

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}

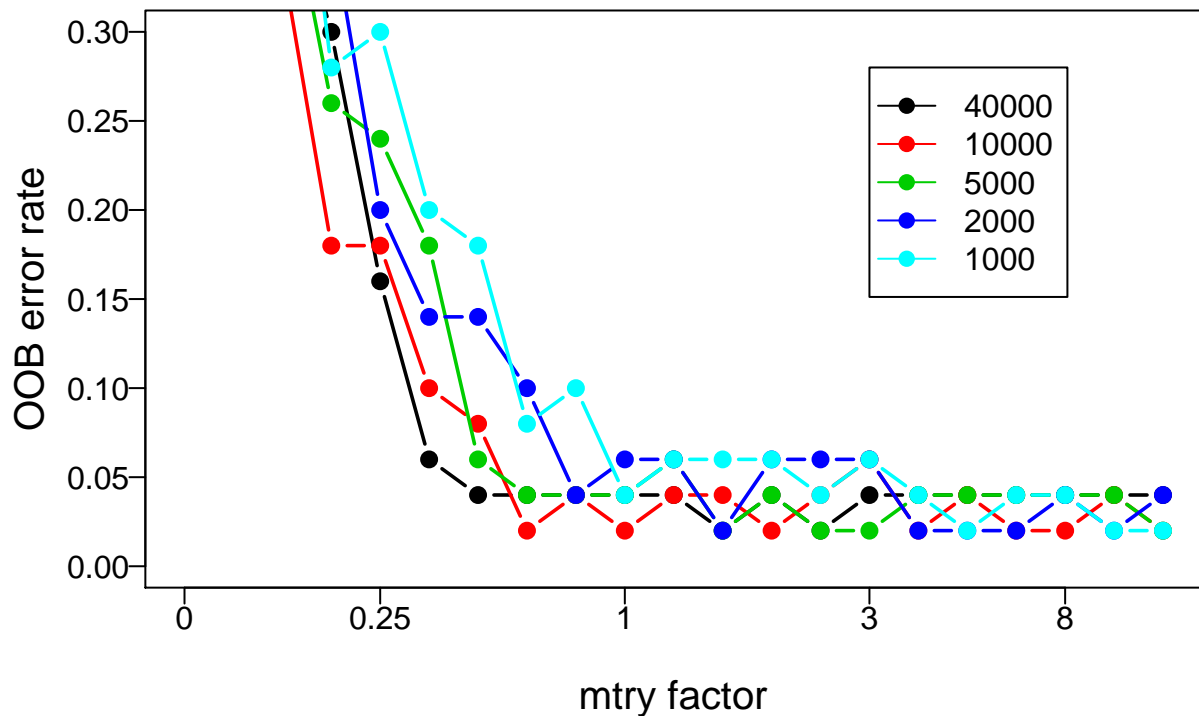
(mtry factors of 0 means mtry = 1)

I: Simulated data sets:

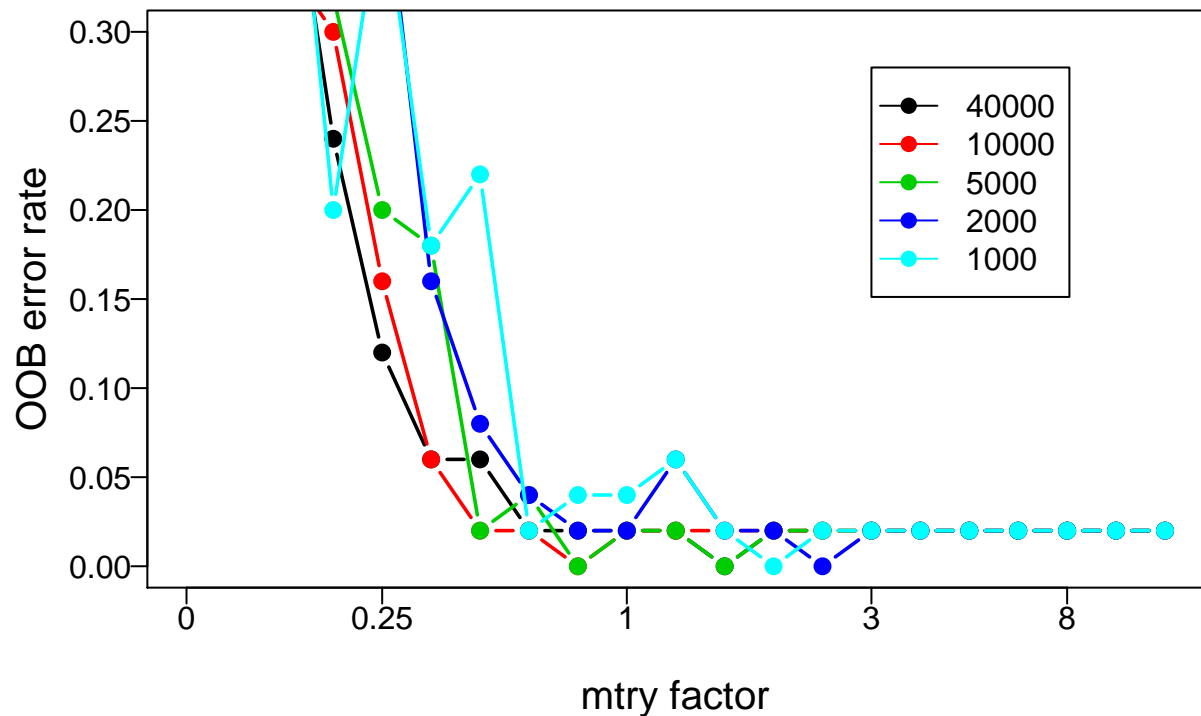
signal + 4000 noise random variables

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

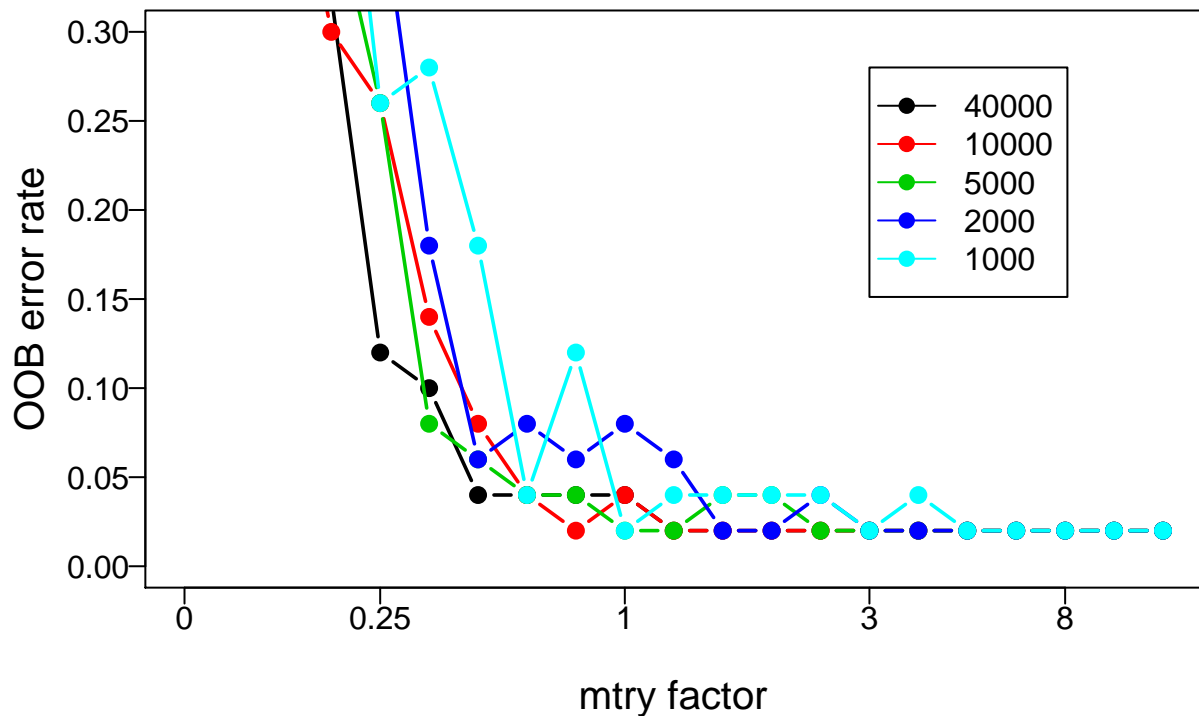
2 classes; 1 dimensions; 5 genes/dimen.; nodesize = 1



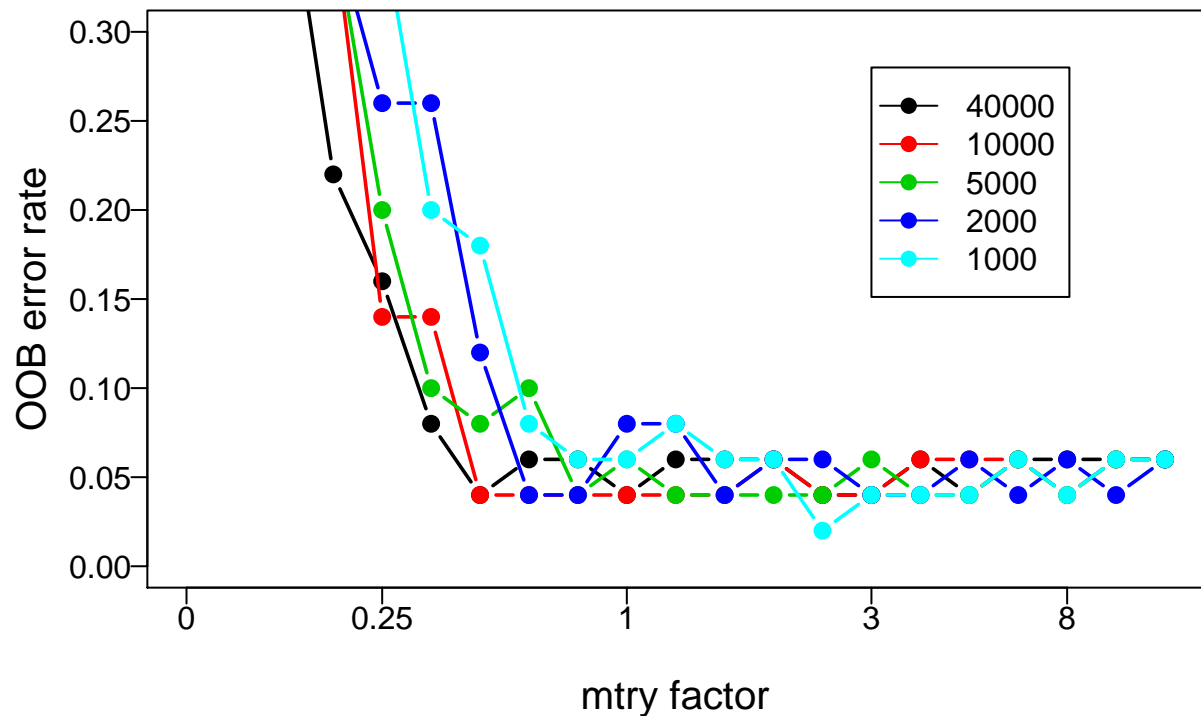
2 classes; 1 dimensions; 5 genes/dimen.; nodesize = 1



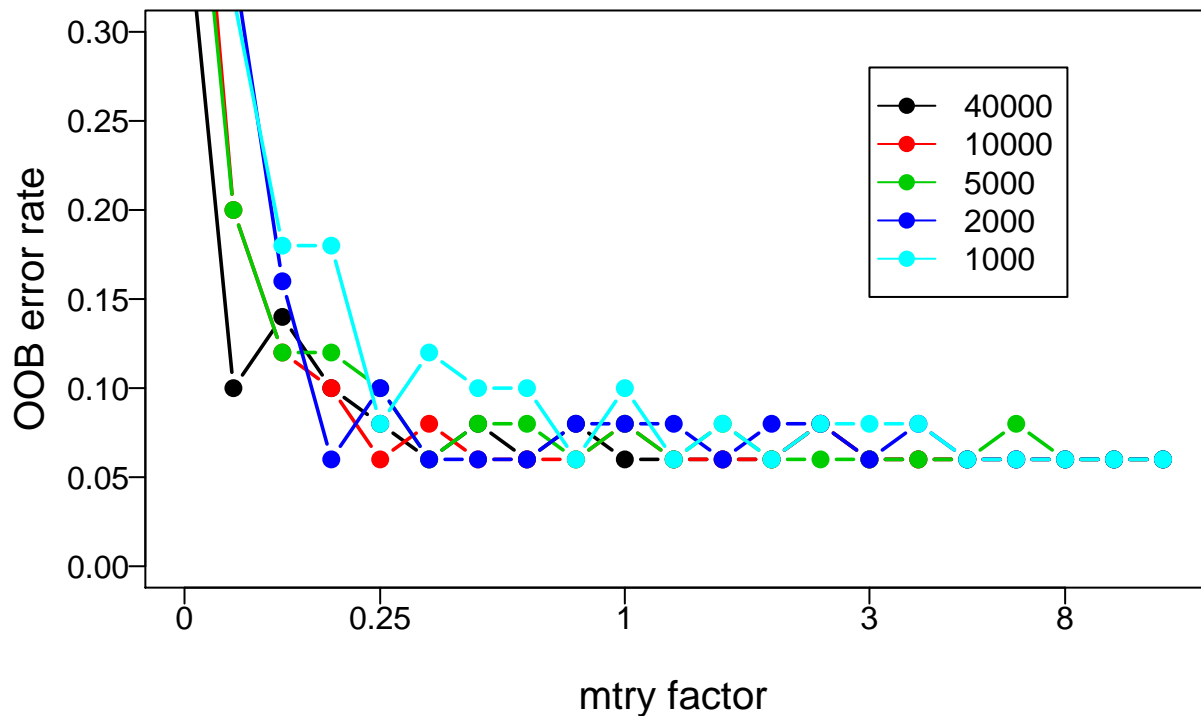
2 classes; 1 dimensions; 5 genes/dimen.; nodesize = 1



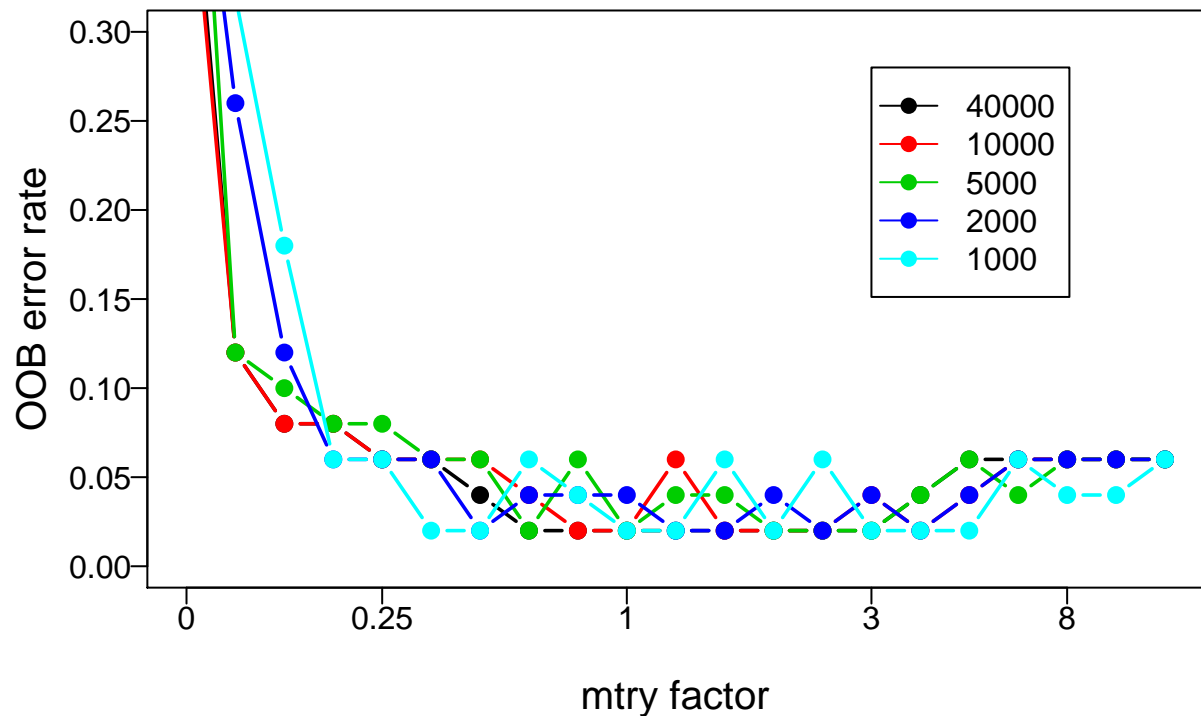
2 classes; 1 dimensions; 5 genes/dimen.; nodesize = 1



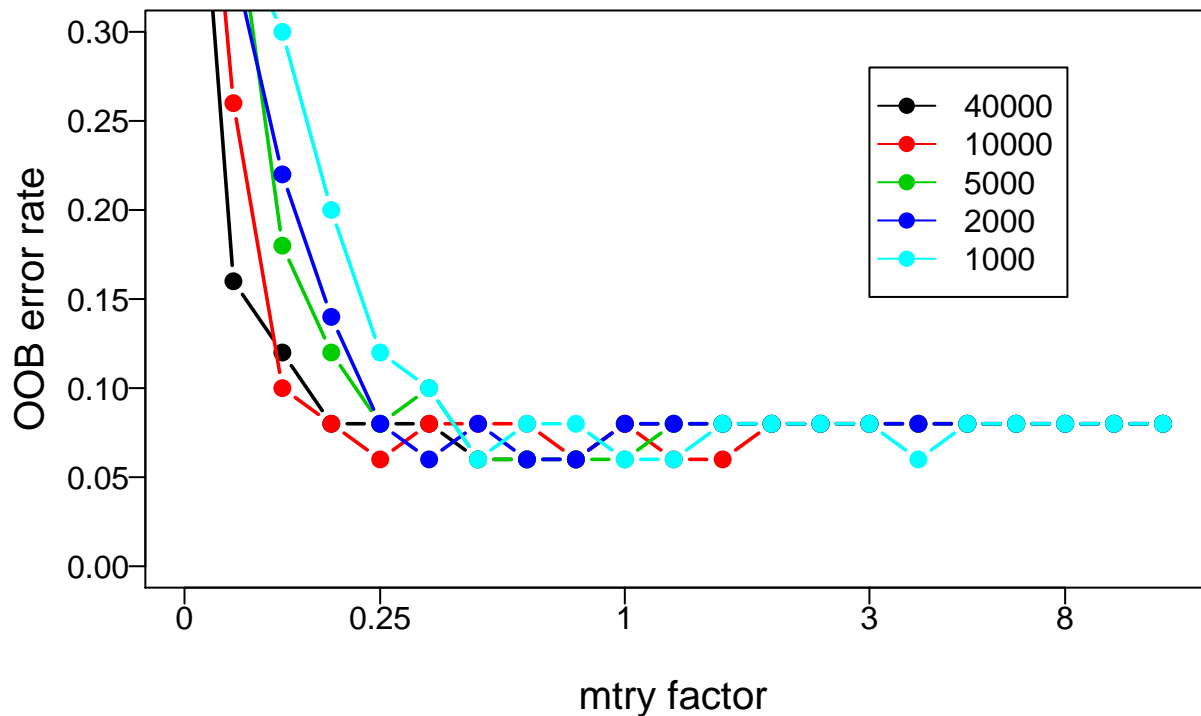
2 classes; 1 dimensions; 20 genes/dimen.; nodesize = 1



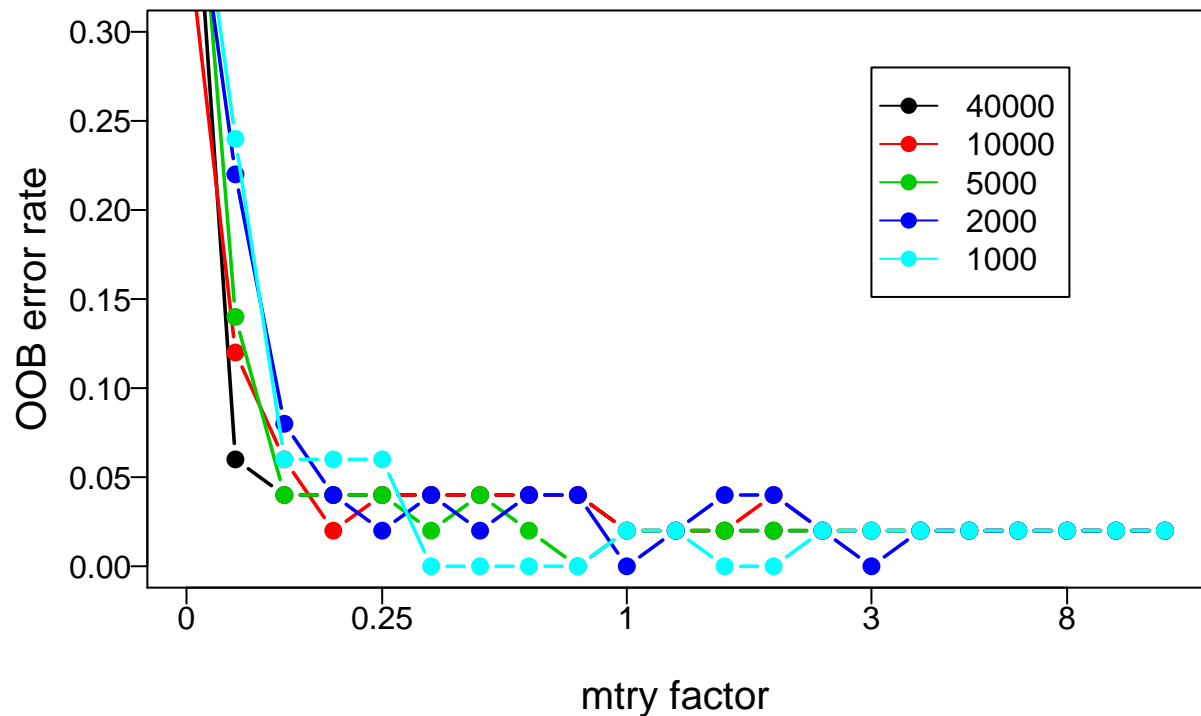
2 classes; 1 dimensions; 20 genes/dimen.; nodesize = 1



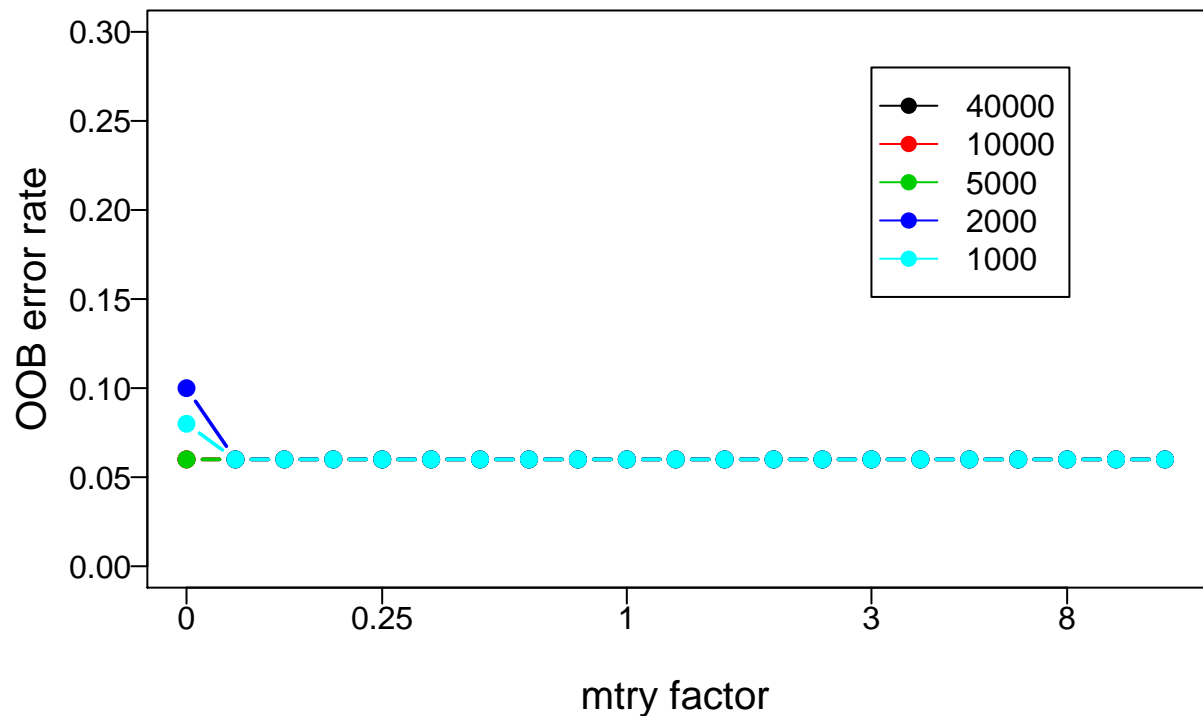
2 classes; 1 dimensions; 20 genes/dimen.; nodesize = 1



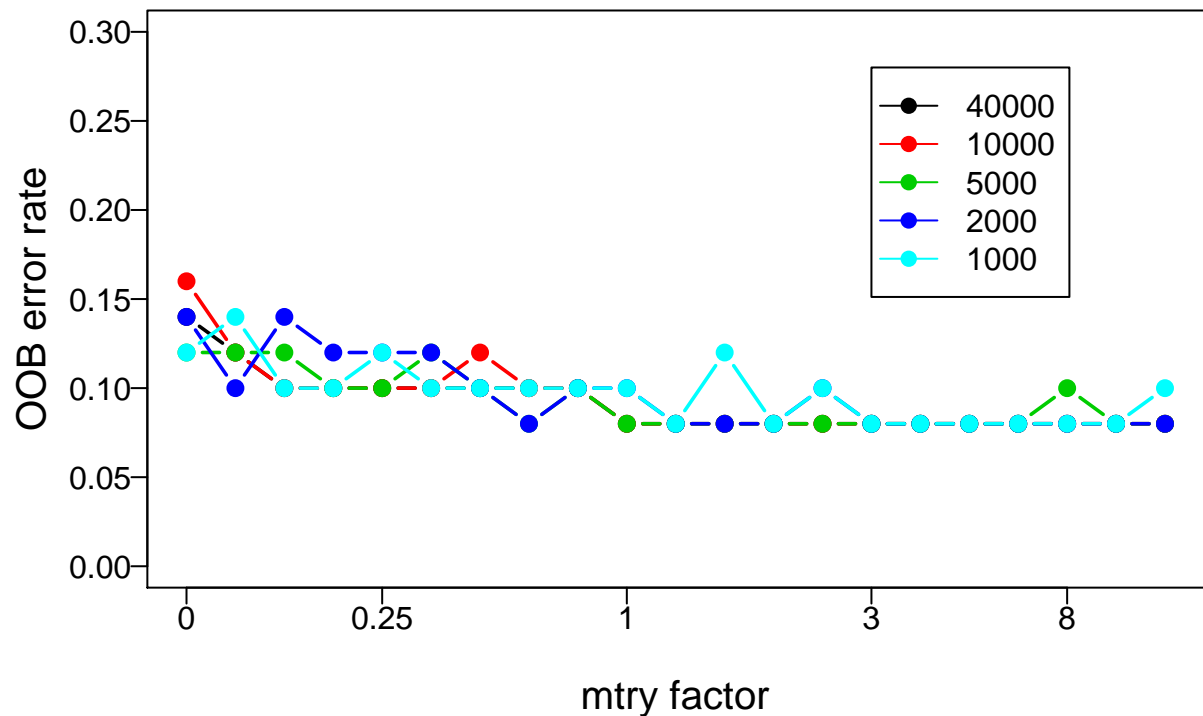
2 classes; 1 dimensions; 20 genes/dimen.; nodesize = 1



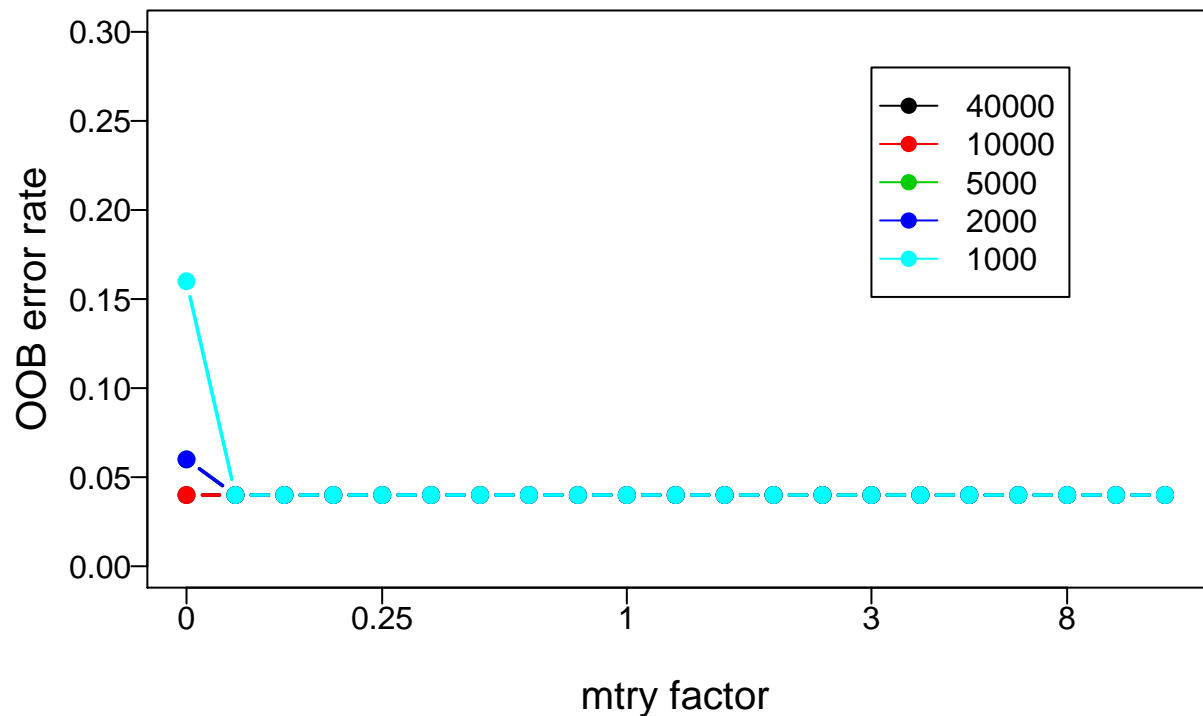
2 classes; 1 dimensions; 100 genes/dimen.; nodesize = 1



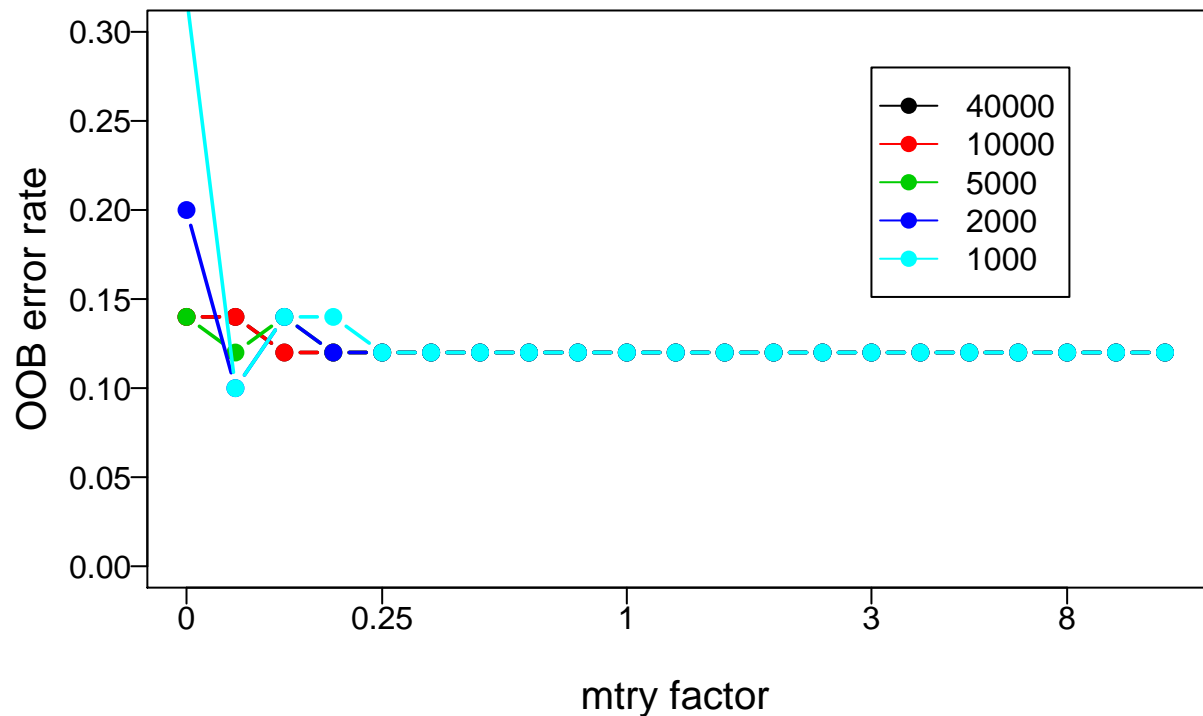
2 classes; 1 dimensions; 100 genes/dimen.; nodesize = 1



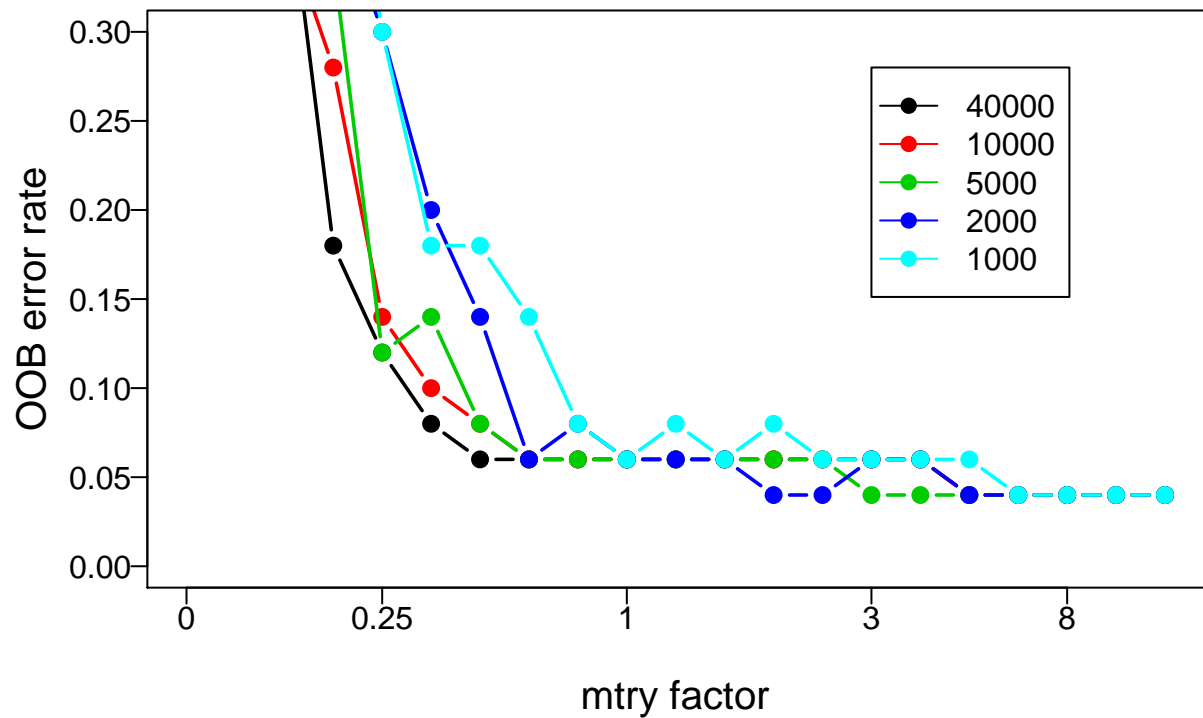
2 classes; 1 dimensions; 100 genes/dimen.; nodesize = 1



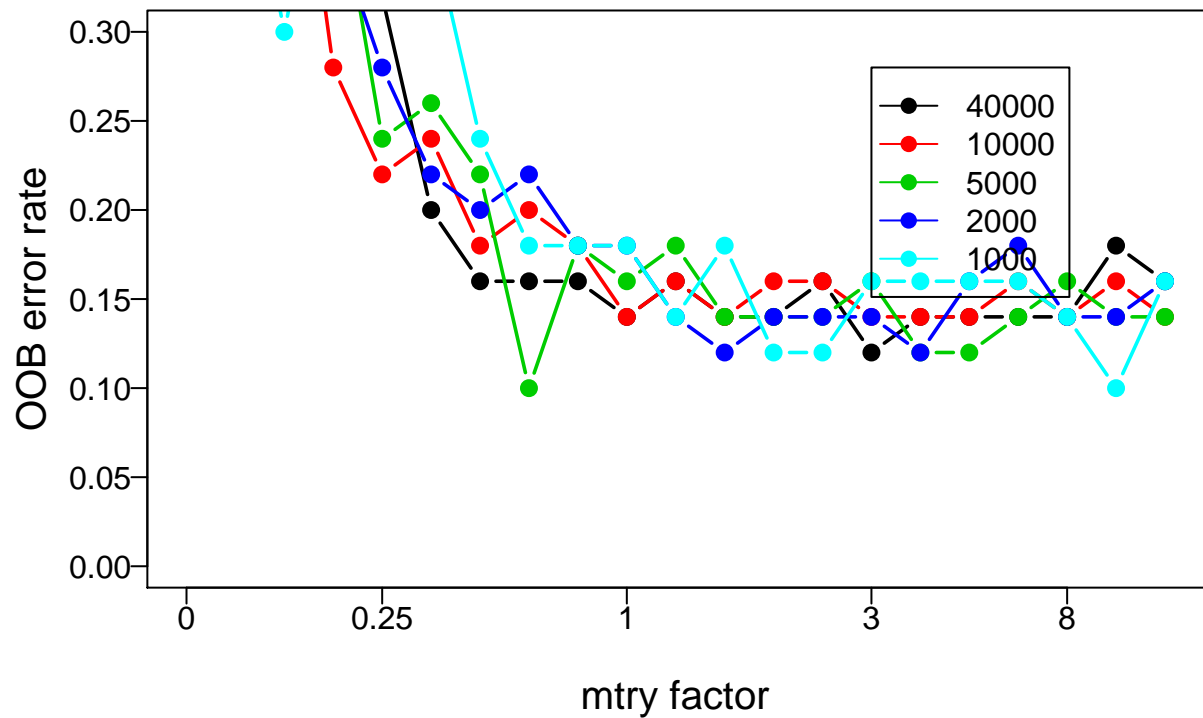
2 classes; 1 dimensions; 100 genes/dimen.; nodesize = 1



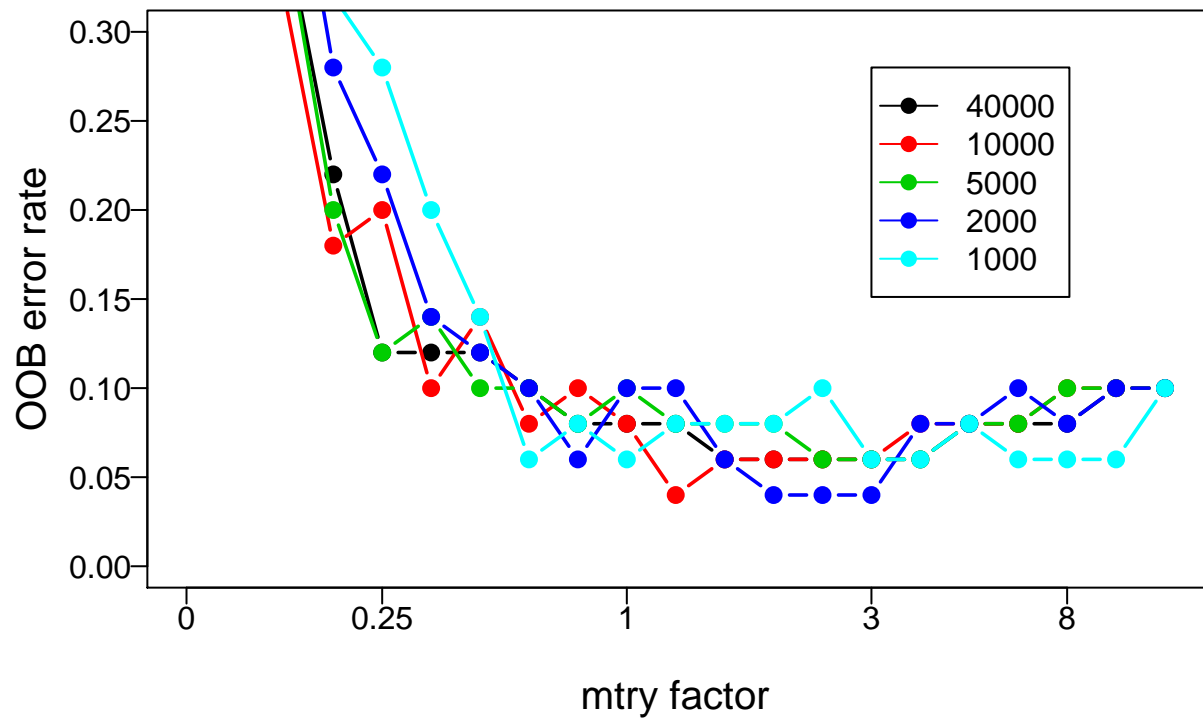
2 classes; 2 dimensions; 5 genes/dimen.; nodesize = 1



