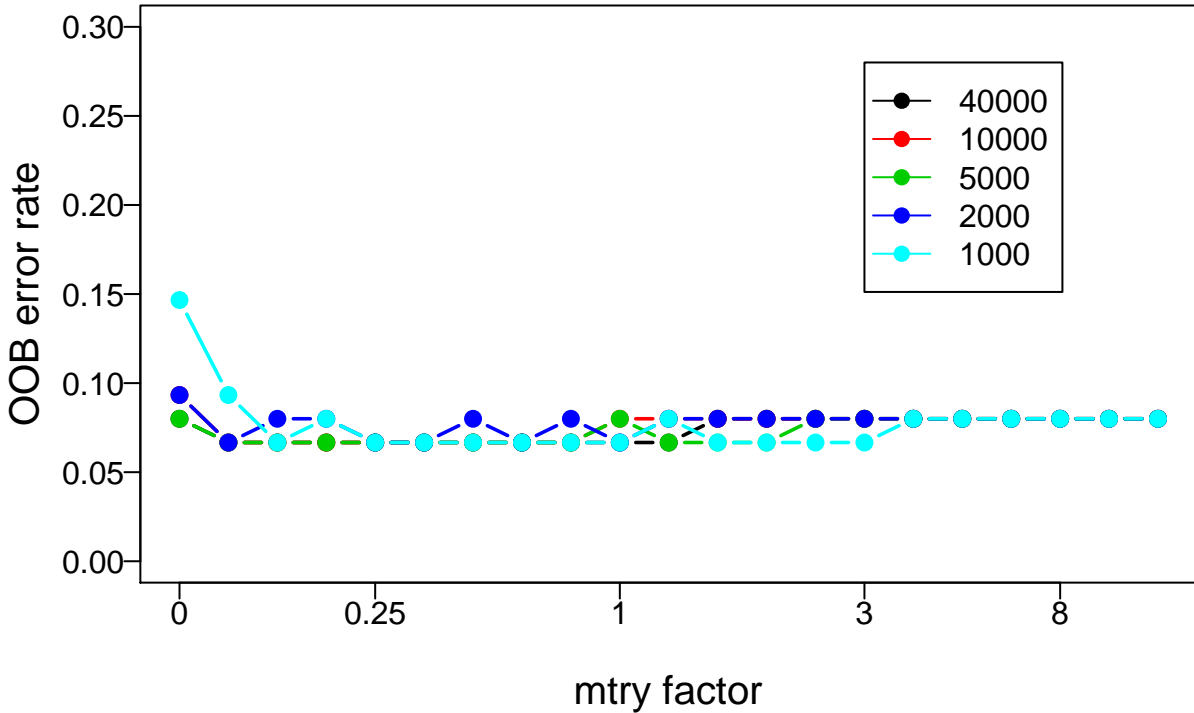
The plot shows that for all sample sizes, the number of iterations is relatively low (below 1000) for mtry factors from 0.25 to 10. For mtry factor 0, the number of iterations increases significantly with sample size, reaching approximately 8000 for 40000 samples and 1000 for 1000 samples.



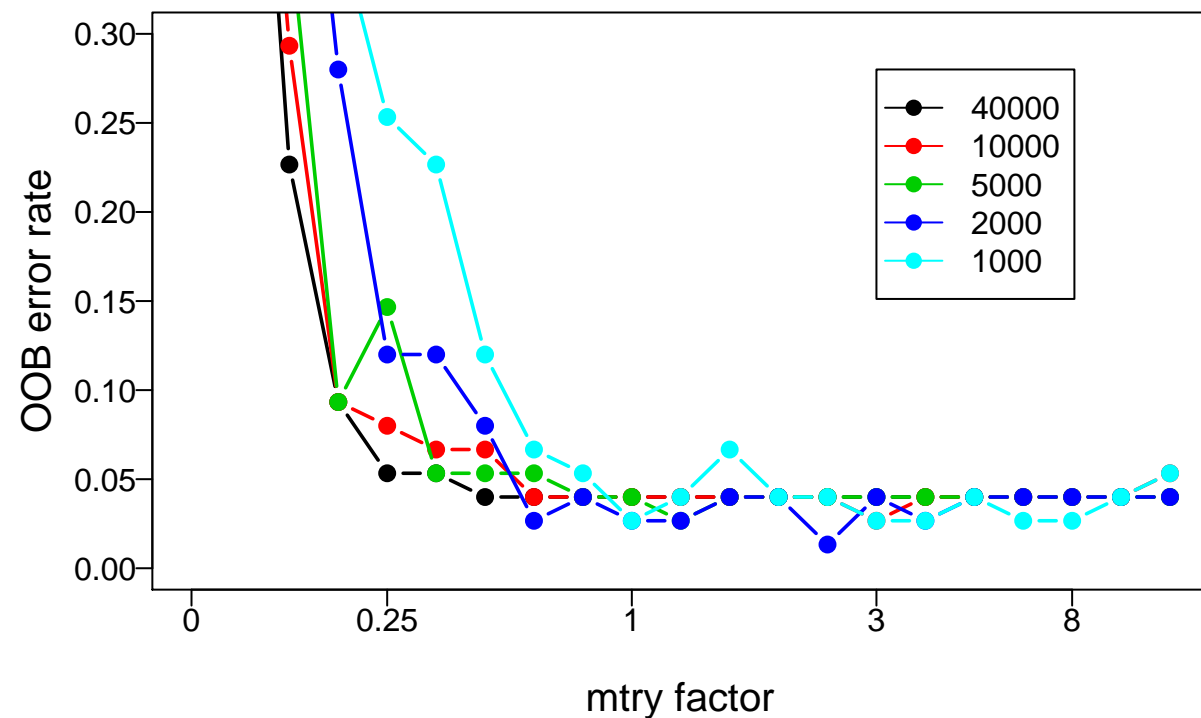
The graph displays the relationship between the mtry factor and a metric for five different sample sizes. The x-axis, labeled 'mtry factor', has major ticks at 0, 0.25, 1, 3, and 8. The y-axis is on a logarithmic scale. The legend indicates the following series:

- 40000 (black line)
- 10000 (red line)
- 5000 (green line)
- 2000 (blue line)
- 1000 (cyan line)

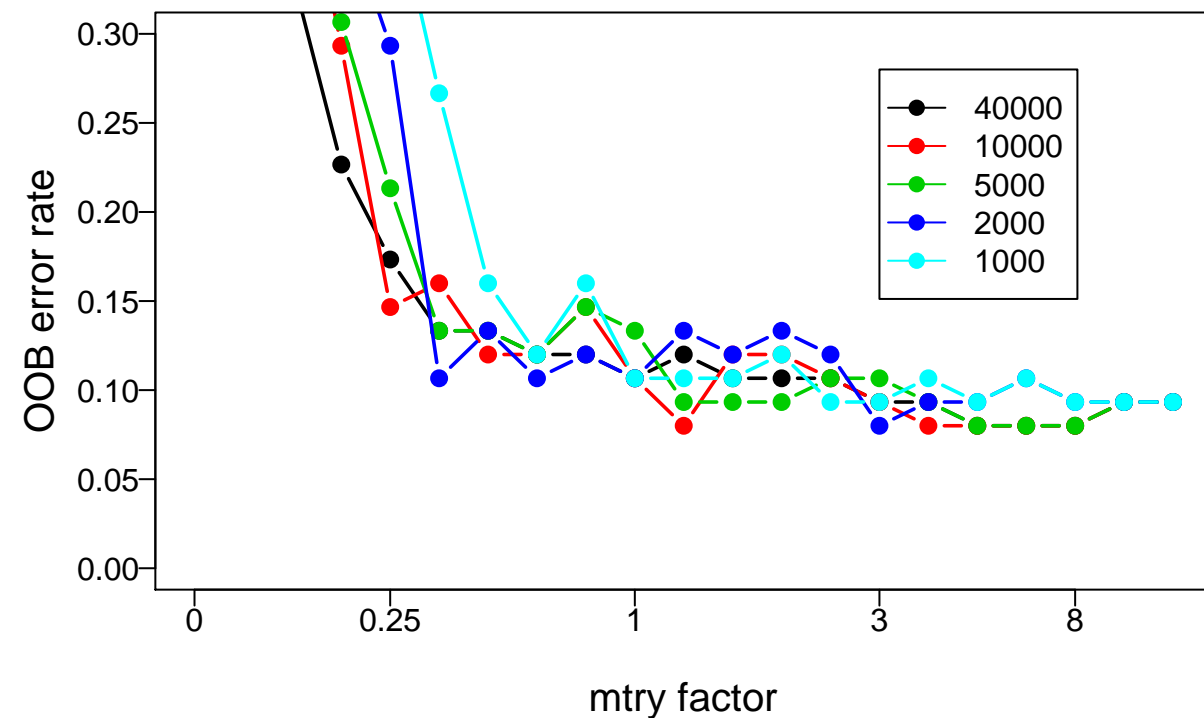
All series show a sharp initial drop from mtry factor 0 to 0.25, followed by fluctuations at a lower level. The 1000 sample size series starts at a significantly higher value than the others at mtry factor 0.



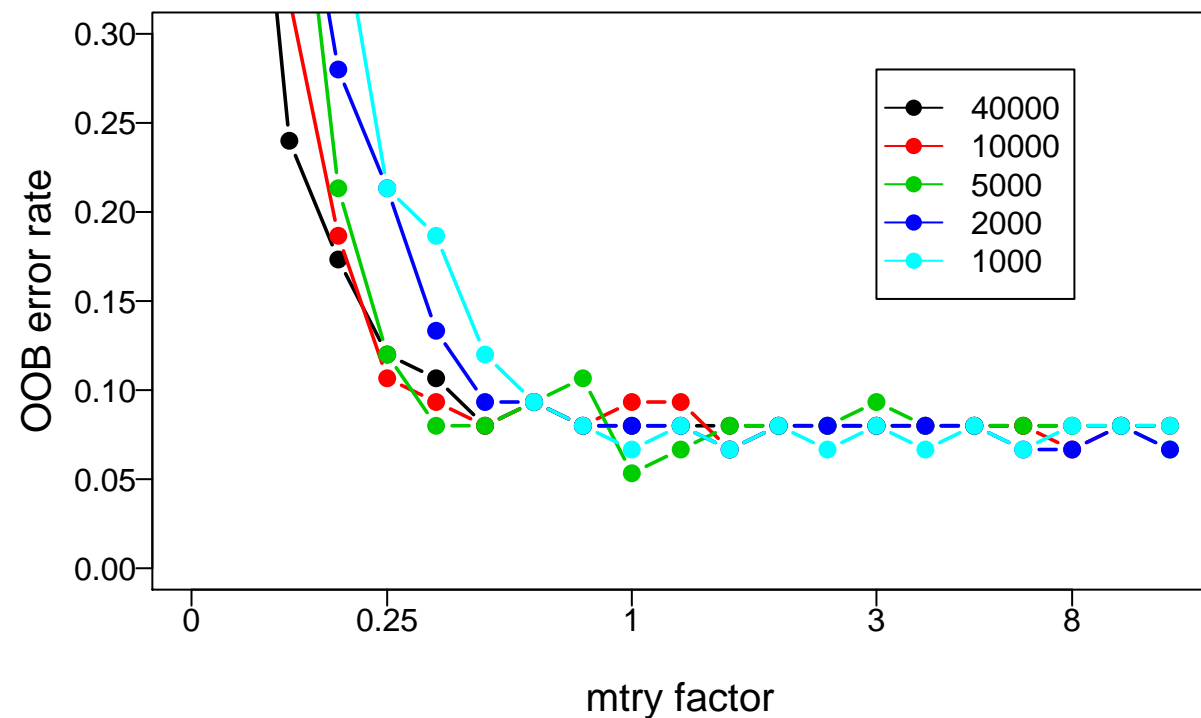
3 classes; 3 dimensions; 5 genes/dimen.; nodesize = 1



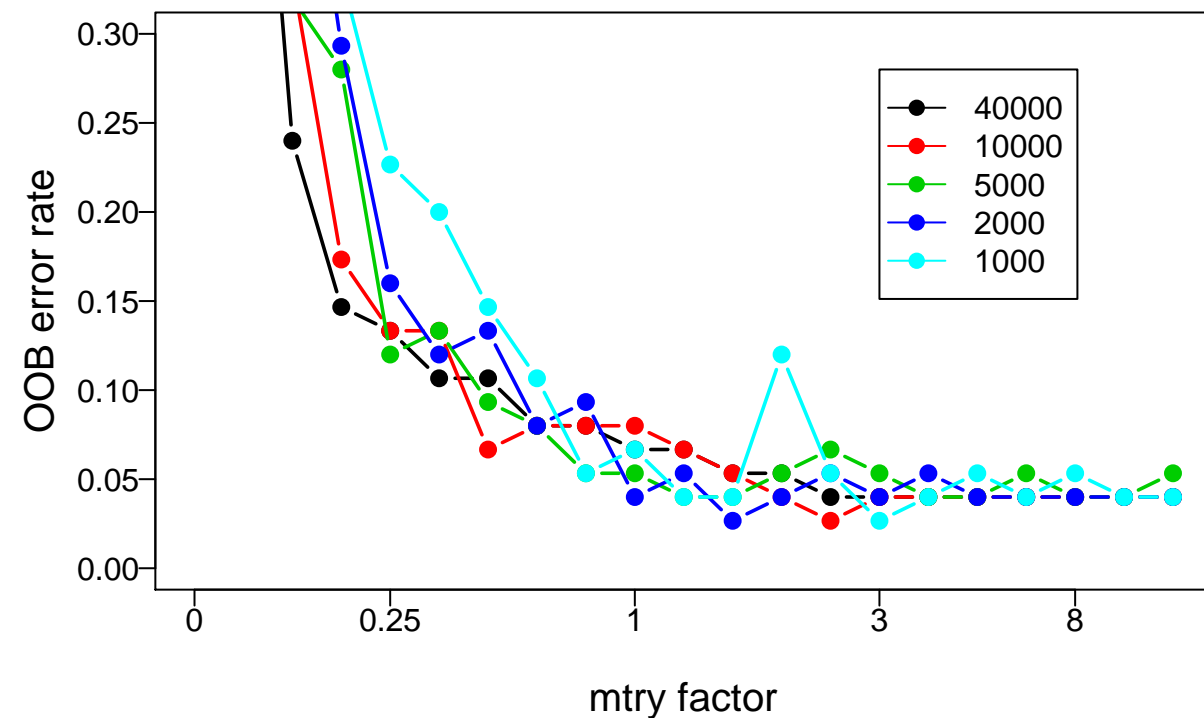
3 classes; 3 dimensions; 5 genes/dimen.; nodesize = 1



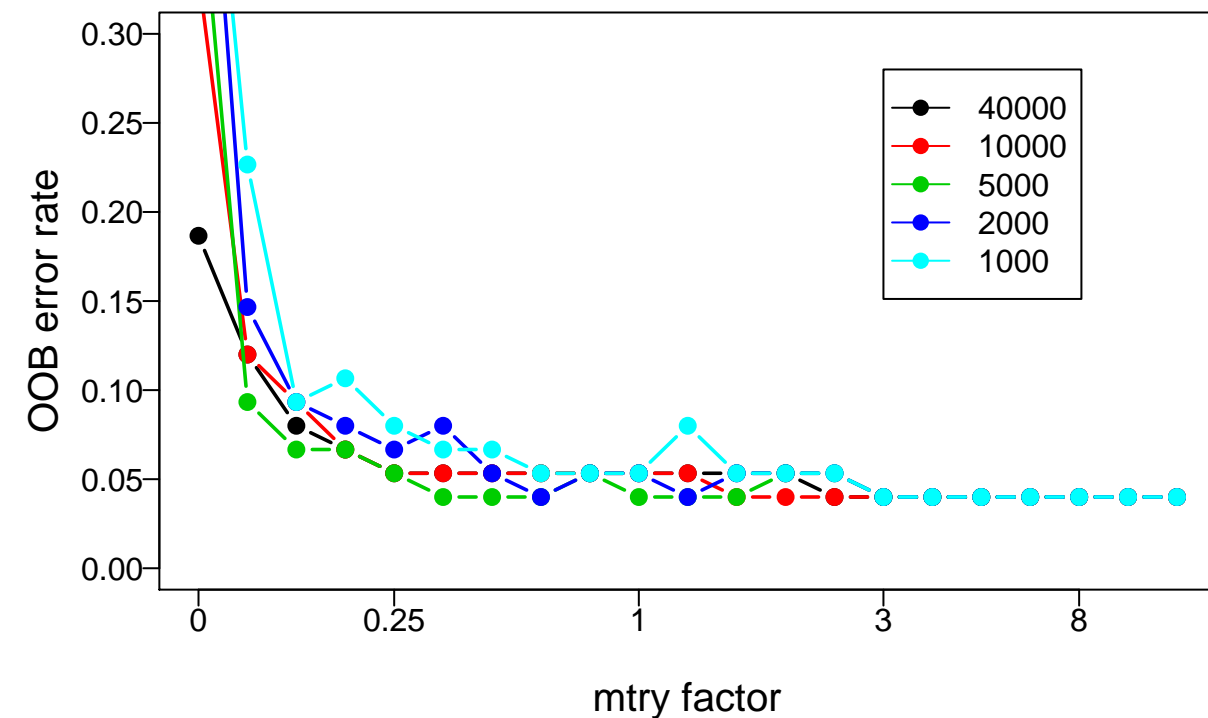
3 classes; 3 dimensions; 5 genes/dimen.; nodesize = 1



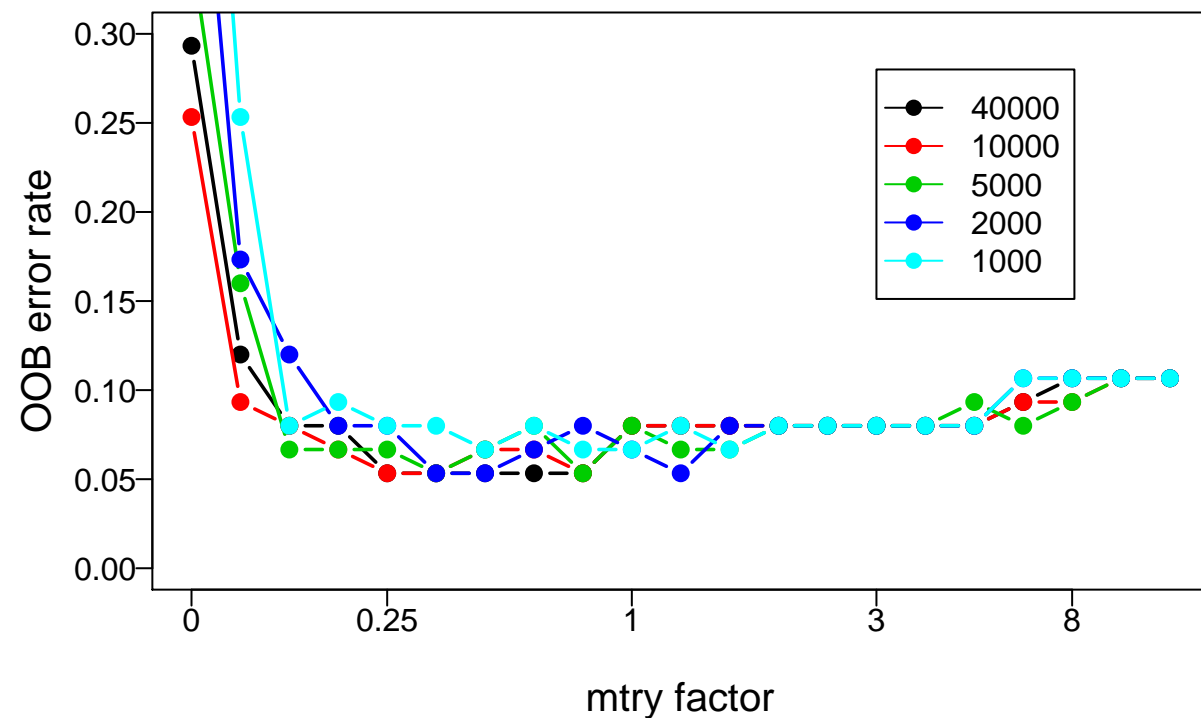
3 classes; 3 dimensions; 5 genes/dimen.; nodesize = 1



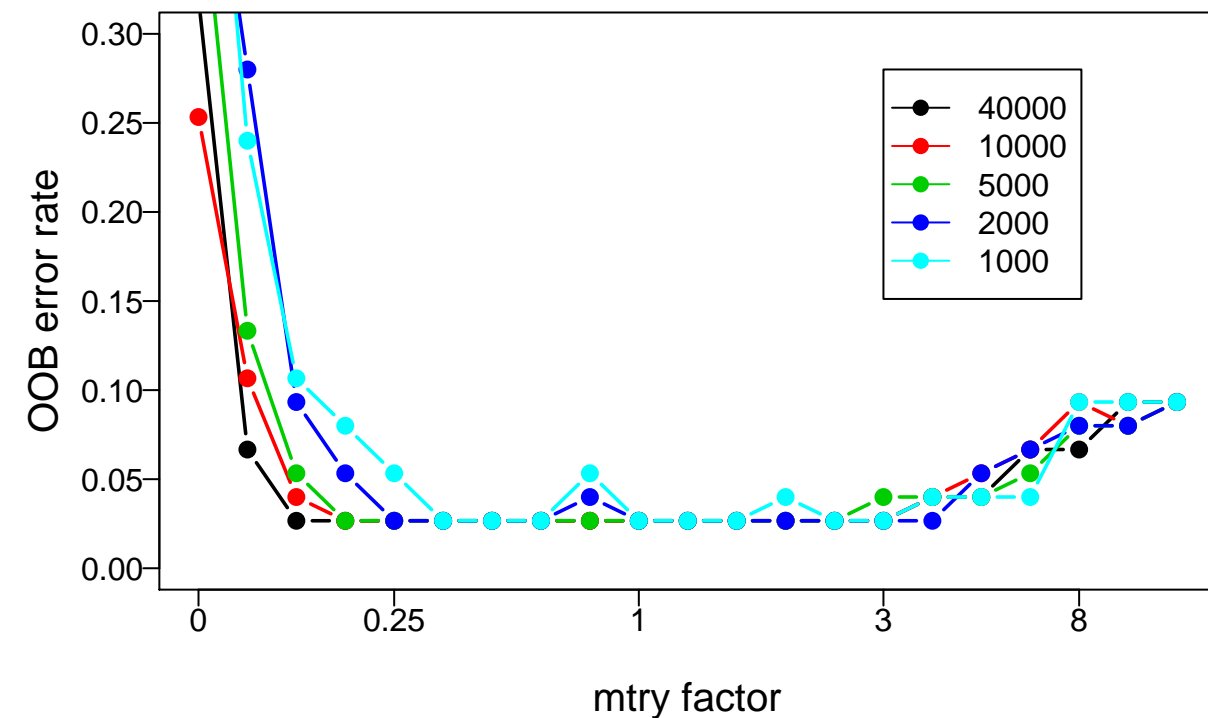
3 classes; 3 dimensions; 20 genes/dimen.; nodesize = 1



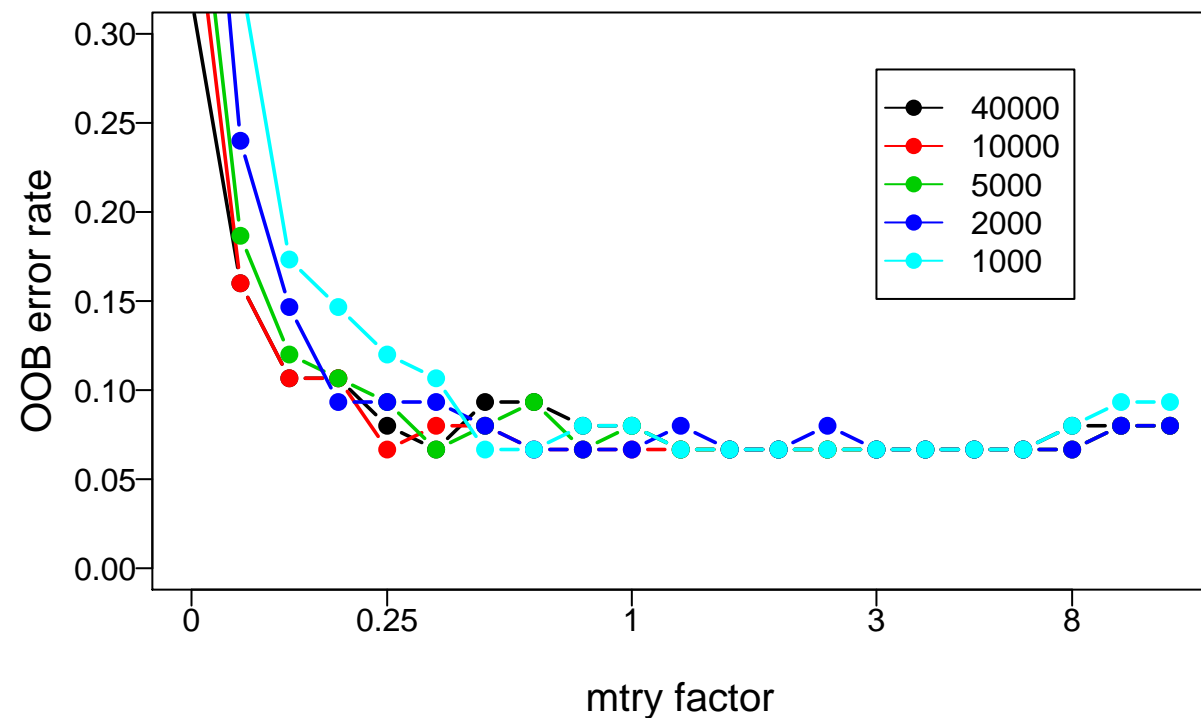
3 classes; 3 dimensions; 20 genes/dimen.; nodesize = 1



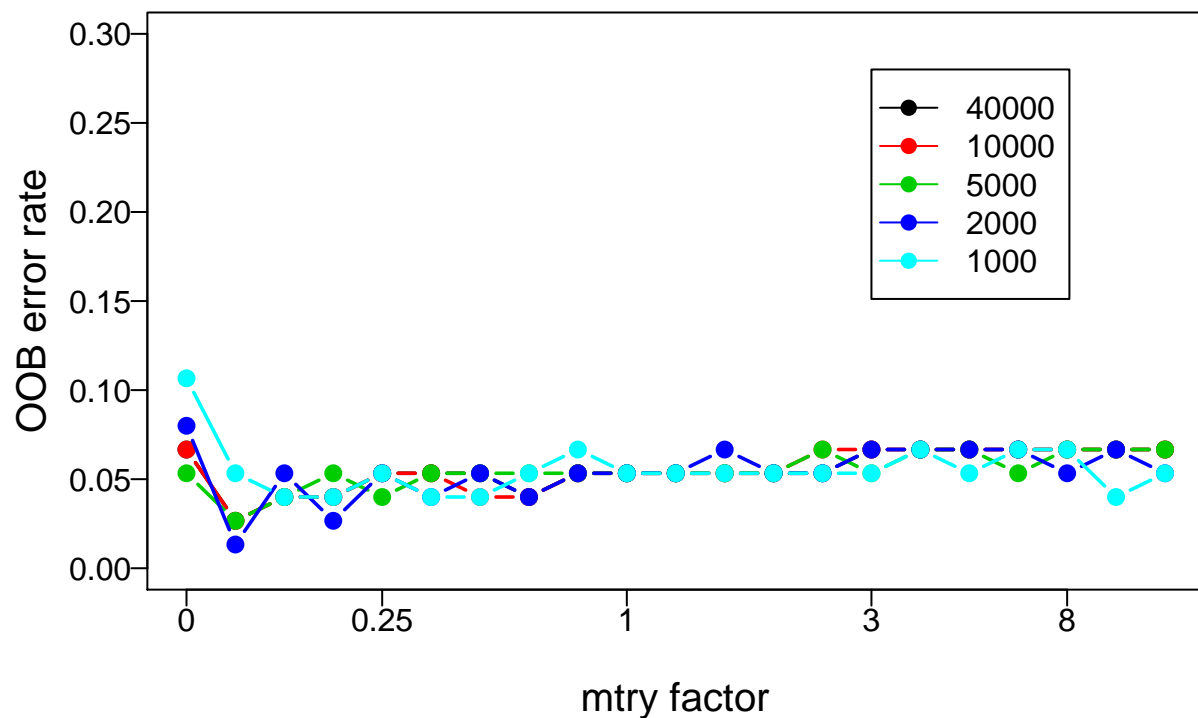
3 classes; 3 dimensions; 20 genes/dimen.; nodesize = 1



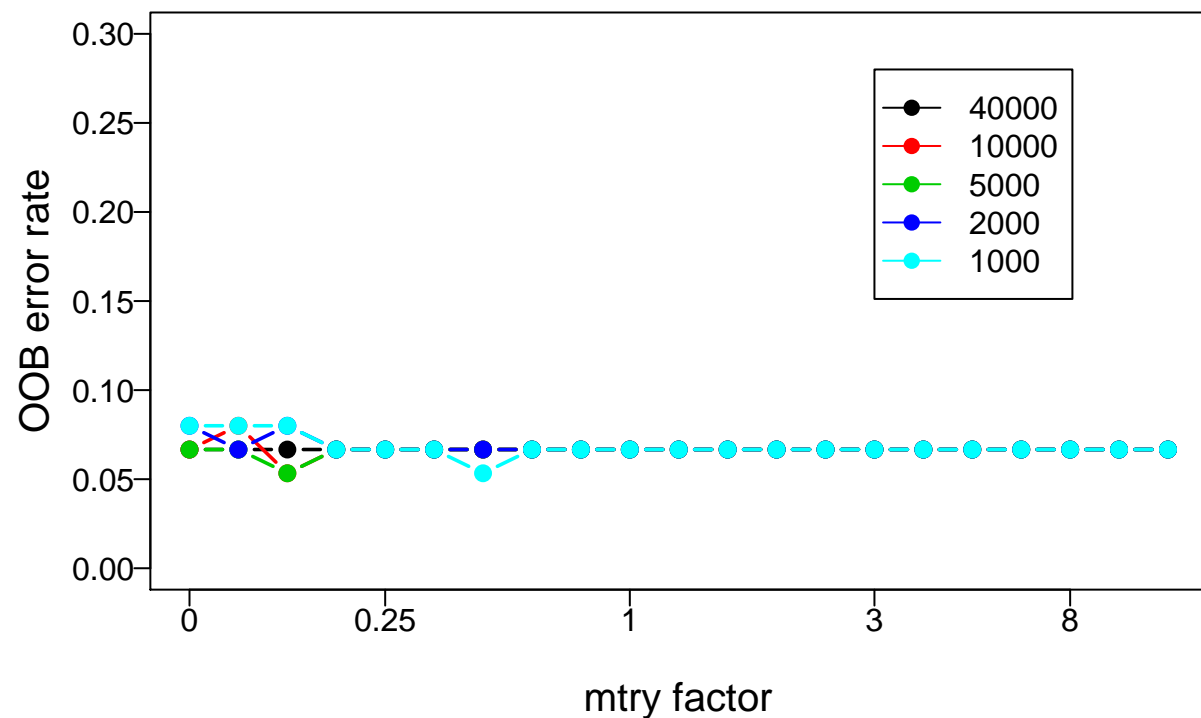
3 classes; 3 dimensions; 20 genes/dimen.; nodesize = 1



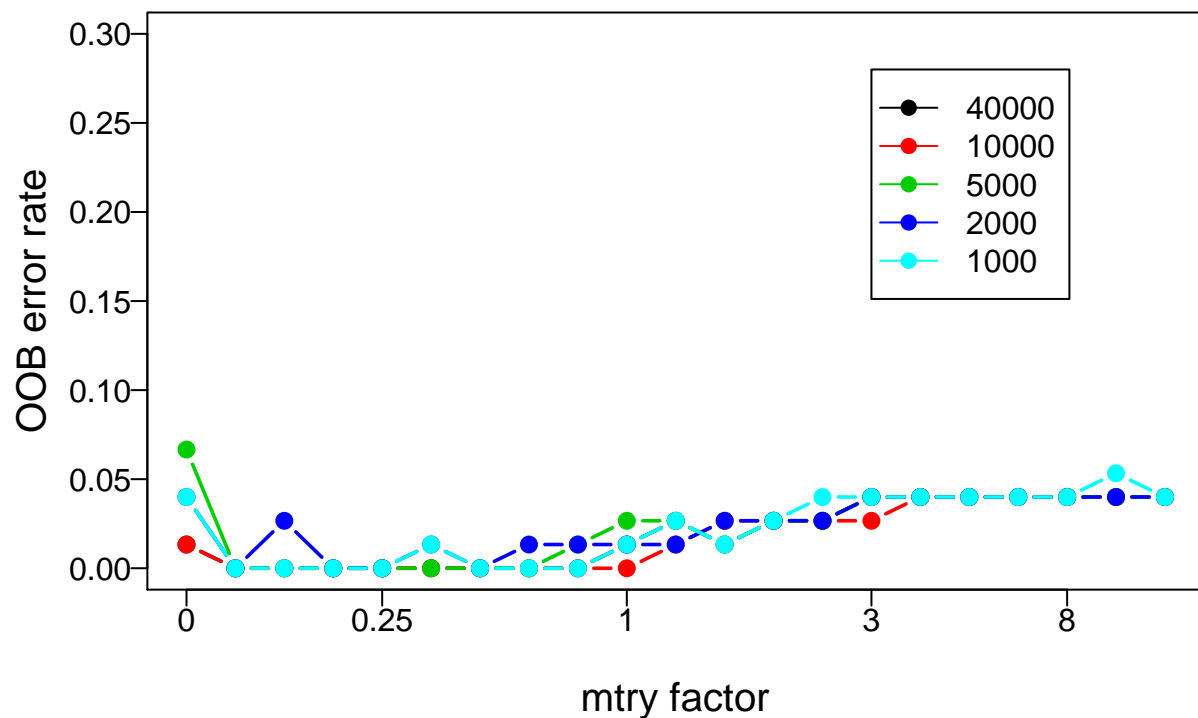
3 classes; 3 dimensions; 100 genes/dimen.; nodesize = 1



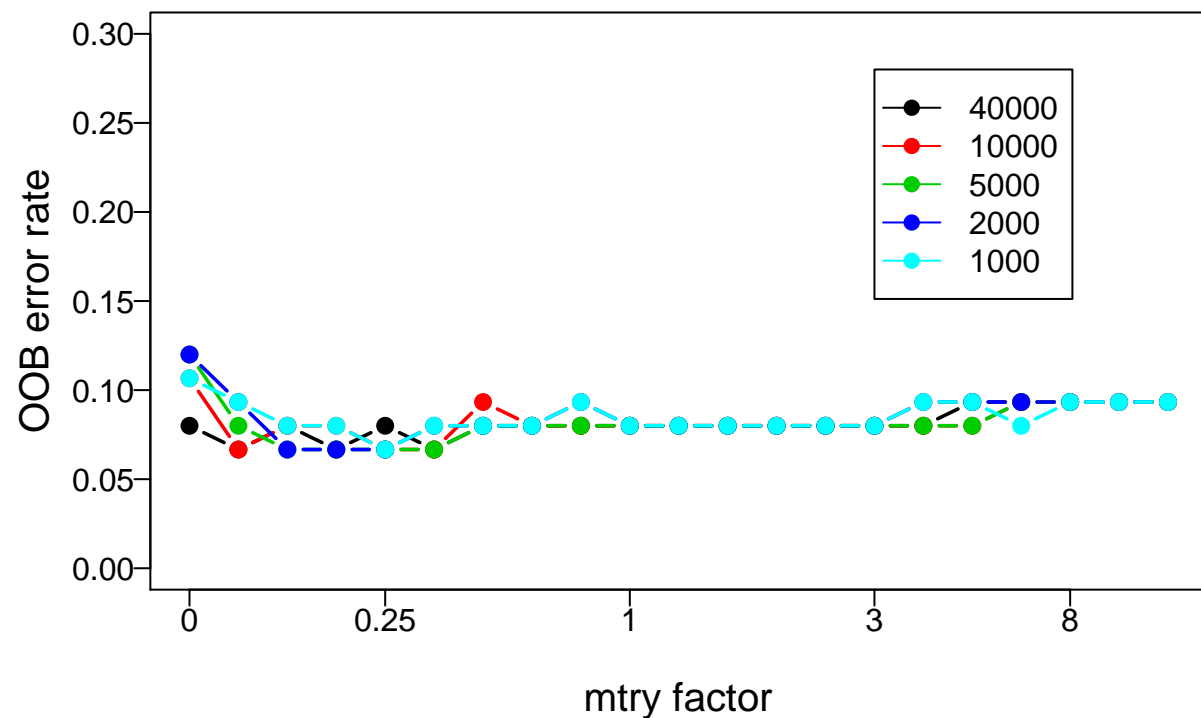
3 classes; 3 dimensions; 100 genes/dimen.; nodesize = 1



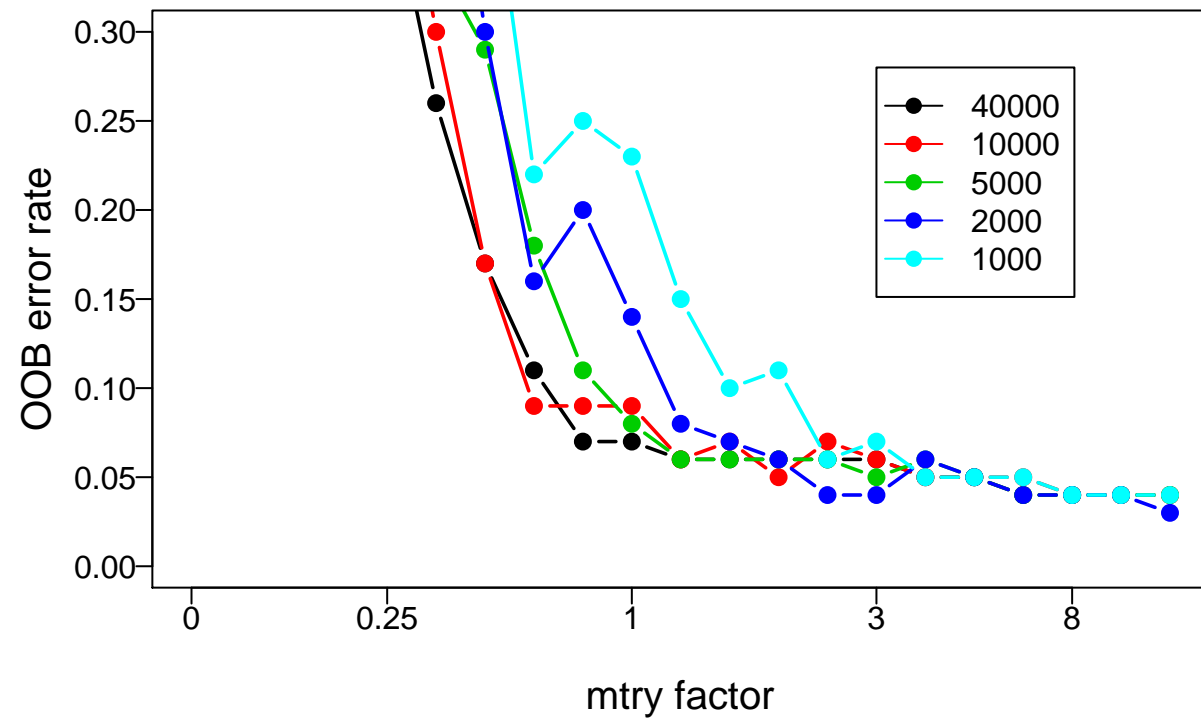
3 classes; 3 dimensions; 100 genes/dimen.; nodesize = 1



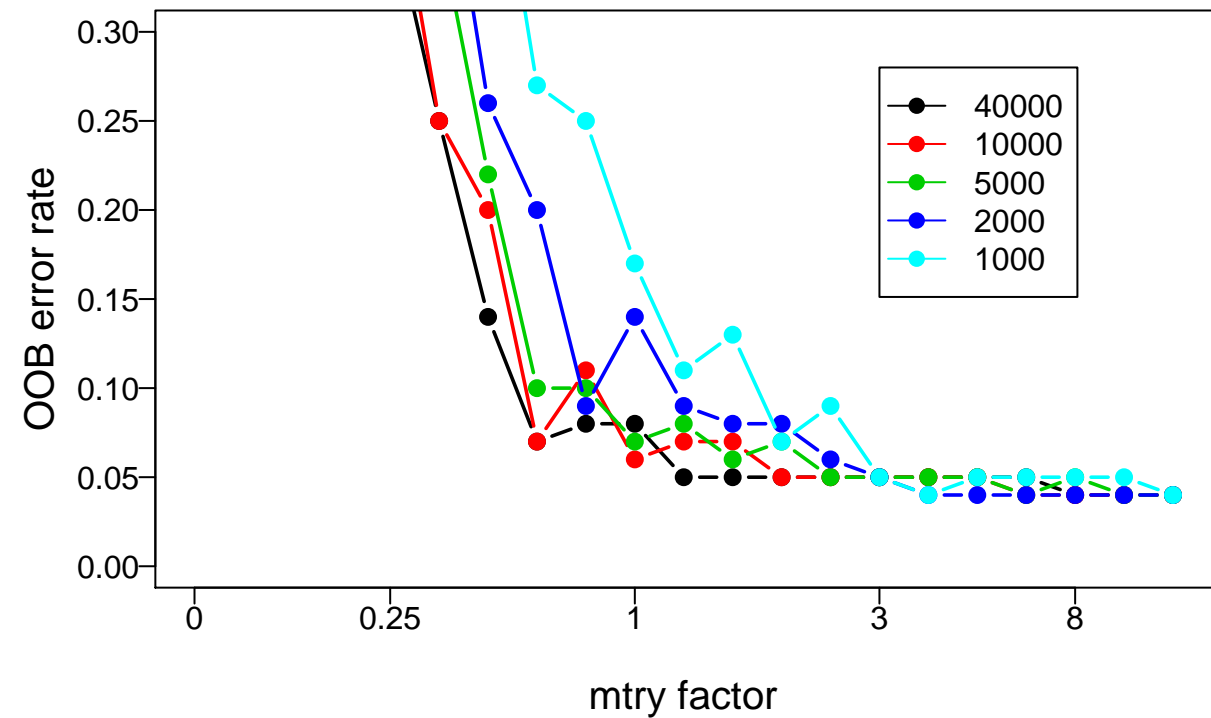
3 classes; 3 dimensions; 100 genes/dimen.; nodesize = 1



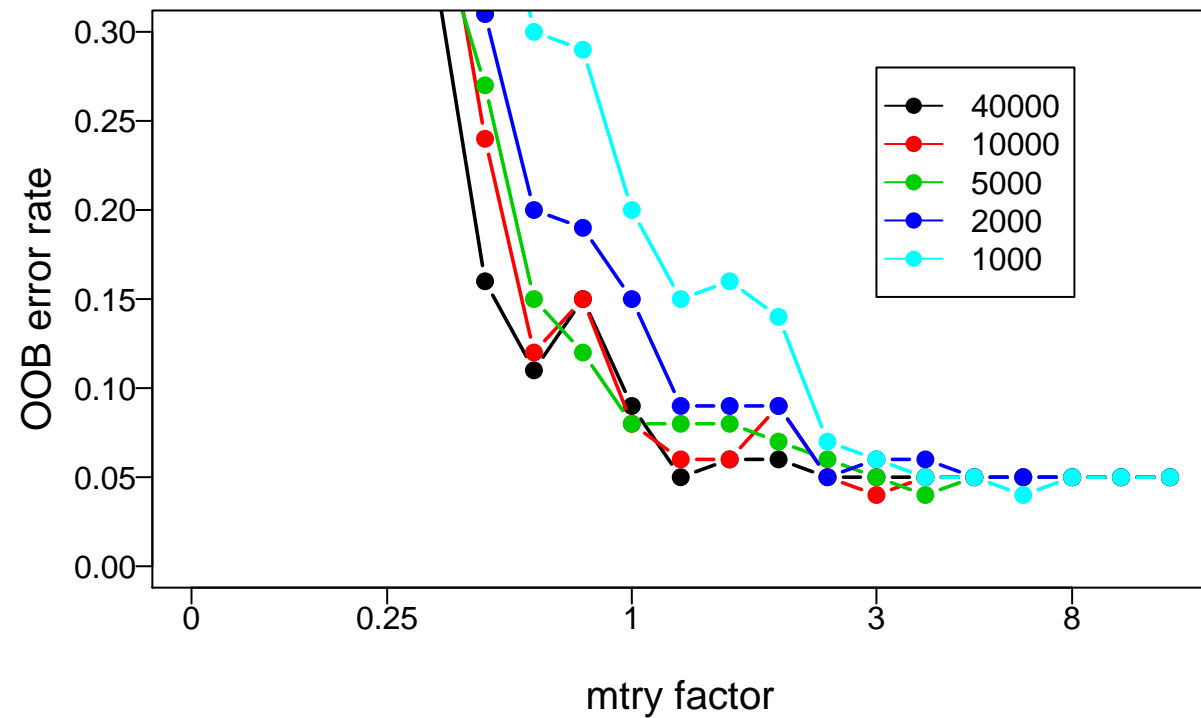
4 classes; 1 dimensions; 5 genes/dimen.; nodesize = 1



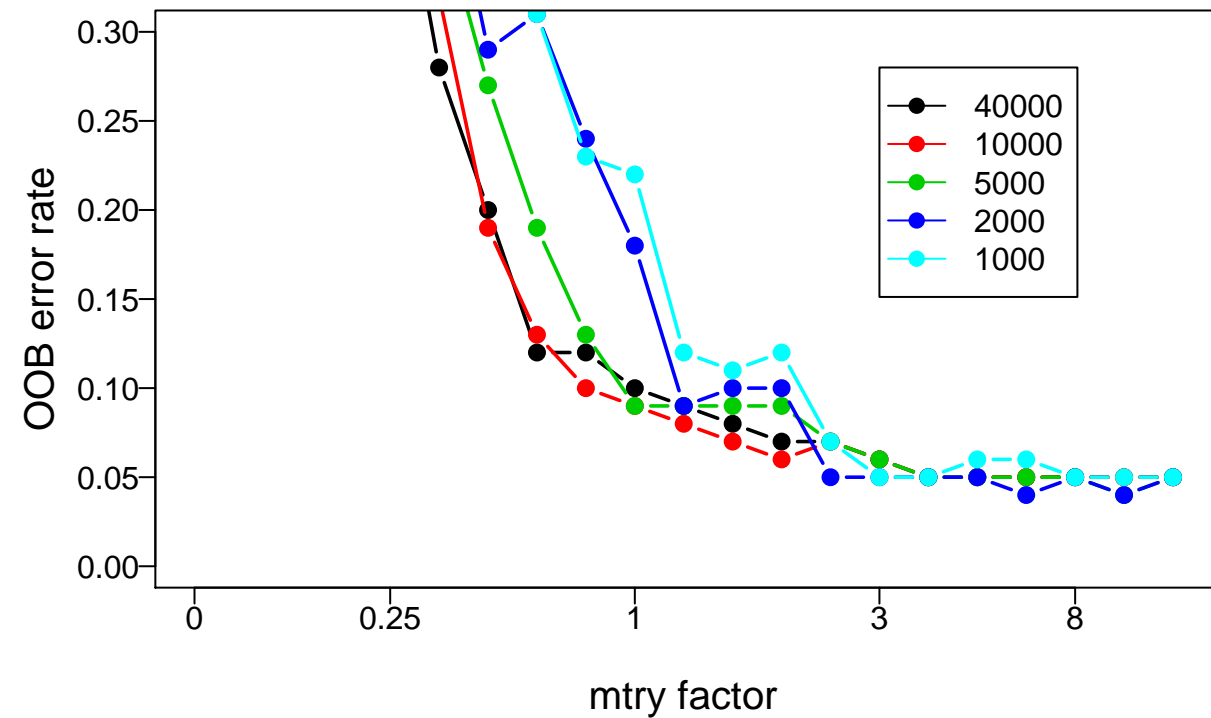
4 classes; 1 dimensions; 5 genes/dimen.; nodesize = 1



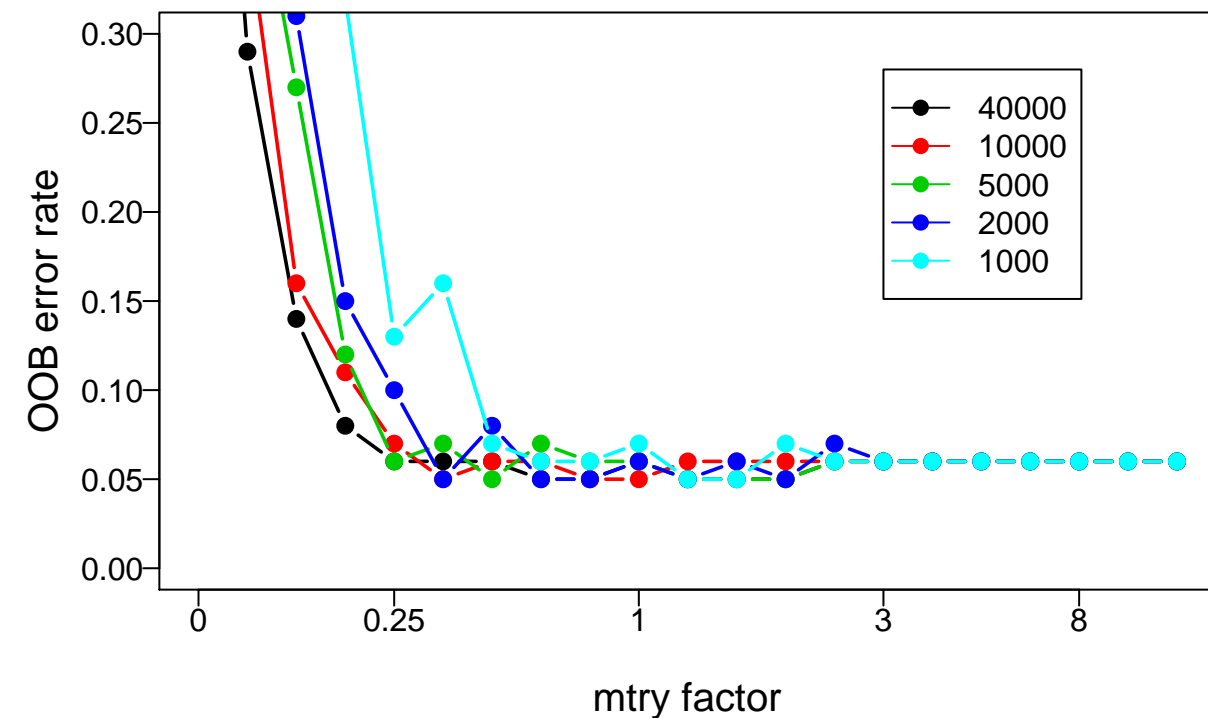
4 classes; 1 dimensions; 5 genes/dimen.; nodesize = 1



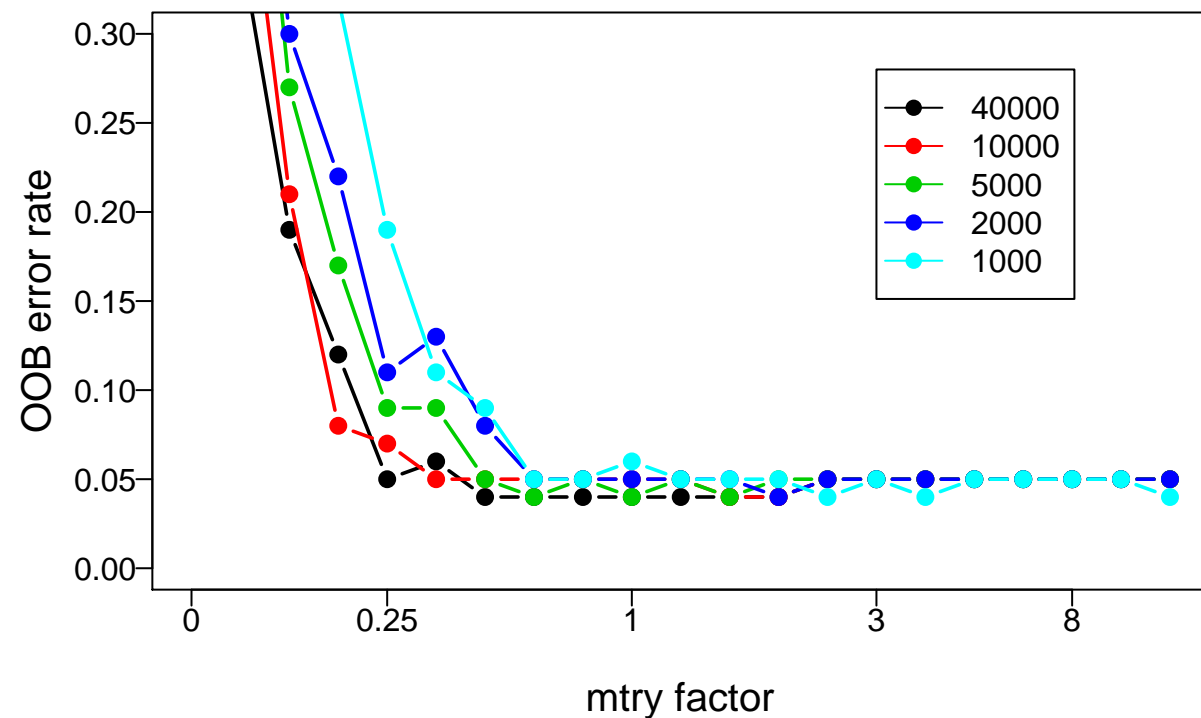
4 classes; 1 dimensions; 5 genes/dimen.; nodesize = 1



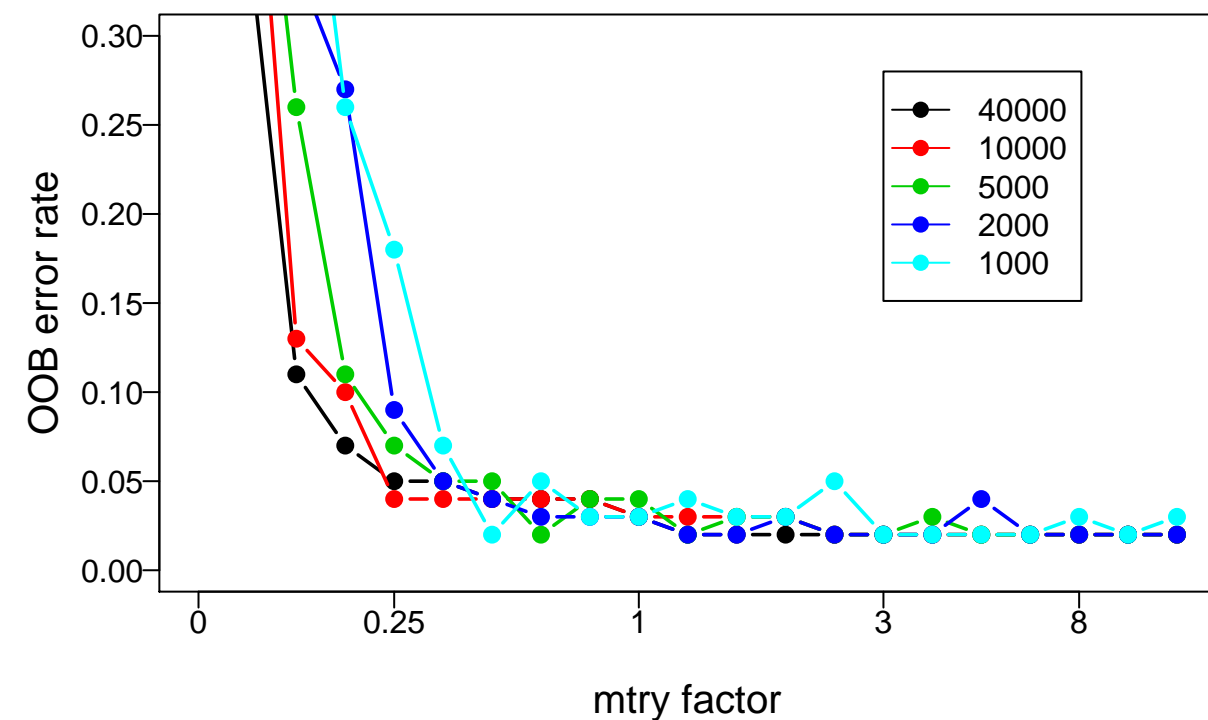
4 classes; 1 dimensions; 20 genes/dimen.; nodesize = 1



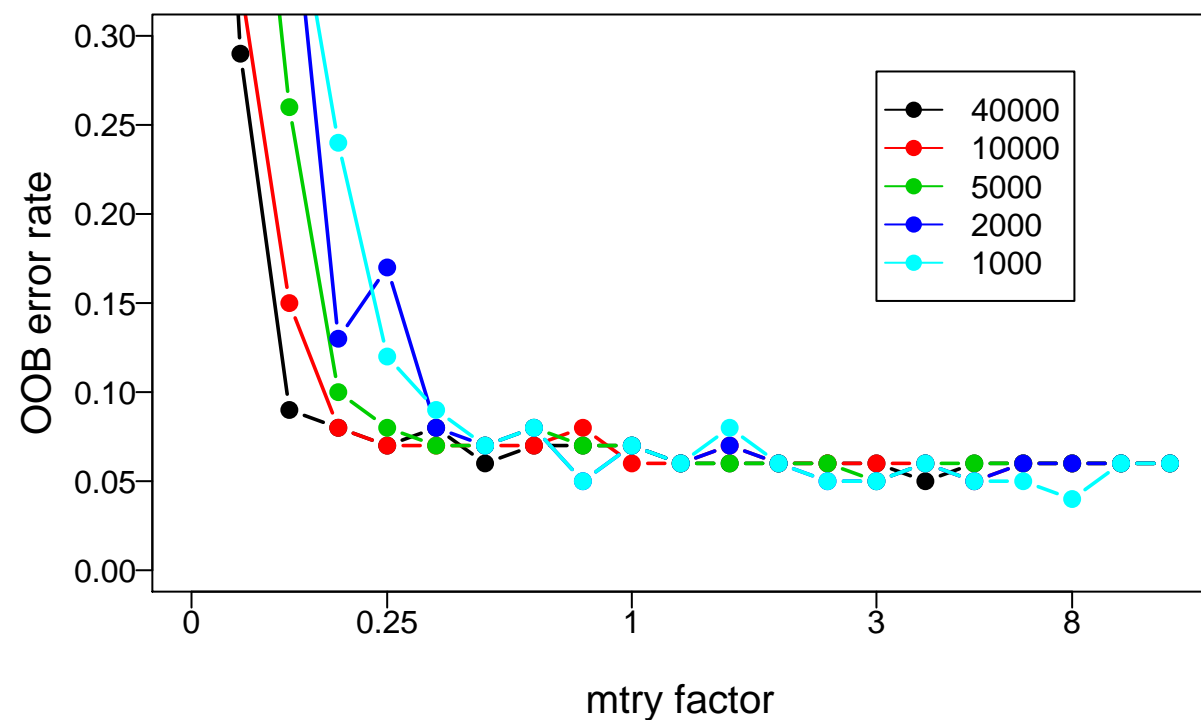
4 classes; 1 dimensions; 20 genes/dimen.; nodesize = 1



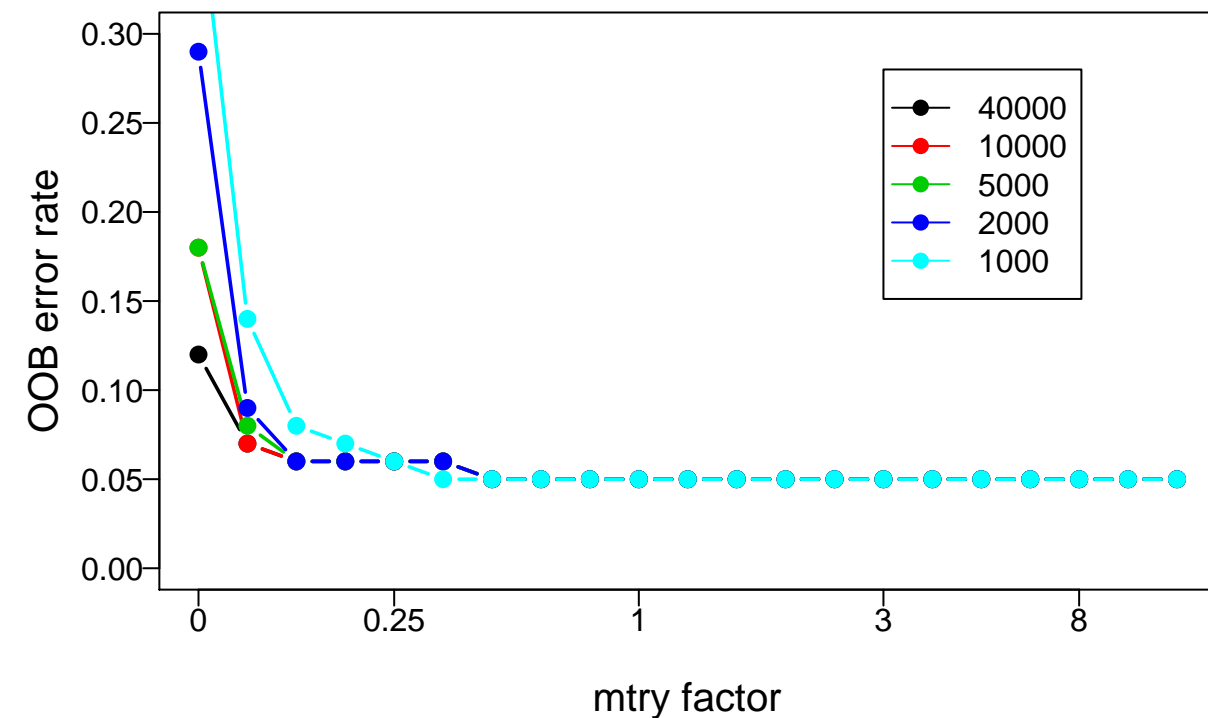
4 classes; 1 dimensions; 20 genes/dimen.; nodesize = 1



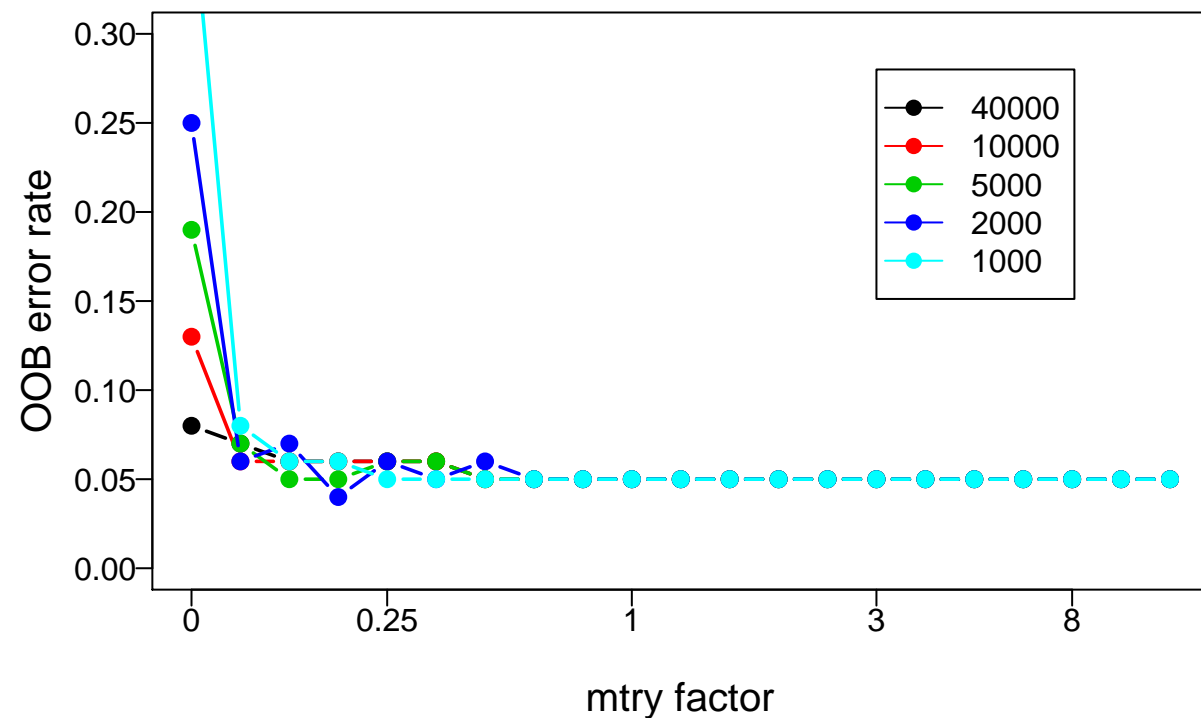
4 classes; 1 dimensions; 20 genes/dimen.; nodesize = 1



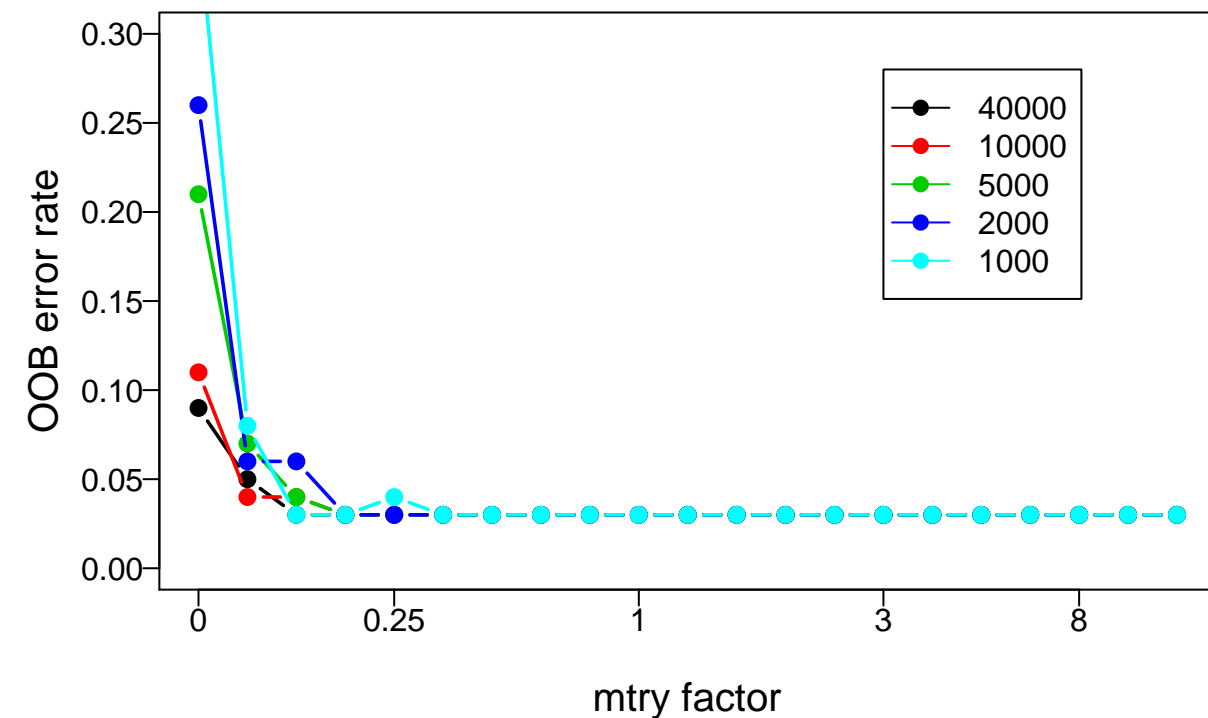
4 classes; 1 dimensions; 100 genes/dimen.; nodesize = 1



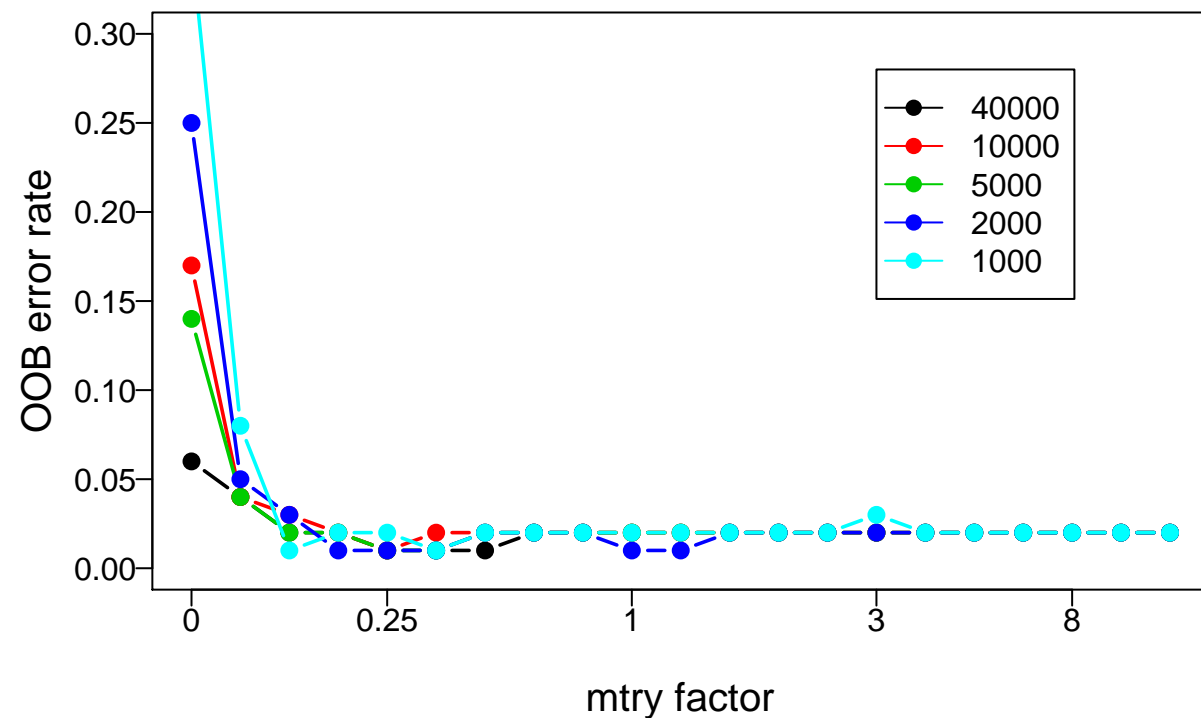
4 classes; 1 dimensions; 100 genes/dimen.; nodesize = 1