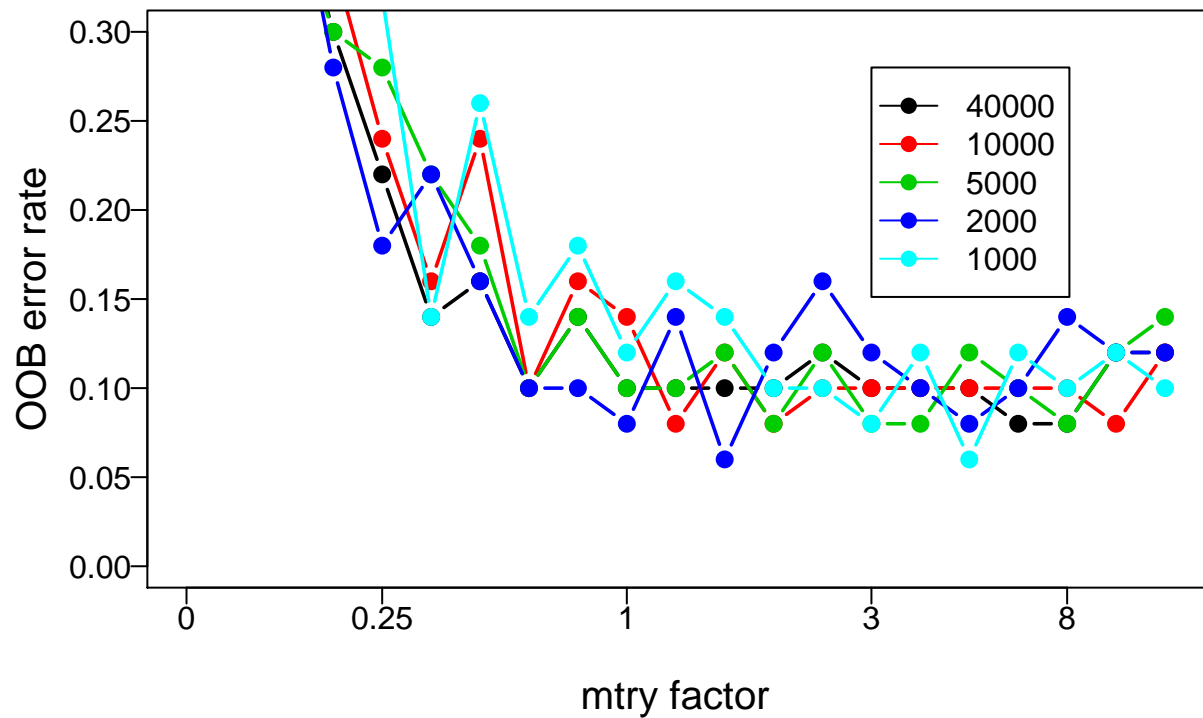
2 classes; 2 dimensions; 5 genes/dimen.; nodesize = 1



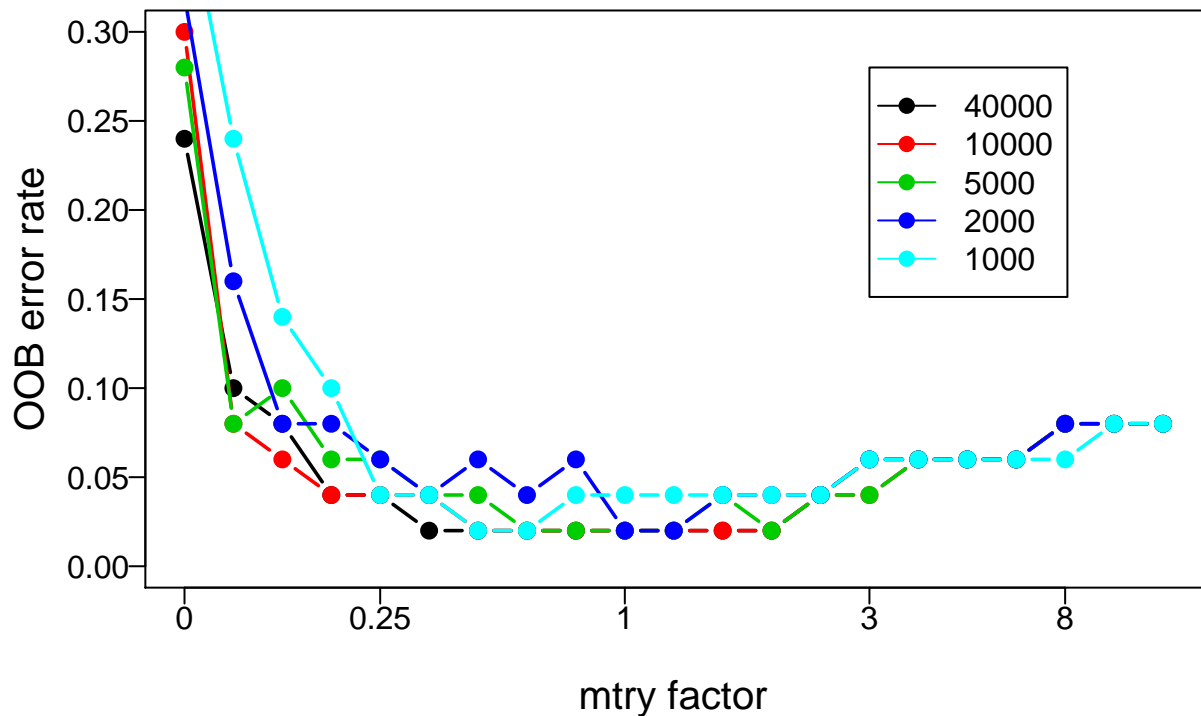
2 classes; 2 dimensions; 5 genes/dimen.; nodesize = 1



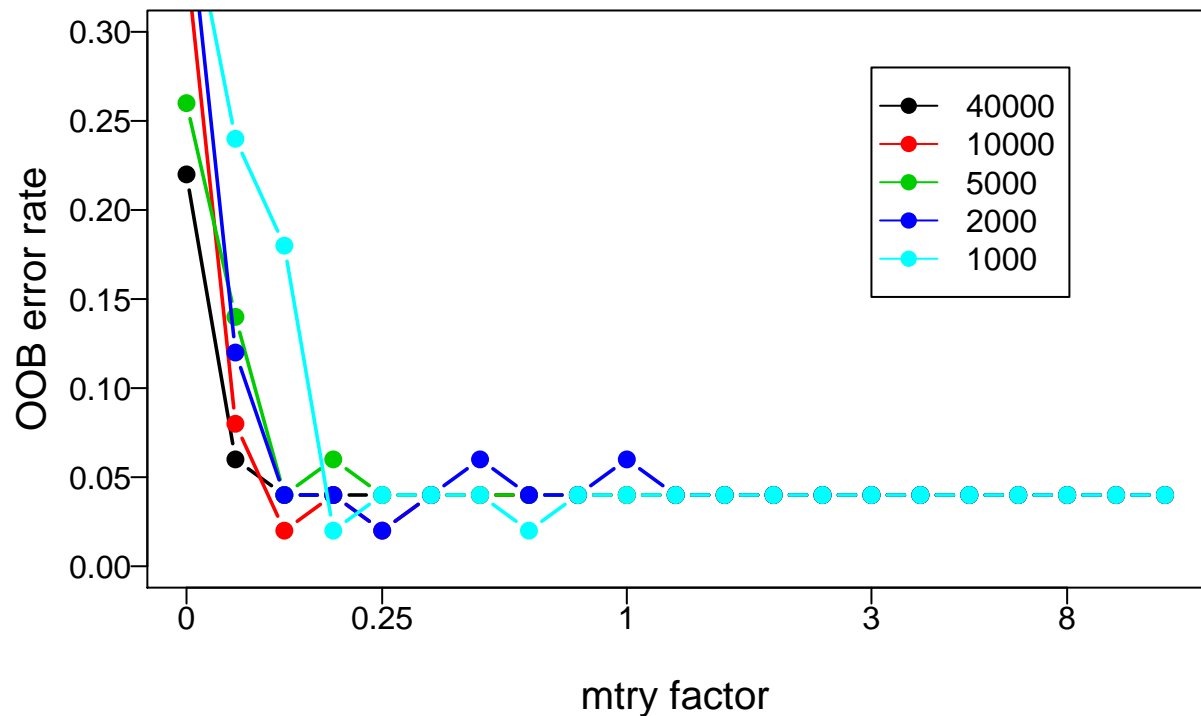
2 classes; 2 dimensions; 5 genes/dimen.; nodesize = 1



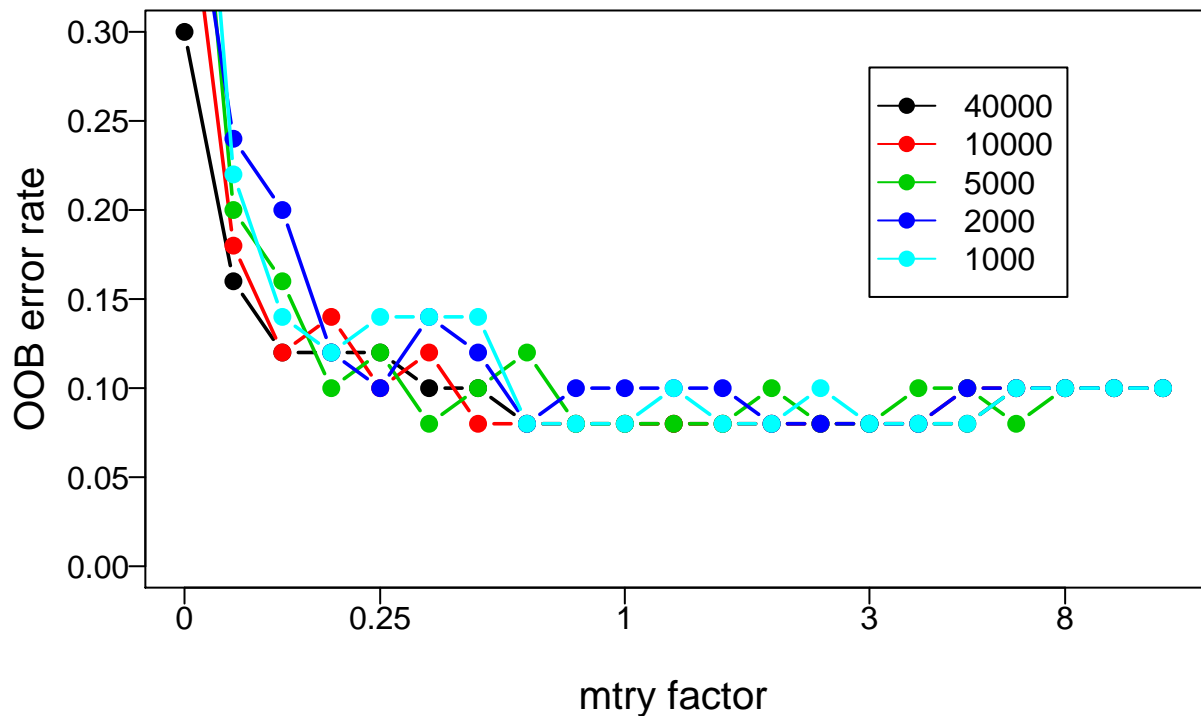
2 classes; 2 dimensions; 20 genes/dimen.; nodesize = 1



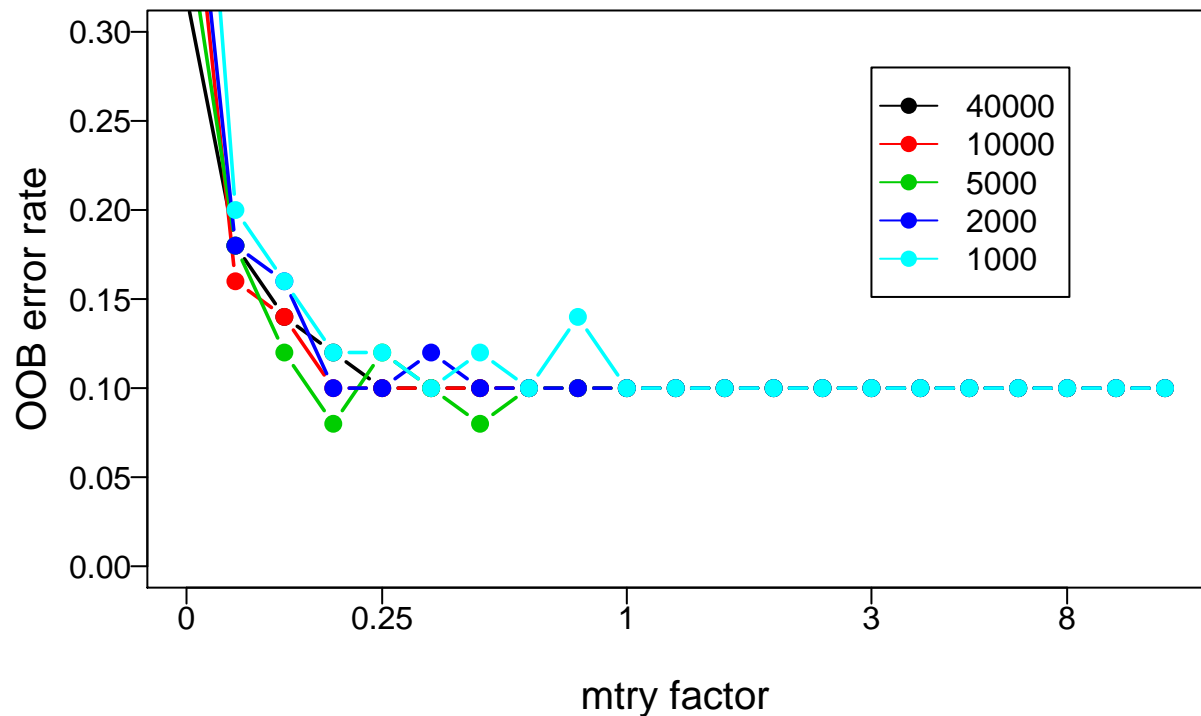
2 classes; 2 dimensions; 20 genes/dimen.; nodesize = 1



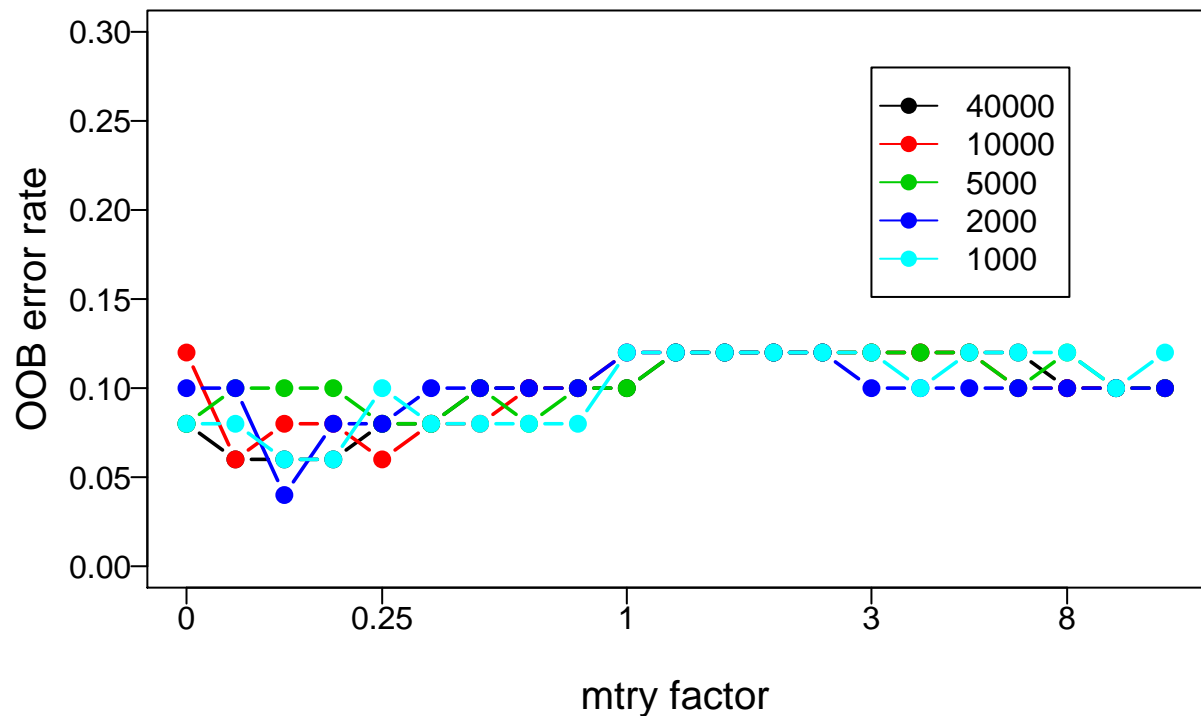
2 classes; 2 dimensions; 20 genes/dimen.; nodesize = 1



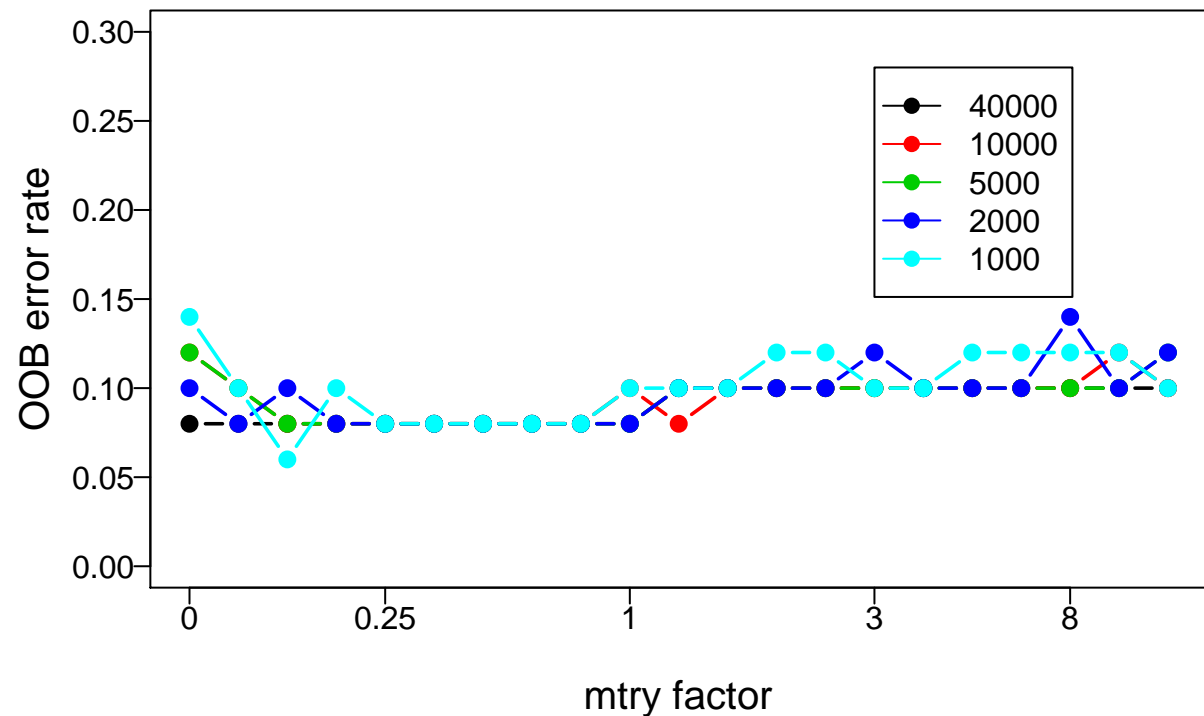
2 classes; 2 dimensions; 20 genes/dimen.; nodesize = 1



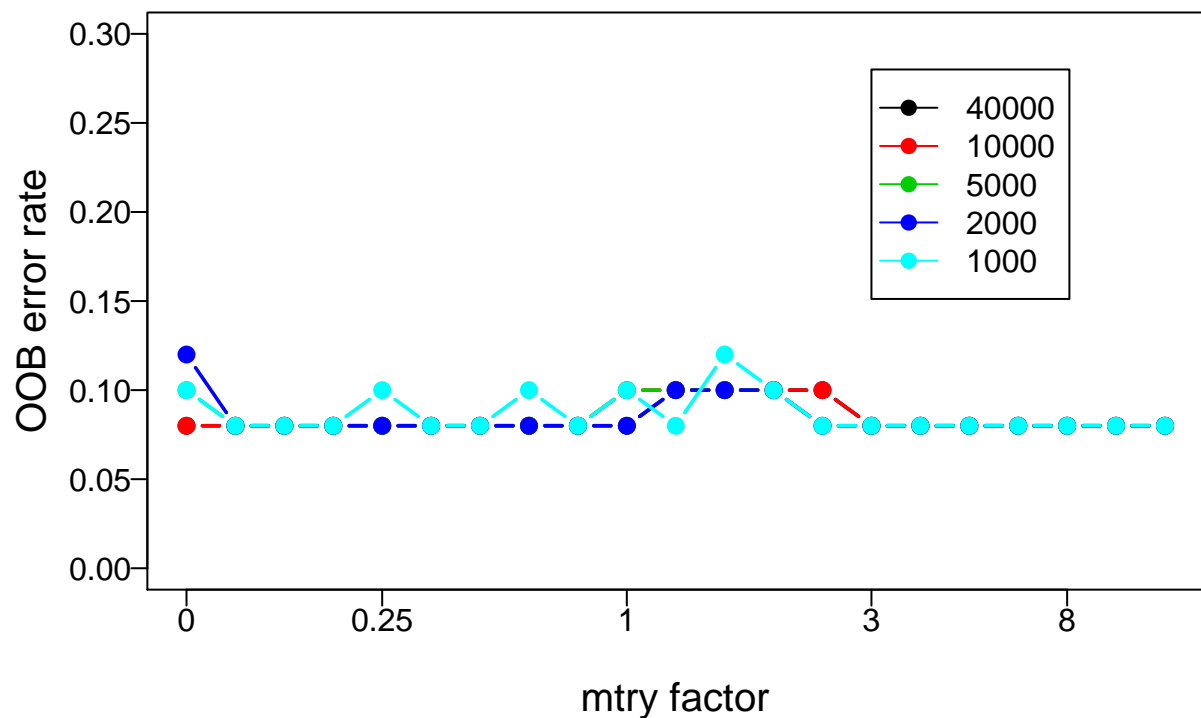
2 classes; 2 dimensions; 100 genes/dimen.; nodesize = 1



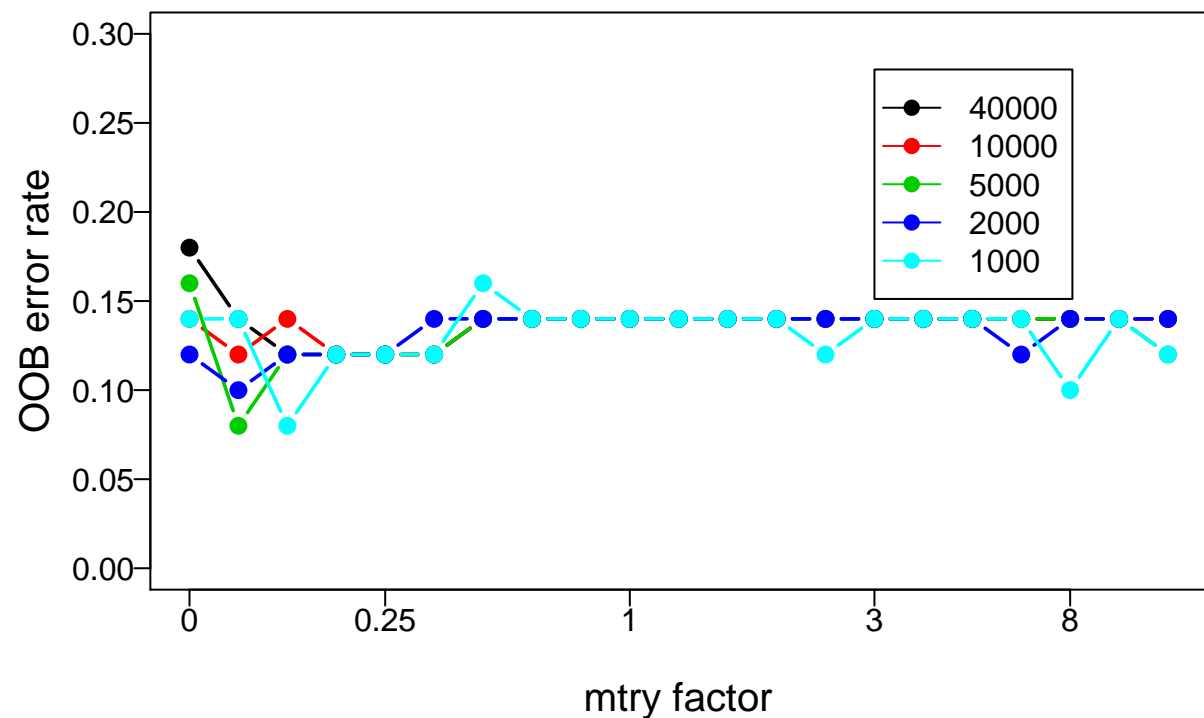
2 classes; 2 dimensions; 100 genes/dimen.; nodesize = 1



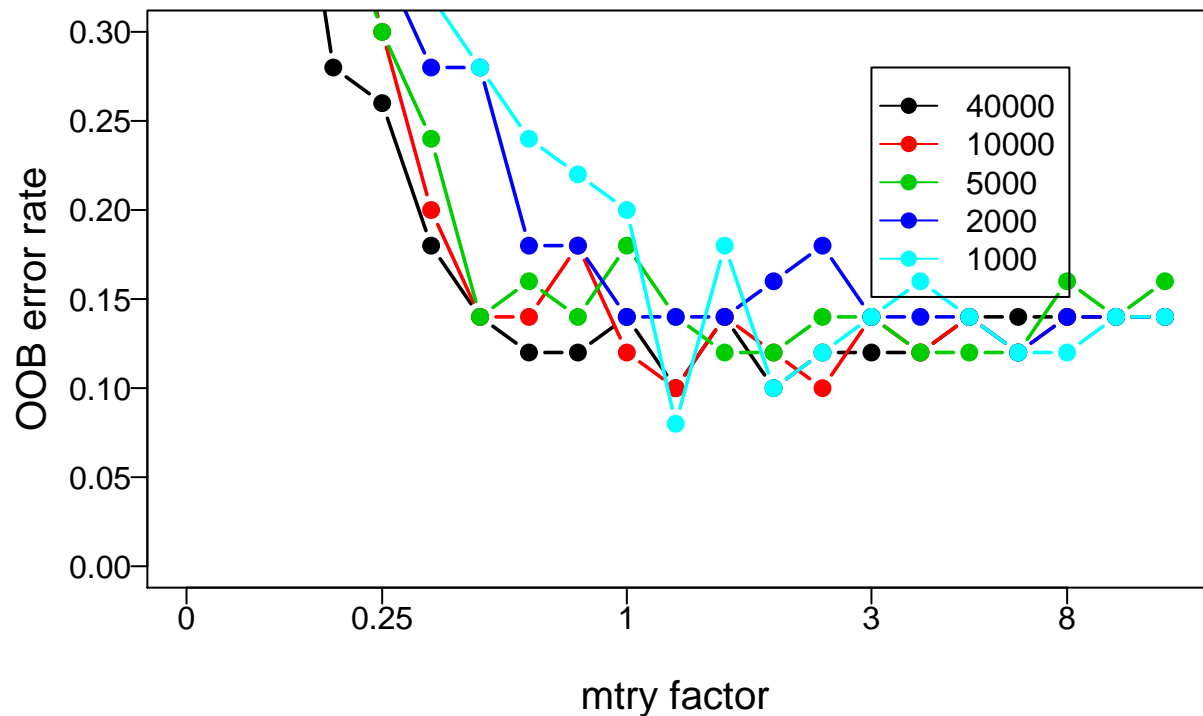
2 classes; 2 dimensions; 100 genes/dimen.; nodesize = 1



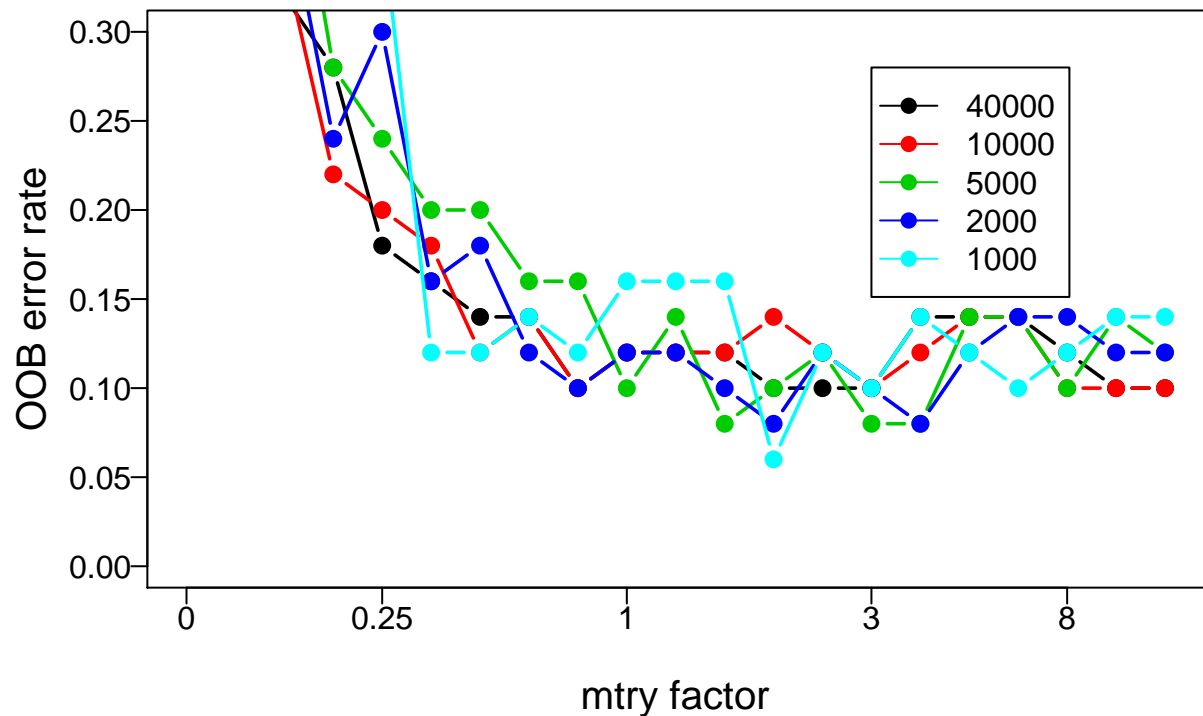
2 classes; 2 dimensions; 100 genes/dimen.; nodesize = 1



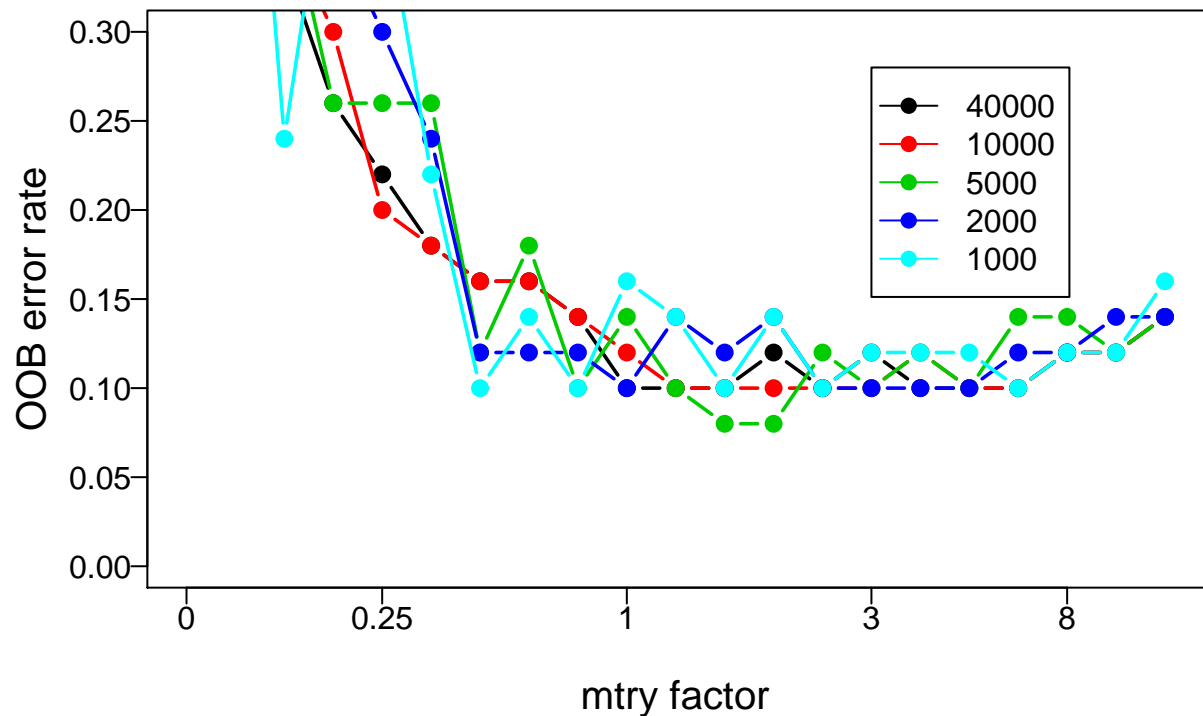
2 classes; 3 dimensions; 5 genes/dimen.; nodesize = 1



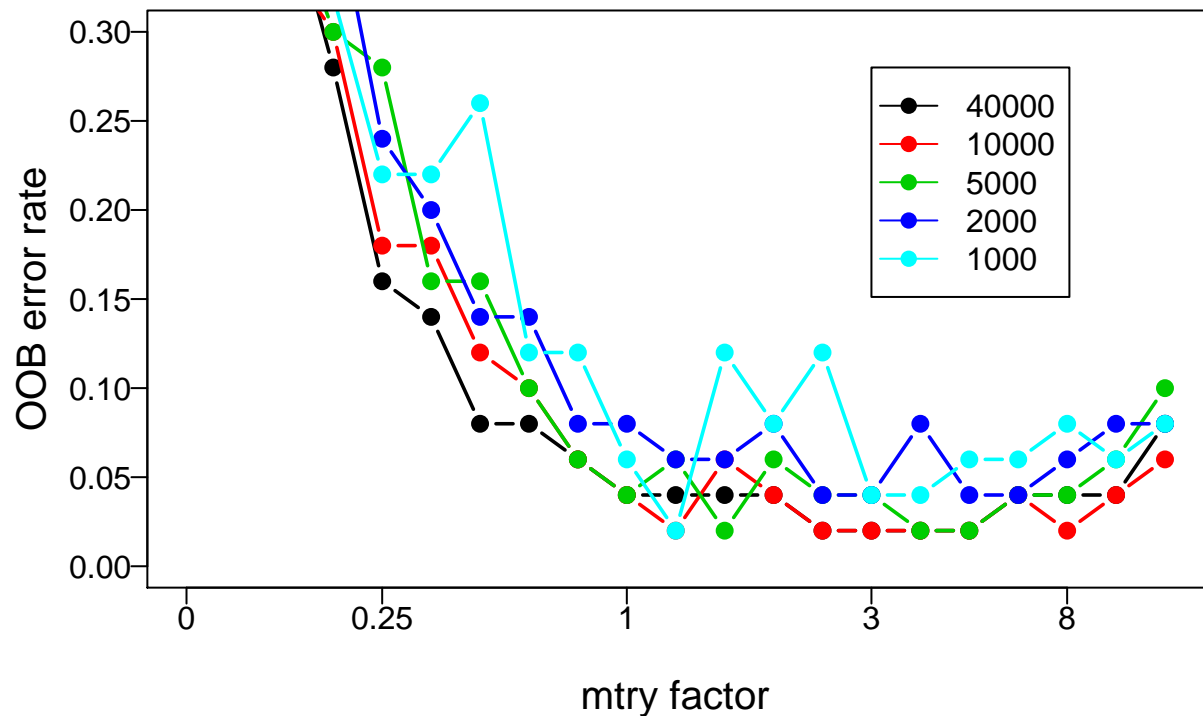
2 classes; 3 dimensions; 5 genes/dimen.; nodesize = 1



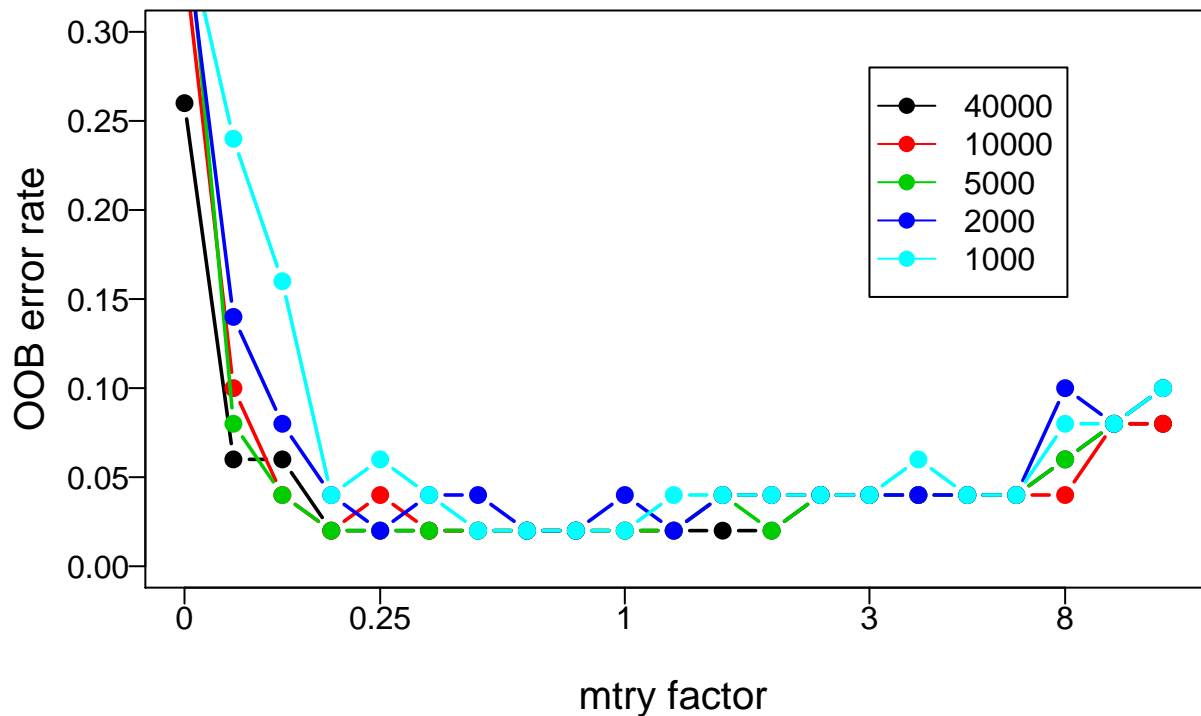
2 classes; 3 dimensions; 5 genes/dimen.; nodesize = 1



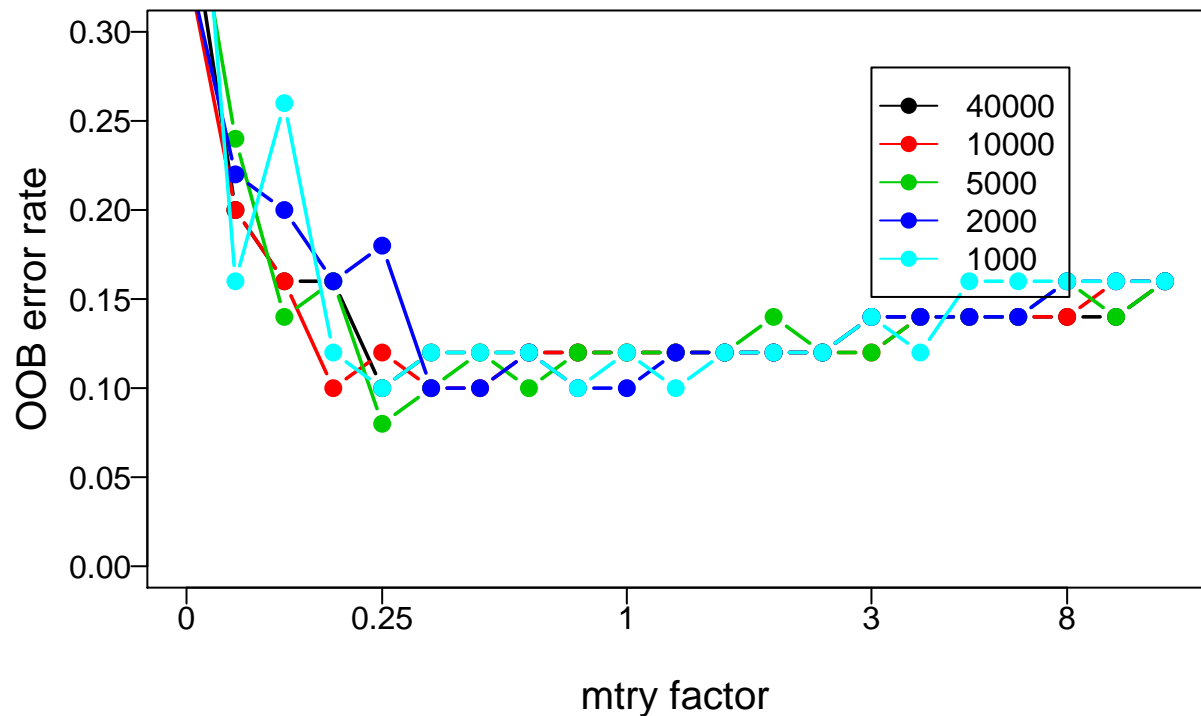
2 classes; 3 dimensions; 5 genes/dimen.; nodesize = 1