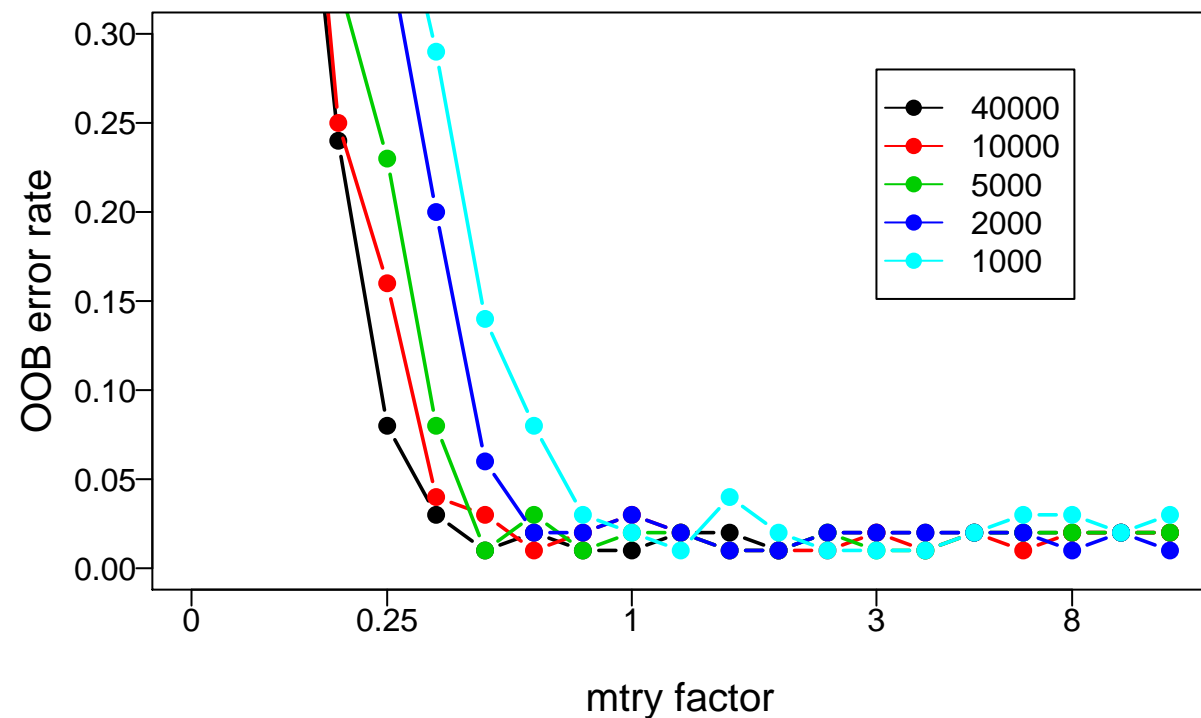
4 classes; 1 dimensions; 100 genes/dimen.; nodesize = 1



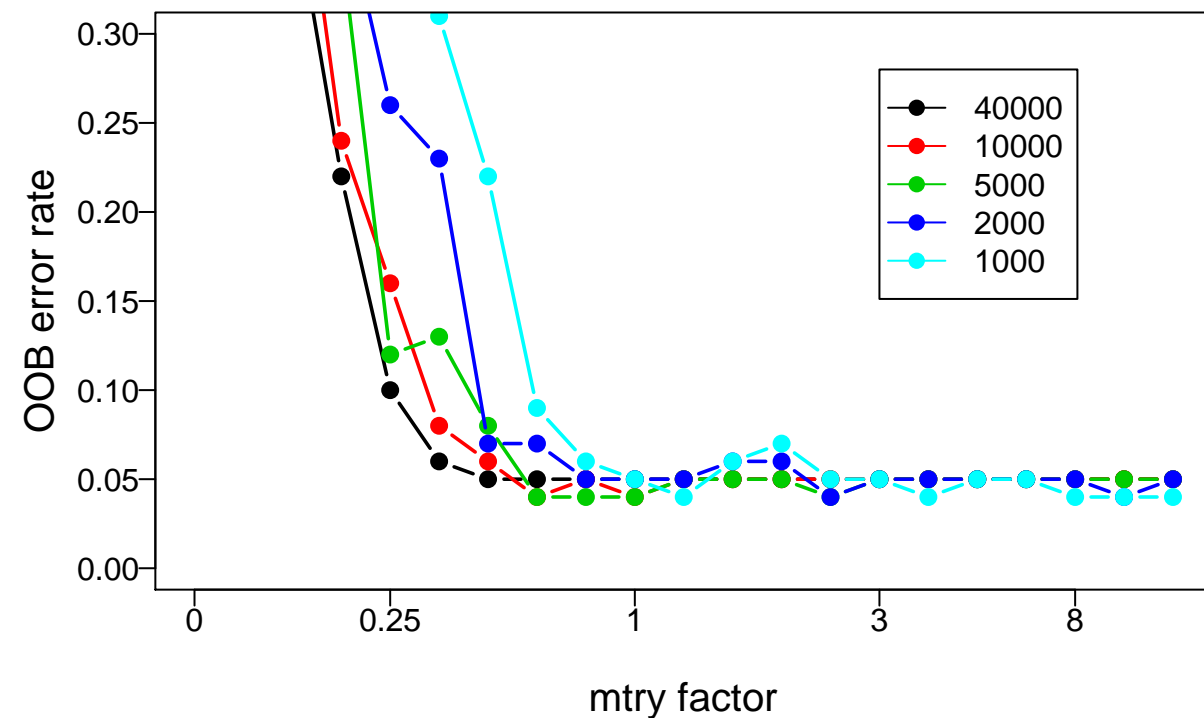
4 classes; 1 dimensions; 100 genes/dimen.; nodesize = 1



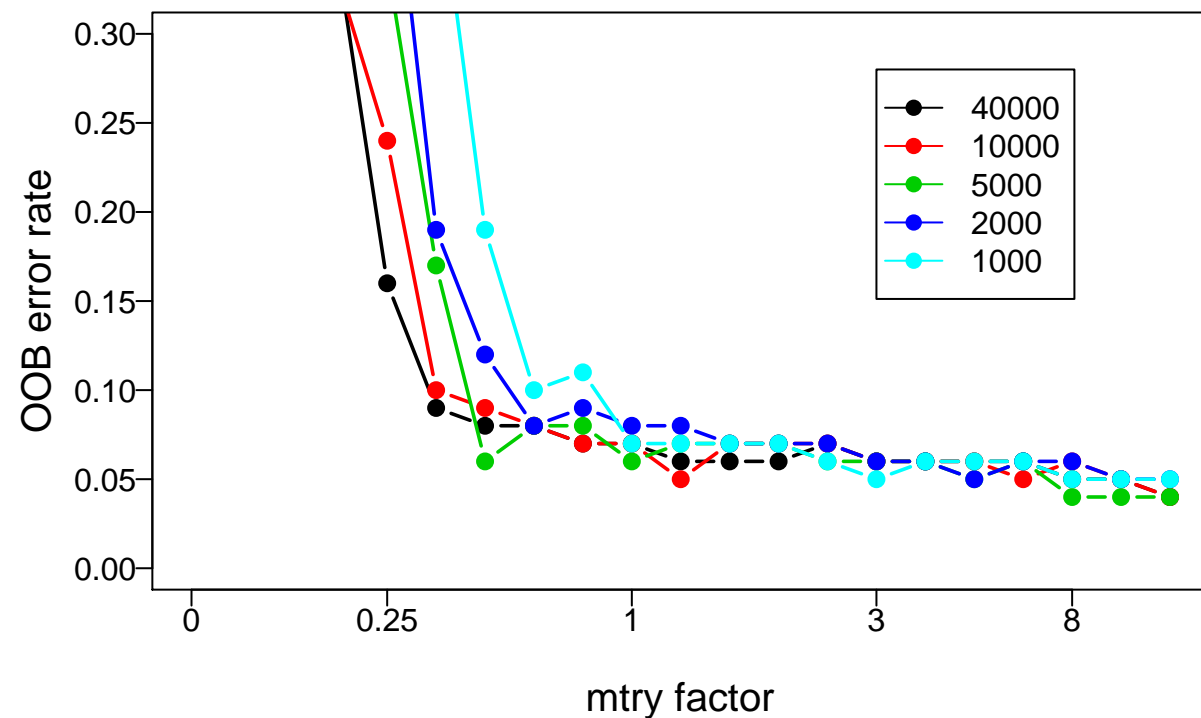
4 classes; 2 dimensions; 5 genes/dimen.; nodesize = 1



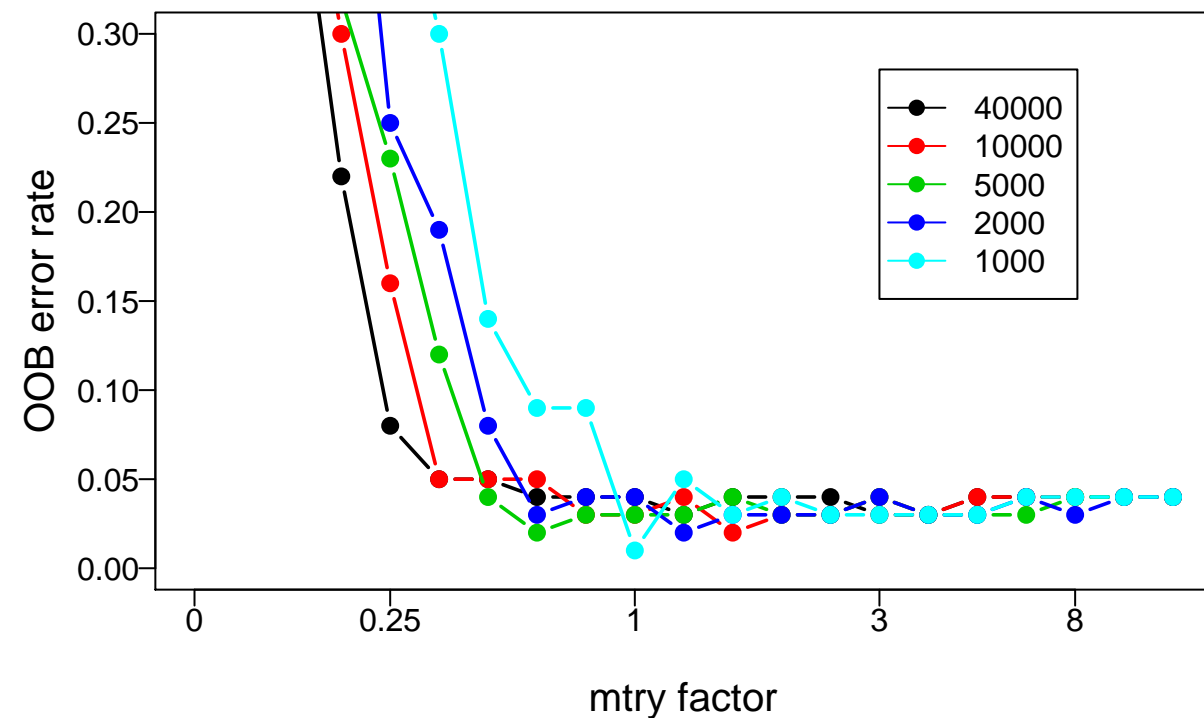
4 classes; 2 dimensions; 5 genes/dimen.; nodesize = 1



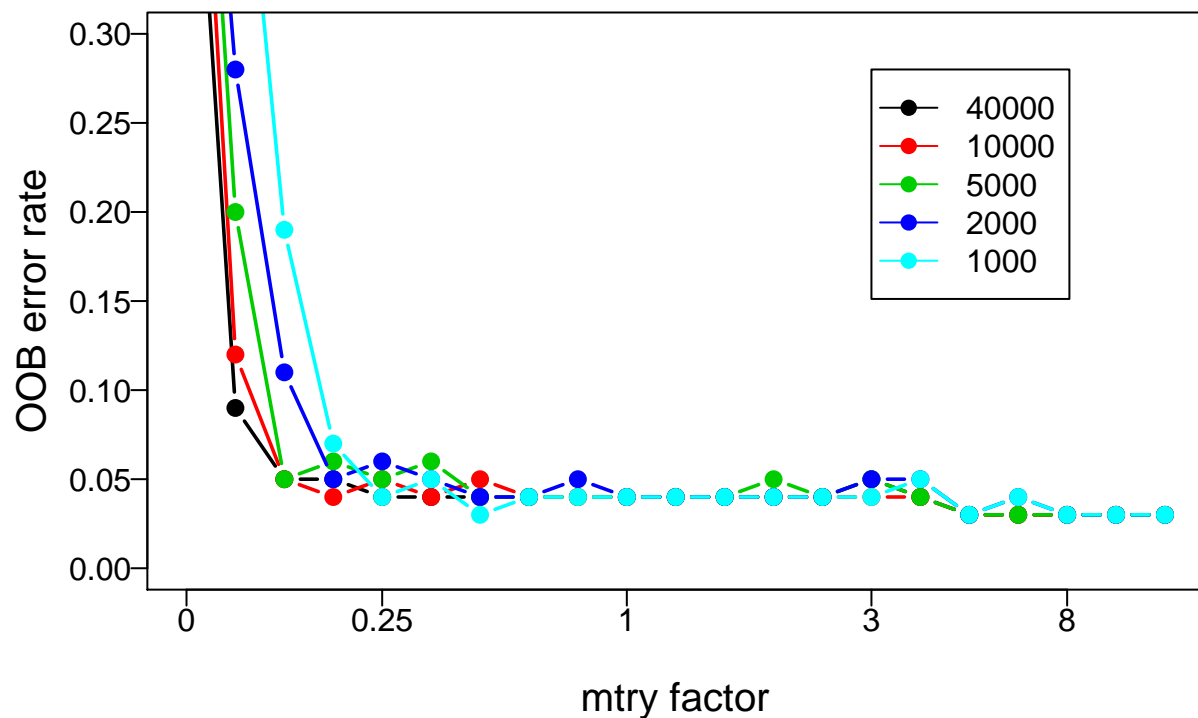
4 classes; 2 dimensions; 5 genes/dimen.; nodesize = 1



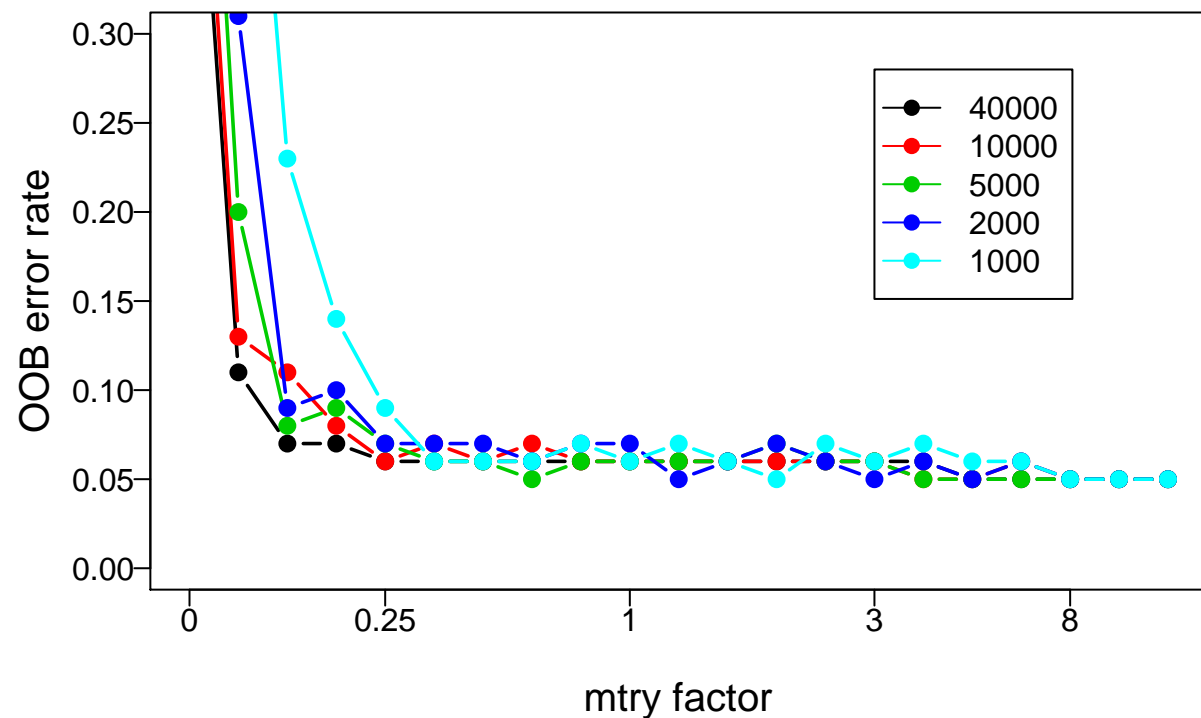
4 classes; 2 dimensions; 5 genes/dimen.; nodesize = 1



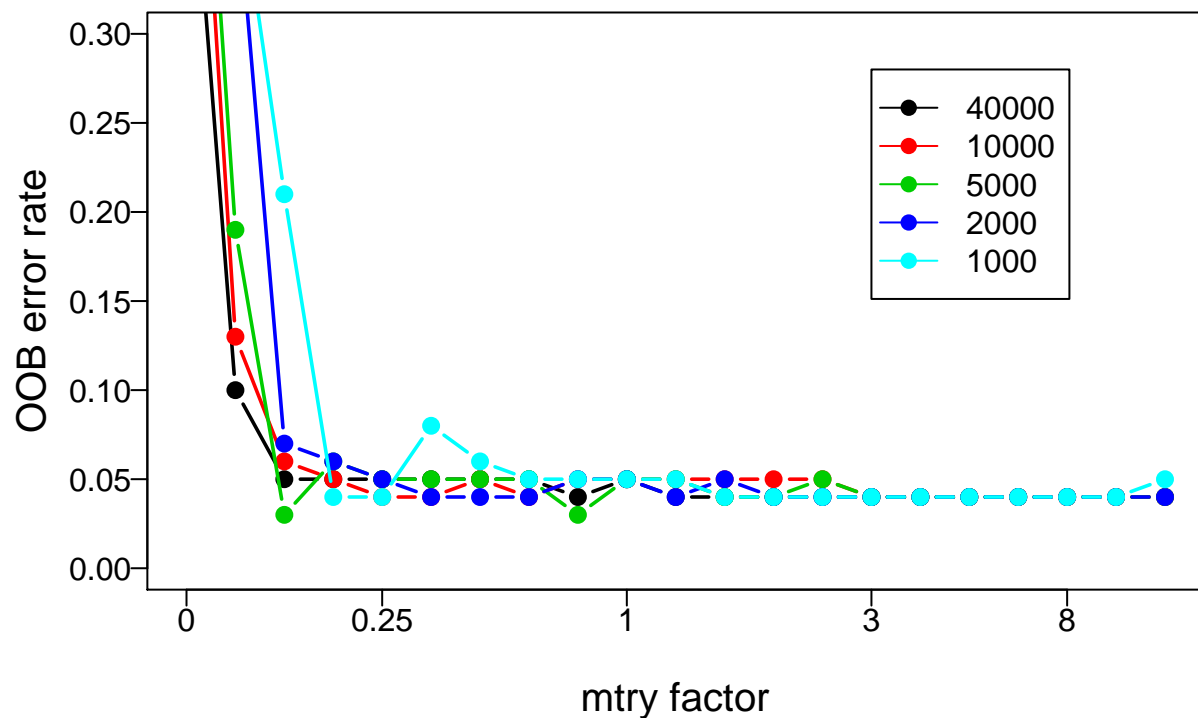
4 classes; 2 dimensions; 20 genes/dimen.; nodesize = 1



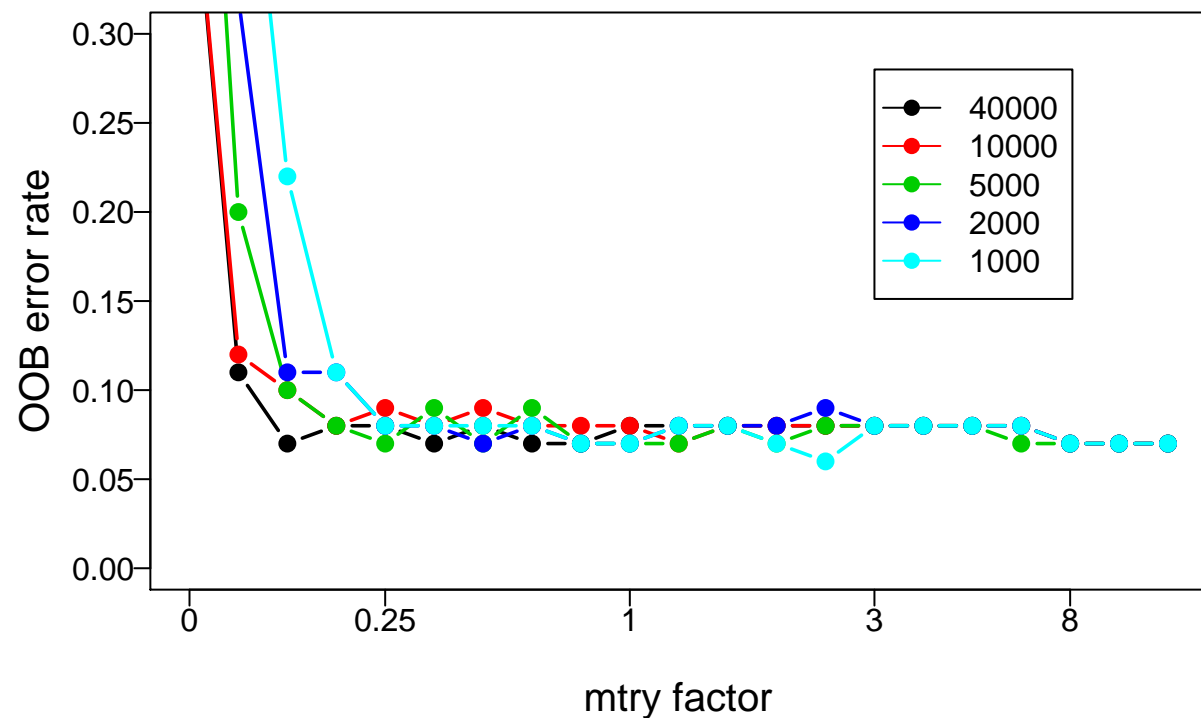
4 classes; 2 dimensions; 20 genes/dimen.; nodesize = 1



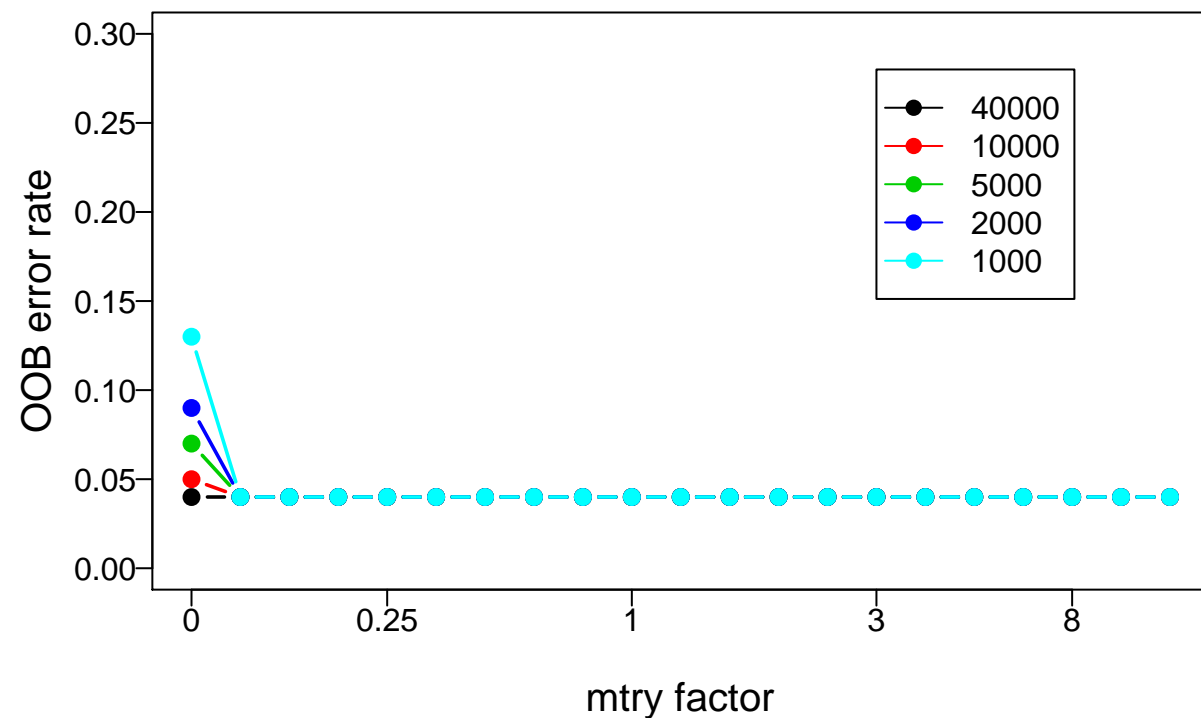
4 classes; 2 dimensions; 20 genes/dimen.; nodesize = 1



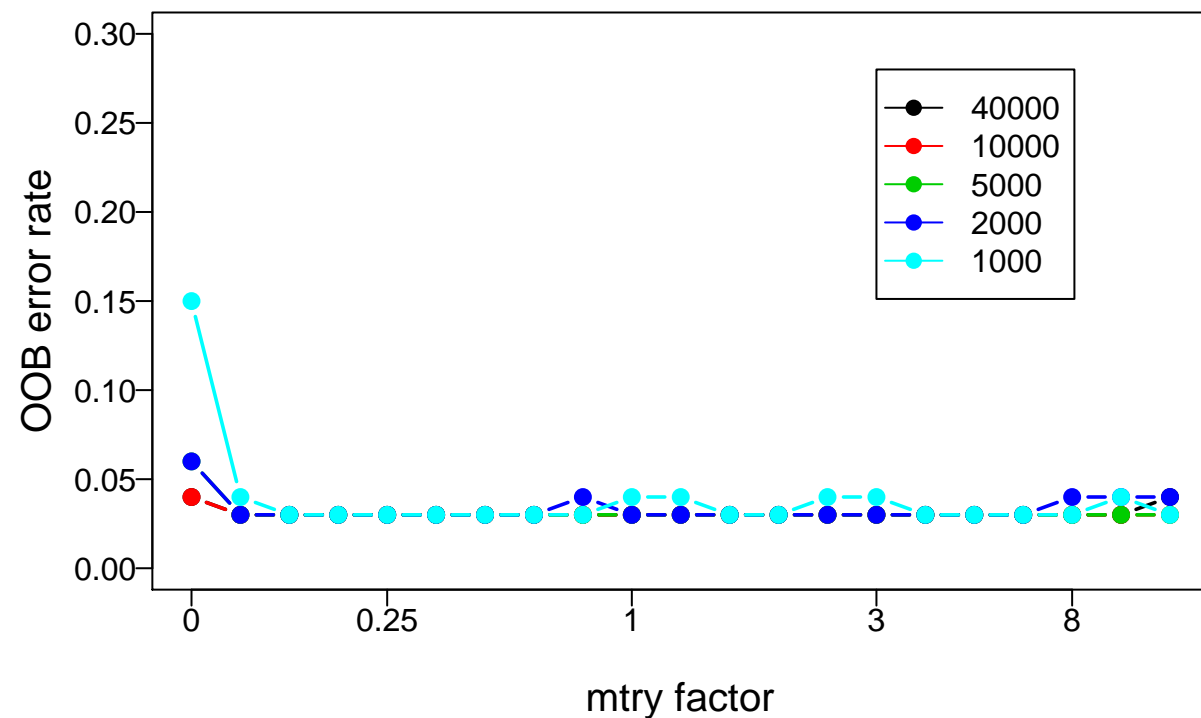
4 classes; 2 dimensions; 20 genes/dimen.; nodesize = 1



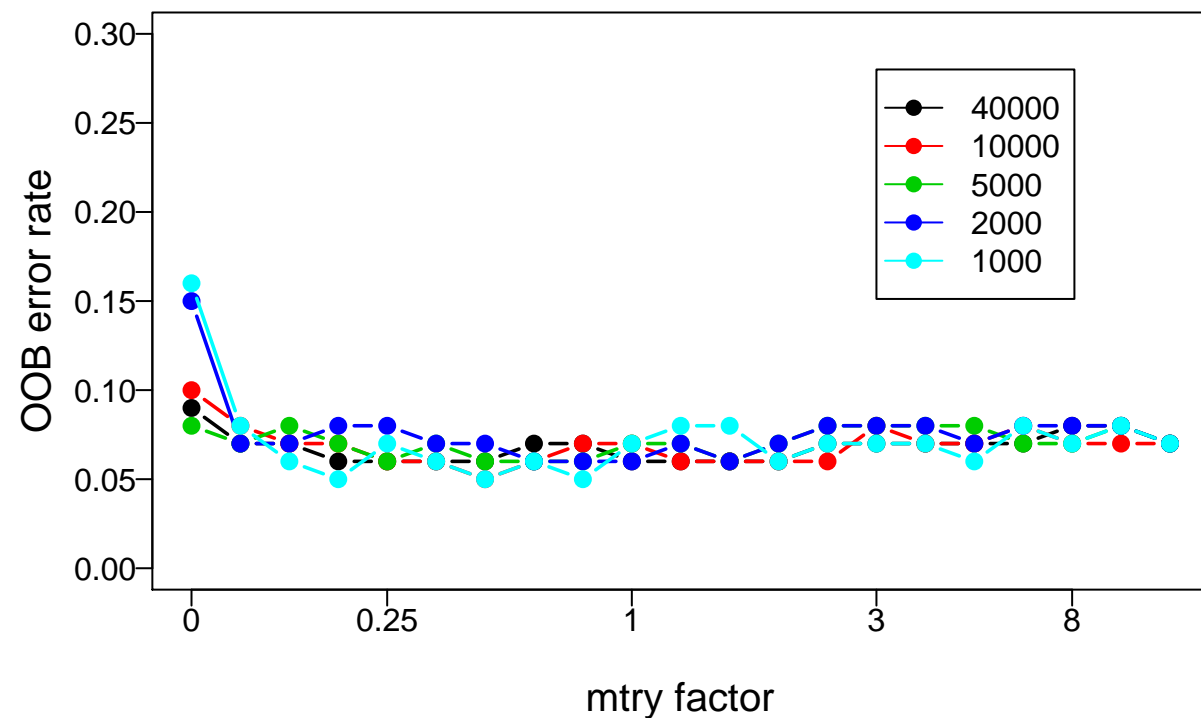
4 classes; 2 dimensions; 100 genes/dimen.; nodesize = 1



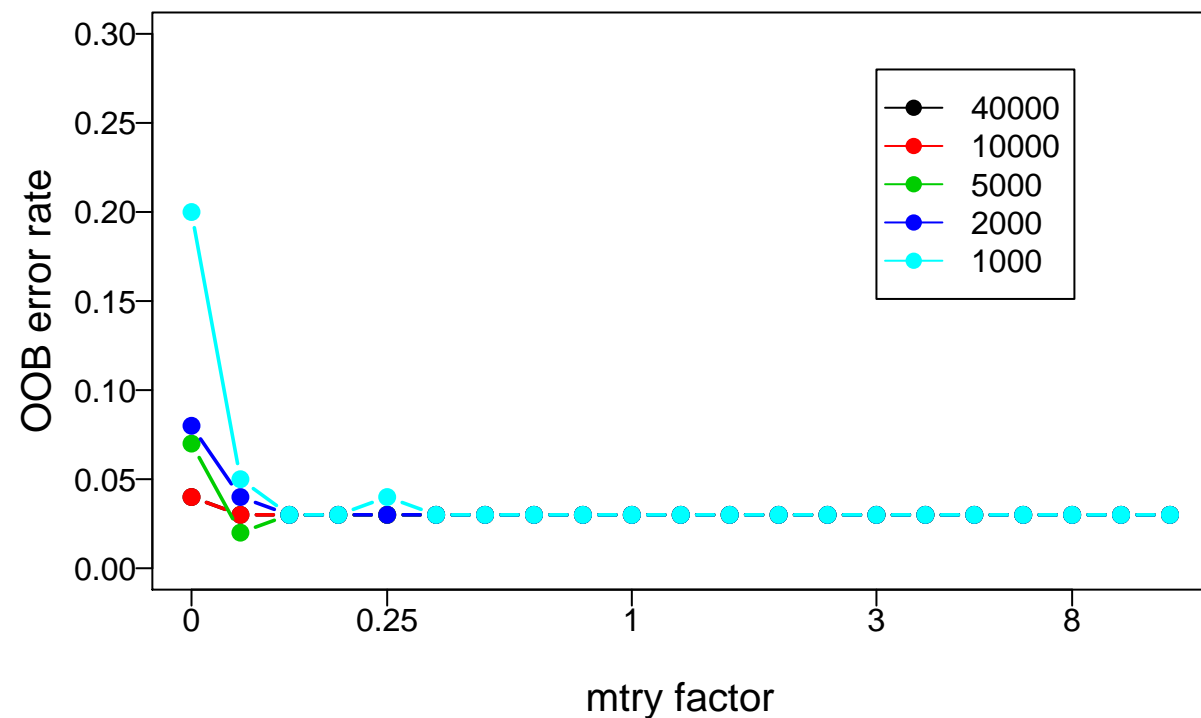
4 classes; 2 dimensions; 100 genes/dimen.; nodesize = 1



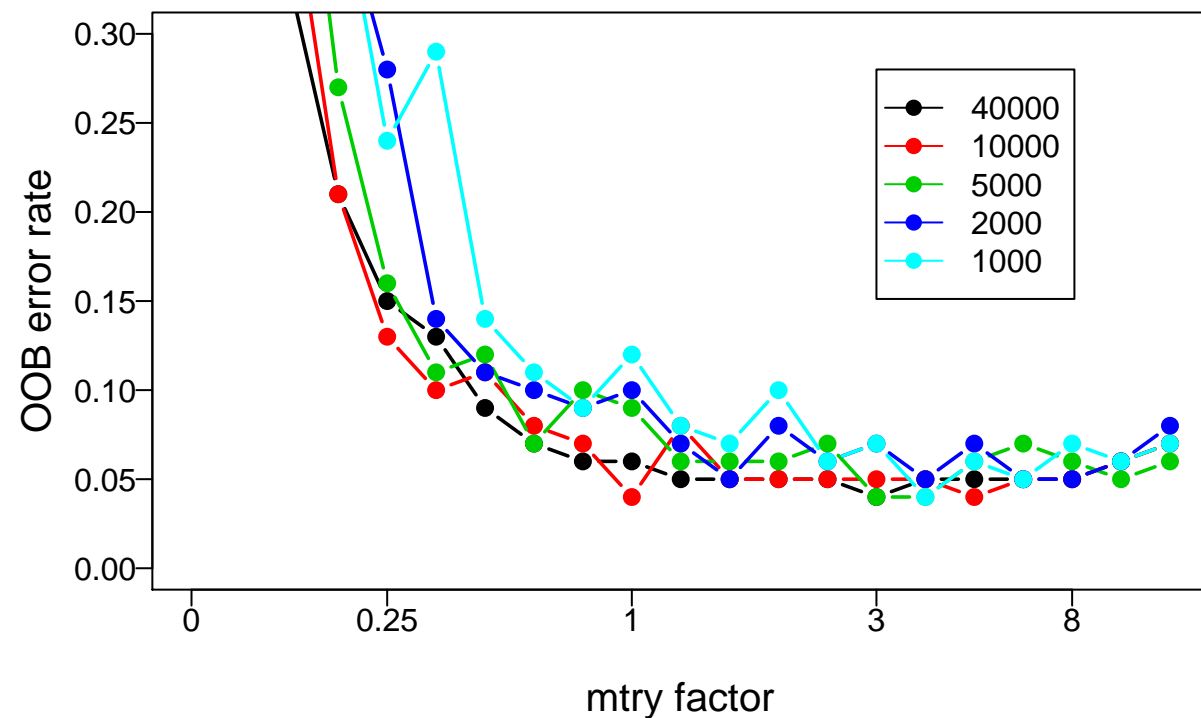
4 classes; 2 dimensions; 100 genes/dimen.; nodesize = 1



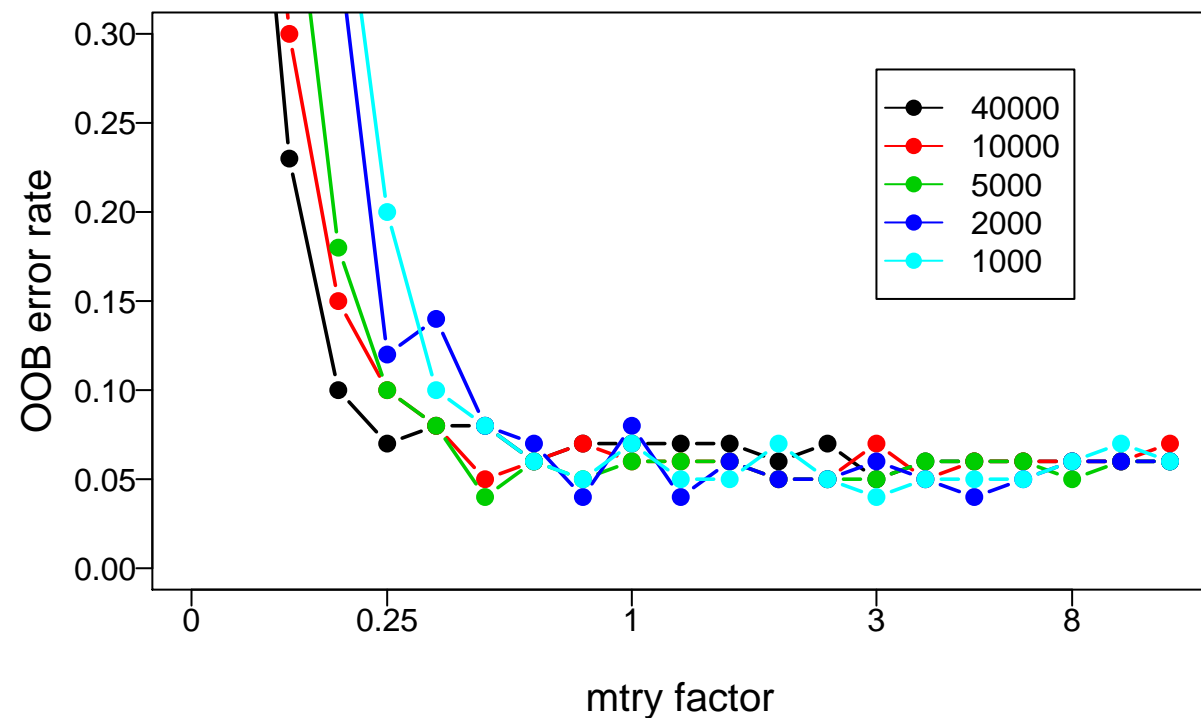
4 classes; 2 dimensions; 100 genes/dimen.; nodesize = 1



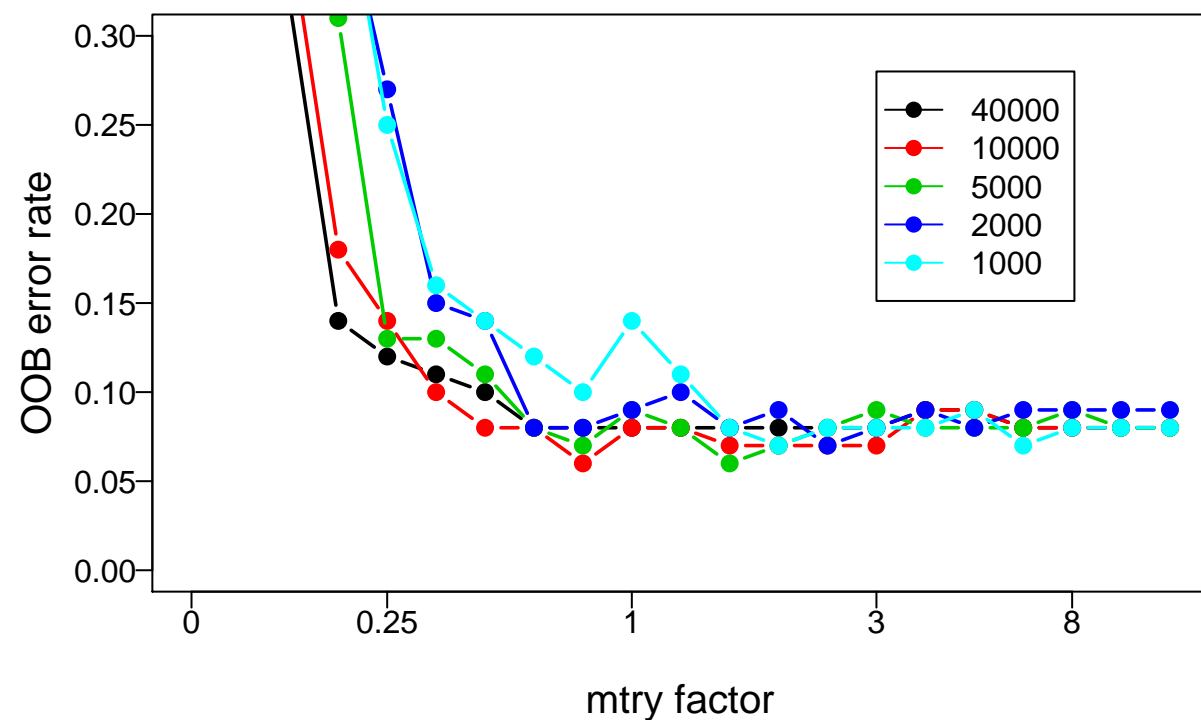
4 classes; 3 dimensions; 5 genes/dimen.; nodesize = 1



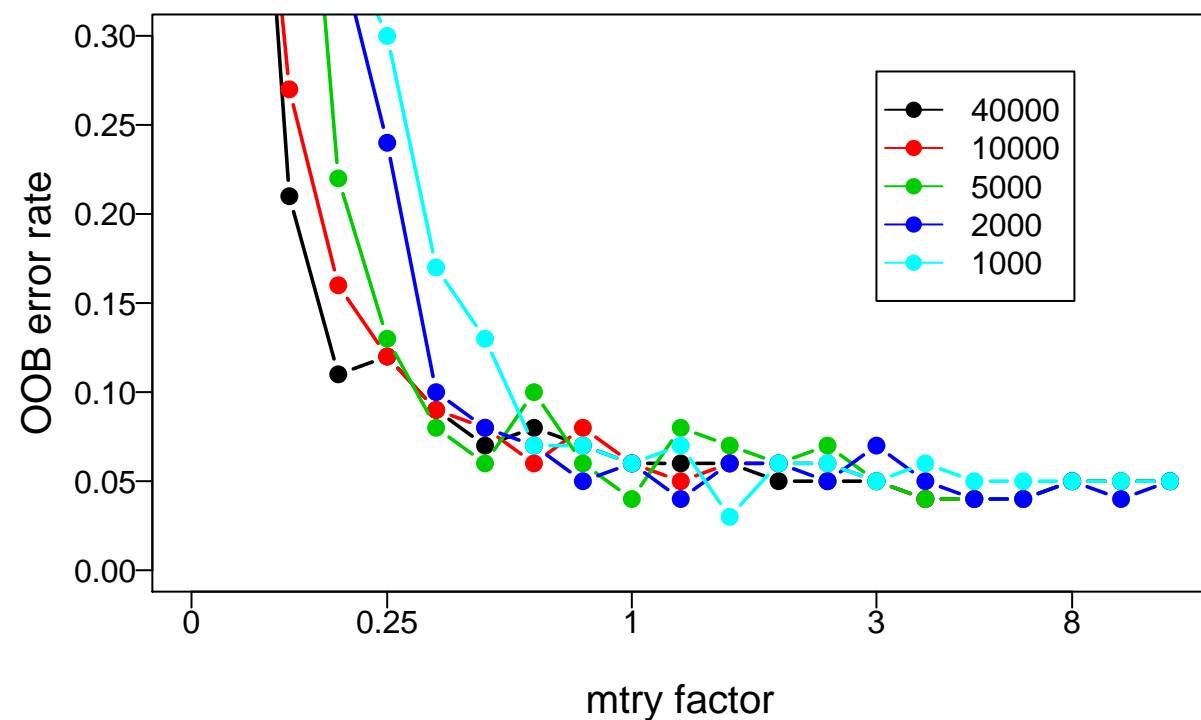
4 classes; 3 dimensions; 5 genes/dimen.; nodesize = 1



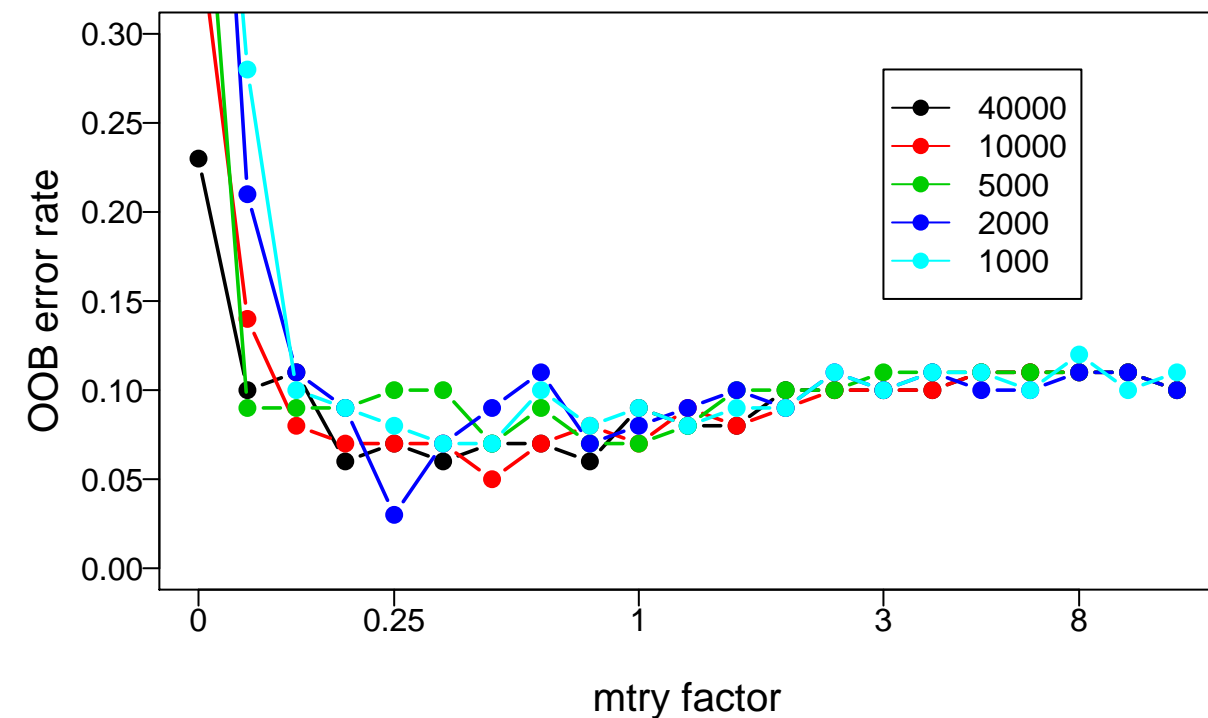
4 classes; 3 dimensions; 5 genes/dimen.; nodesize = 1



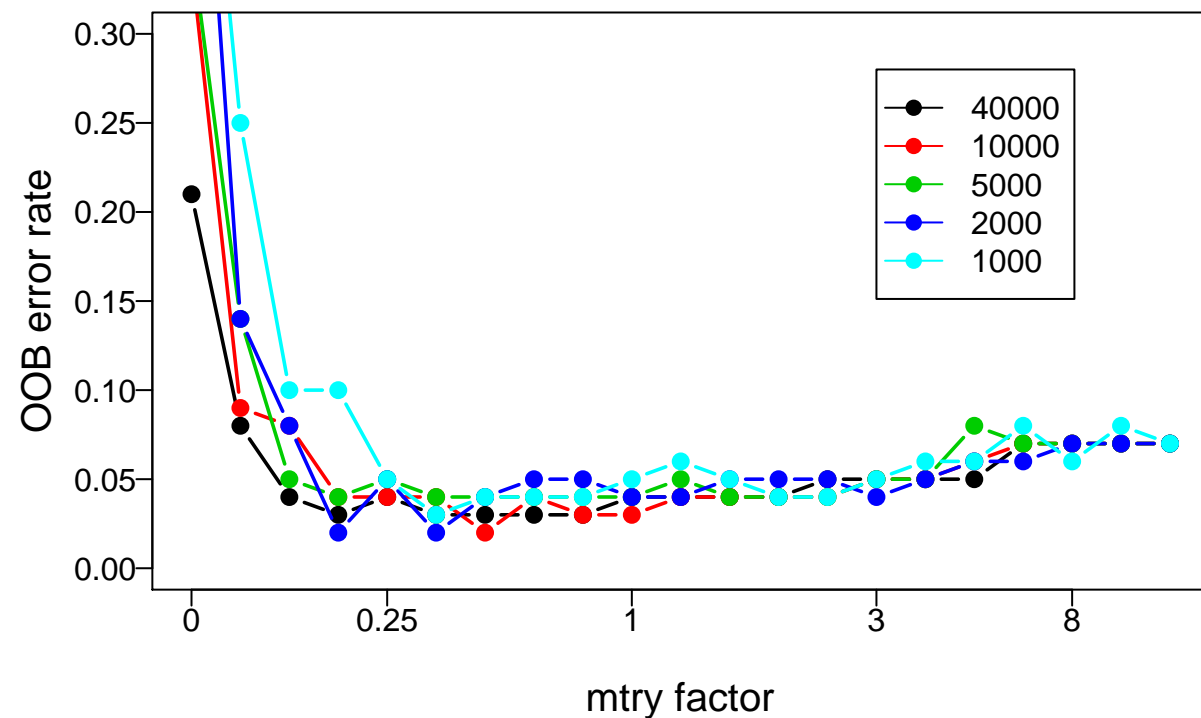
4 classes; 3 dimensions; 5 genes/dimen.; nodesize = 1



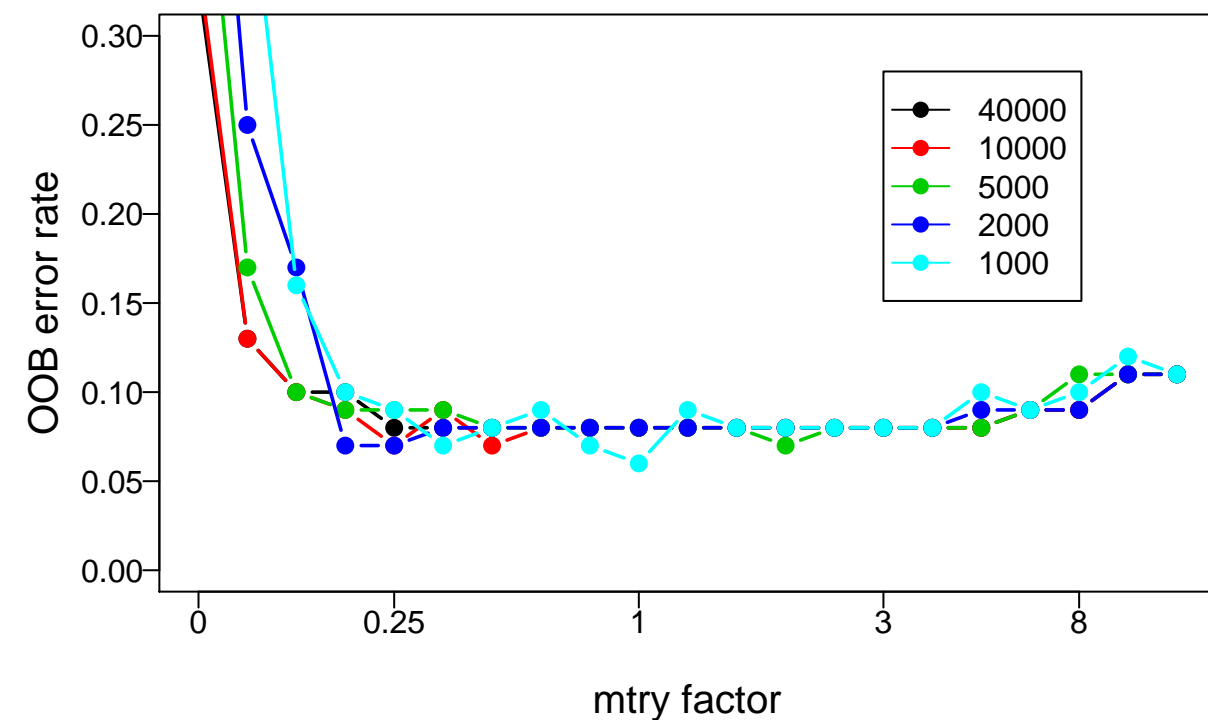
4 classes; 3 dimensions; 20 genes/dimen.; nodesize = 1



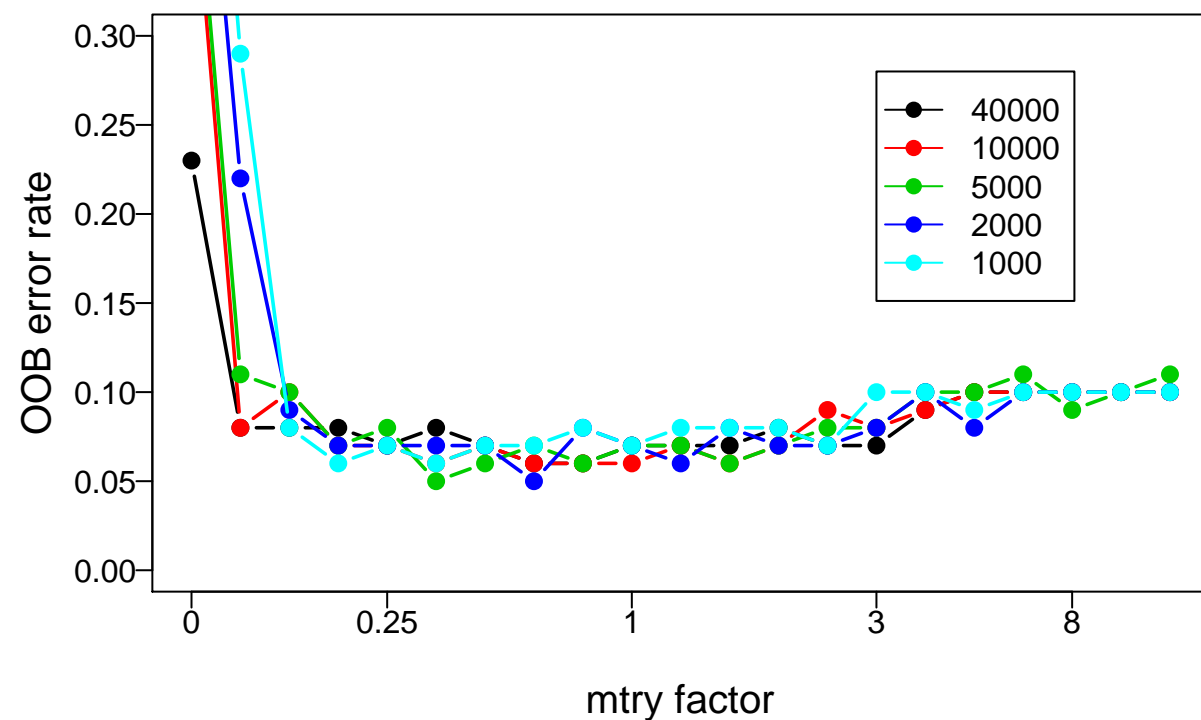
4 classes; 3 dimensions; 20 genes/dimen.; nodesize = 1



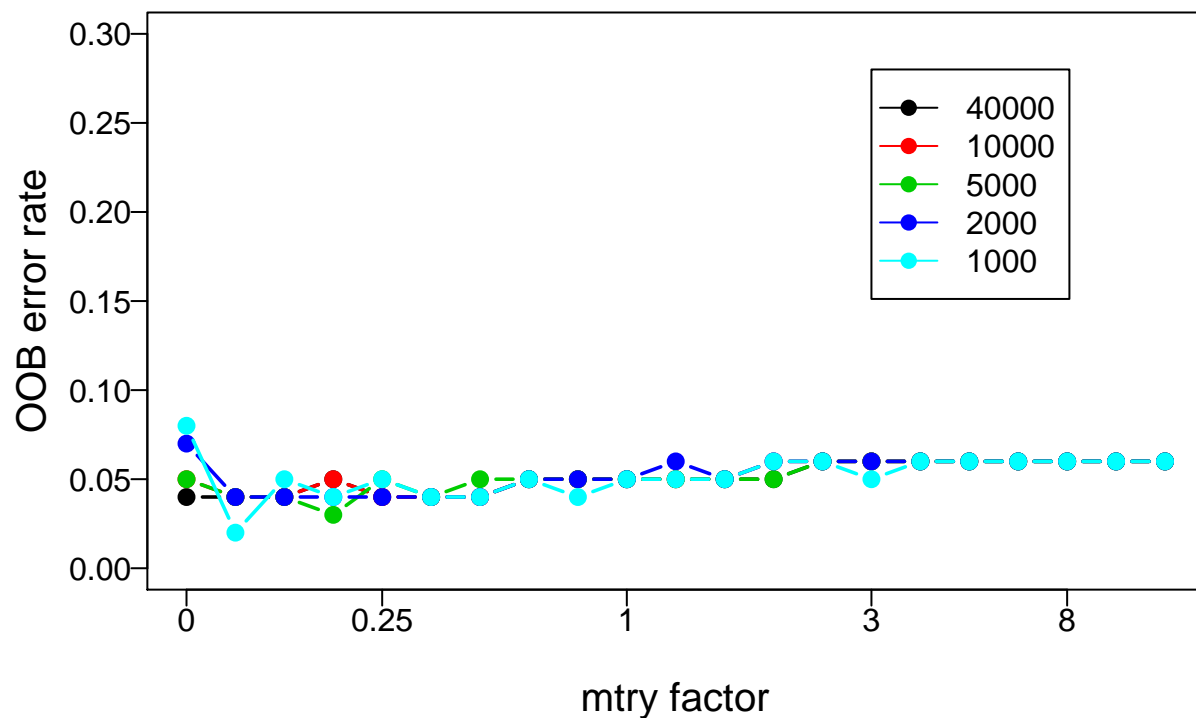
4 classes; 3 dimensions; 20 genes/dimen.; nodesize = 1



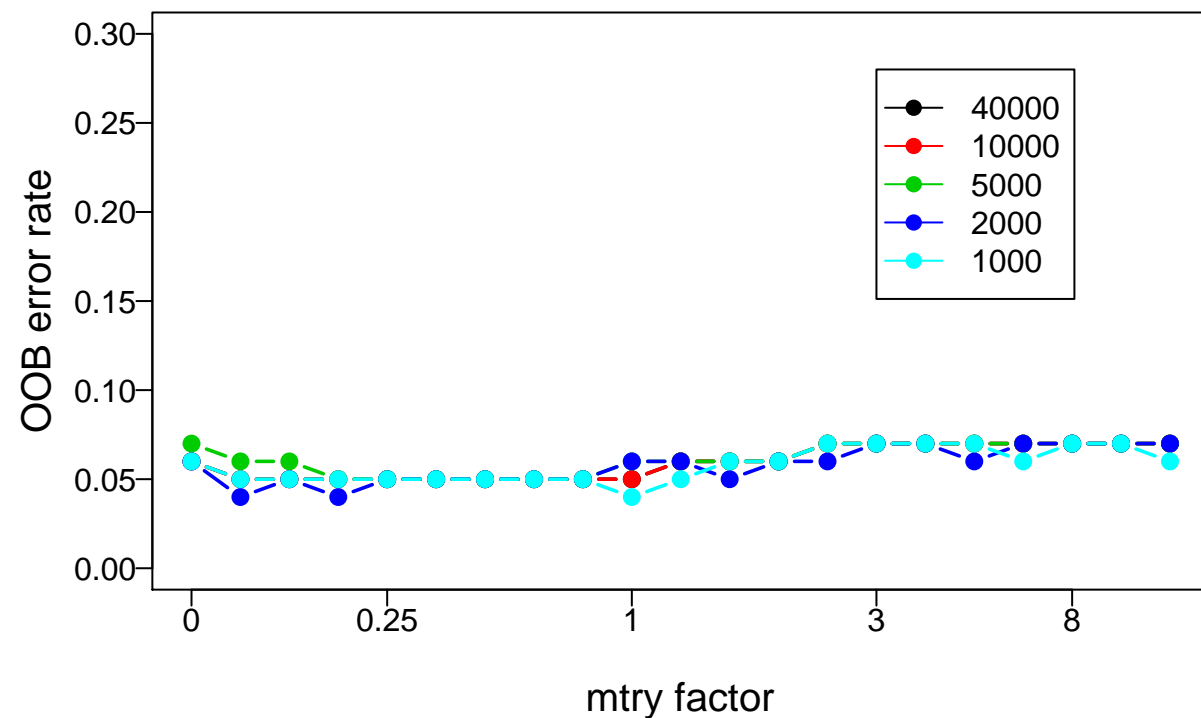
4 classes; 3 dimensions; 20 genes/dimen.; nodesize = 1



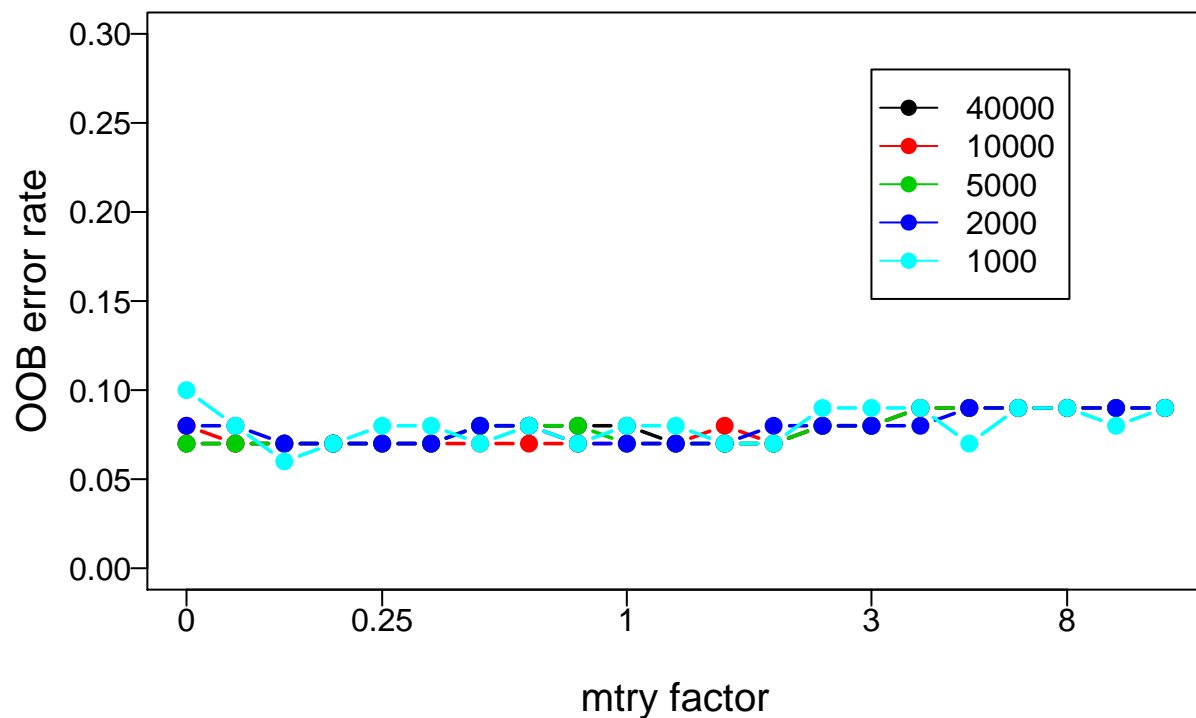
4 classes; 3 dimensions; 100 genes/dimen.; nodesize = 1



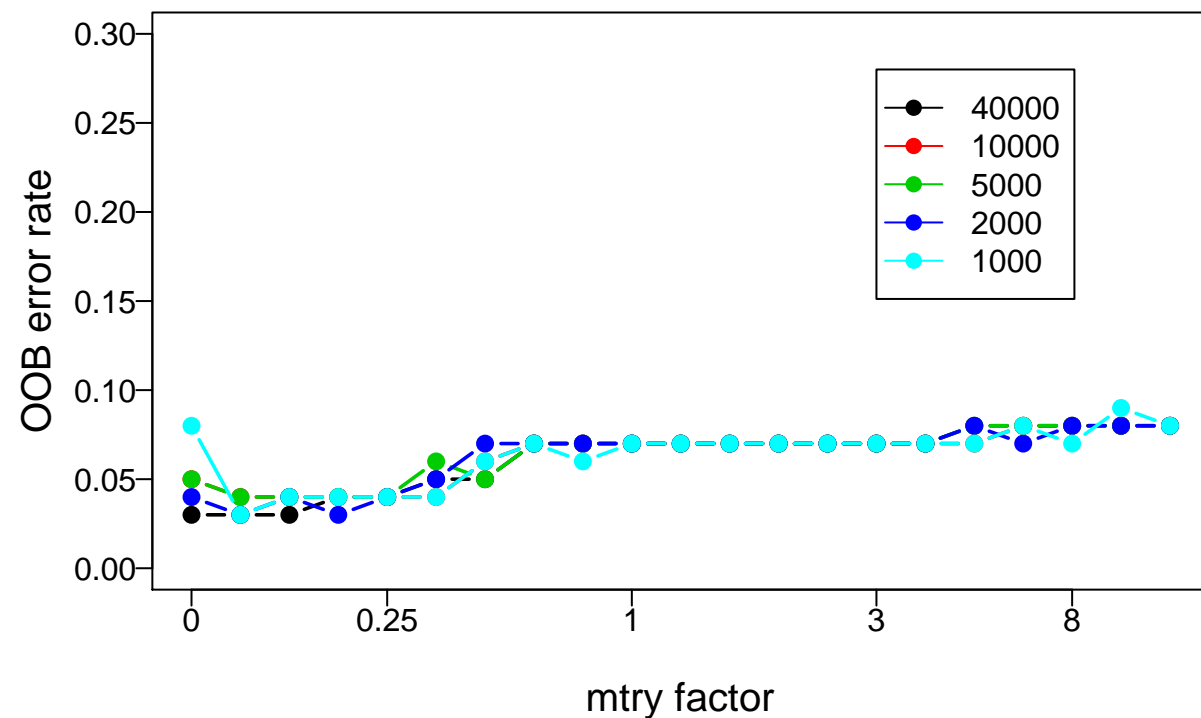
4 classes; 3 dimensions; 100 genes/dimen.; nodesize = 1



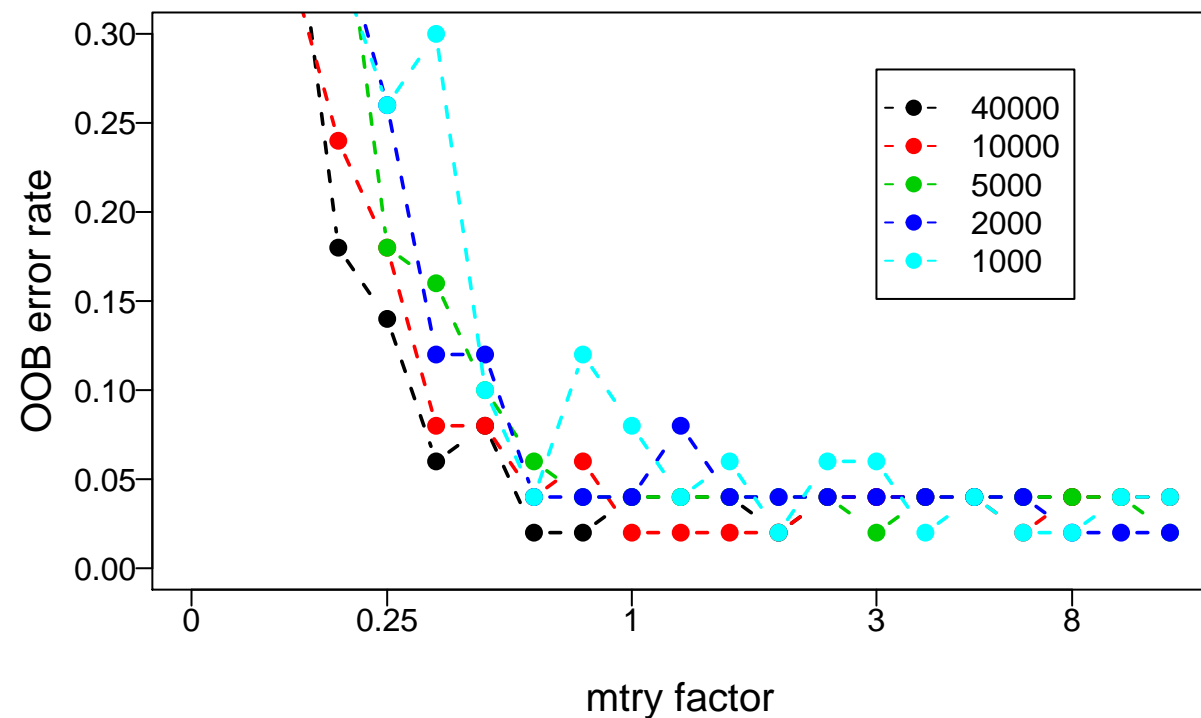
4 classes; 3 dimensions; 100 genes/dimen.; nodesize = 1