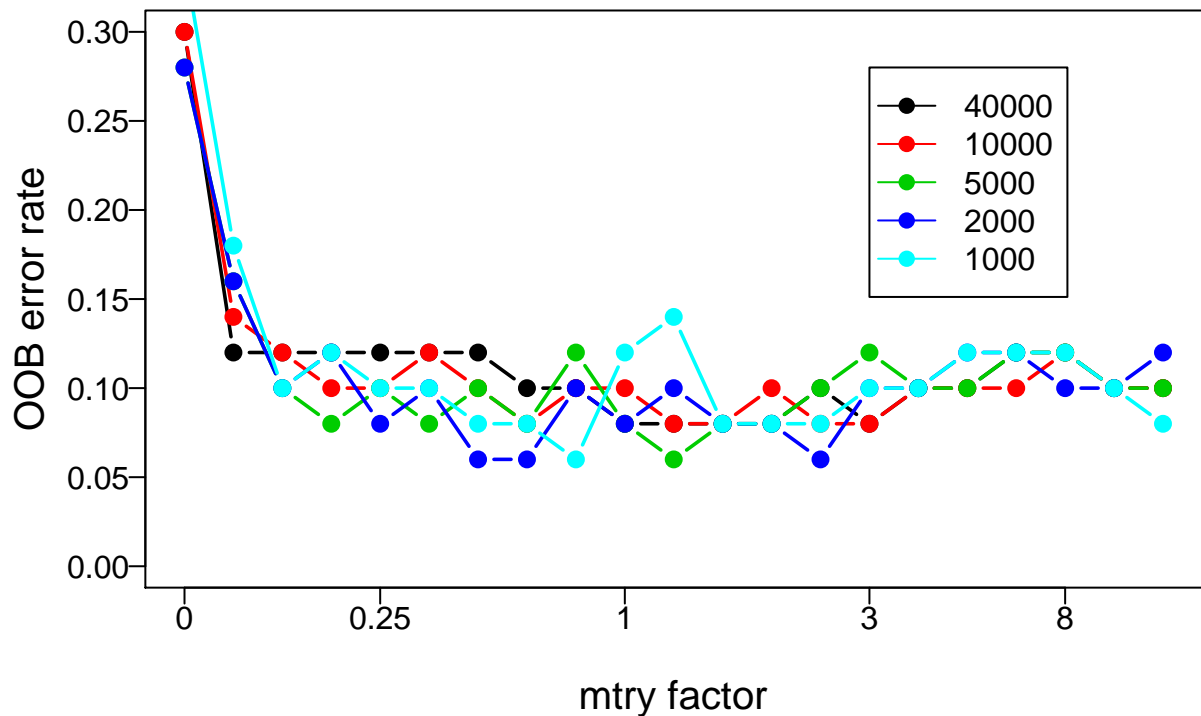
2 classes; 3 dimensions; 20 genes/dimen.; nodesize = 1



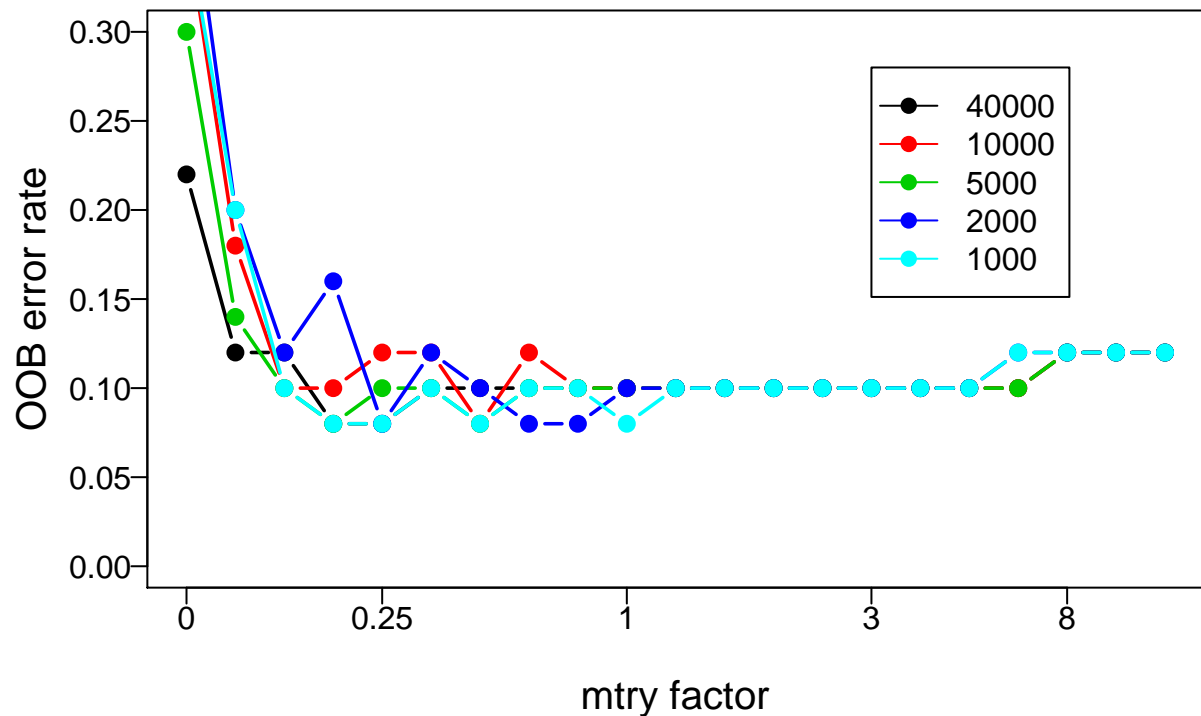
2 classes; 3 dimensions; 20 genes/dimen.; nodesize = 1



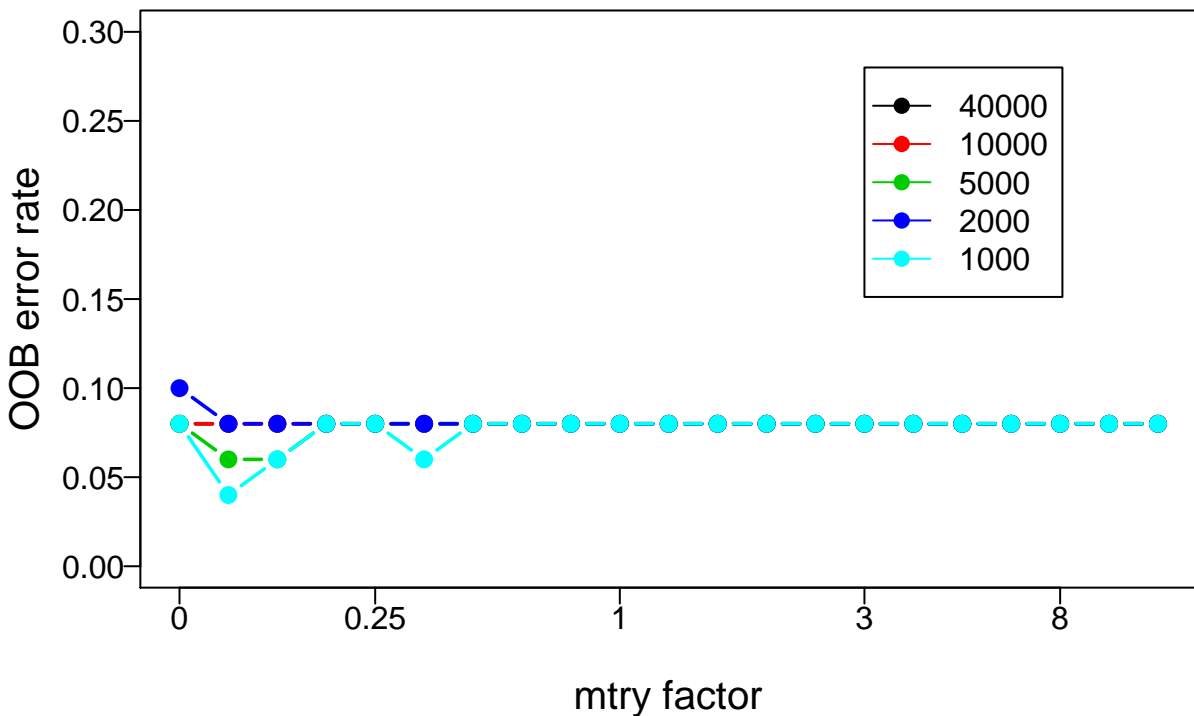
2 classes; 3 dimensions; 20 genes/dimen.; nodesize = 1



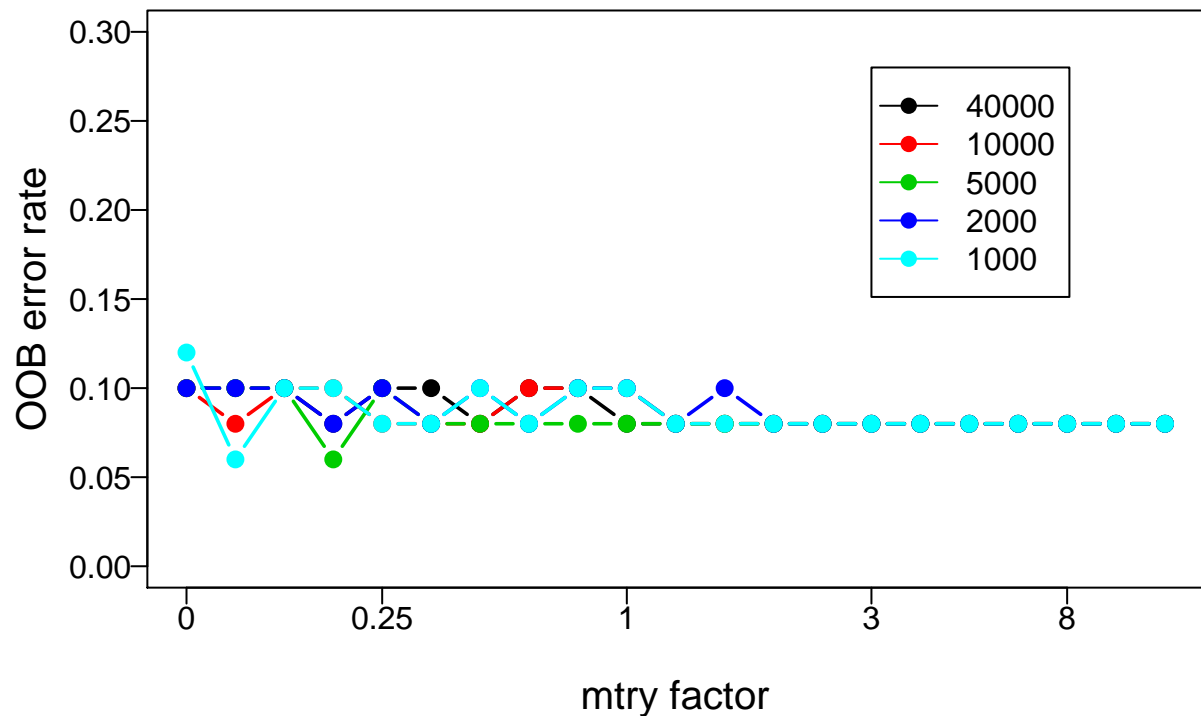
2 classes; 3 dimensions; 20 genes/dimen.; nodesize = 1



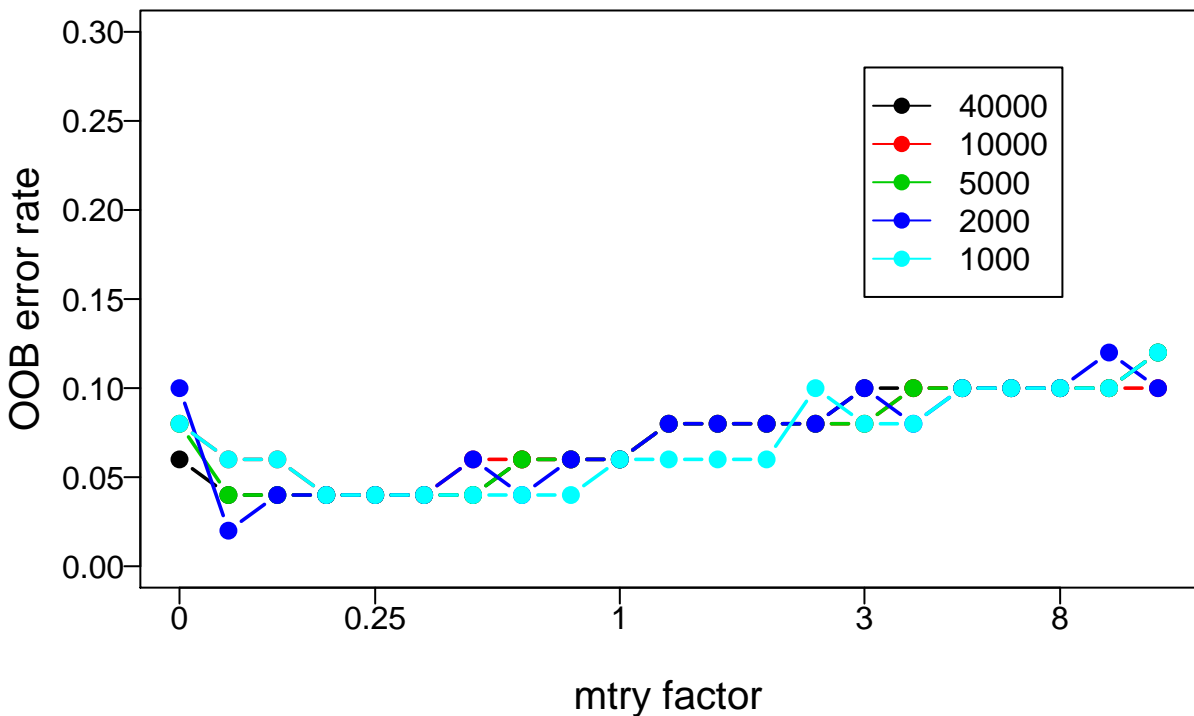
2 classes; 3 dimensions; 100 genes/dimen.; nodesize = 1



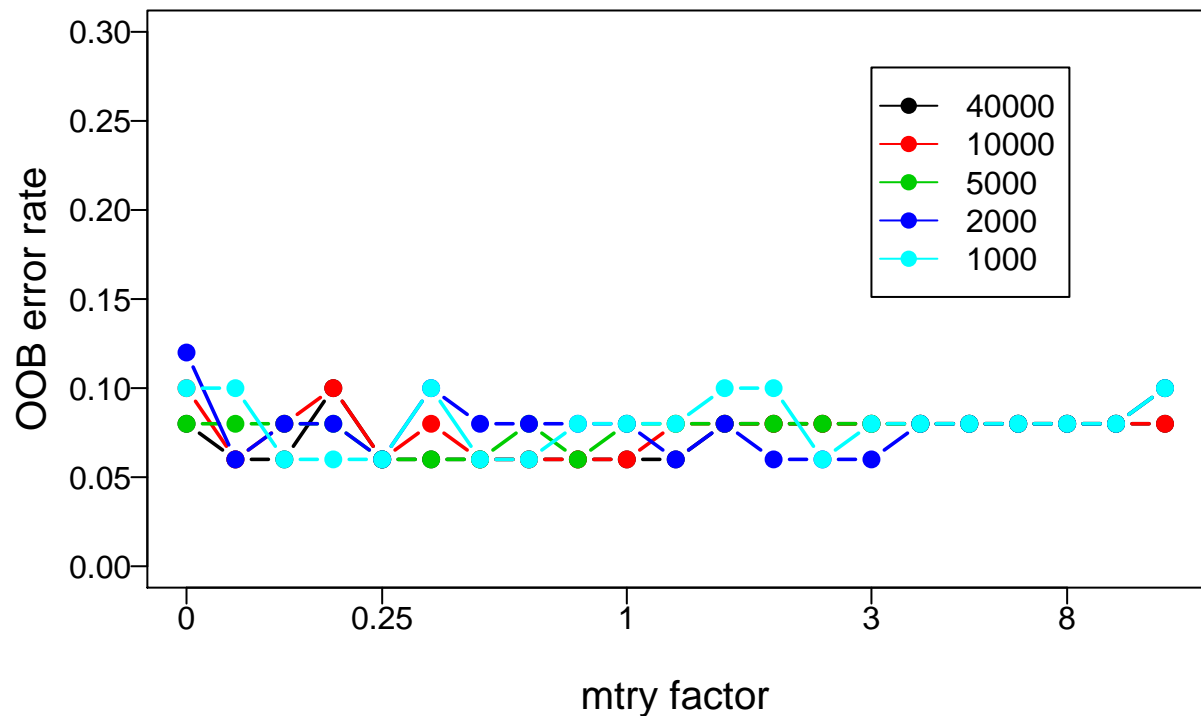
2 classes; 3 dimensions; 100 genes/dimen.; nodesize = 1



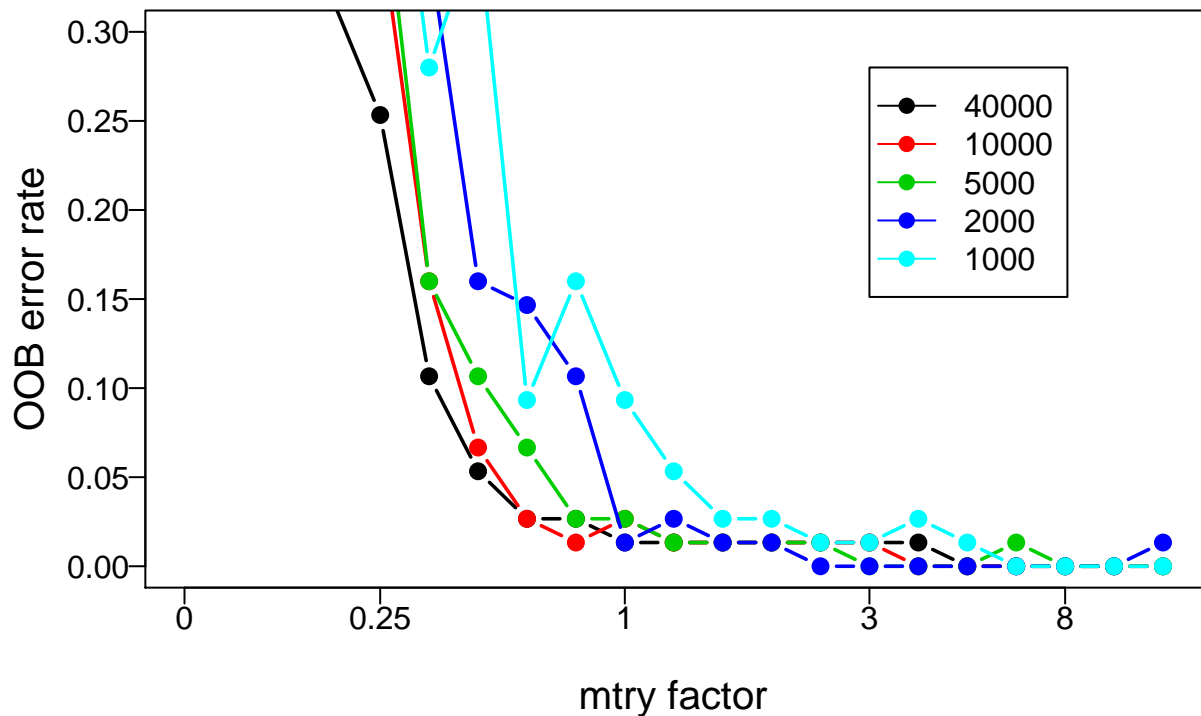
2 classes; 3 dimensions; 100 genes/dimen.; nodesize = 1



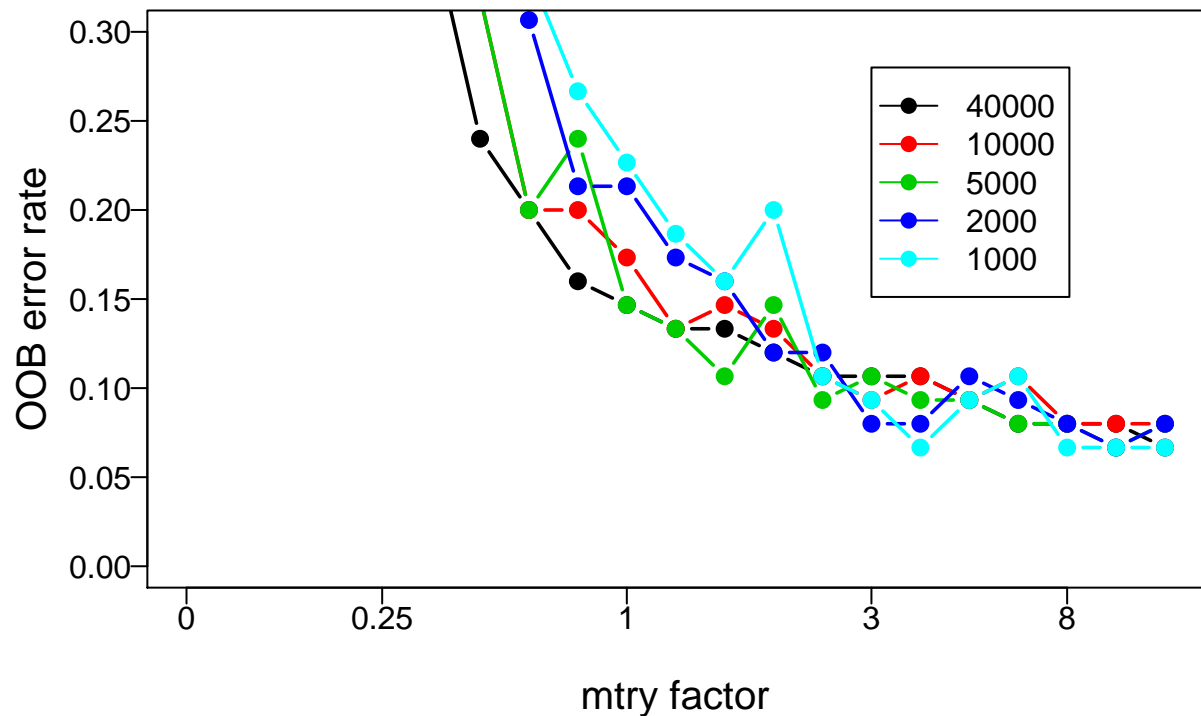
2 classes; 3 dimensions; 100 genes/dimen.; nodesize = 1



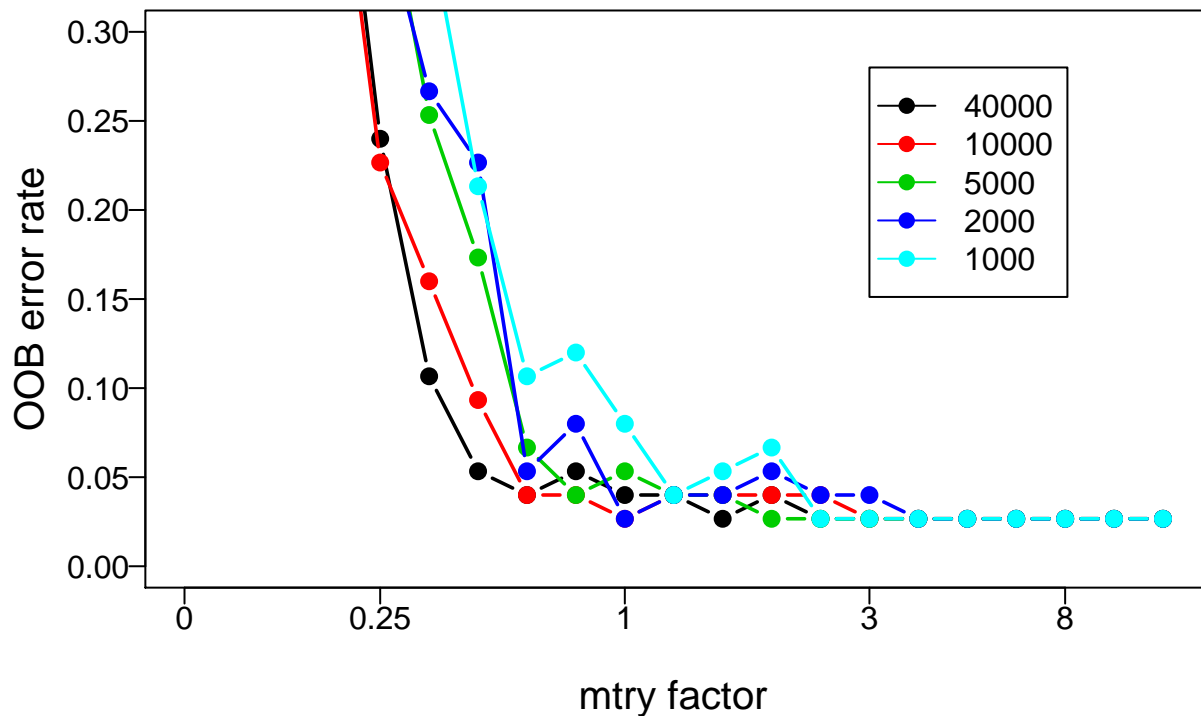
3 classes; 1 dimensions; 5 genes/dimen.; nodesize = 1



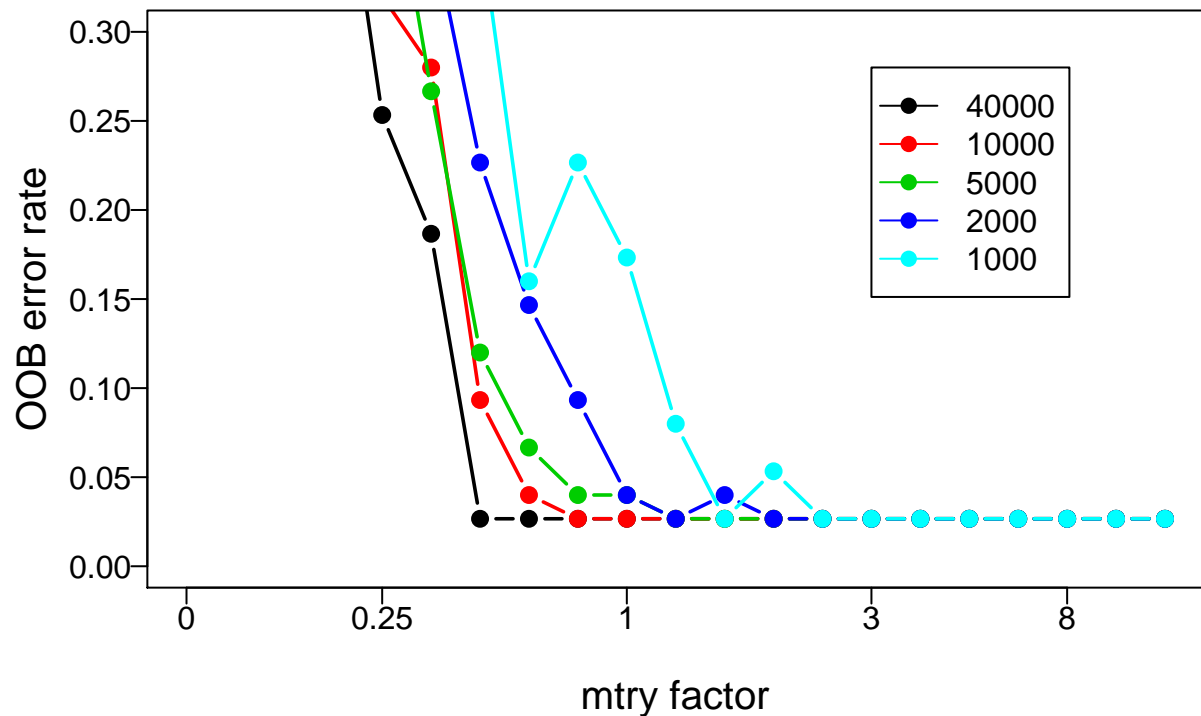
3 classes; 1 dimensions; 5 genes/dimen.; nodesize = 1



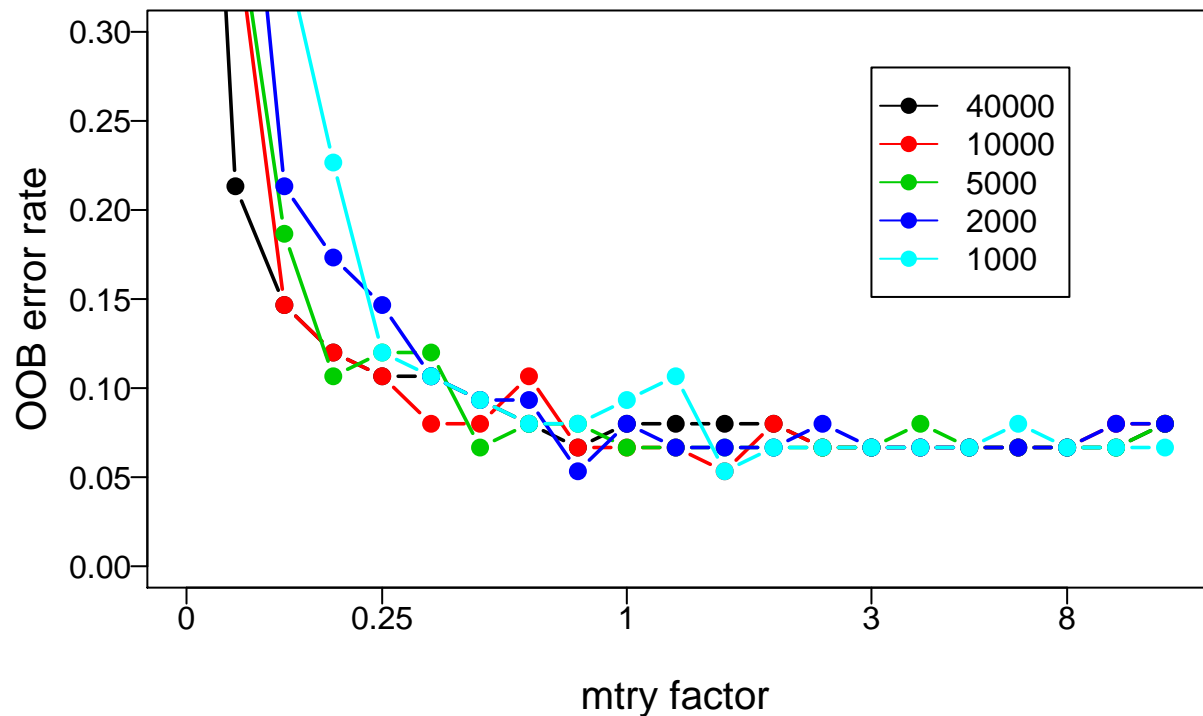
3 classes; 1 dimensions; 5 genes/dimen.; nodesize = 1



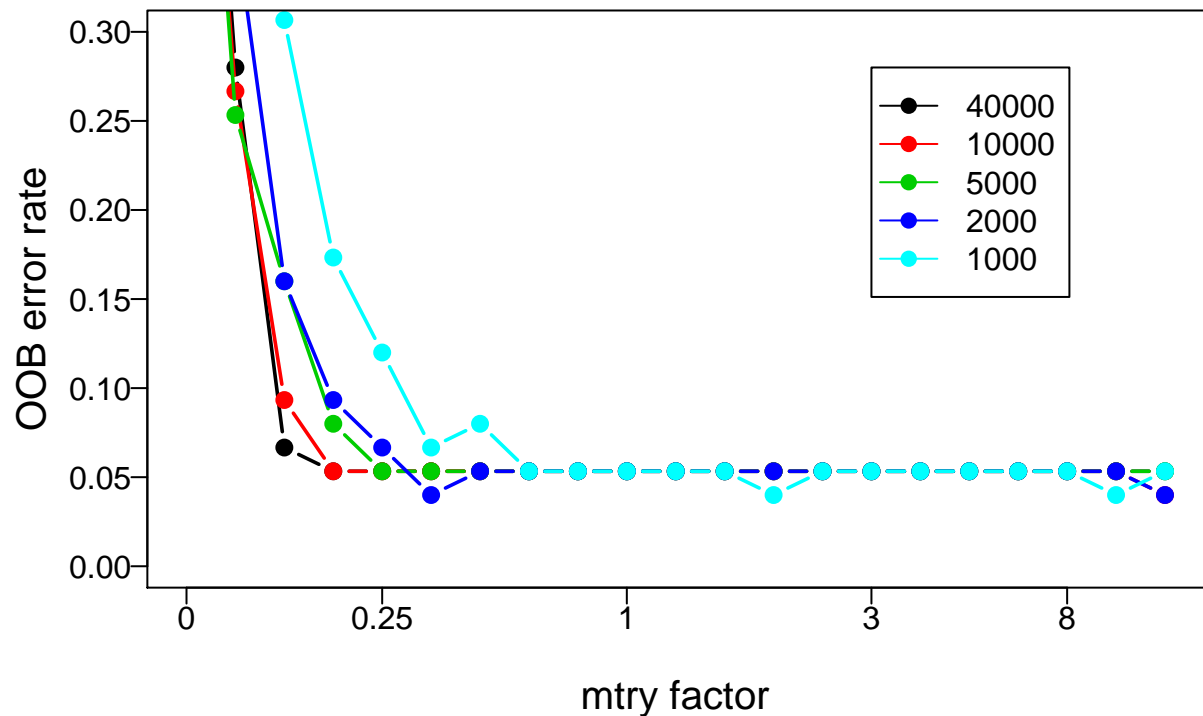
3 classes; 1 dimensions; 5 genes/dimen.; nodesize = 1



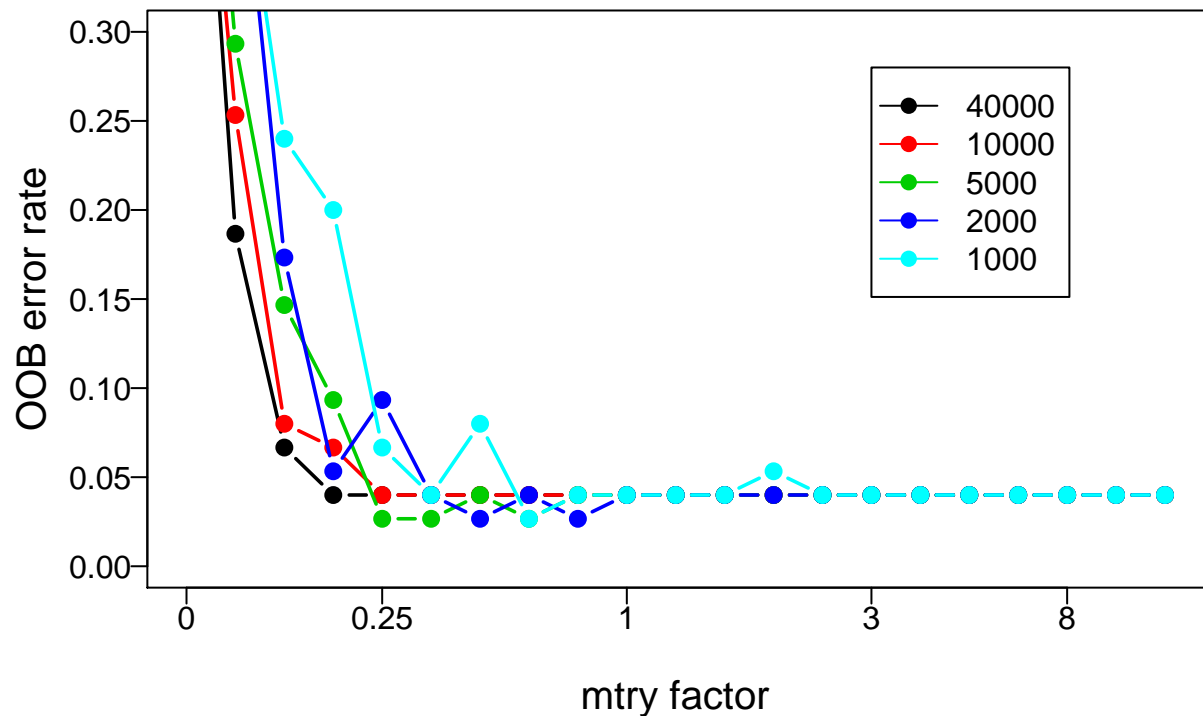
3 classes; 1 dimensions; 20 genes/dimen.; nodesize = 1



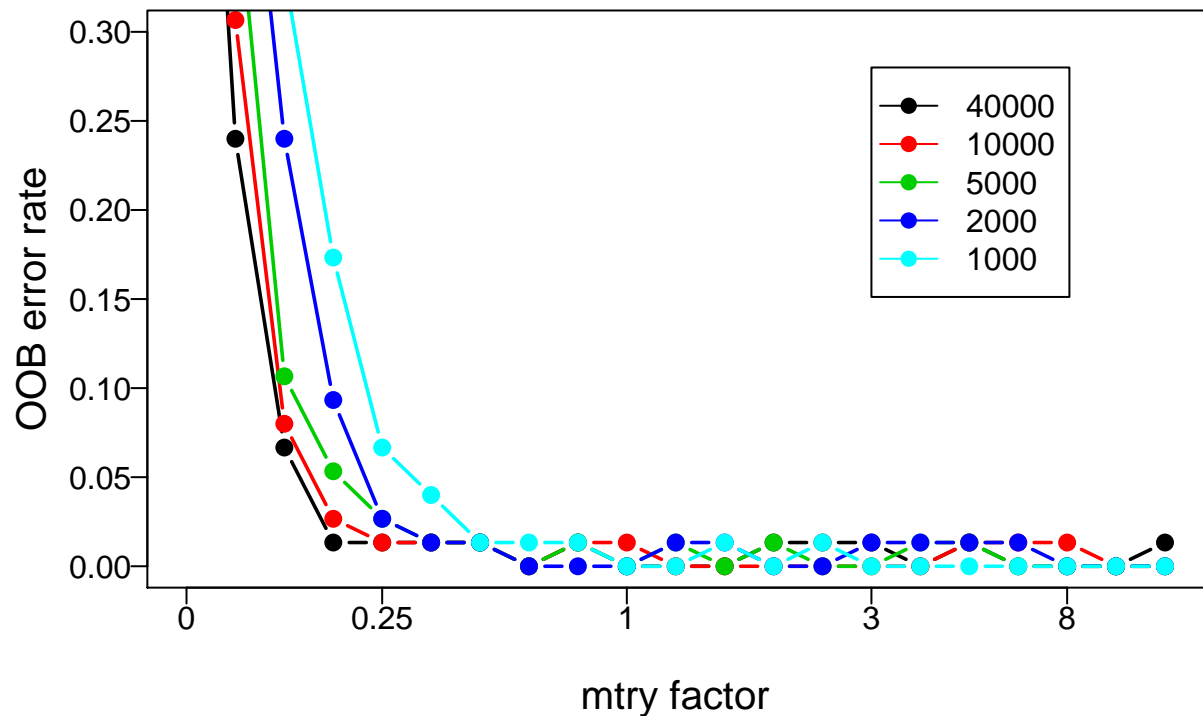
3 classes; 1 dimensions; 20 genes/dimen.; nodesize = 1



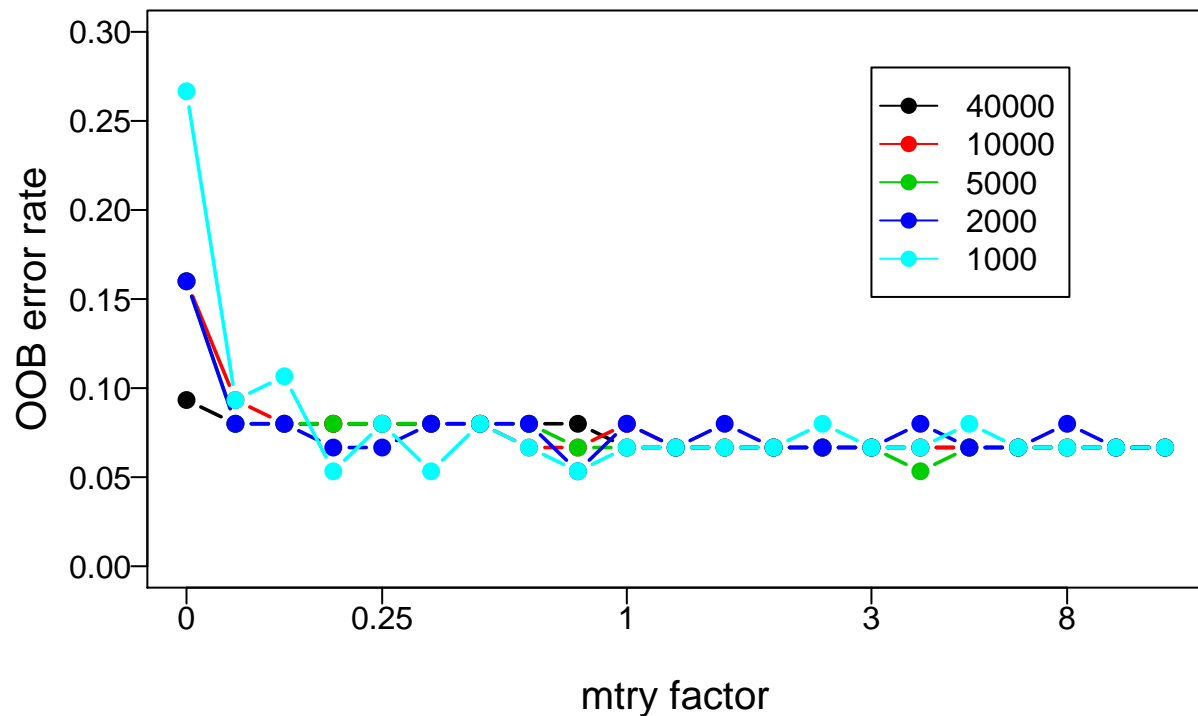
3 classes; 1 dimensions; 20 genes/dimen.; nodesize = 1



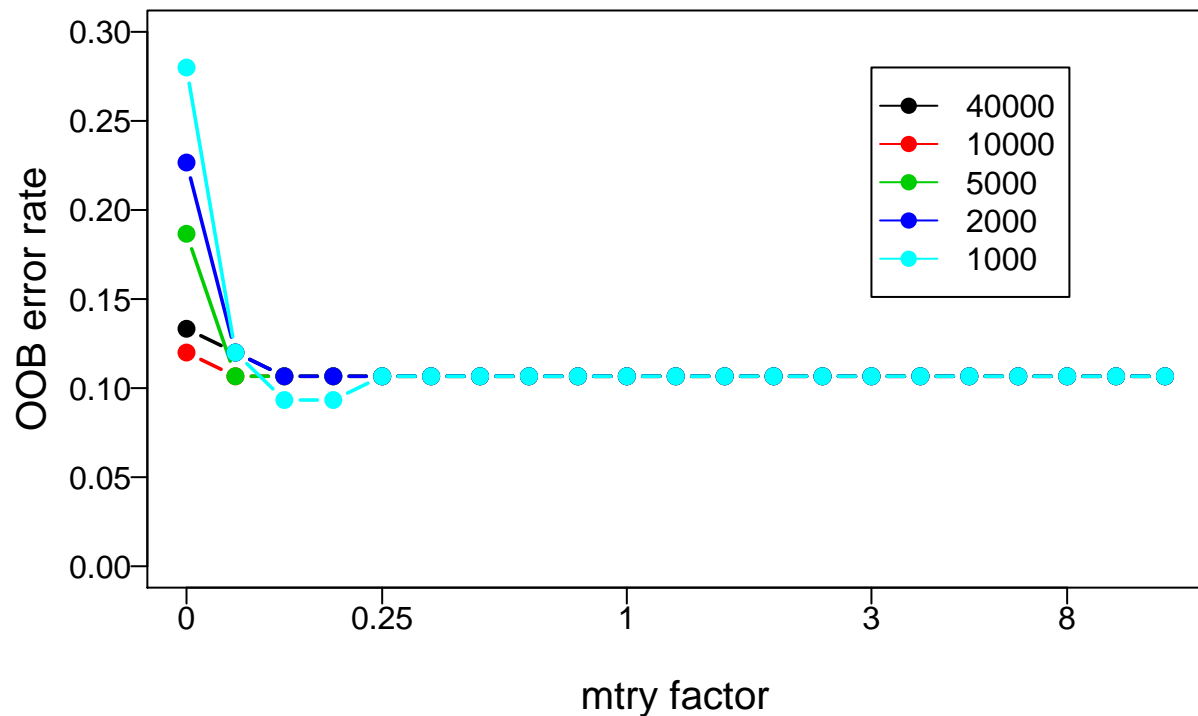
3 classes; 1 dimensions; 20 genes/dimen.; nodesize = 1



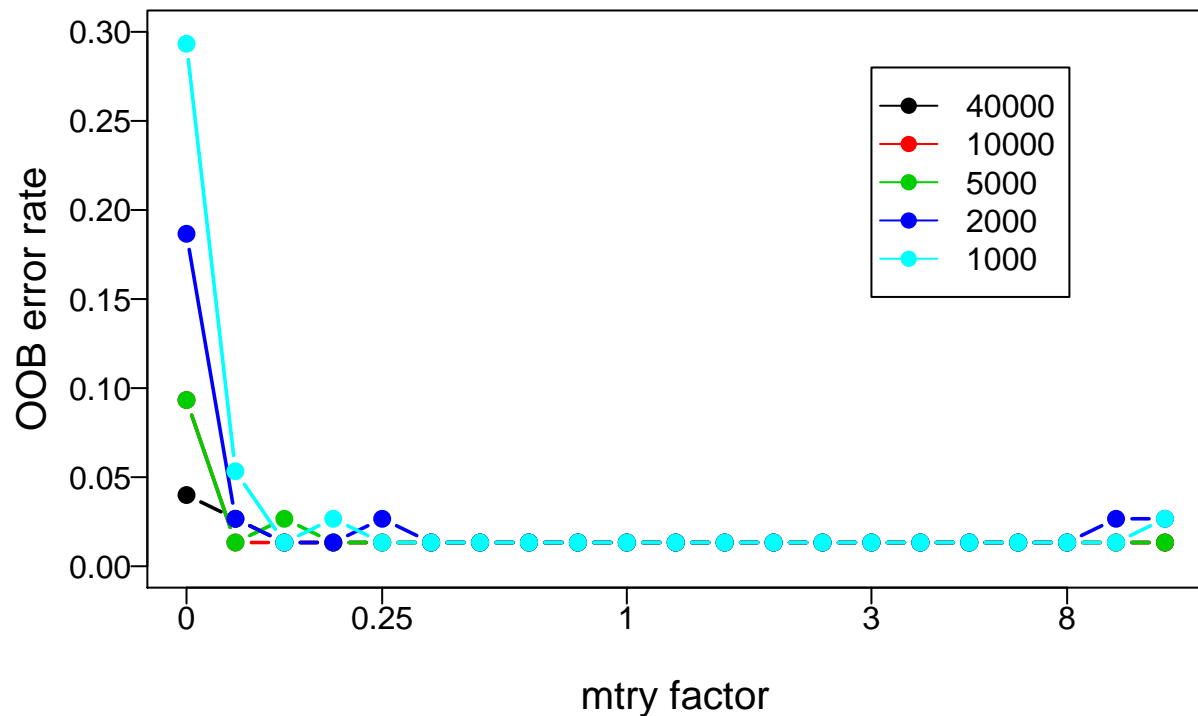
3 classes; 1 dimensions; 100 genes/dimen.; nodesize = 1



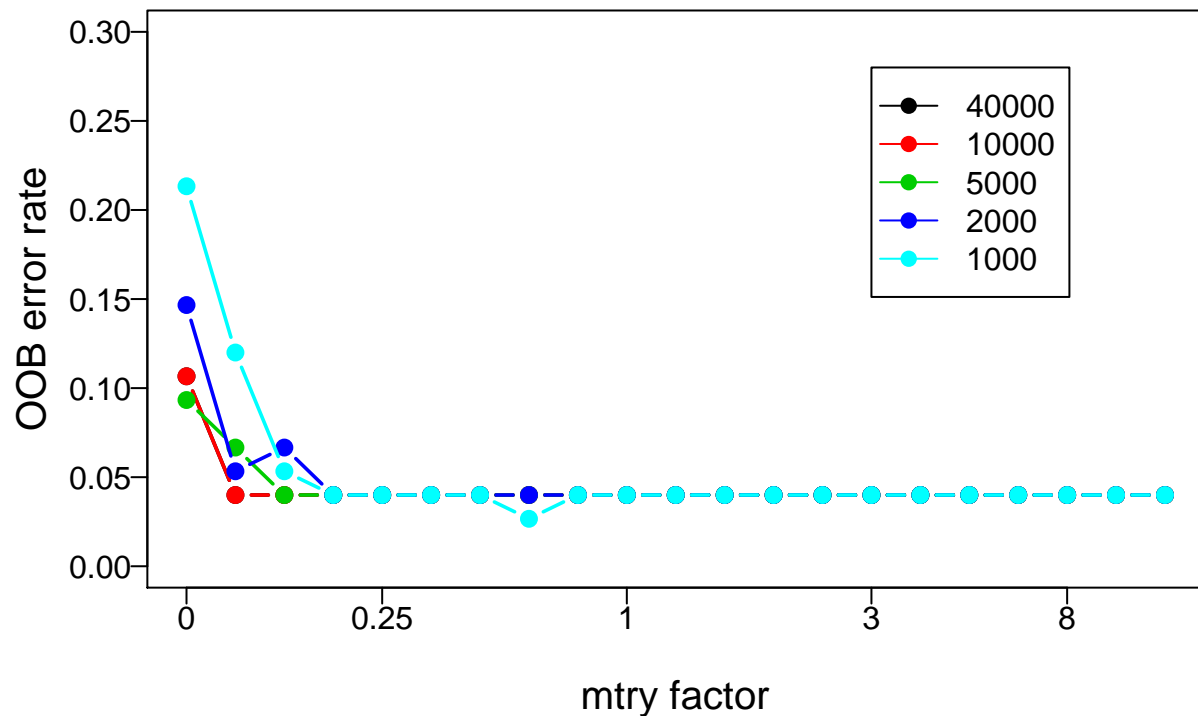
3 classes; 1 dimensions; 100 genes/dimen.; nodesize = 1



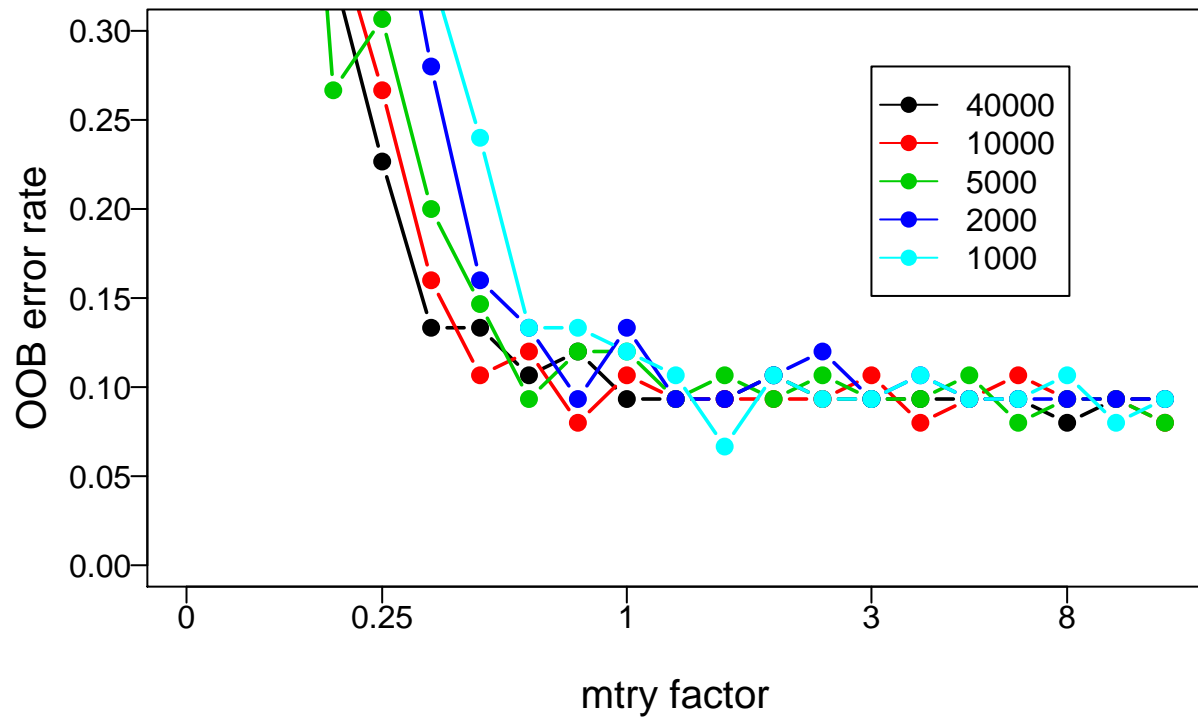
3 classes; 1 dimensions; 100 genes/dimen.; nodesize = 1



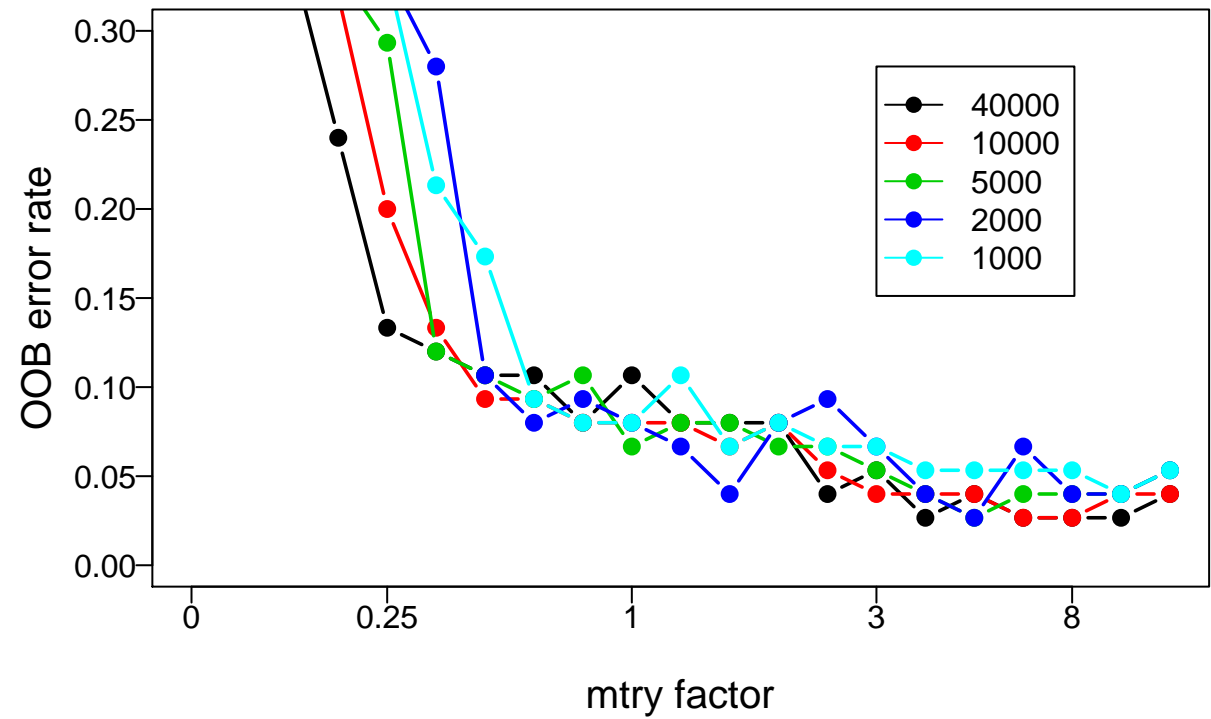
3 classes; 1 dimensions; 100 genes/dimen.; nodesize = 1



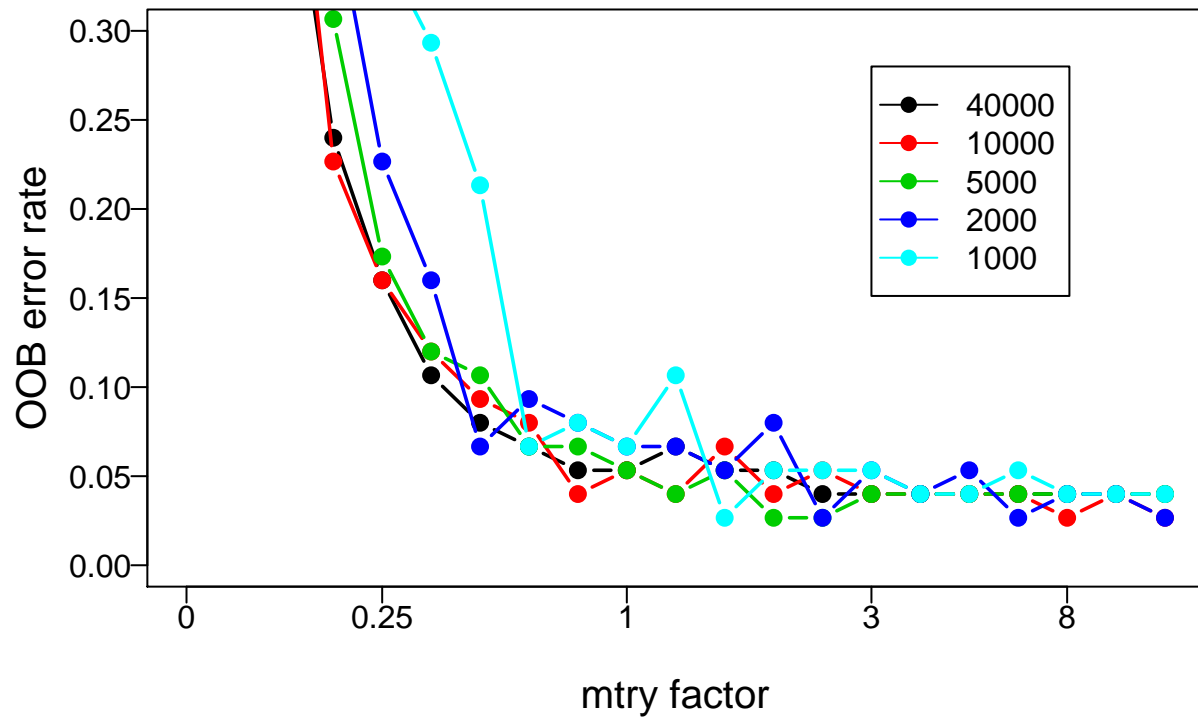
3 classes; 2 dimensions; 5 genes/dimen.; nodesize = 1



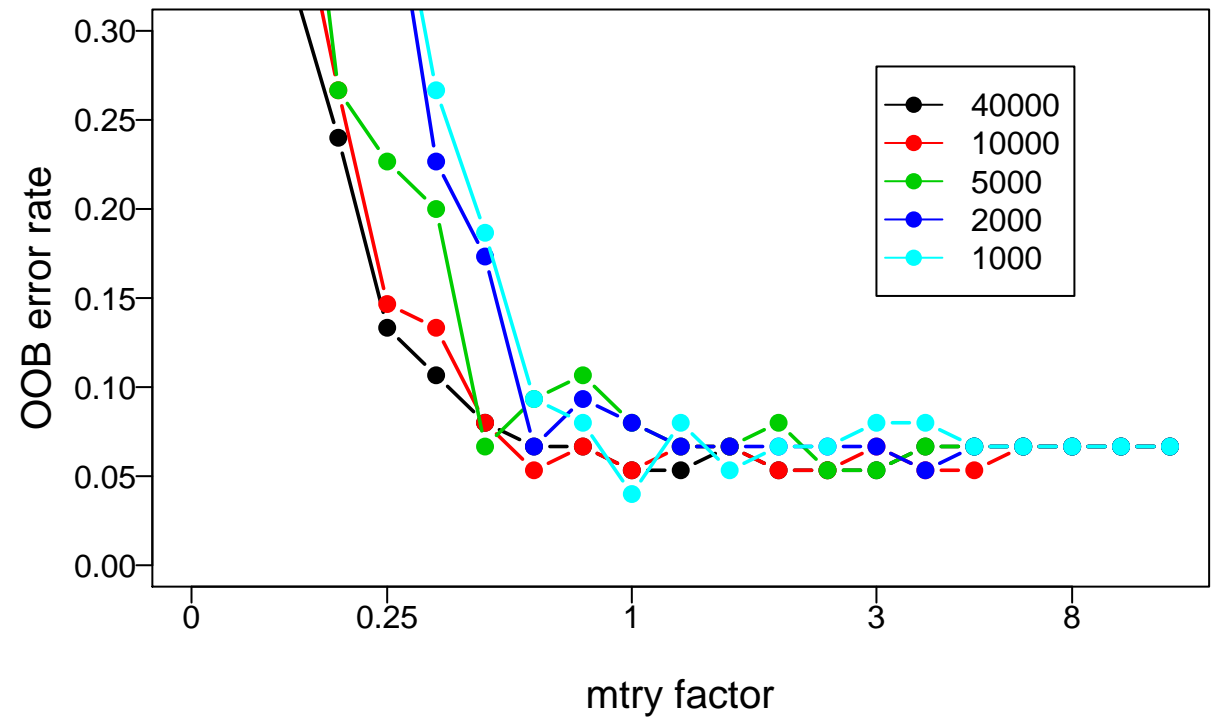
3 classes; 2 dimensions; 5 genes/dimen.; nodesize = 1



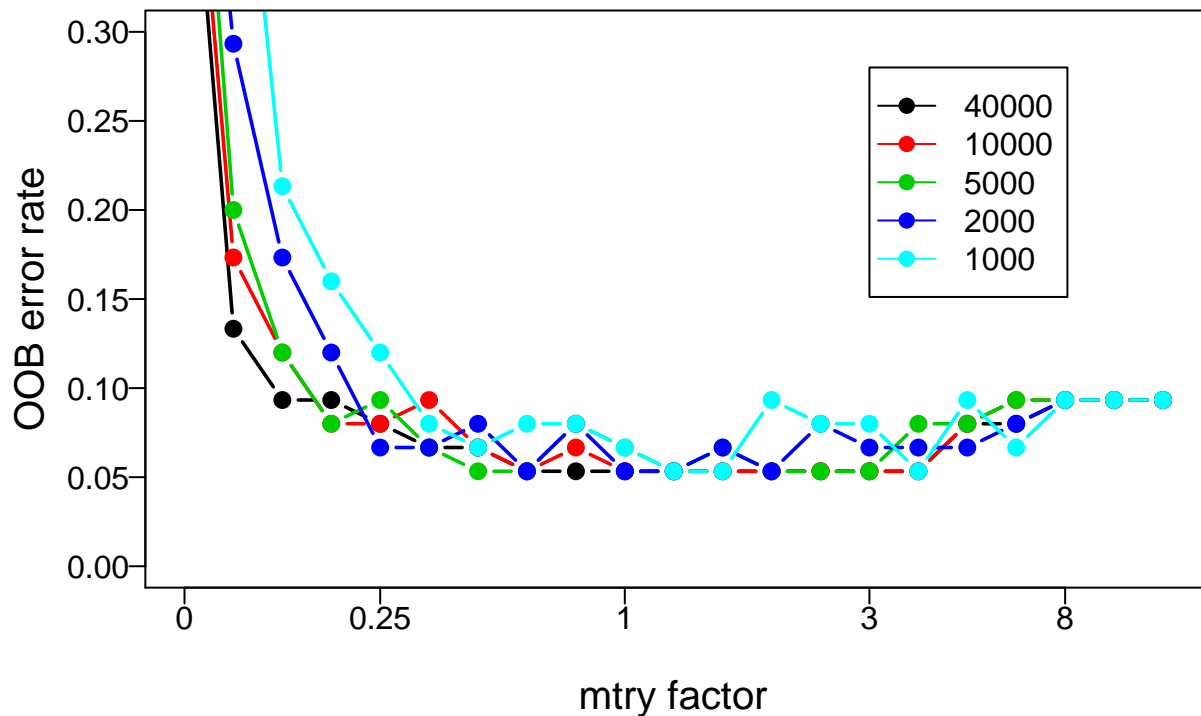
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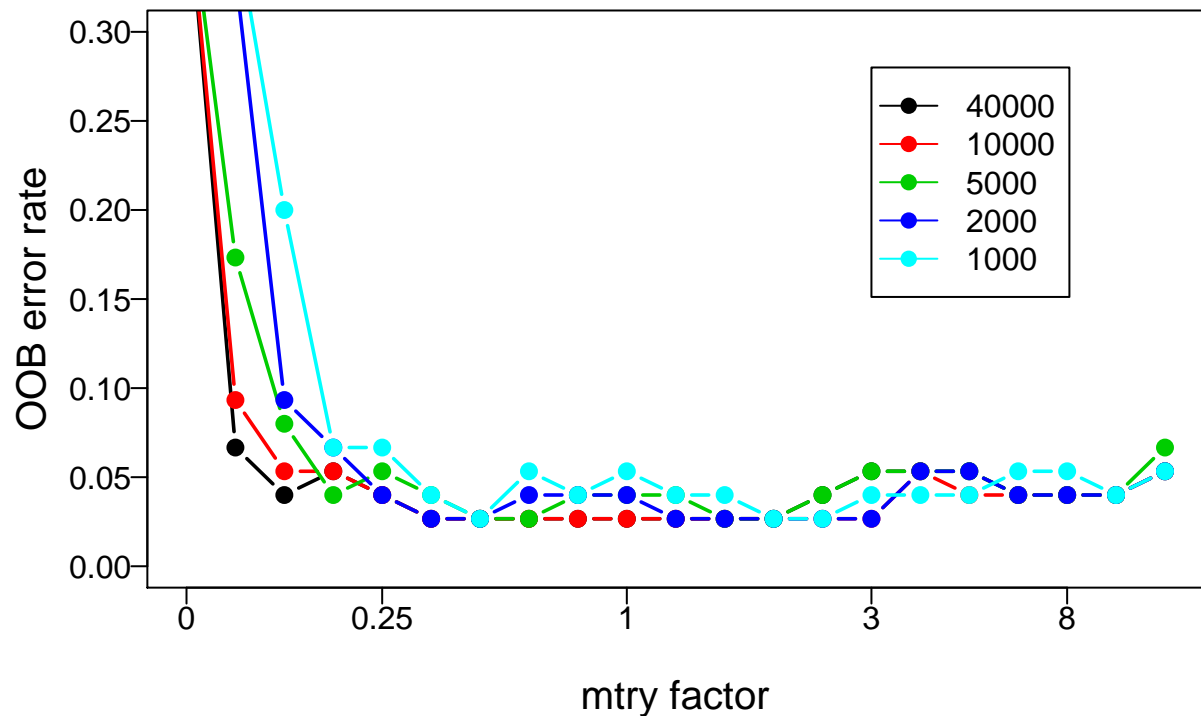
3 classes; 2 dimensions; 5 genes/dimen.; nodesize = 1



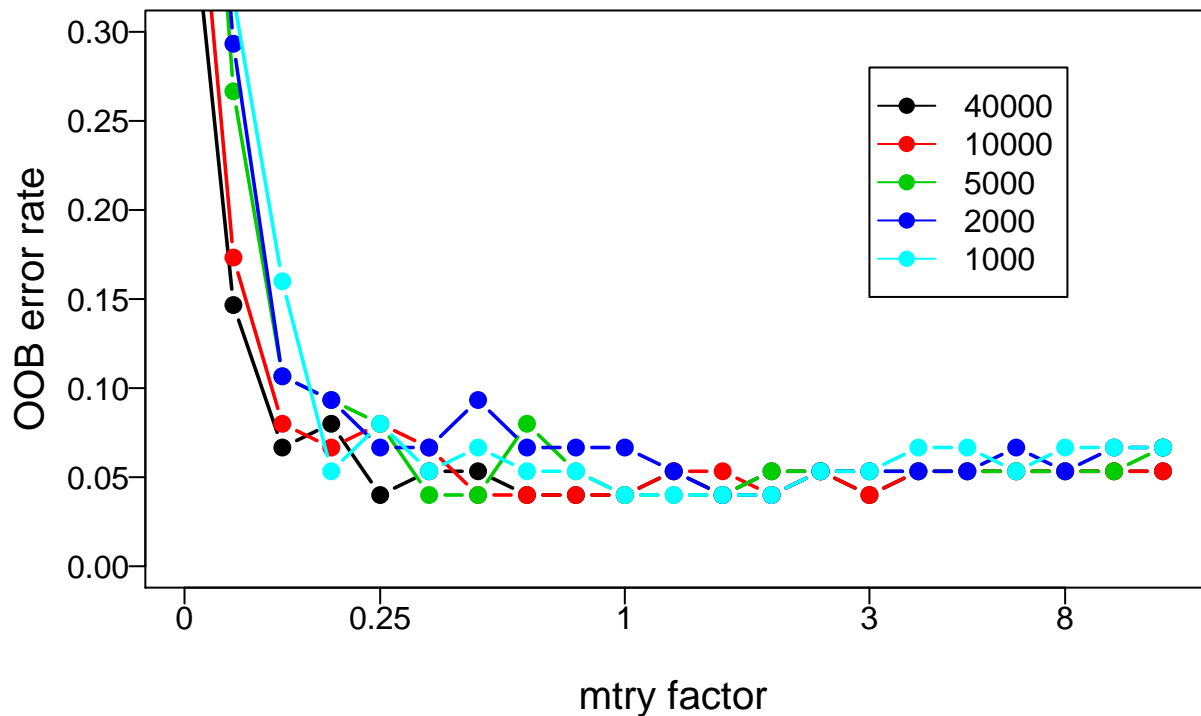
3 classes; 2 dimensions; 20 genes/dimen.; nodesize = 1



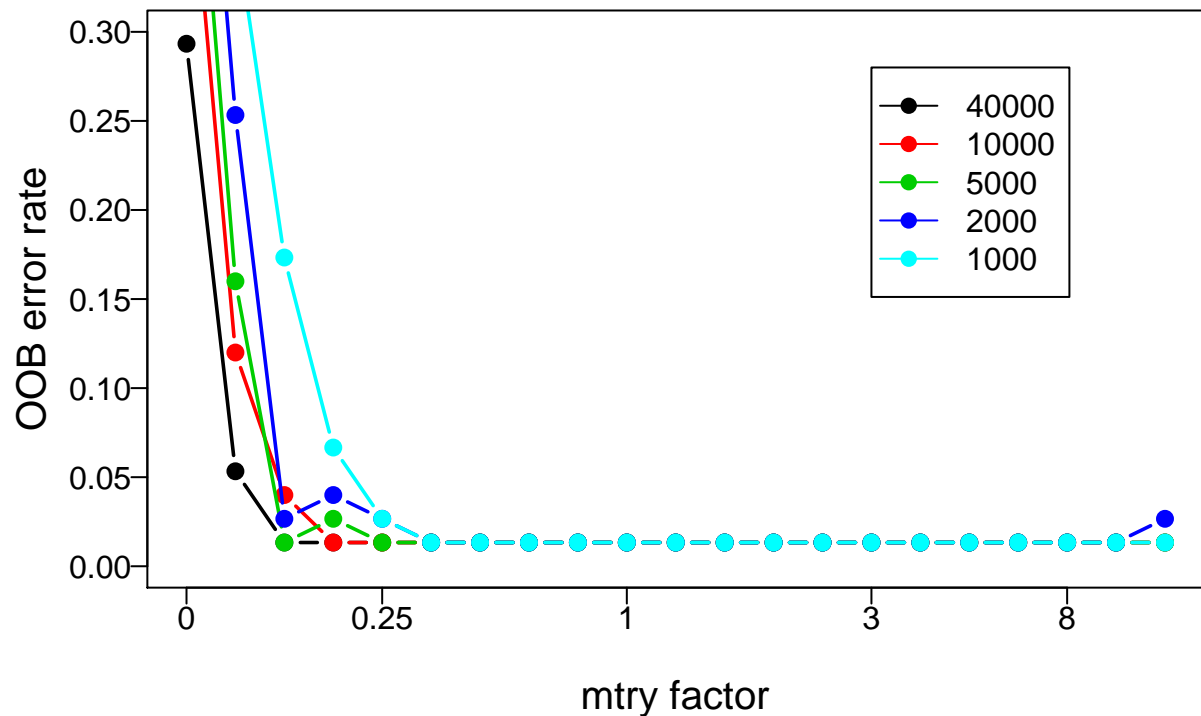
3 classes; 2 dimensions; 20 genes/dimen.; nodesize = 1



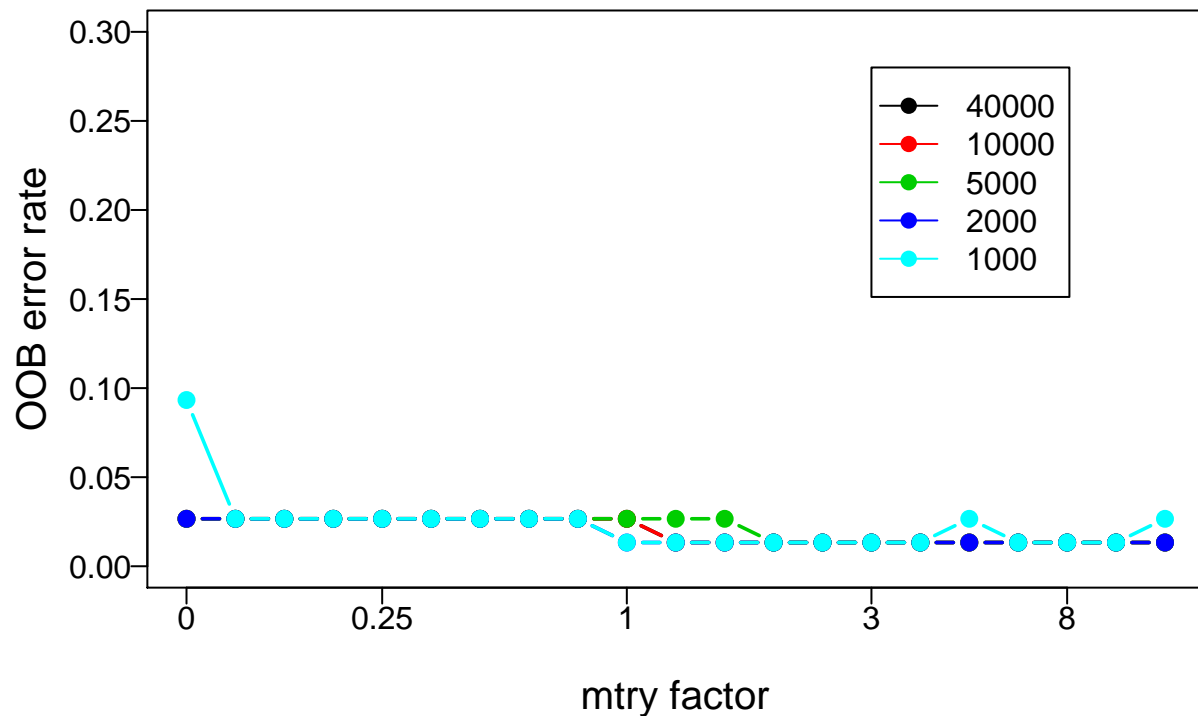
3 classes; 2 dimensions; 20 genes/dimen.; nodesize = 1



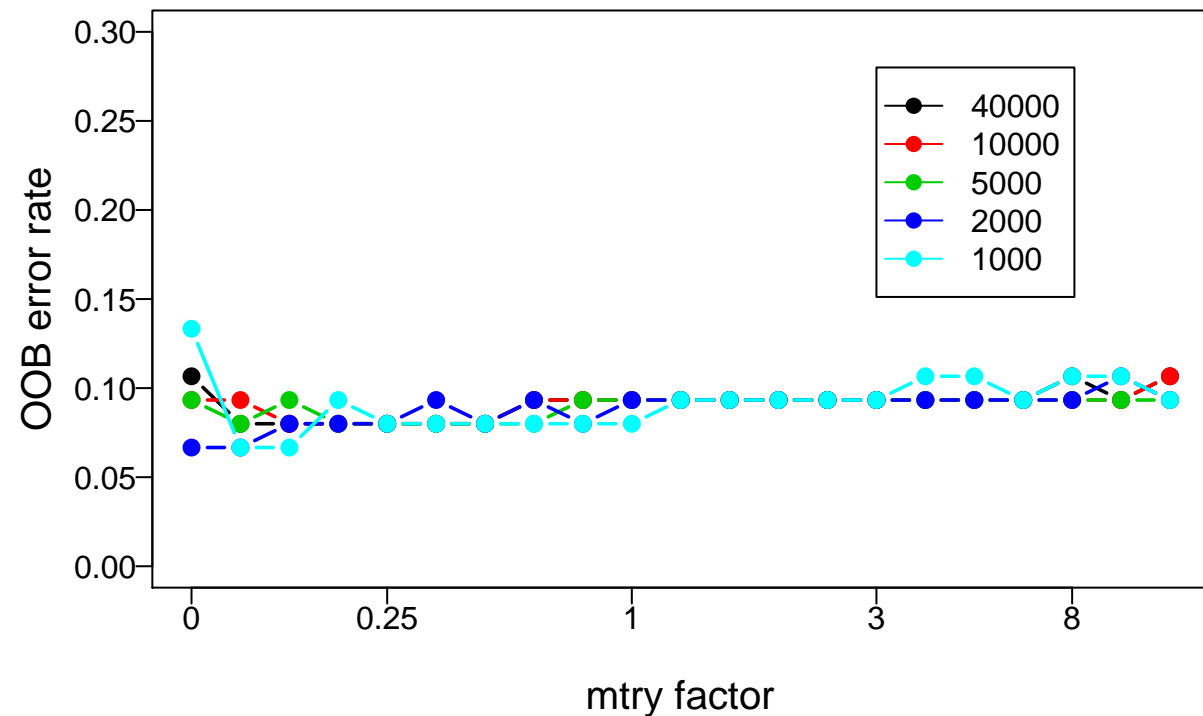
3 classes; 2 dimensions; 20 genes/dimen.; nodesize = 1



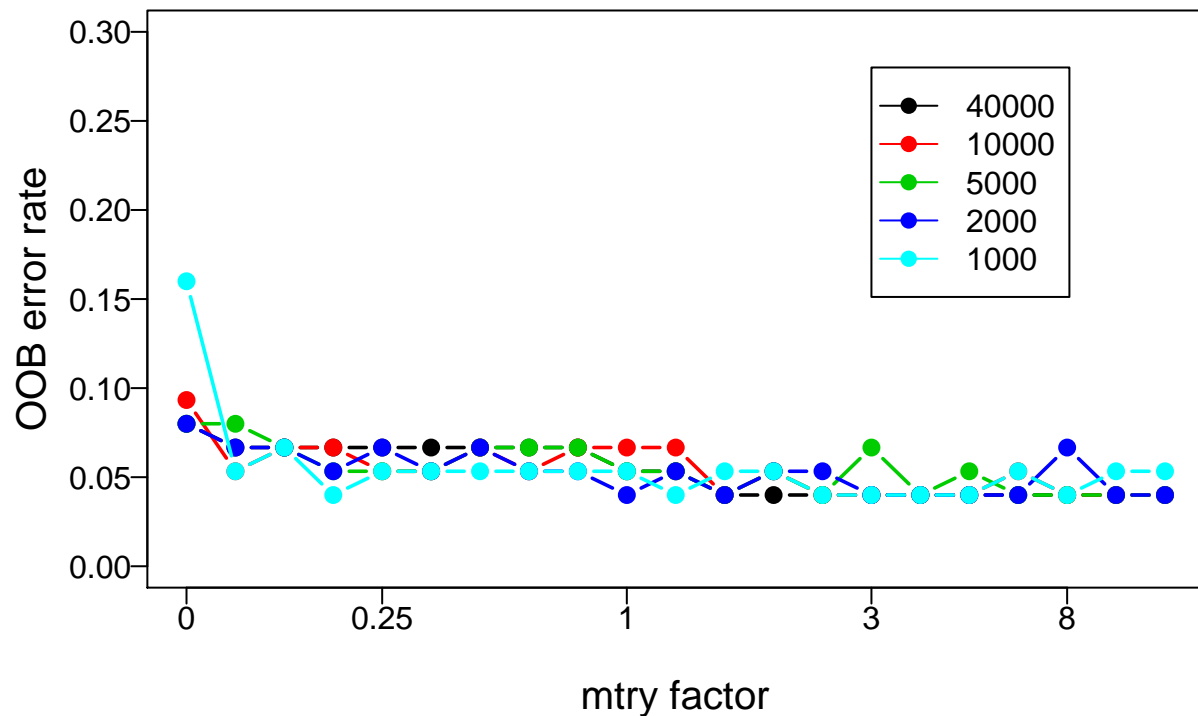
3 classes; 2 dimensions; 100 genes/dimen.; nodesize = 1



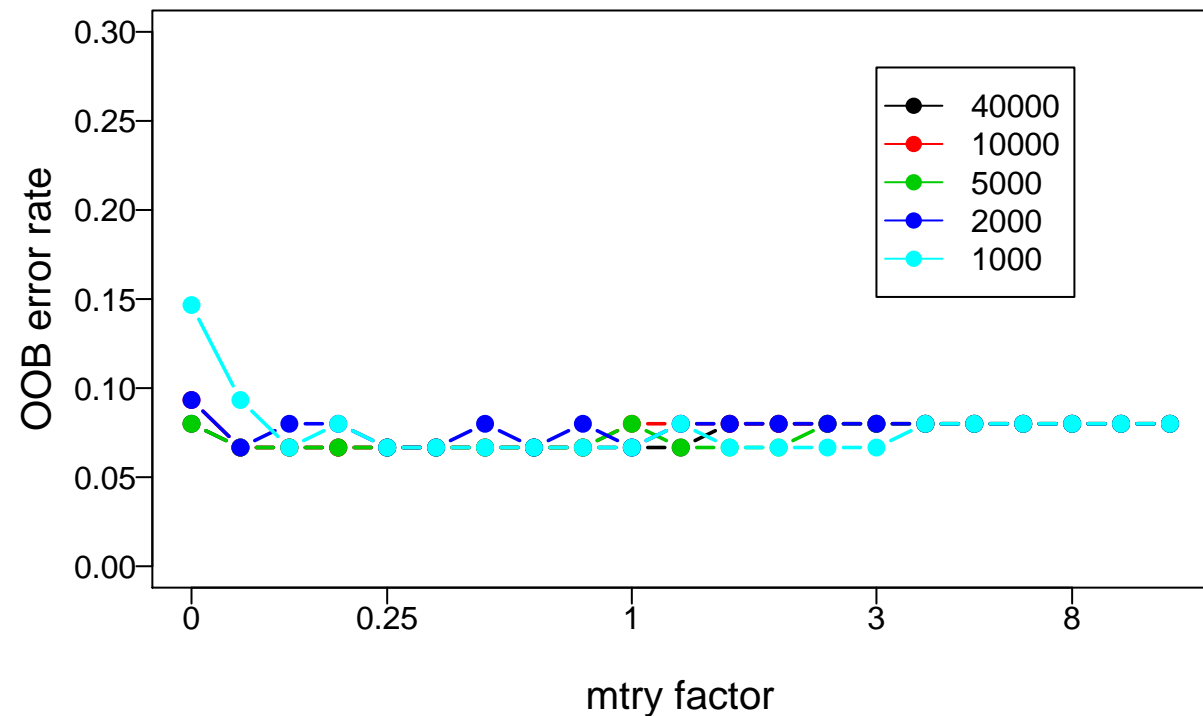
3 classes; 2 dimensions; 100 genes/dimen.; nodesize = 1



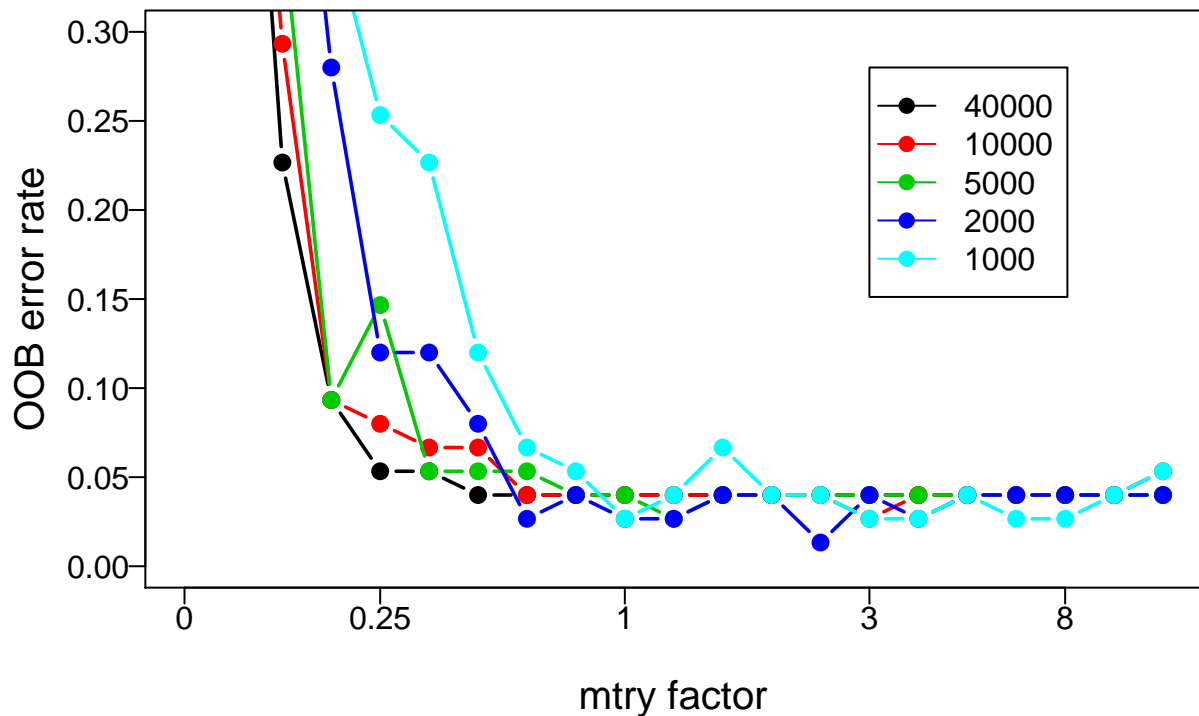
3 classes; 2 dimensions; 100 genes/dimen.; nodesize = 1