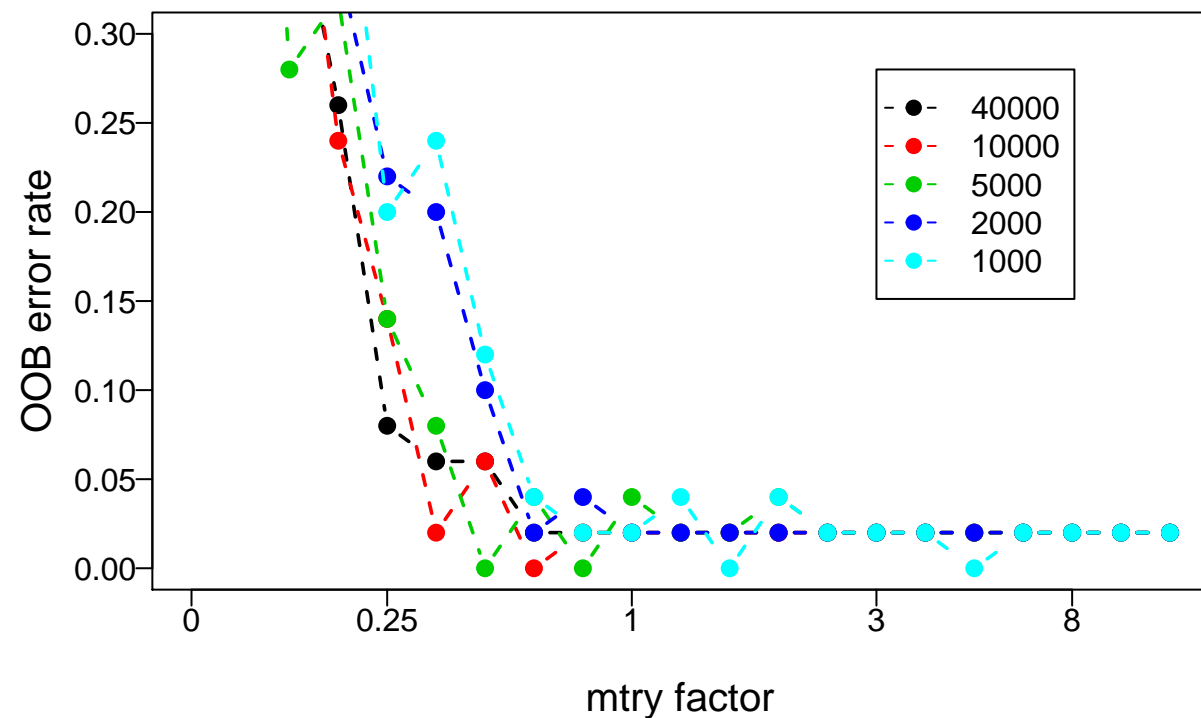
4 classes; 3 dimensions; 100 genes/dimen.; nodesize = 1



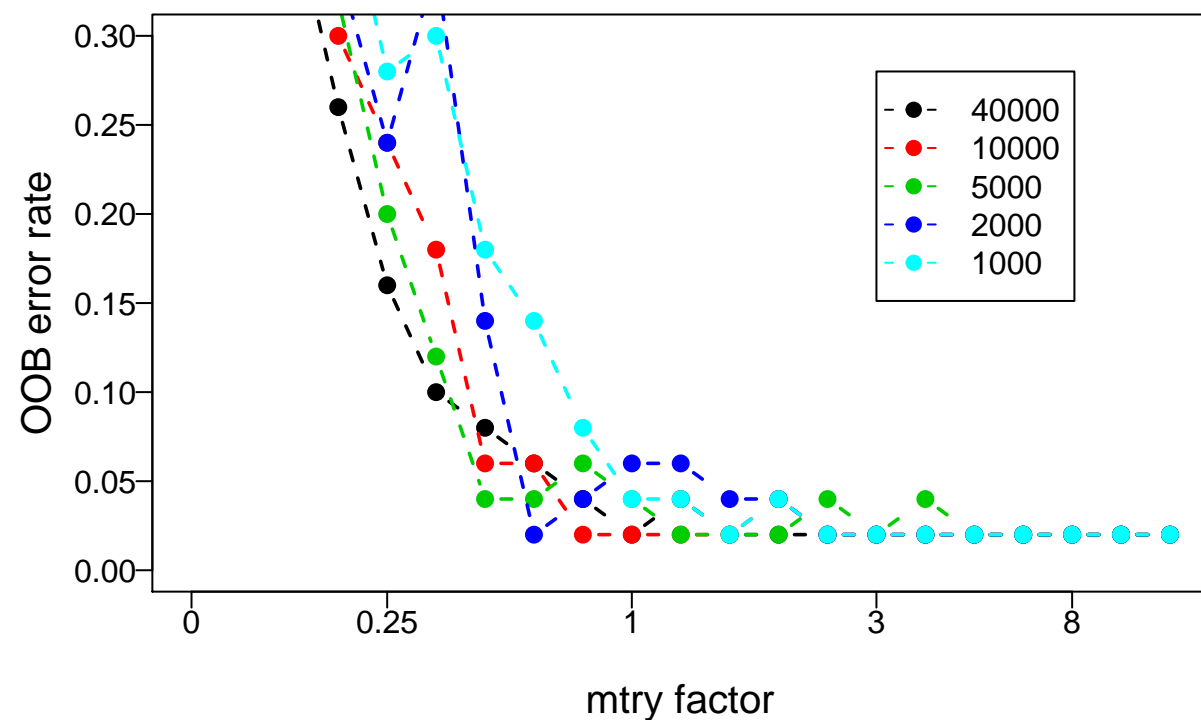
2 classes; 1 dimensions; 5 genes/dimen.; nodesize = 5



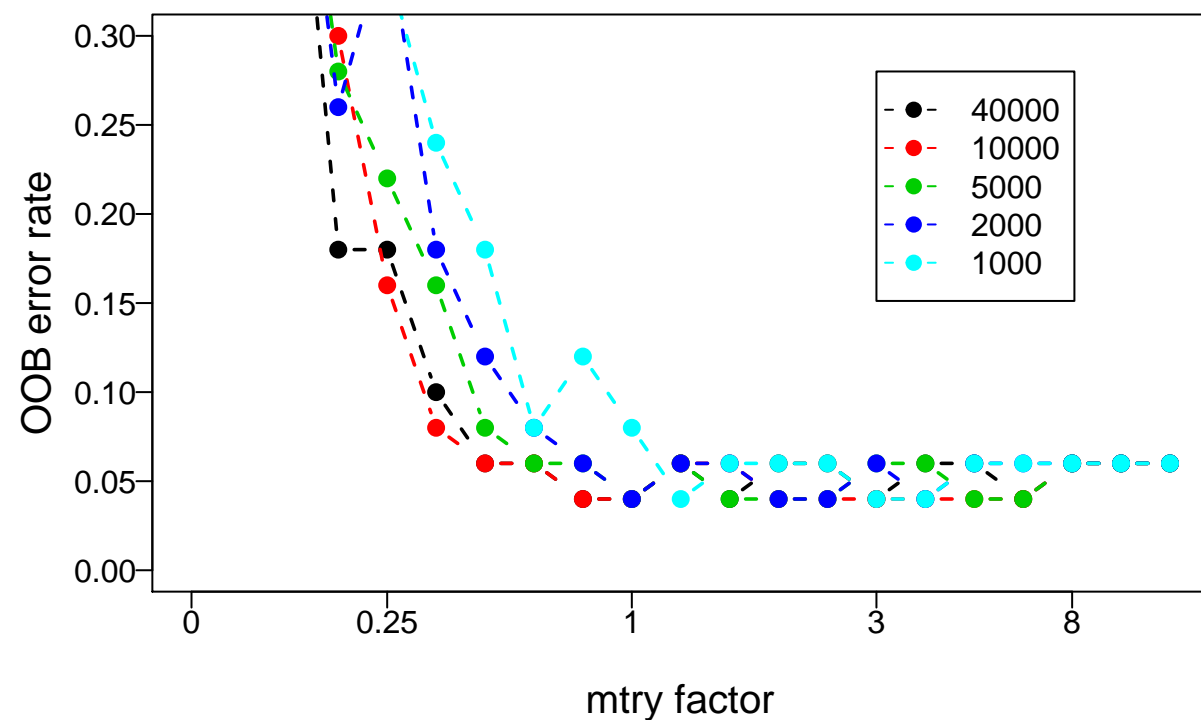
2 classes; 1 dimensions; 5 genes/dimen.; nodesize = 5



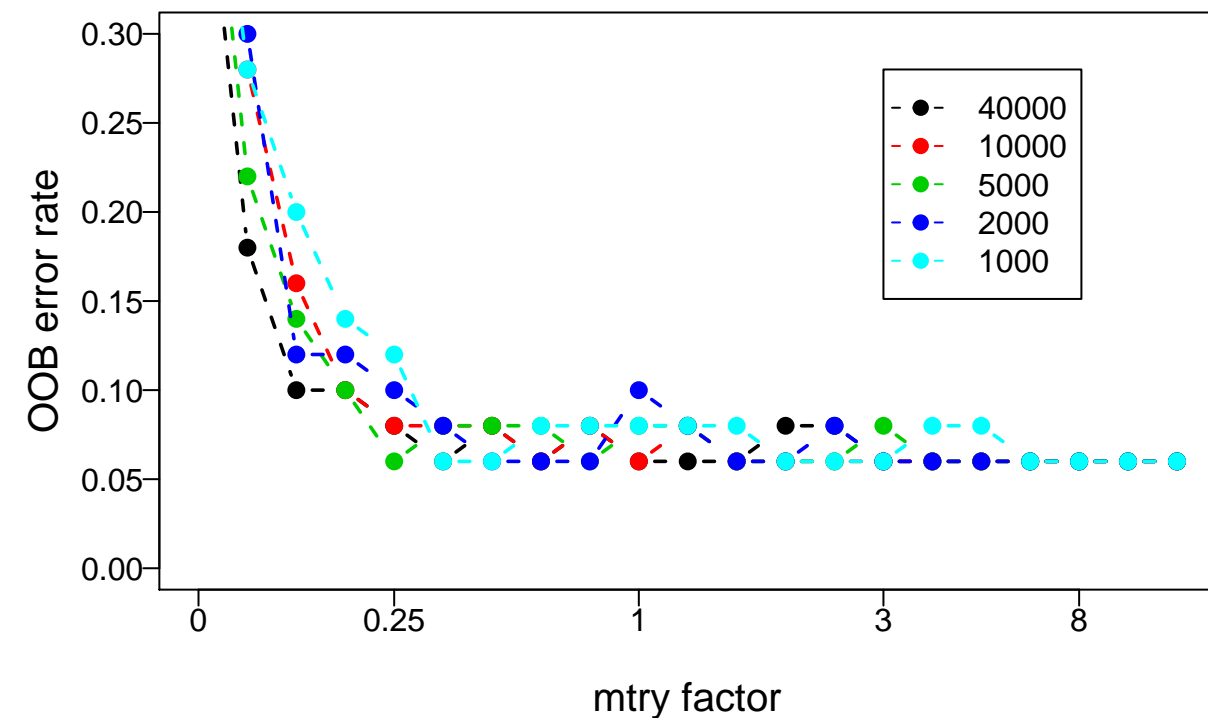
2 classes; 1 dimensions; 5 genes/dimen.; nodesize = 5



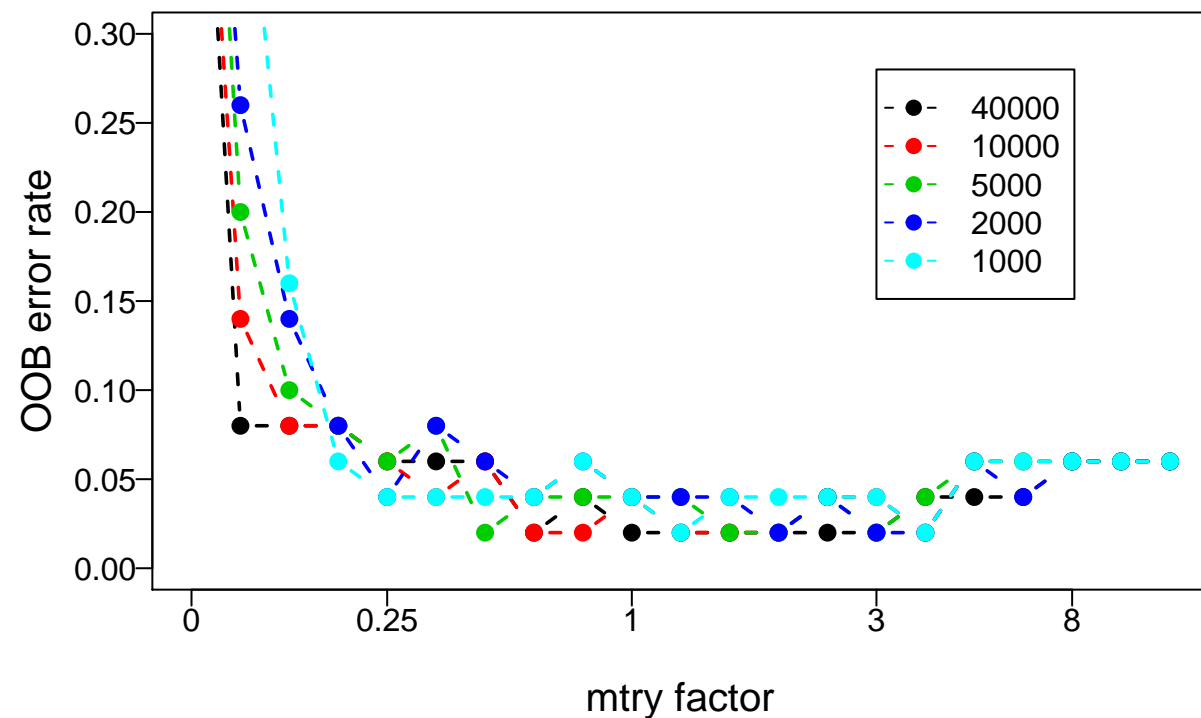
2 classes; 1 dimensions; 5 genes/dimen.; nodesize = 5



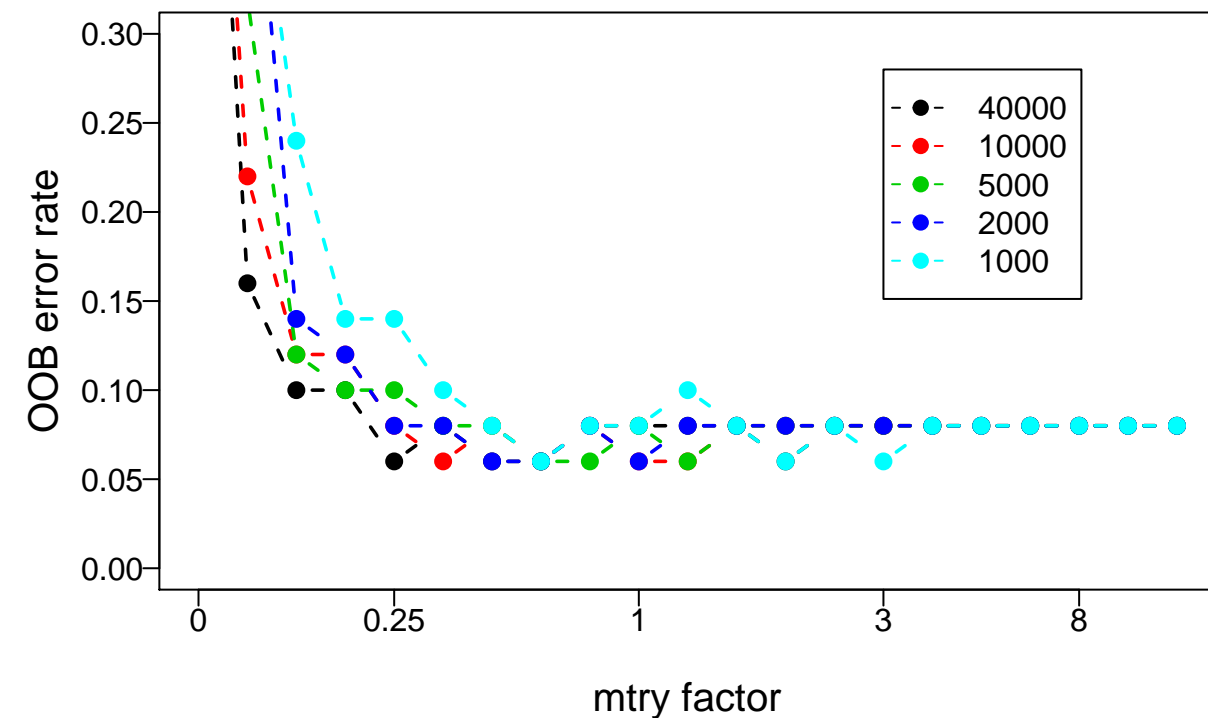
2 classes; 1 dimensions; 20 genes/dimen.; nodesize = 5



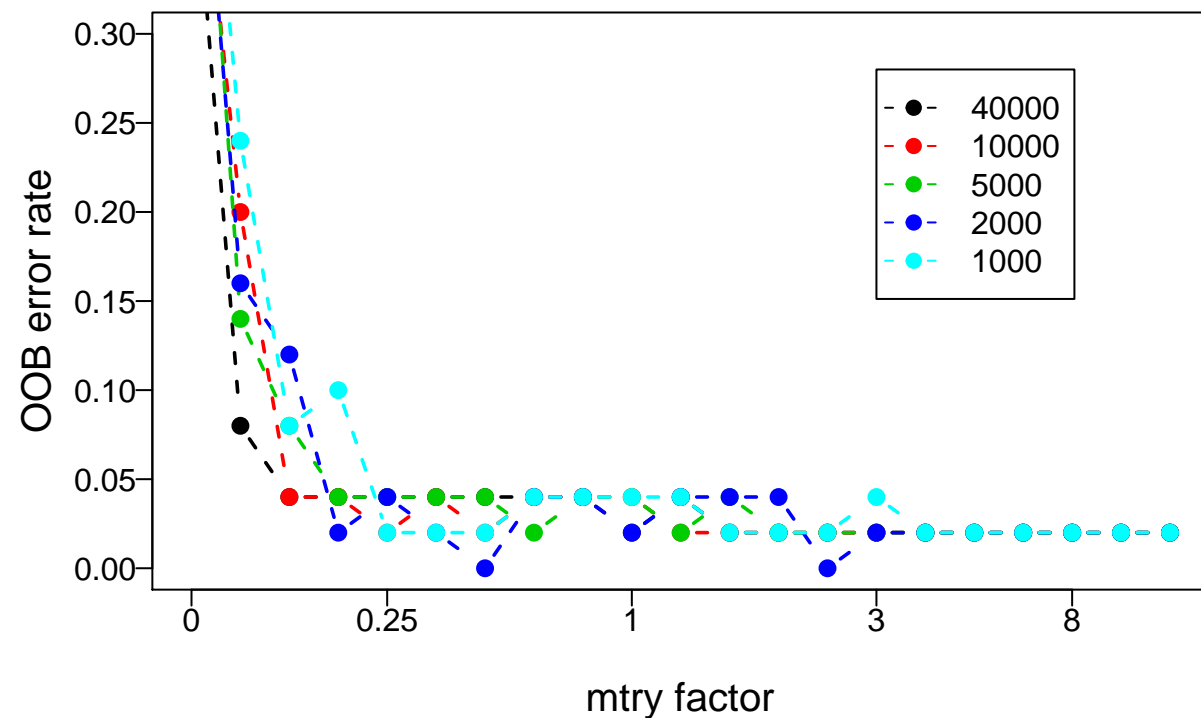
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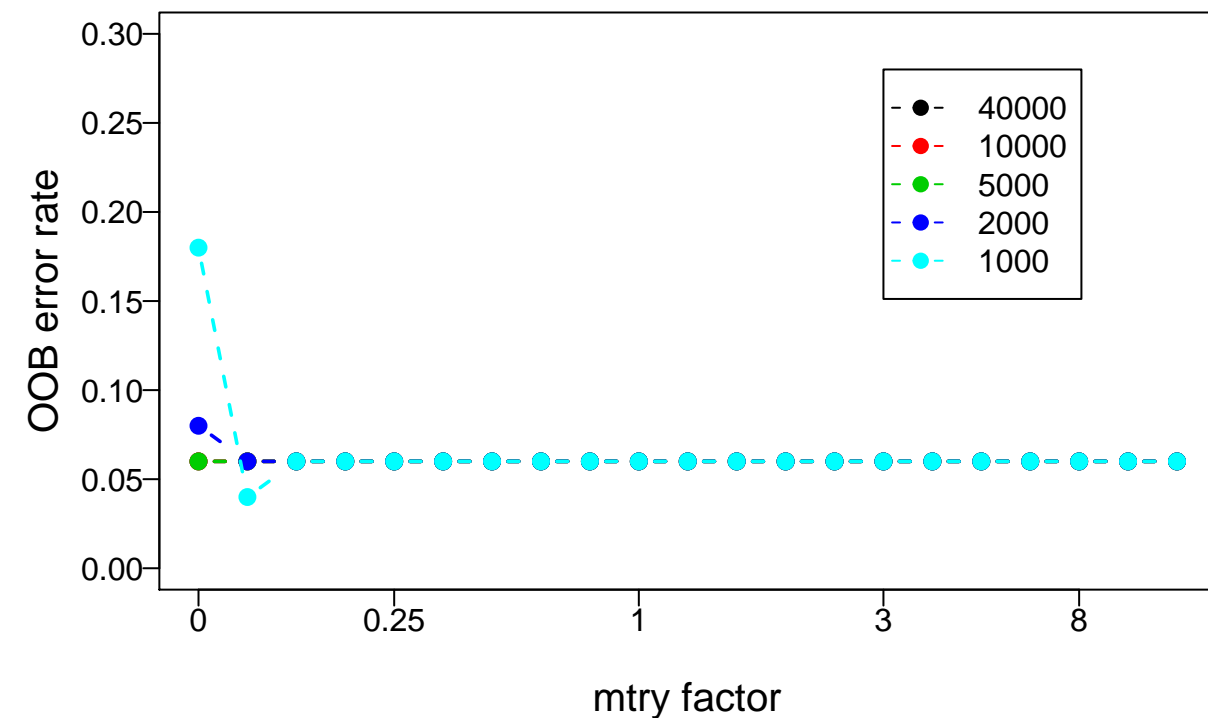
2 classes; 1 dimensions; 20 genes/dimen.; nodesize = 5



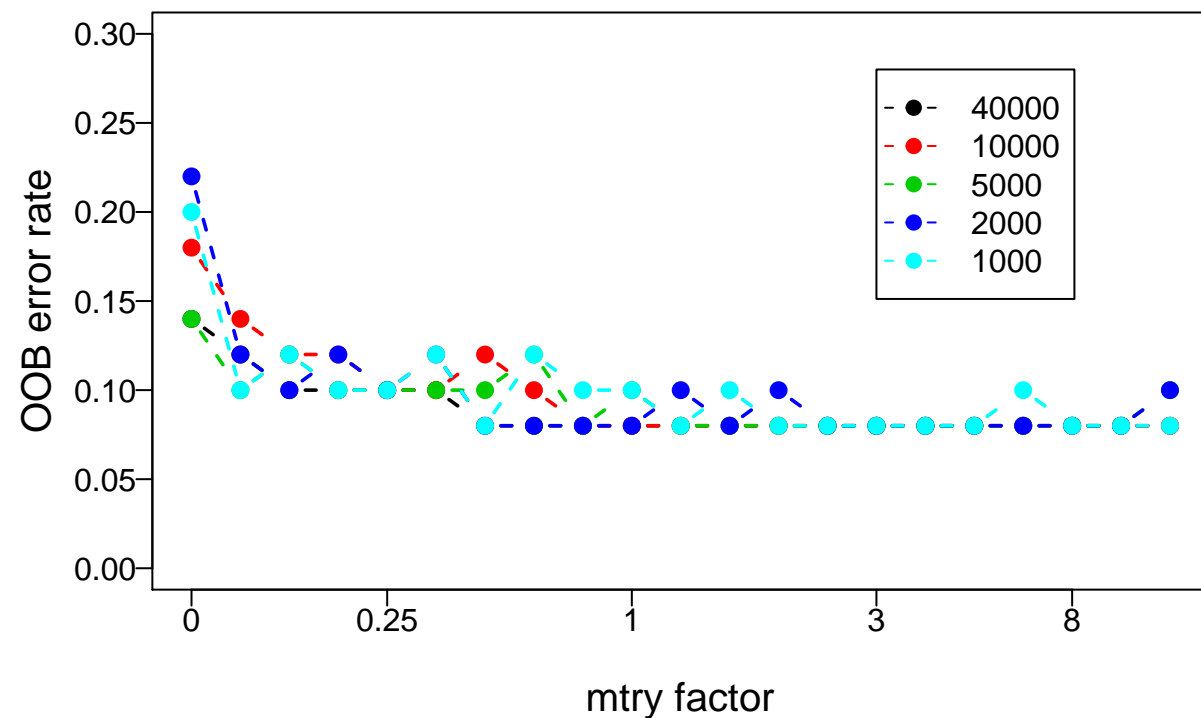
2 classes; 1 dimensions; 20 genes/dimen.; nodesize = 5



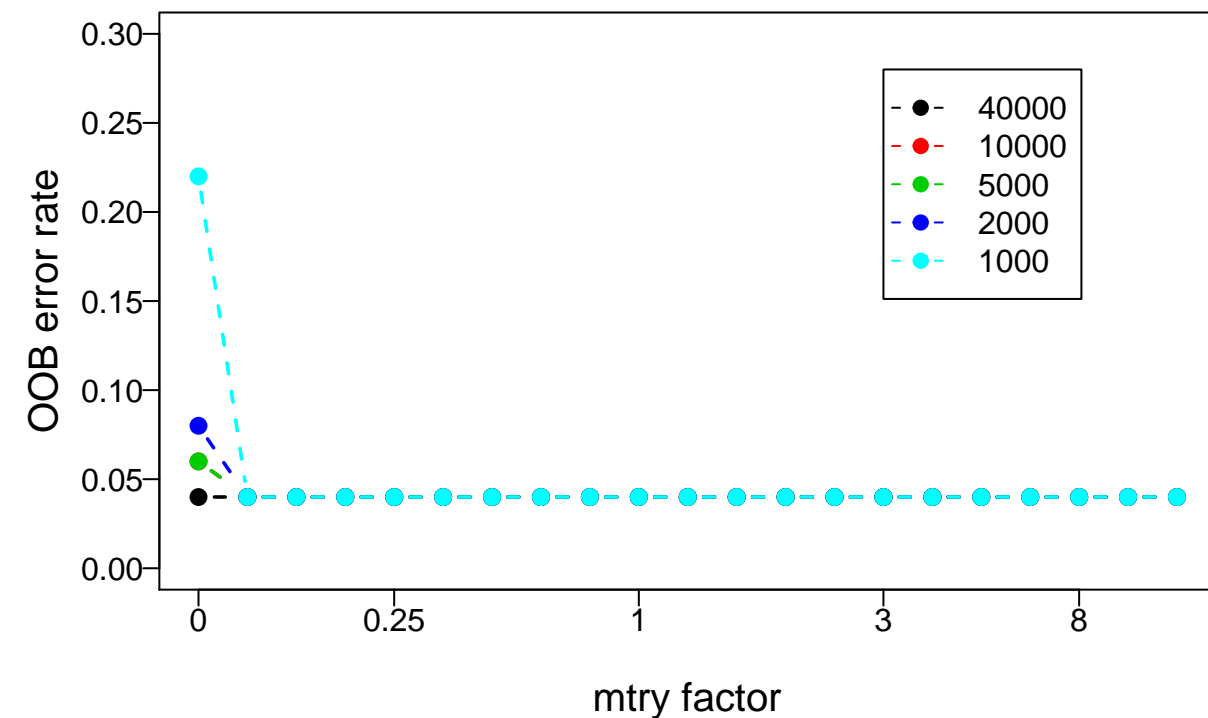
2 classes; 1 dimensions; 100 genes/dimen.; nodesize = 5



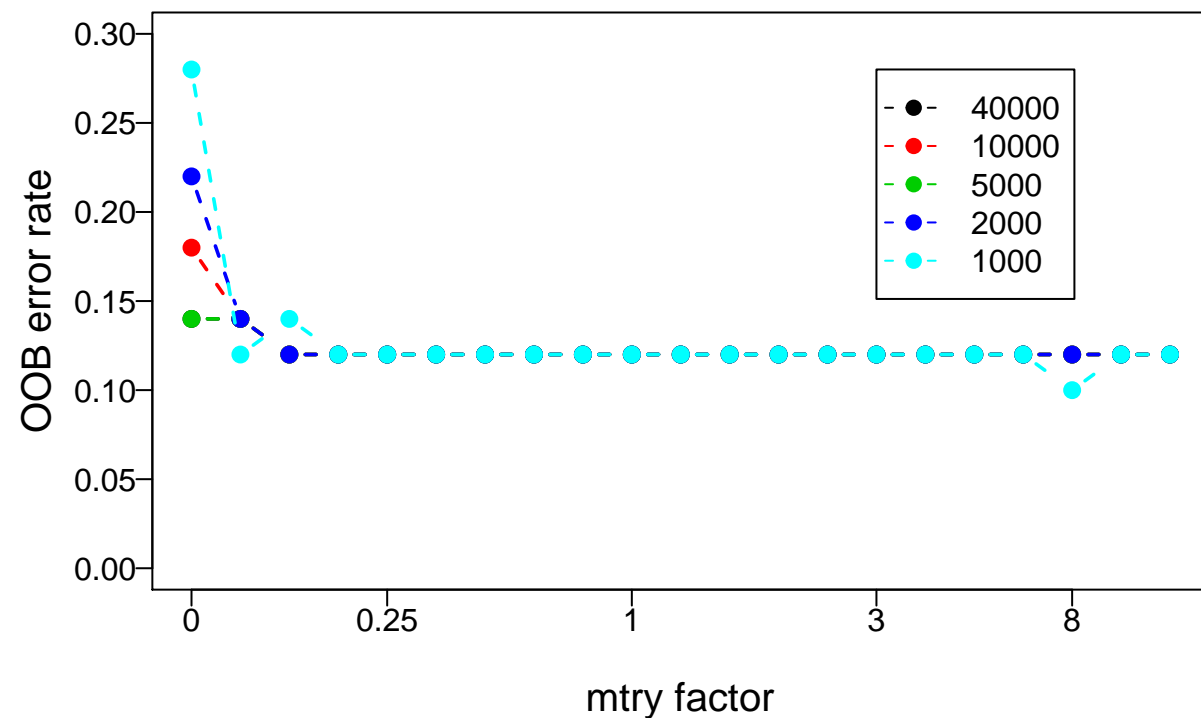
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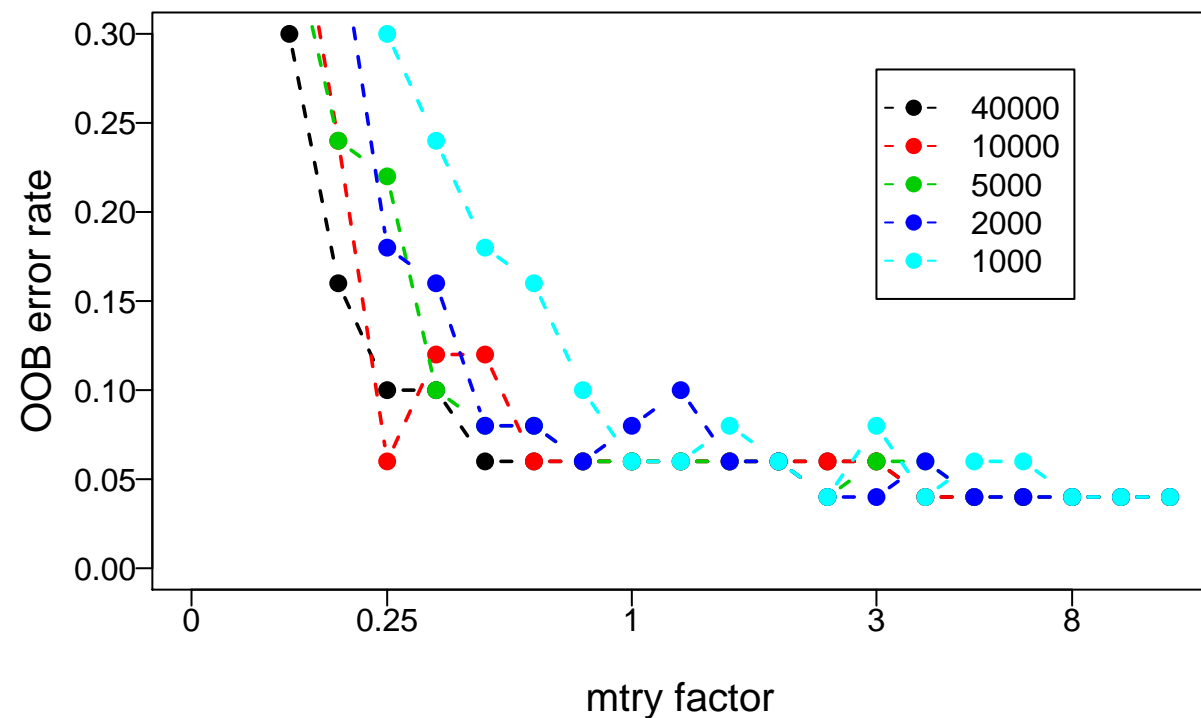
2 classes; 1 dimensions; 100 genes/dimen.; nodesize = 5



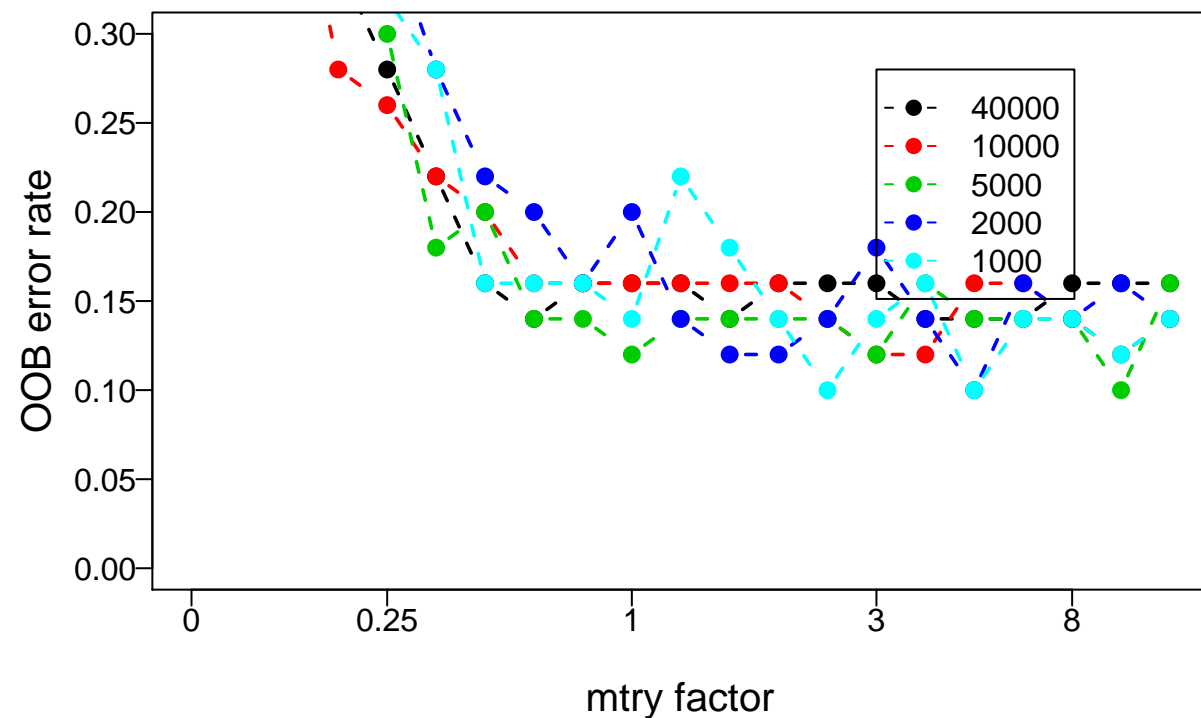
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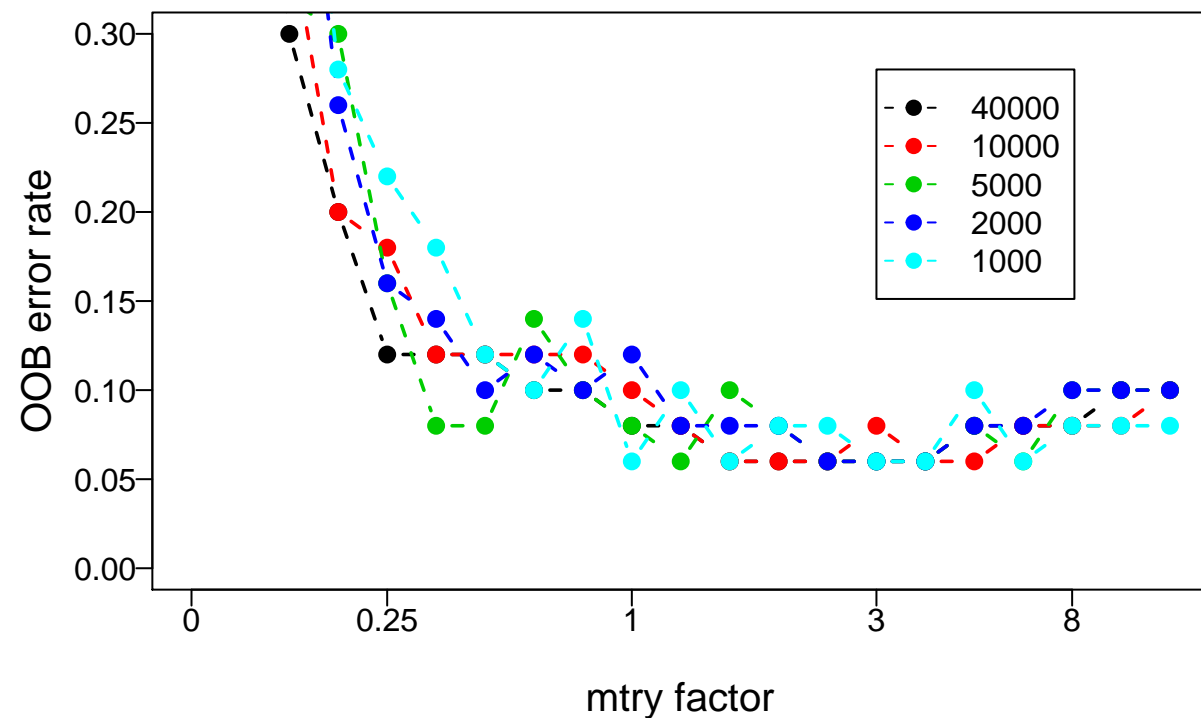
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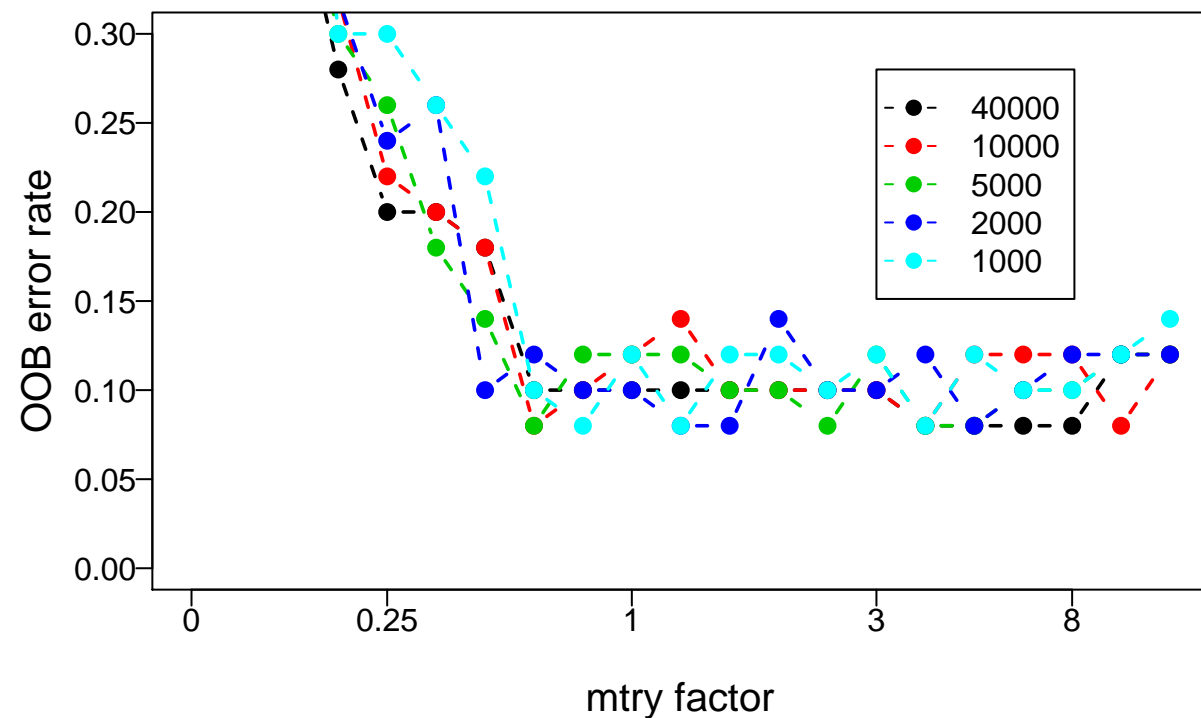
2 classes; 2 dimensions; 5 genes/dimen.; nodesize = 5



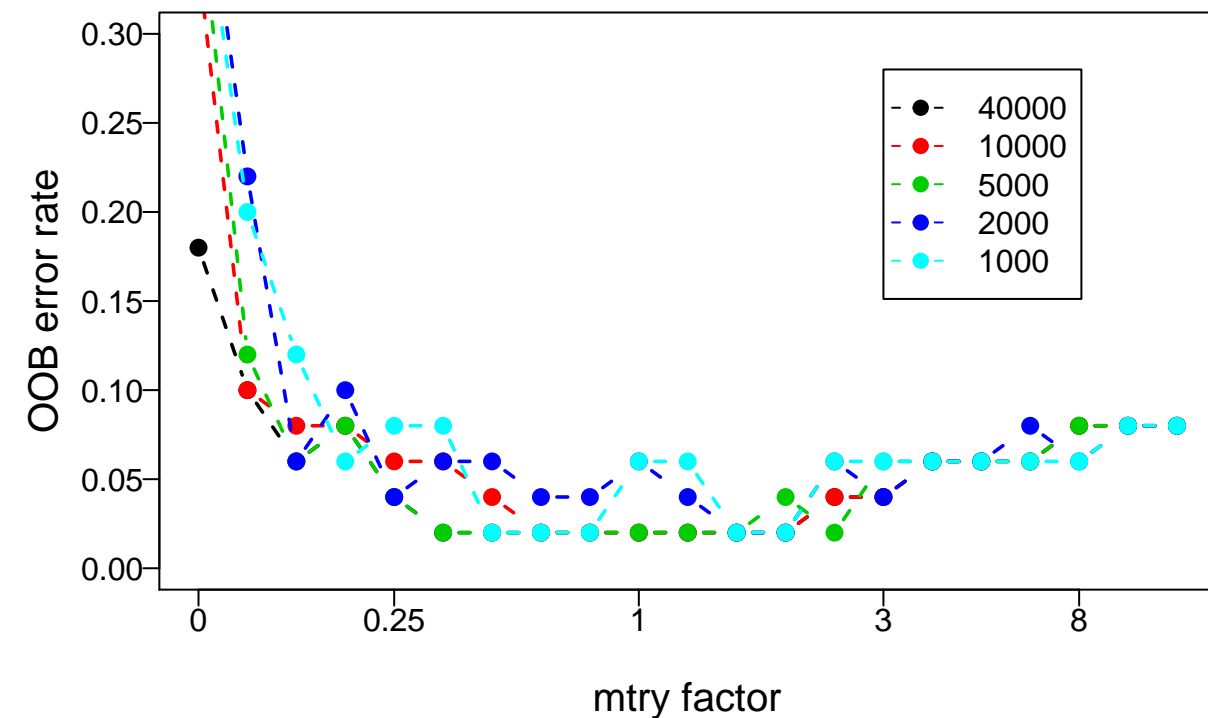
2 classes; 2 dimensions; 5 genes/dimen.; nodesize = 5



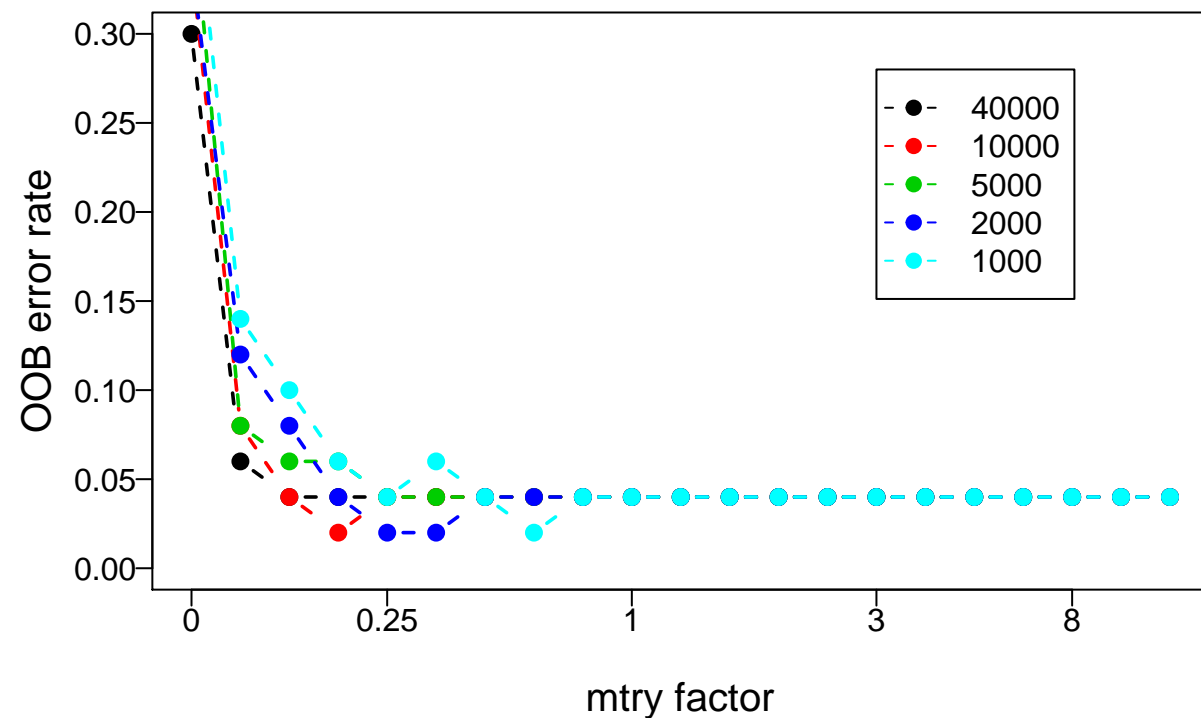
2 classes; 2 dimensions; 5 genes/dimen.; nodesize = 5



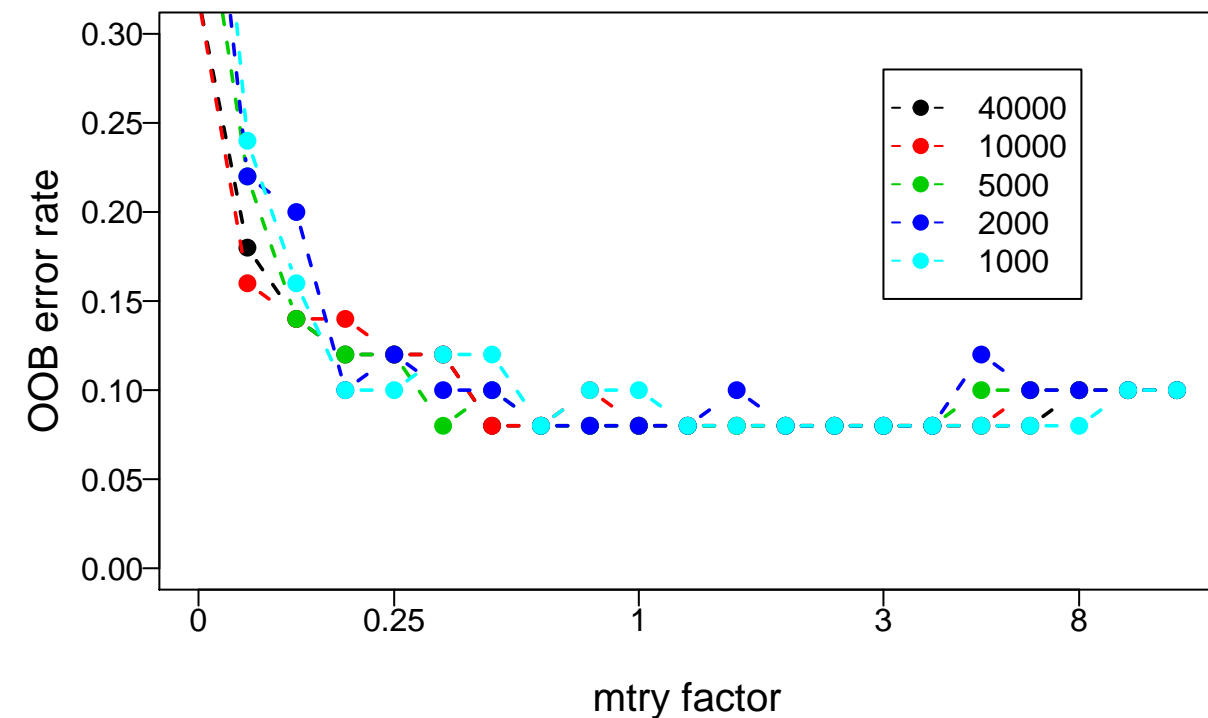
2 classes; 2 dimensions; 20 genes/dimen.; nodesize = 5



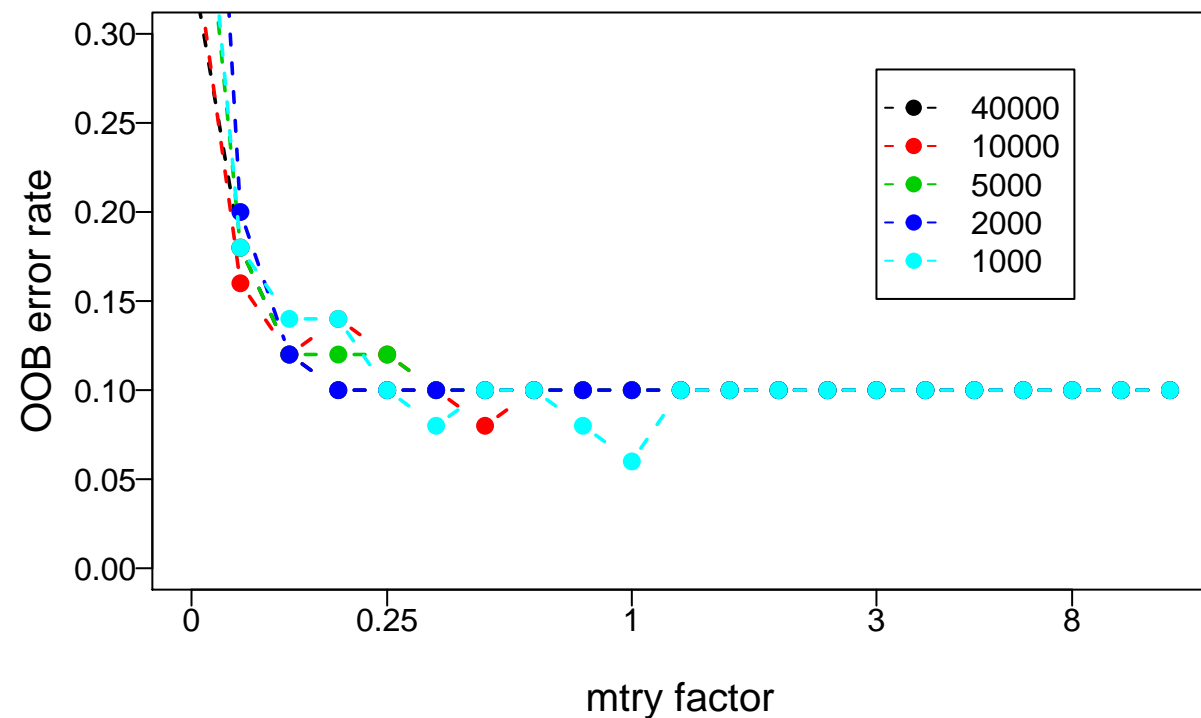
2 classes; 2 dimensions; 20 genes/dimen.; nodesize = 5



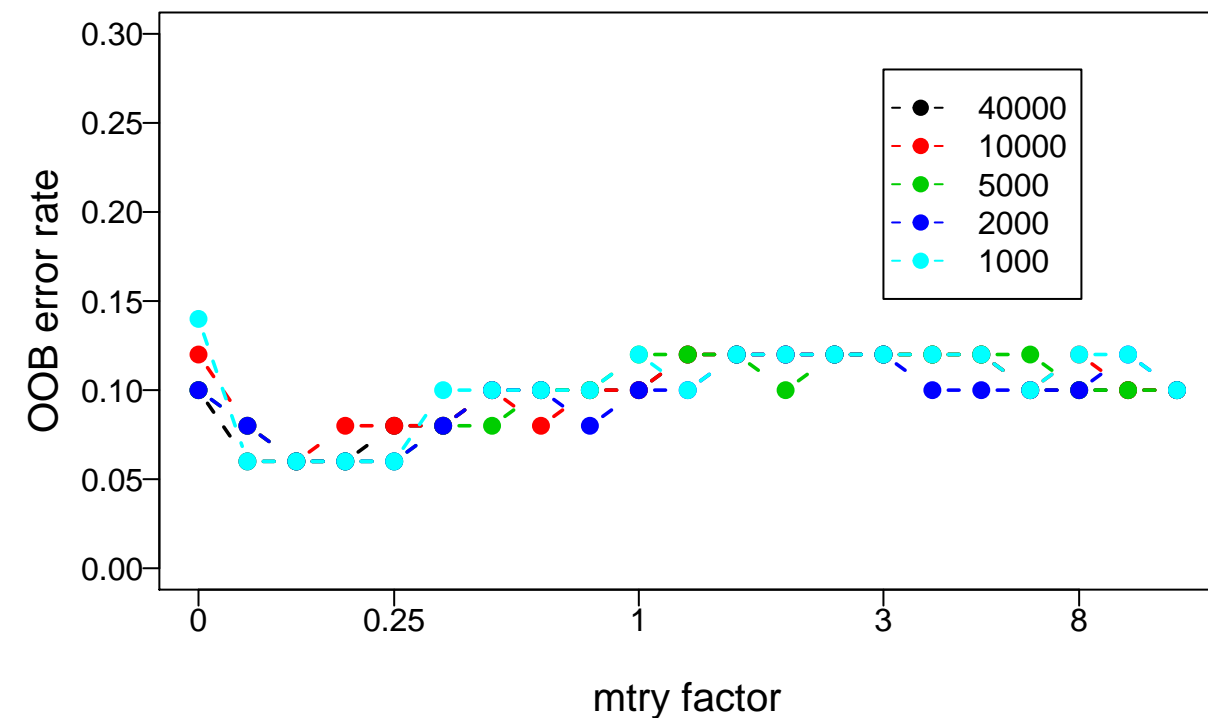
2 classes; 2 dimensions; 20 genes/dimen.; nodesize = 5



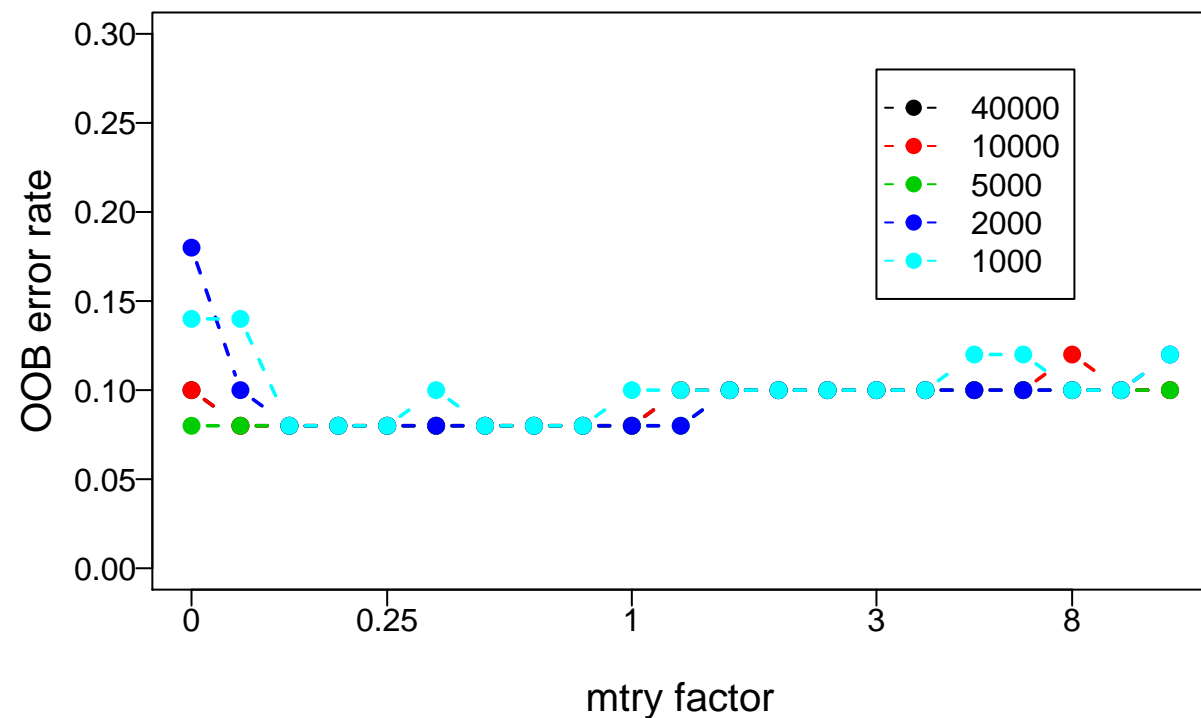
2 classes; 2 dimensions; 20 genes/dimen.; nodesize = 5



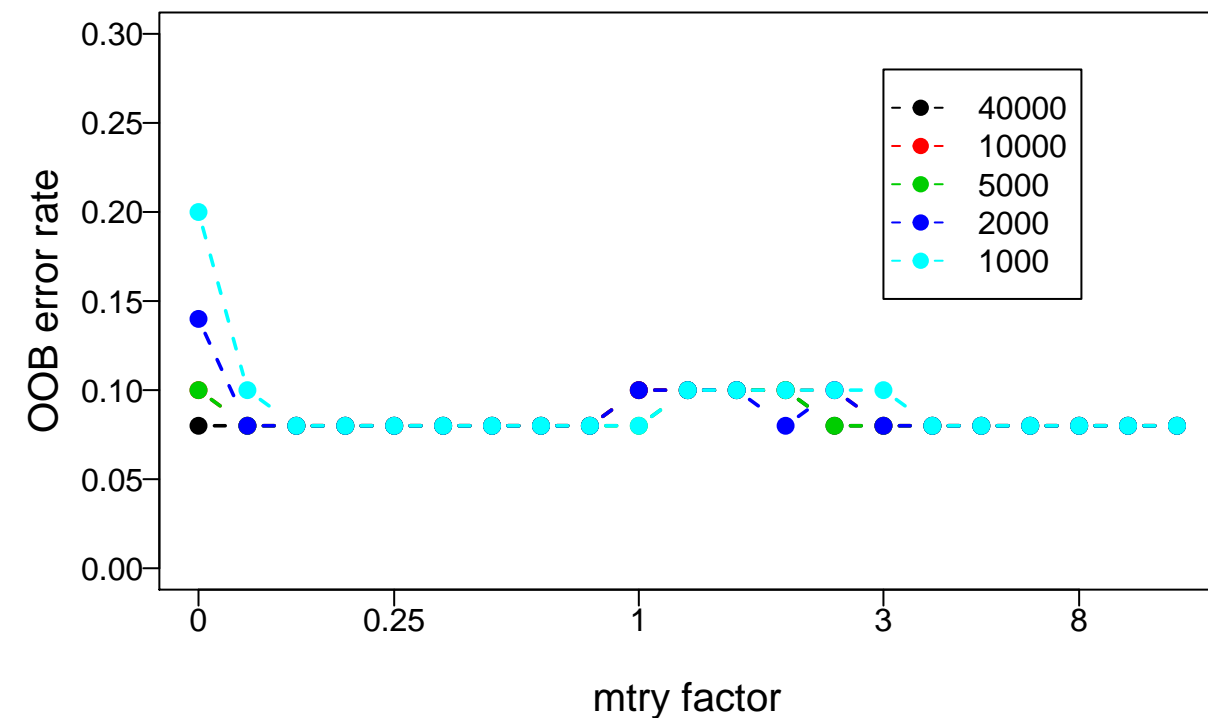
2 classes; 2 dimensions; 100 genes/dimen.; nodesize = 5



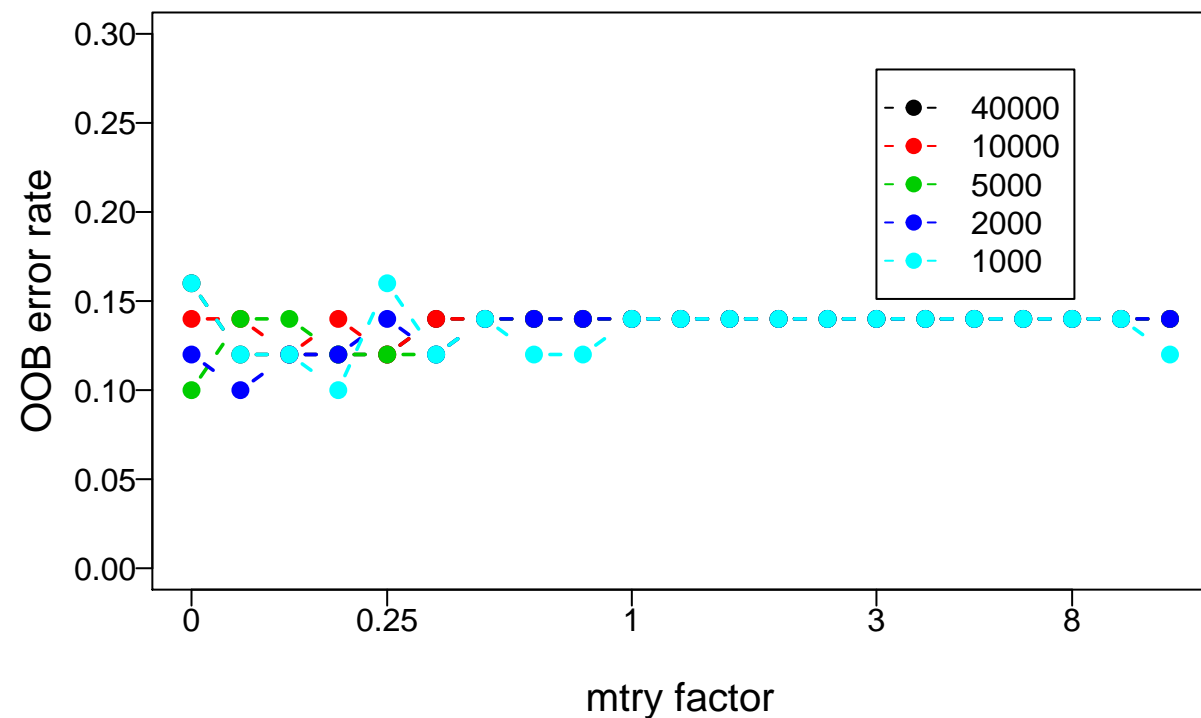
2 classes; 2 dimensions; 100 genes/dimen.; nodesize = 5



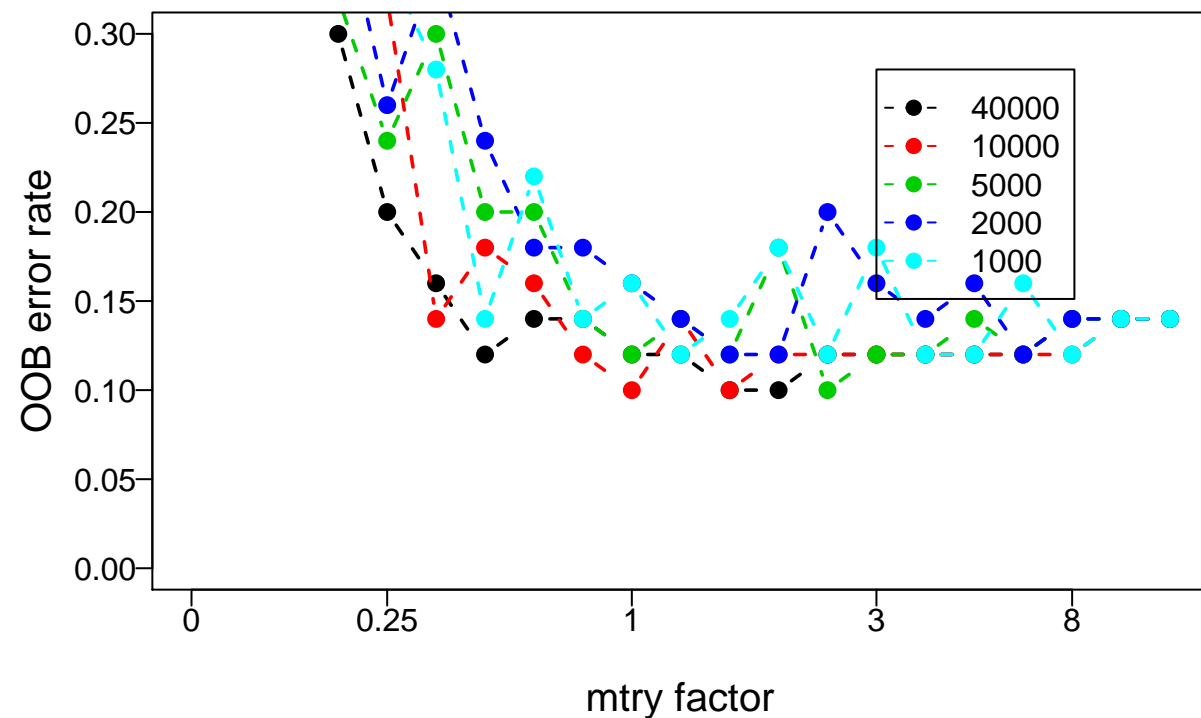
2 classes; 2 dimensions; 100 genes/dimen.; nodesize = 5



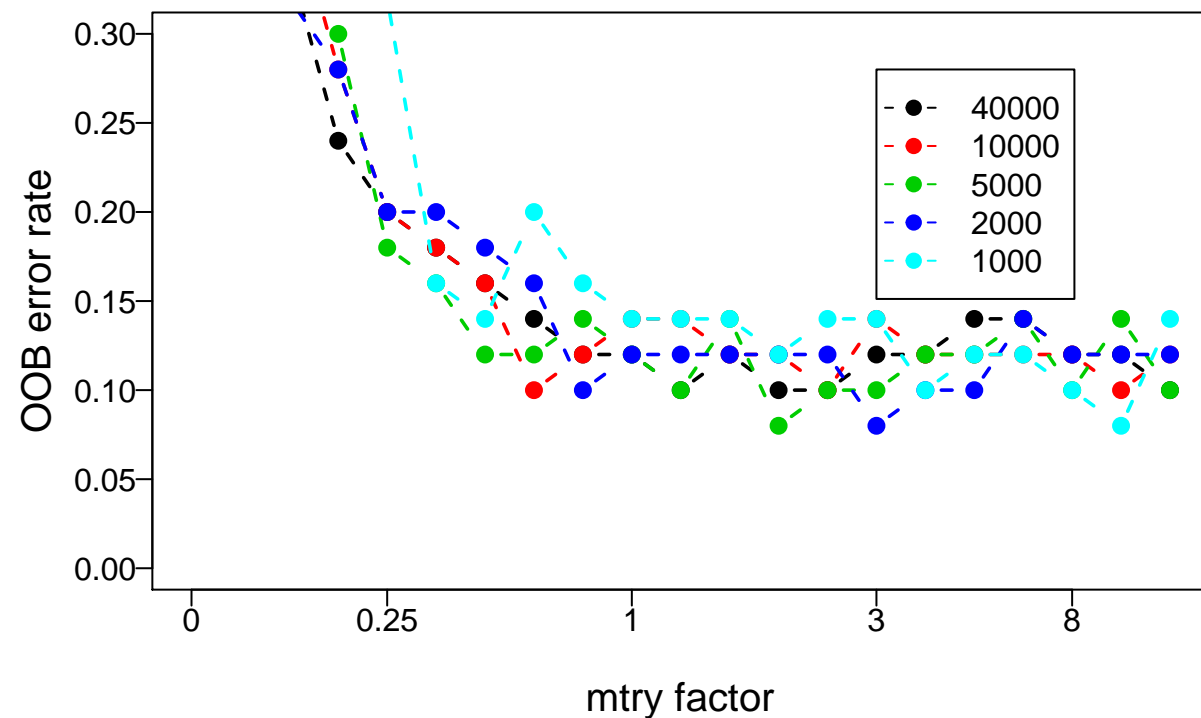
2 classes; 2 dimensions; 100 genes/dimen.; nodesize = 5