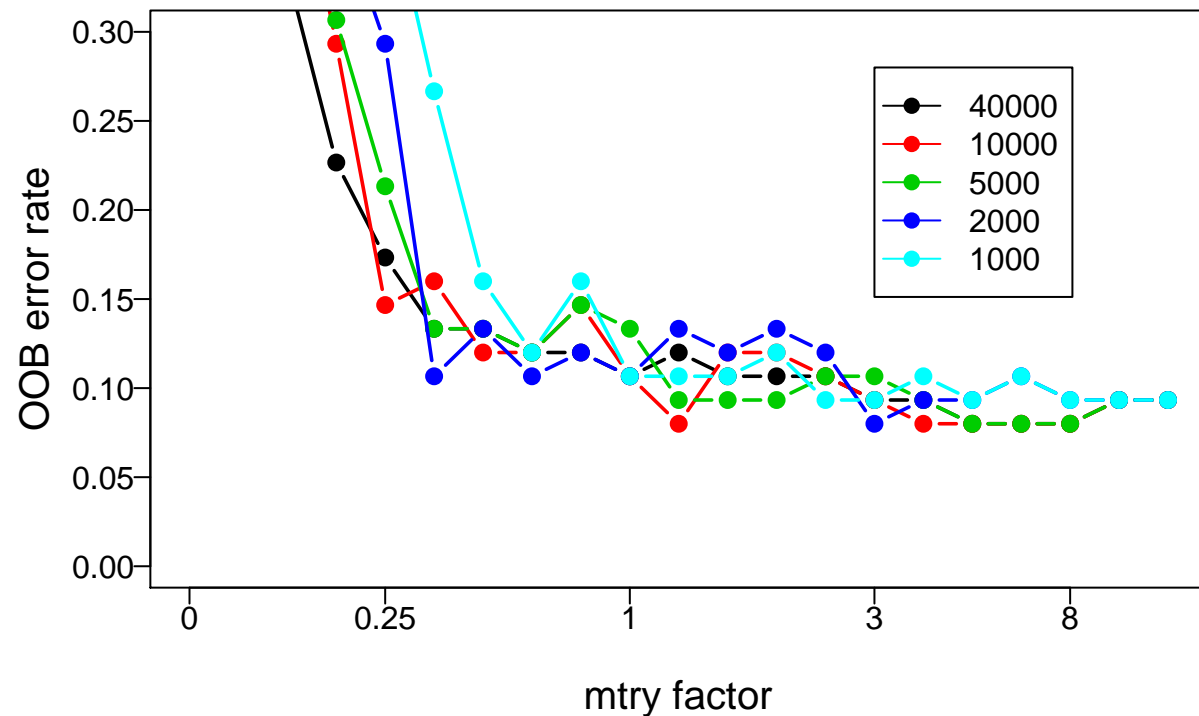
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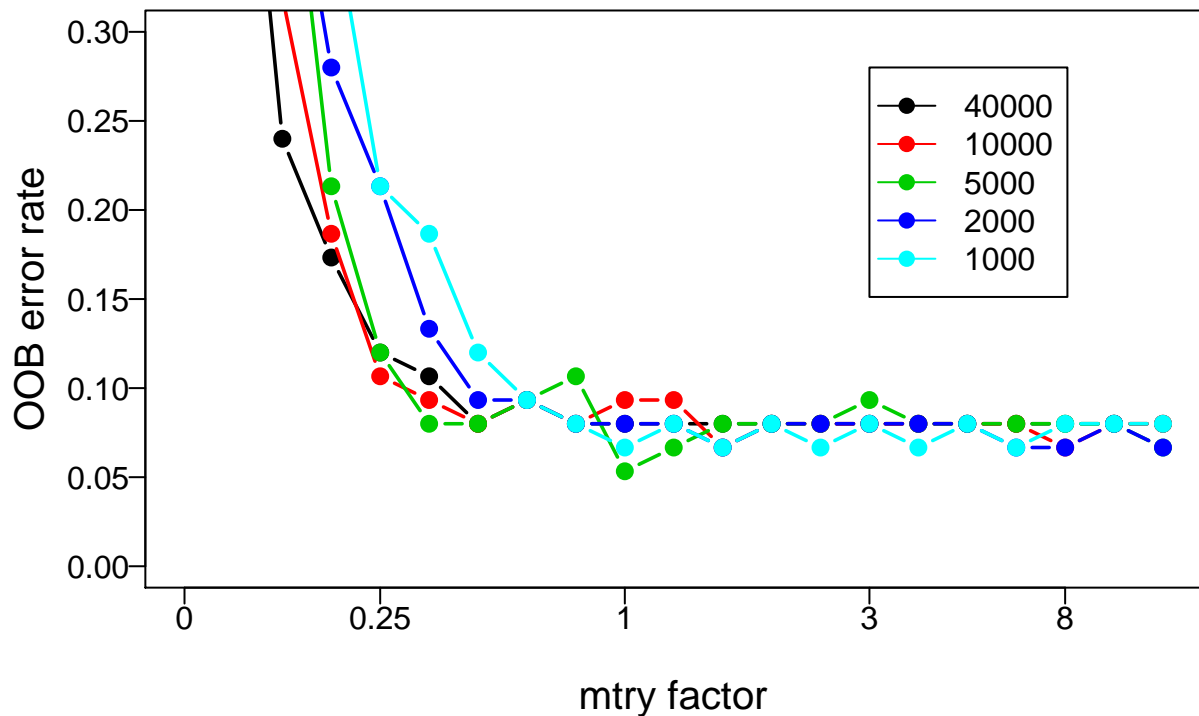
3 classes; 3 dimensions; 5 genes/dimen.; nodesize = 1



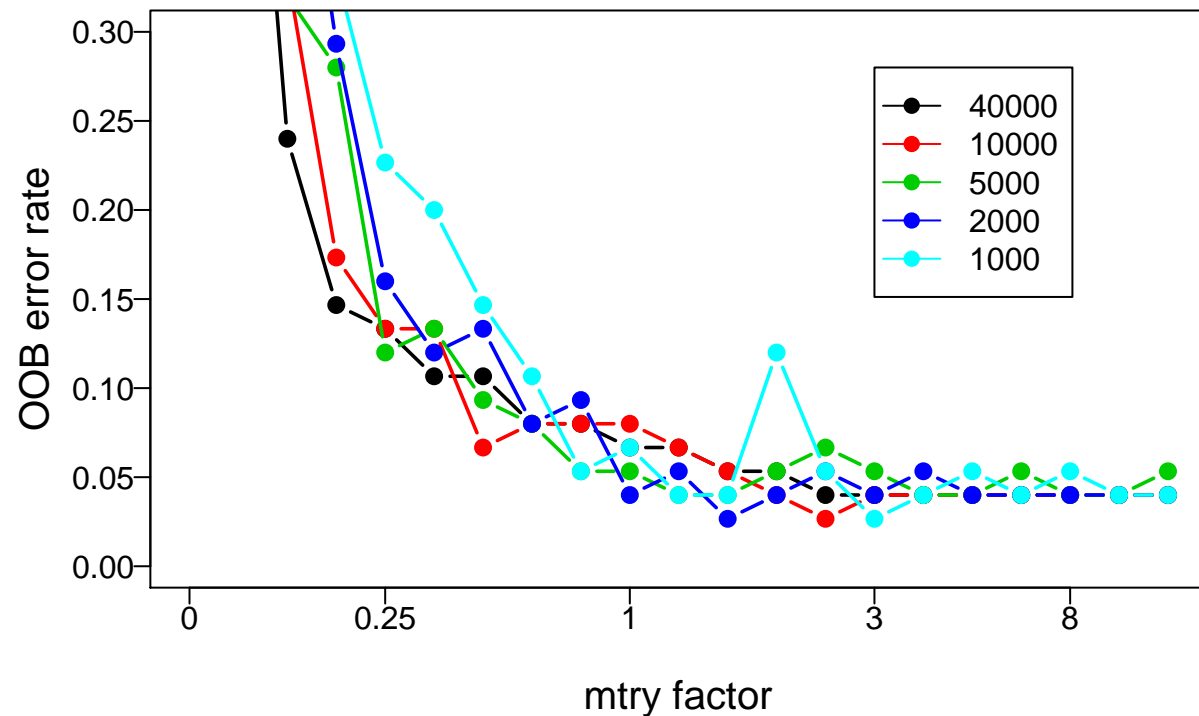
3 classes; 3 dimensions; 5 genes/dimen.; nodesize = 1



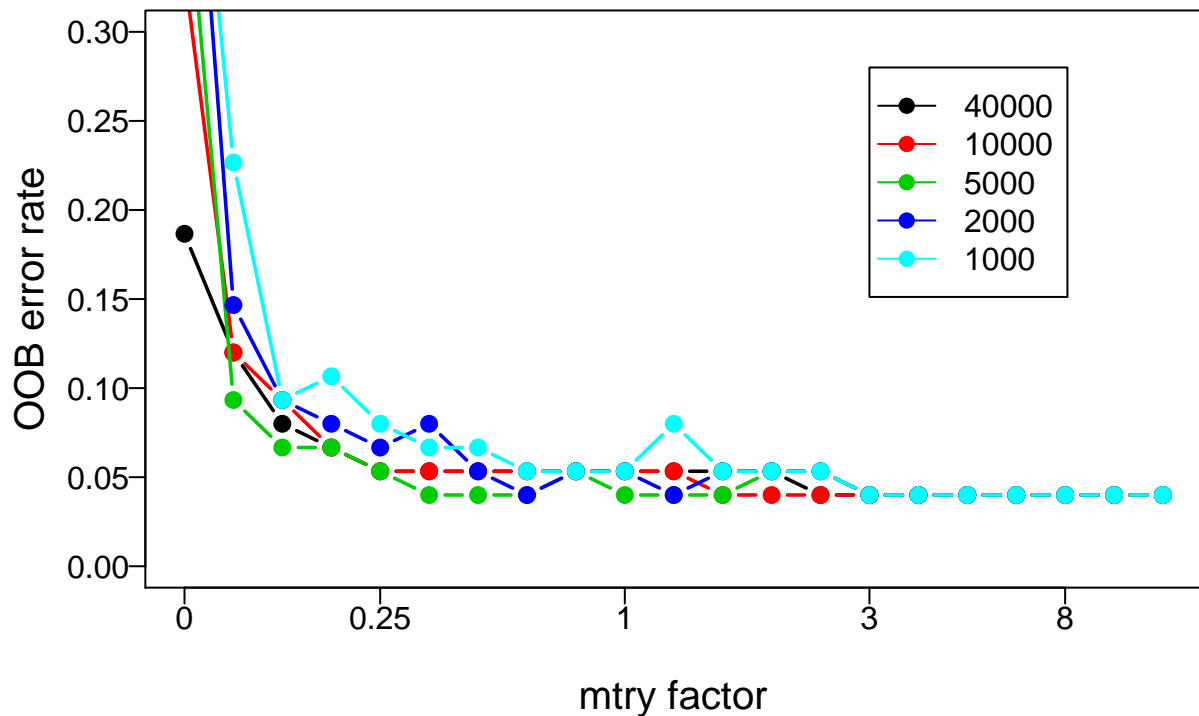
3 classes; 3 dimensions; 5 genes/dimen.; nodesize = 1



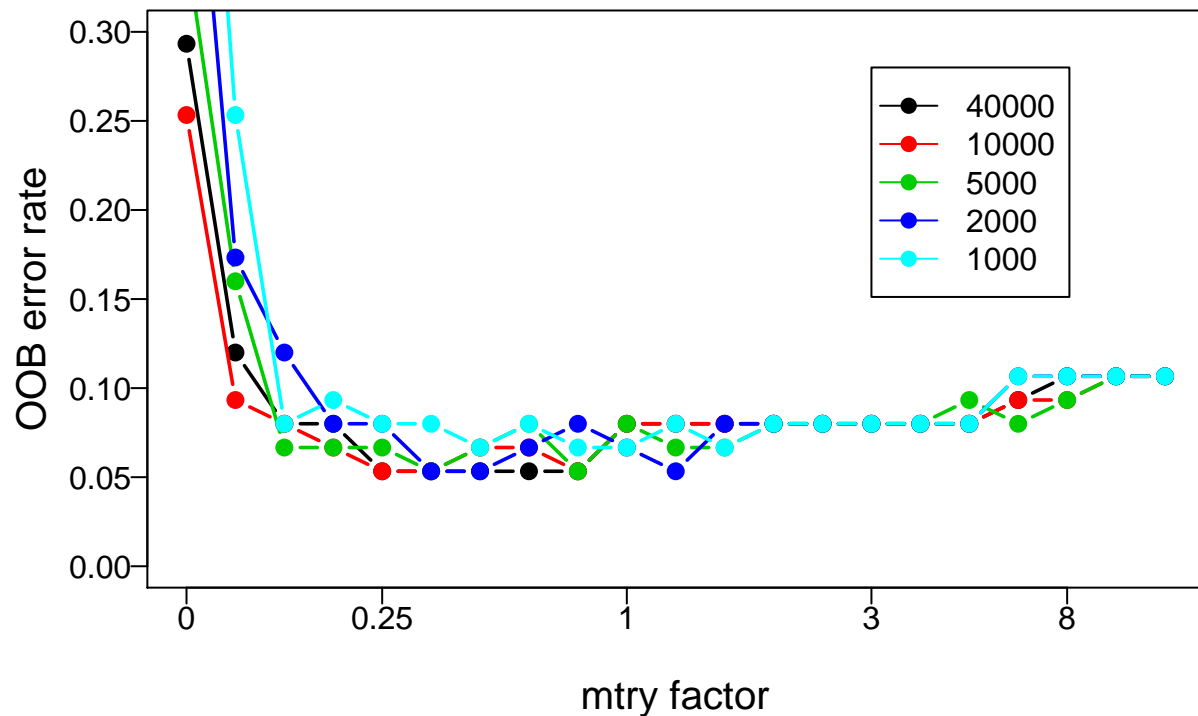
3 classes; 3 dimensions; 5 genes/dimen.; nodesize = 1



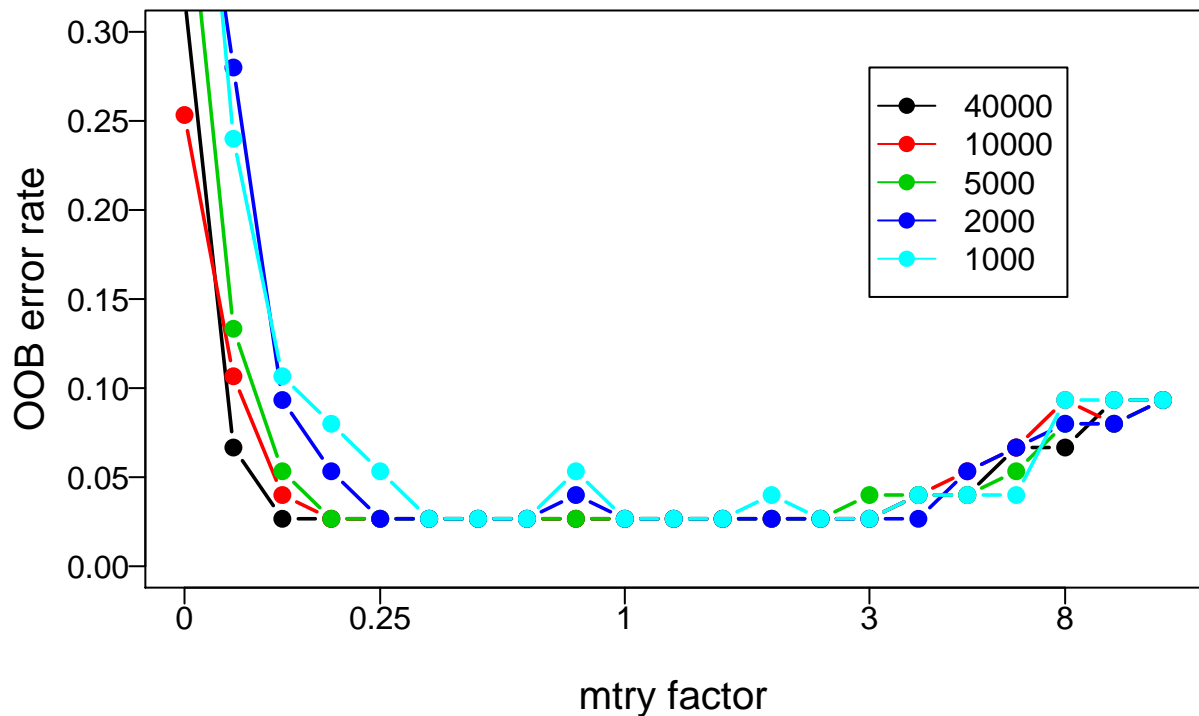
3 classes; 3 dimensions; 20 genes/dimen.; nodesize = 1



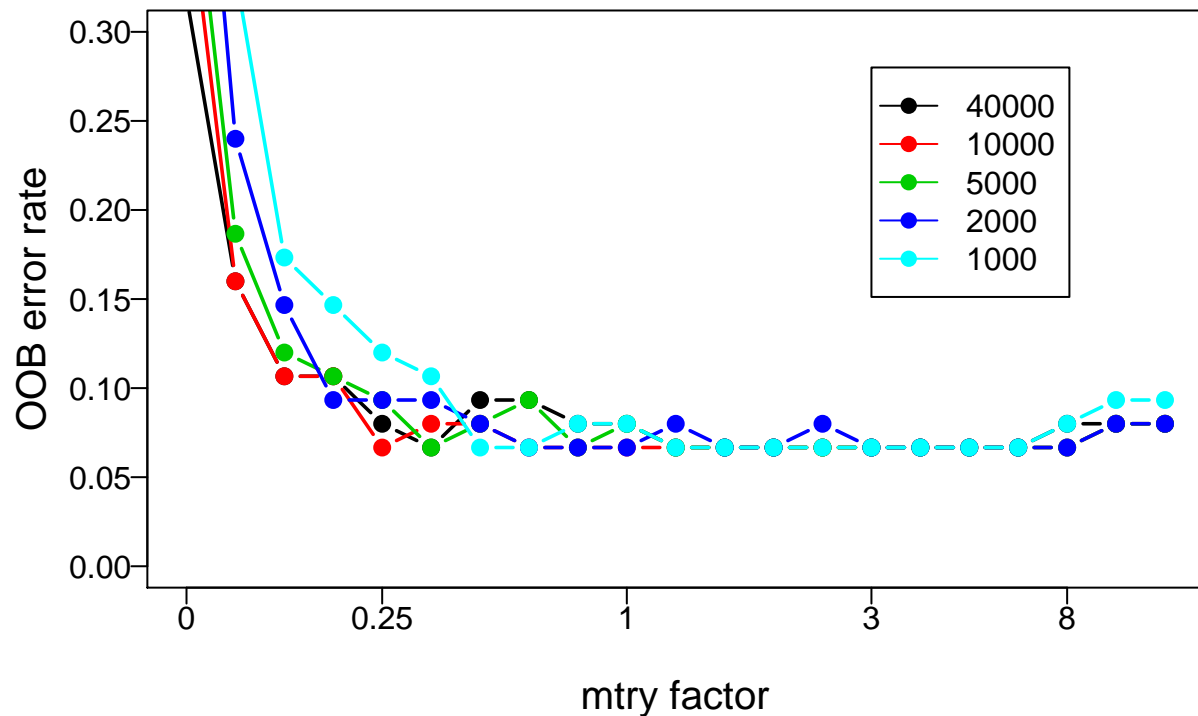
3 classes; 3 dimensions; 20 genes/dimen.; nodesize = 1



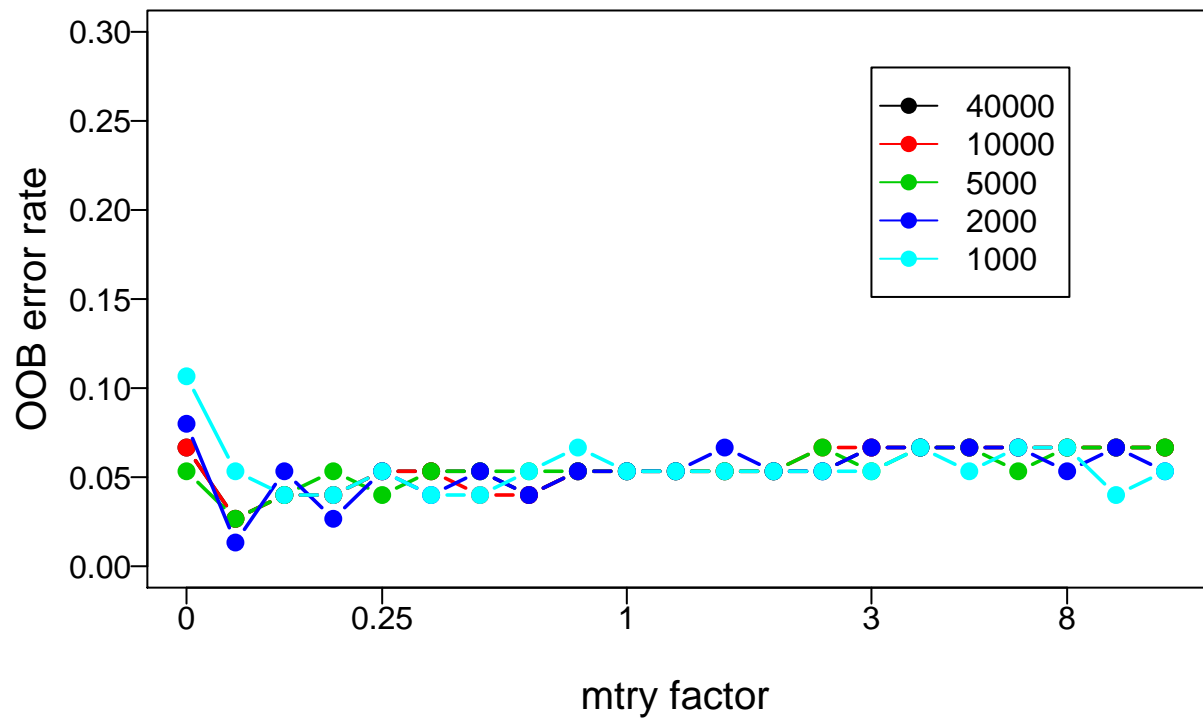
3 classes; 3 dimensions; 20 genes/dimen.; nodesize = 1



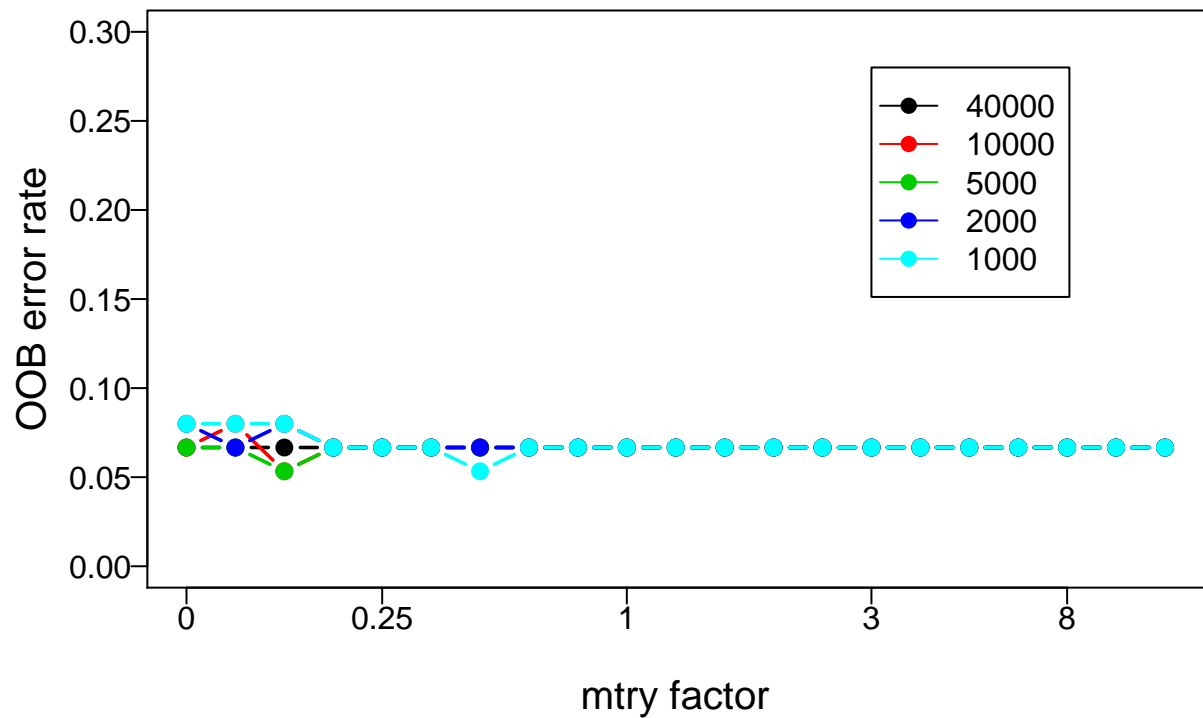
3 classes; 3 dimensions; 20 genes/dimen.; nodesize = 1



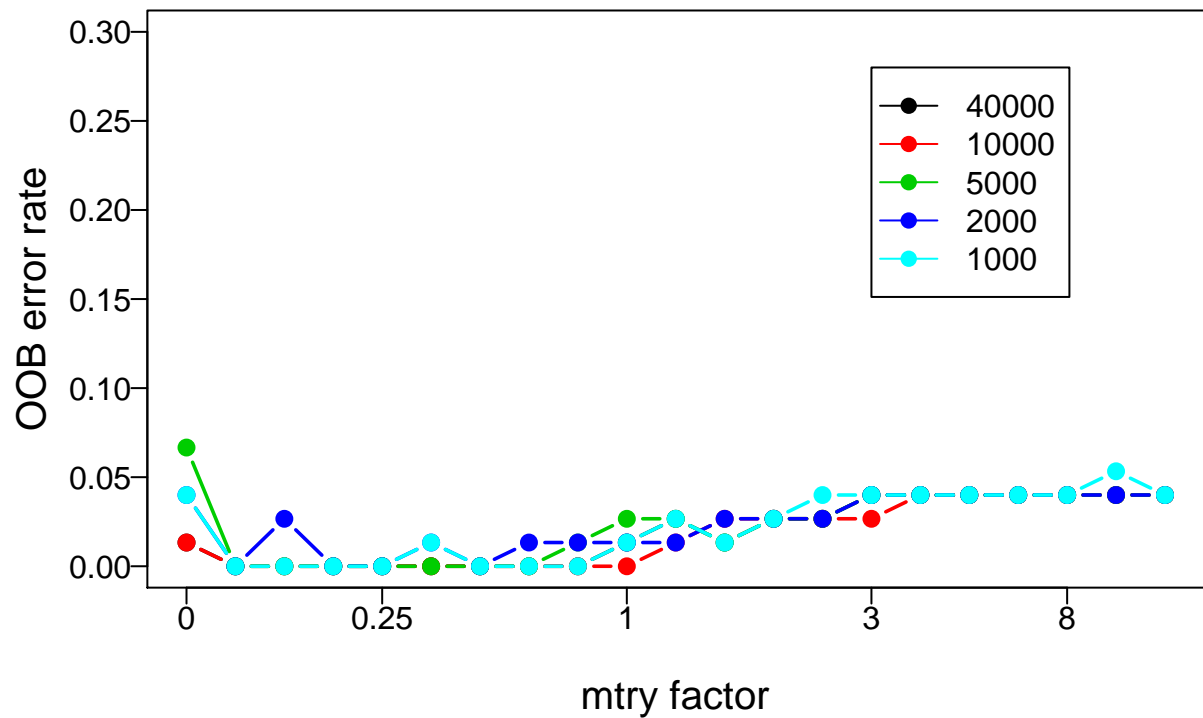
3 classes; 3 dimensions; 100 genes/dimen.; nodesize = 1



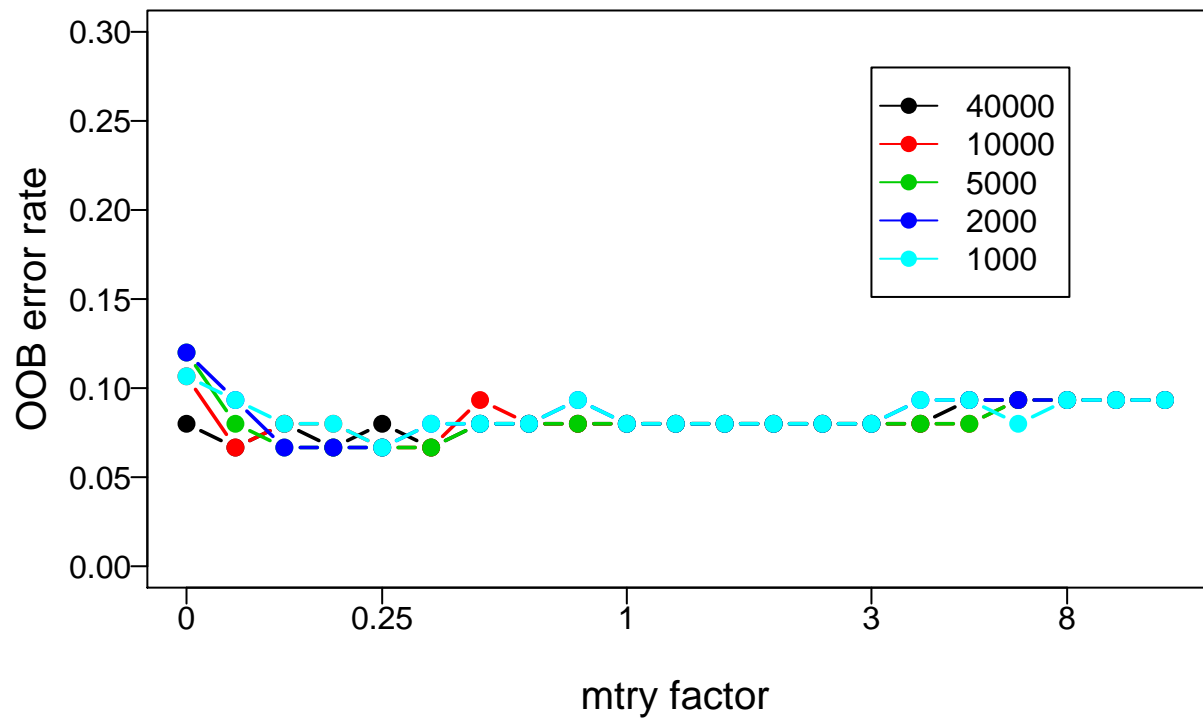
3 classes; 3 dimensions; 100 genes/dimen.; nodesize = 1



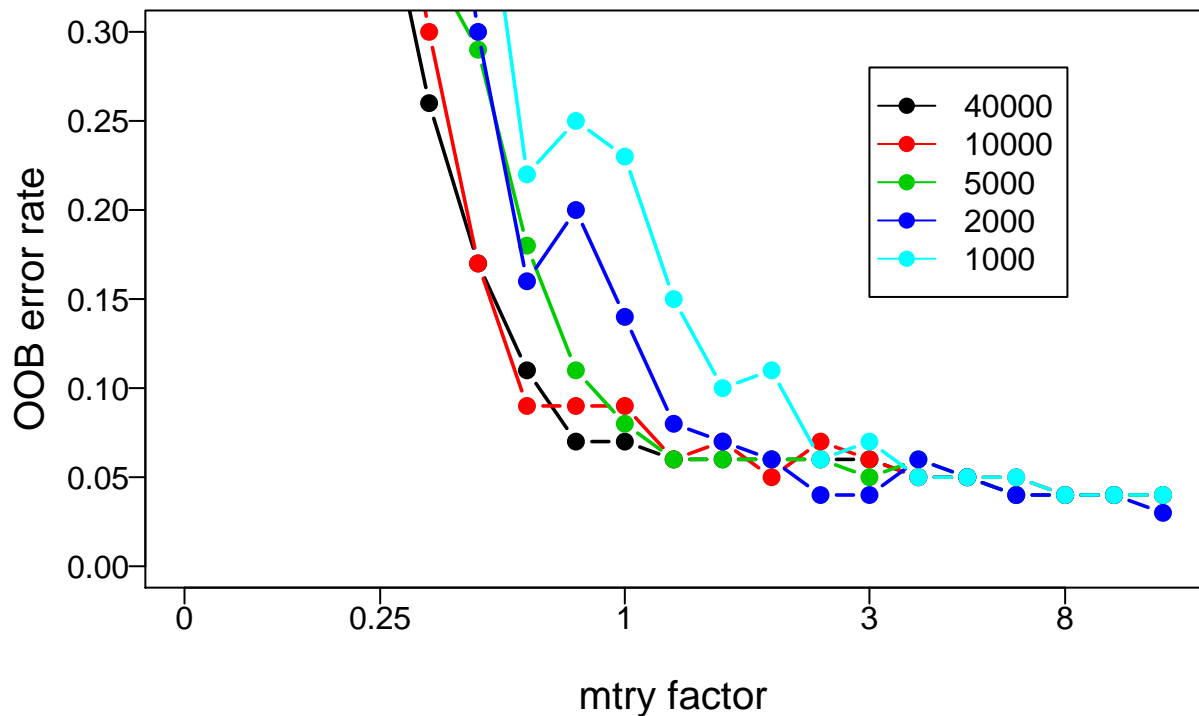
3 classes; 3 dimensions; 100 genes/dimen.; nodesize = 1



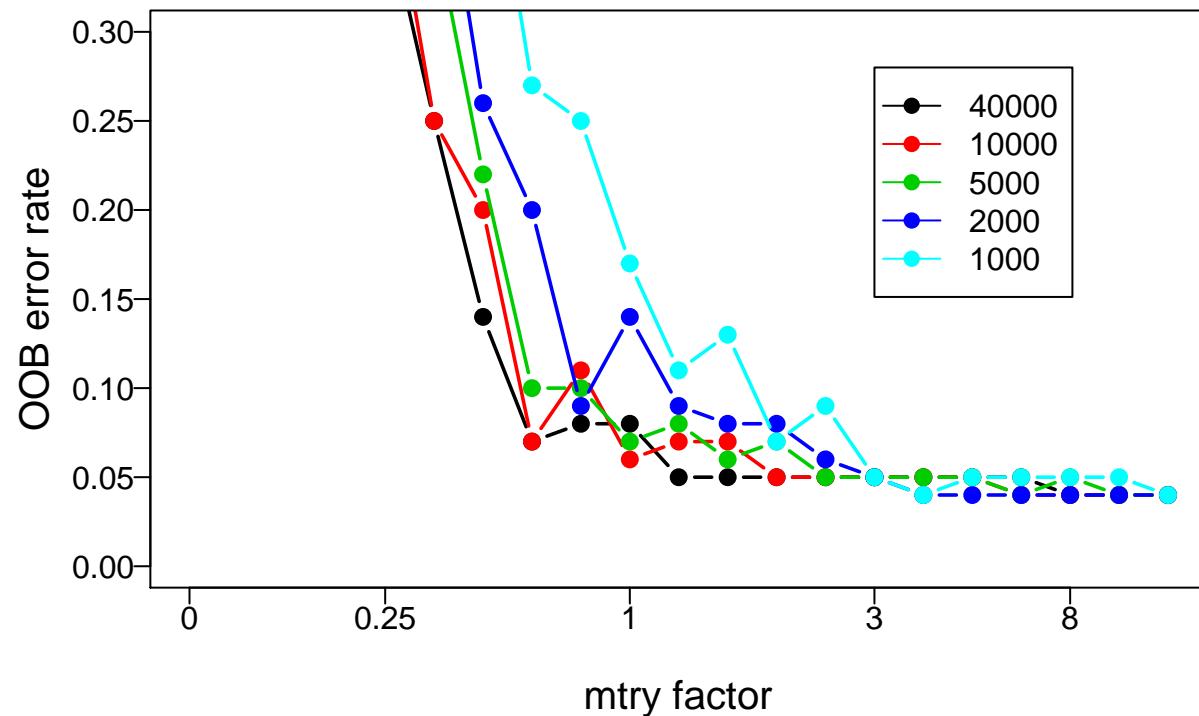
3 classes; 3 dimensions; 100 genes/dimen.; nodesize = 1



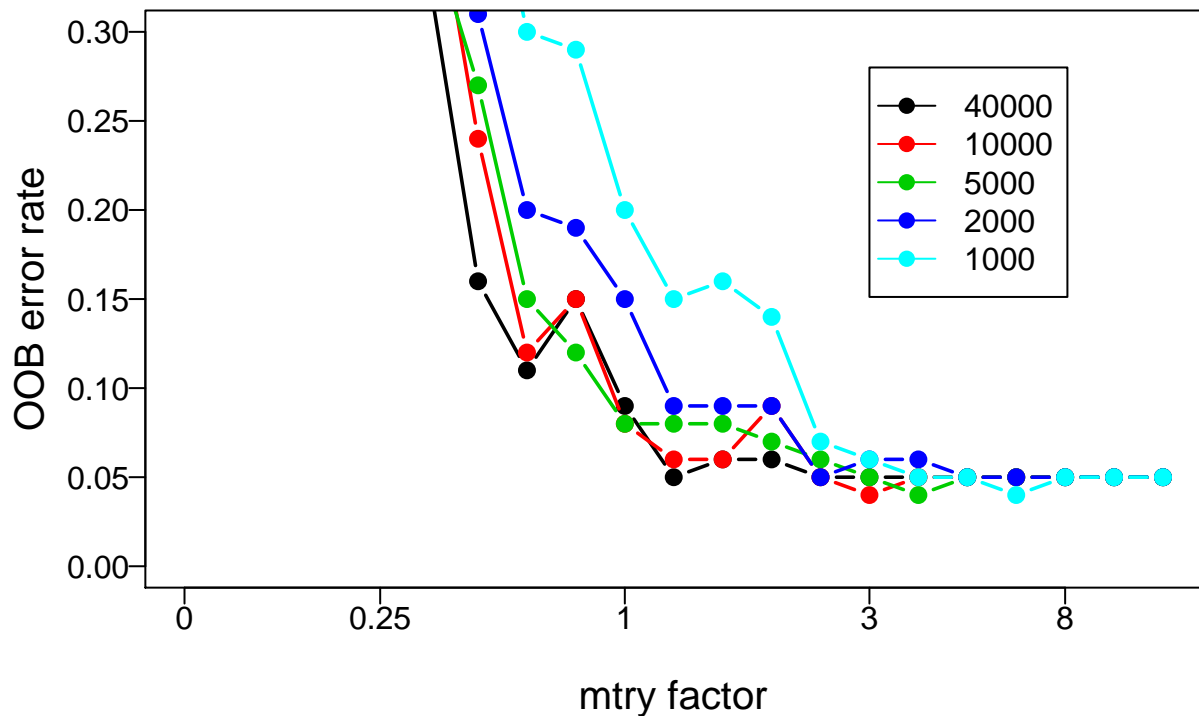
4 classes; 1 dimensions; 5 genes/dimen.; nodesize = 1



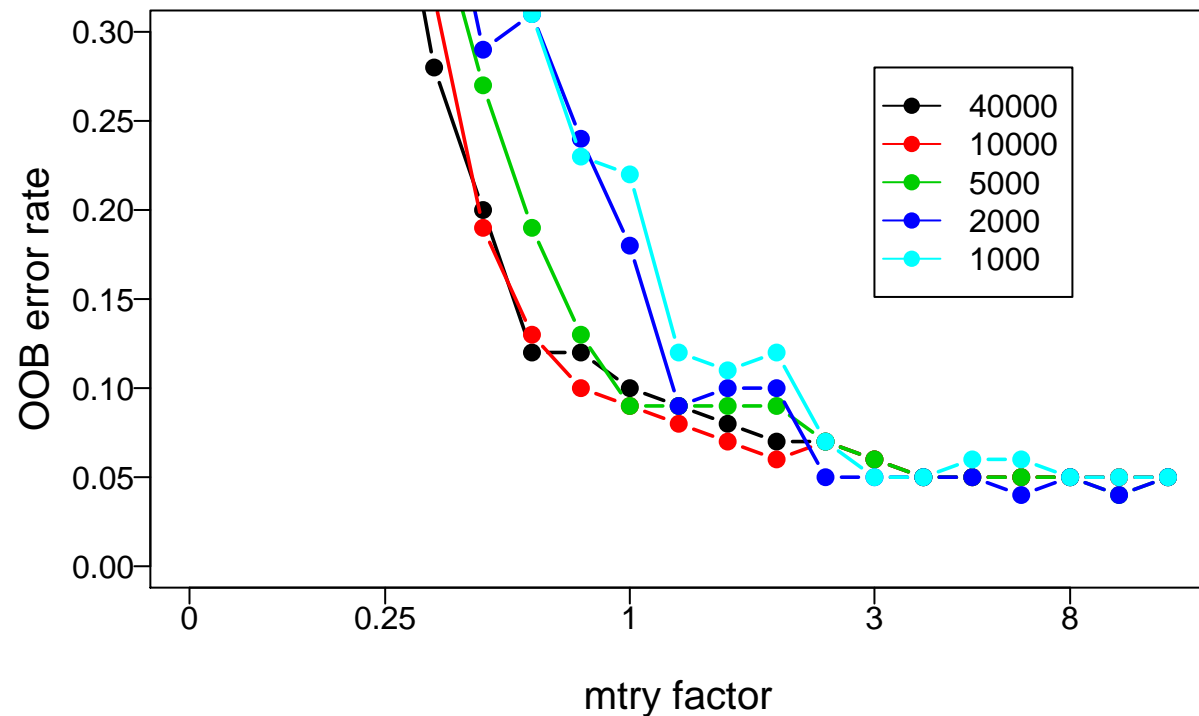
4 classes; 1 dimensions; 5 genes/dimen.; nodesize = 1



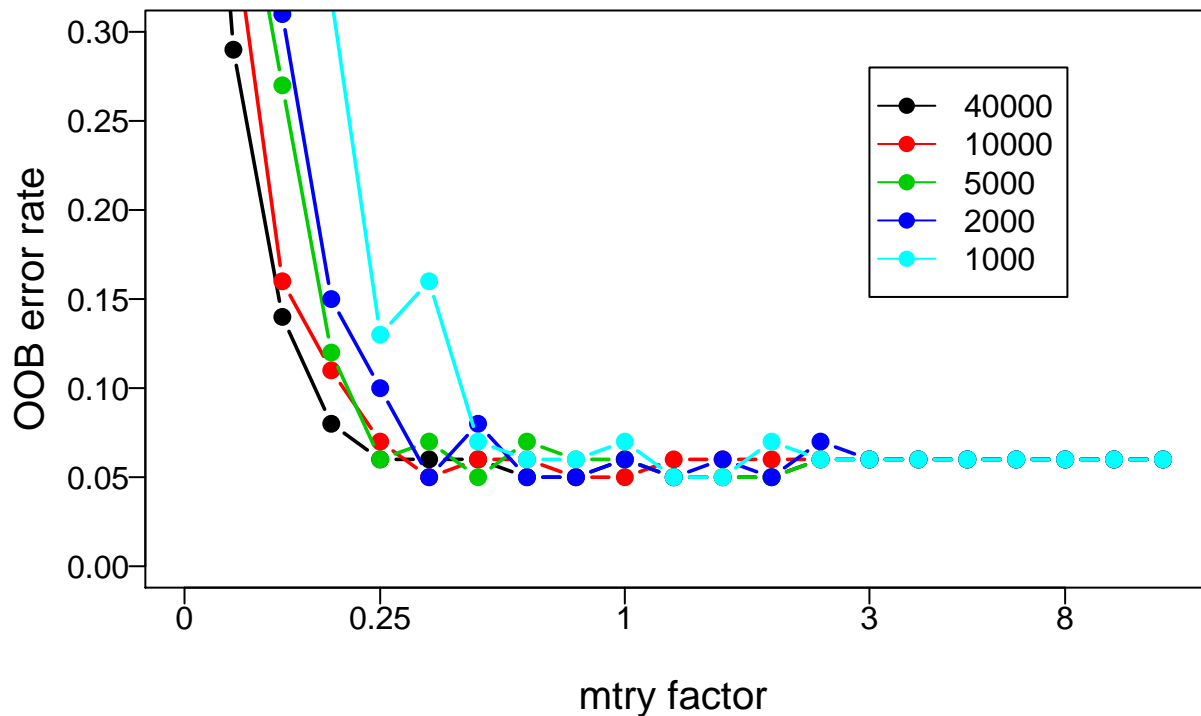
4 classes; 1 dimensions; 5 genes/dimen.; nodesize = 1



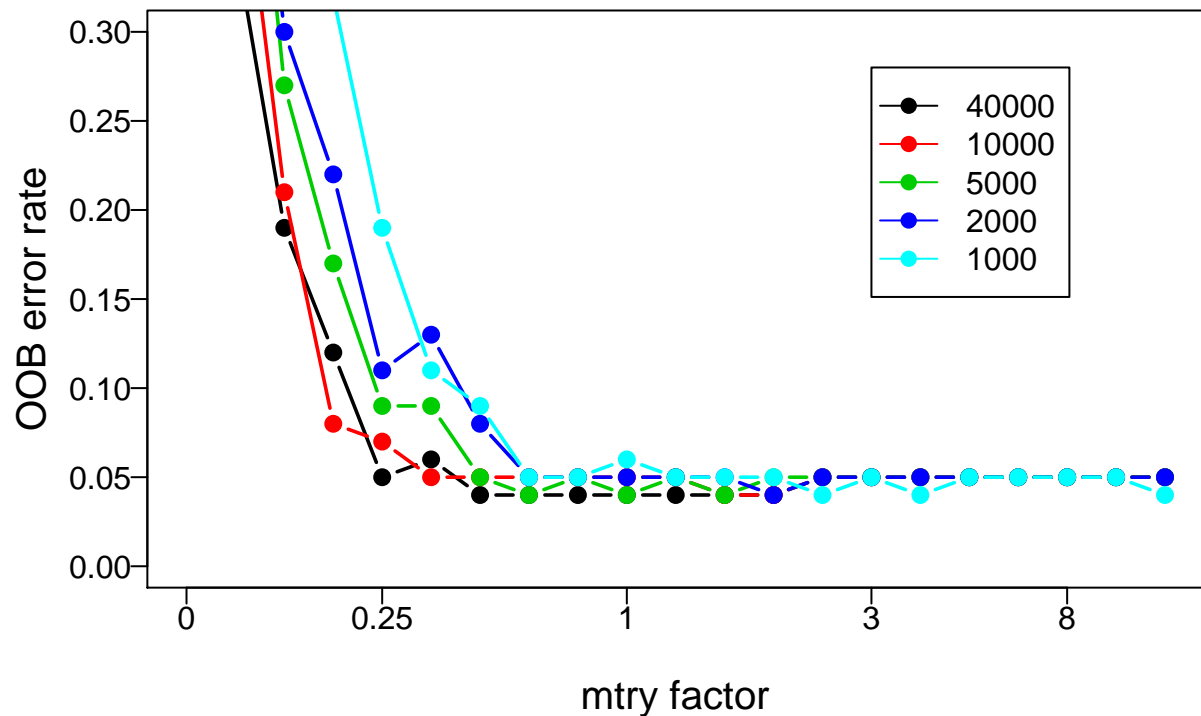
4 classes; 1 dimensions; 5 genes/dimen.; nodesize = 1



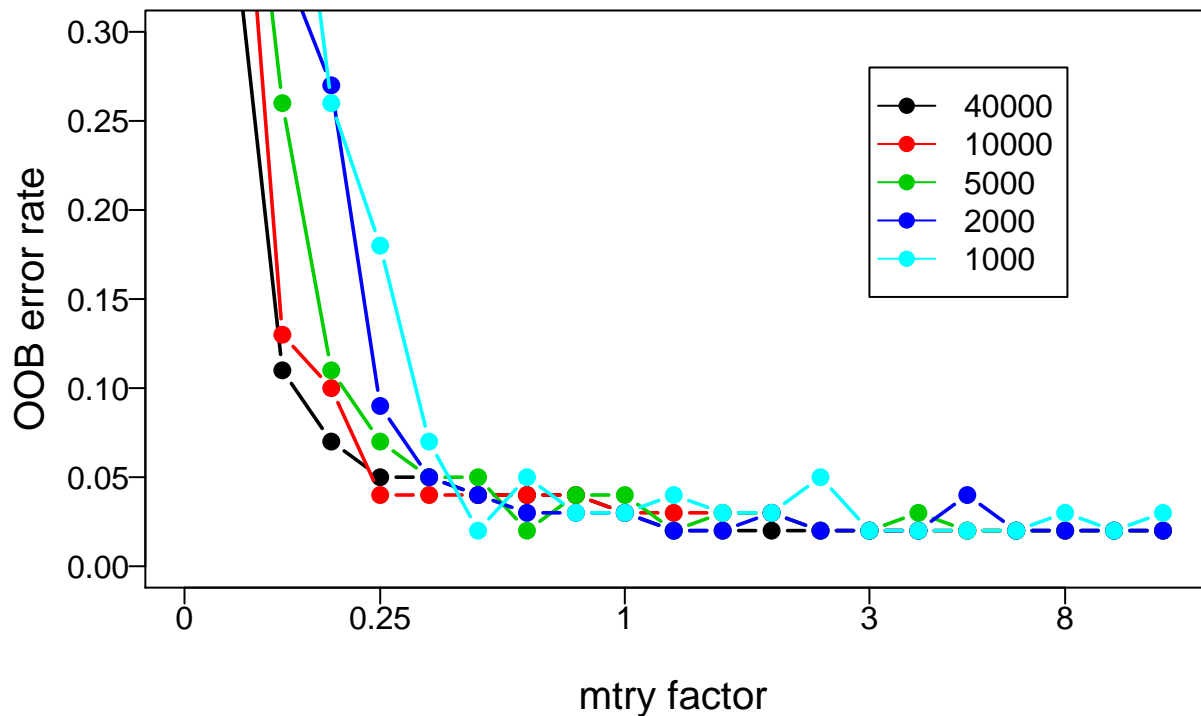
4 classes; 1 dimensions; 20 genes/dimen.; nodesize = 1



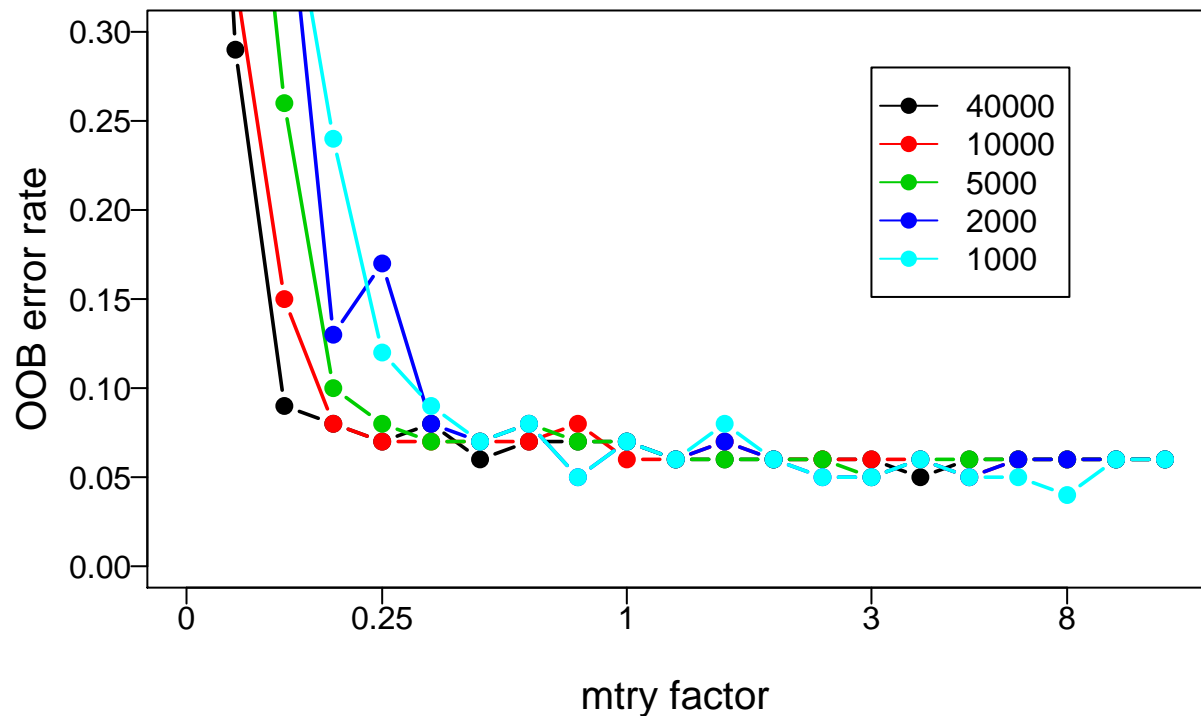
4 classes; 1 dimensions; 20 genes/dimen.; nodesize = 1



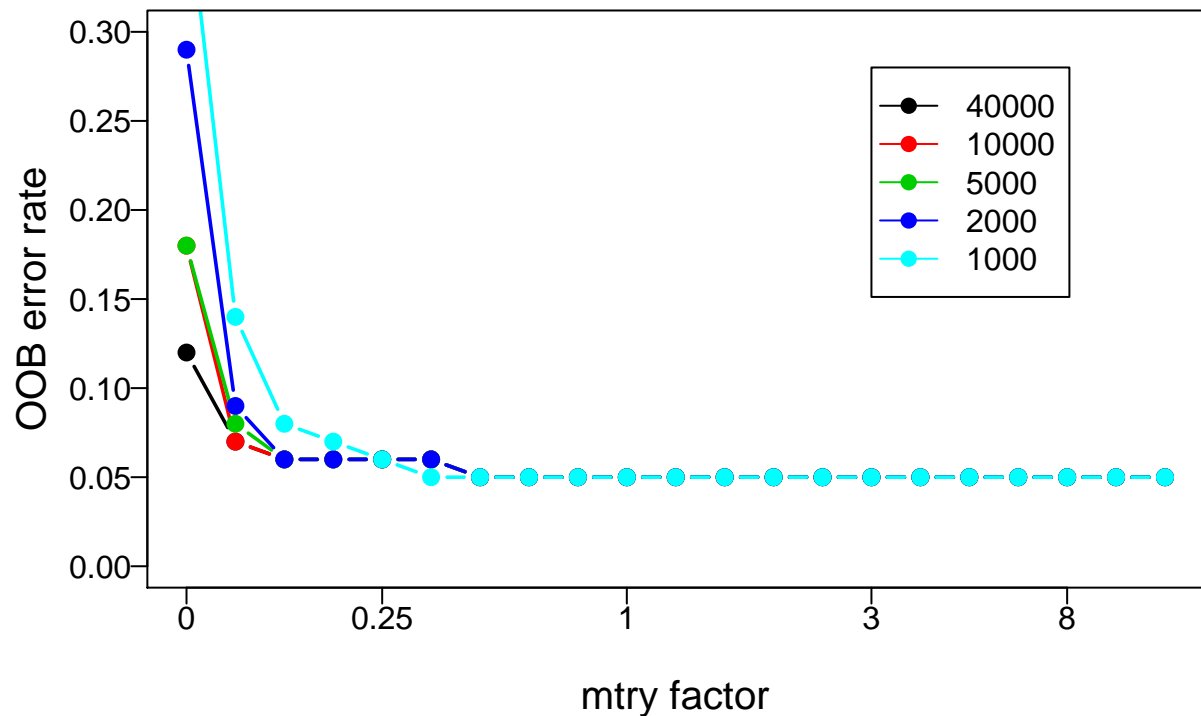
4 classes; 1 dimensions; 20 genes/dimen.; nodesize = 1