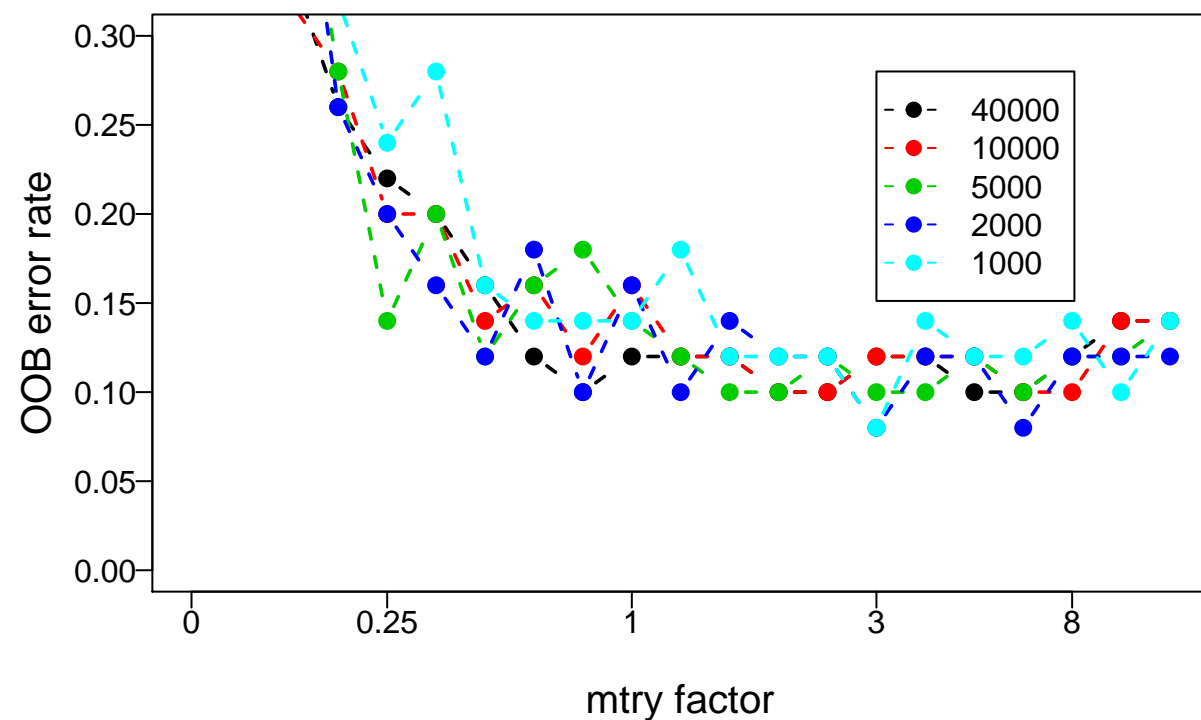
2 classes; 3 dimensions; 5 genes/dimen.; nodesize = 5



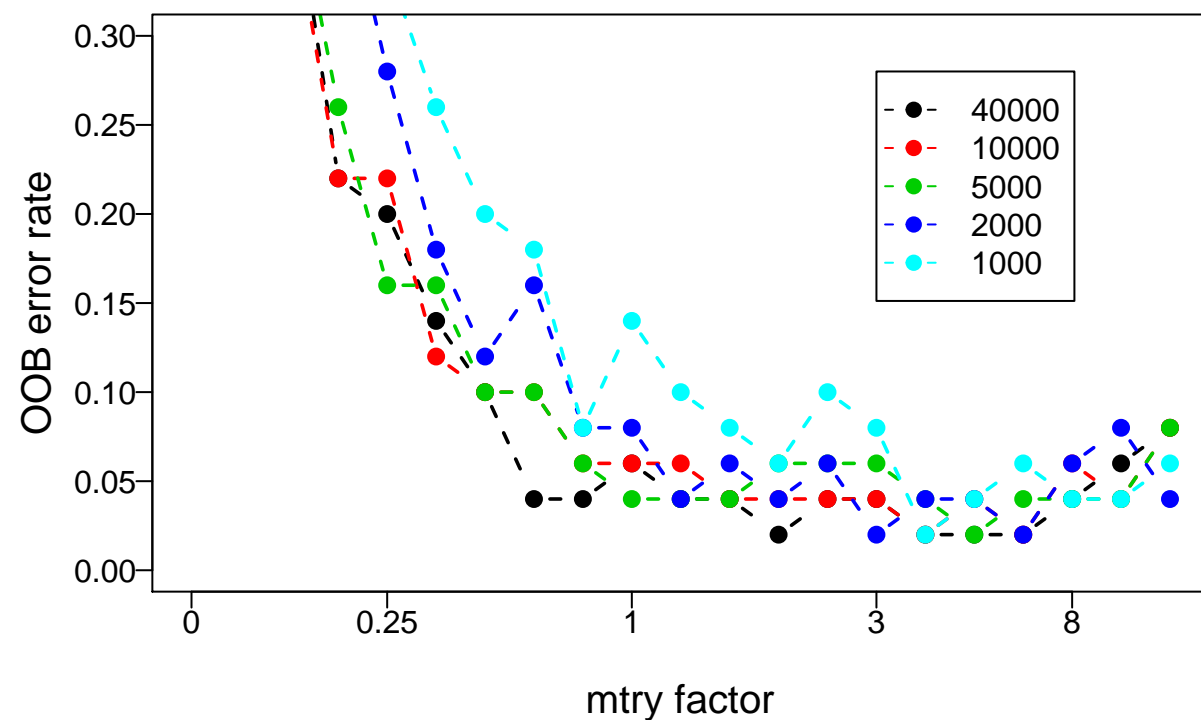
2 classes; 3 dimensions; 5 genes/dimen.; nodesize = 5



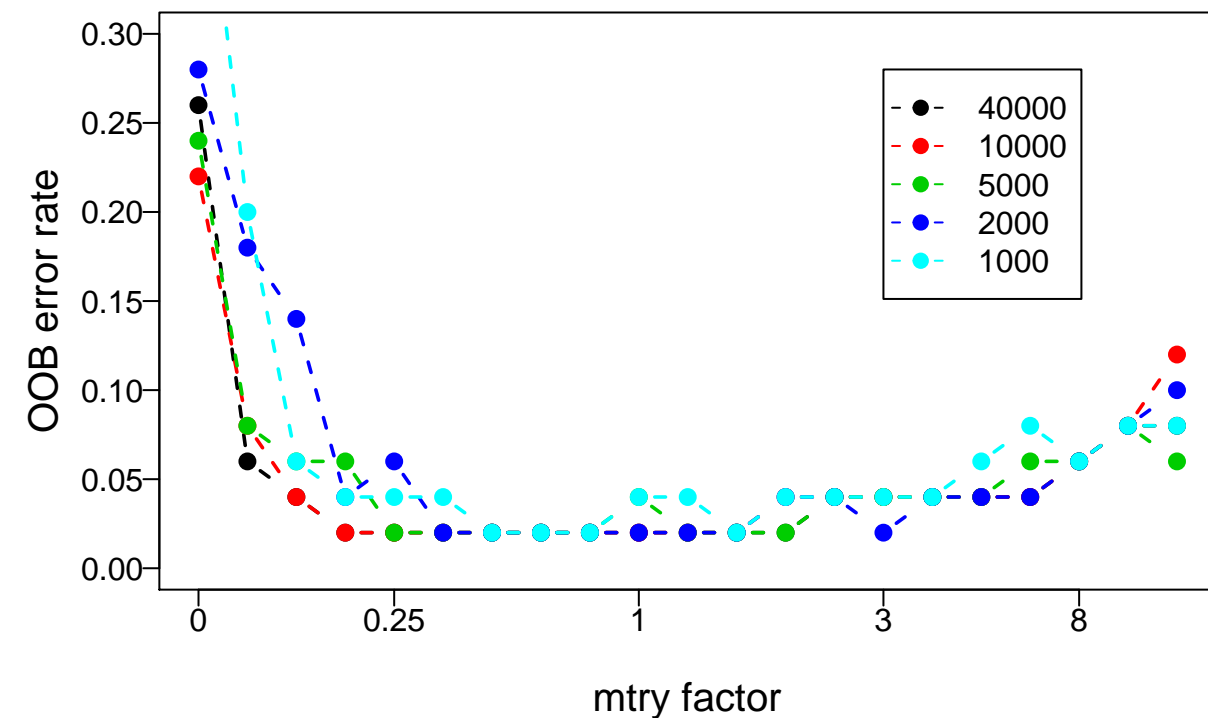
2 classes; 3 dimensions; 5 genes/dimen.; nodesize = 5



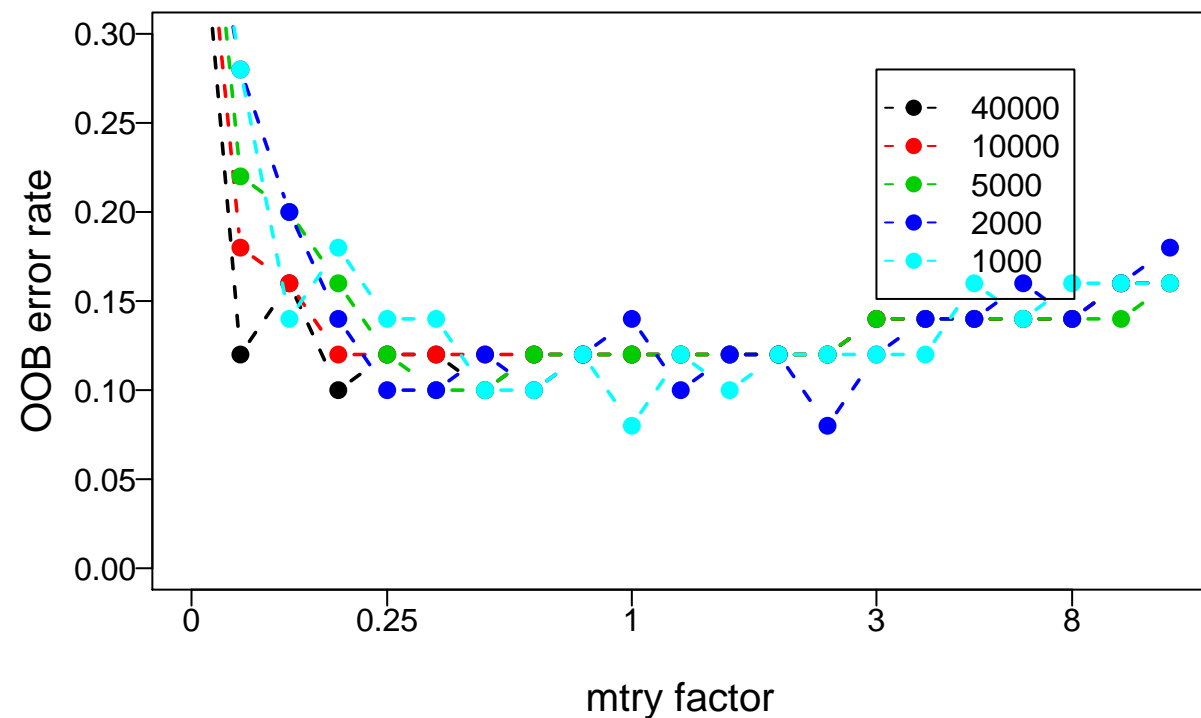
2 classes; 3 dimensions; 5 genes/dimen.; nodesize = 5



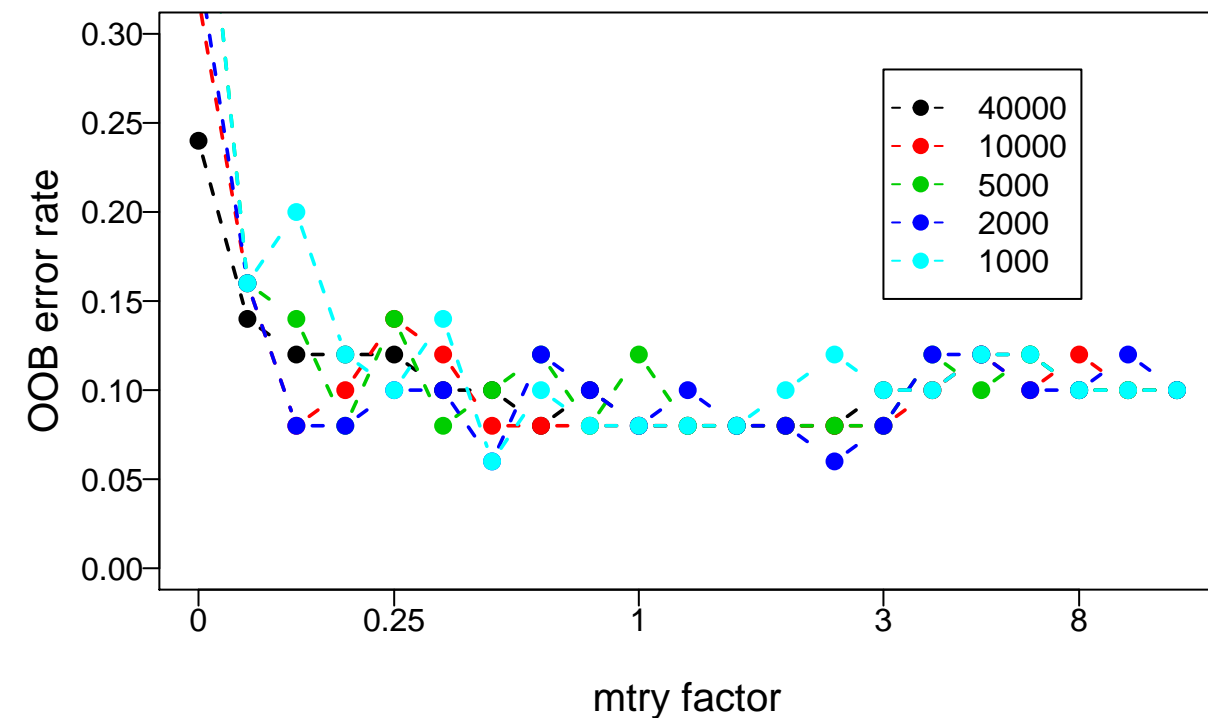
2 classes; 3 dimensions; 20 genes/dimen.; nodesize = 5



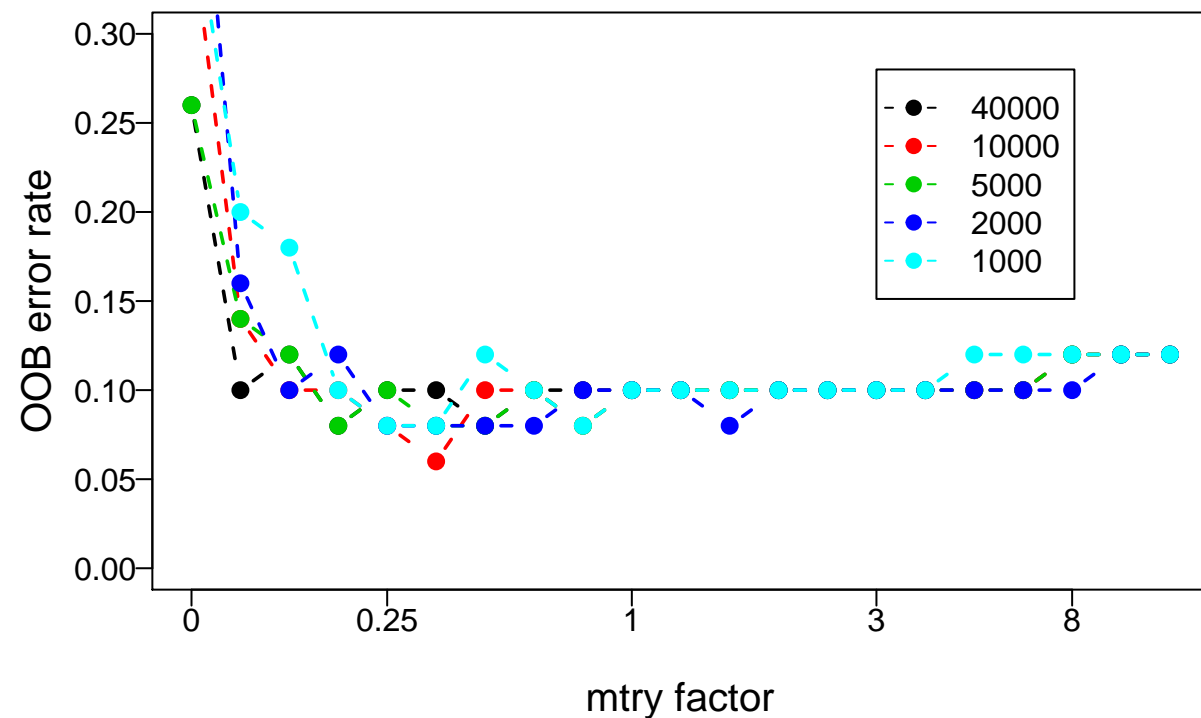
2 classes; 3 dimensions; 20 genes/dimen.; nodesize = 5



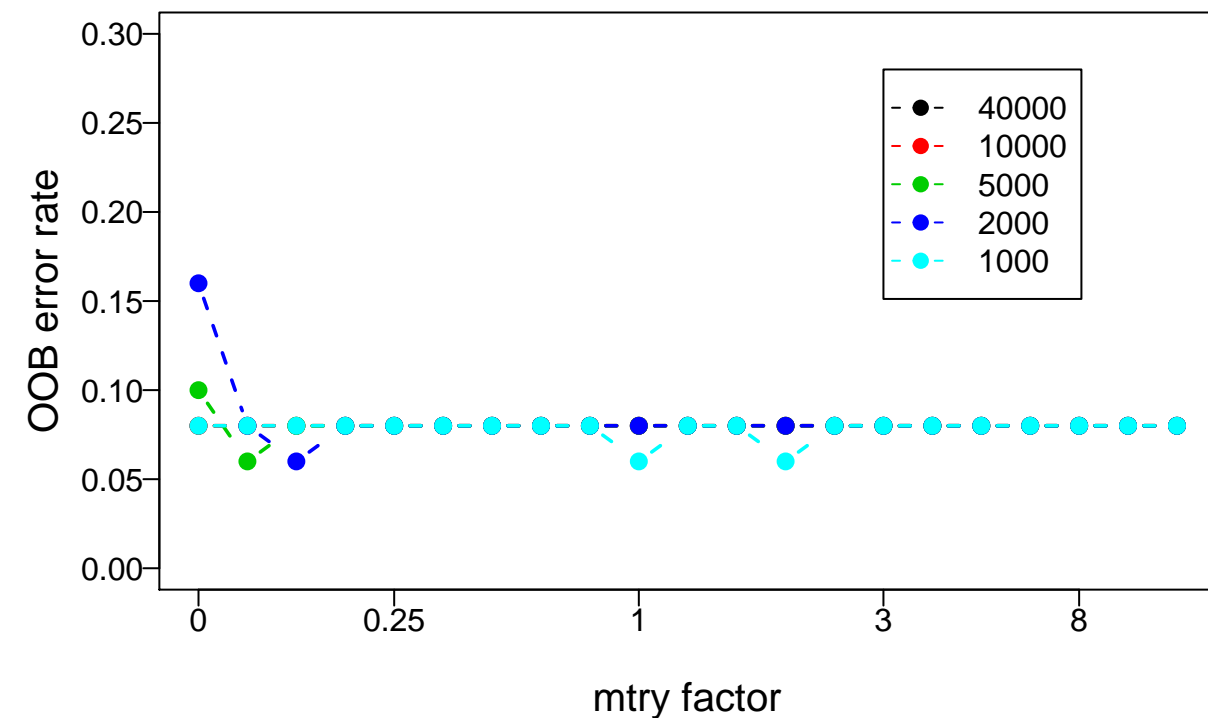
2 classes; 3 dimensions; 20 genes/dimen.; nodesize = 5



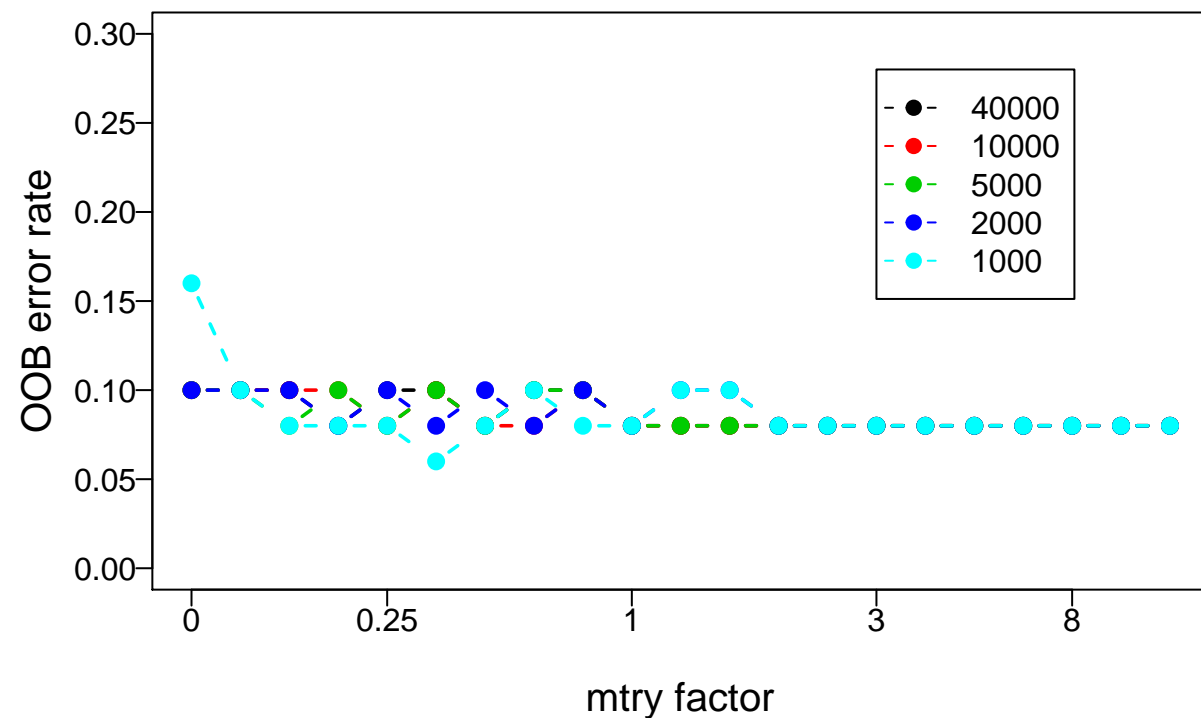
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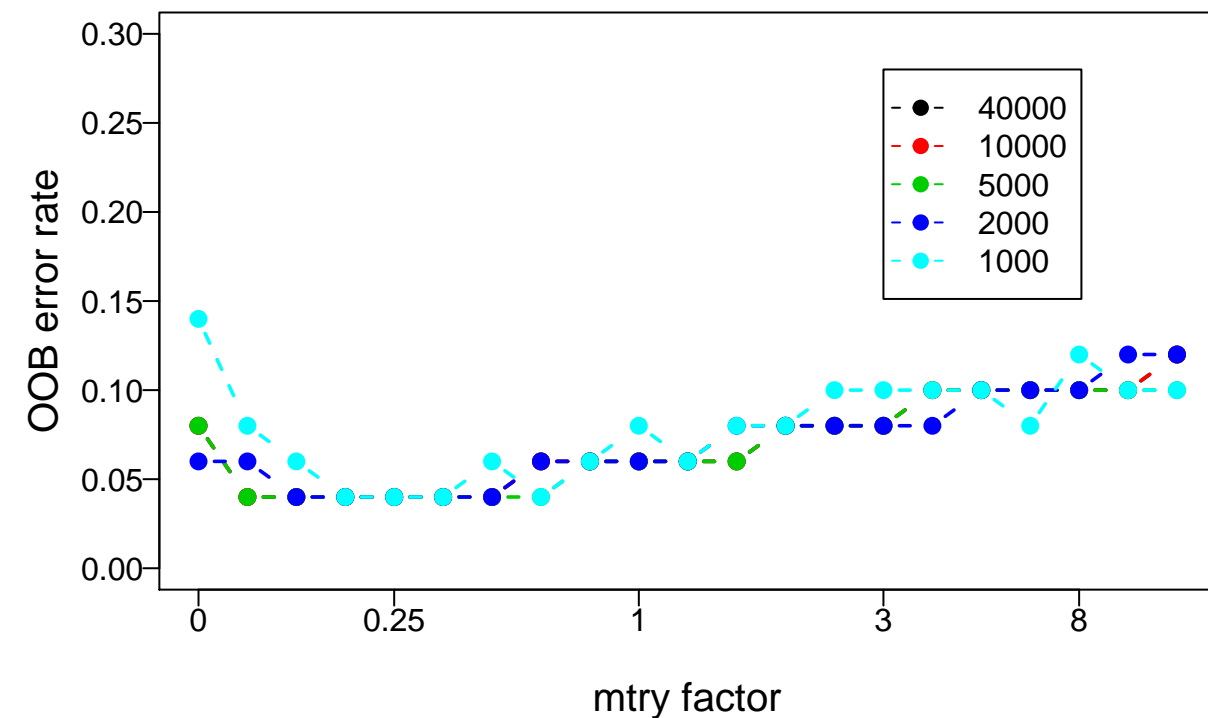
2 classes; 3 dimensions; 100 genes/dimen.; nodesize = 5



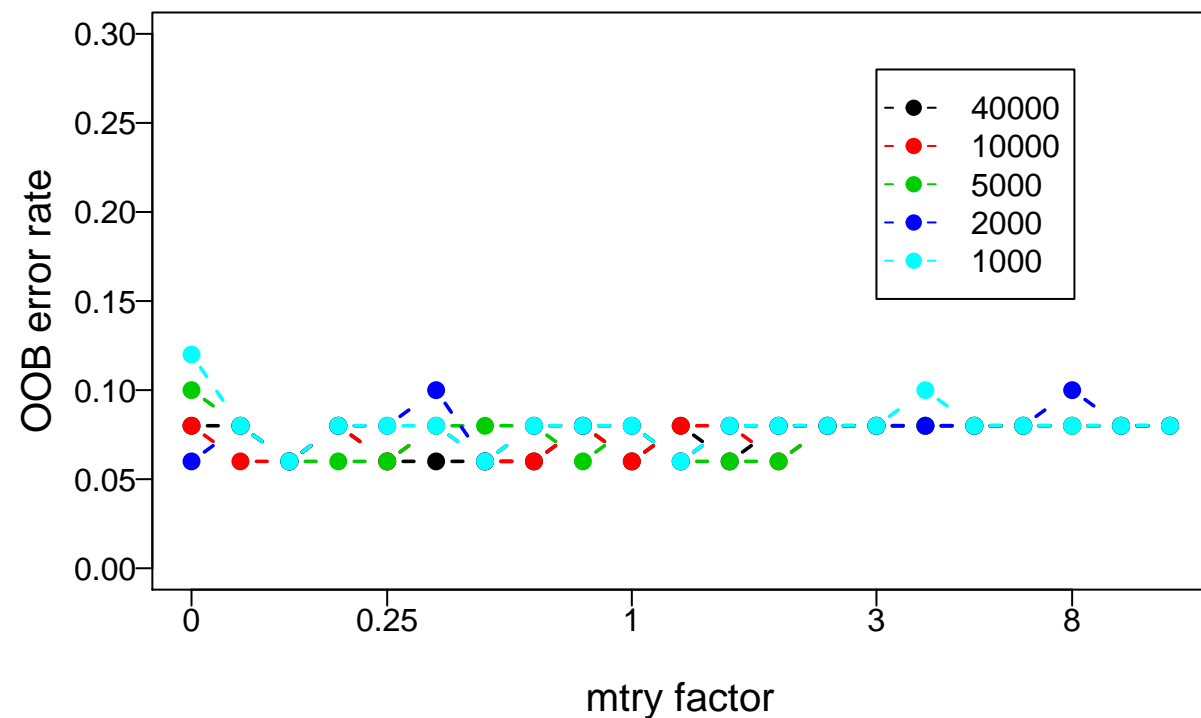
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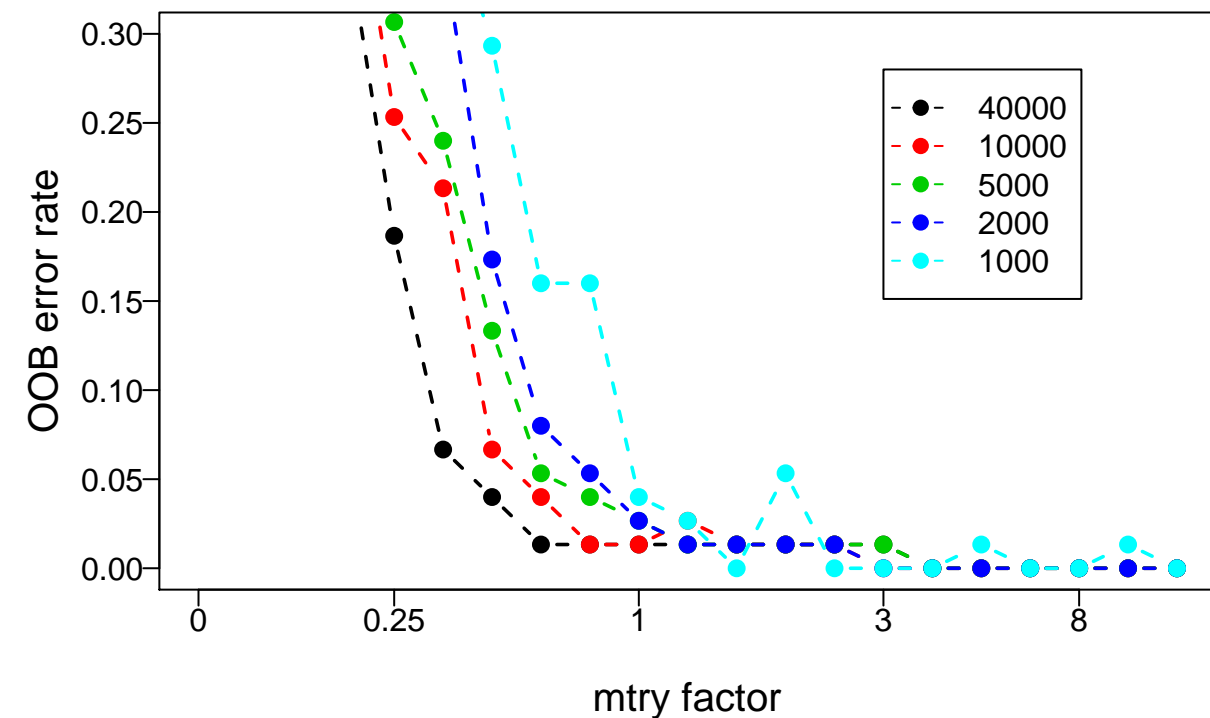
2 classes; 3 dimensions; 100 genes/dimen.; nodesize = 5



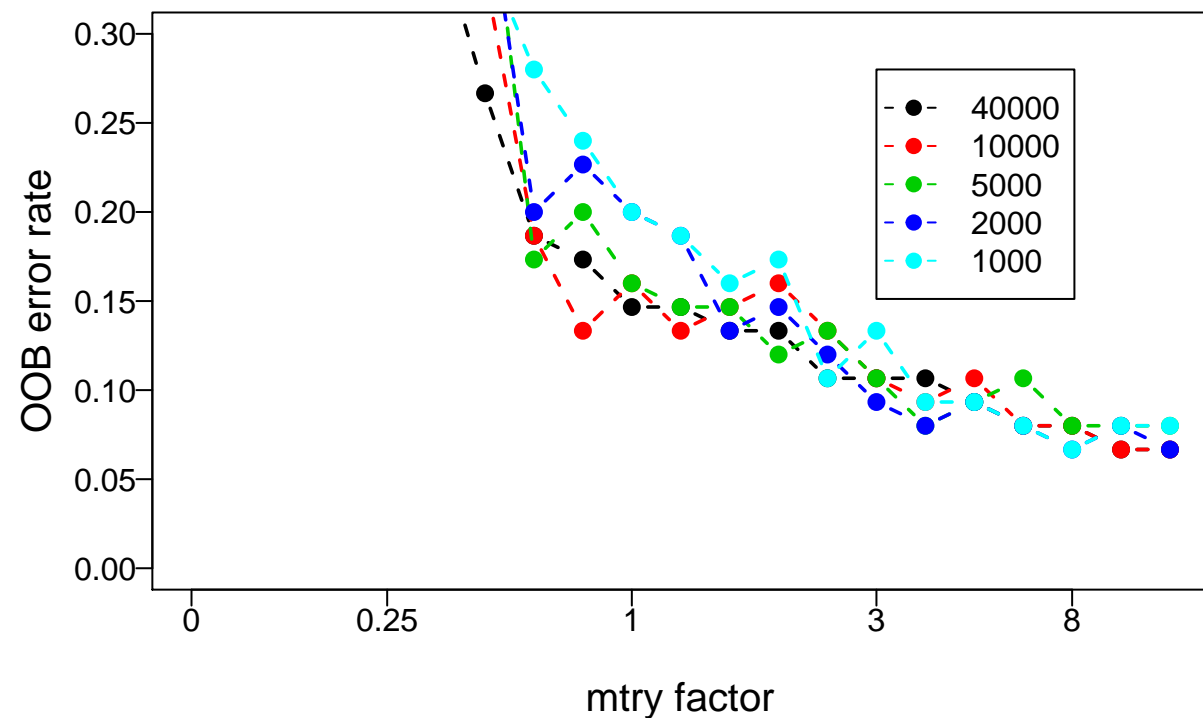
2 classes; 3 dimensions; 100 genes/dimen.; nodesize = 5



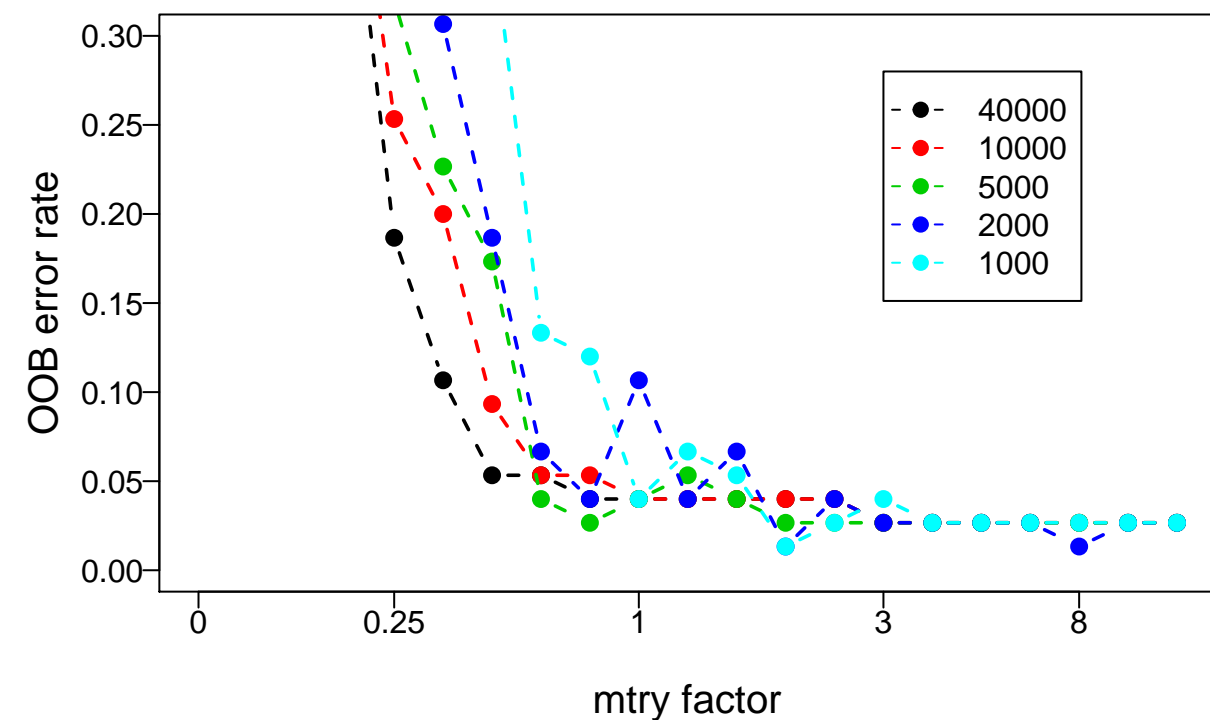
3 classes; 1 dimensions; 5 genes/dimen.; nodesize = 5



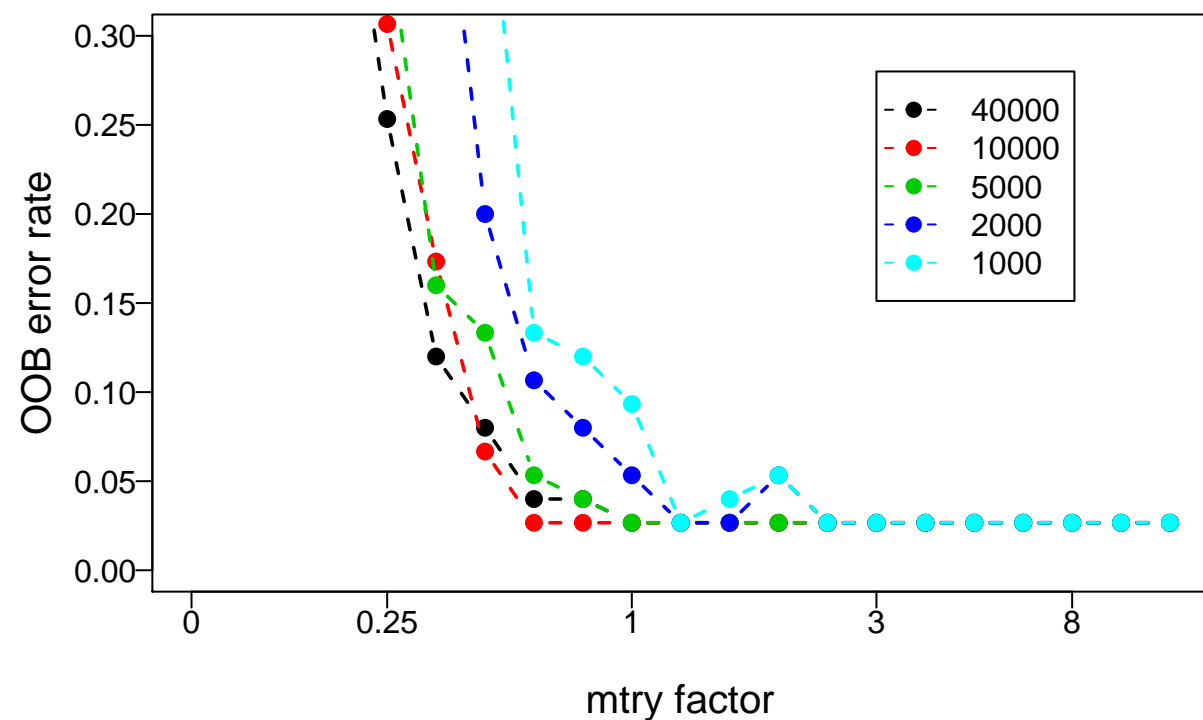
3 classes; 1 dimensions; 5 genes/dimen.; nodesize = 5



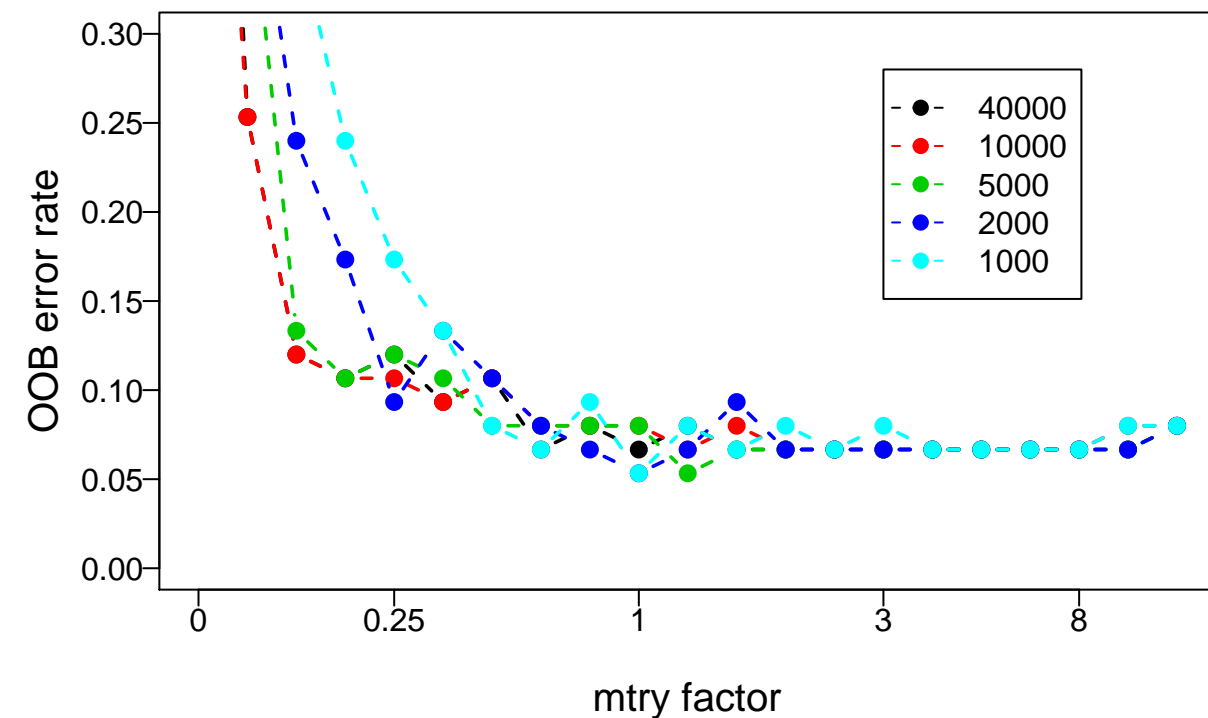
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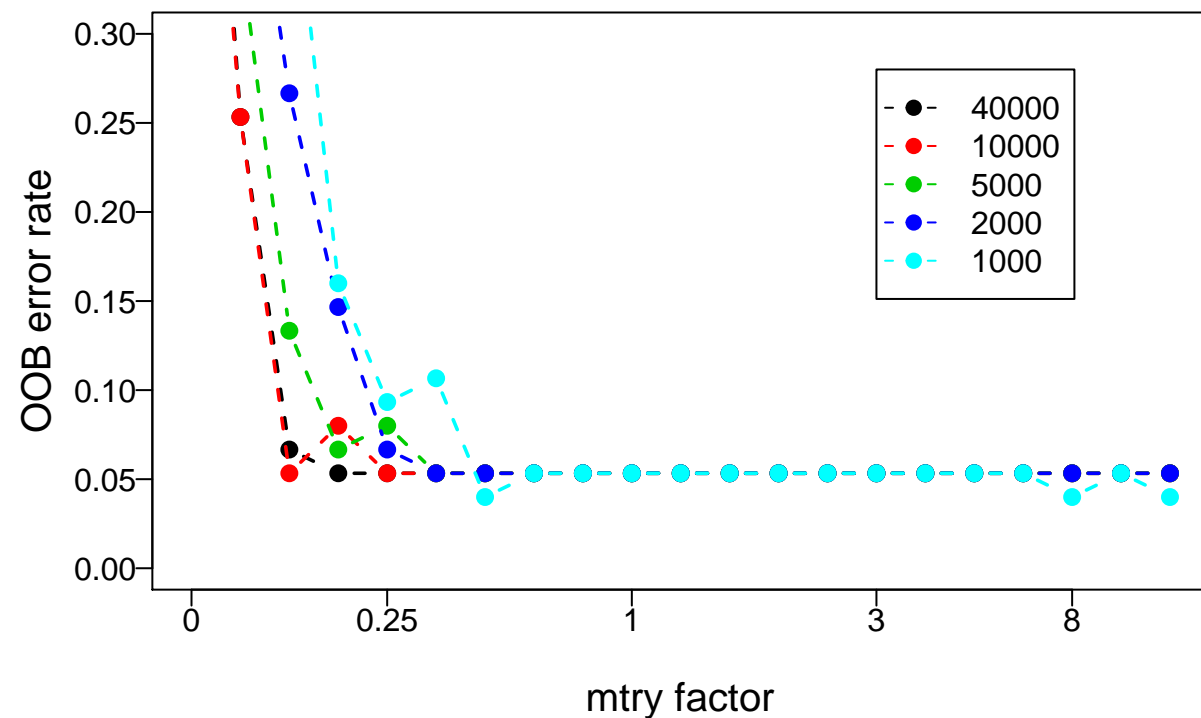
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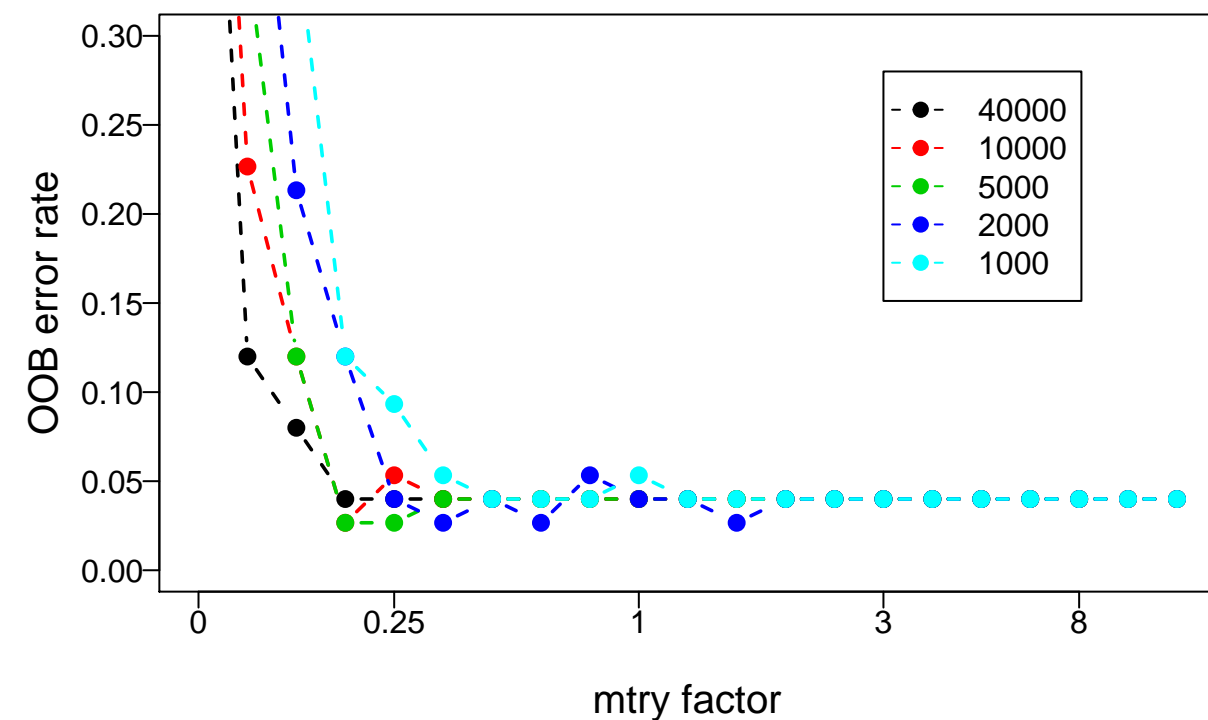
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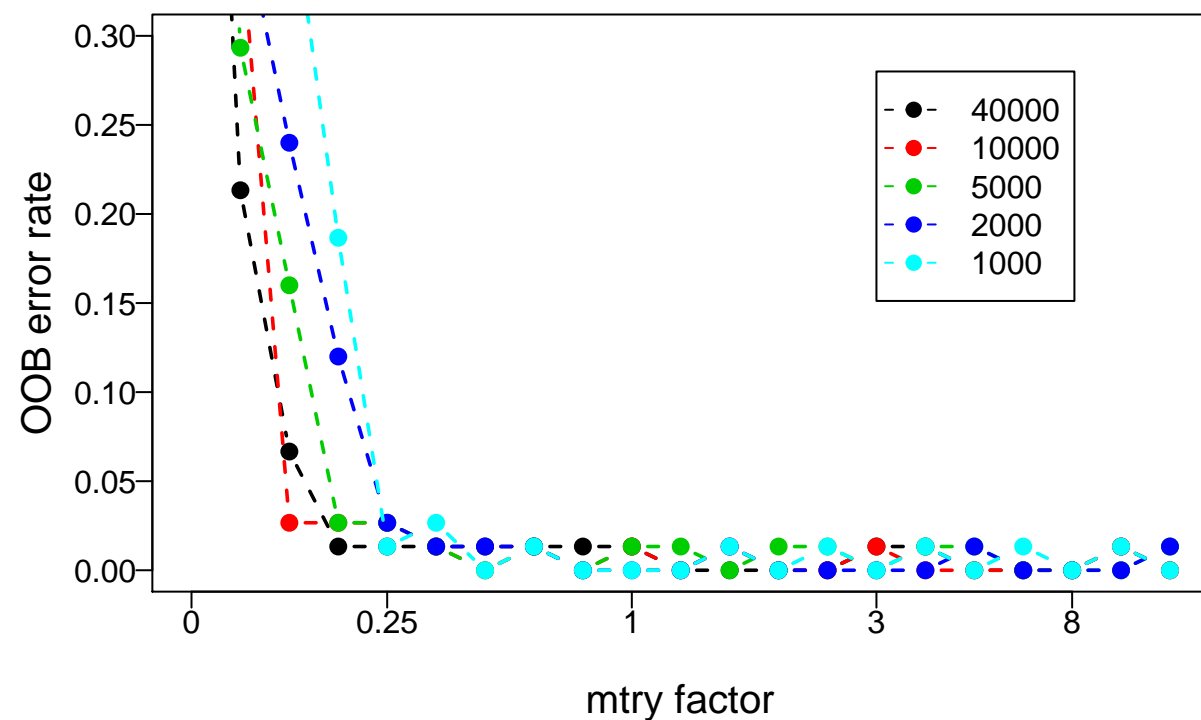
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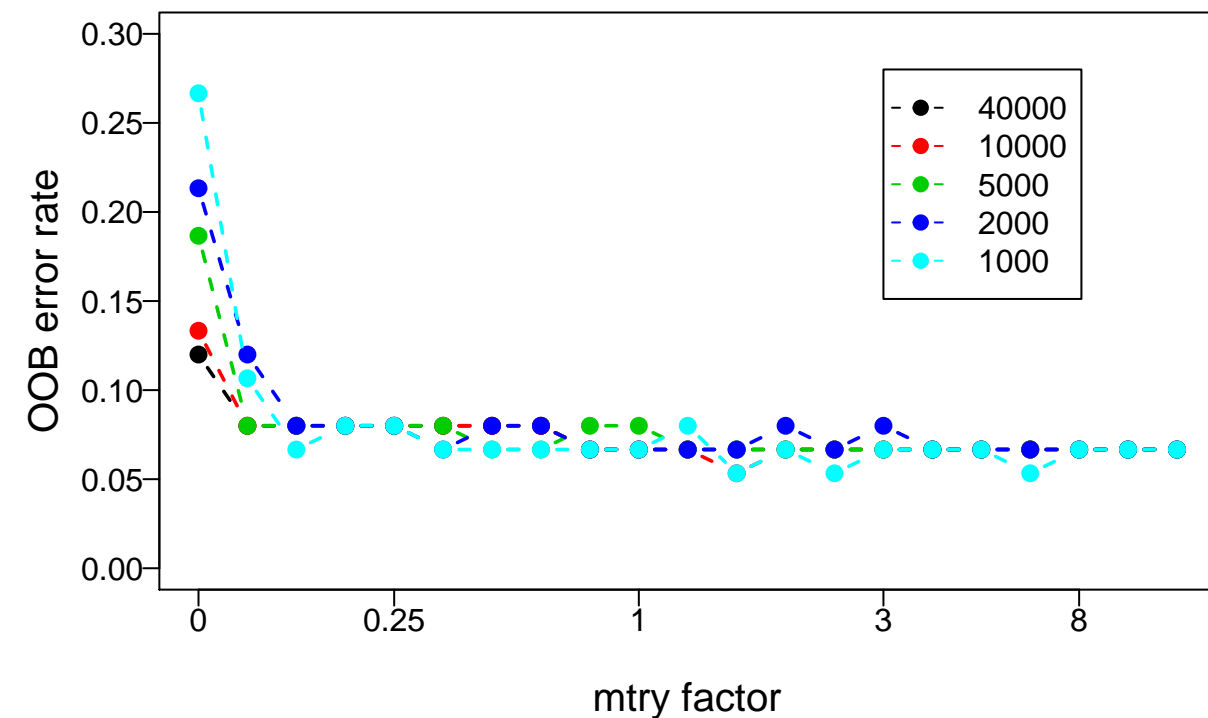
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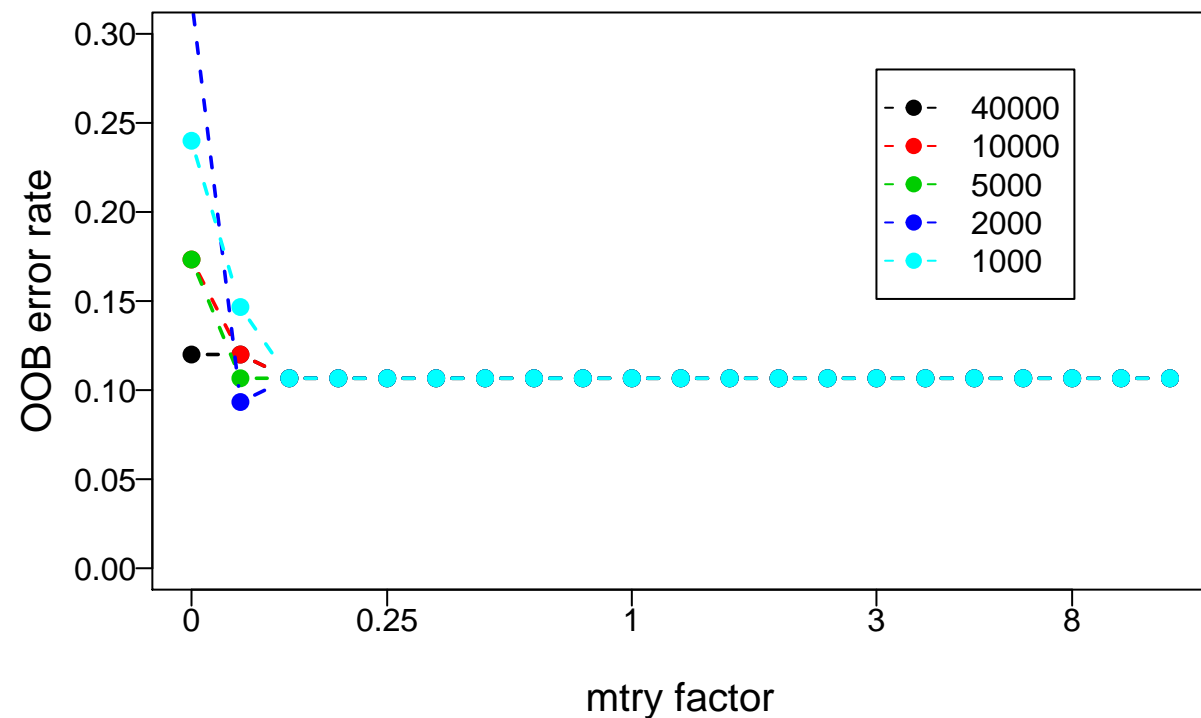
3 classes; 1 dimensions; 20 genes/dimen.; nodesize = 5



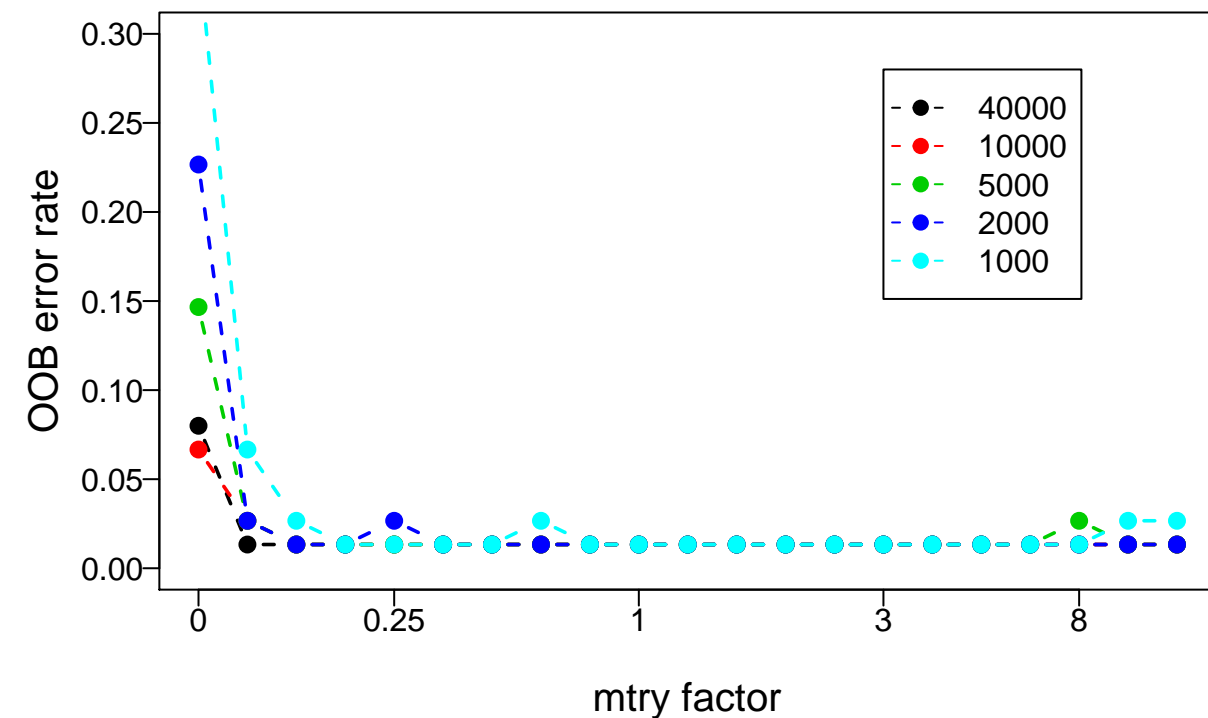
3 classes; 1 dimensions; 100 genes/dimen.; nodesize = 5



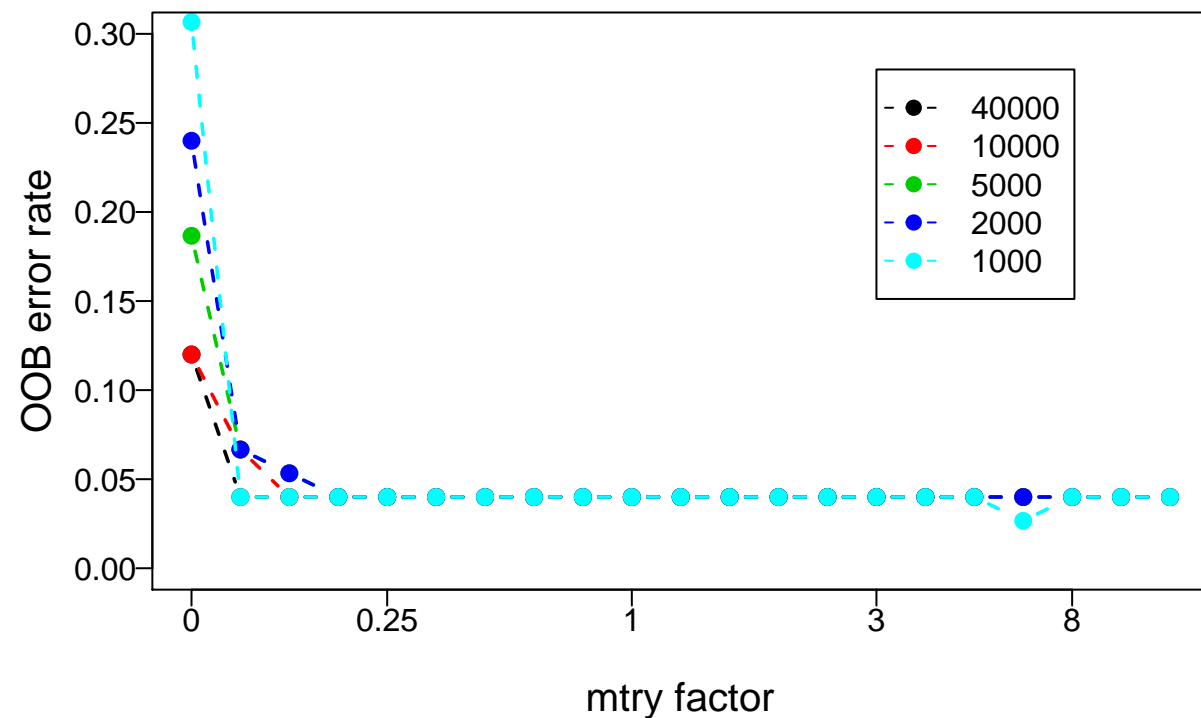
3 classes; 1 dimensions; 100 genes/dimen.; nodesize = 5



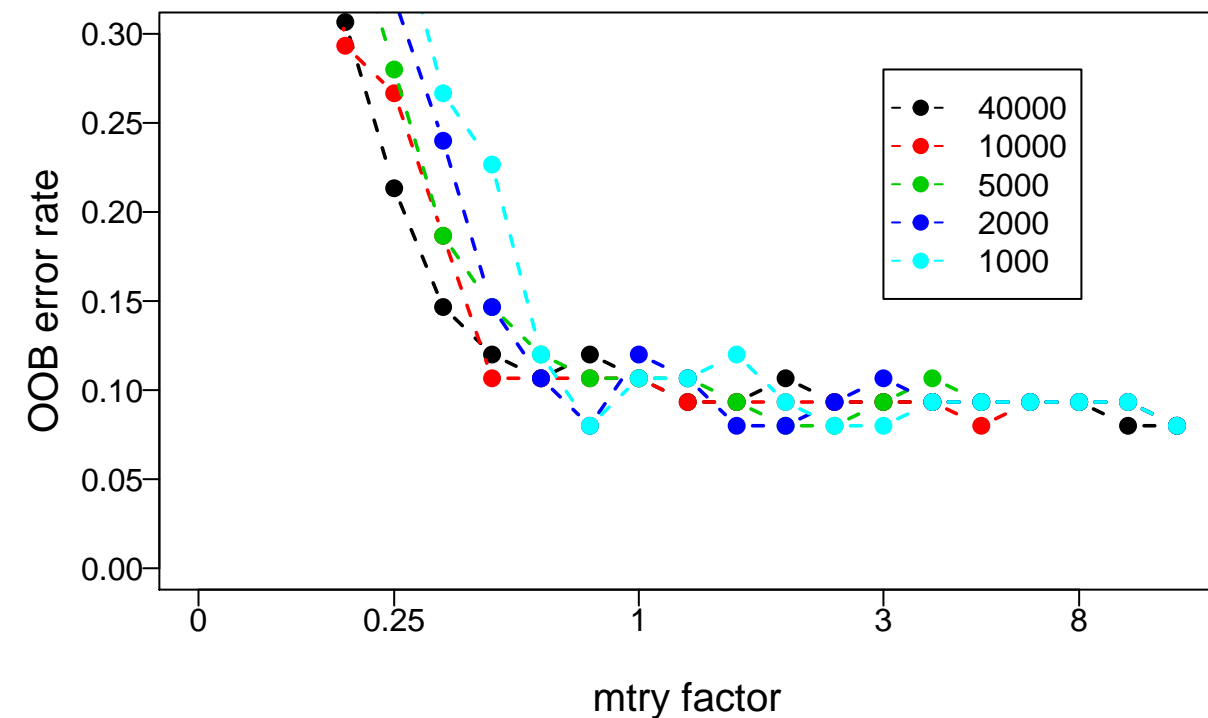
3 classes; 1 dimensions; 100 genes/dimen.; nodesize = 5



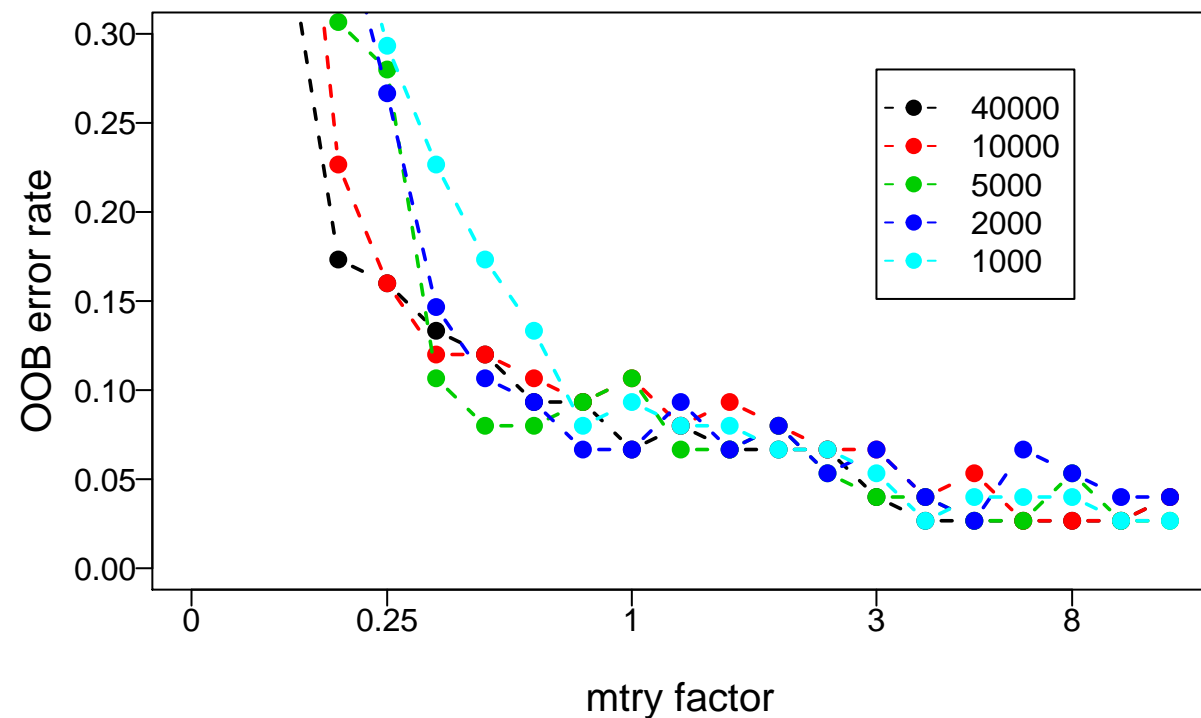
3 classes; 1 dimensions; 100 genes/dimen.; nodesize = 5



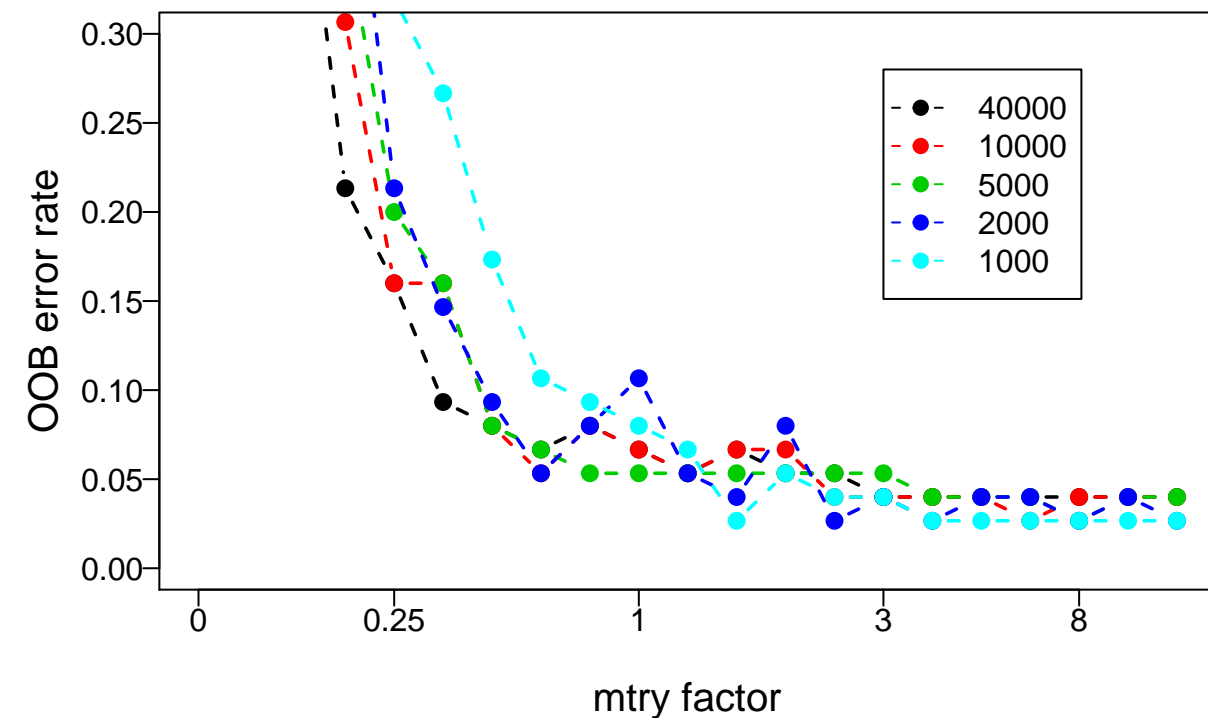
3 classes; 2 dimensions; 5 genes/dimen.; nodesize = 5



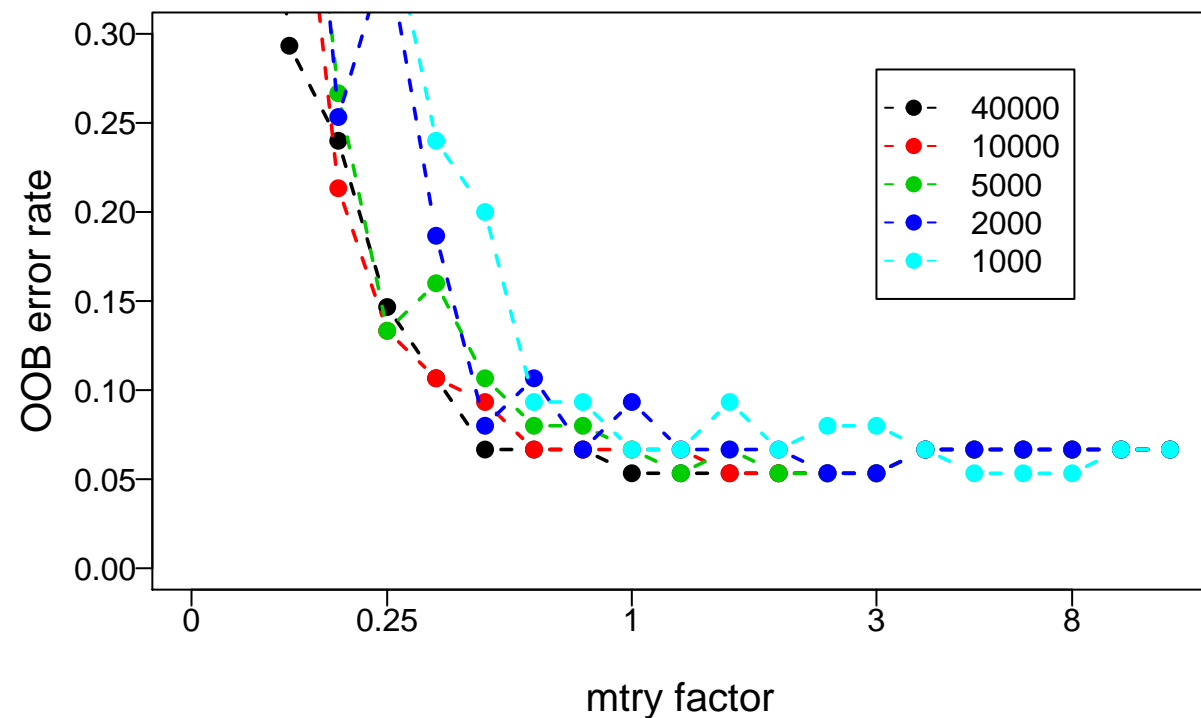
3 classes; 2 dimensions; 5 genes/dimen.; nodesize = 5