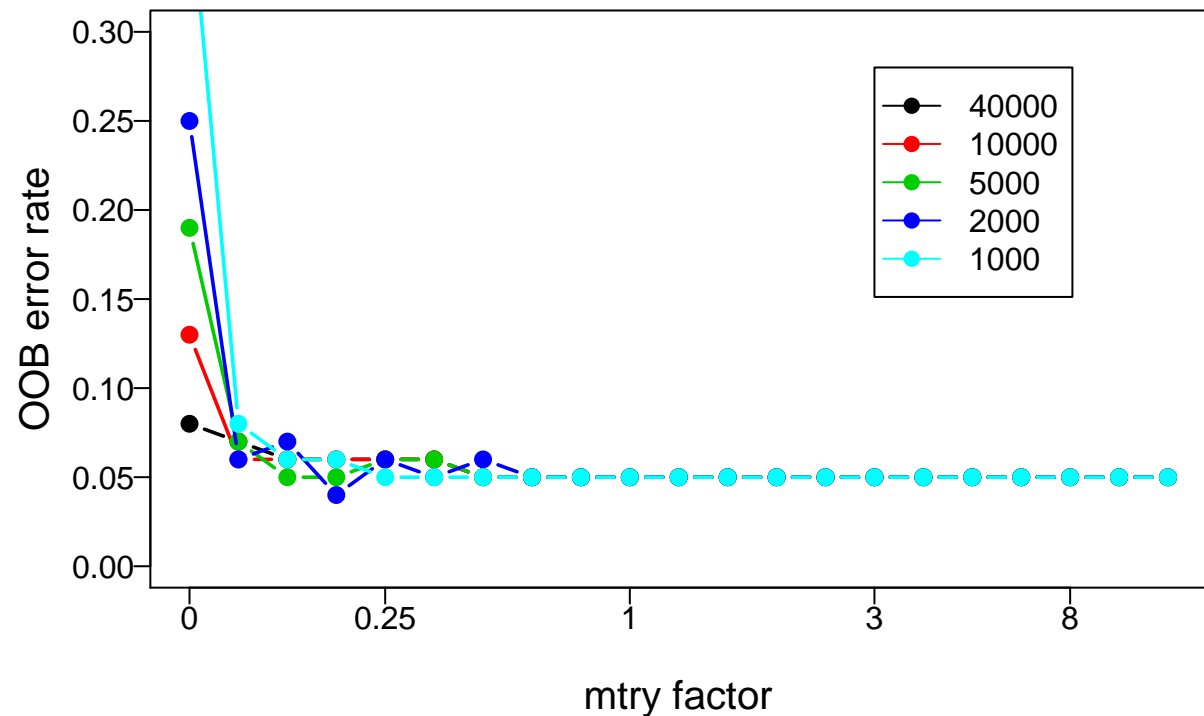
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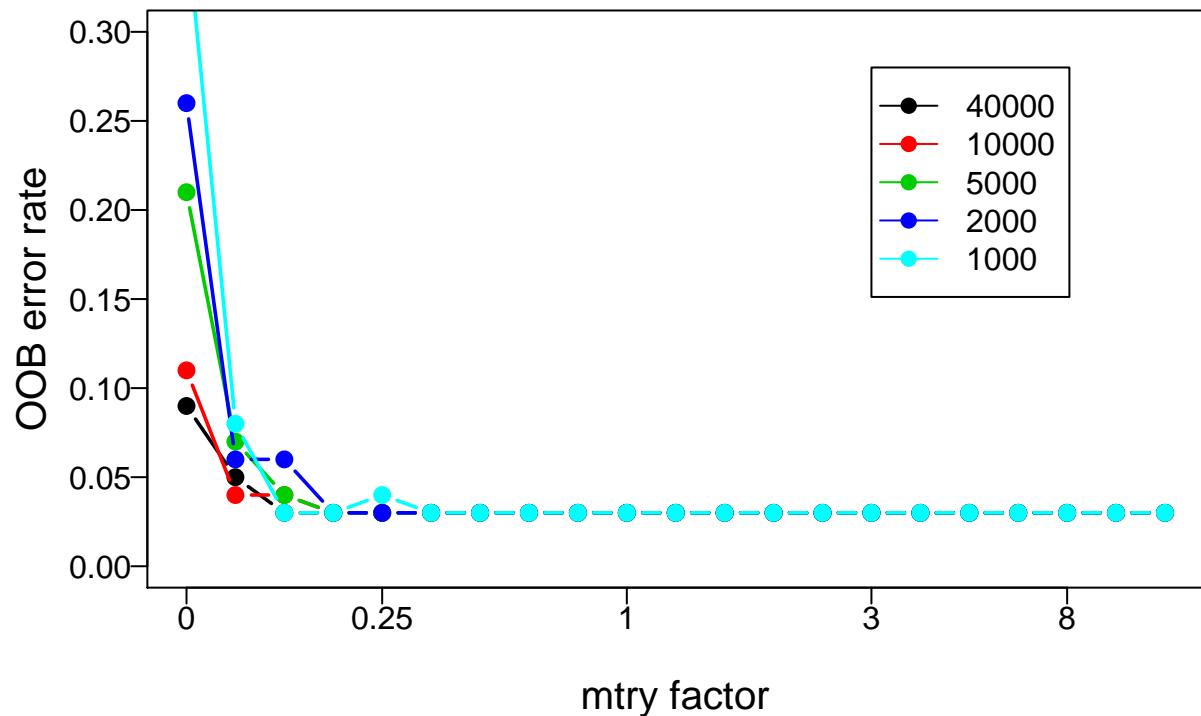
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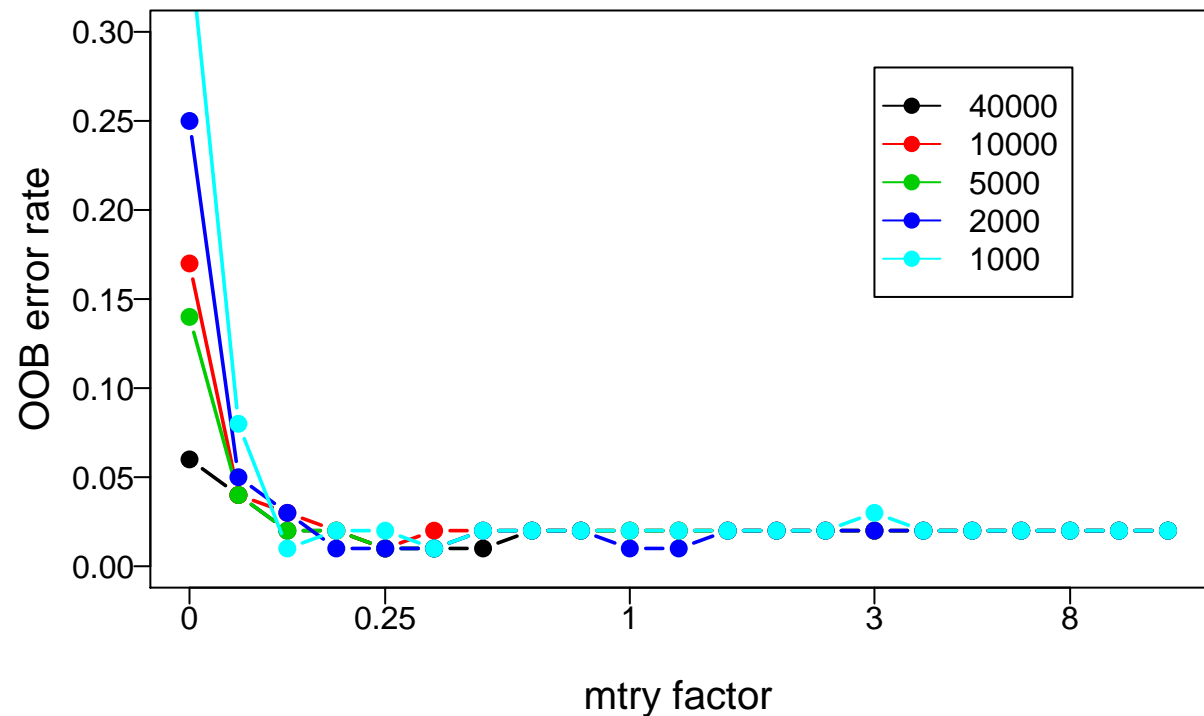
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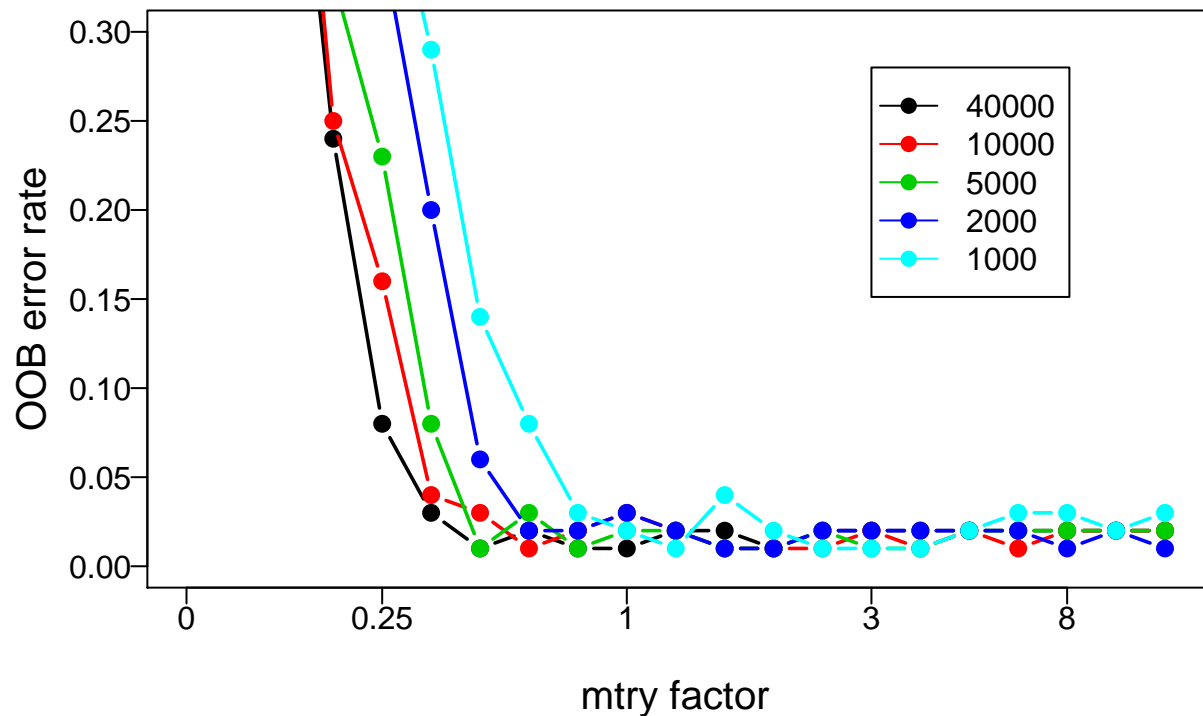
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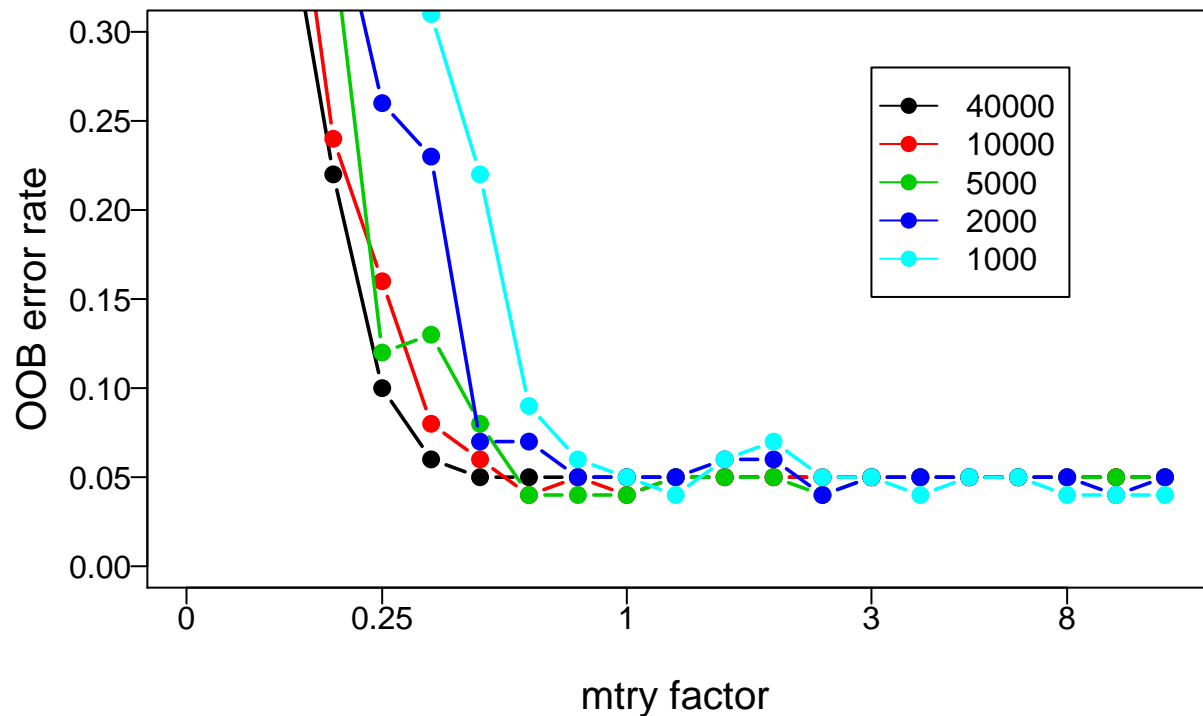
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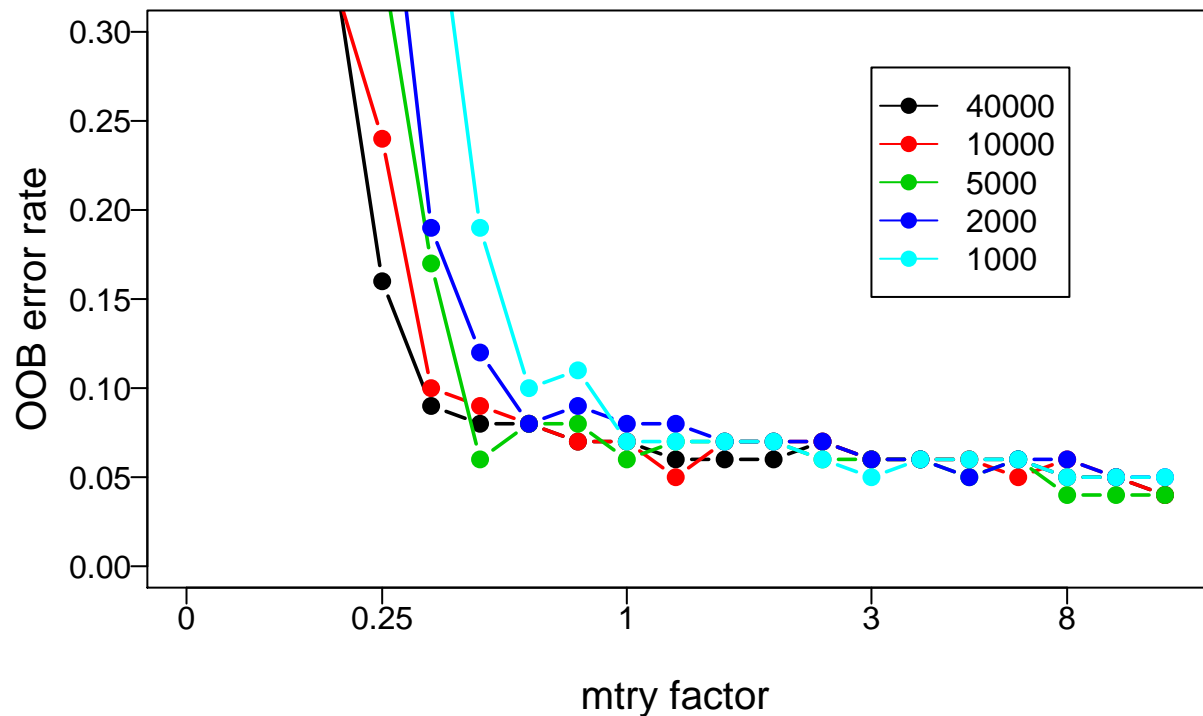
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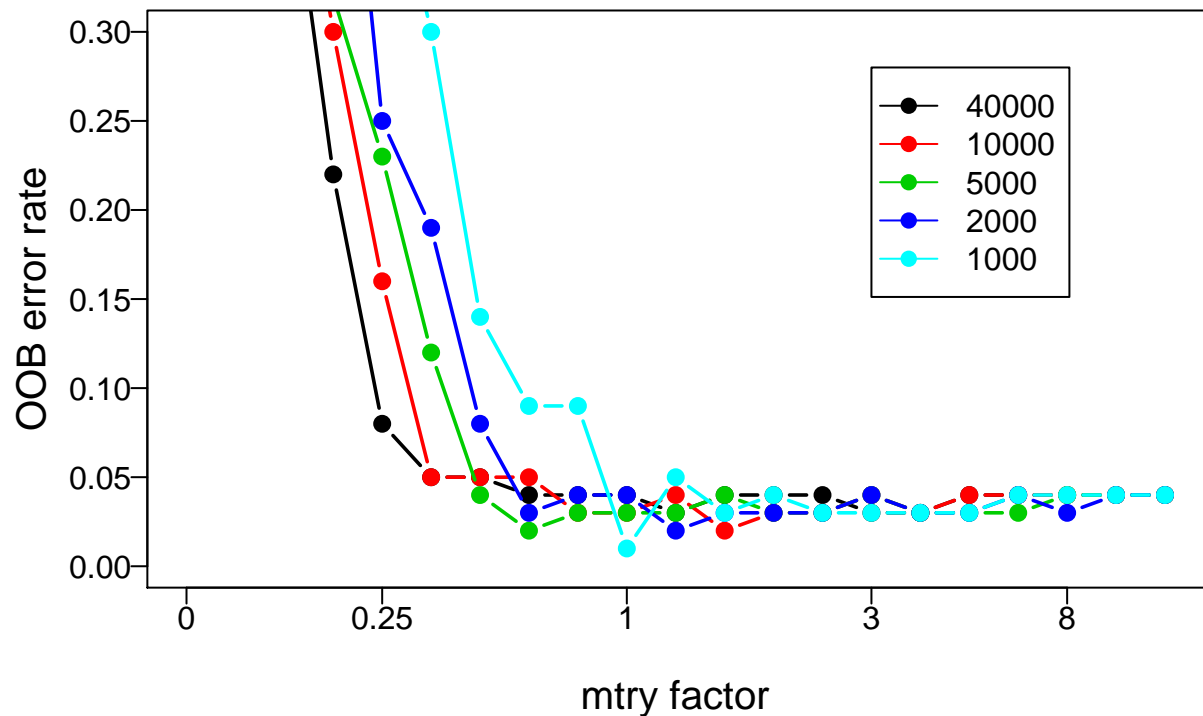
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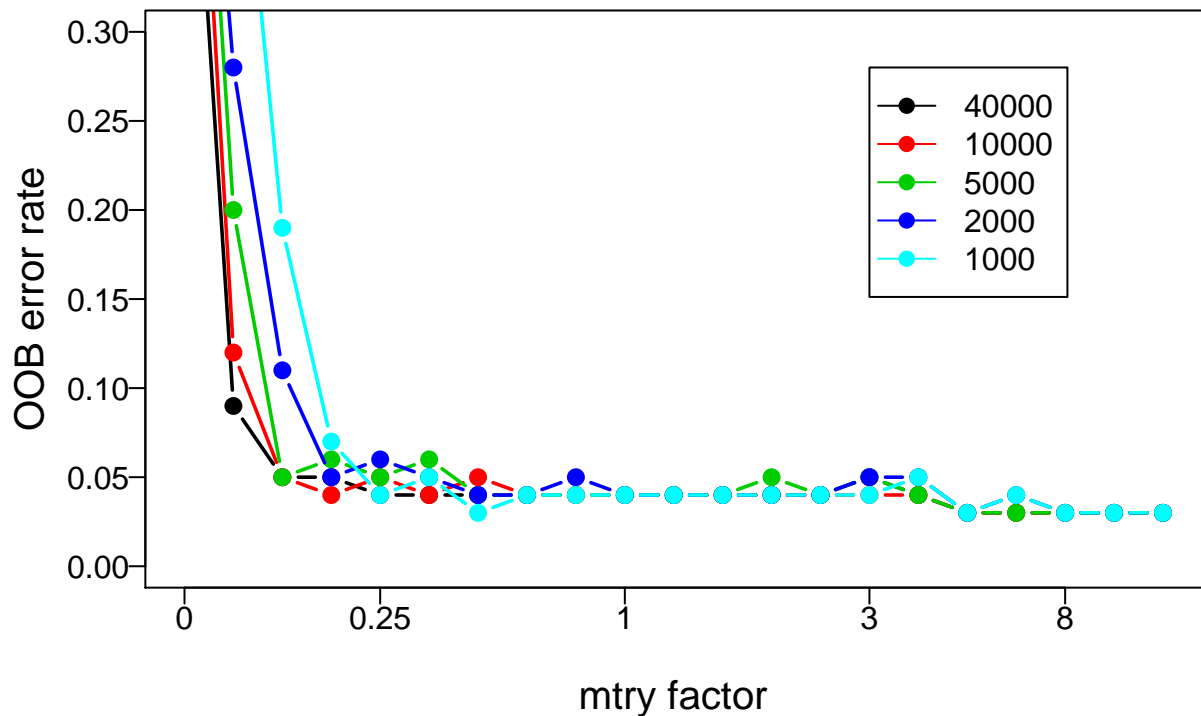
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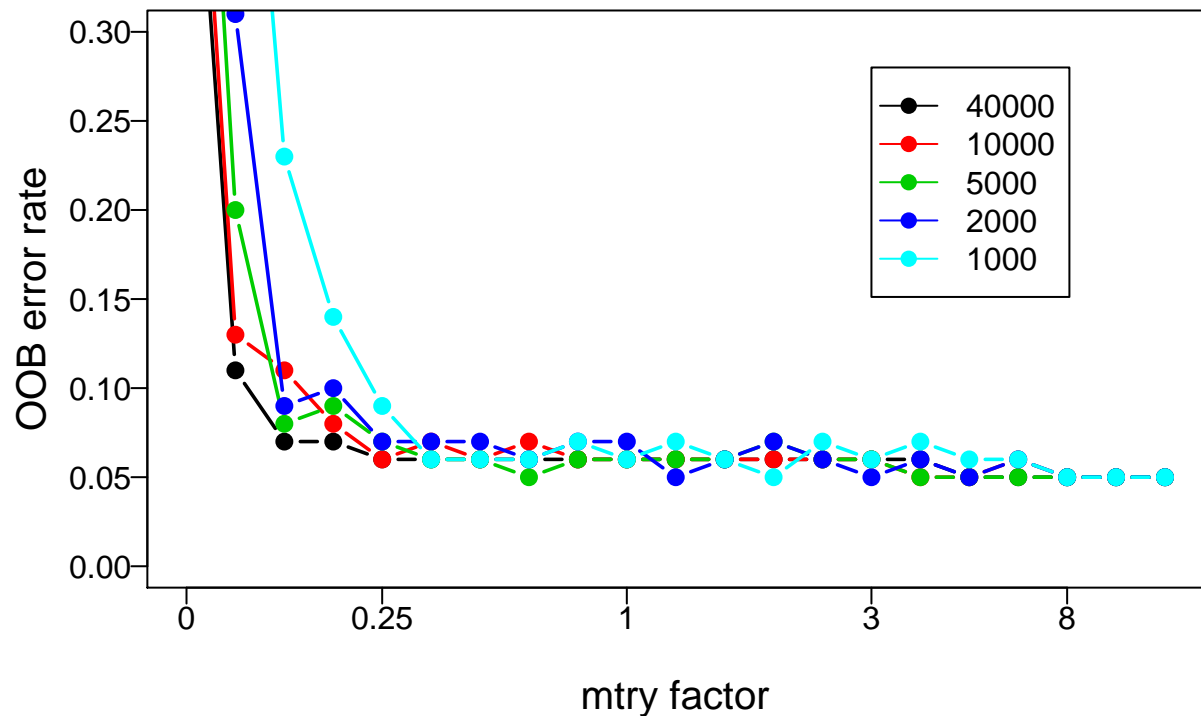
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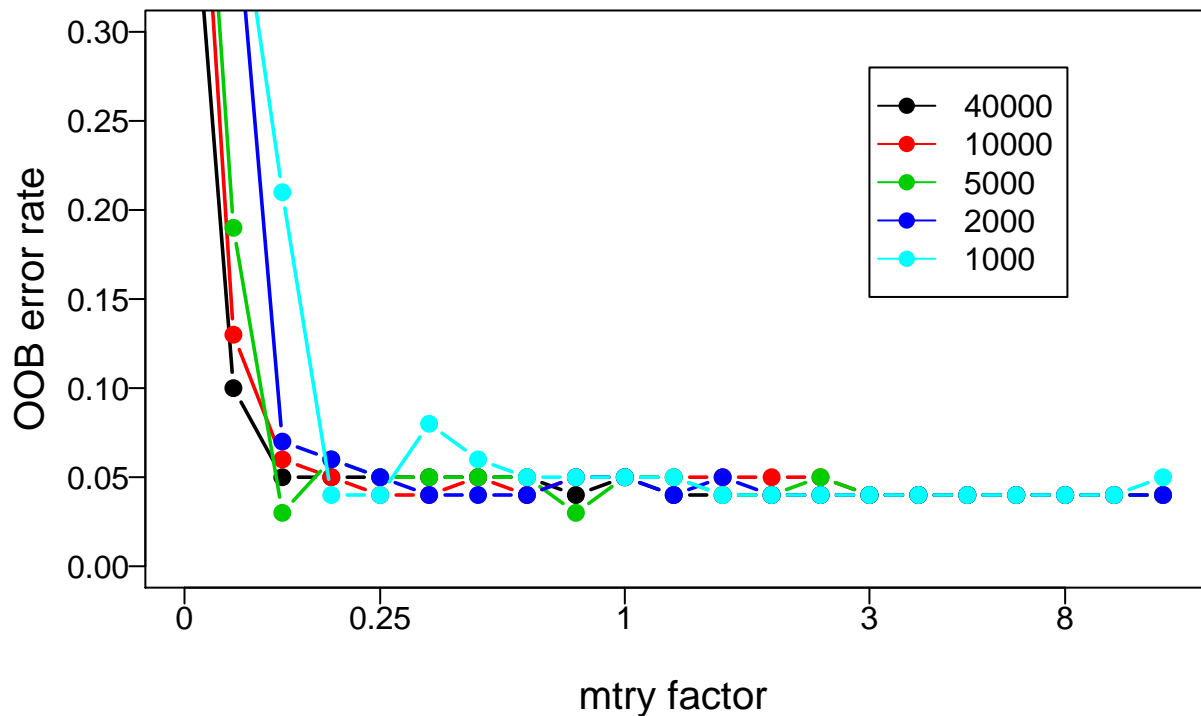
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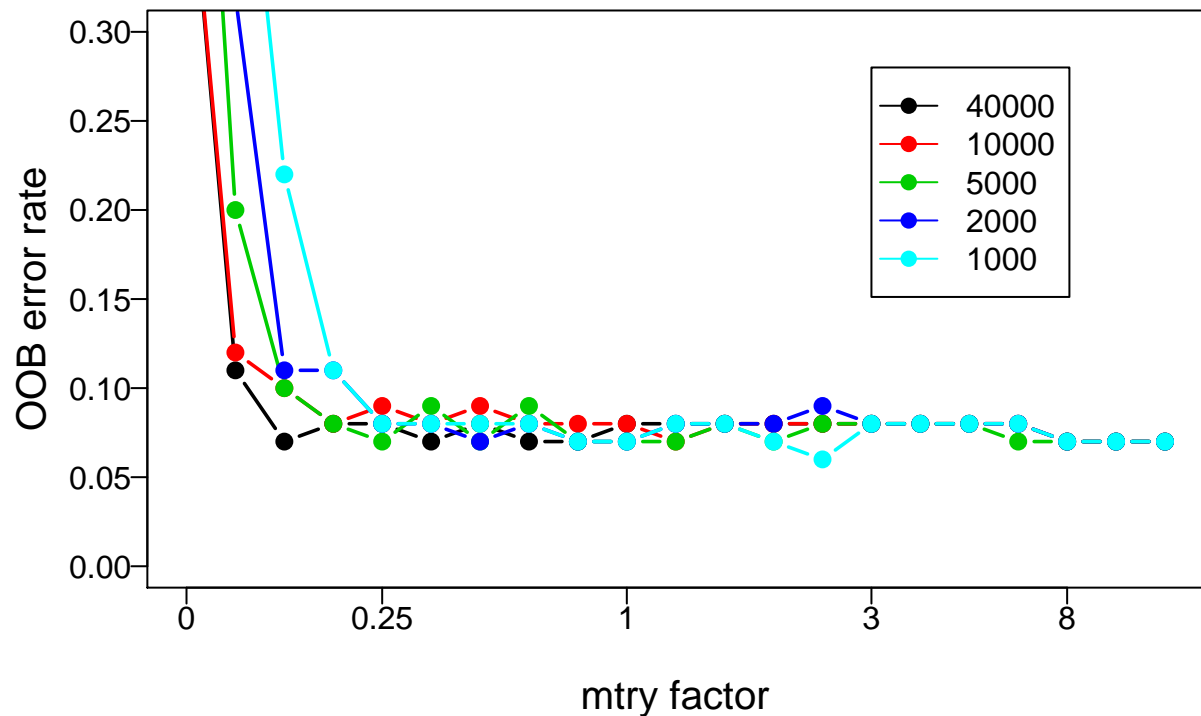
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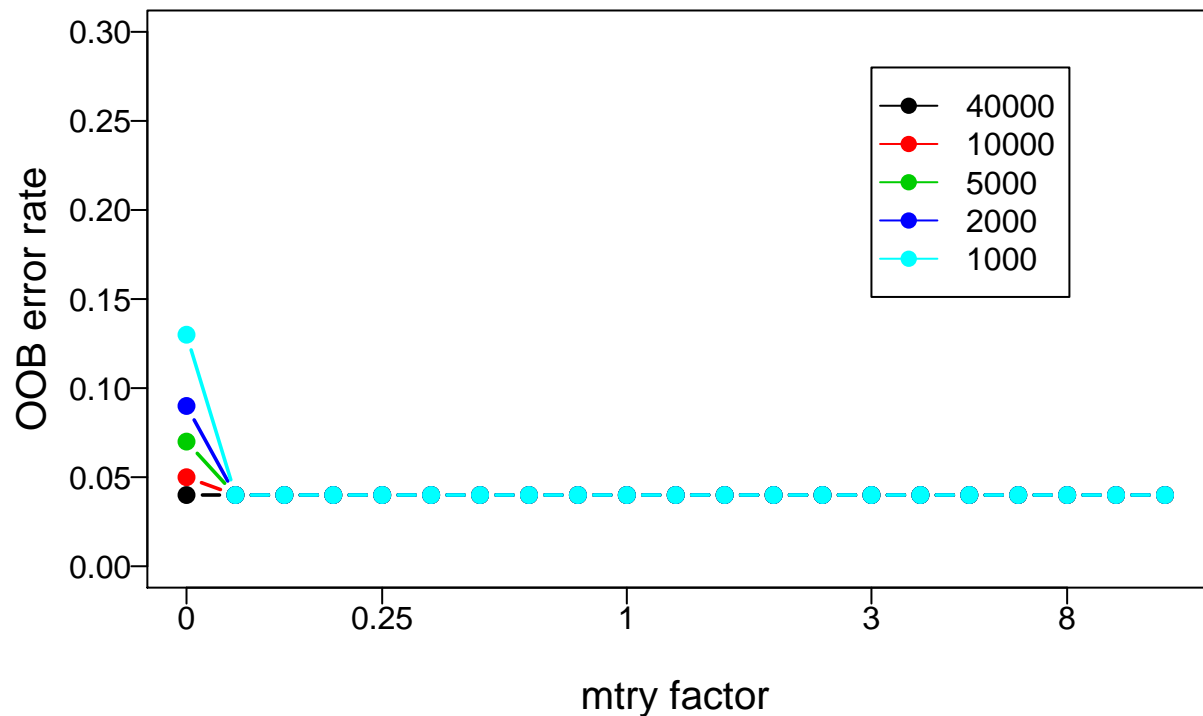
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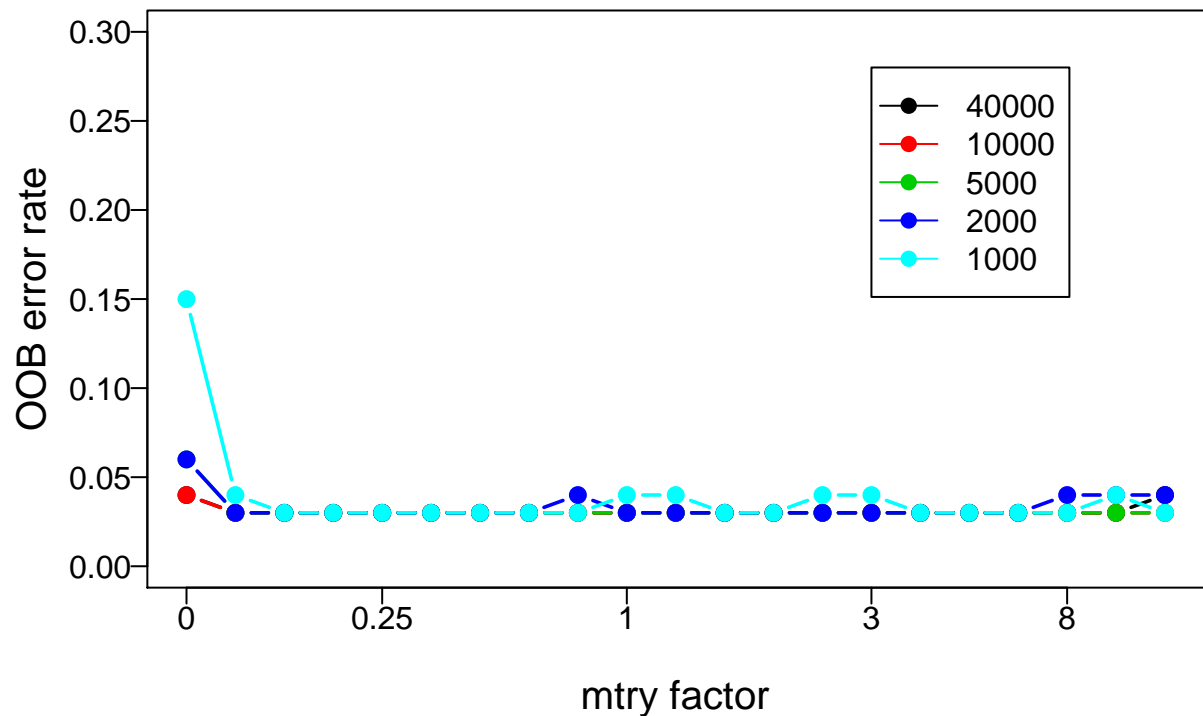
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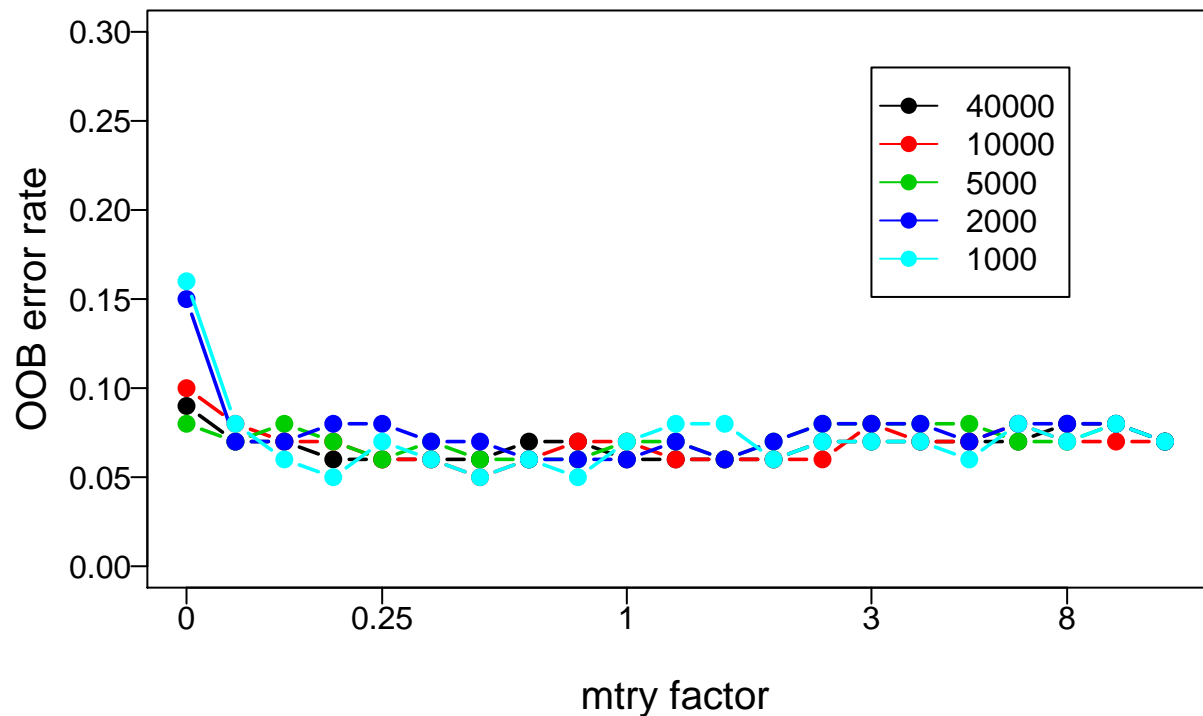
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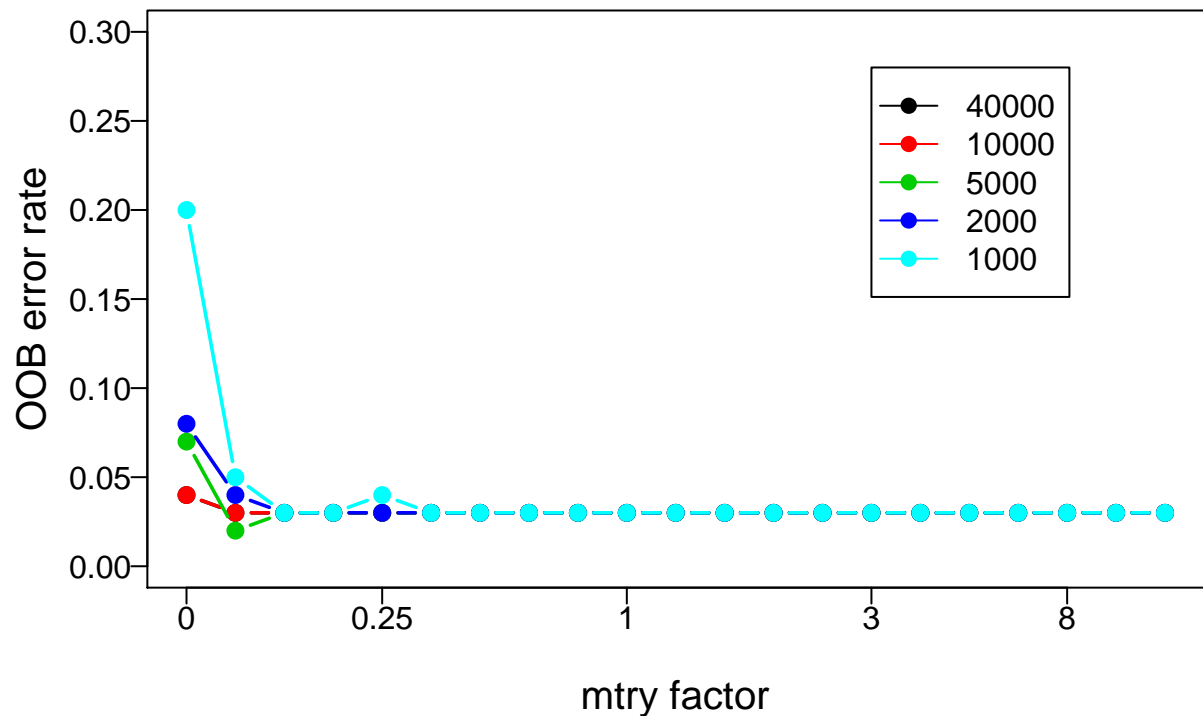
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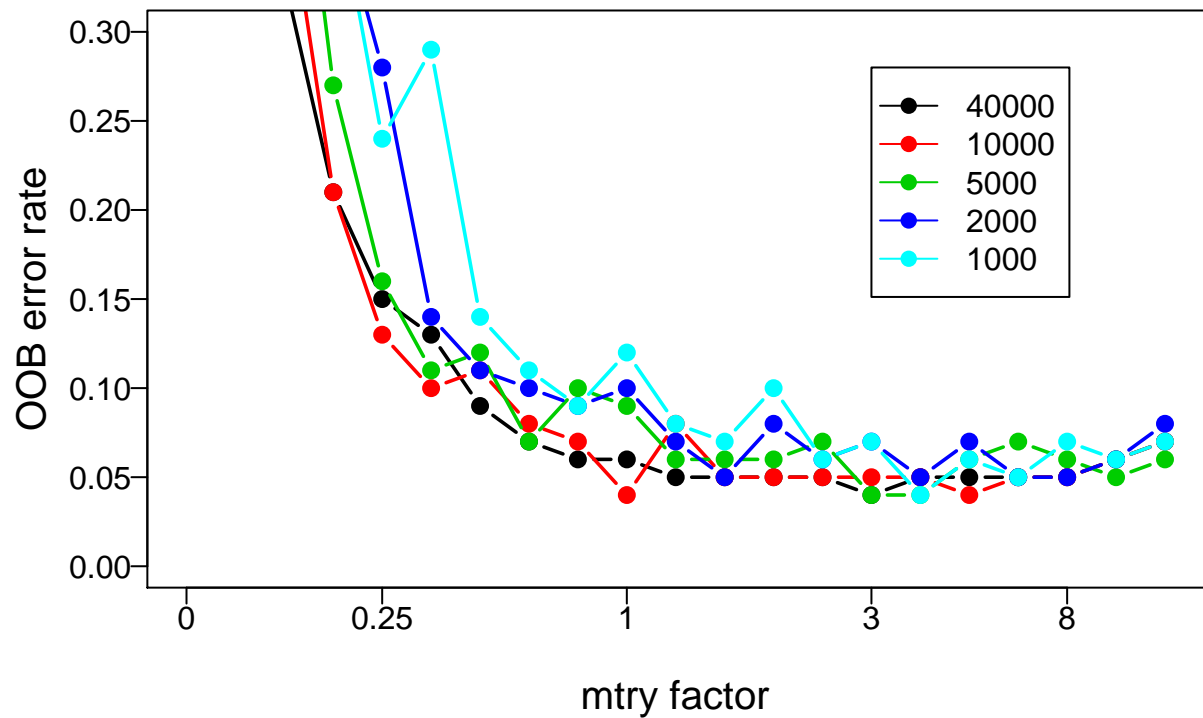
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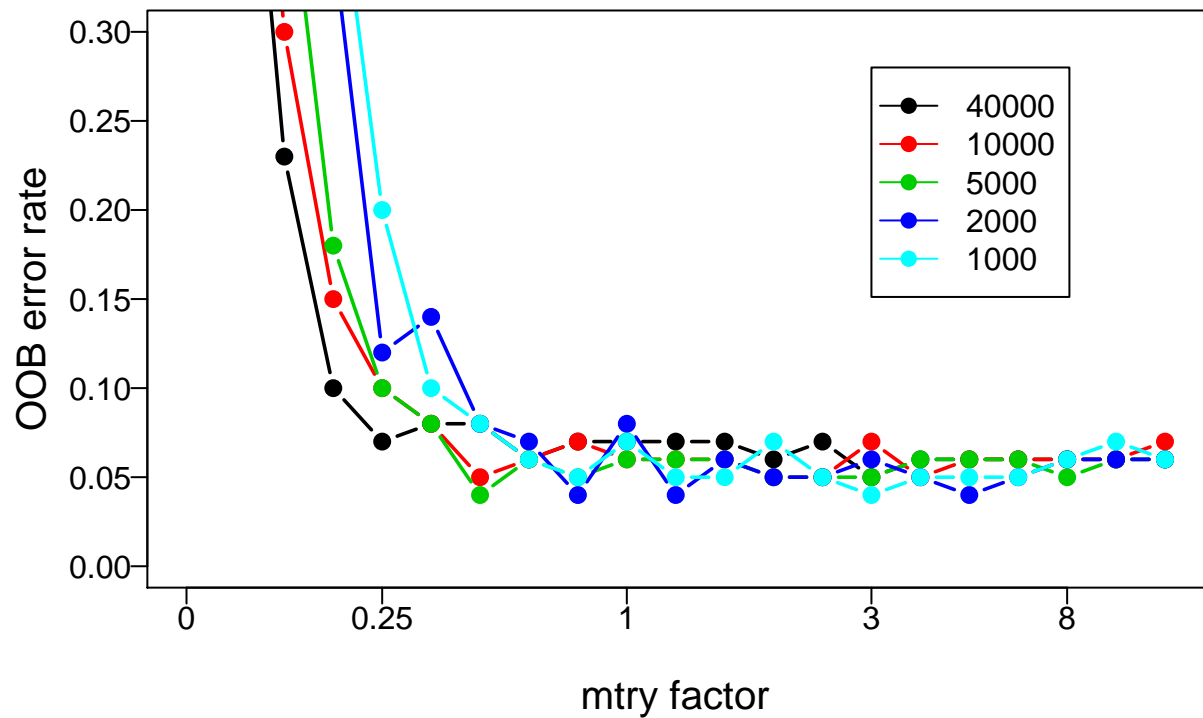
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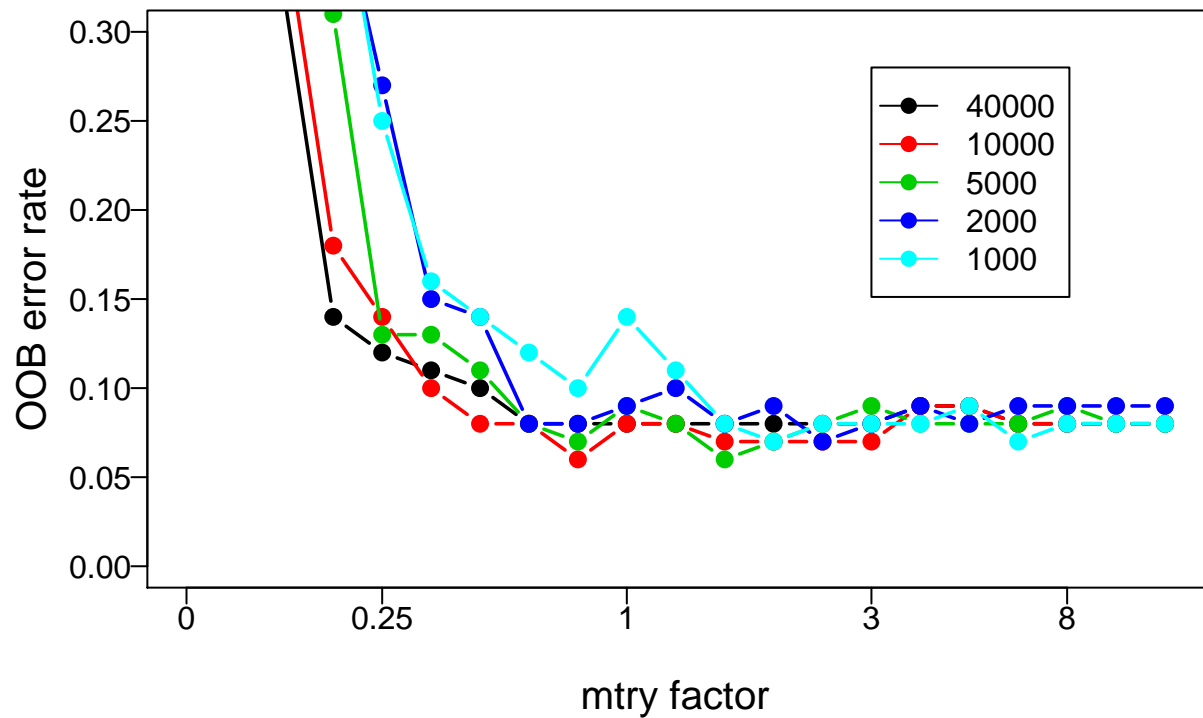
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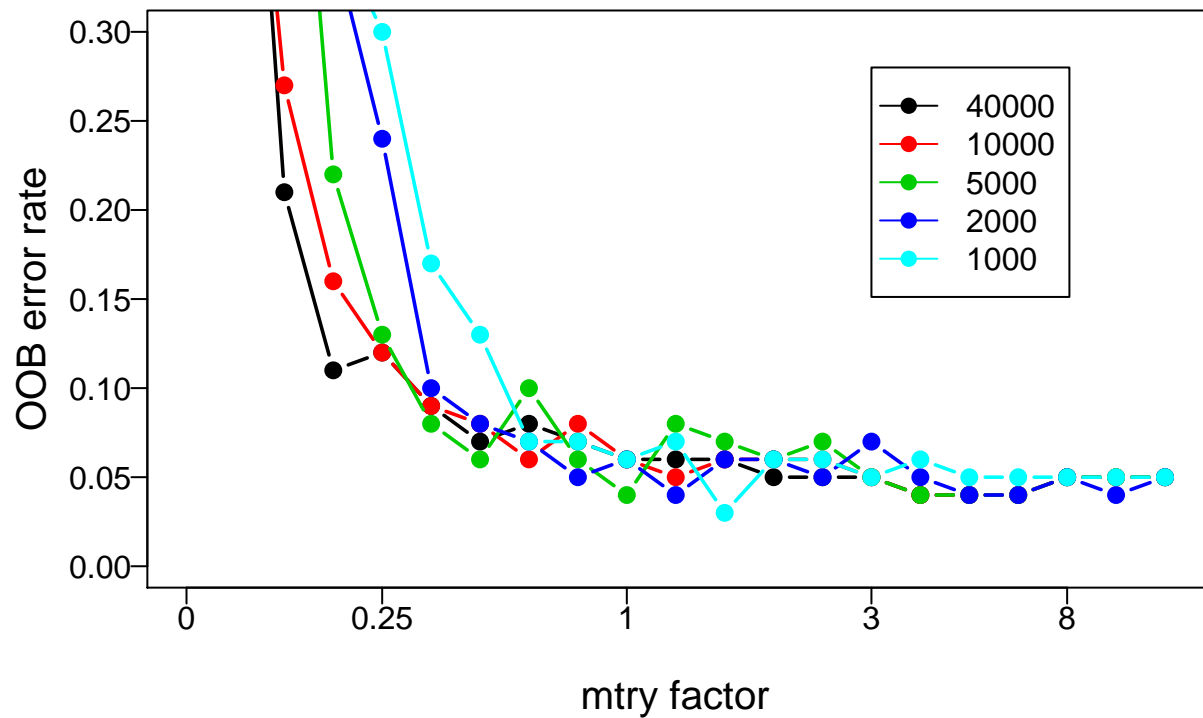
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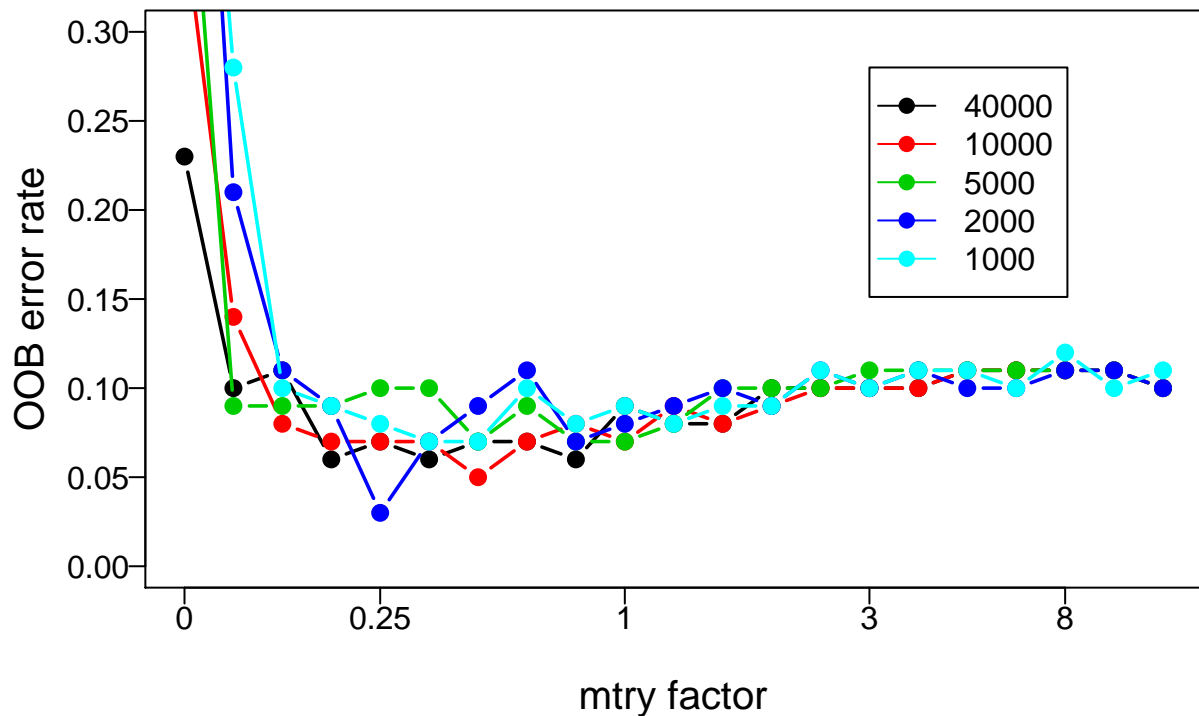
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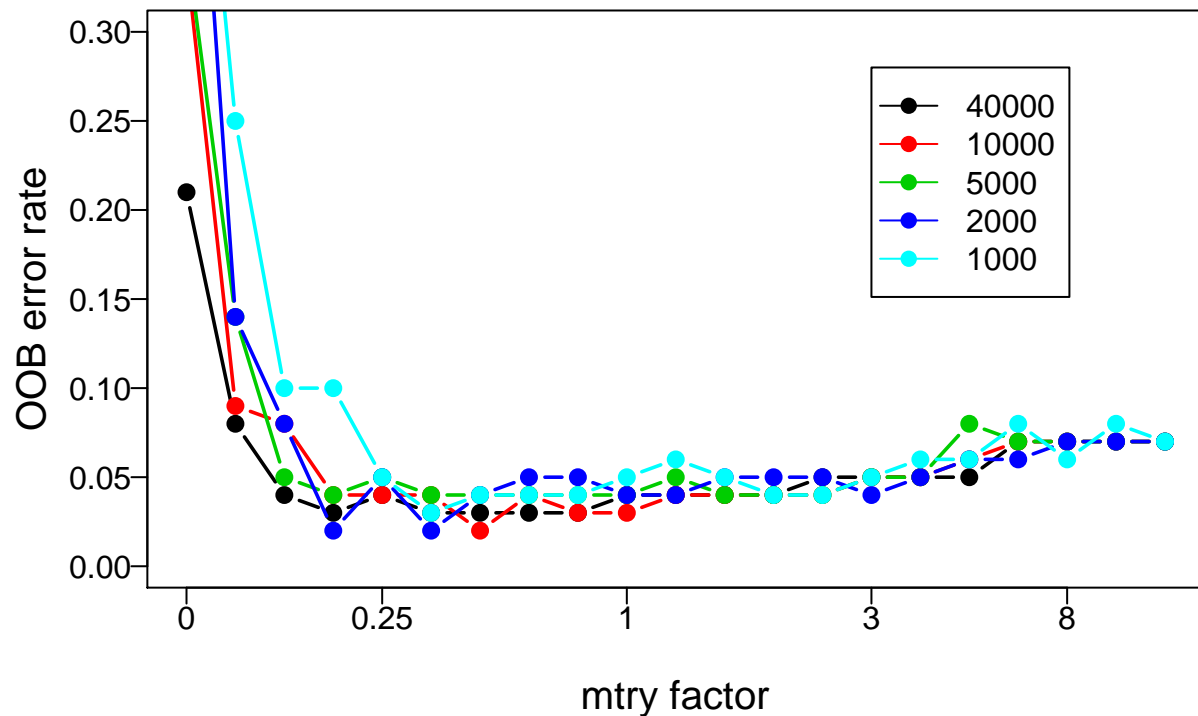
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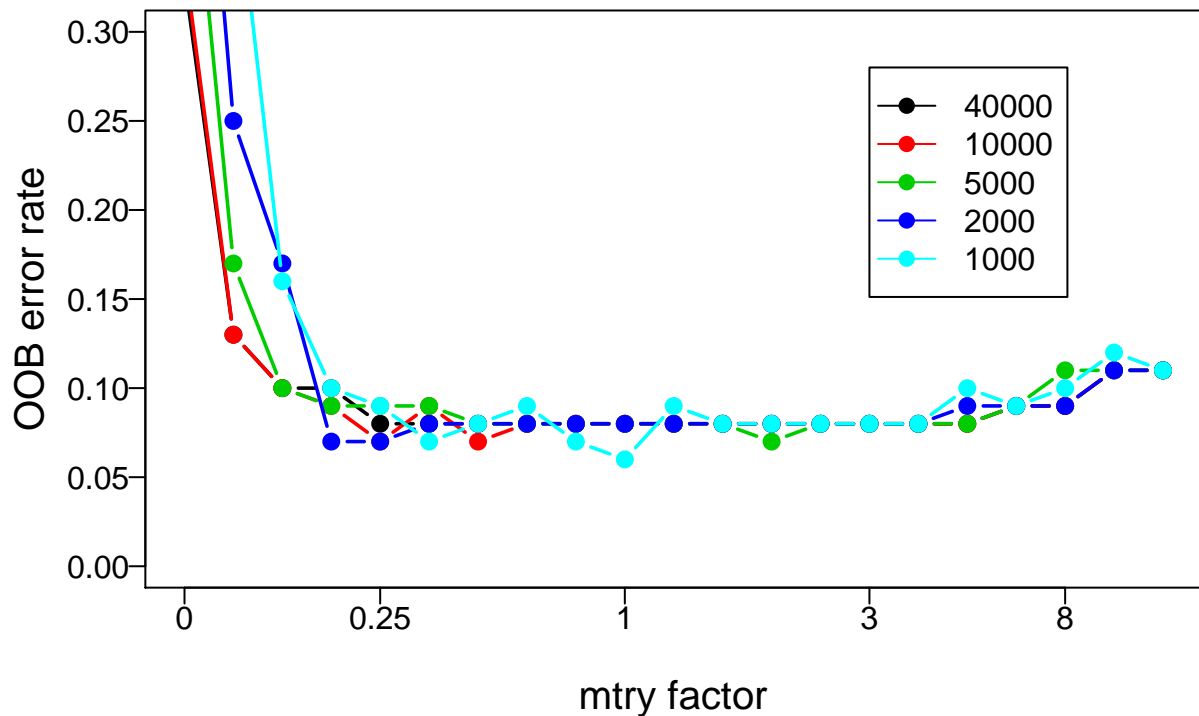