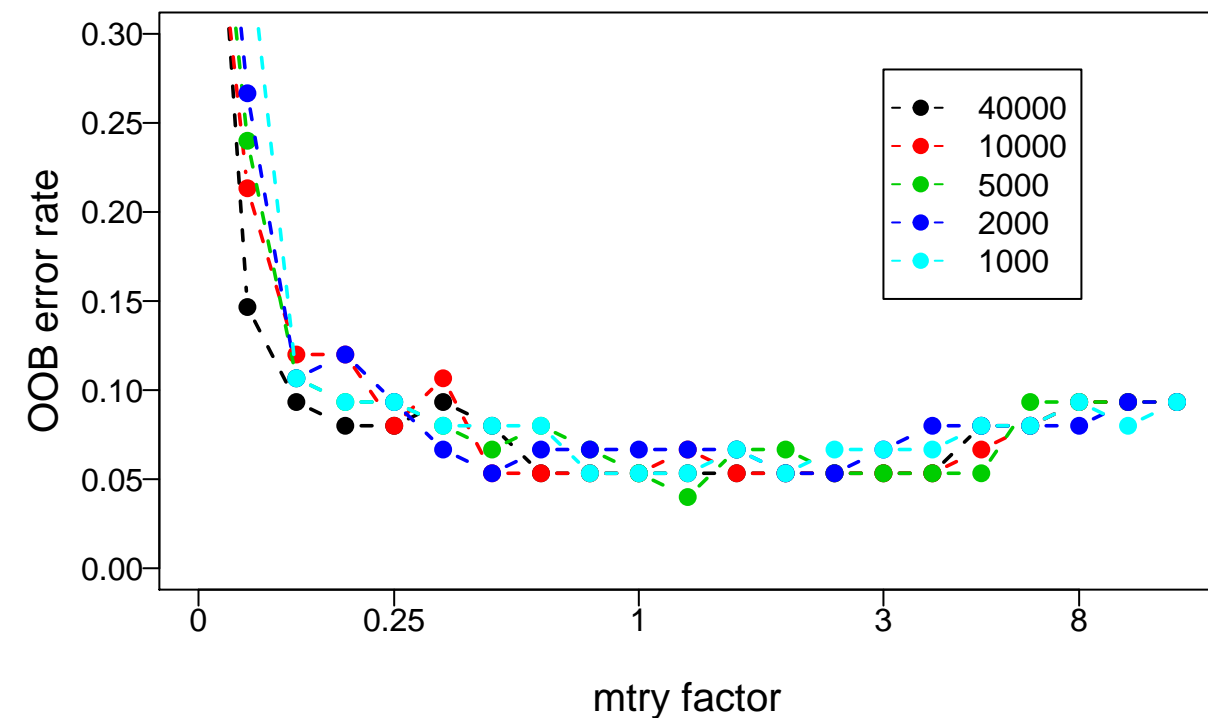
3 classes; 2 dimensions; 5 genes/dimen.; nodesize = 5



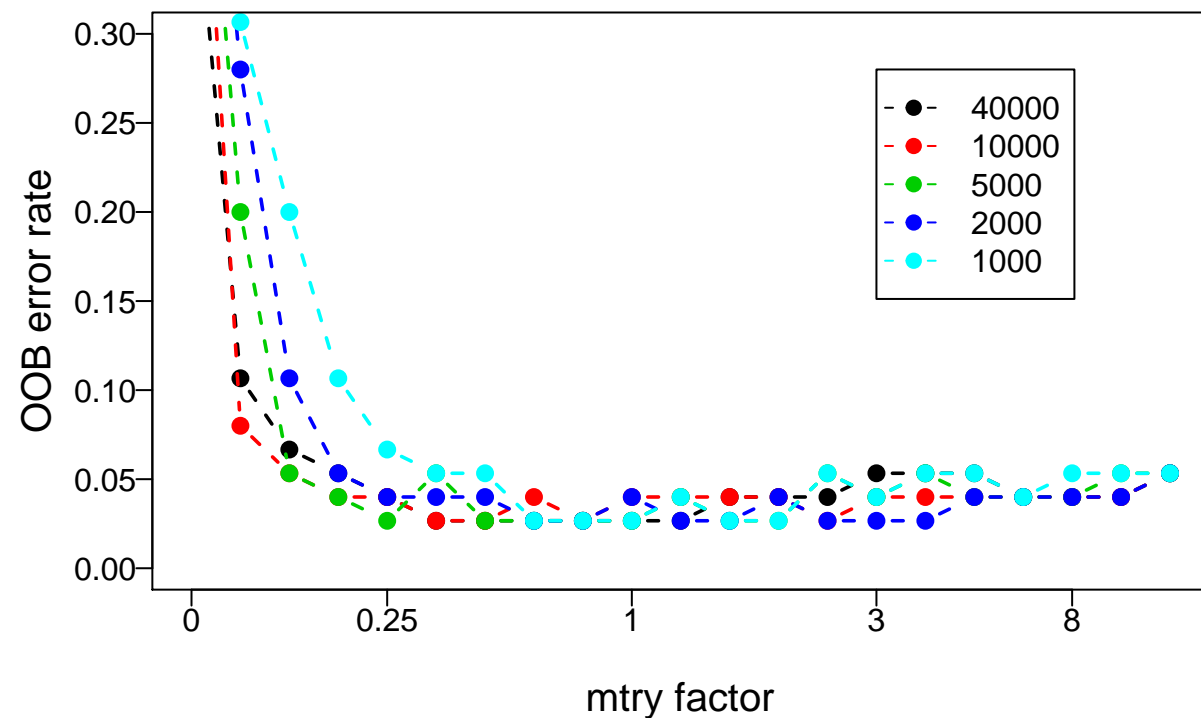
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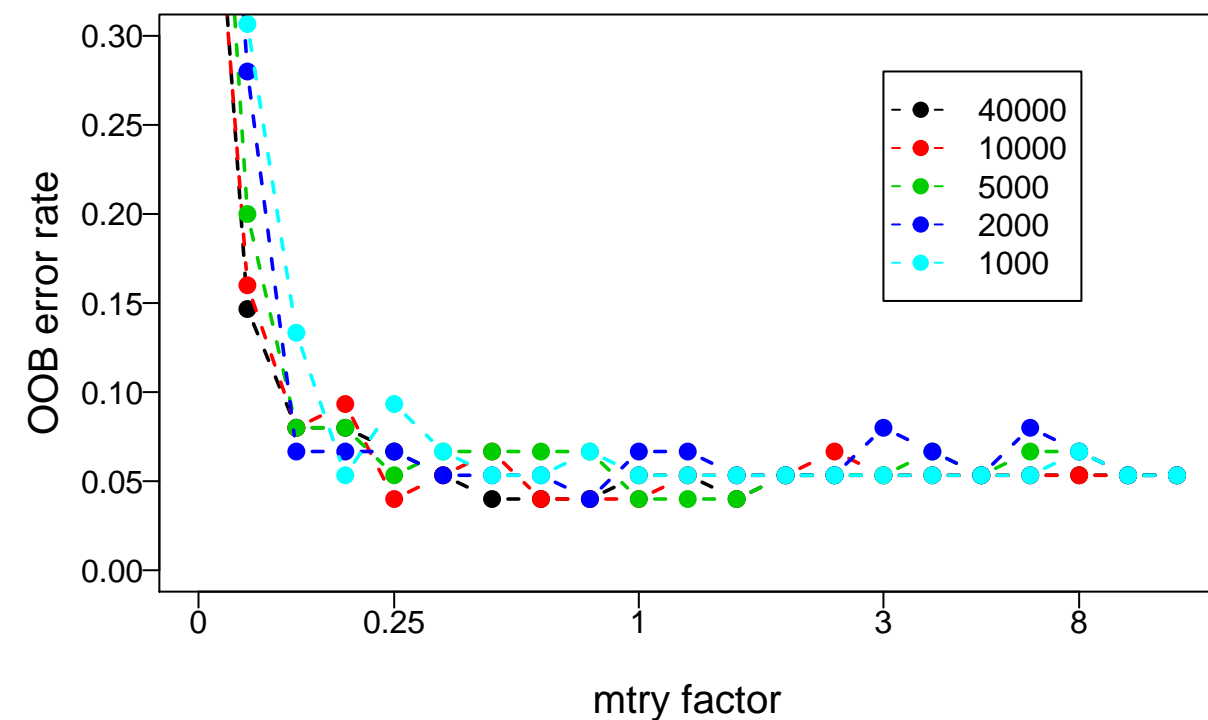
3 classes; 2 dimensions; 20 genes/dimen.; nodesize = 5



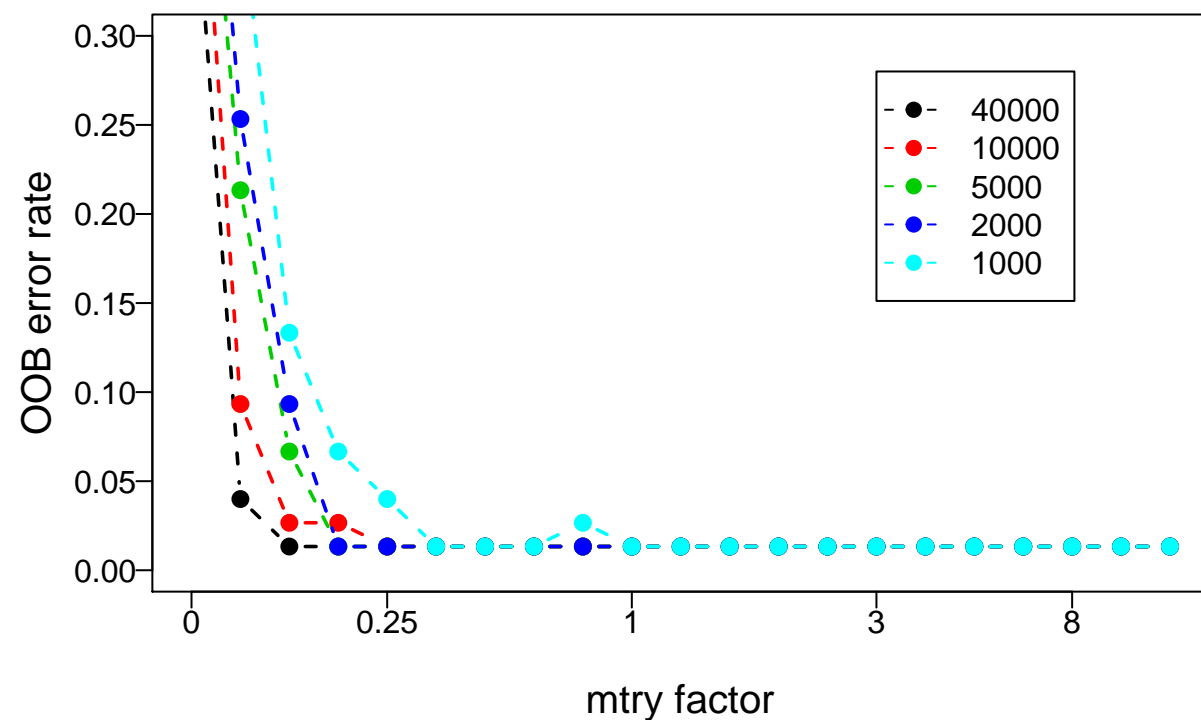
3 classes; 2 dimensions; 20 genes/dimen.; nodesize = 5



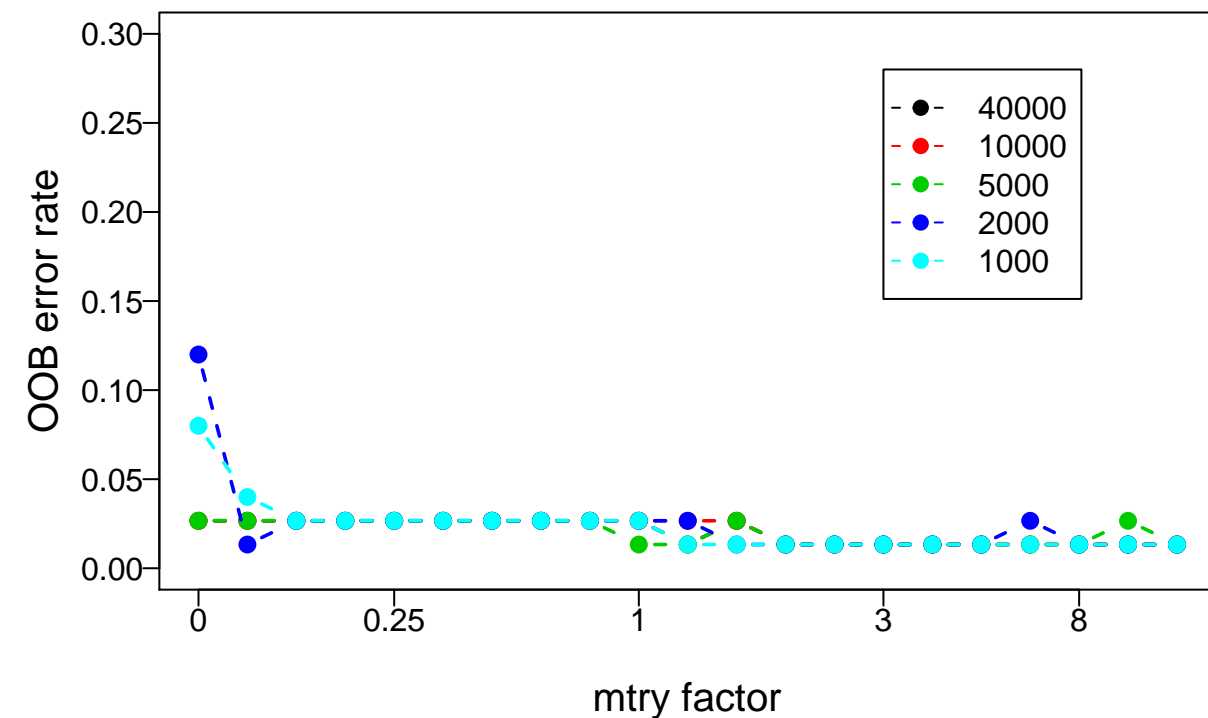
3 classes; 2 dimensions; 20 genes/dimen.; nodesize = 5



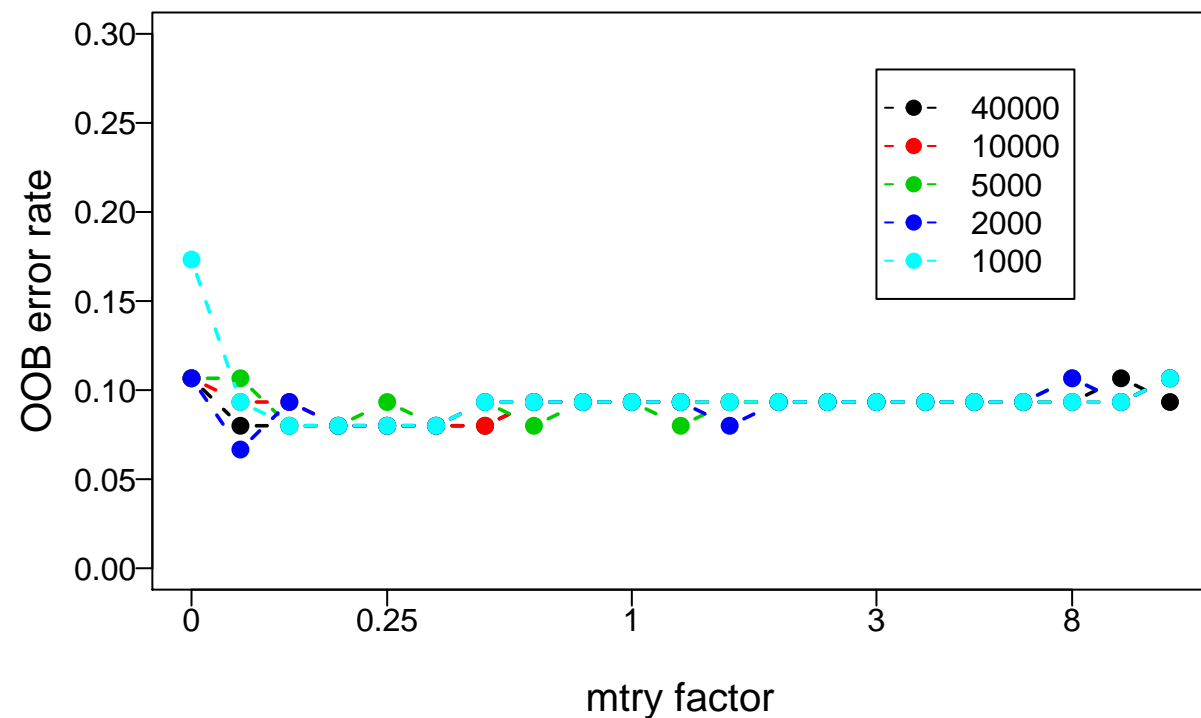
3 classes; 2 dimensions; 20 genes/dimen.; nodesize = 5



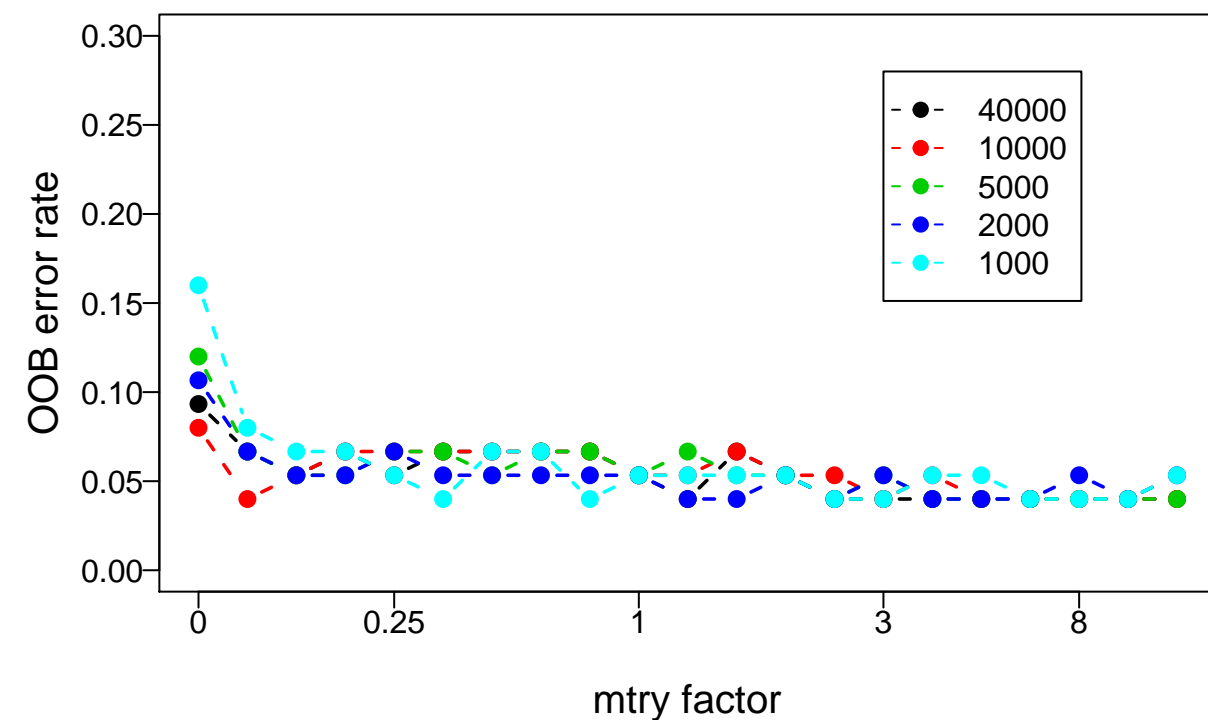
3 classes; 2 dimensions; 100 genes/dimen.; nodesize = 5



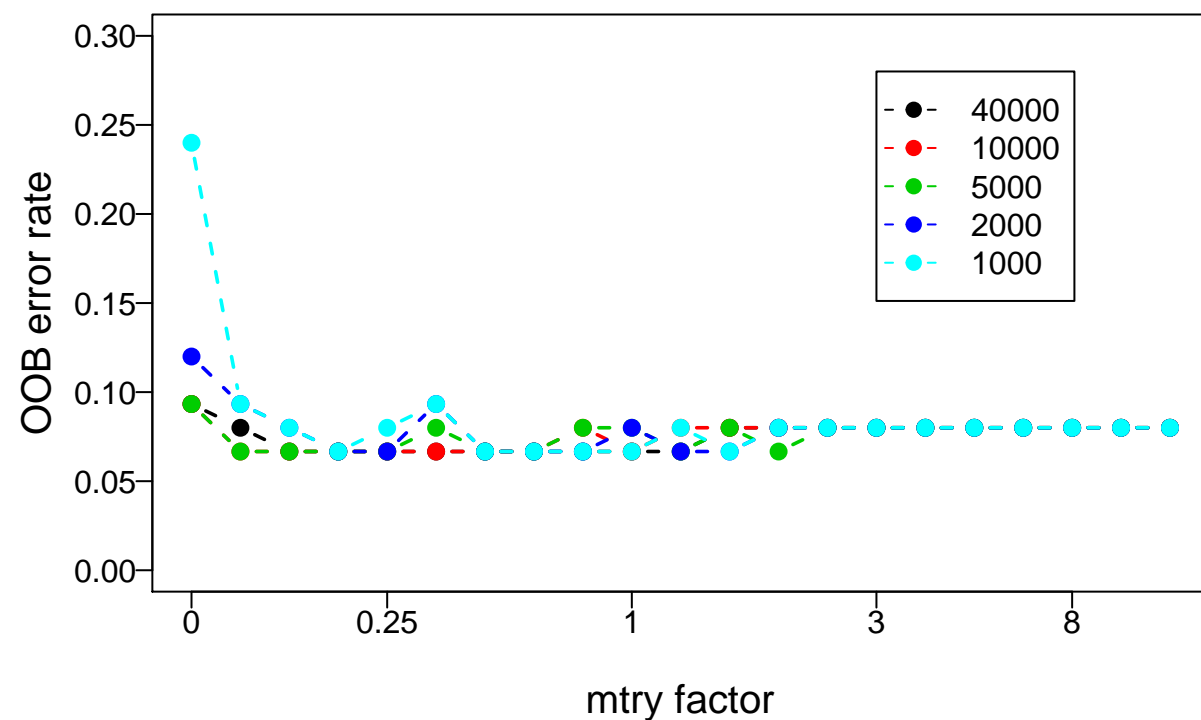
3 classes; 2 dimensions; 100 genes/dimen.; nodesize = 5



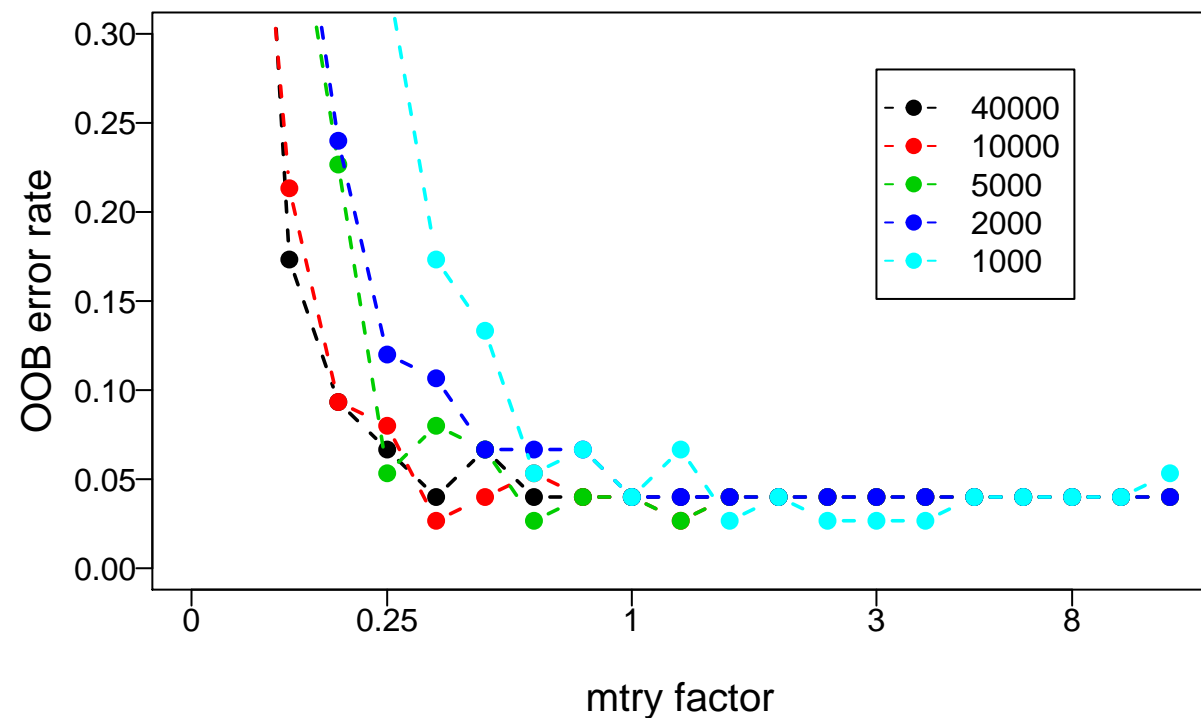
3 classes; 2 dimensions; 100 genes/dimen.; nodesize = 5



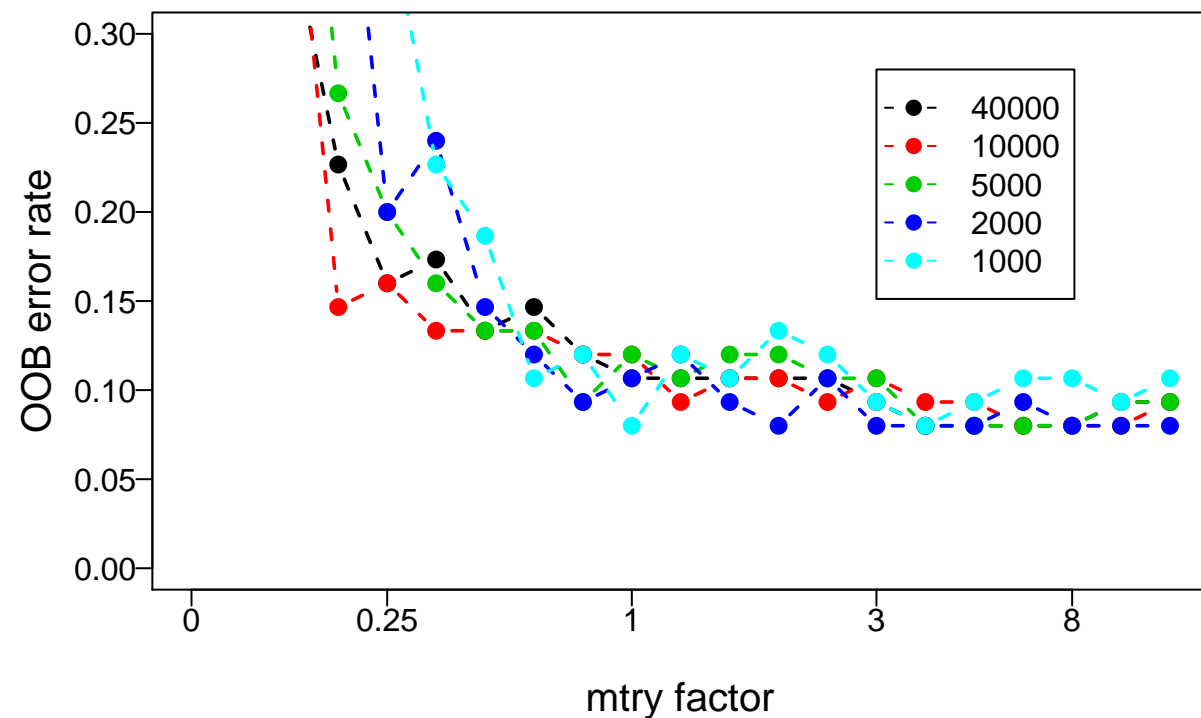
3 classes; 2 dimensions; 100 genes/dimen.; nodesize = 5



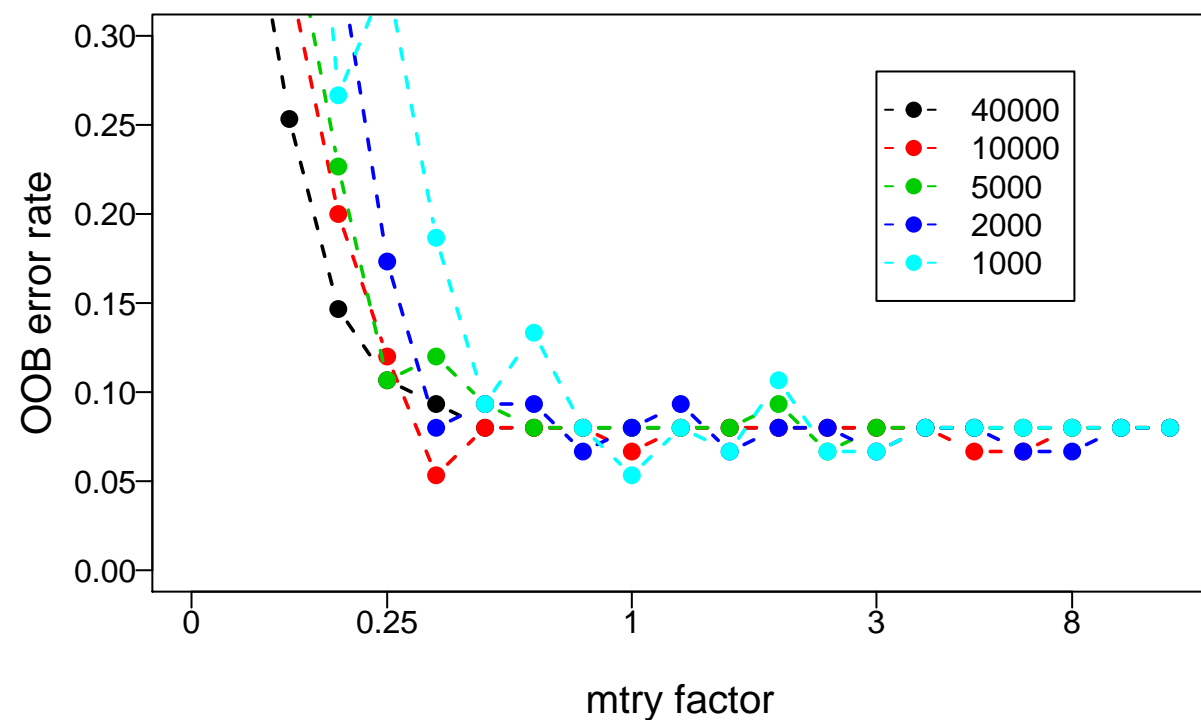
3 classes; 3 dimensions; 5 genes/dimen.; nodesize = 5



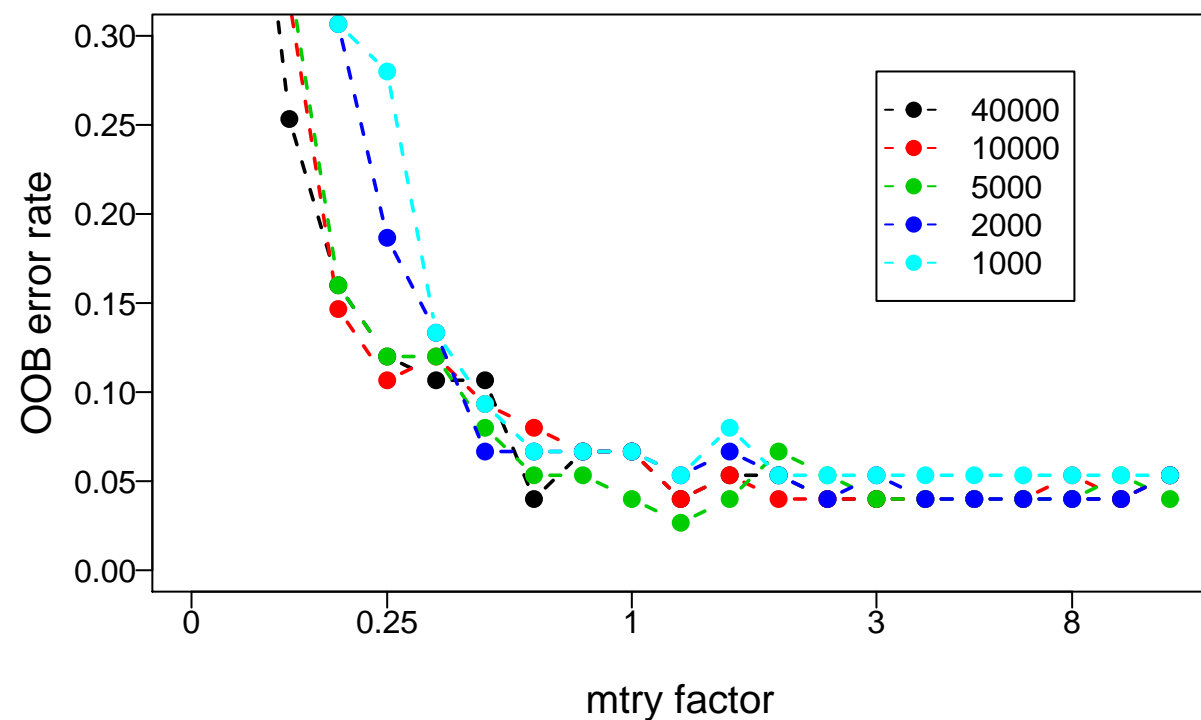
3 classes; 3 dimensions; 5 genes/dimen.; nodesize = 5



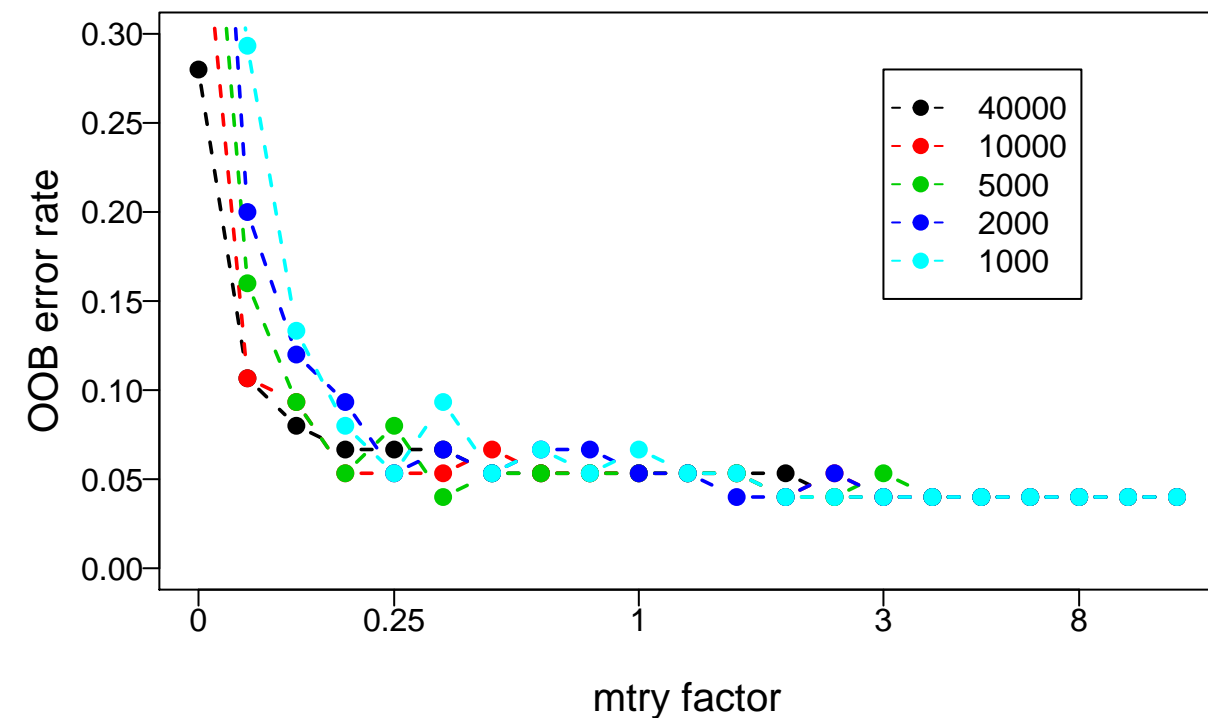
3 classes; 3 dimensions; 5 genes/dimen.; nodesize = 5



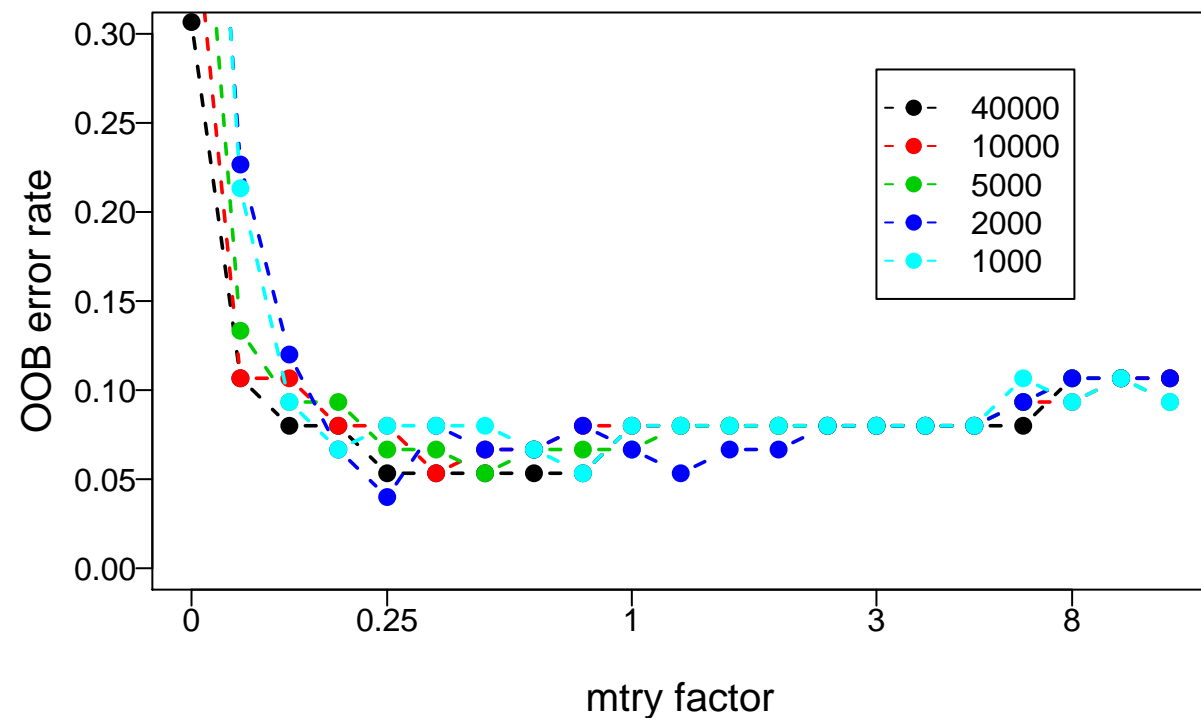
3 classes; 3 dimensions; 5 genes/dimen.; nodesize = 5



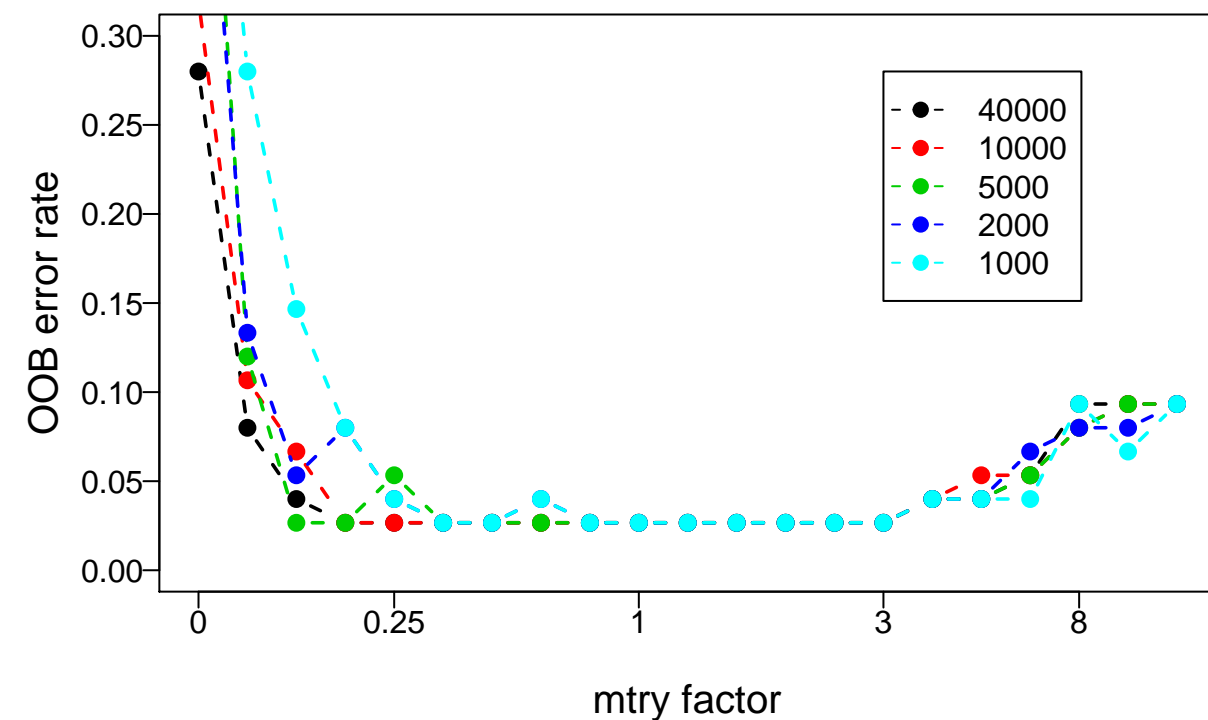
3 classes; 3 dimensions; 20 genes/dimen.; nodesize = 5



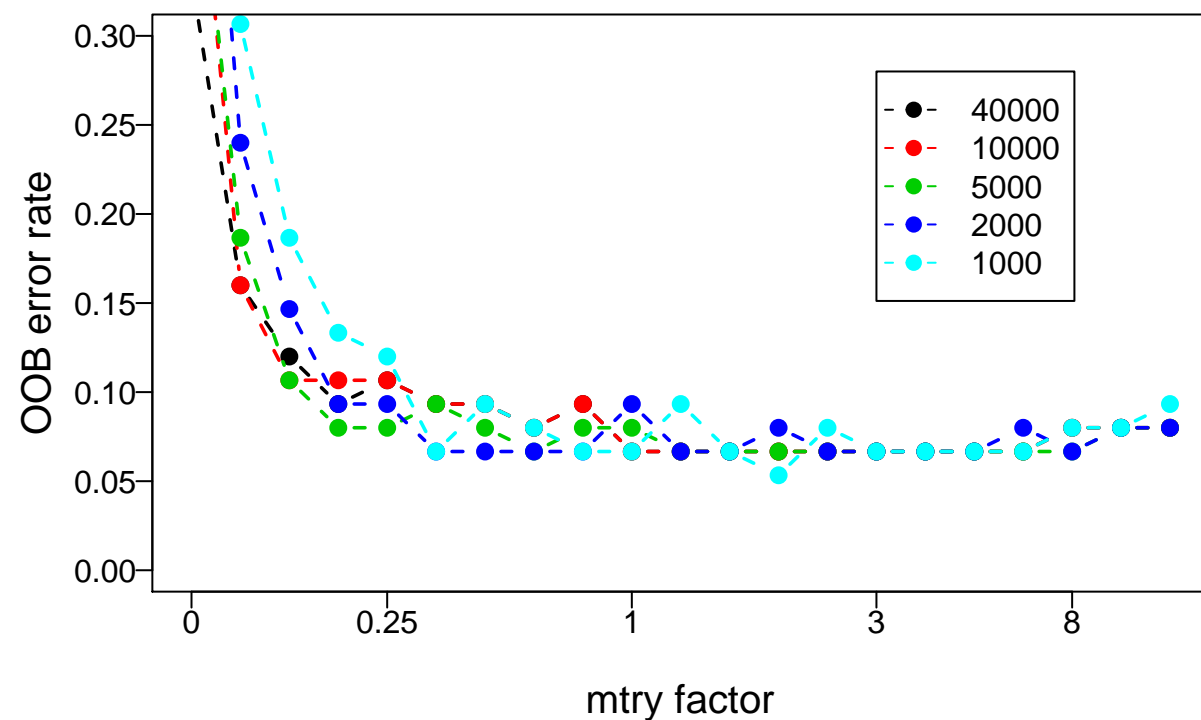
3 classes; 3 dimensions; 20 genes/dimen.; nodesize = 5



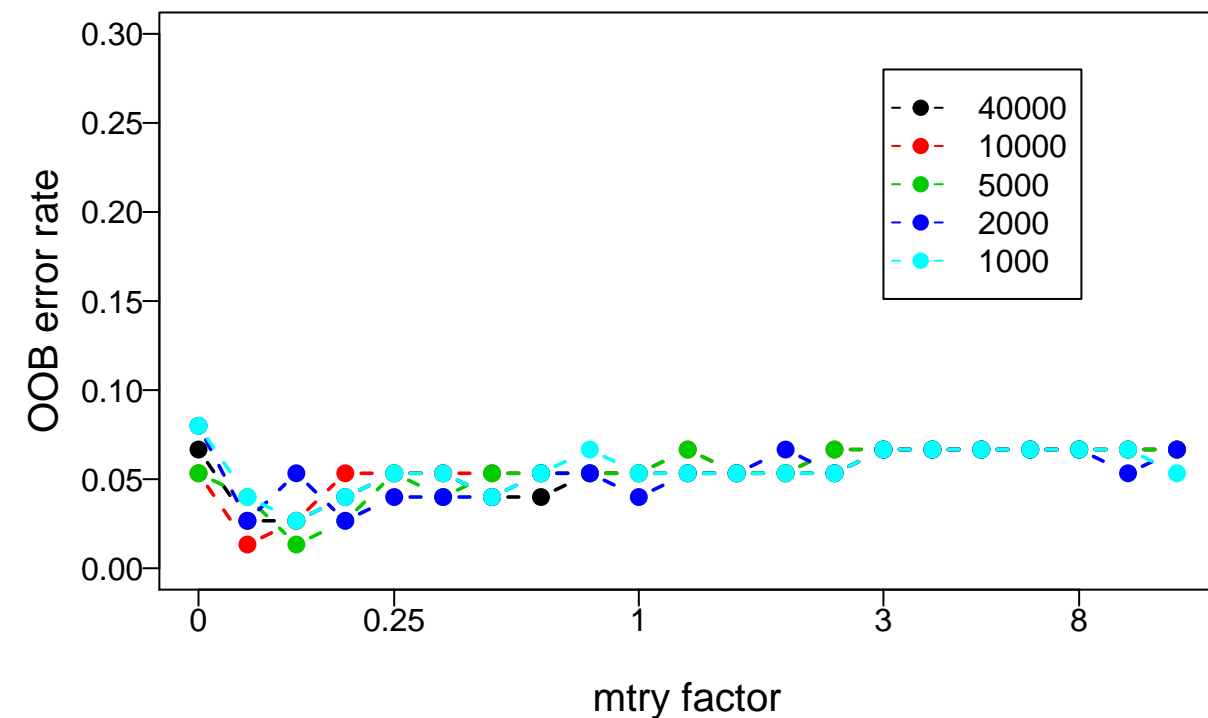
3 classes; 3 dimensions; 20 genes/dimen.; nodesize = 5



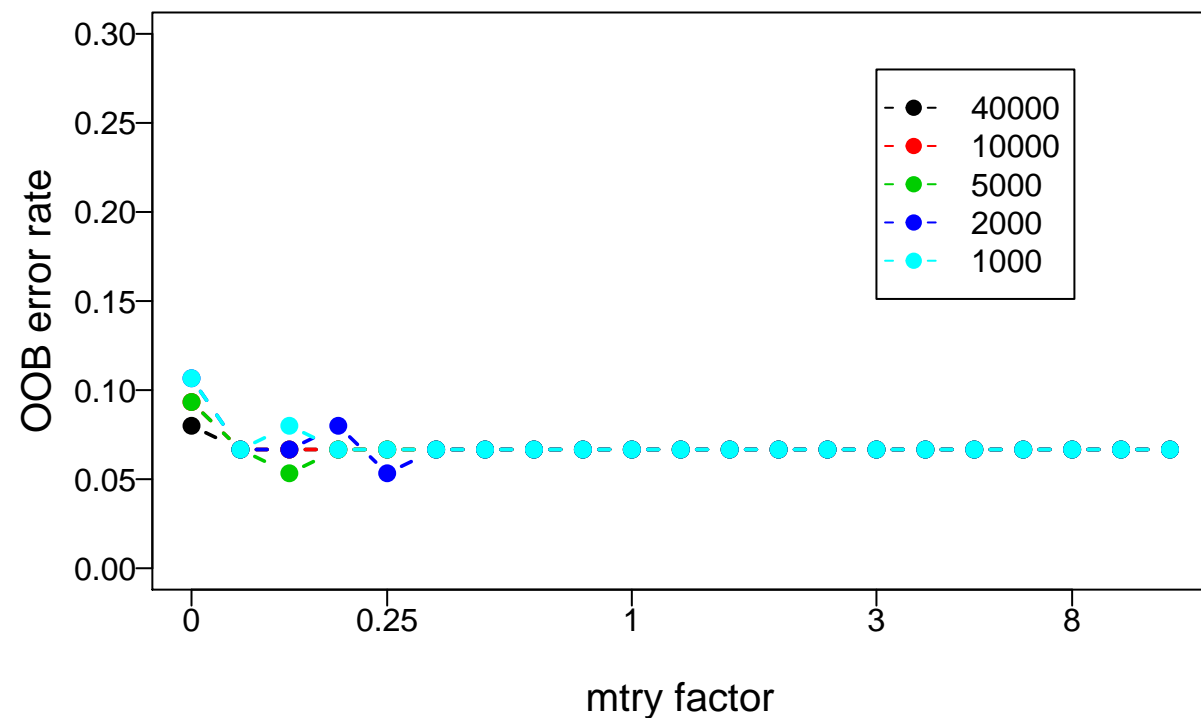
3 classes; 3 dimensions; 20 genes/dimen.; nodesize = 5



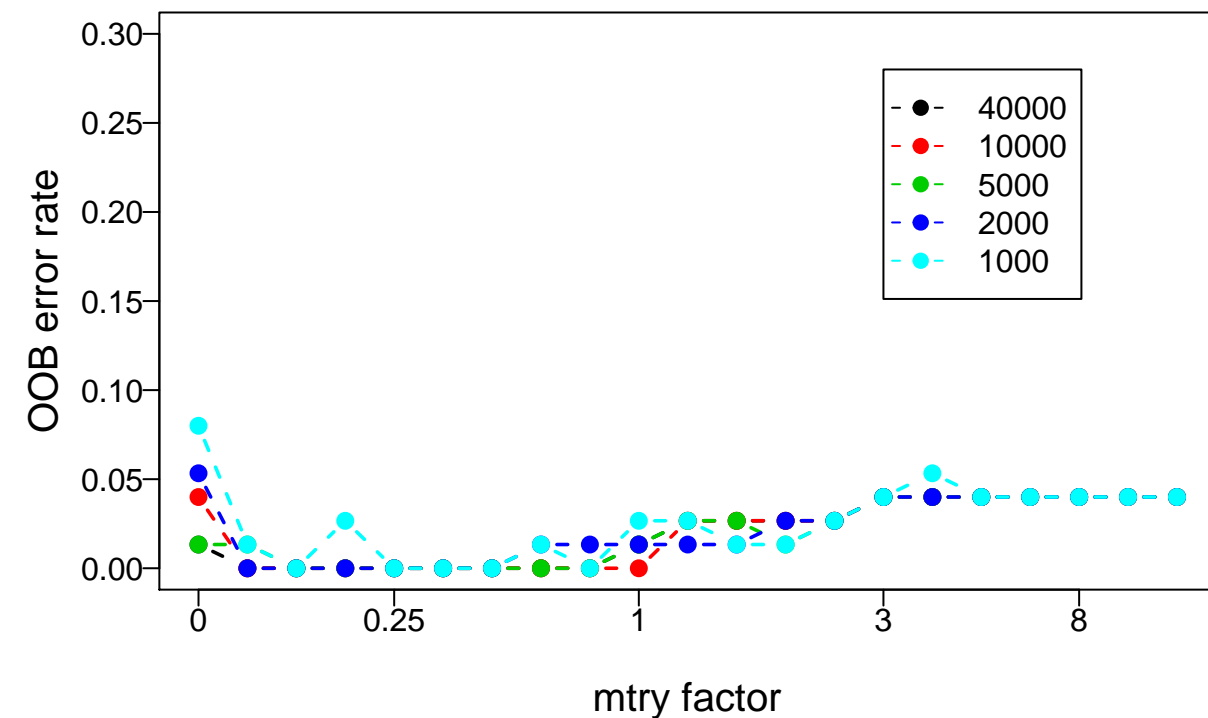
3 classes; 3 dimensions; 100 genes/dimen.; nodesize = 5



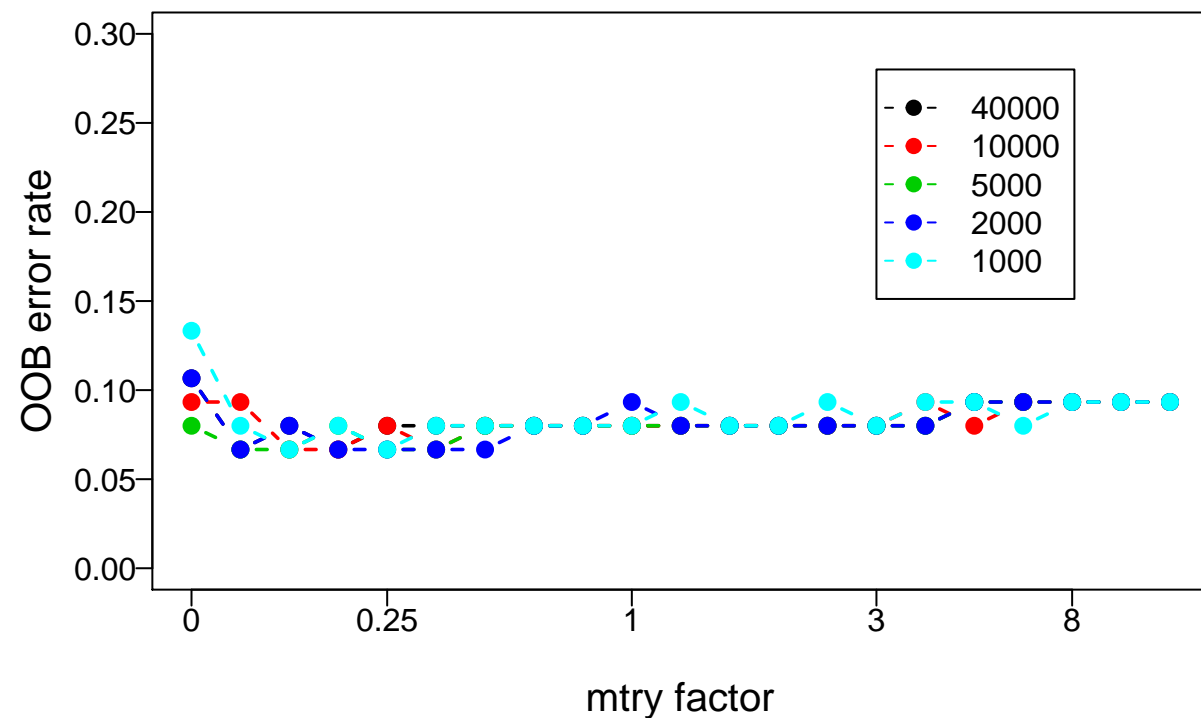
3 classes; 3 dimensions; 100 genes/dimen.; nodesize = 5



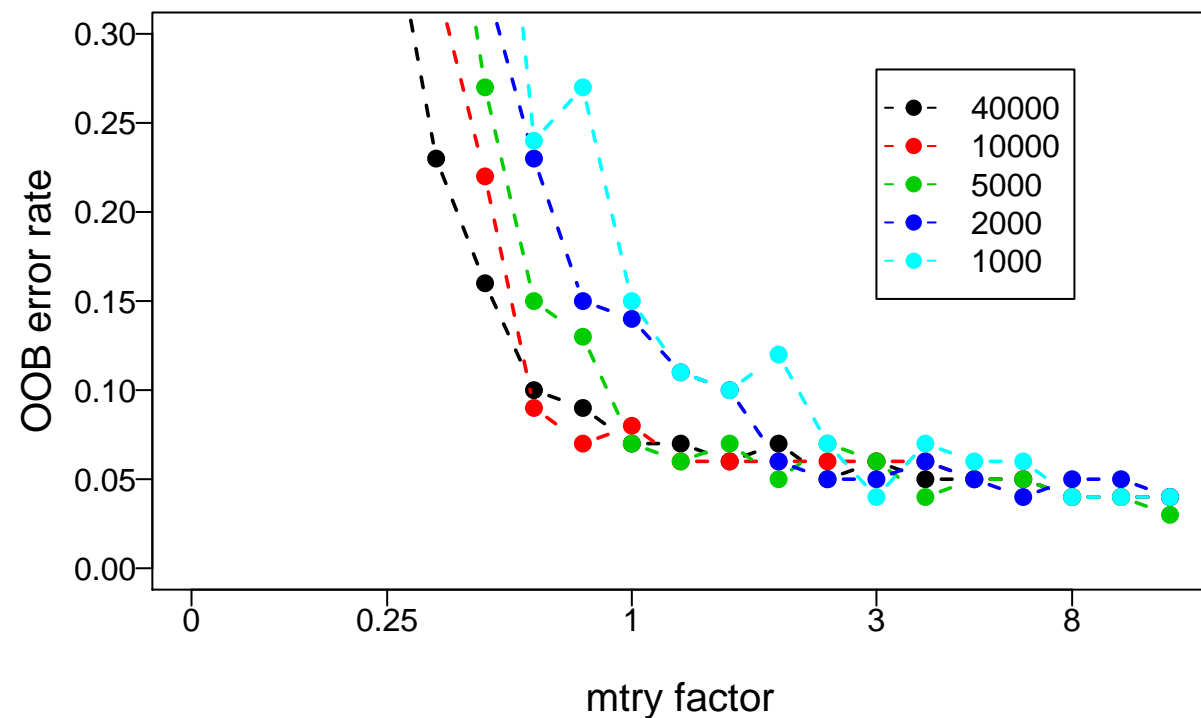
3 classes; 3 dimensions; 100 genes/dimen.; nodesize = 5



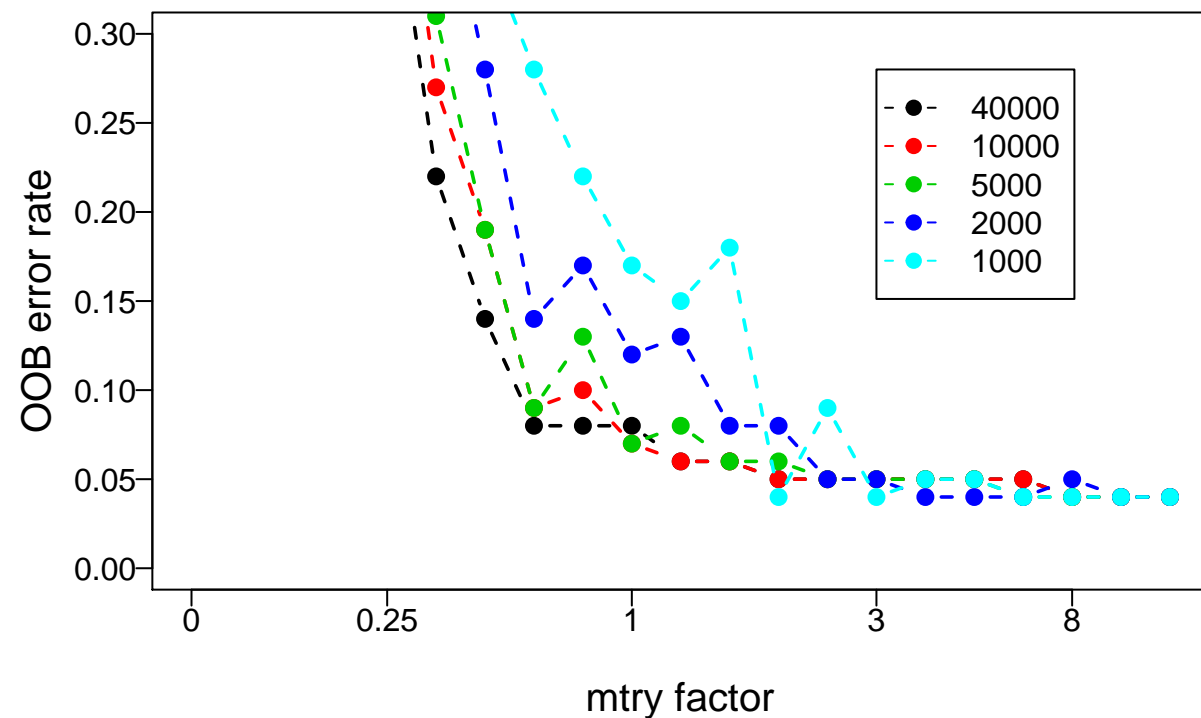
3 classes; 3 dimensions; 100 genes/dimen.; nodesize = 5



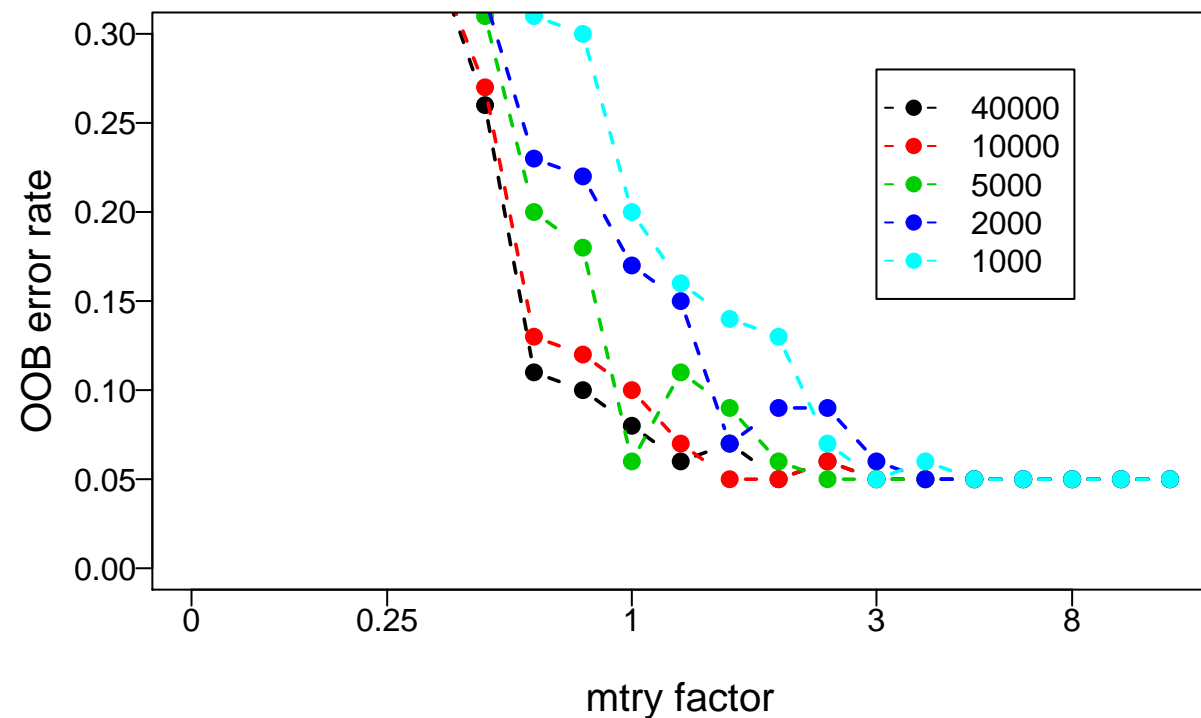
4 classes; 1 dimensions; 5 genes/dimen.; nodesize = 5



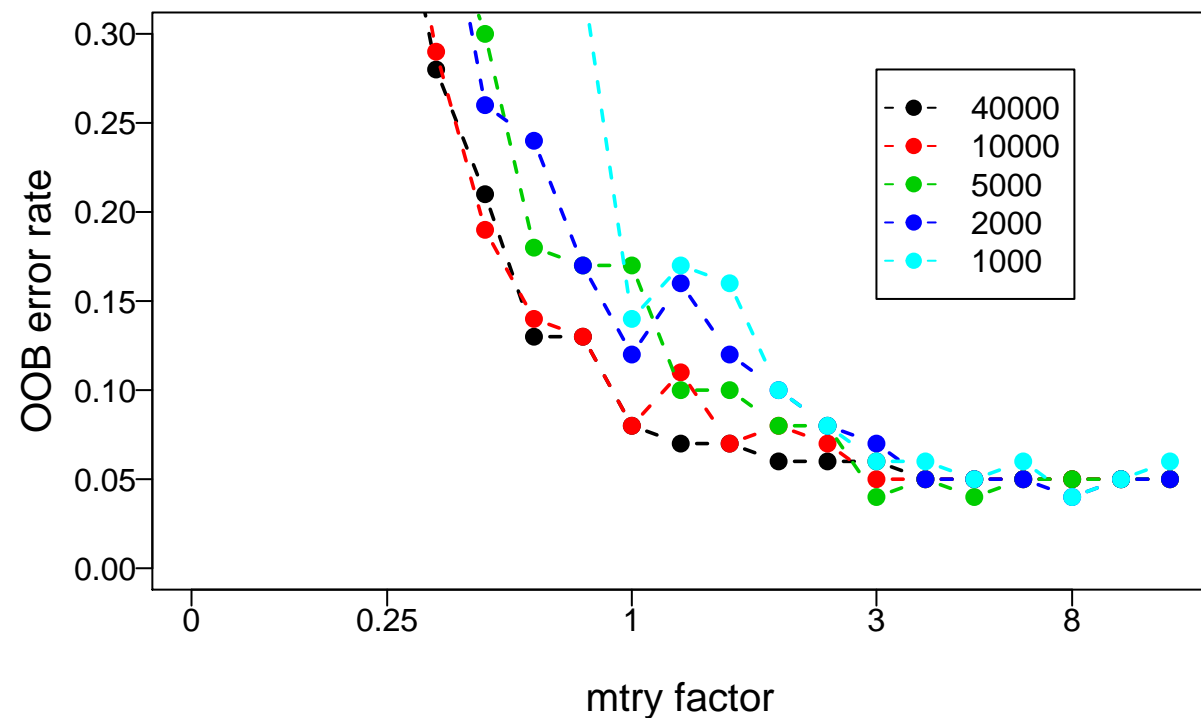
4 classes; 1 dimensions; 5 genes/dimen.; nodesize = 5



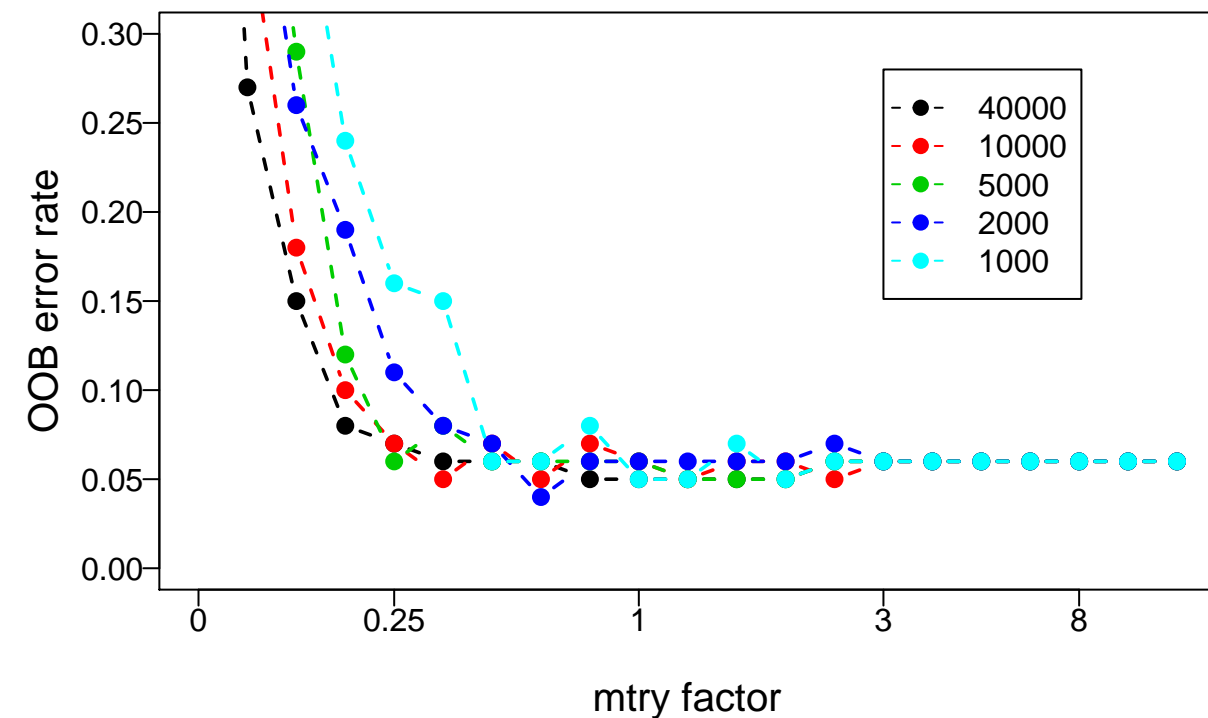
4 classes; 1 dimensions; 5 genes/dimen.; nodesize = 5



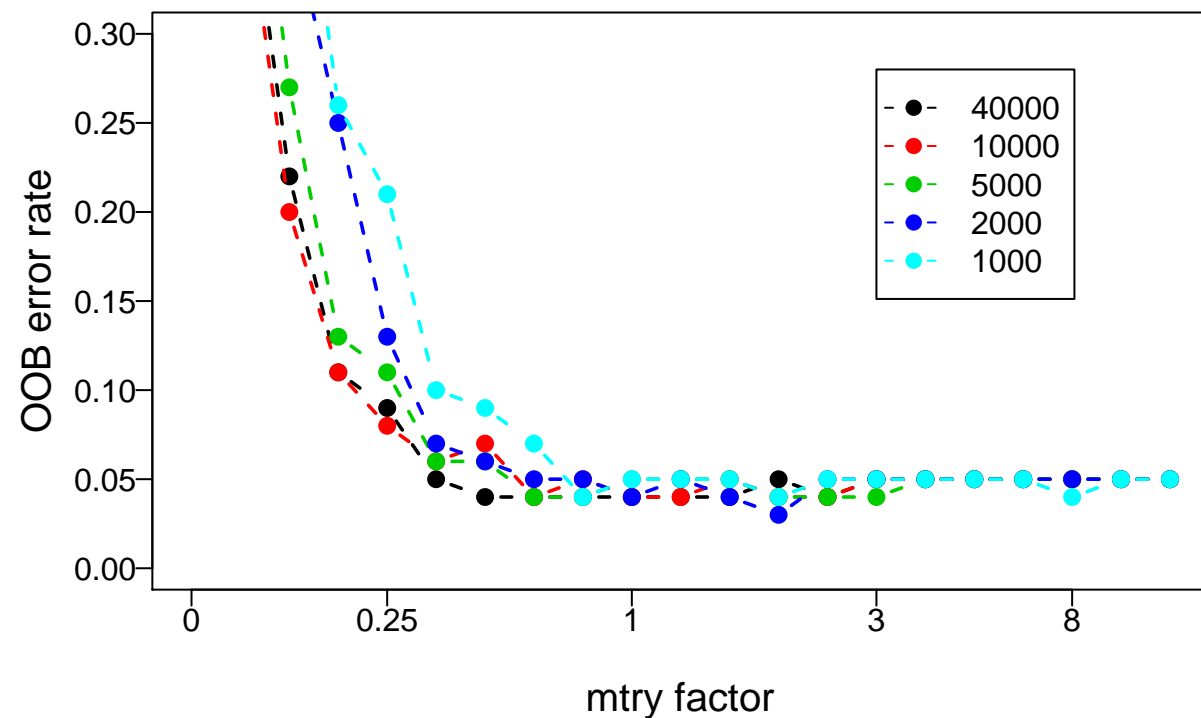
4 classes; 1 dimensions; 5 genes/dimen.; nodesize = 5



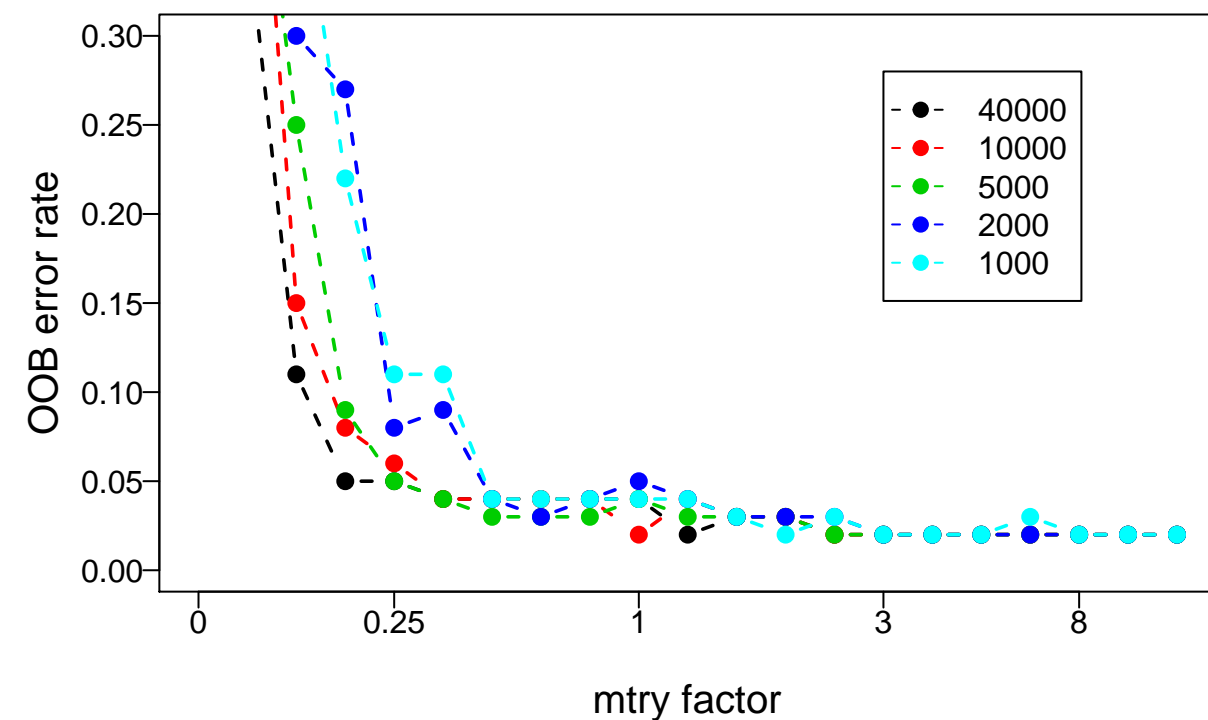
4 classes; 1 dimensions; 20 genes/dimen.; nodesize = 5



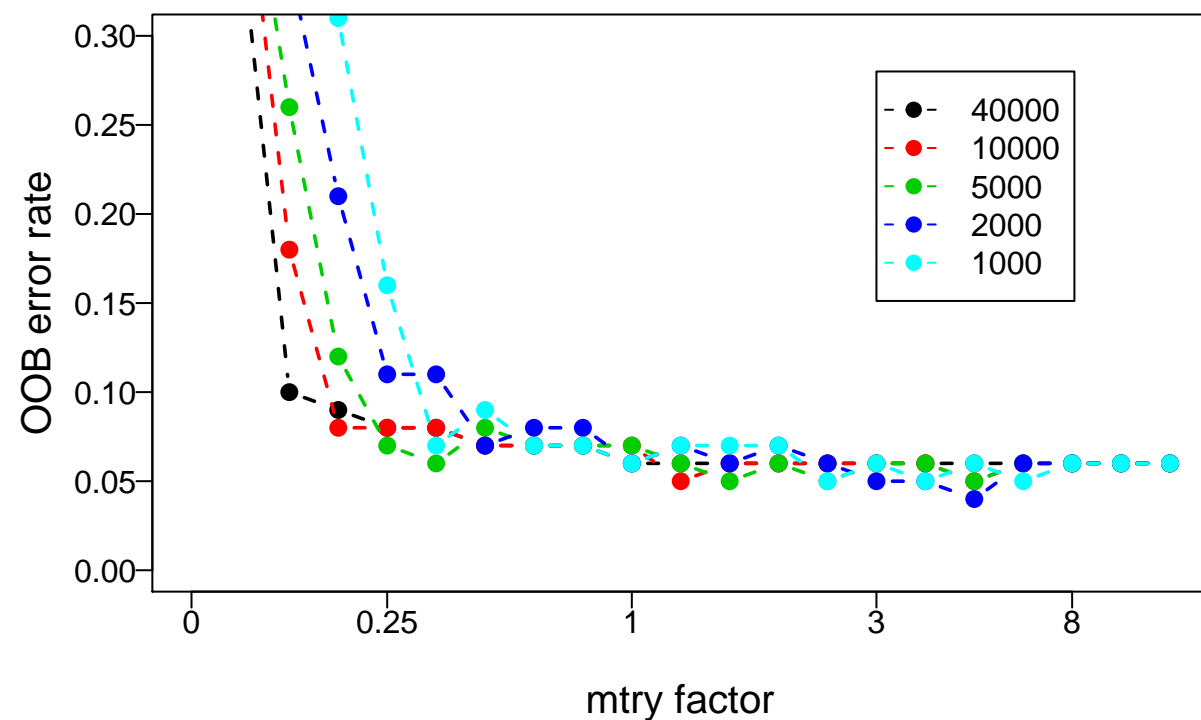
4 classes; 1 dimensions; 20 genes/dimen.; nodesize = 5



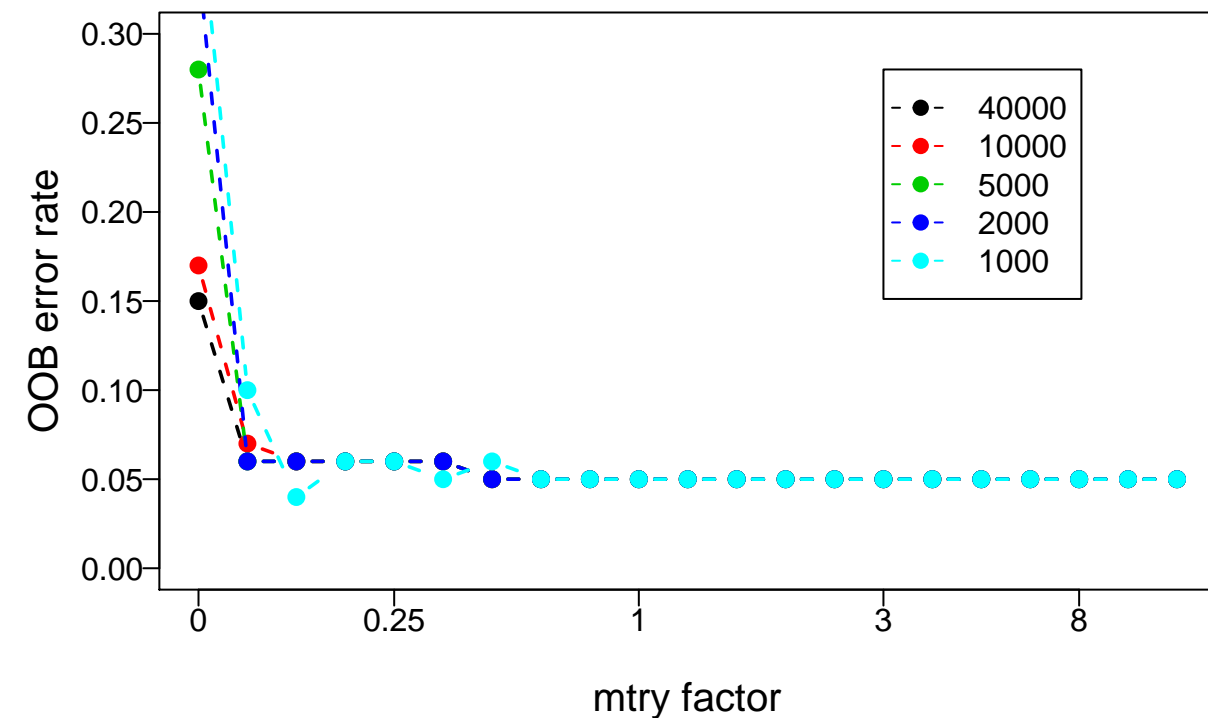
4 classes; 1 dimensions; 20 genes/dimen.; nodesize = 5



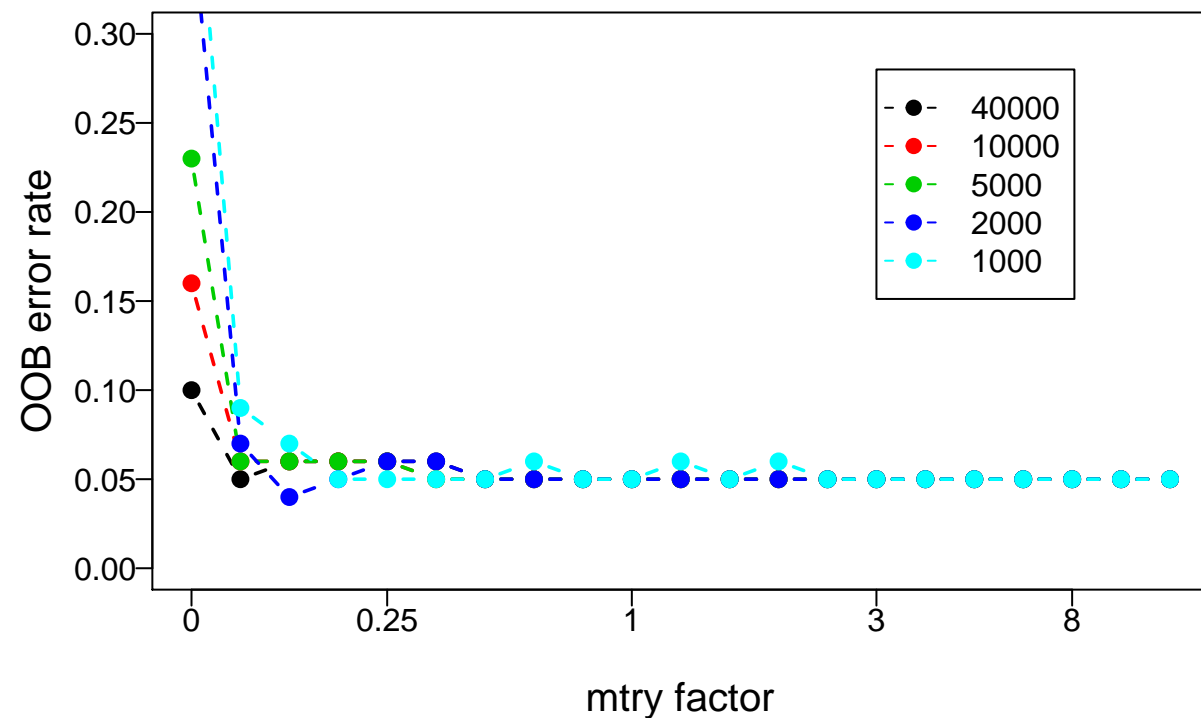
4 classes; 1 dimensions; 20 genes/dimen.; nodesize = 5



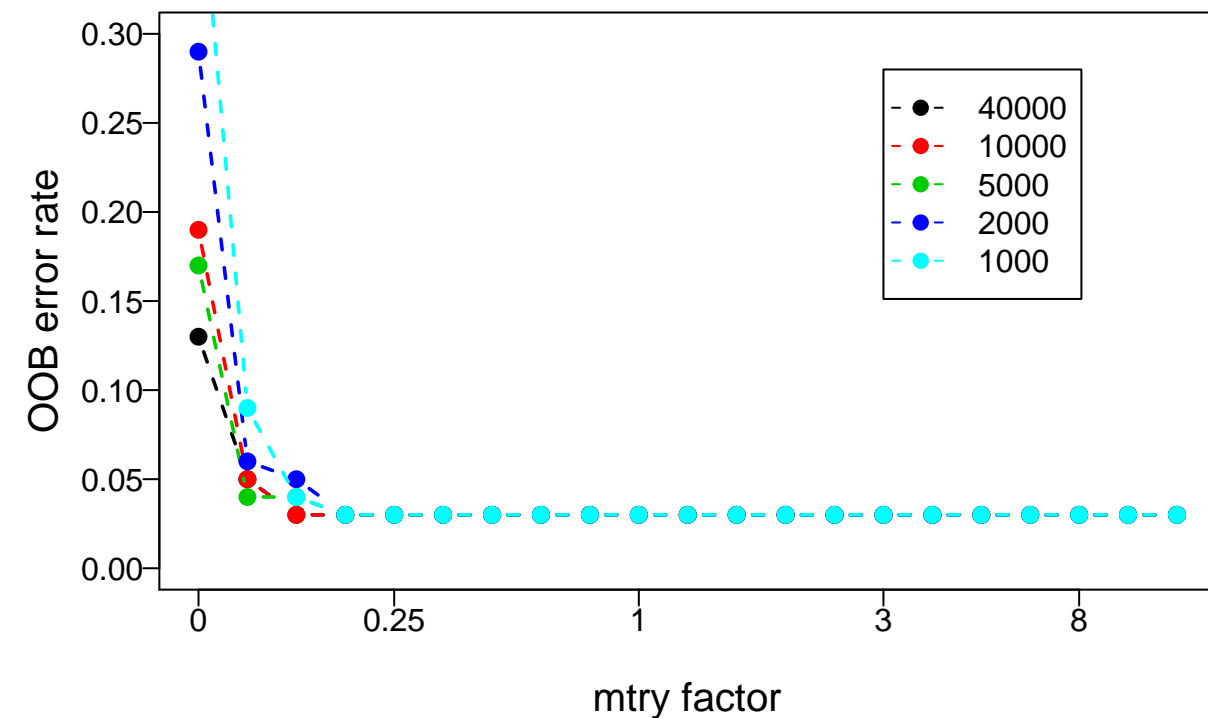
4 classes; 1 dimensions; 100 genes/dimen.; nodesize = 5



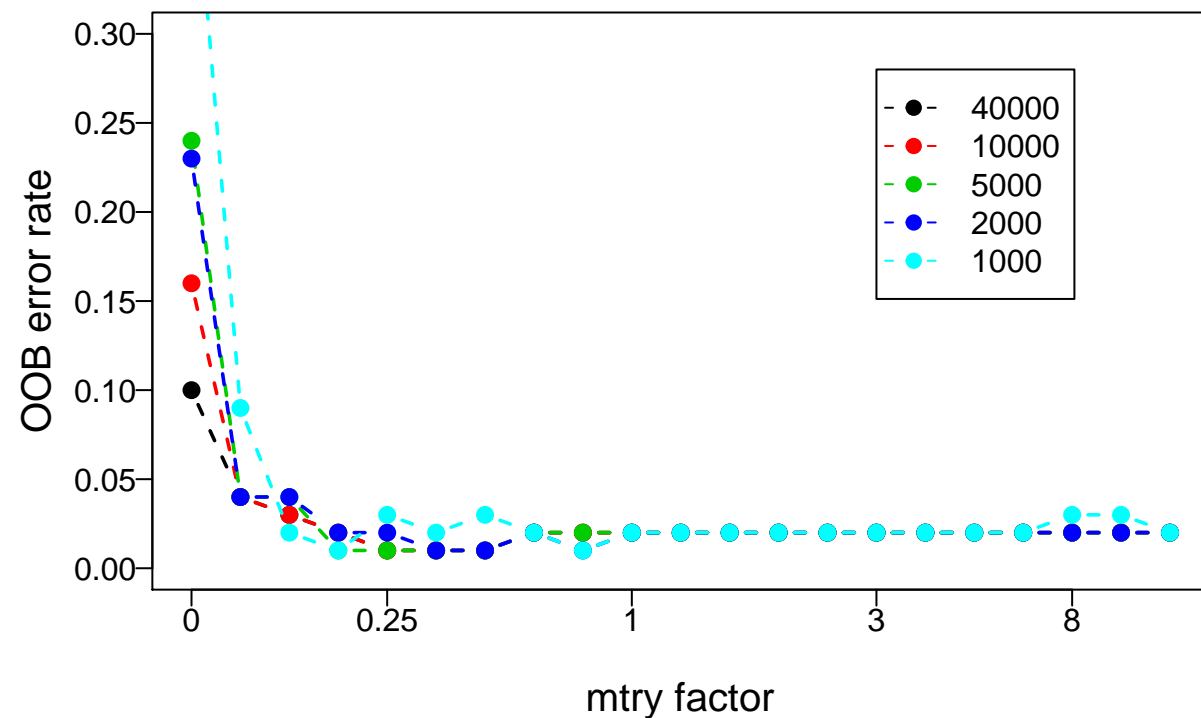
4 classes; 1 dimensions; 100 genes/dimen.; nodesize = 5



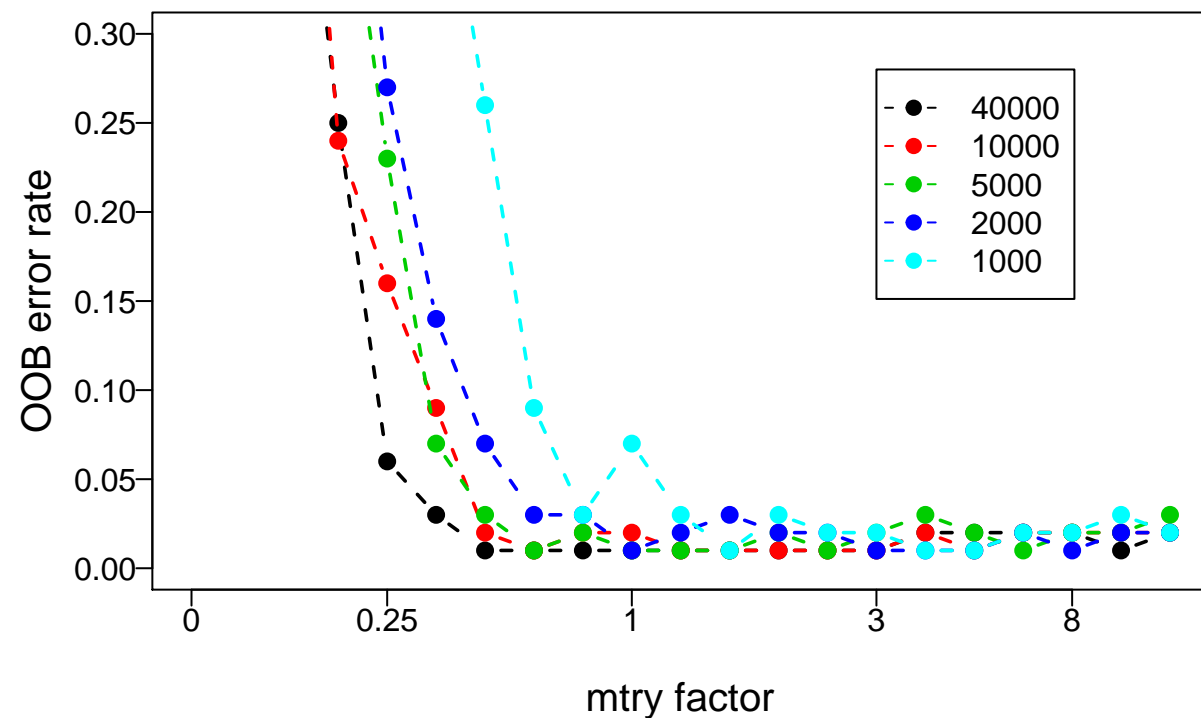
4 classes; 1 dimensions; 100 genes/dimen.; nodesize = 5



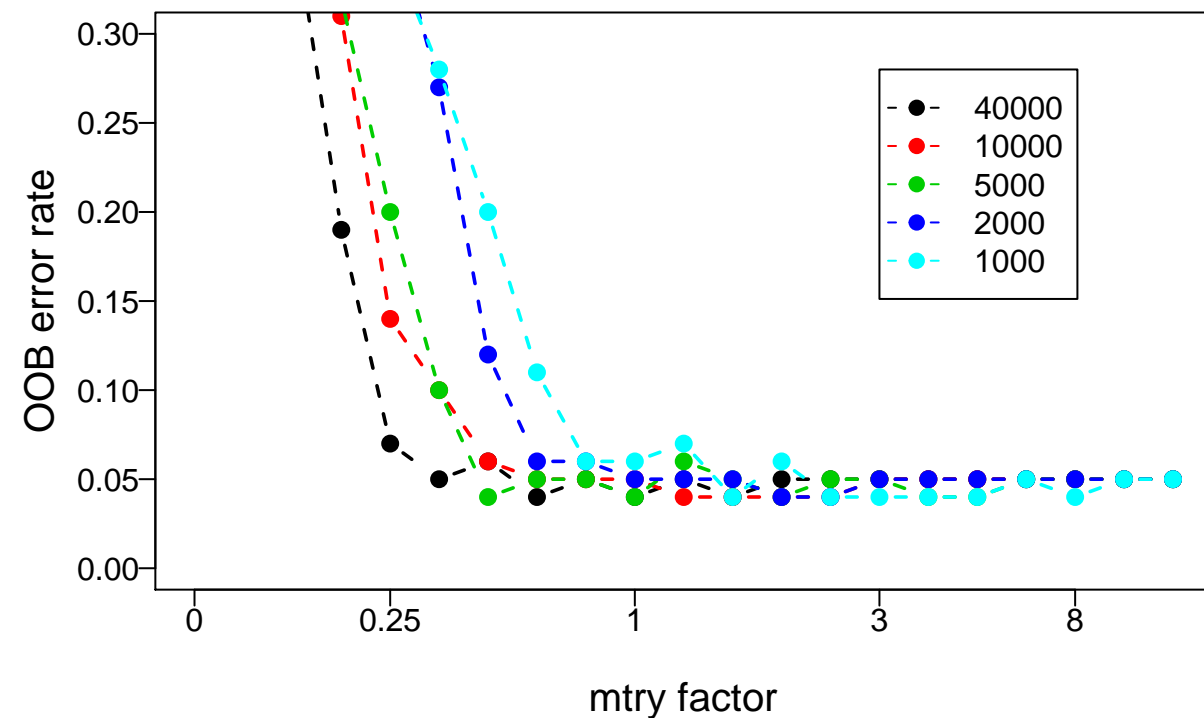
4 classes; 1 dimensions; 100 genes/dimen.; nodesize = 5



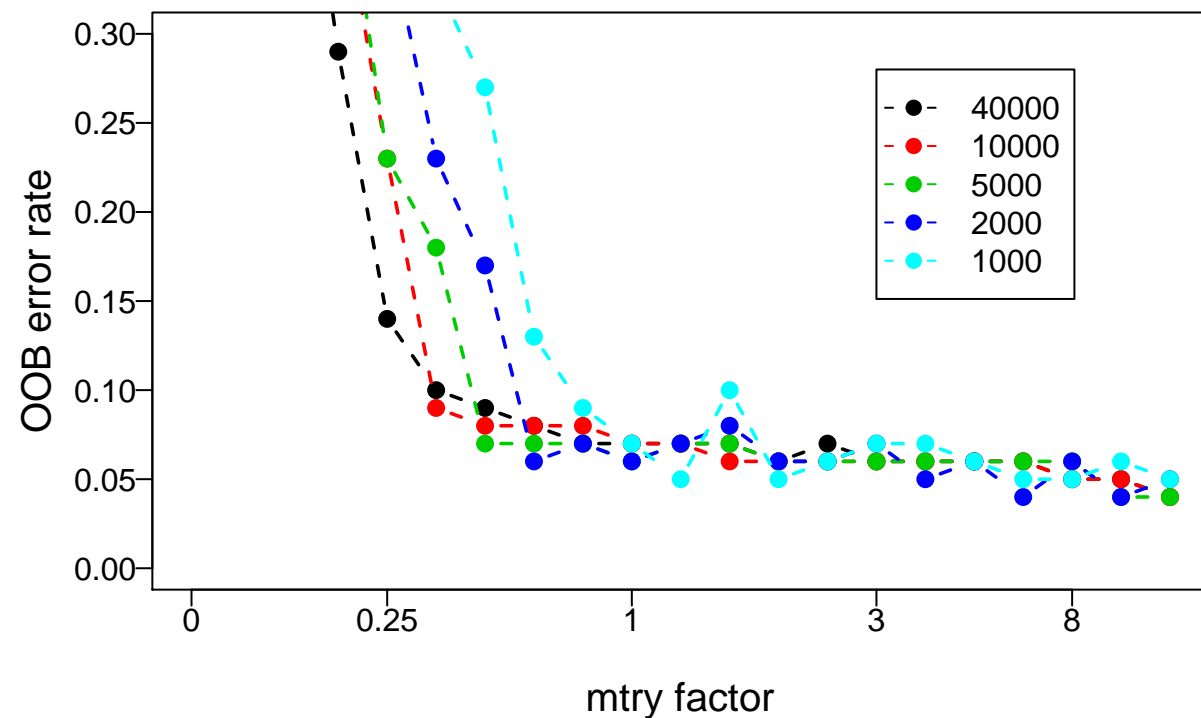
4 classes; 2 dimensions; 5 genes/dimen.; nodesize = 5



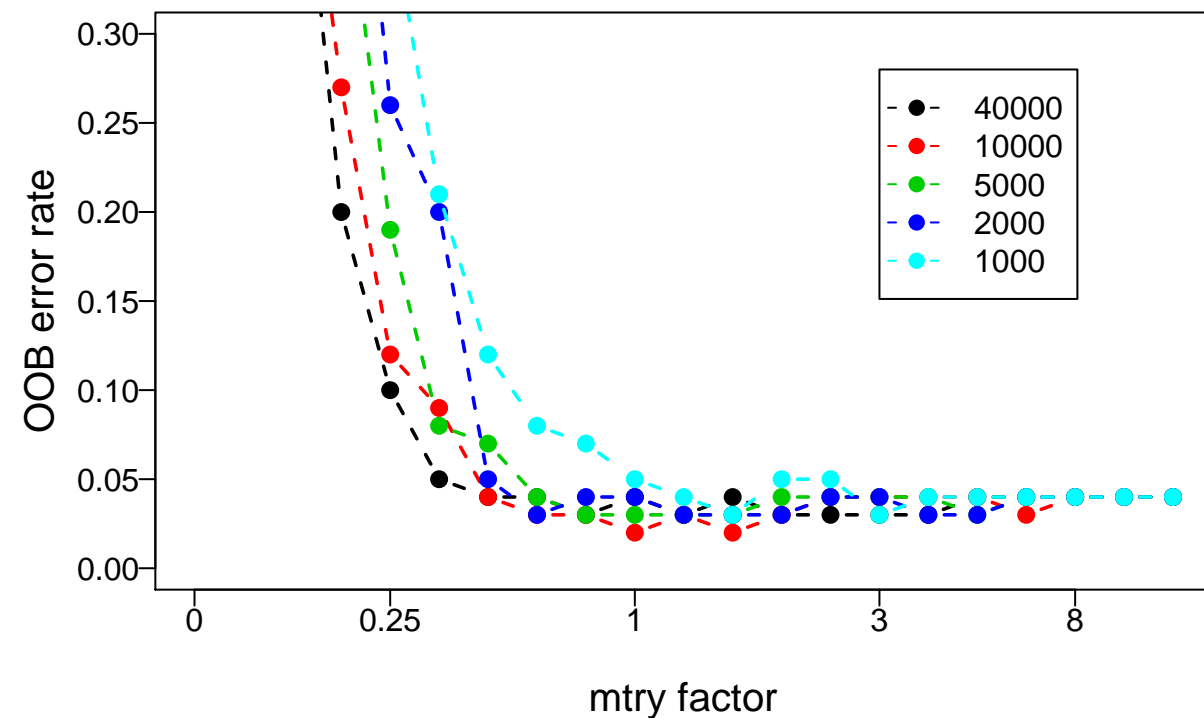
4 classes; 2 dimensions; 5 genes/dimen.; nodesize = 5



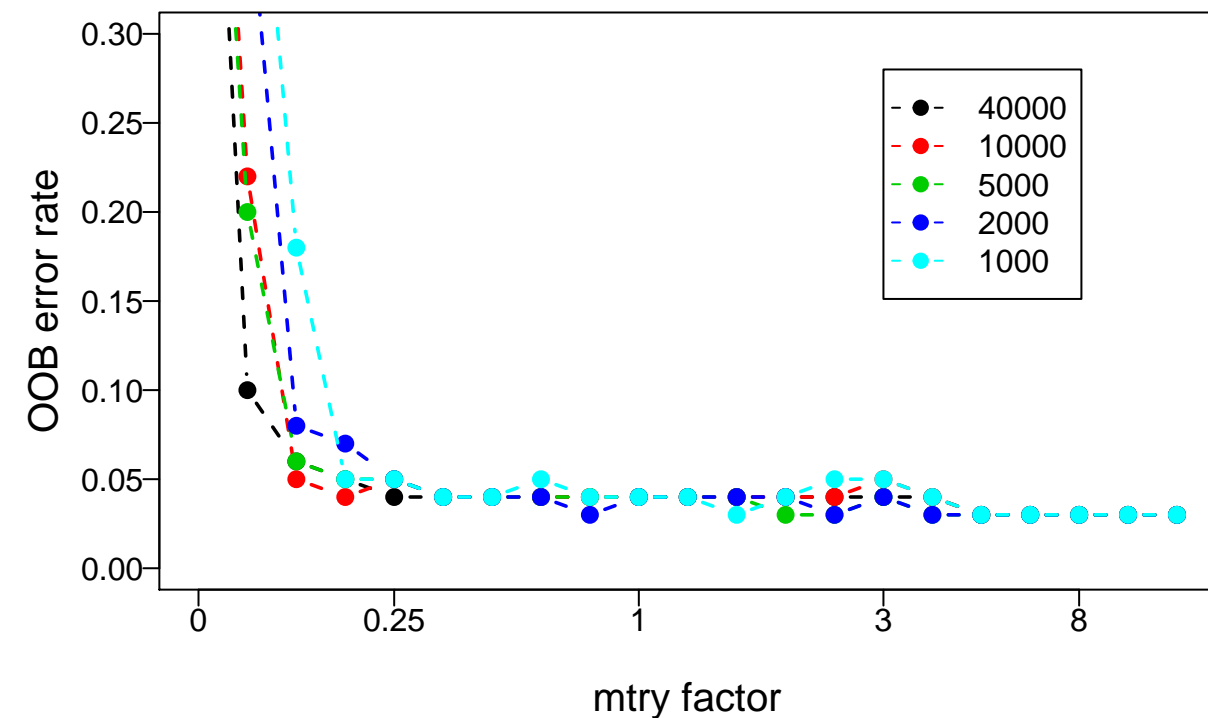
4 classes; 2 dimensions; 5 genes/dimen.; nodesize = 5



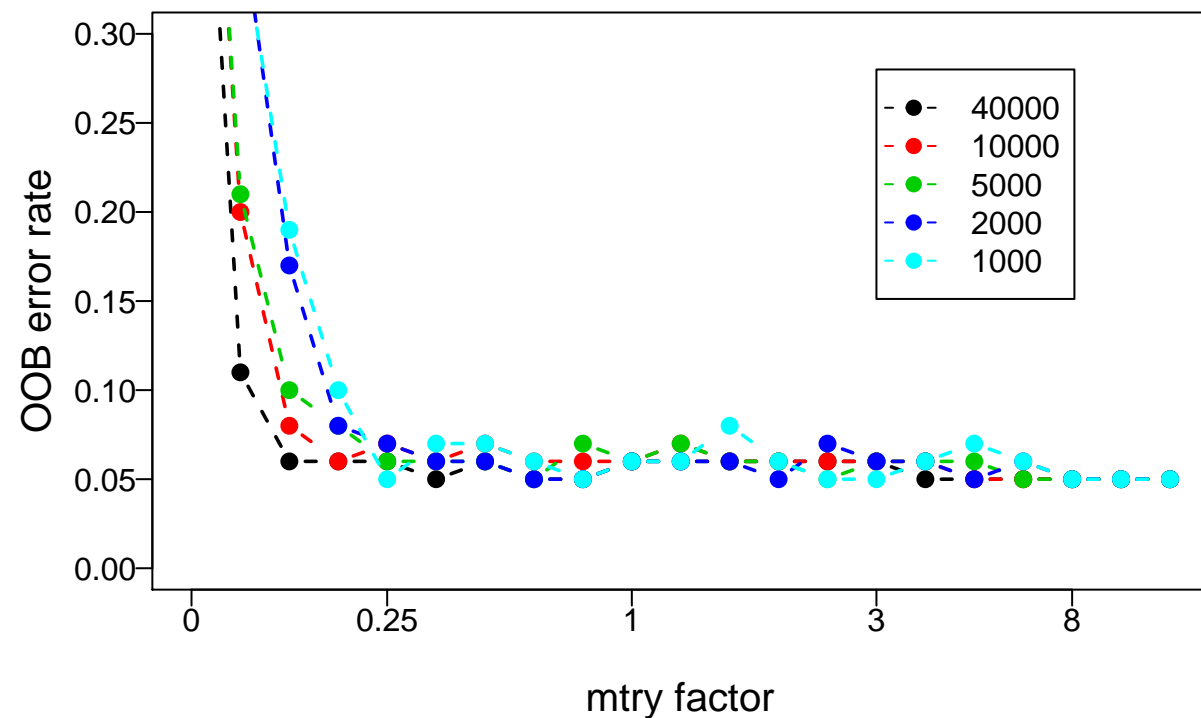
4 classes; 2 dimensions; 5 genes/dimen.; nodesize = 5



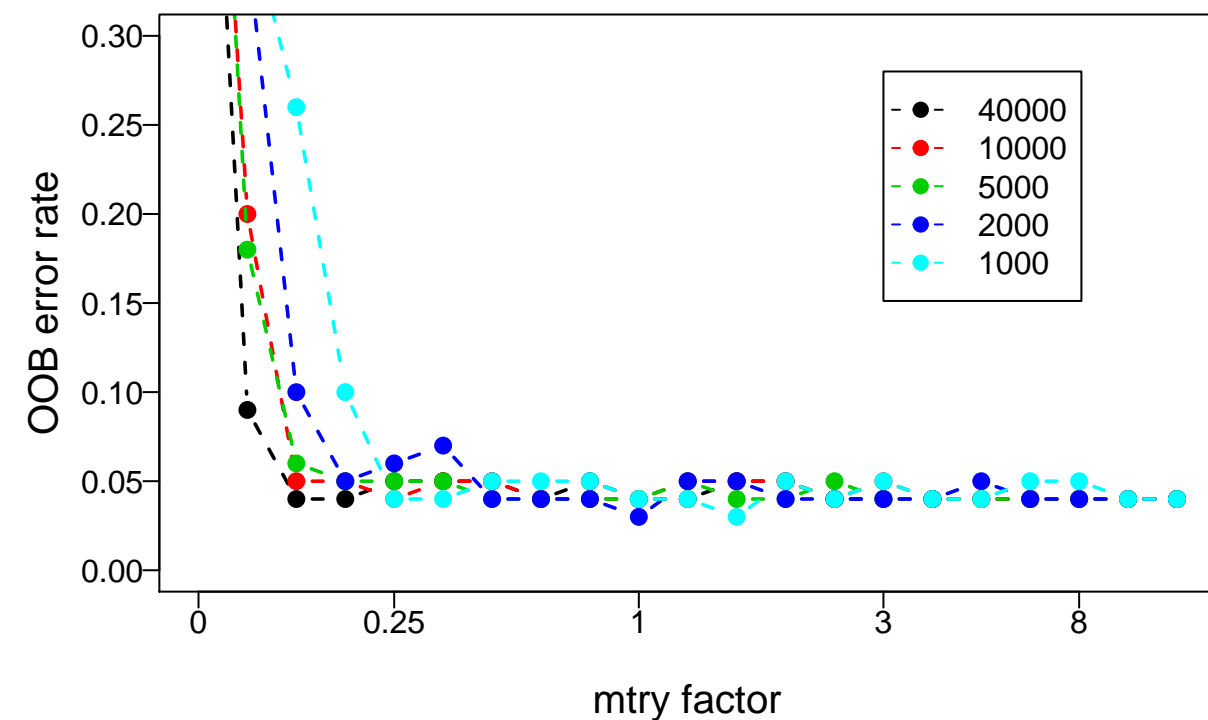
4 classes; 2 dimensions; 20 genes/dimen.; nodesize = 5



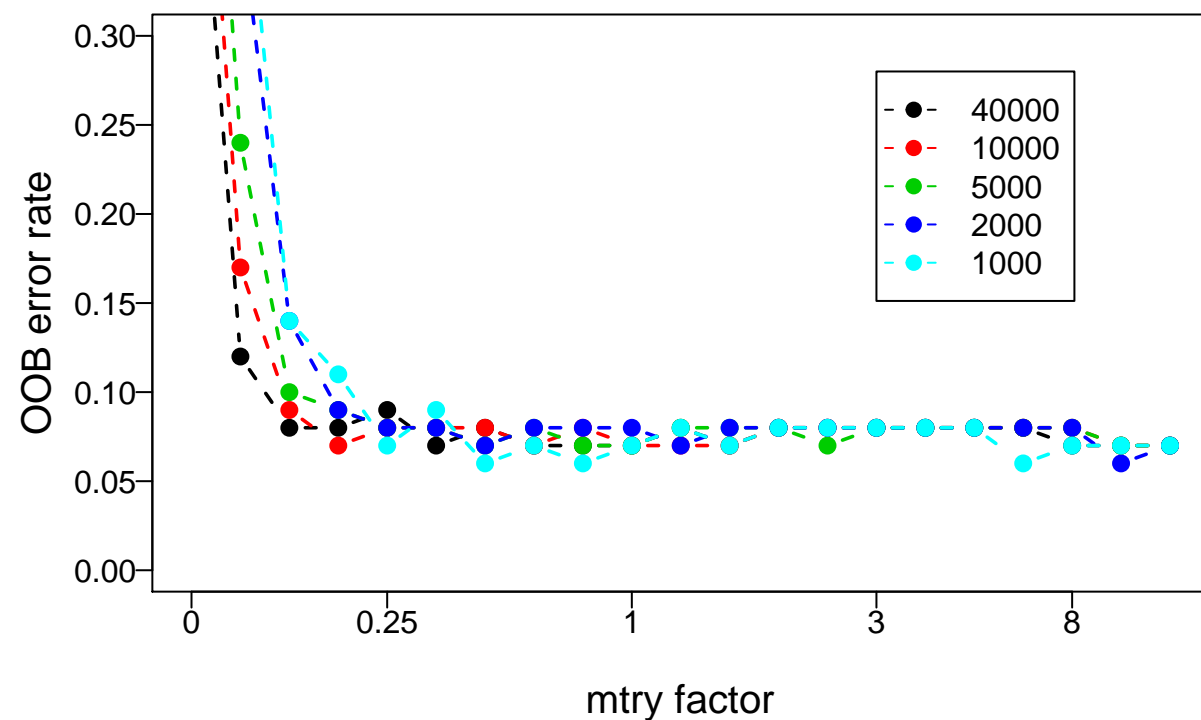
4 classes; 2 dimensions; 20 genes/dimen.; nodesize = 5



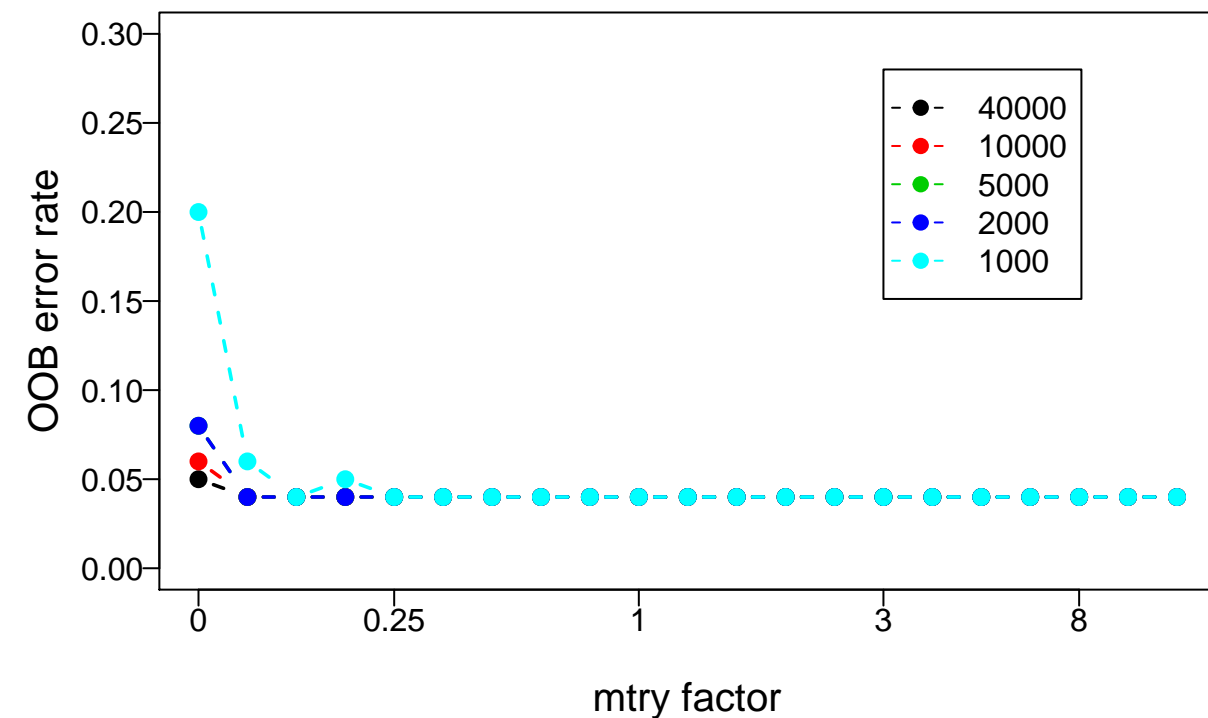
4 classes; 2 dimensions; 20 genes/dimen.; nodesize = 5



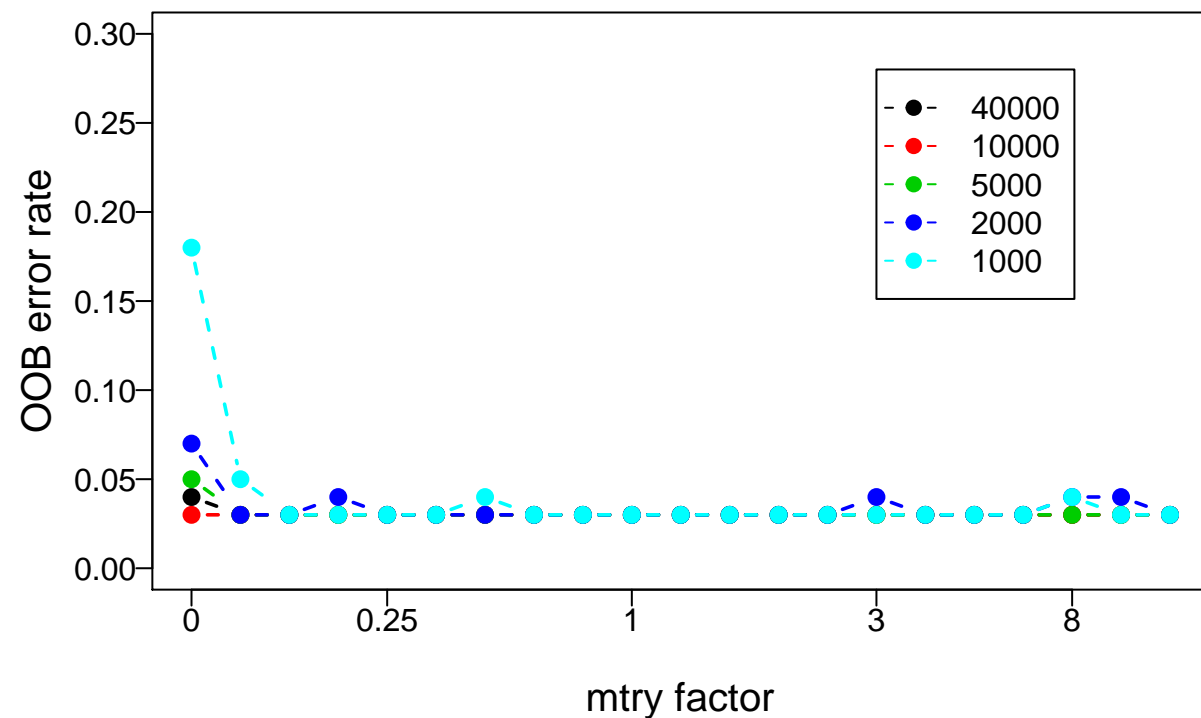
4 classes; 2 dimensions; 20 genes/dimen.; nodesize = 5



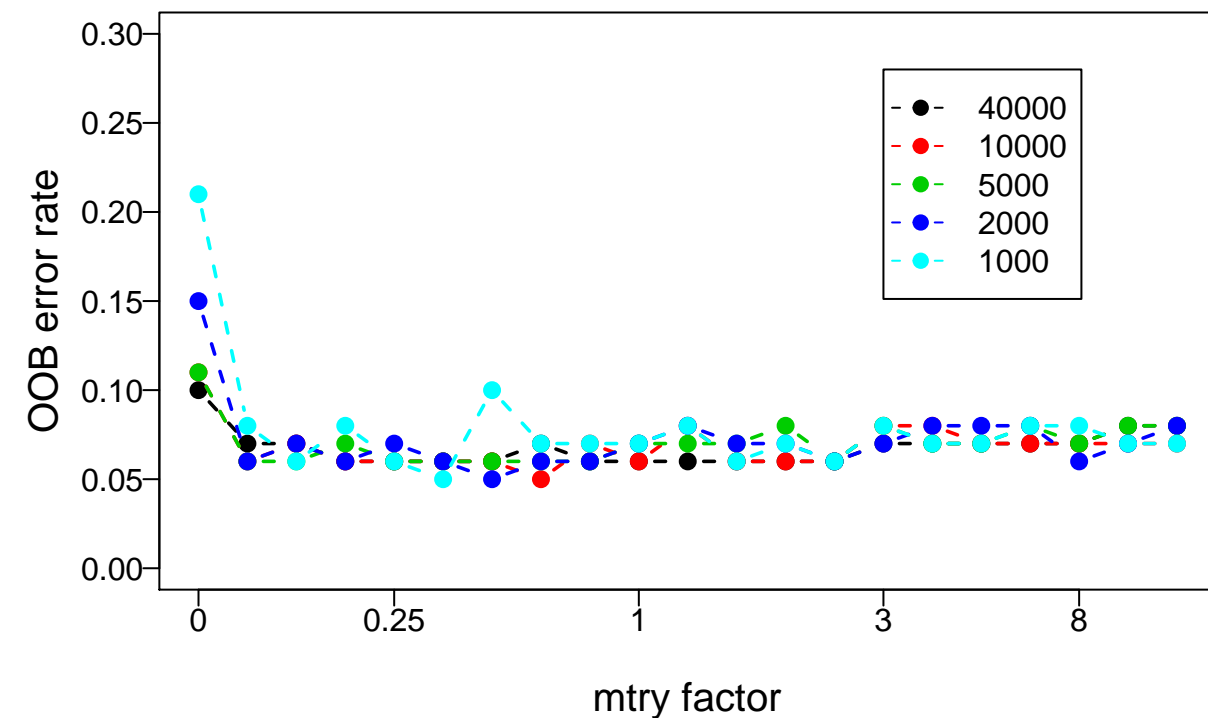
4 classes; 2 dimensions; 100 genes/dimen.; nodesize = 5



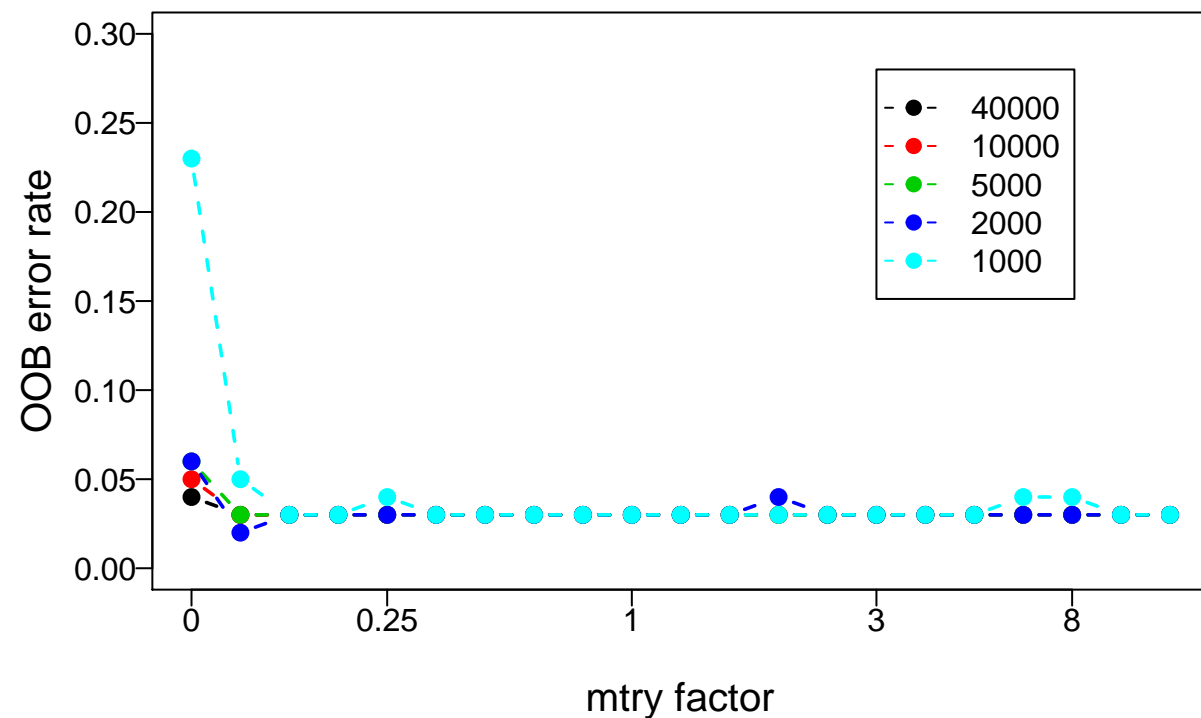
4 classes; 2 dimensions; 100 genes/dimen.; nodesize = 5



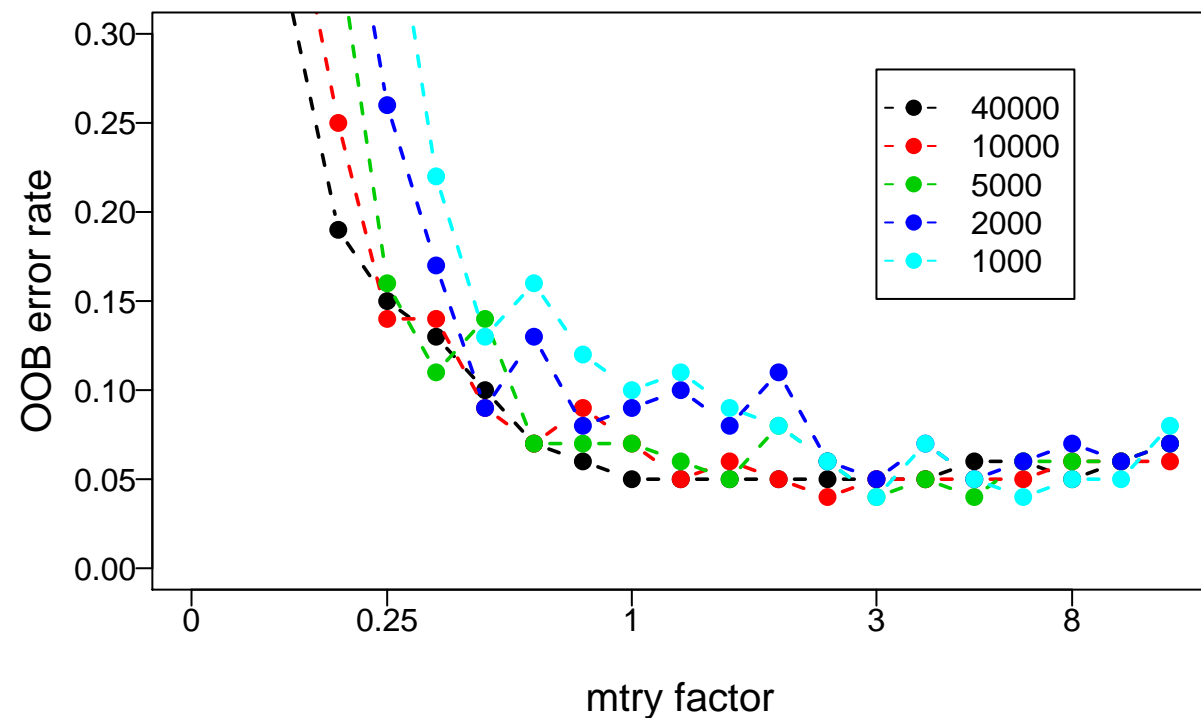
4 classes; 2 dimensions; 100 genes/dimen.; nodesize = 5



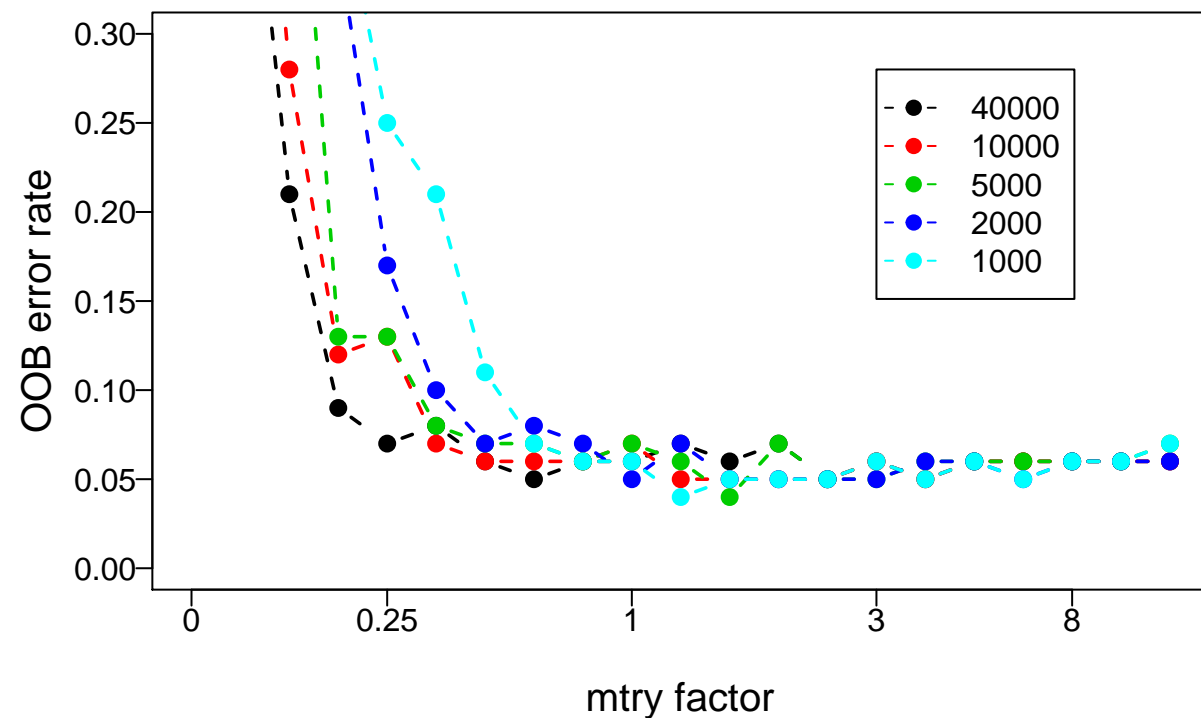
4 classes; 2 dimensions; 100 genes/dimen.; nodesize = 5



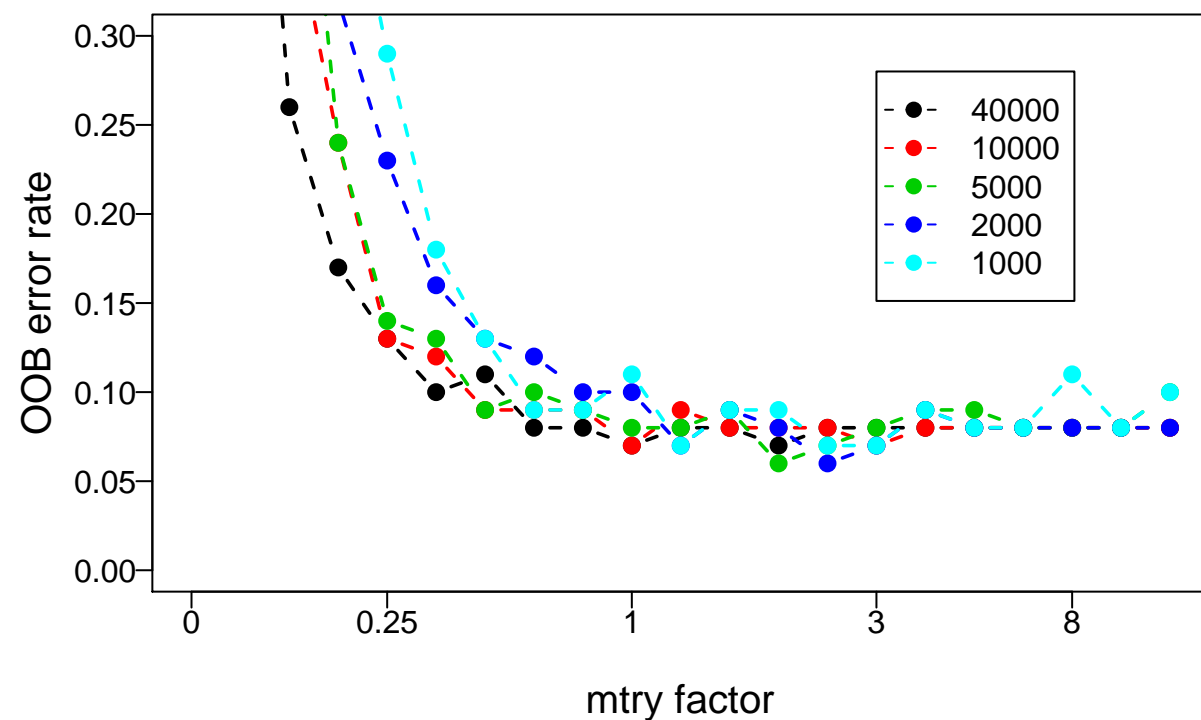
4 classes; 3 dimensions; 5 genes/dimen.; nodesize = 5



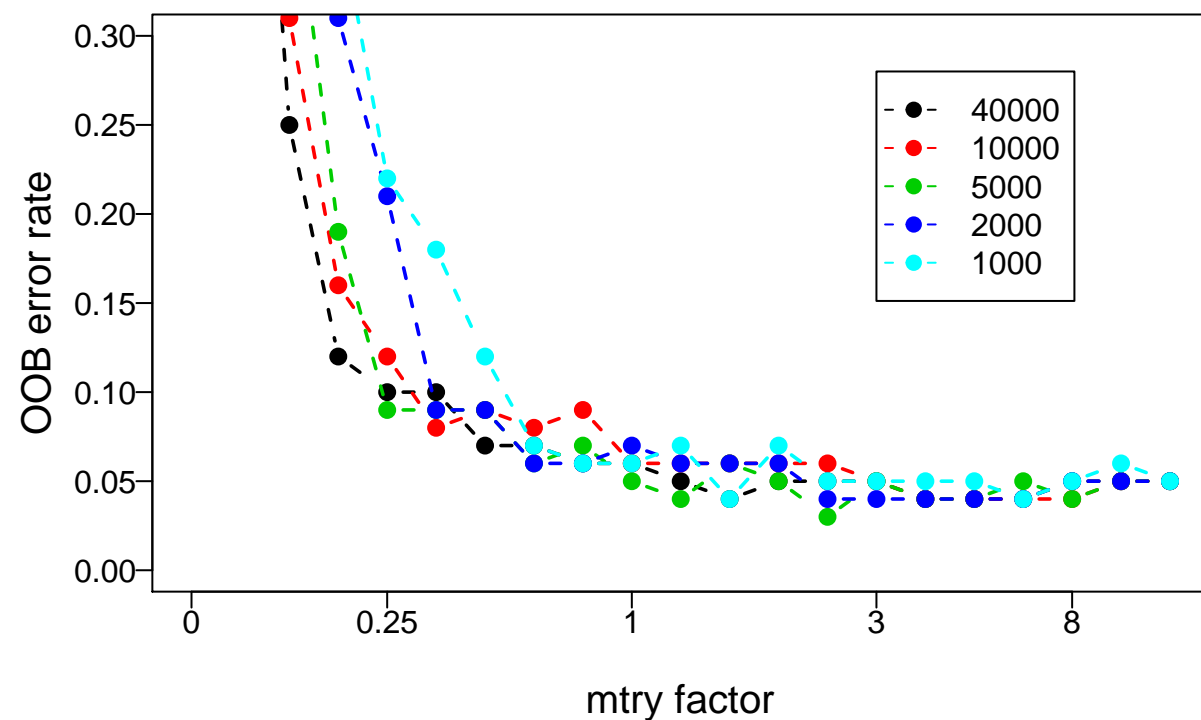
4 classes; 3 dimensions; 5 genes/dimen.; nodesize = 5



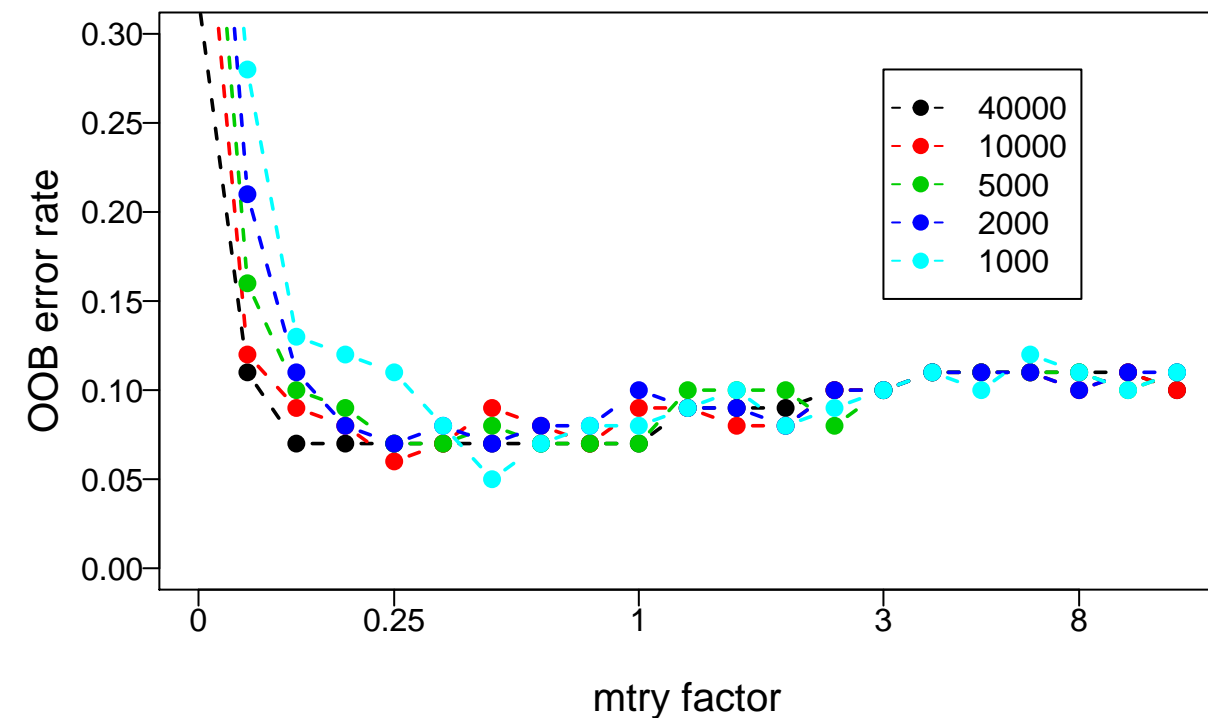
4 classes; 3 dimensions; 5 genes/dimen.; nodesize = 5



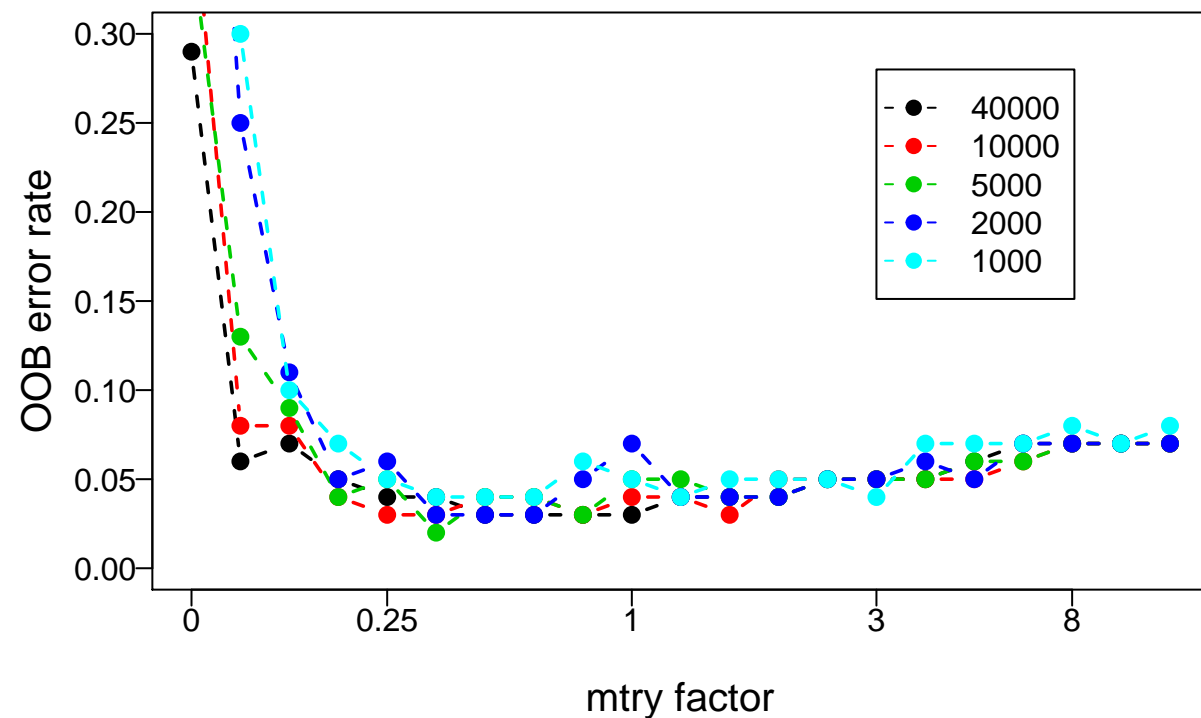
4 classes; 3 dimensions; 5 genes/dimen.; nodesize = 5



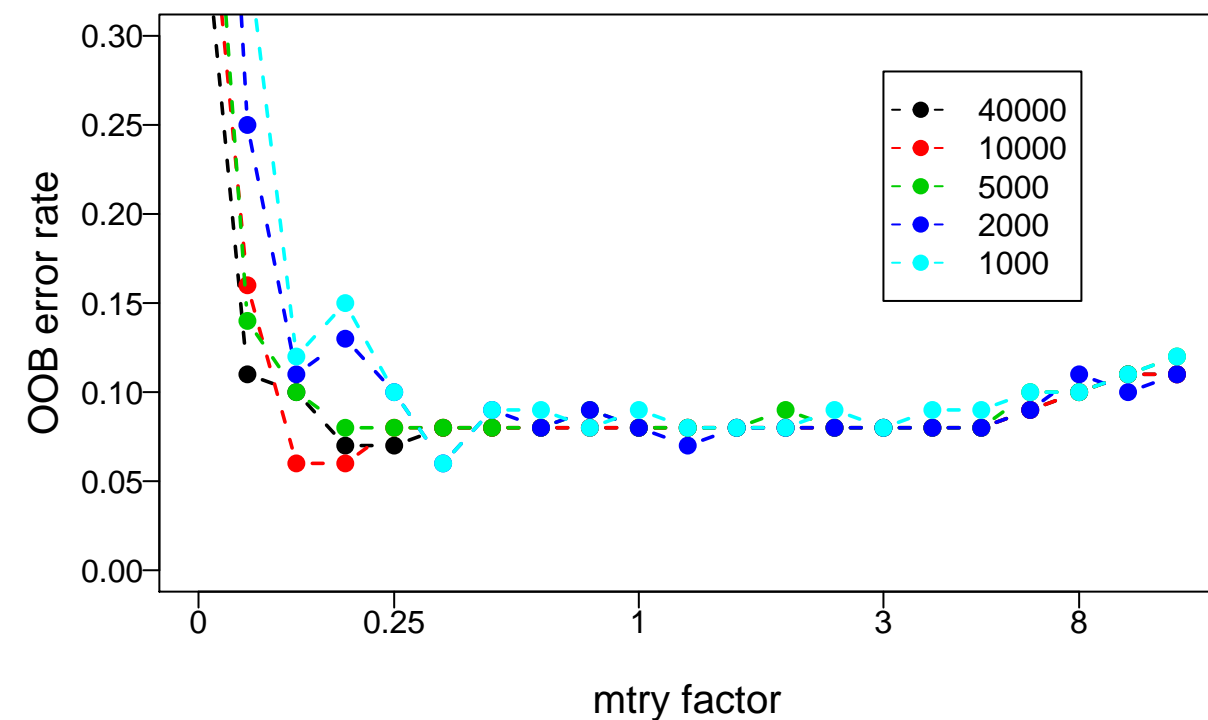
4 classes; 3 dimensions; 20 genes/dimen.; nodesize = 5



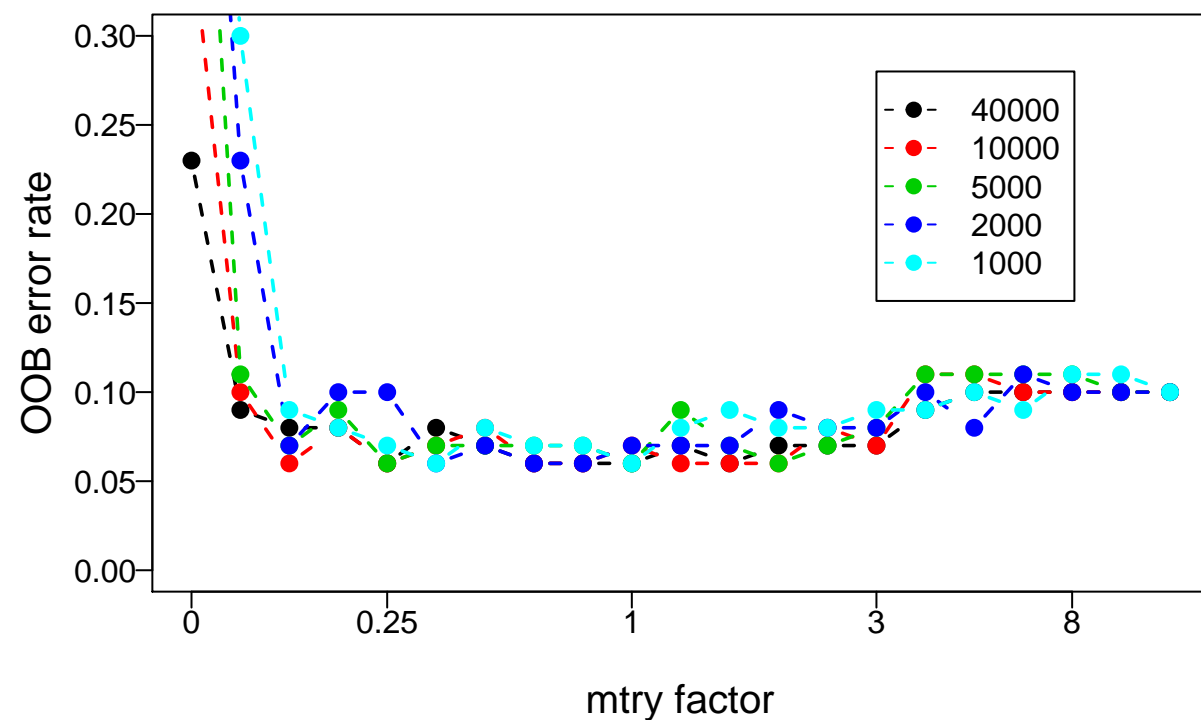
4 classes; 3 dimensions; 20 genes/dimen.; nodesize = 5



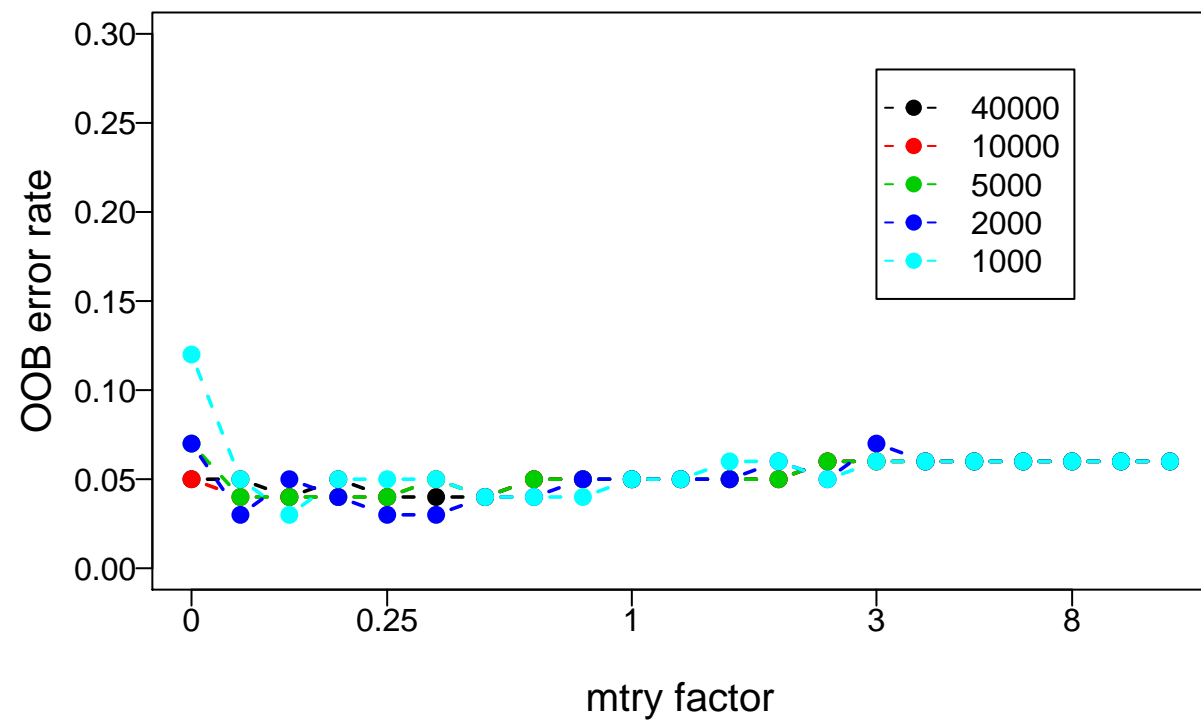
4 classes; 3 dimensions; 20 genes/dimen.; nodesize = 5



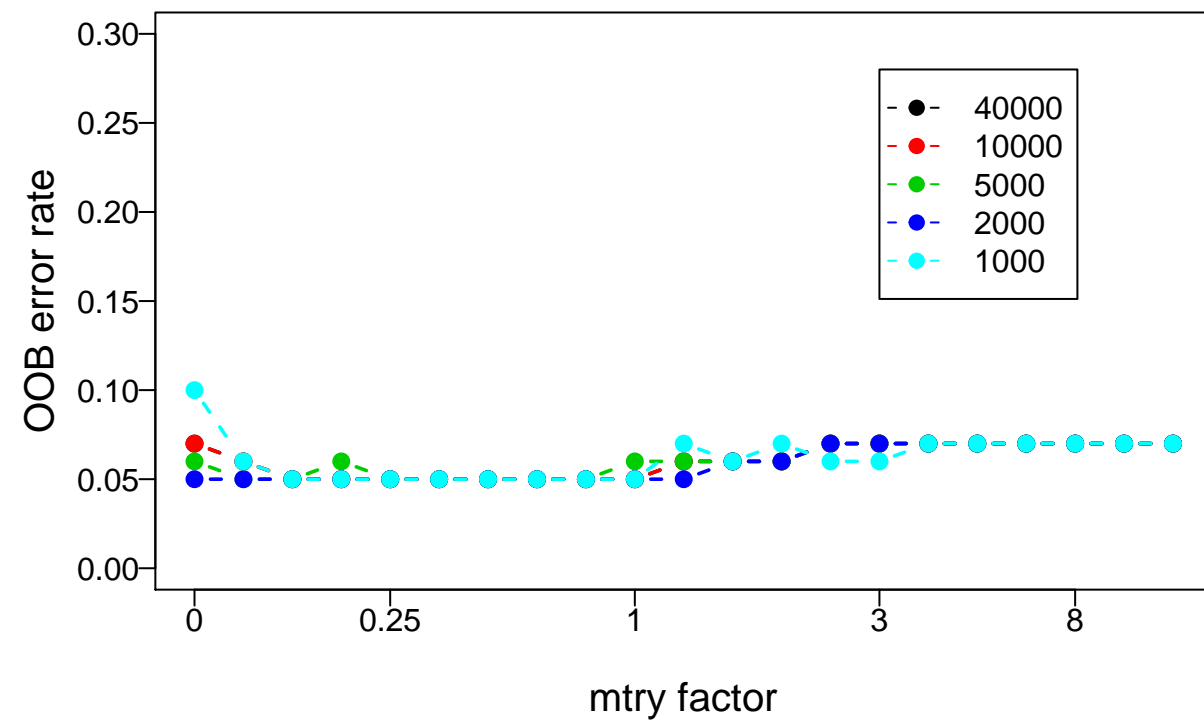
4 classes; 3 dimensions; 20 genes/dimen.; nodesize = 5



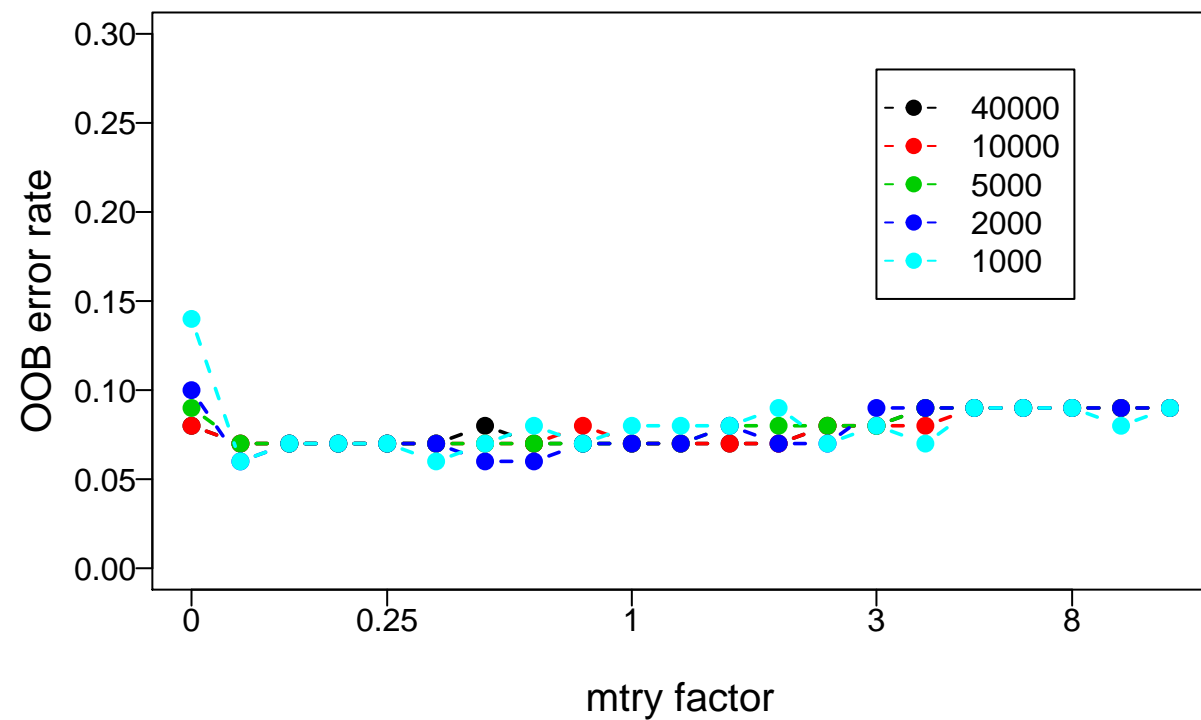
4 classes; 3 dimensions; 100 genes/dimen.; nodesize = 5



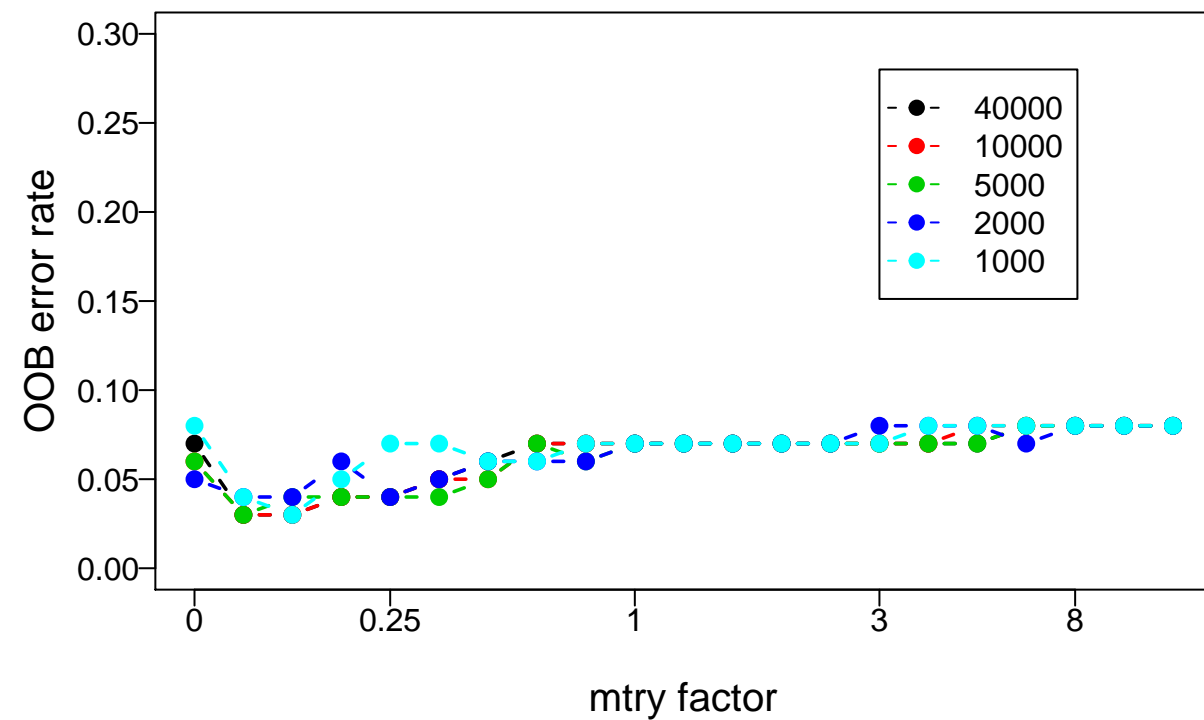
4 classes; 3 dimensions; 100 genes/dimen.; nodesize = 5



4 classes; 3 dimensions; 100 genes/dimen.; nodesize = 5



4 classes; 3 dimensions; 100 genes/dimen.; nodesize = 5

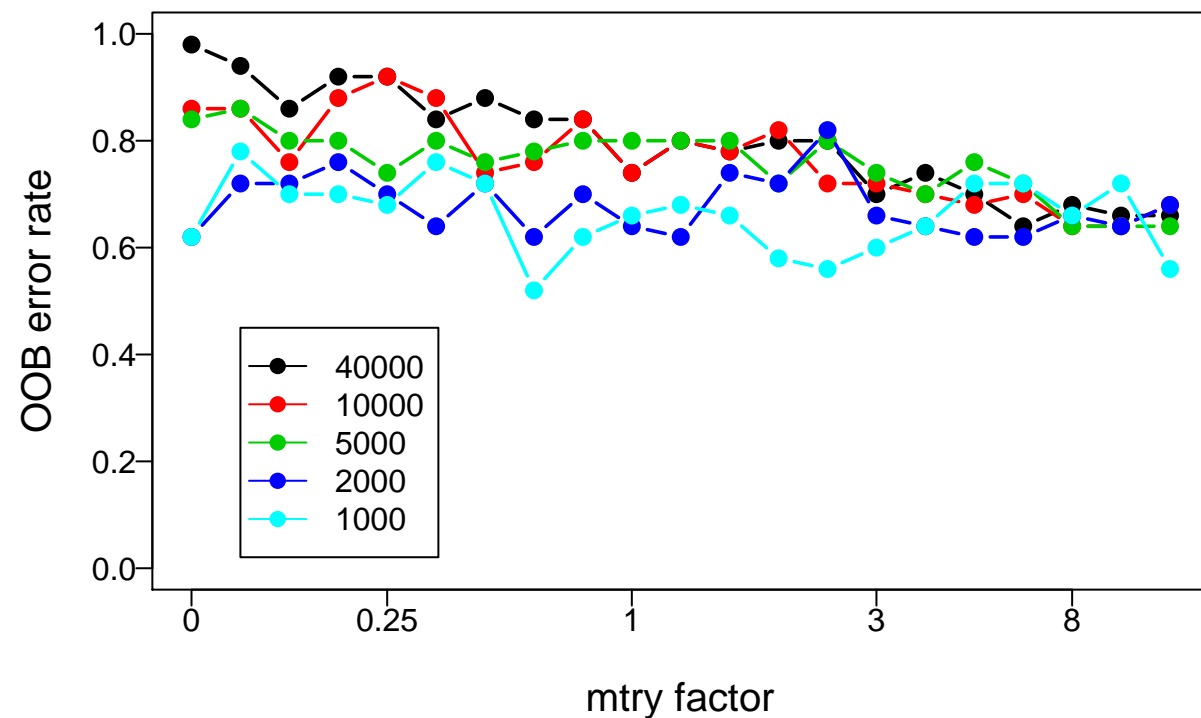


II: Simulated data sets:

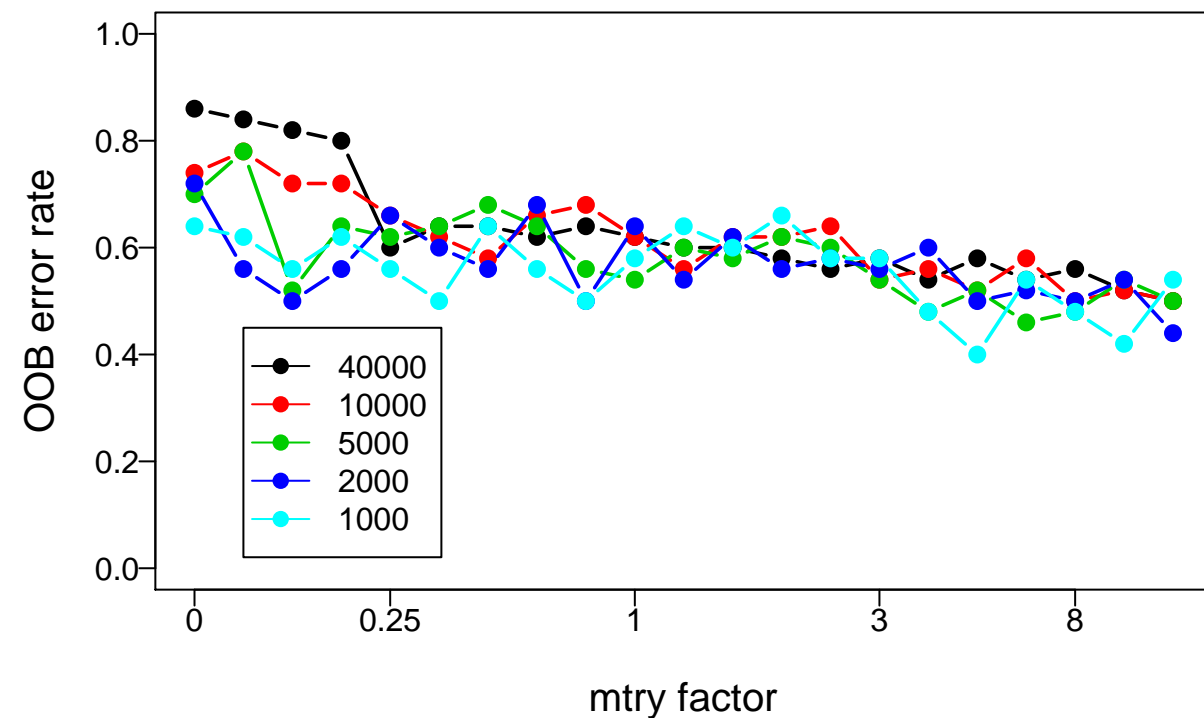
No signal: 4000 noise random variables

(shown first with nodesize = 1, then nodesize = 5)

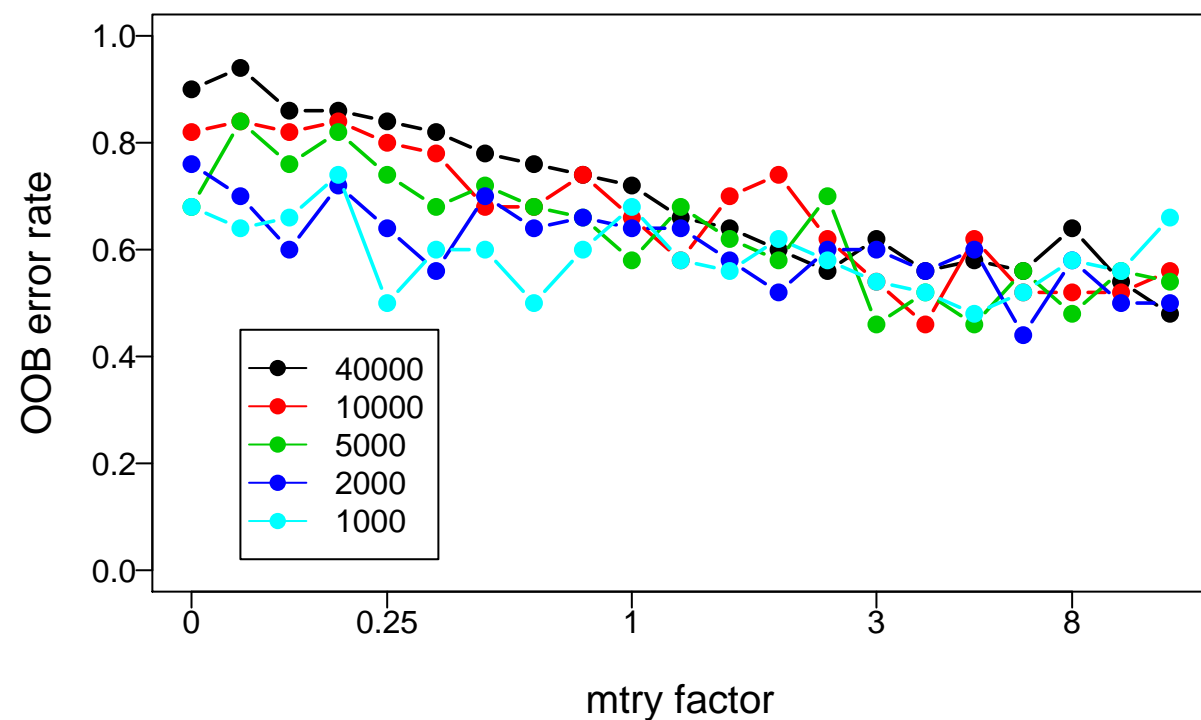
No signal: Classes 2 ; nodesize = 1



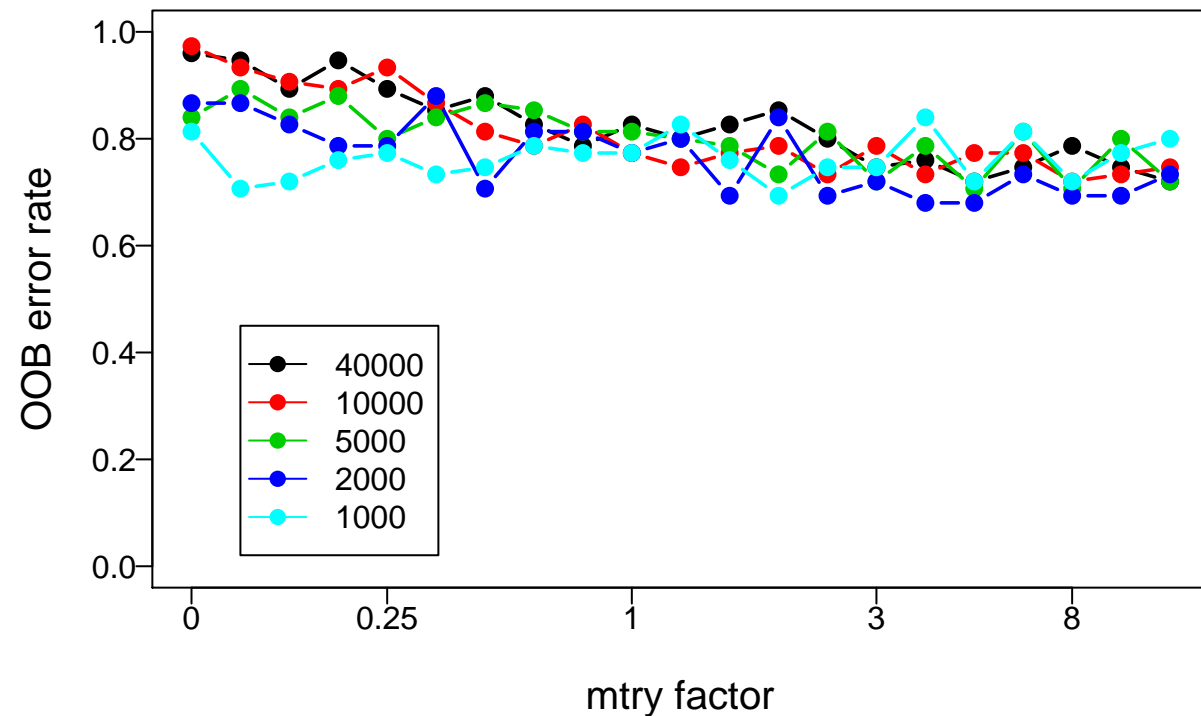
No signal: Classes 2 ; nodesize = 1



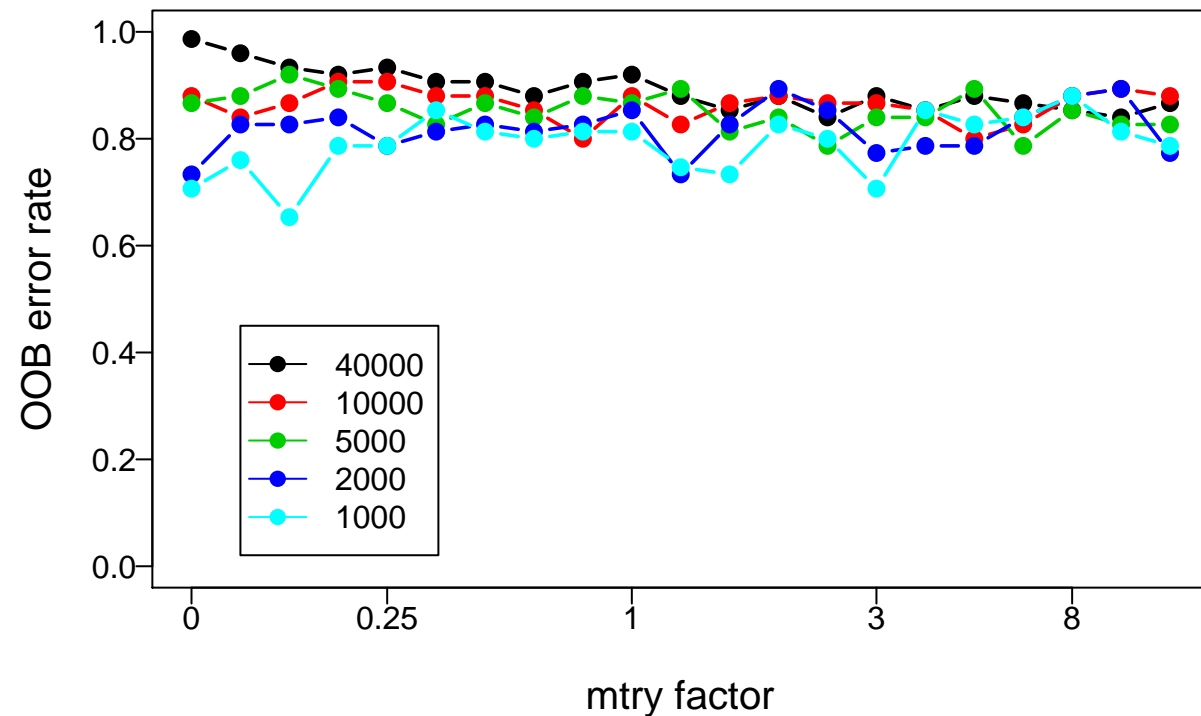
No signal: Classes 2 ; nodesize = 1



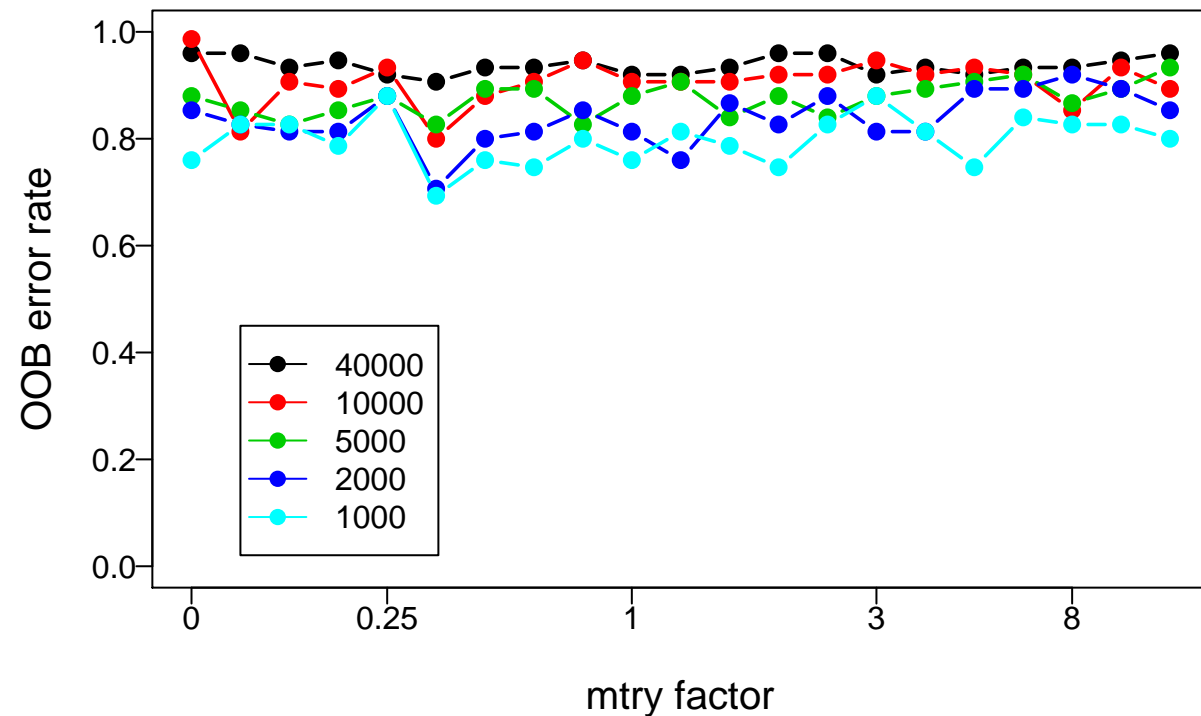
No signal: Classes 3 ; nodesize = 1



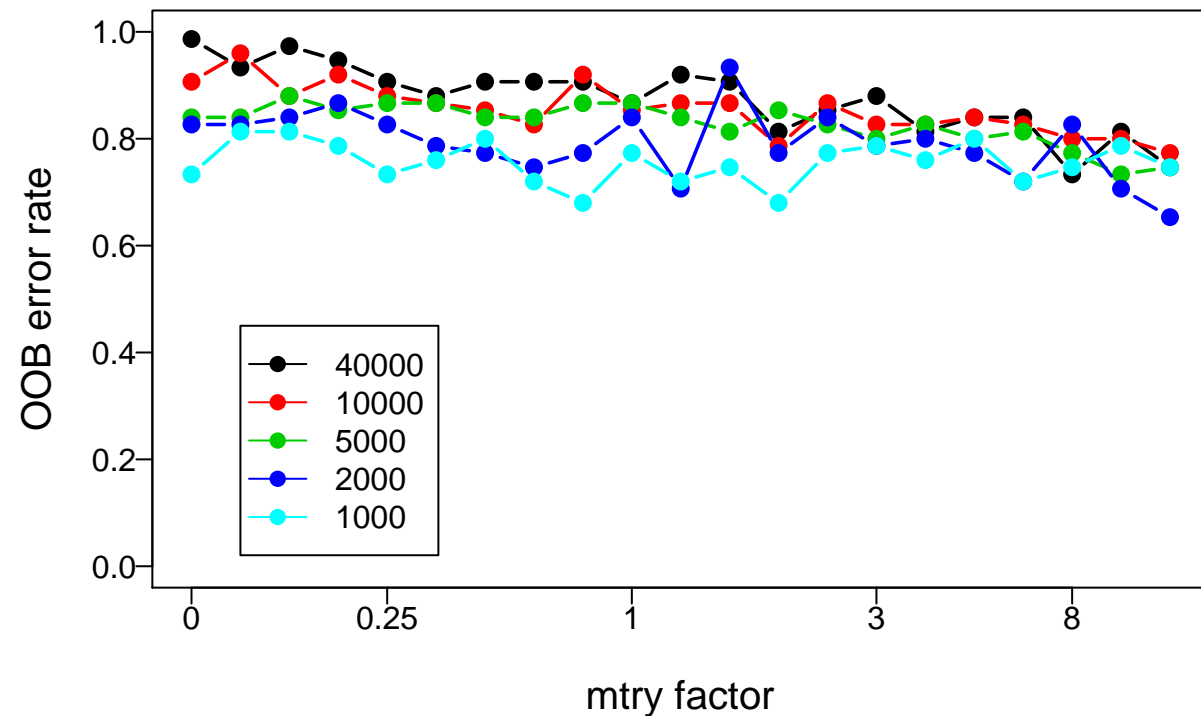
No signal: Classes 3 ; nodesize = 1



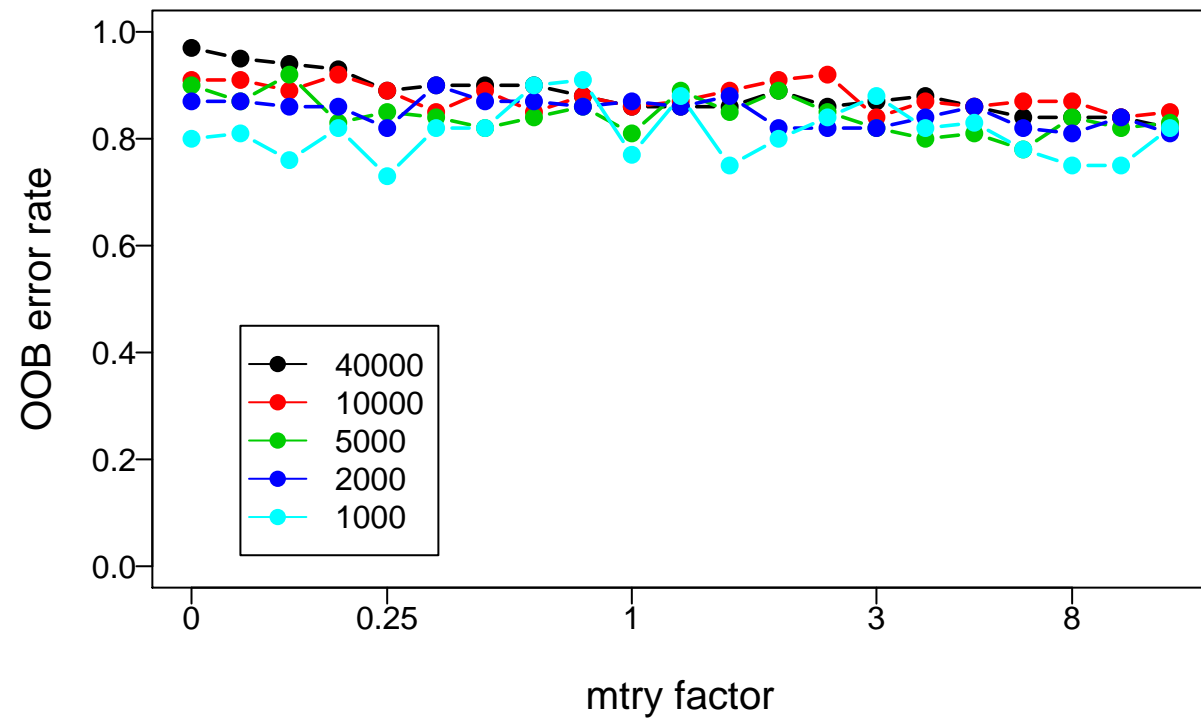
No signal: Classes 3 ; nodesize = 1



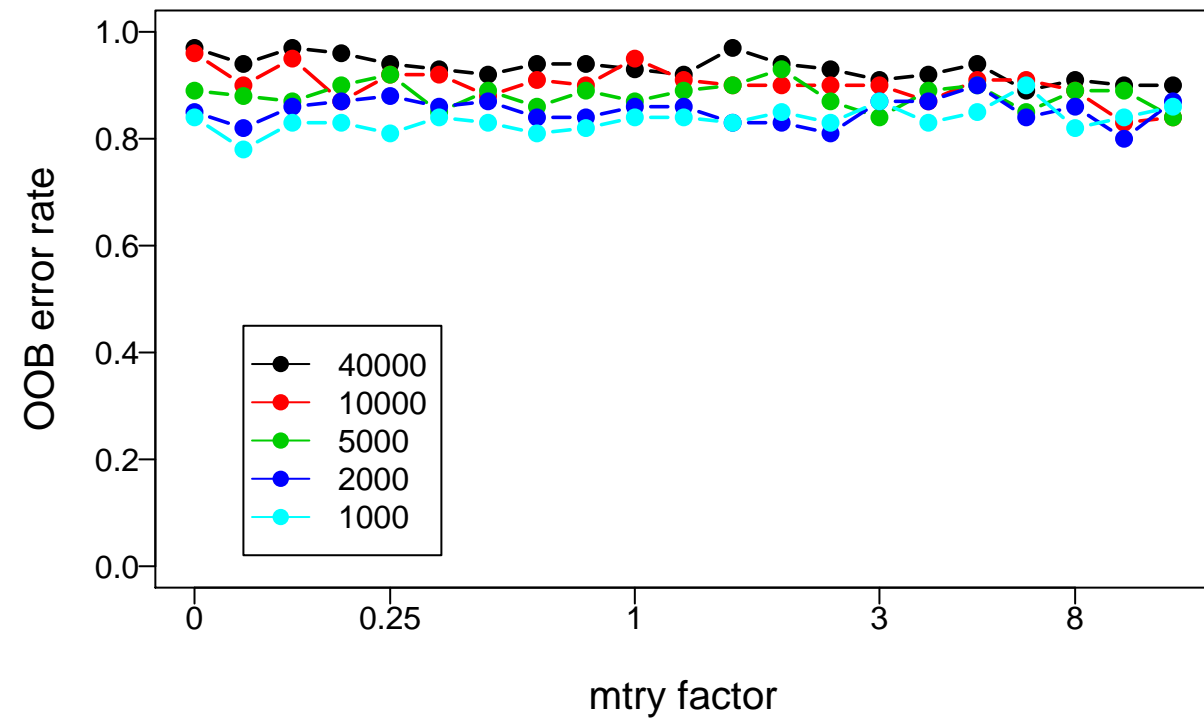
No signal: Classes 3 ; nodesize = 1



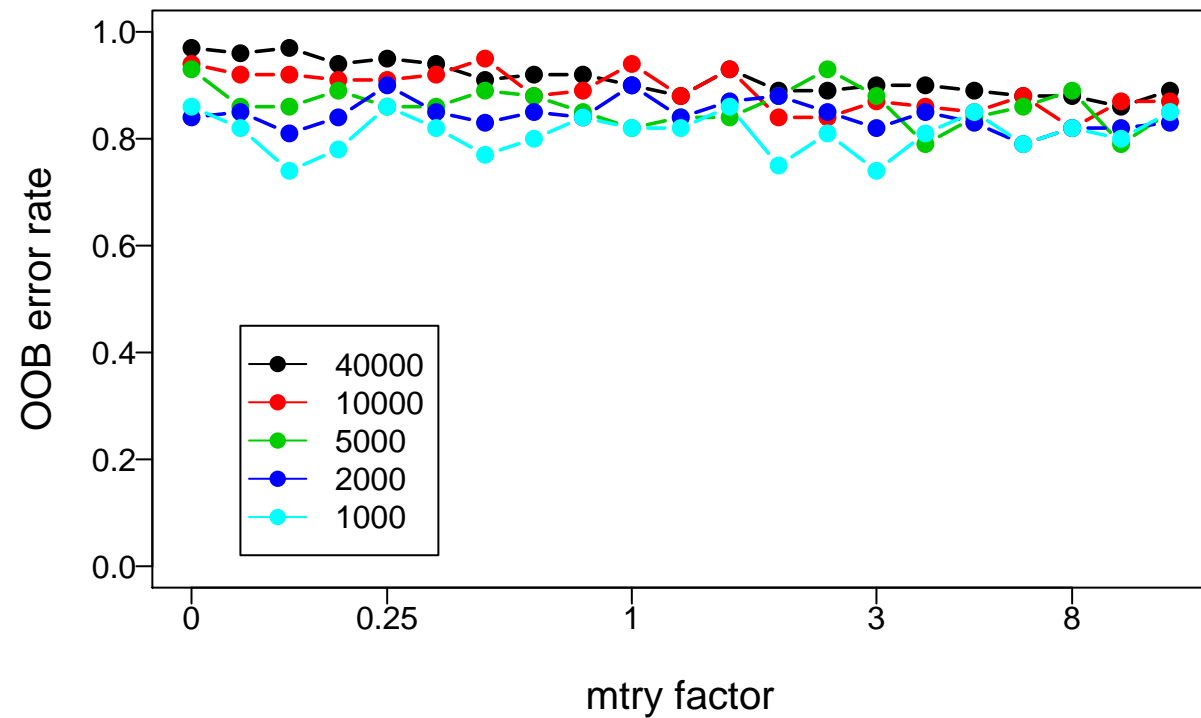
No signal: Classes 4 ; nodesize = 1



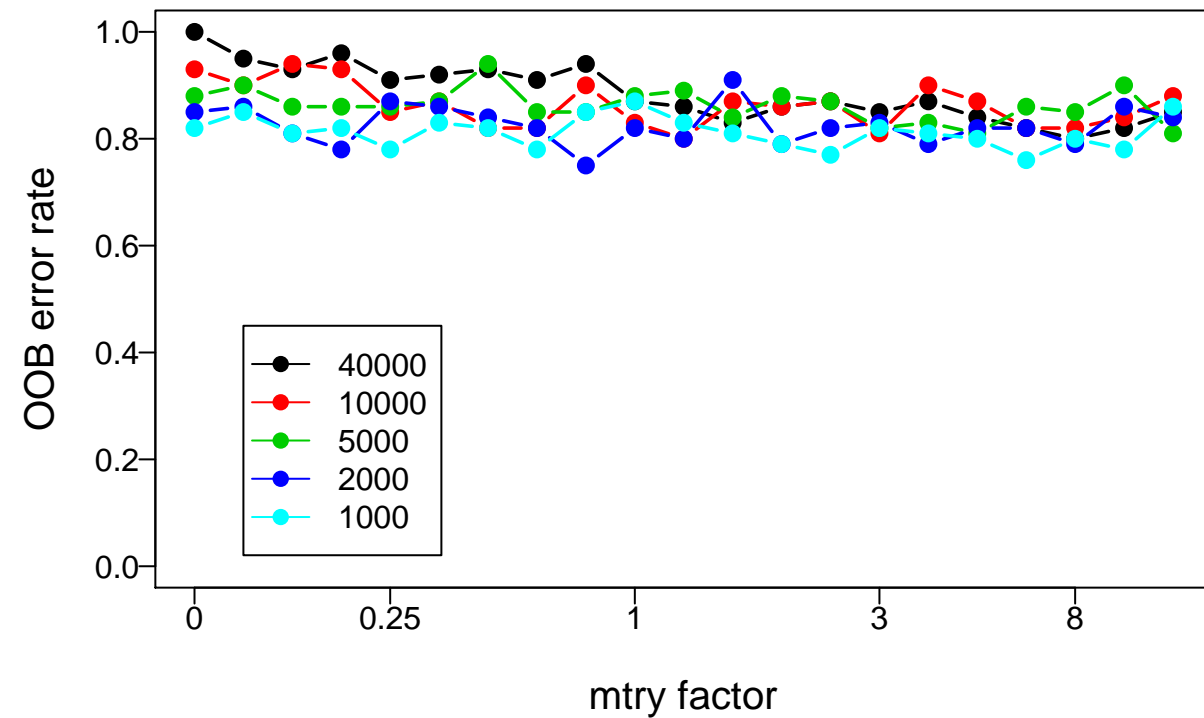
No signal: Classes 4 ; nodesize = 1



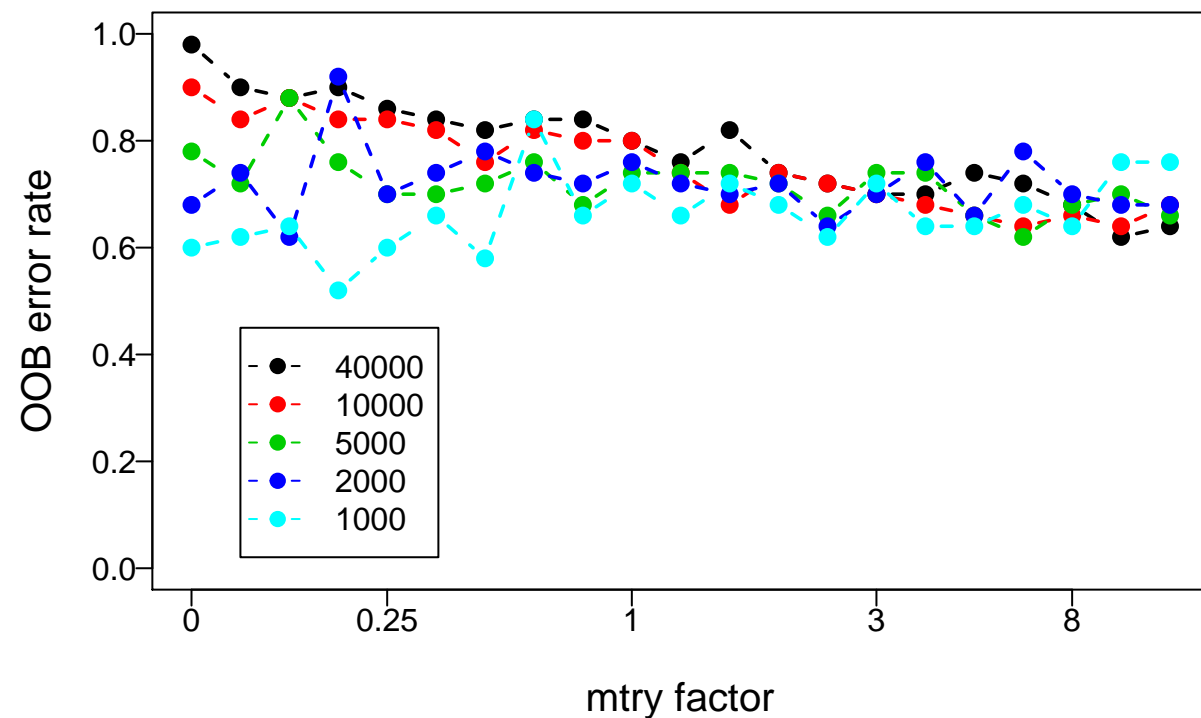
No signal: Classes 4 ; nodesize = 1



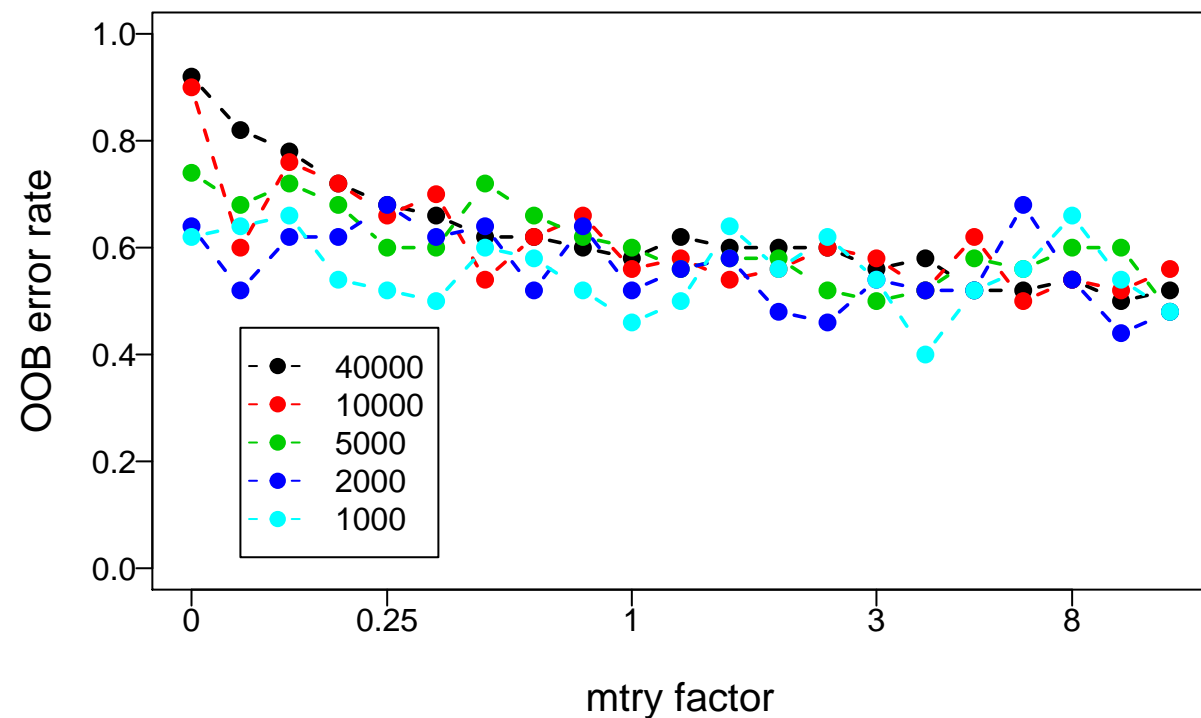
No signal: Classes 4 ; nodesize = 1



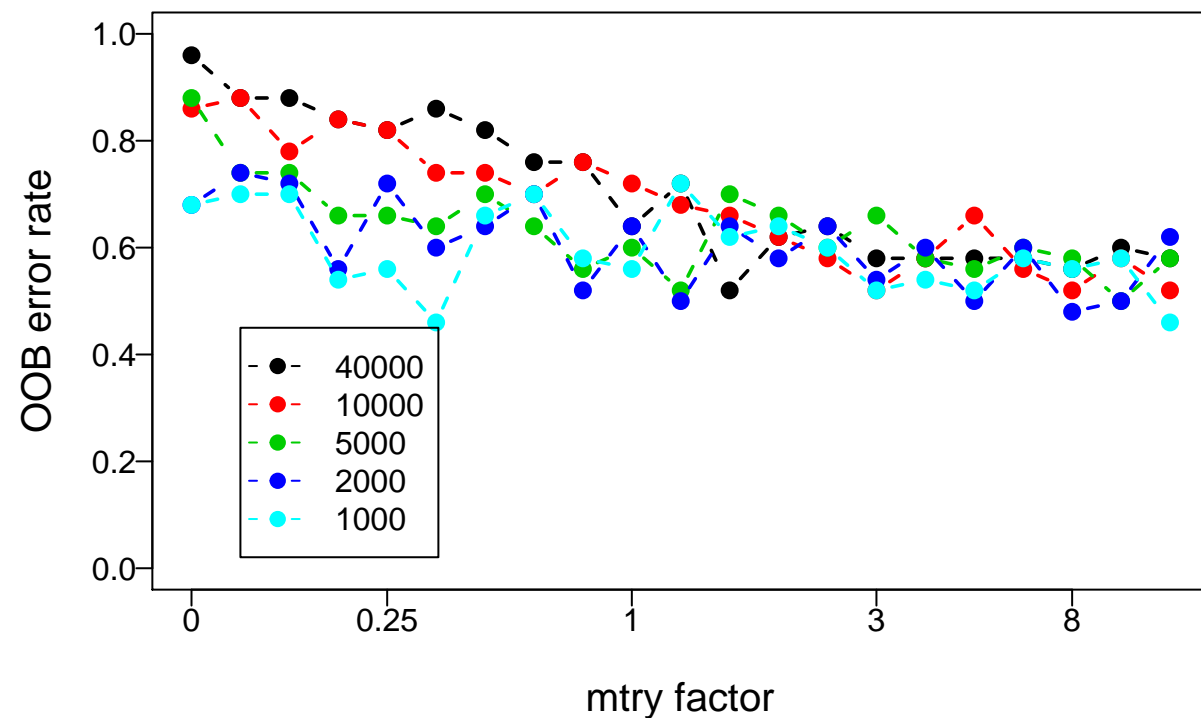
No signal: Classes 2 ; nodesize = 5



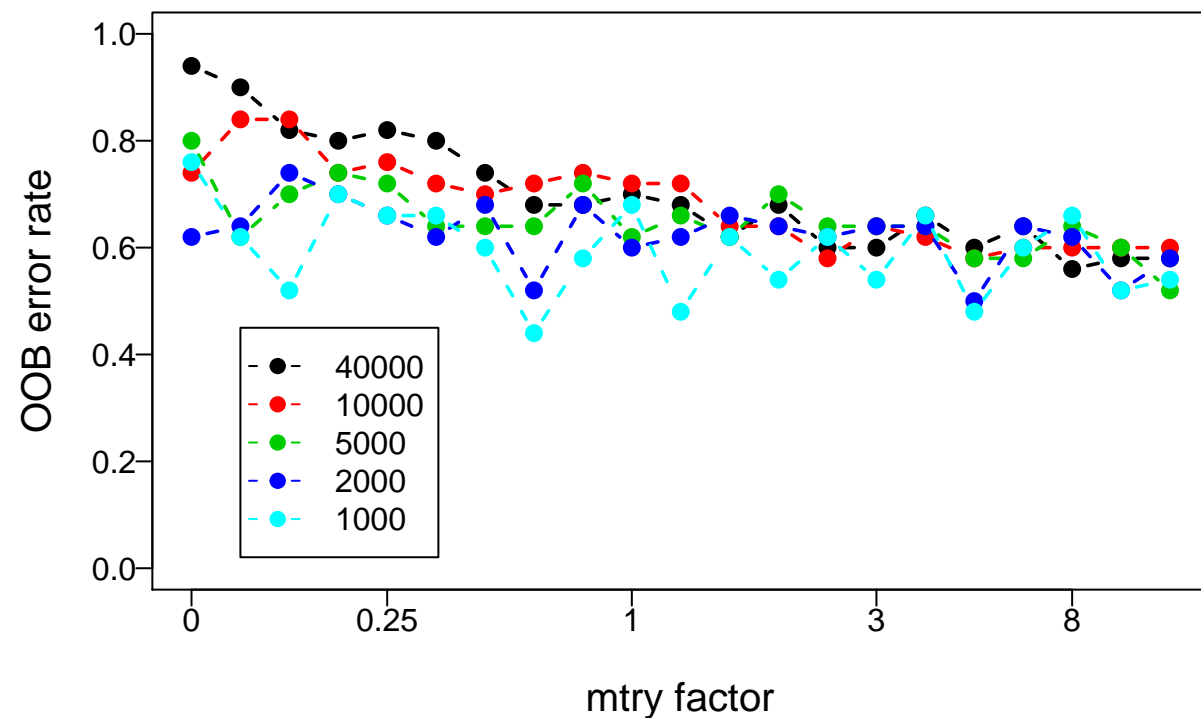
No signal: Classes 2 ; nodesize = 5



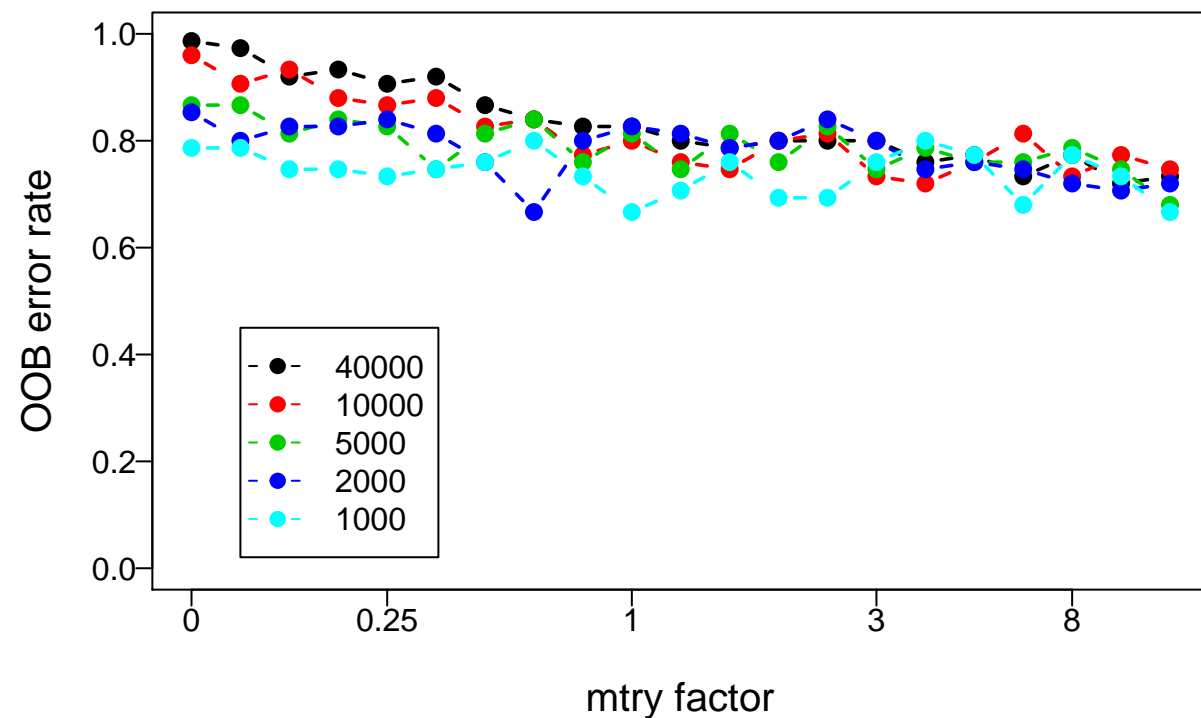
No signal: Classes 2 ; nodesize = 5



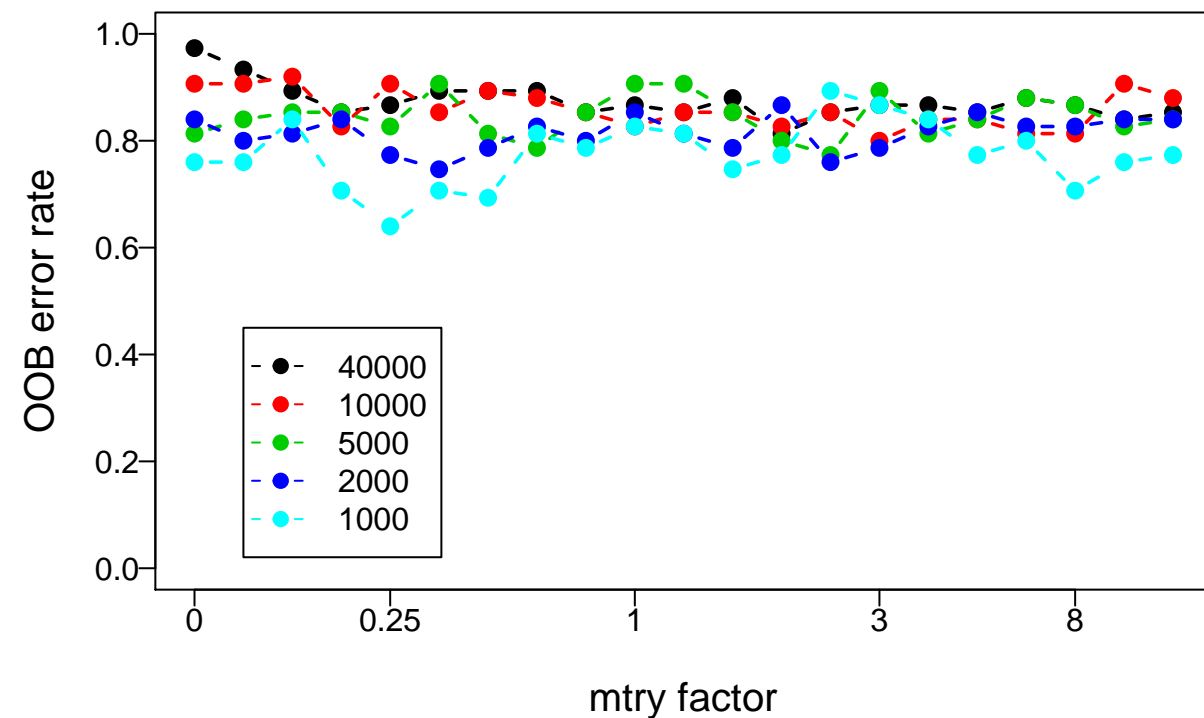
No signal: Classes 2 ; nodesize = 5



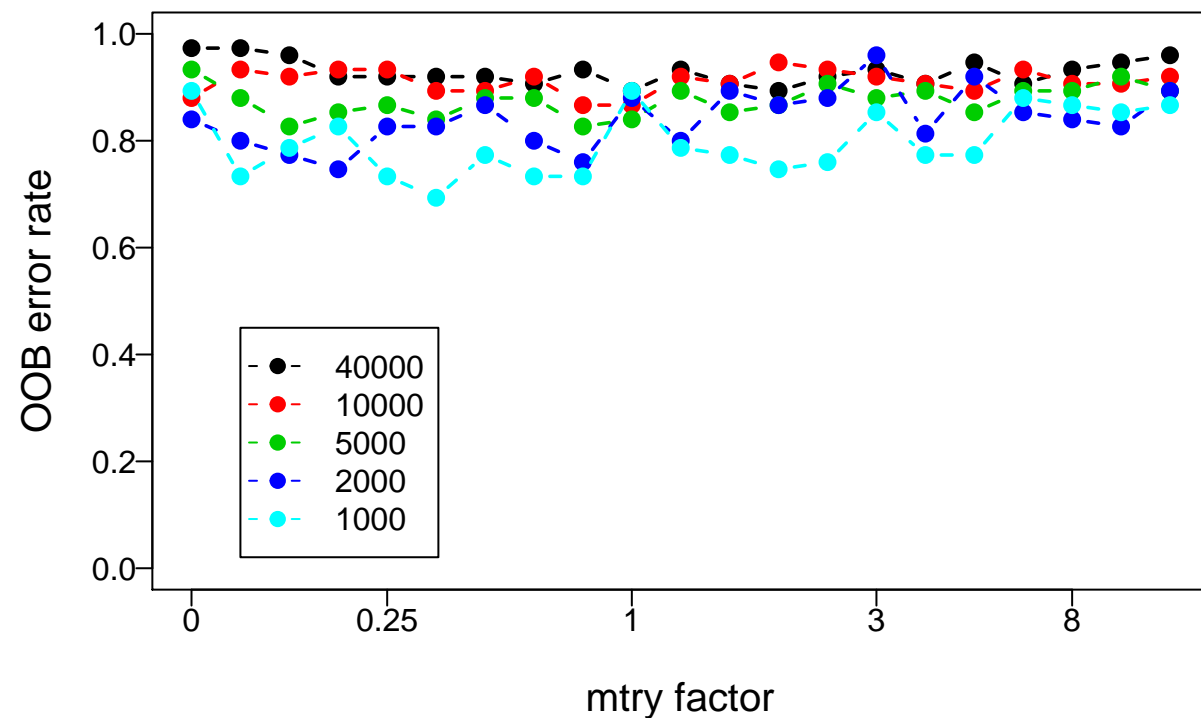
No signal: Classes 3 ; nodesize = 5



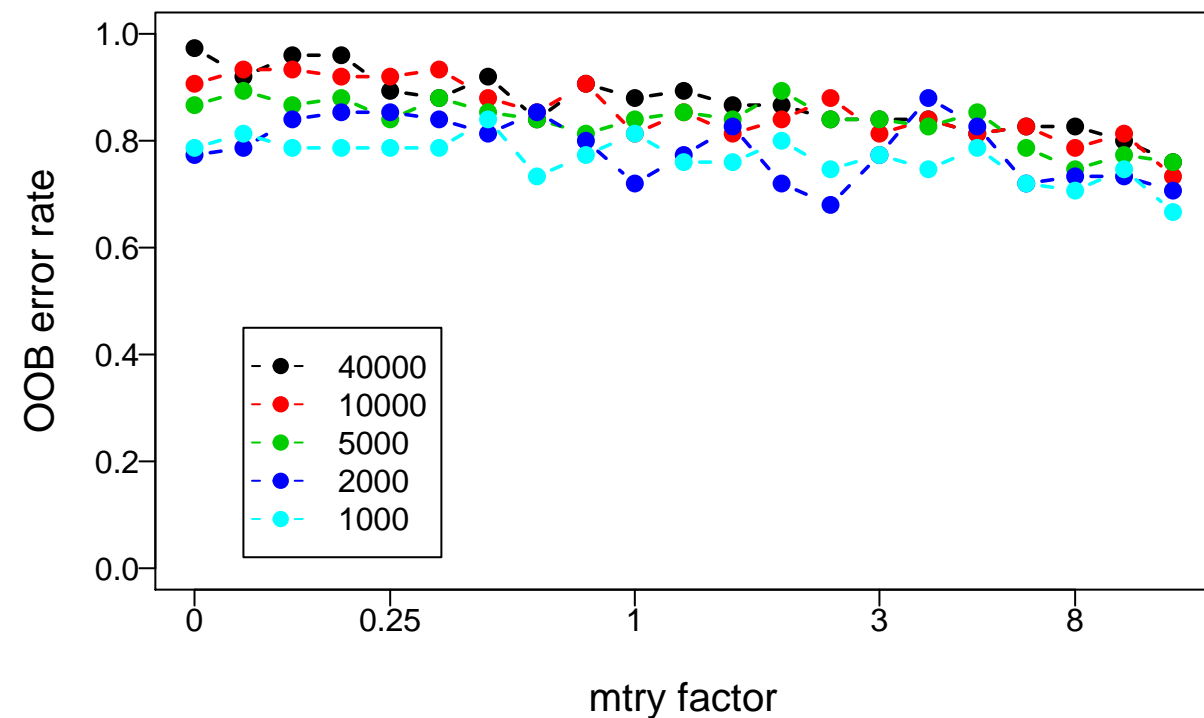
No signal: Classes 3 ; nodesize = 5



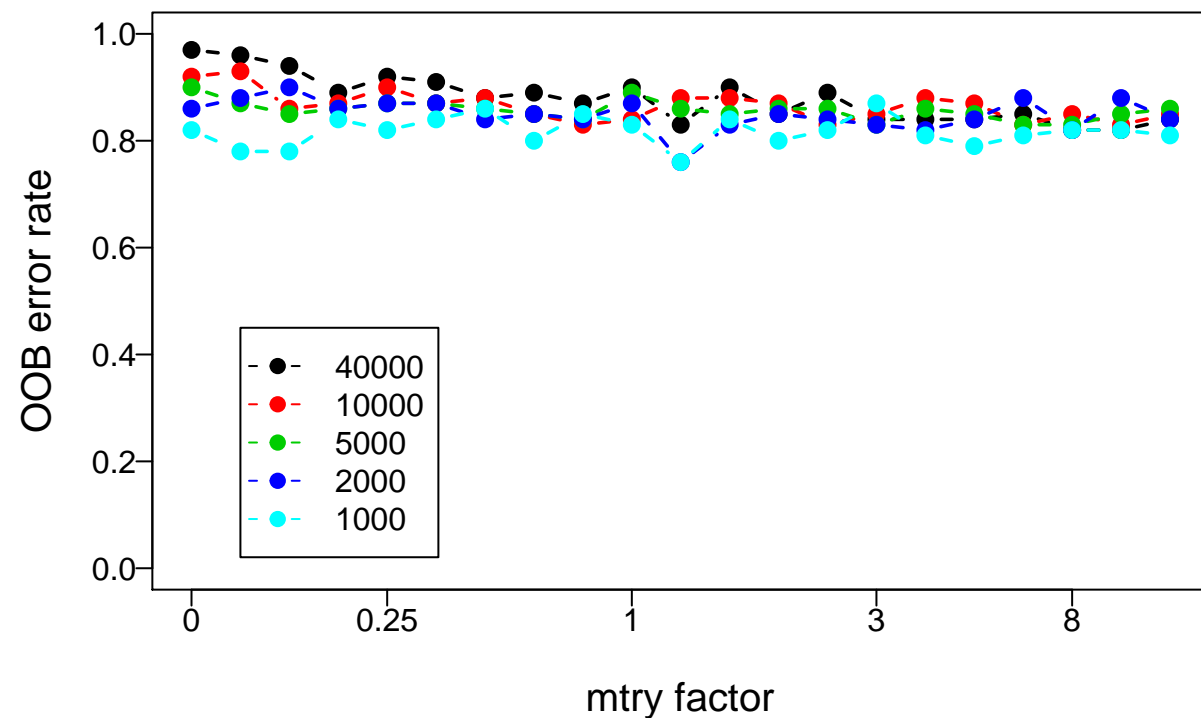
No signal: Classes 3 ; nodesize = 5



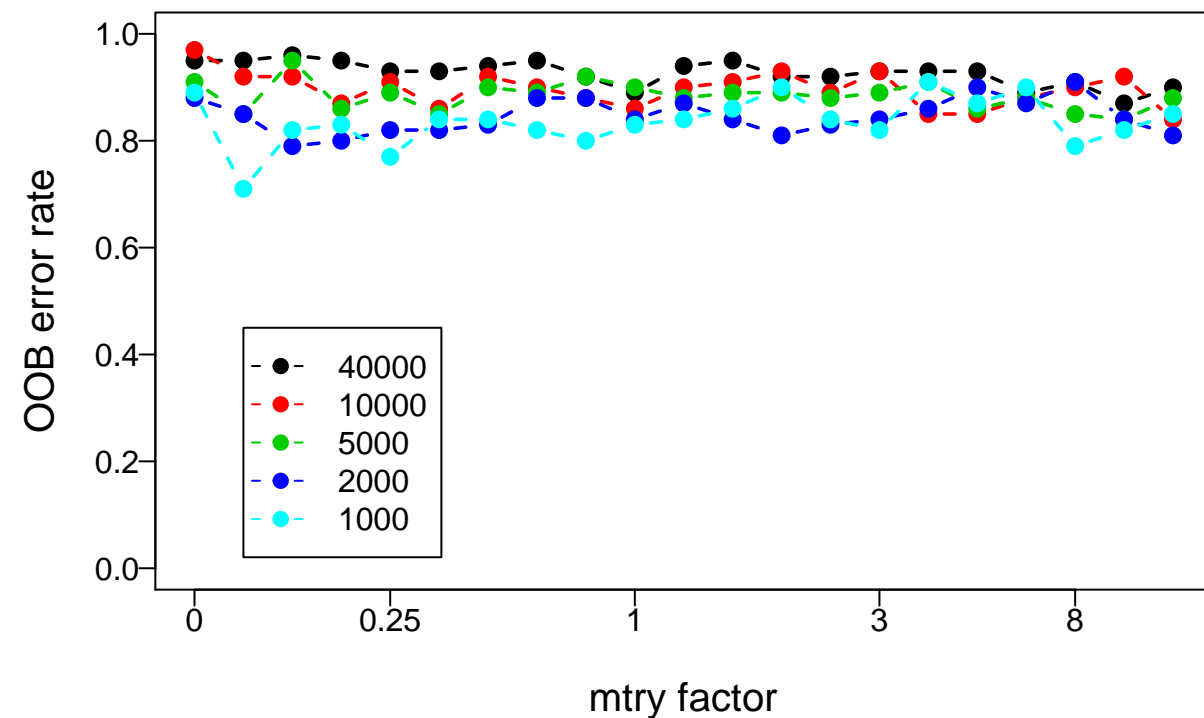
No signal: Classes 3 ; nodesize = 5



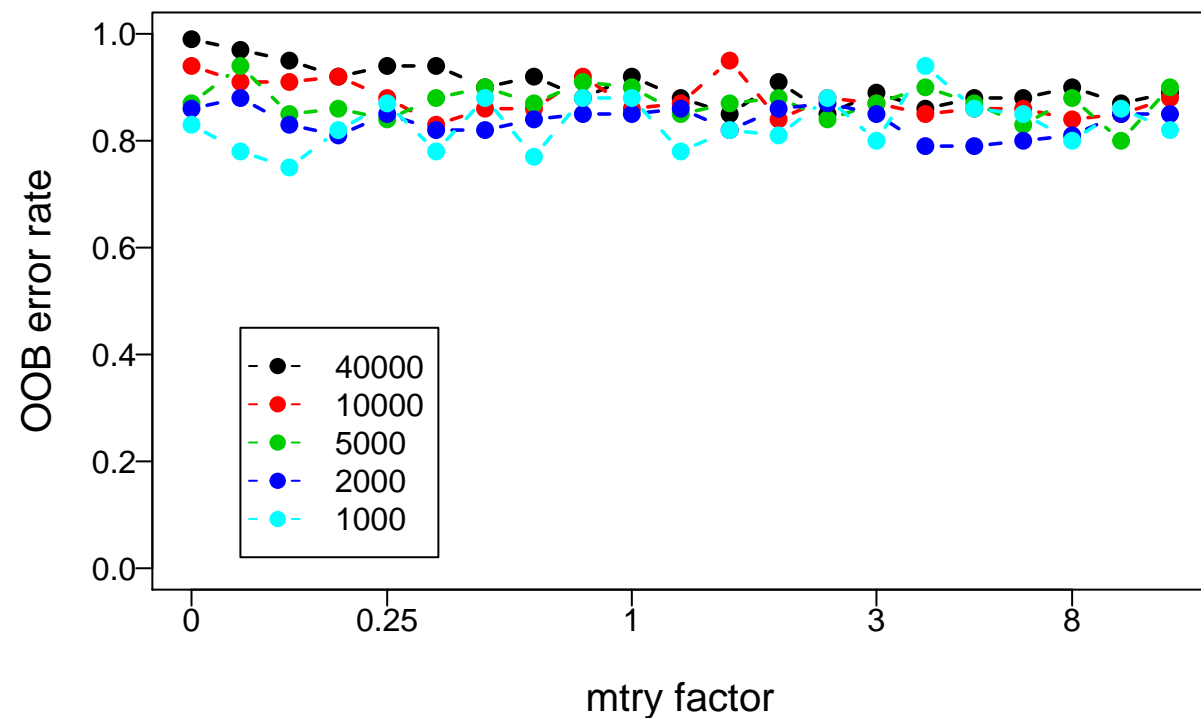
No signal: Classes 4 ; nodesize = 5



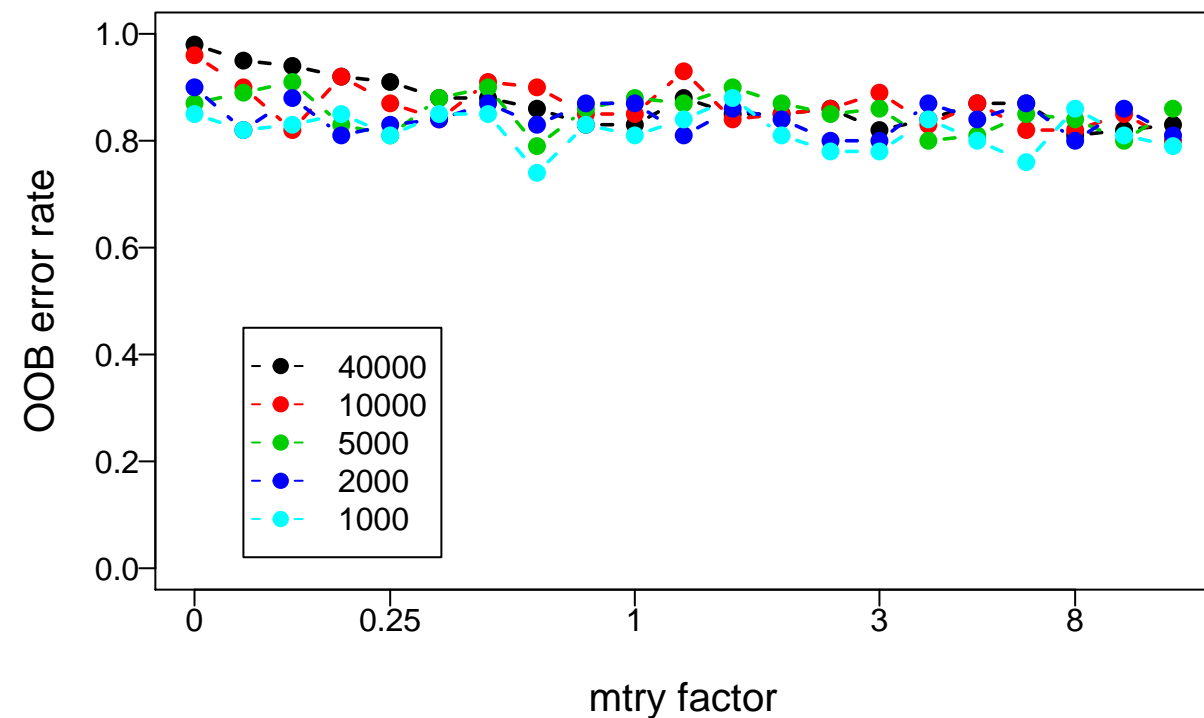
No signal: Classes 4 ; nodesize = 5



No signal: Classes 4 ; nodesize = 5



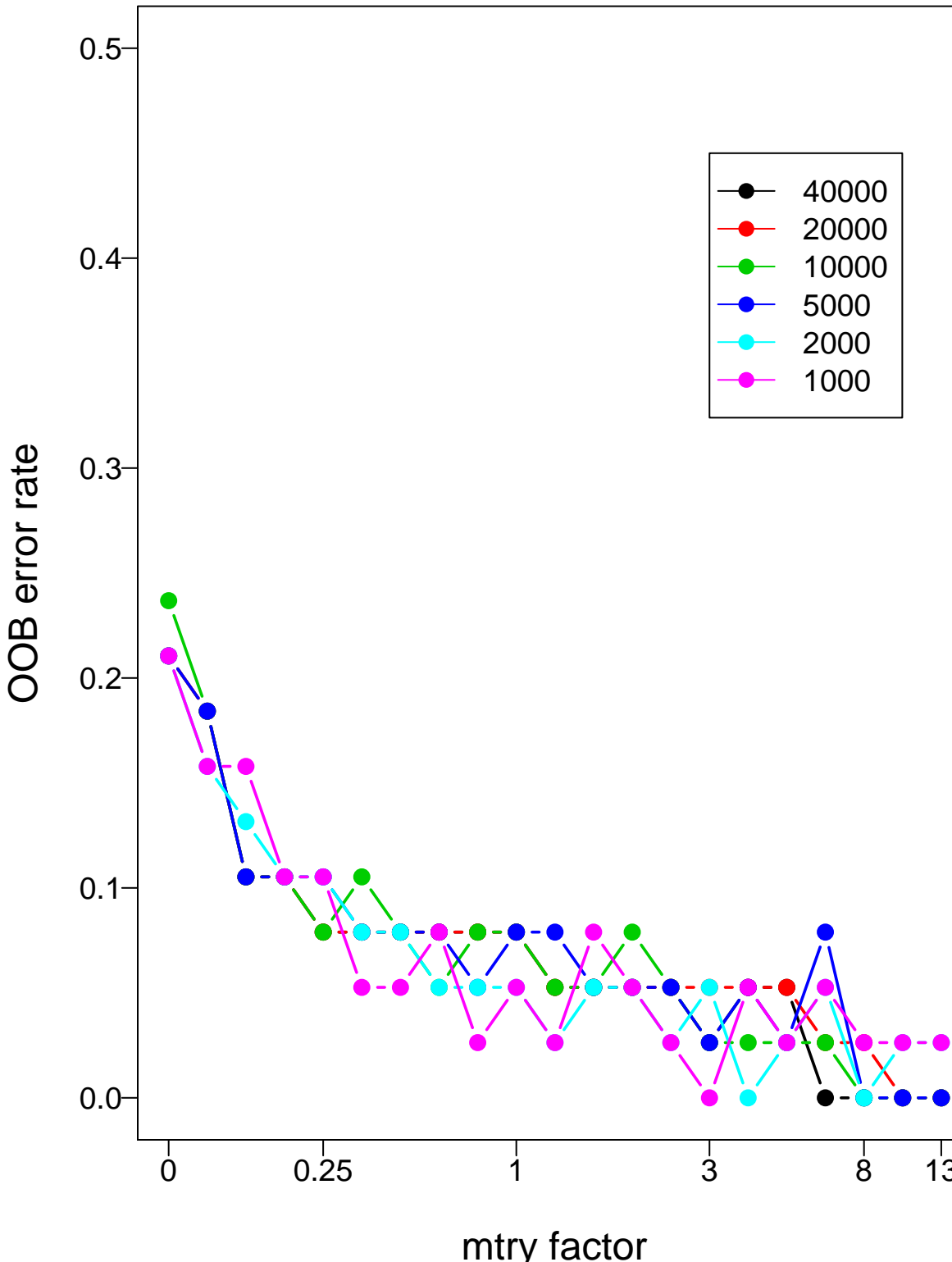
No signal: Classes 4 ; nodesize = 5



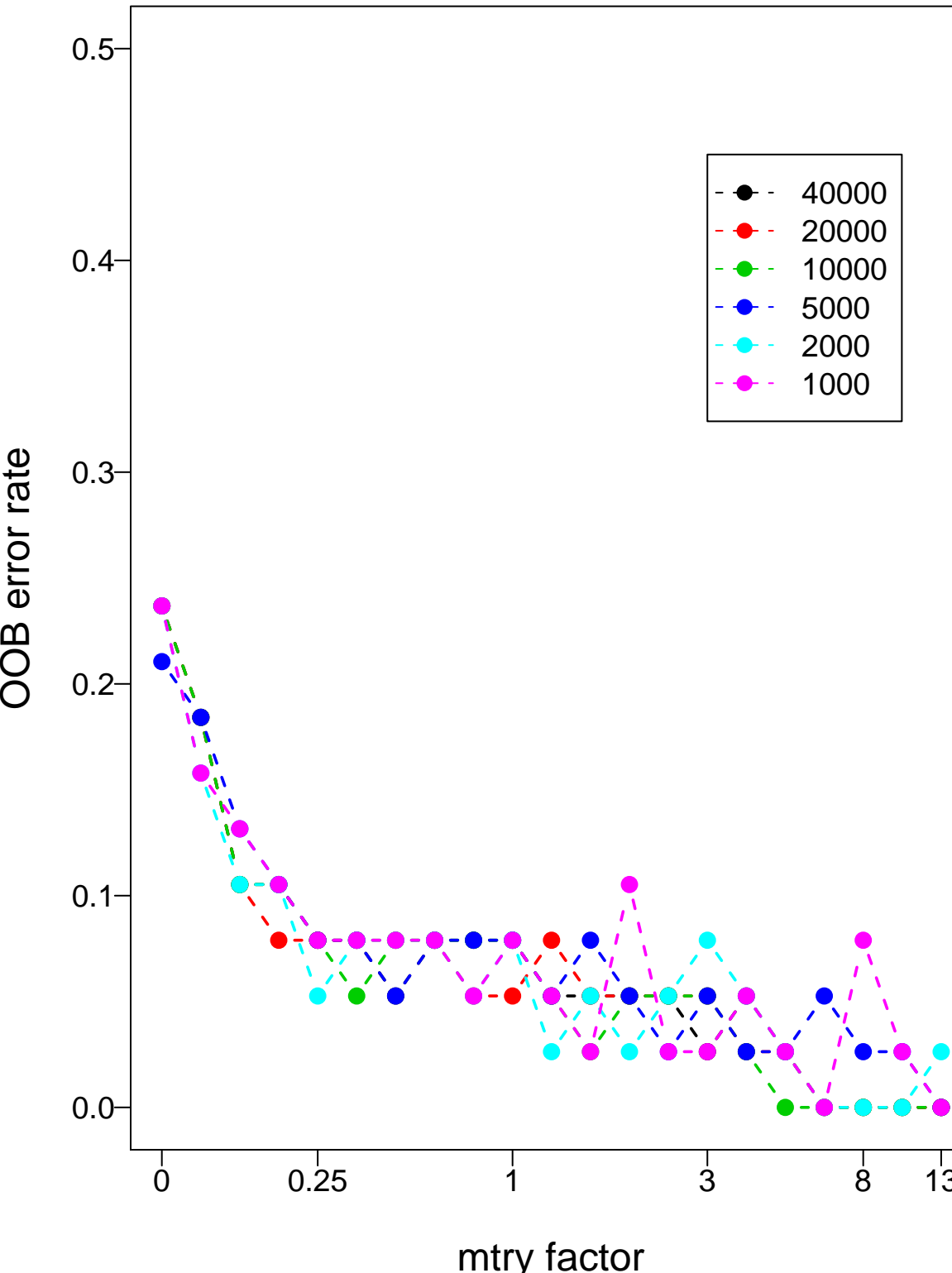
III: Real microarray data sets:

(left: nodesize = 1, right: nodesize = 5)

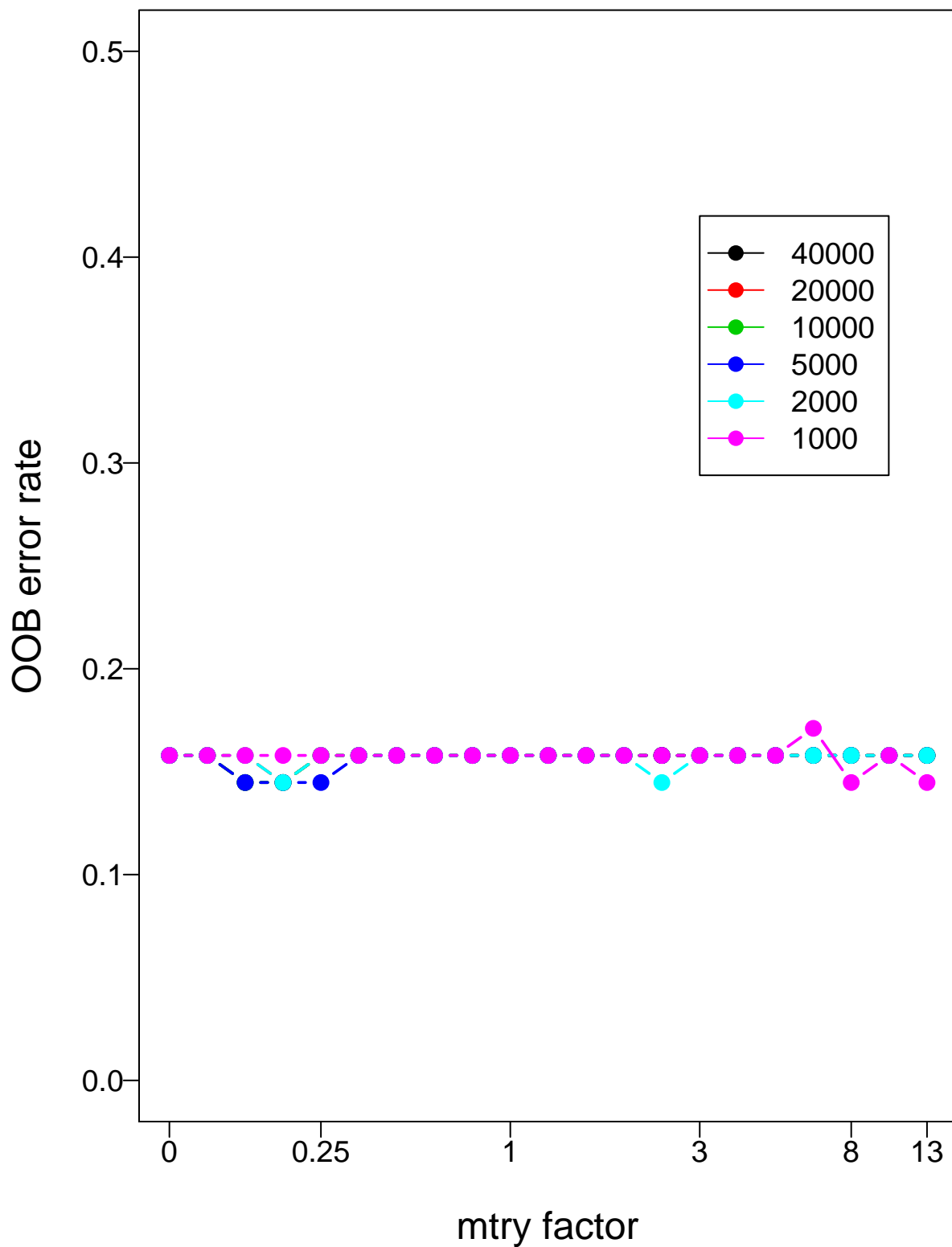
Leukemia; nodesize = 1



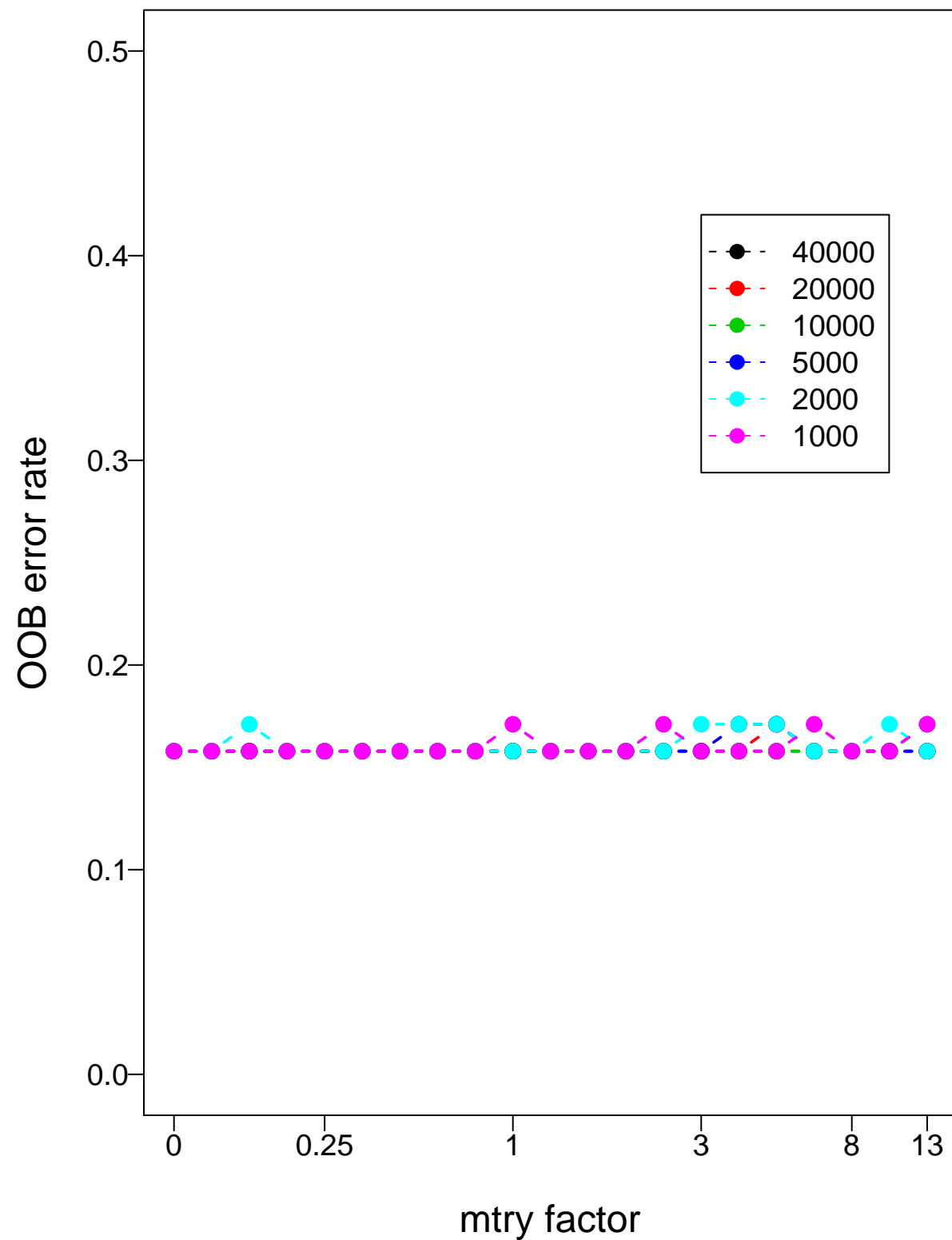
Leukemia; nodesize = 5



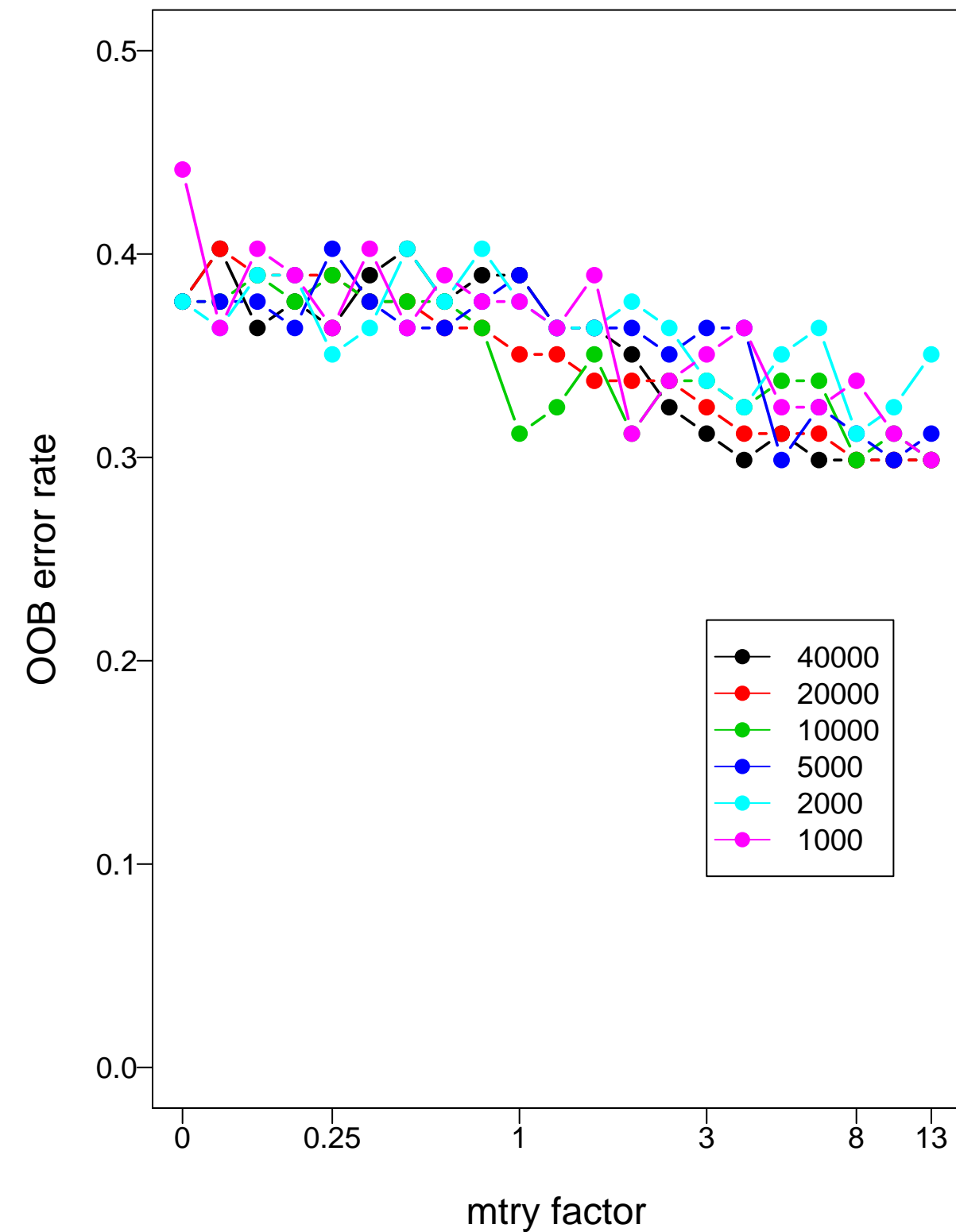
Adenoc.; nodesize = 1



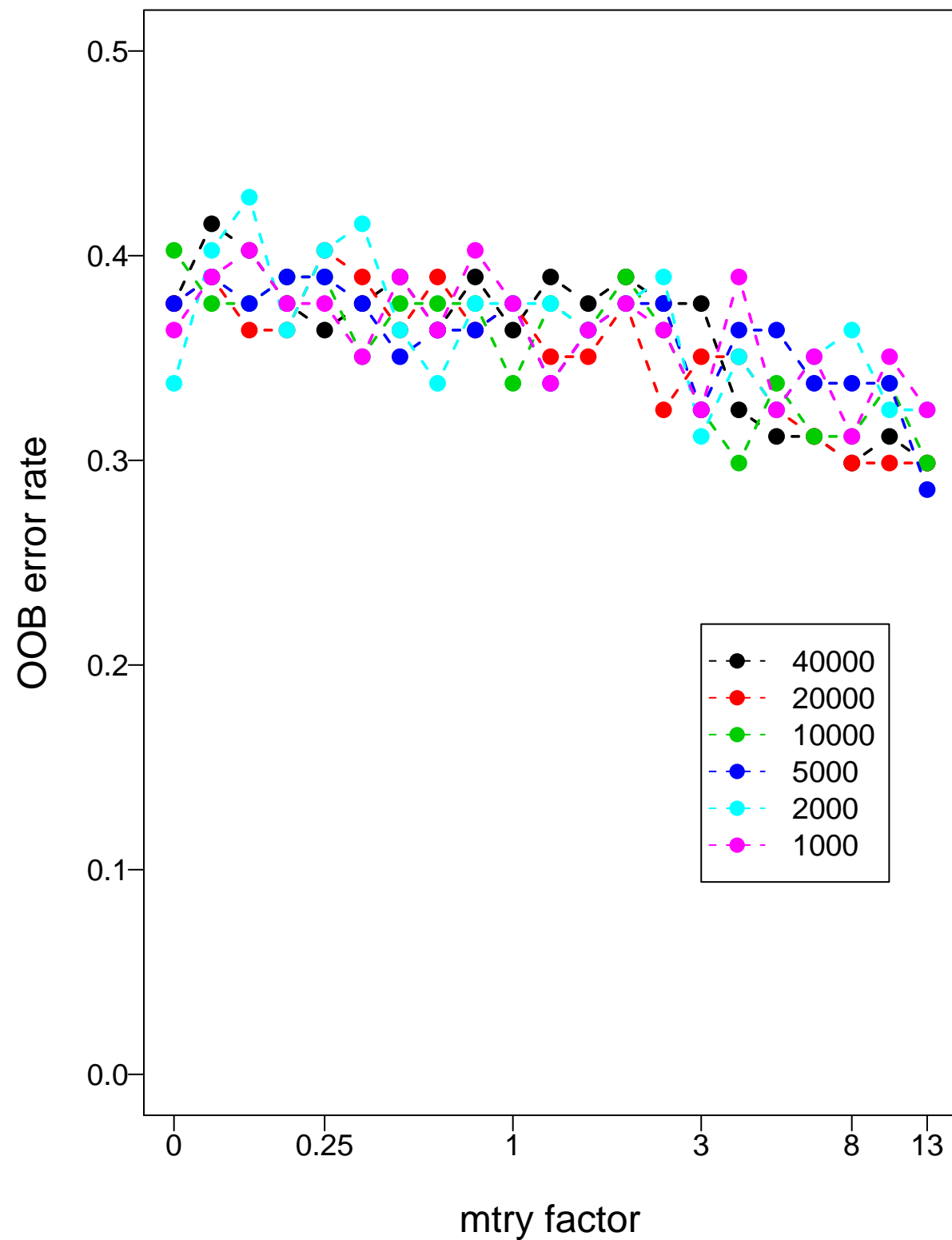
Adenoc.; nodesize = 5



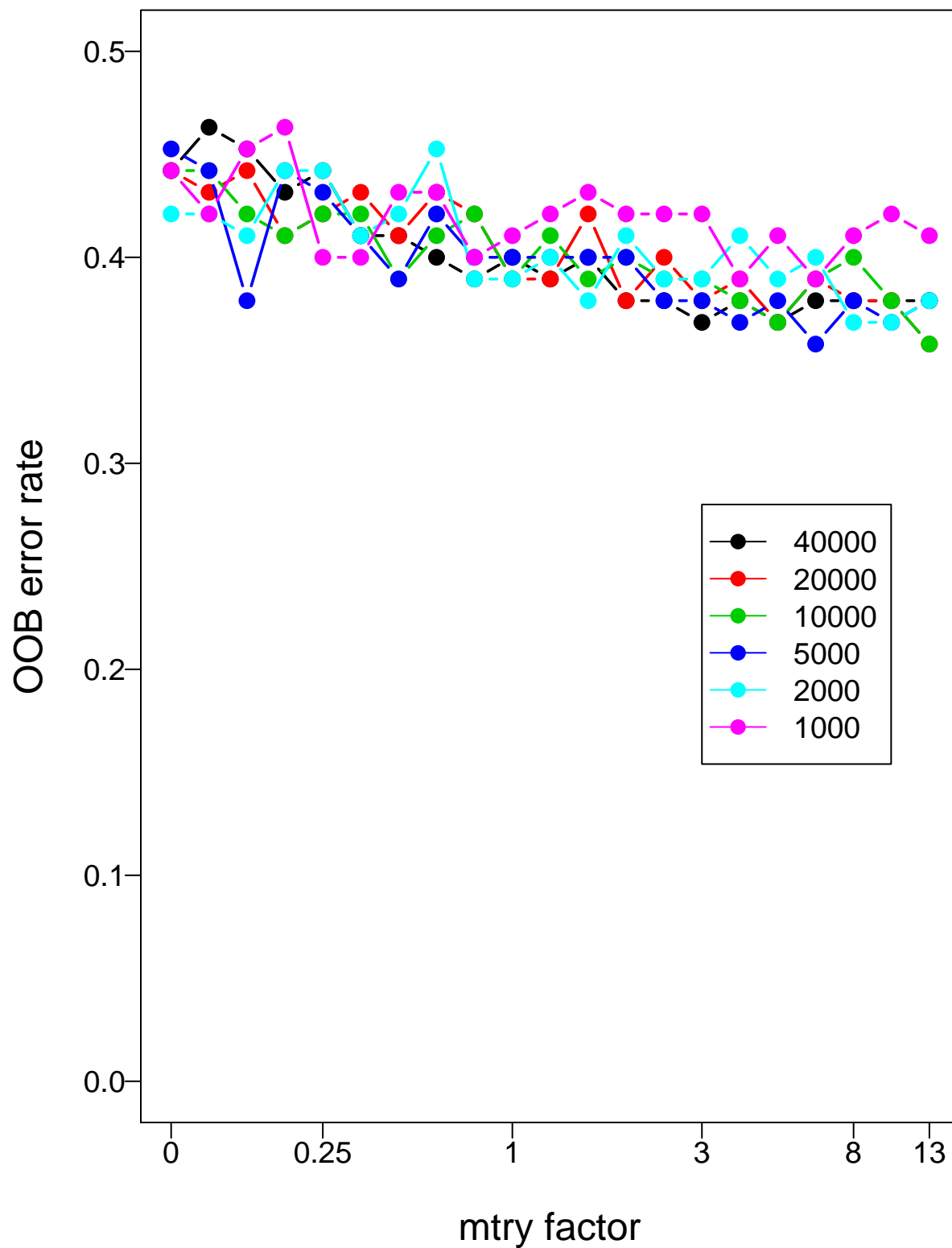
Breast, 2 cl.; nodesize = 1



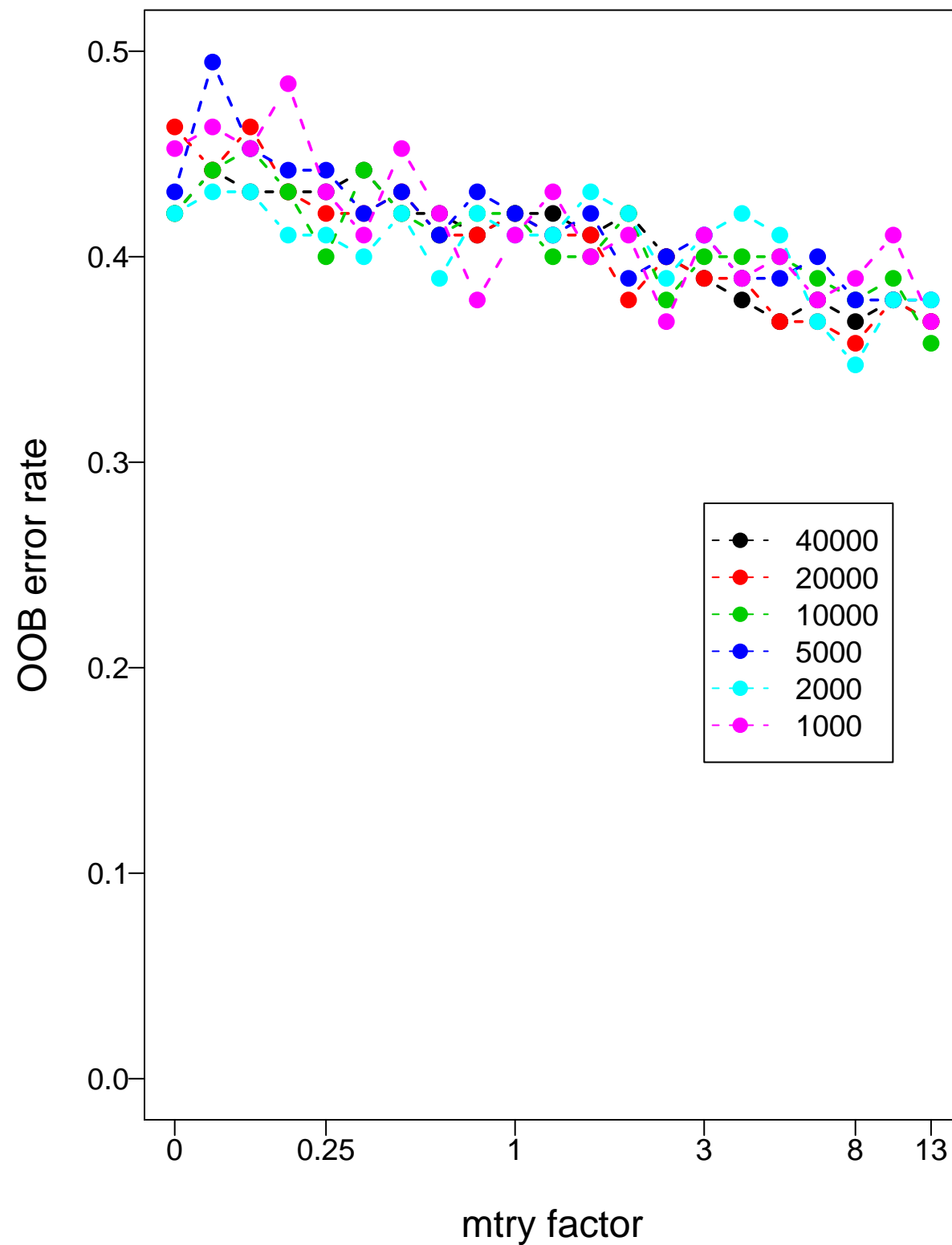
Breast, 2 cl.; nodesize = 5



Breast, 3 cl.; nodesize = 1



Breast, 3 cl.; nodesize = 5



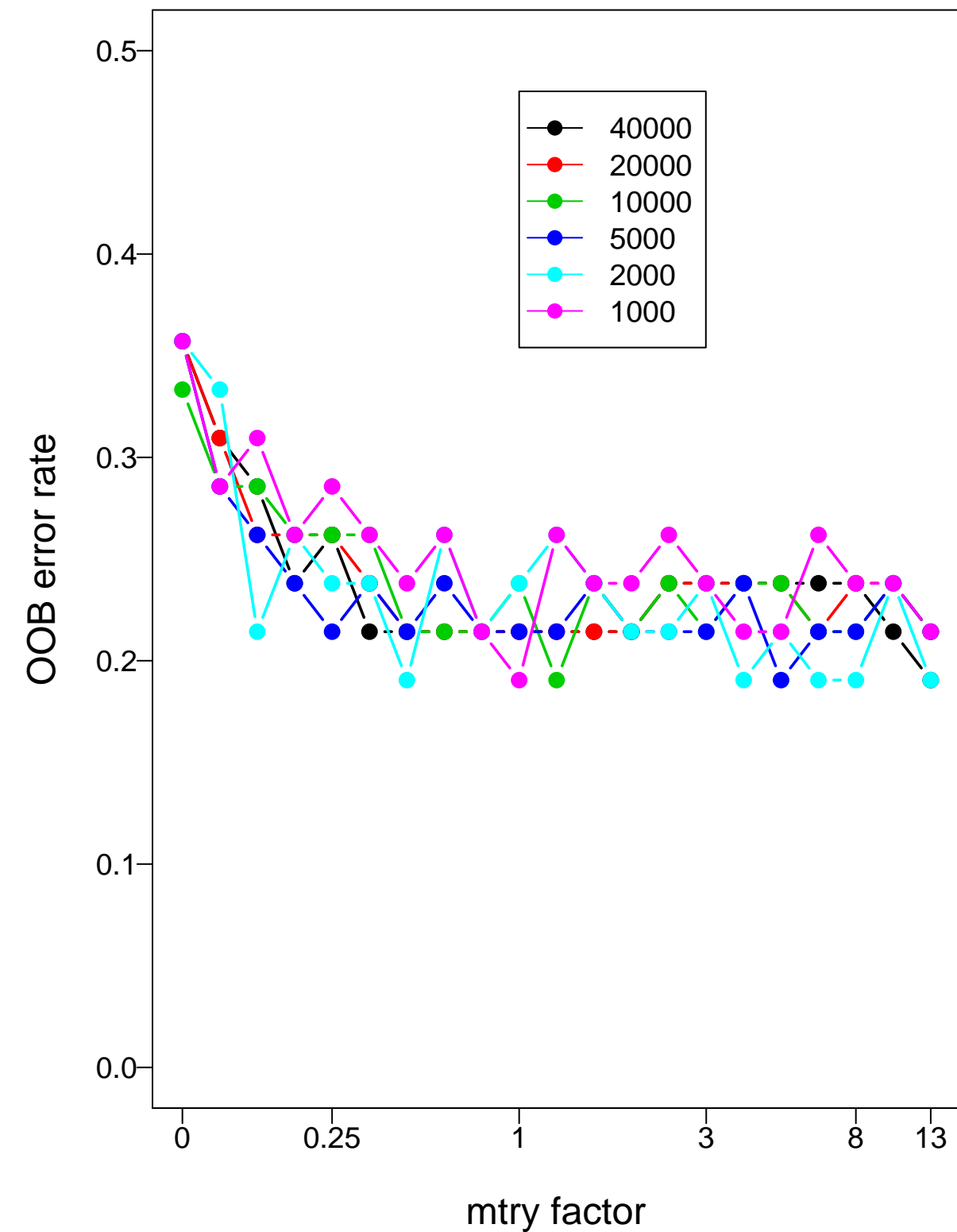
NCI 60; nodesize = 1



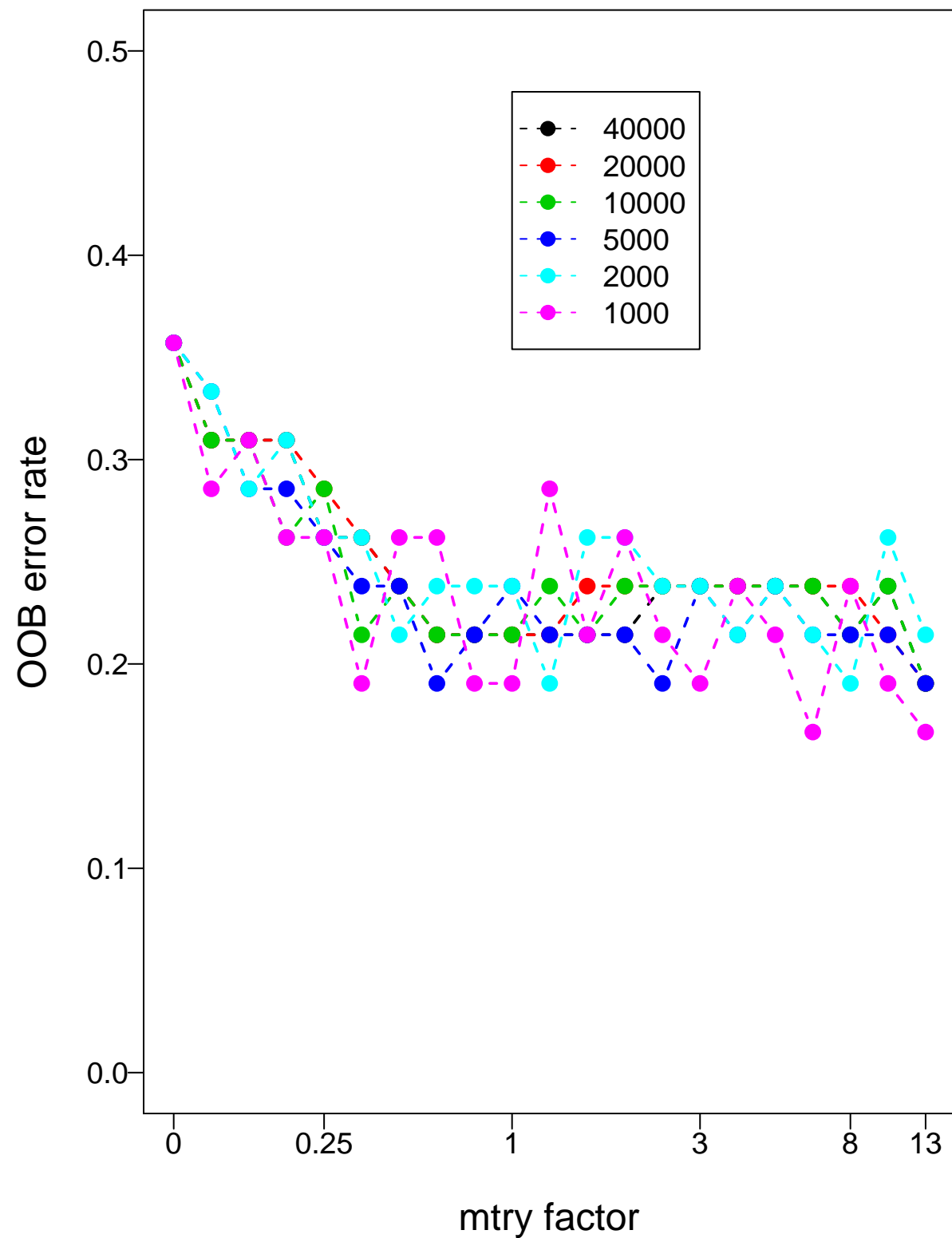
NCI 60; nodesize = 5



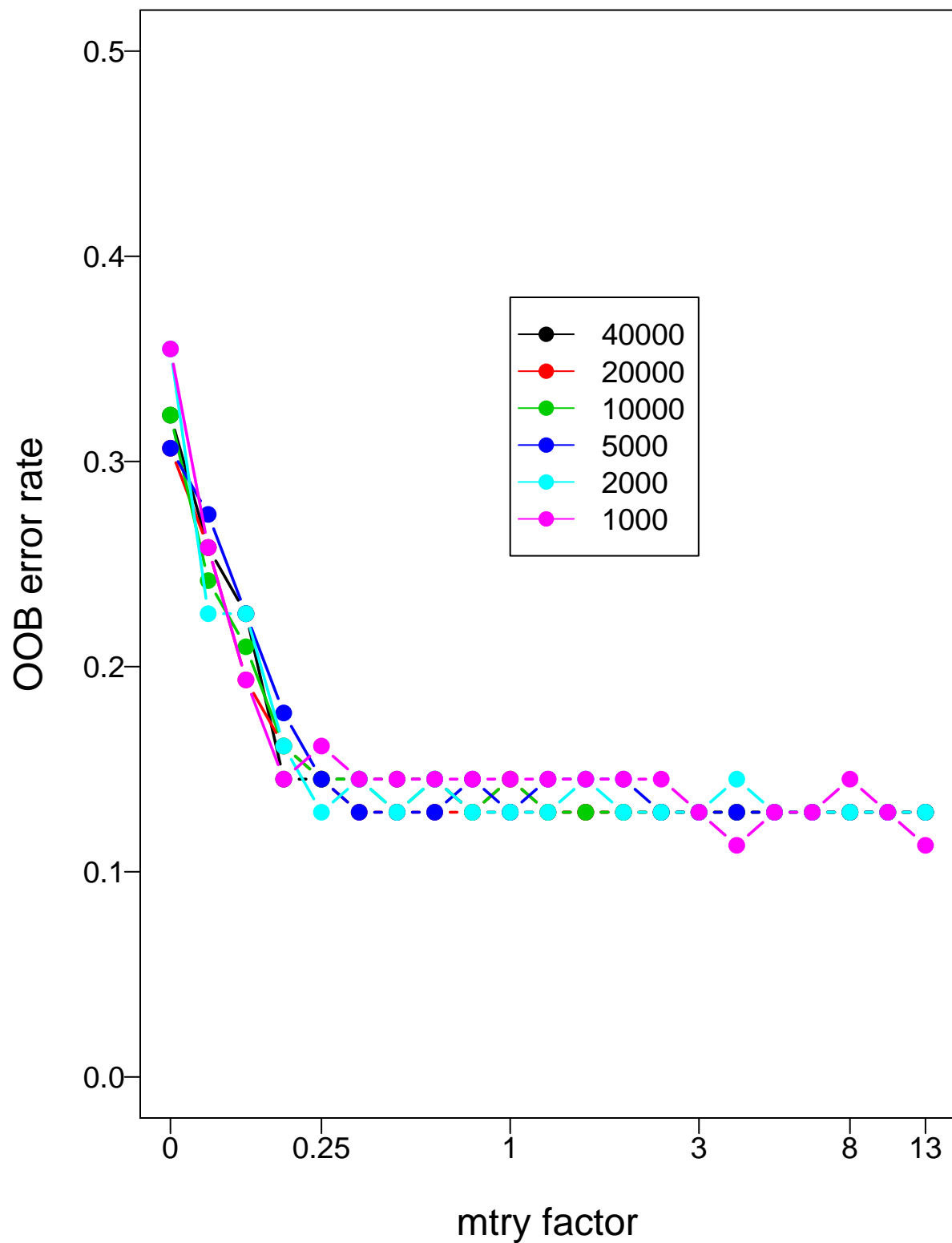
Brain; nodesize = 1



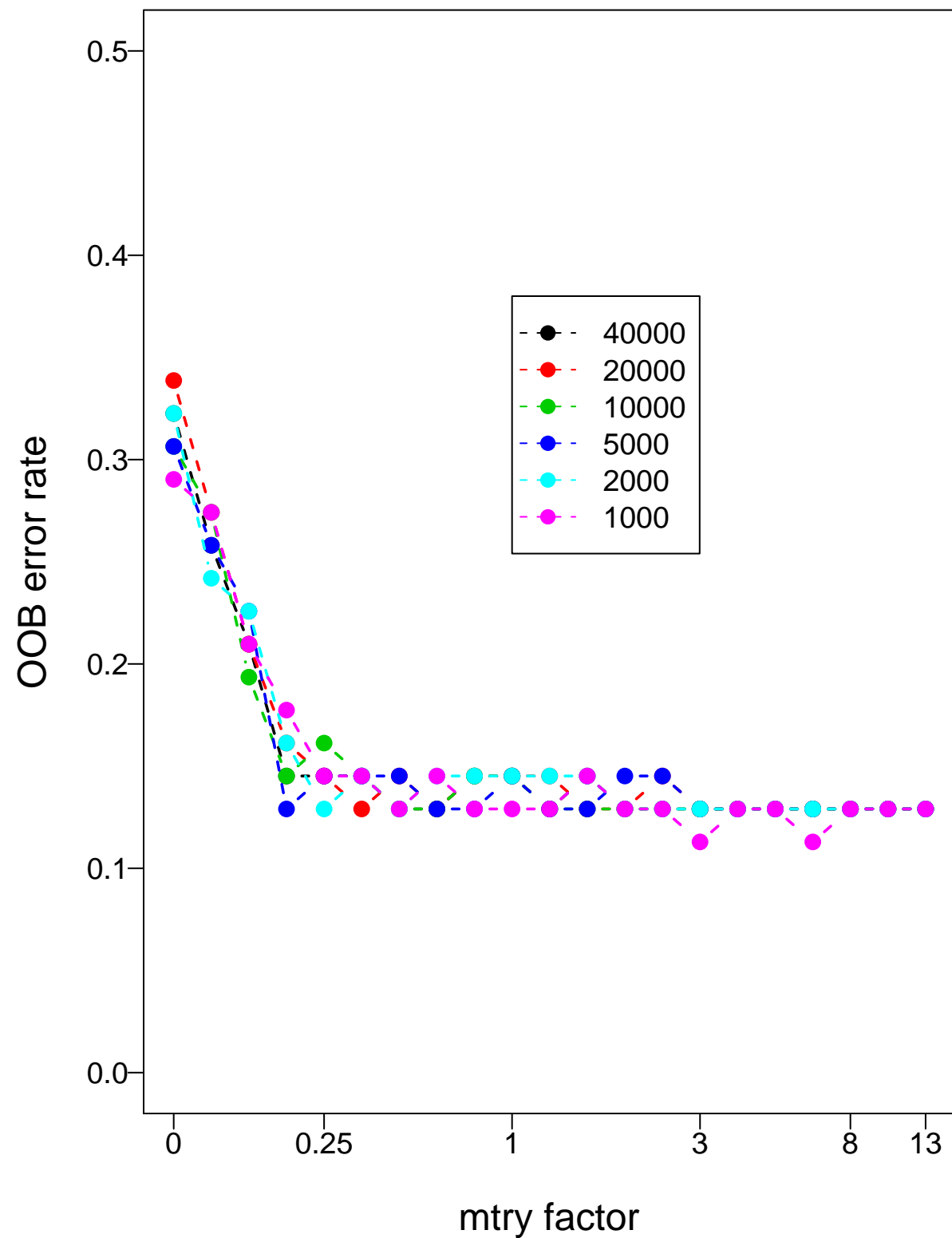
Brain; nodesize = 5



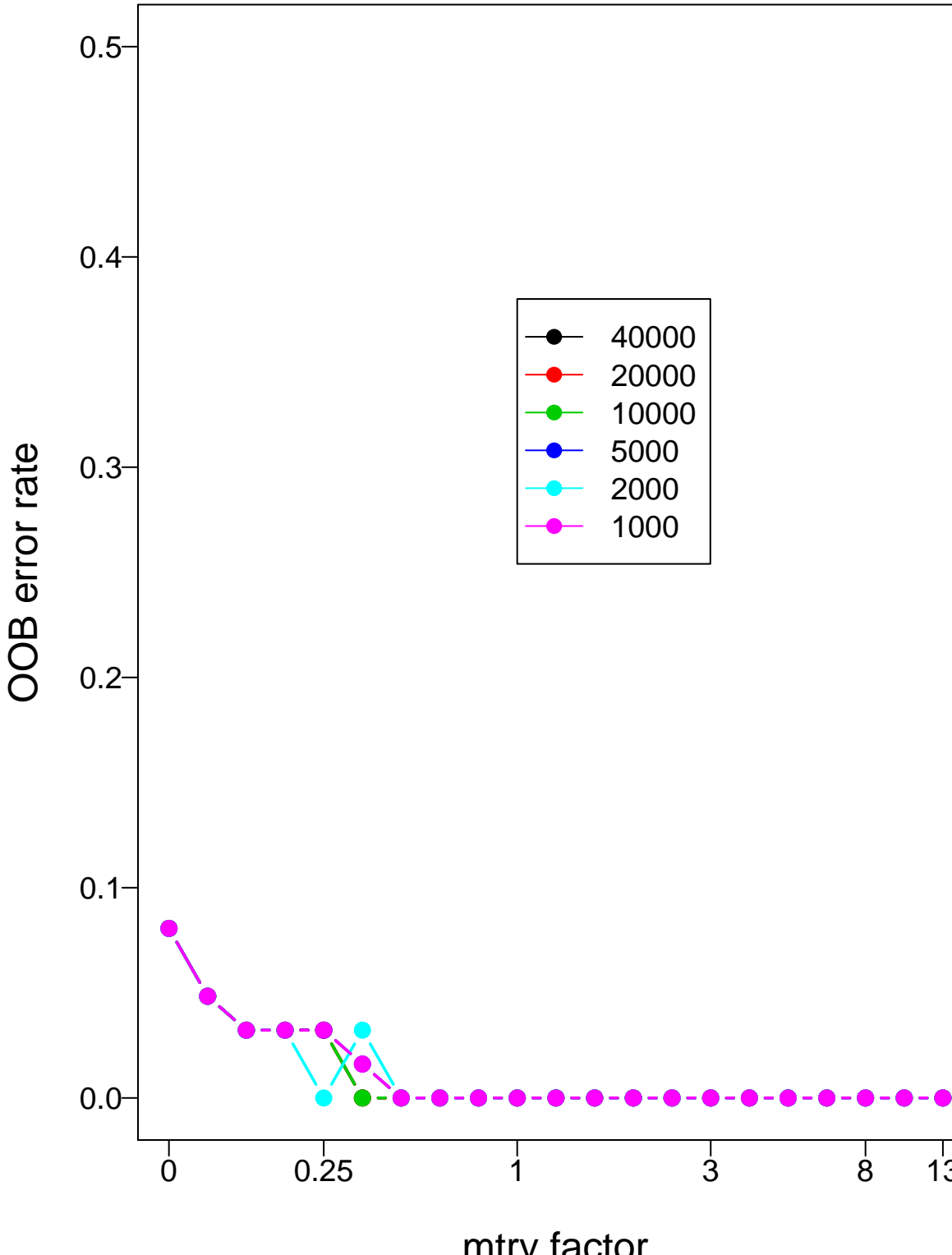
Colon.; nodesize = 1



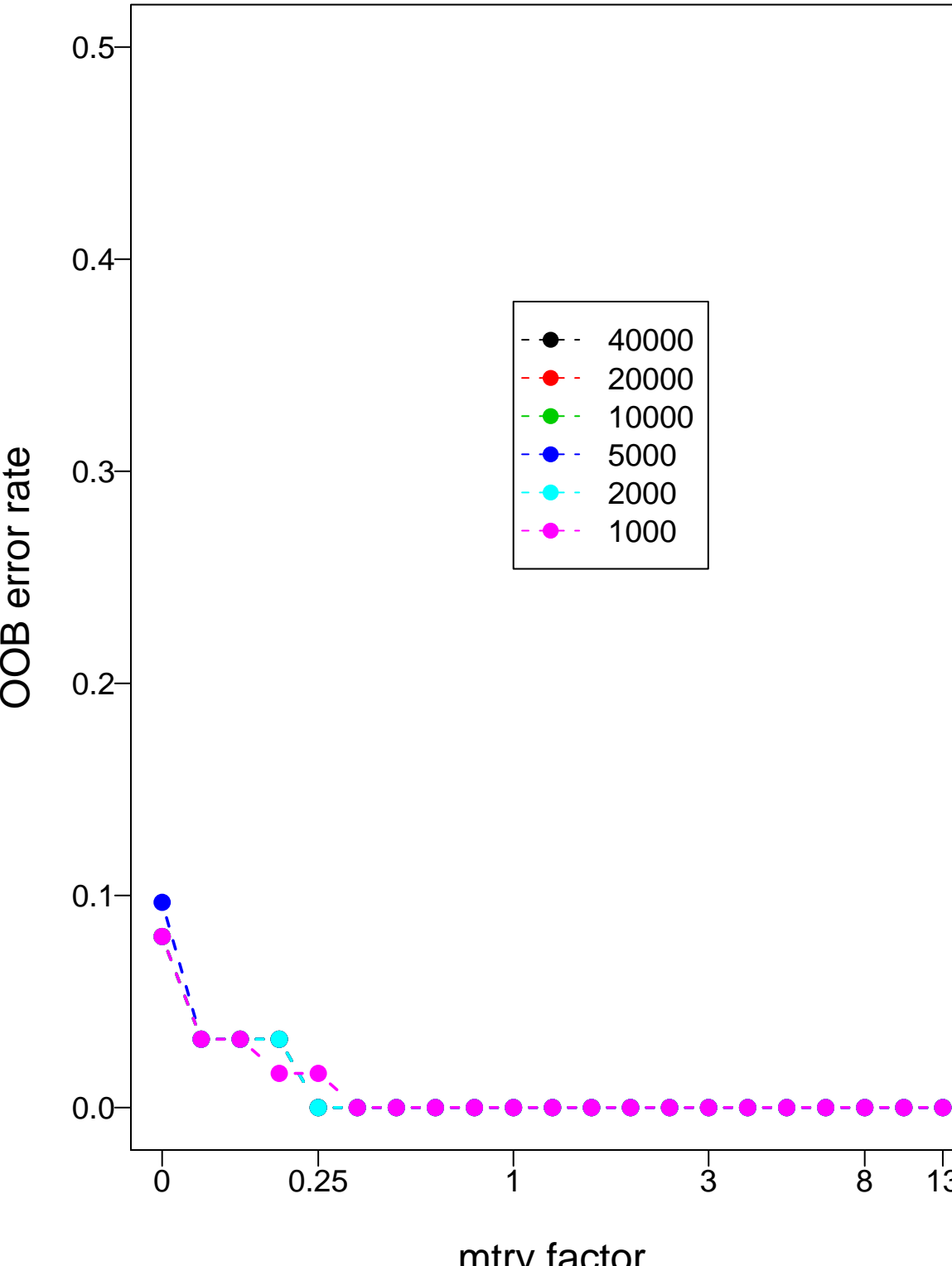
Colon.; nodesize = 5



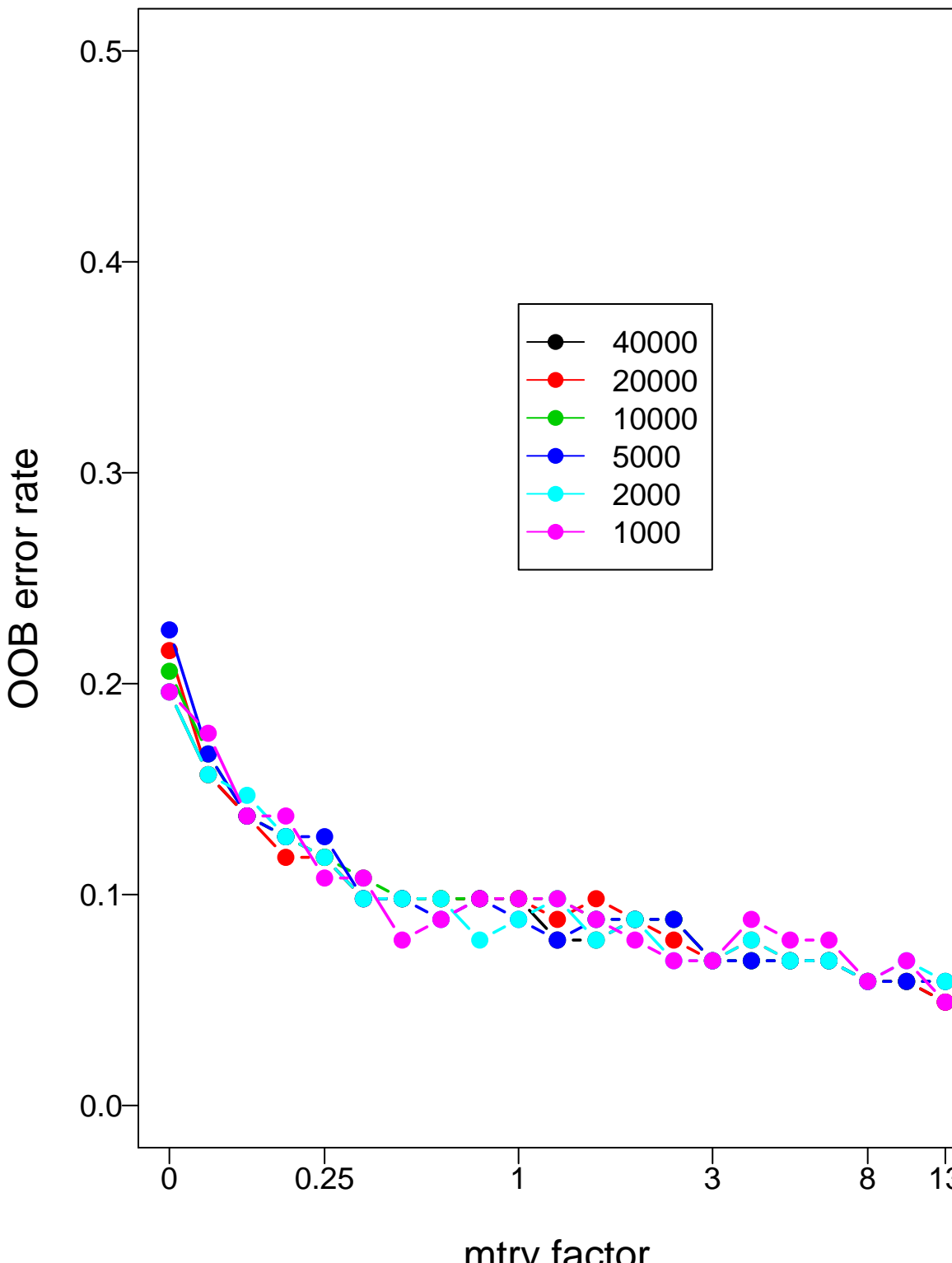
Lymphoma; nodesize = 1



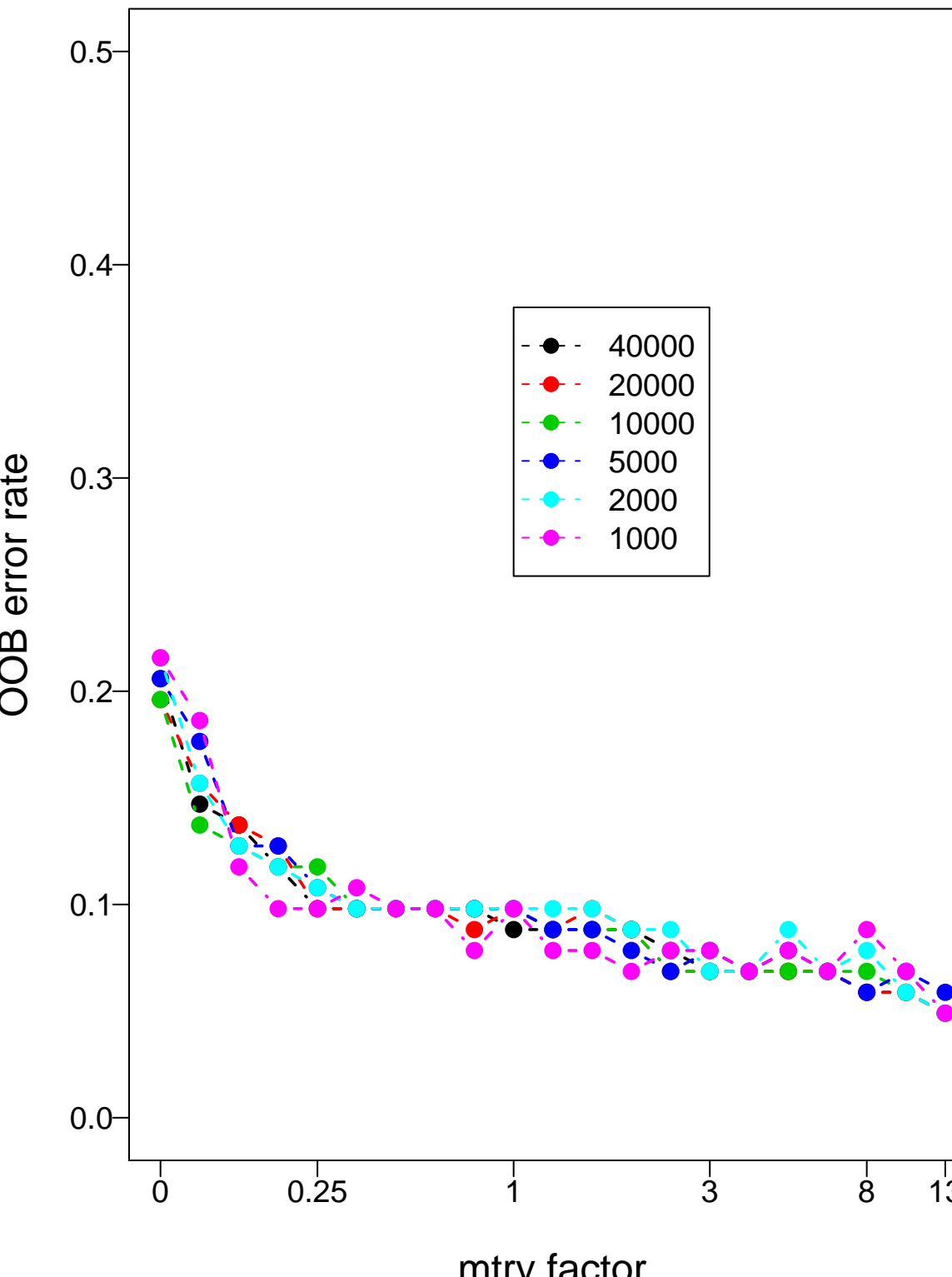
Lymphoma; nodesize = 5



Prostate; nodesize = 1



Prostate; nodesize = 5



SRBCT; nodesize = 1



SRBCT; nodesize = 5