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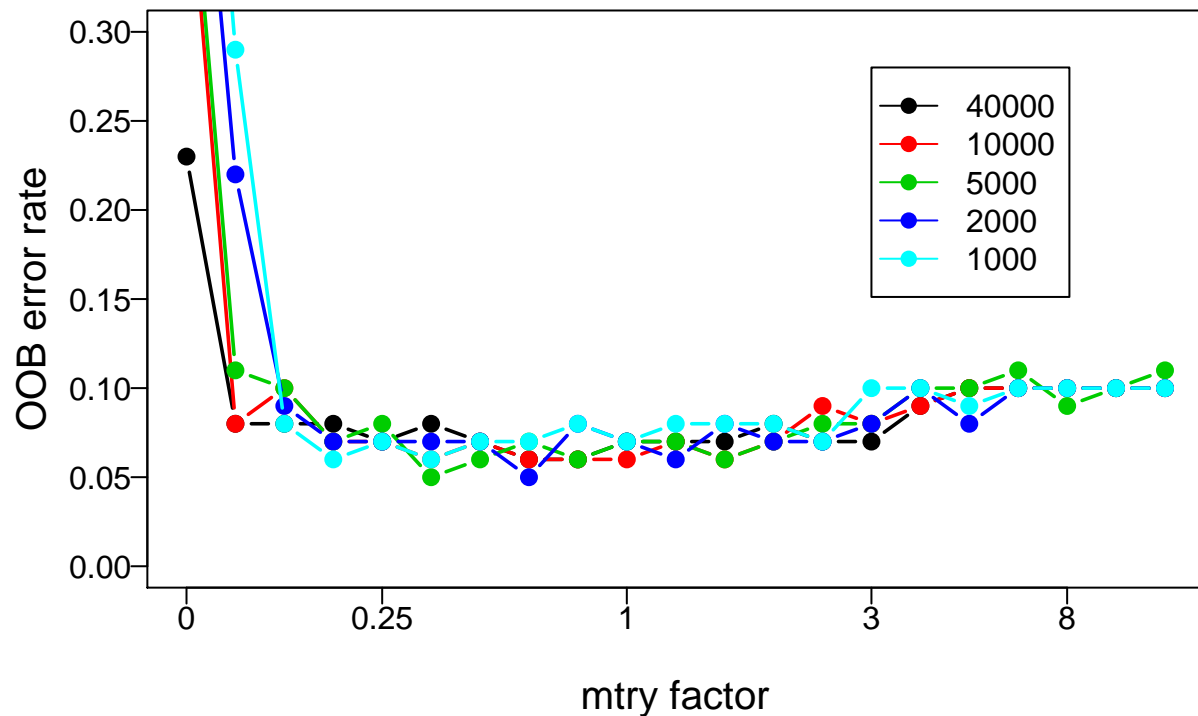
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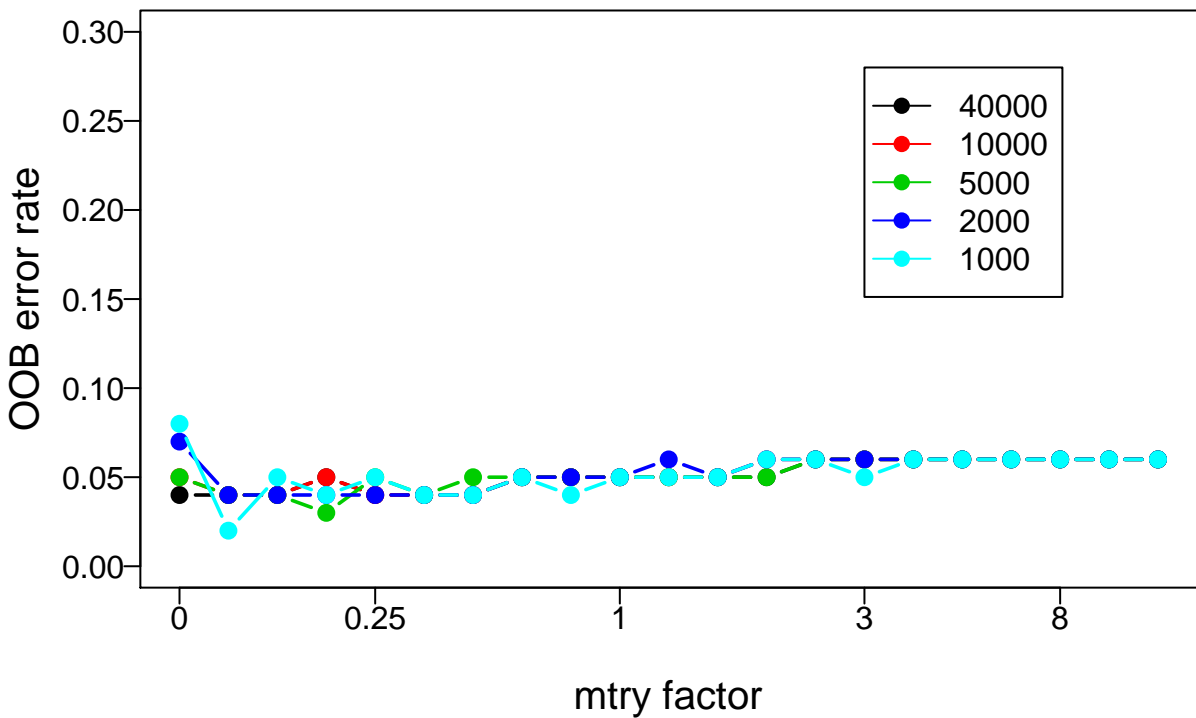
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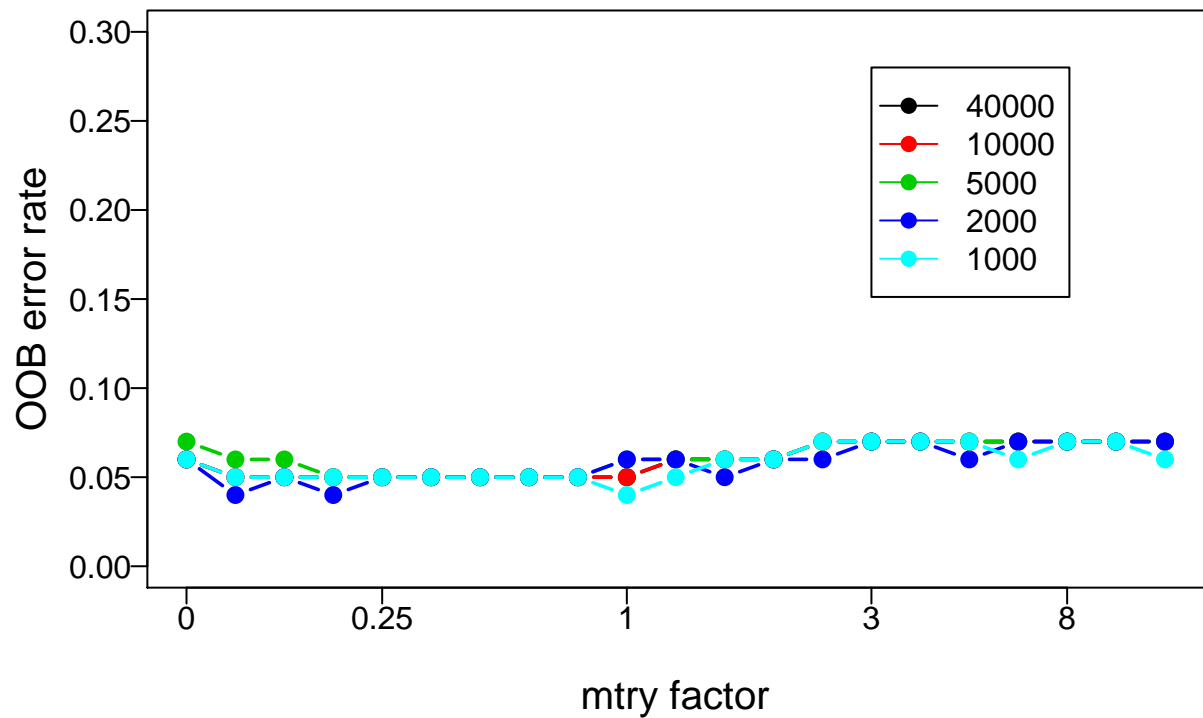
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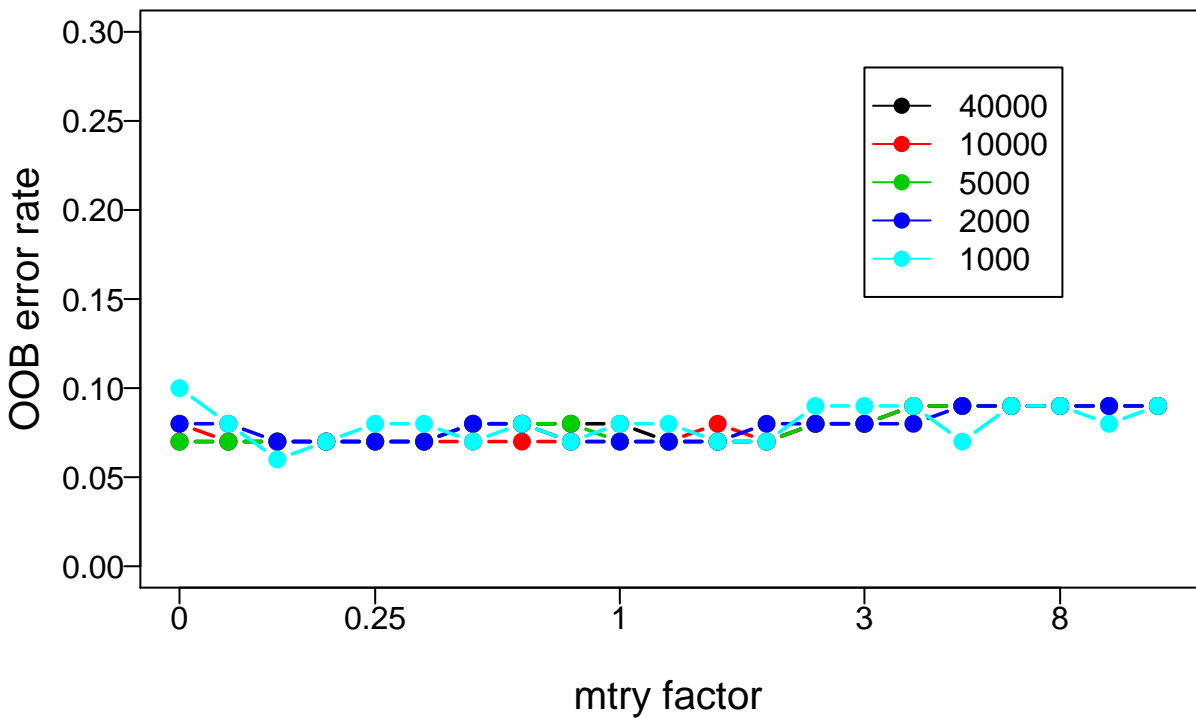
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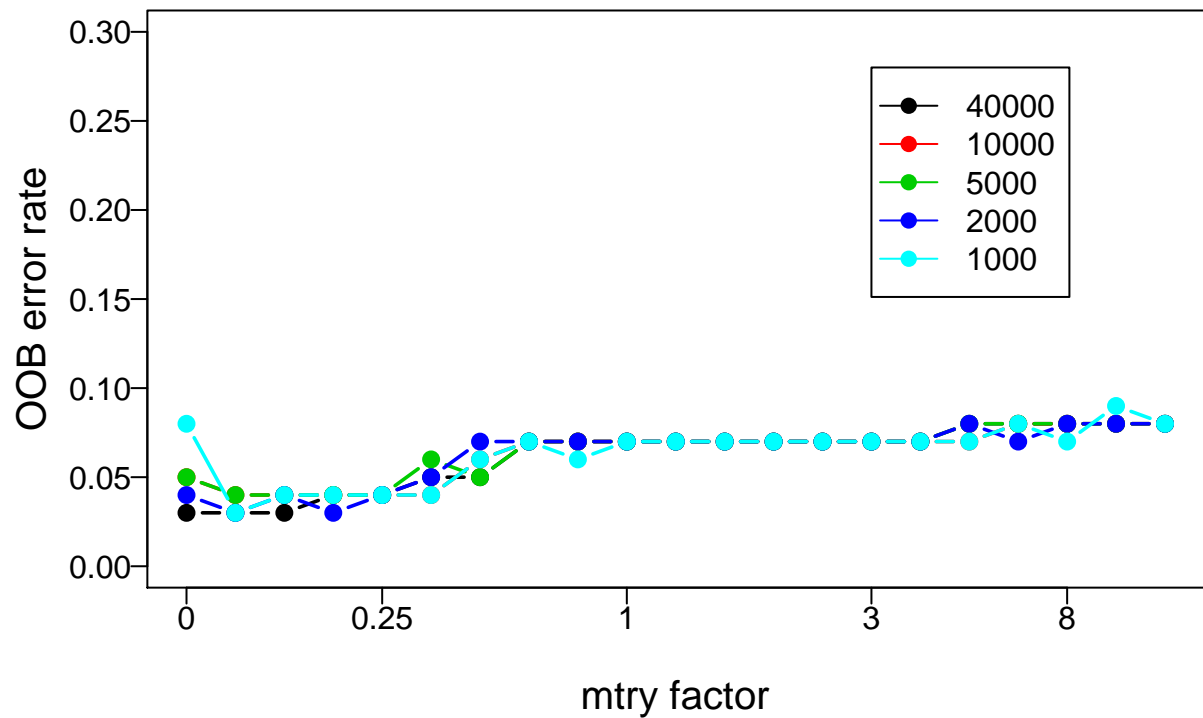
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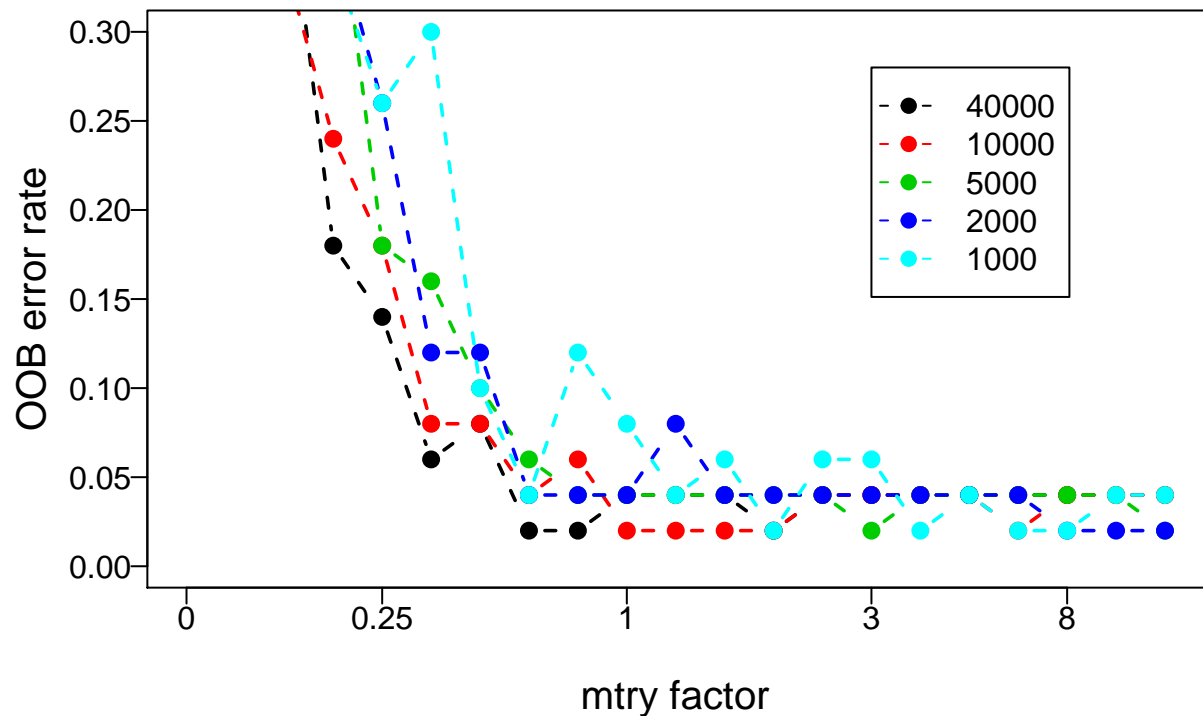
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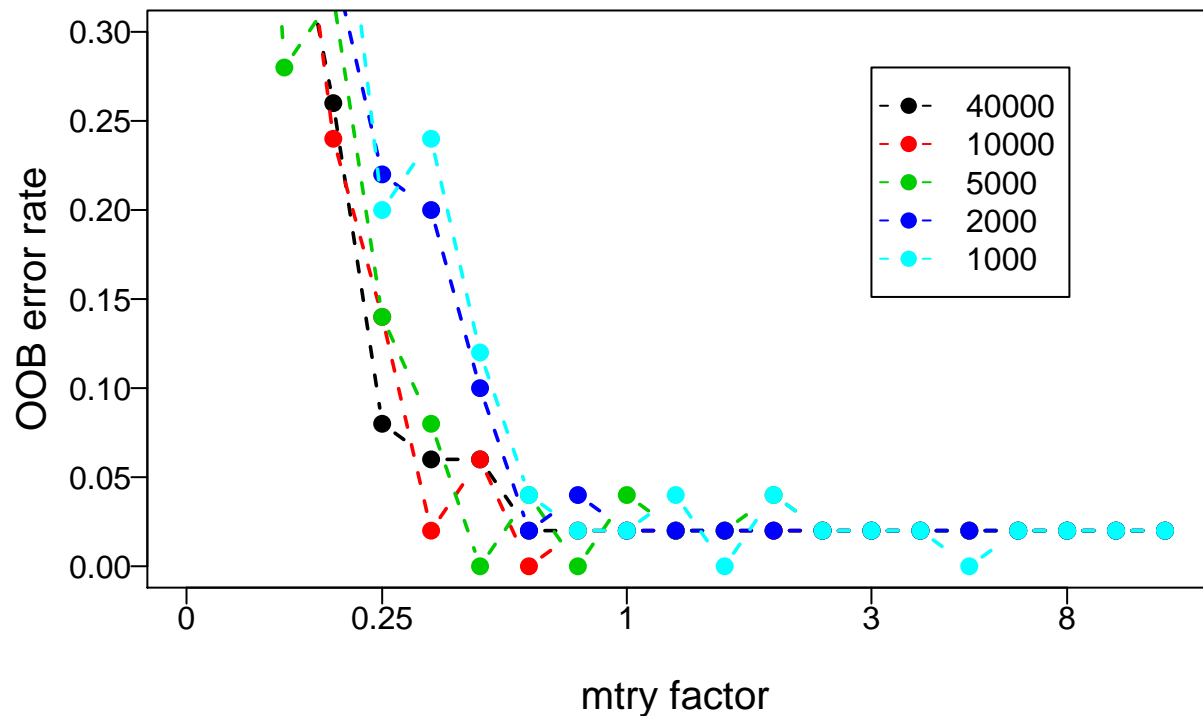
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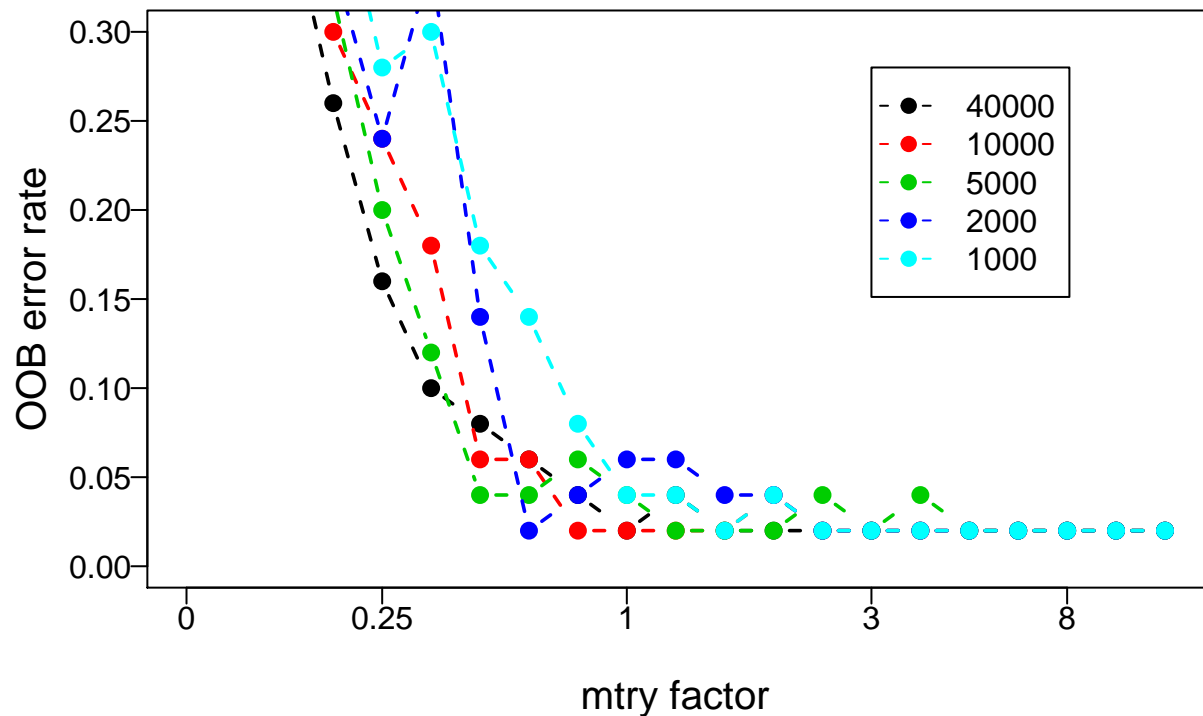
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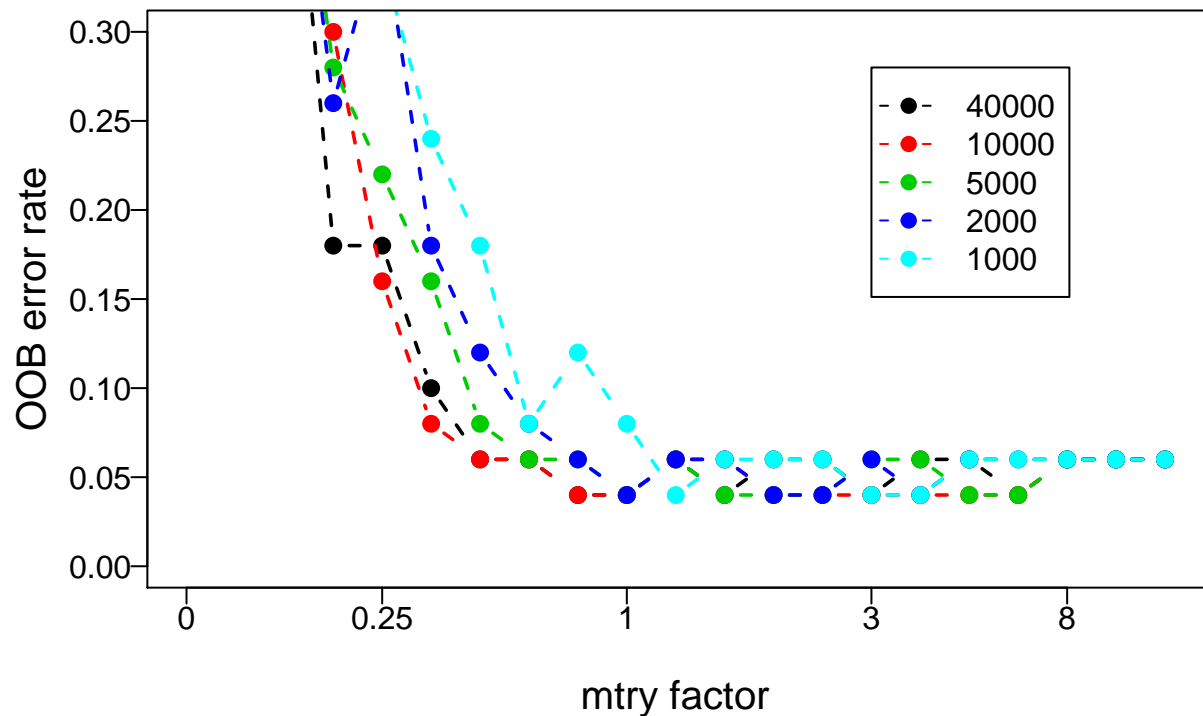
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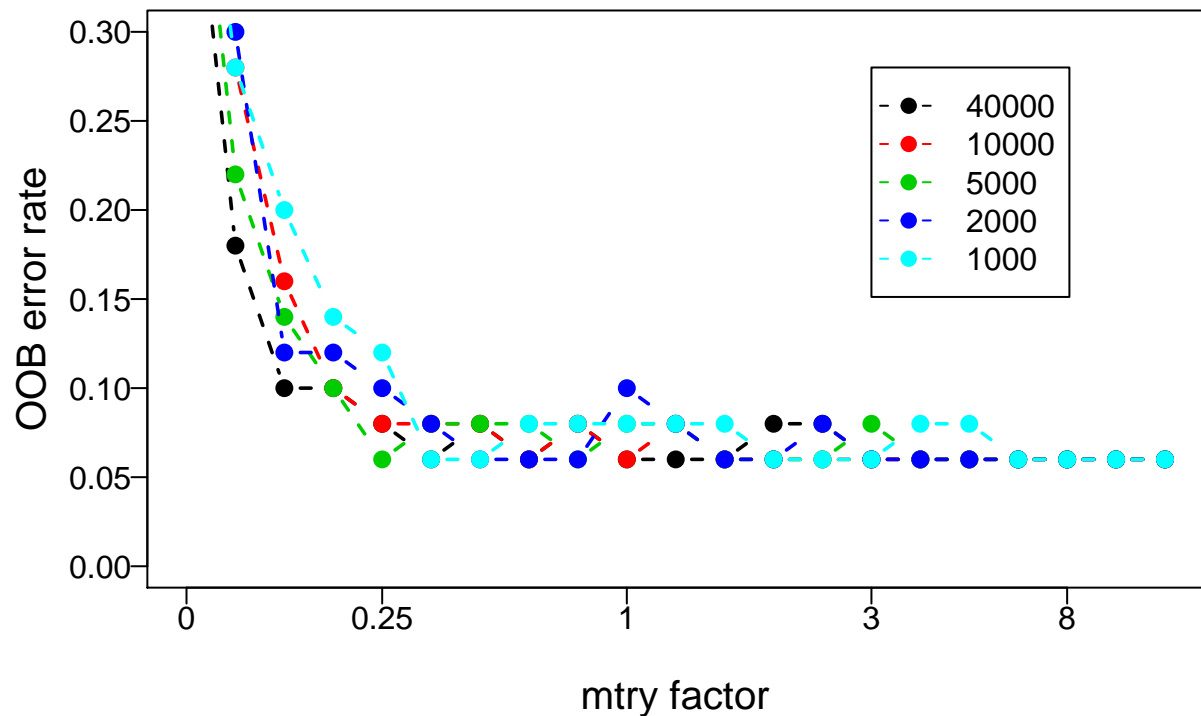
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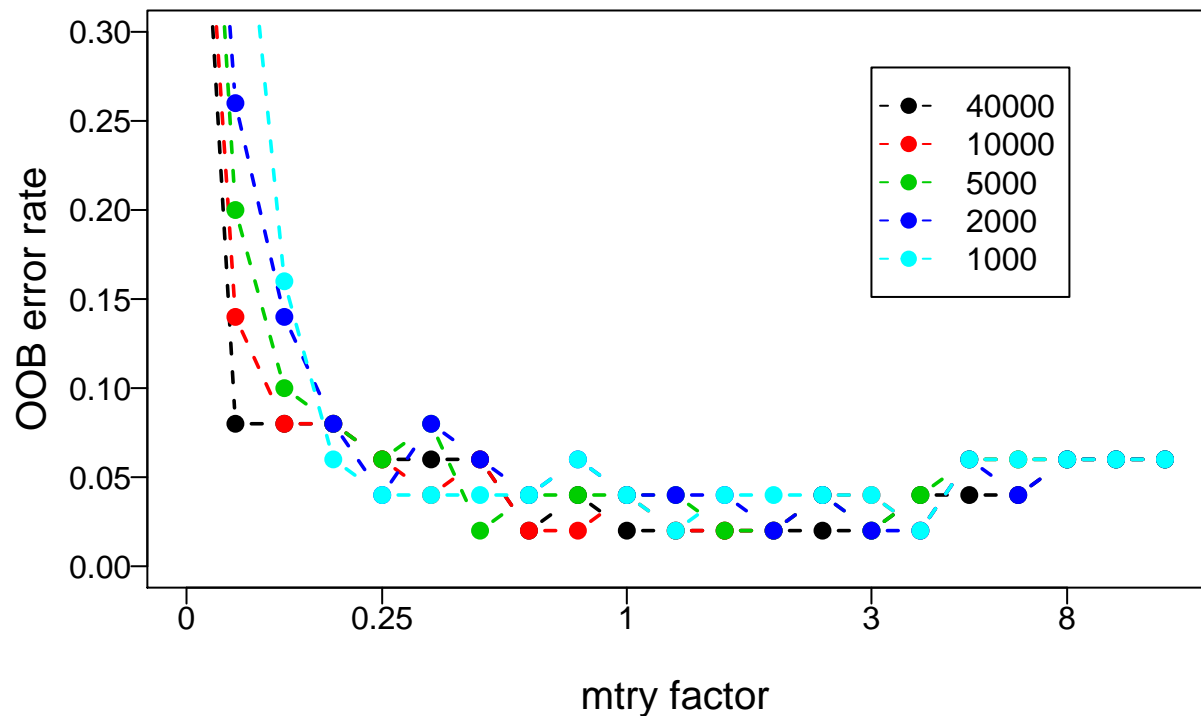
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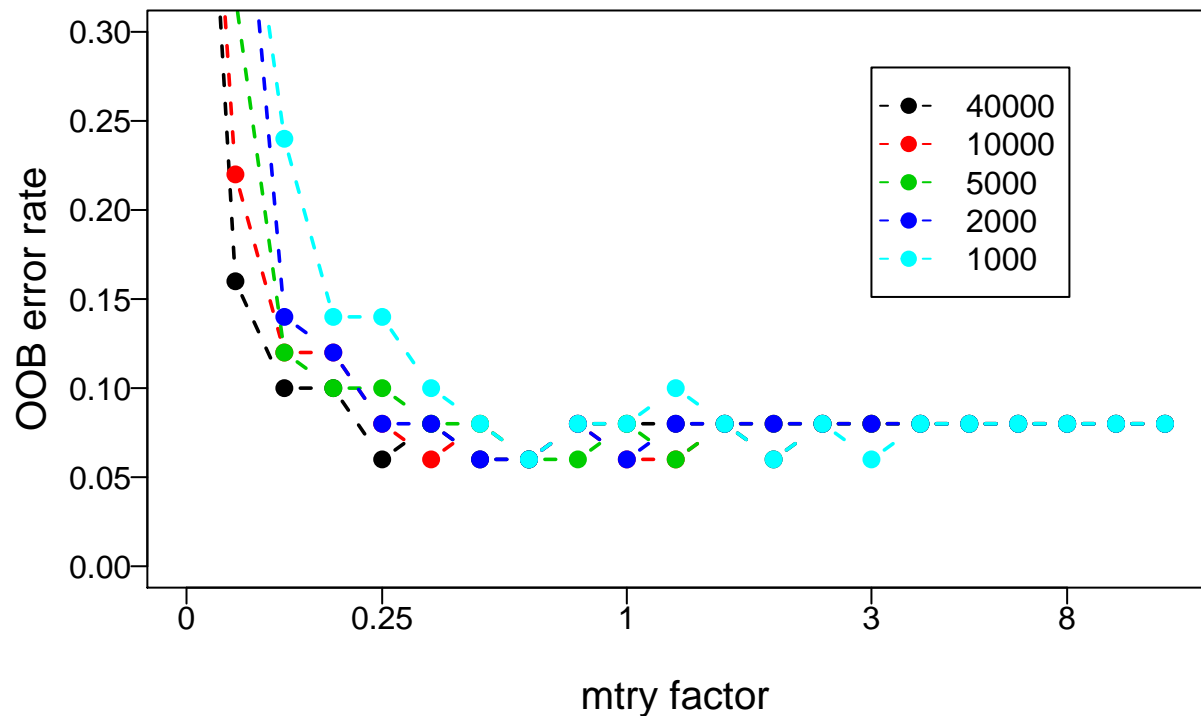
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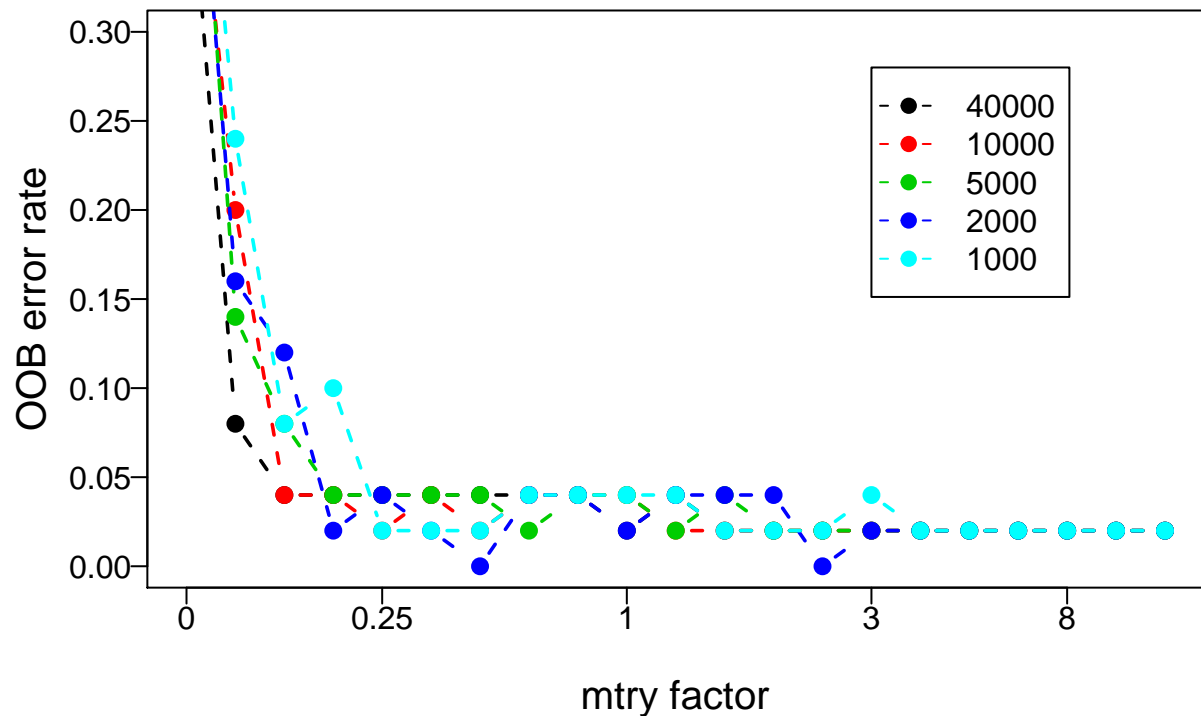
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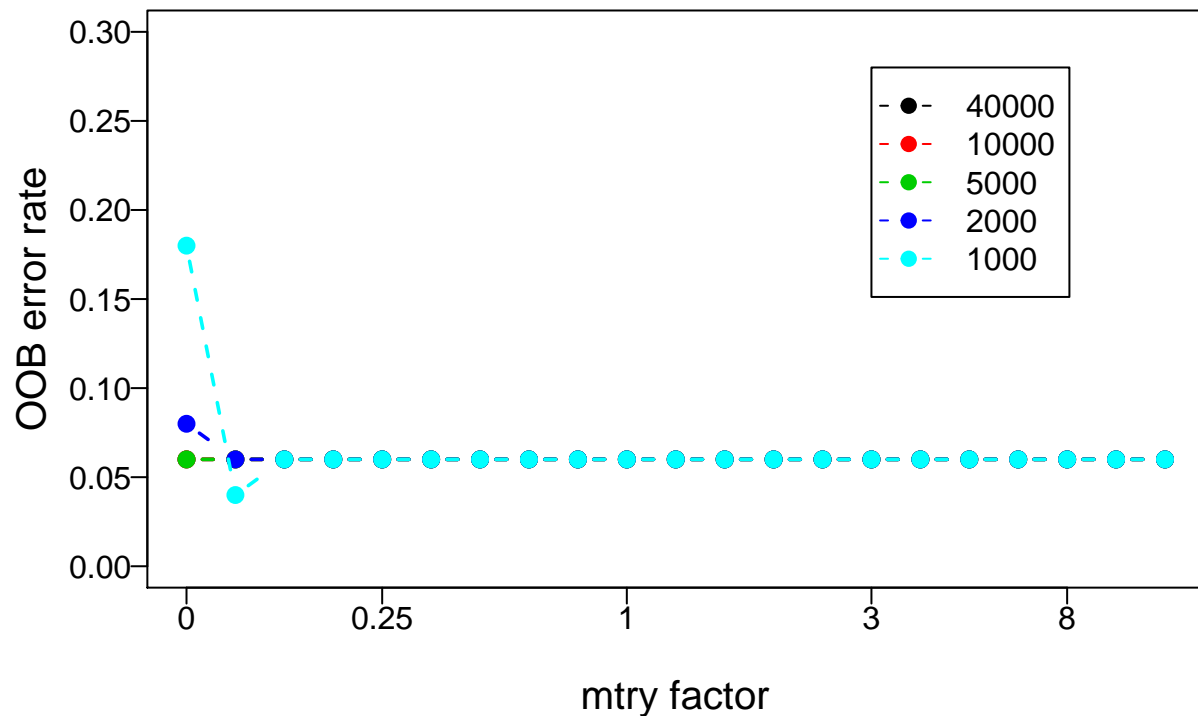
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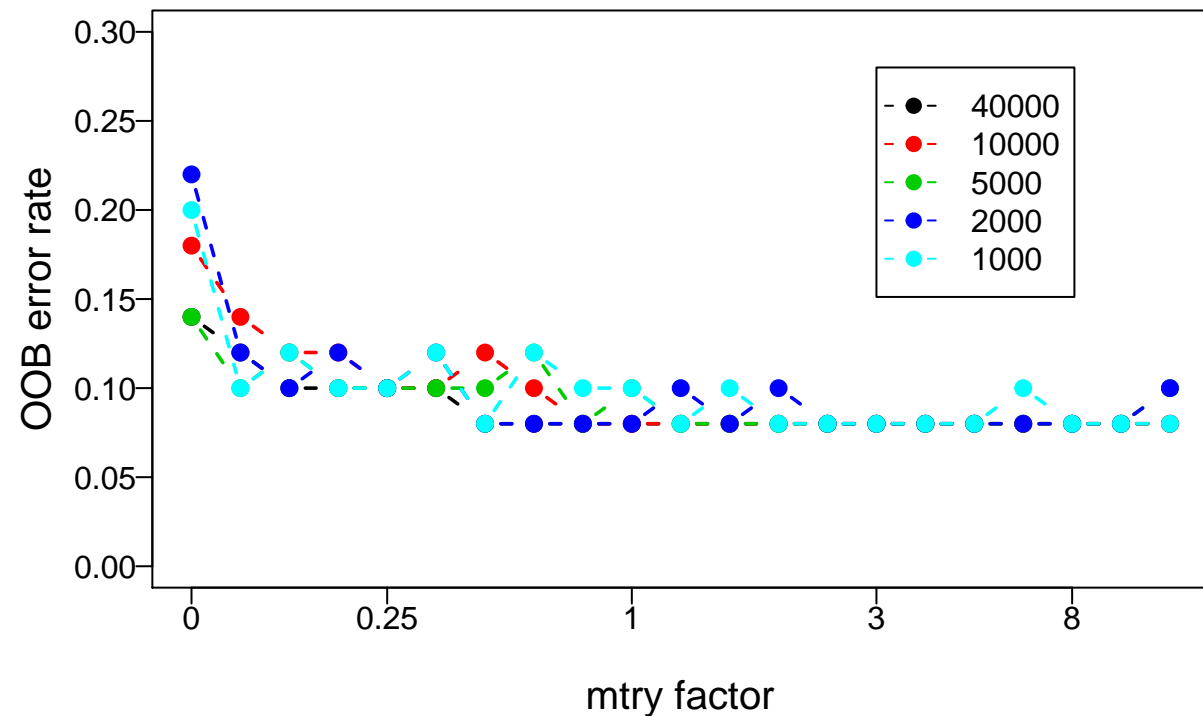
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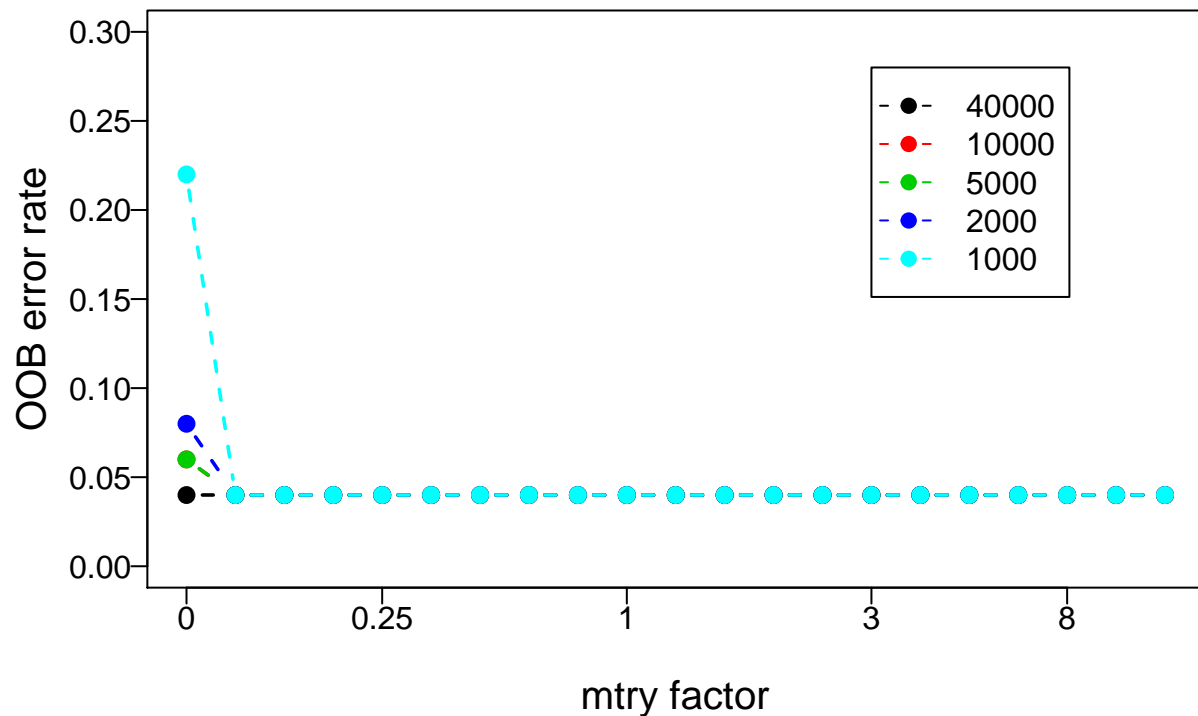
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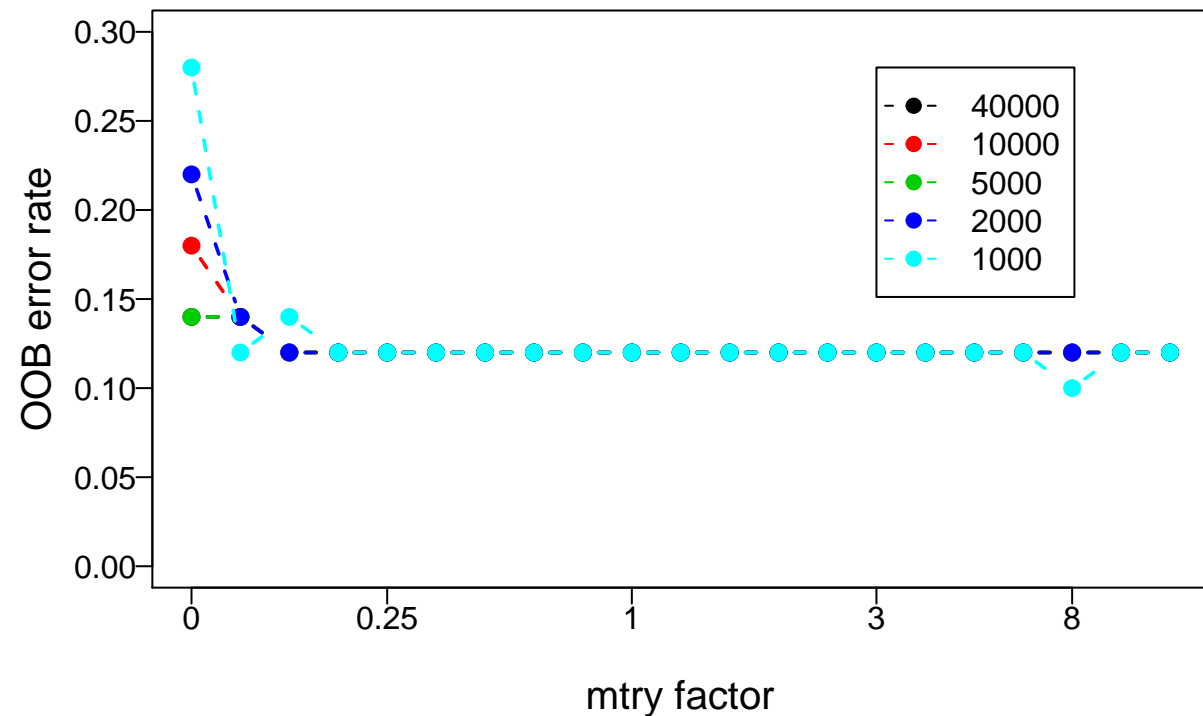
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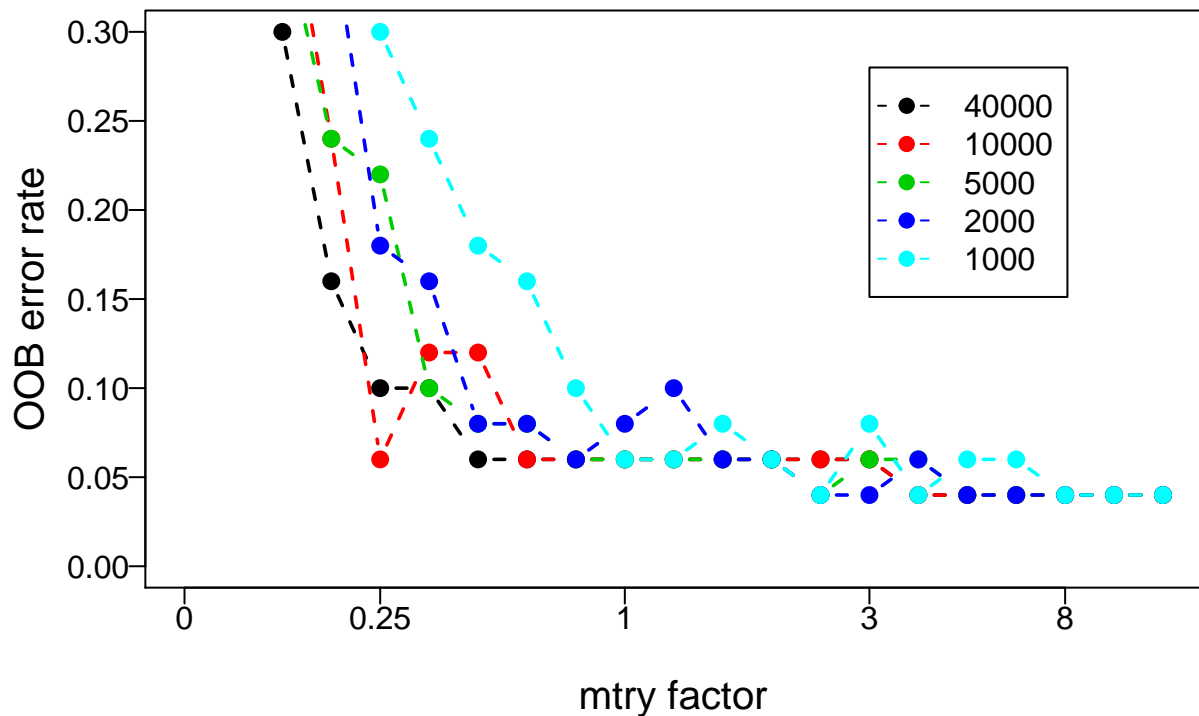
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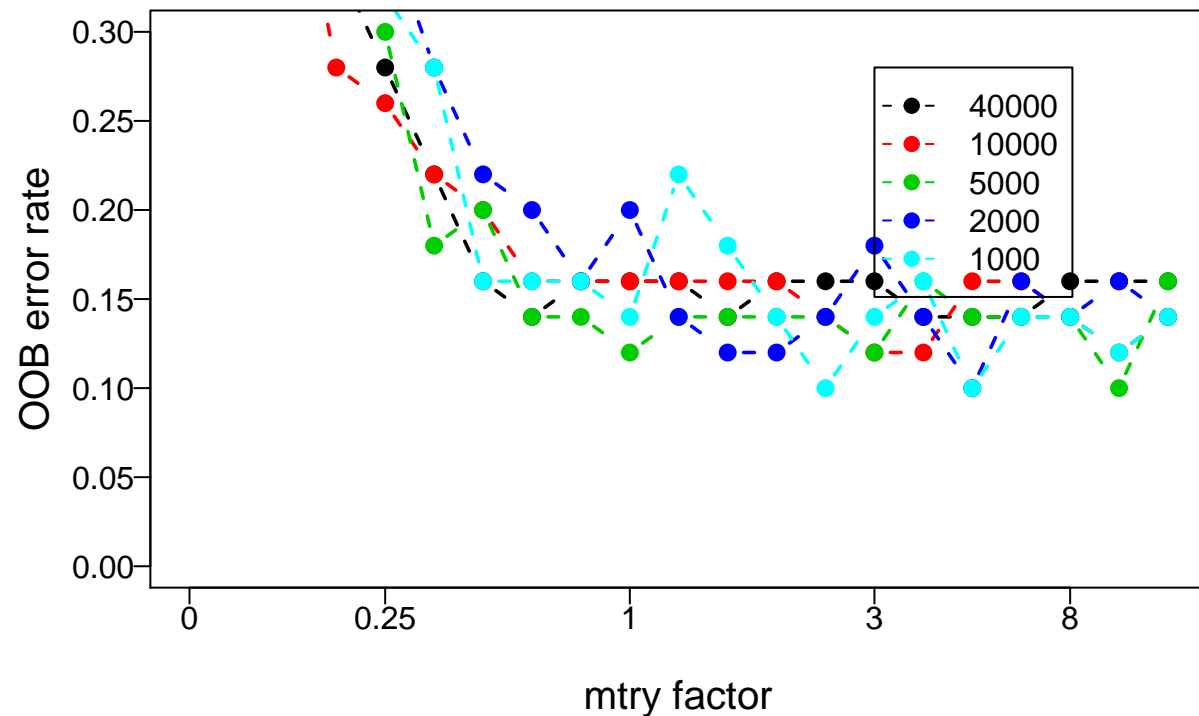
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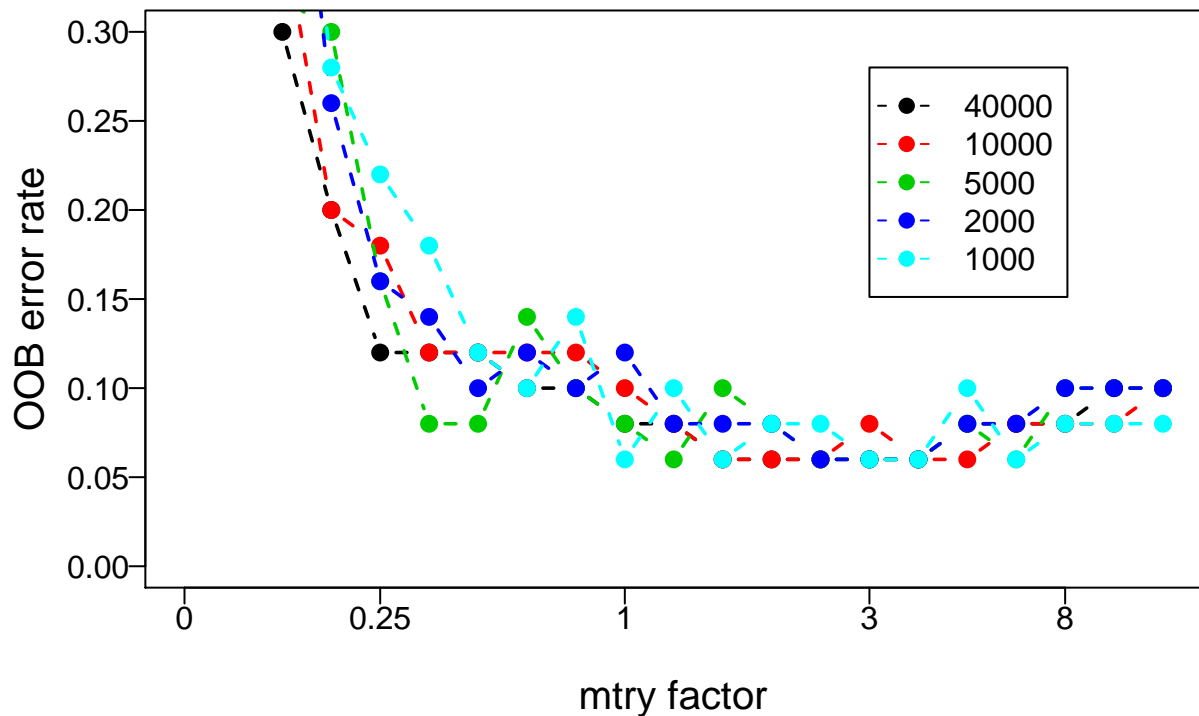
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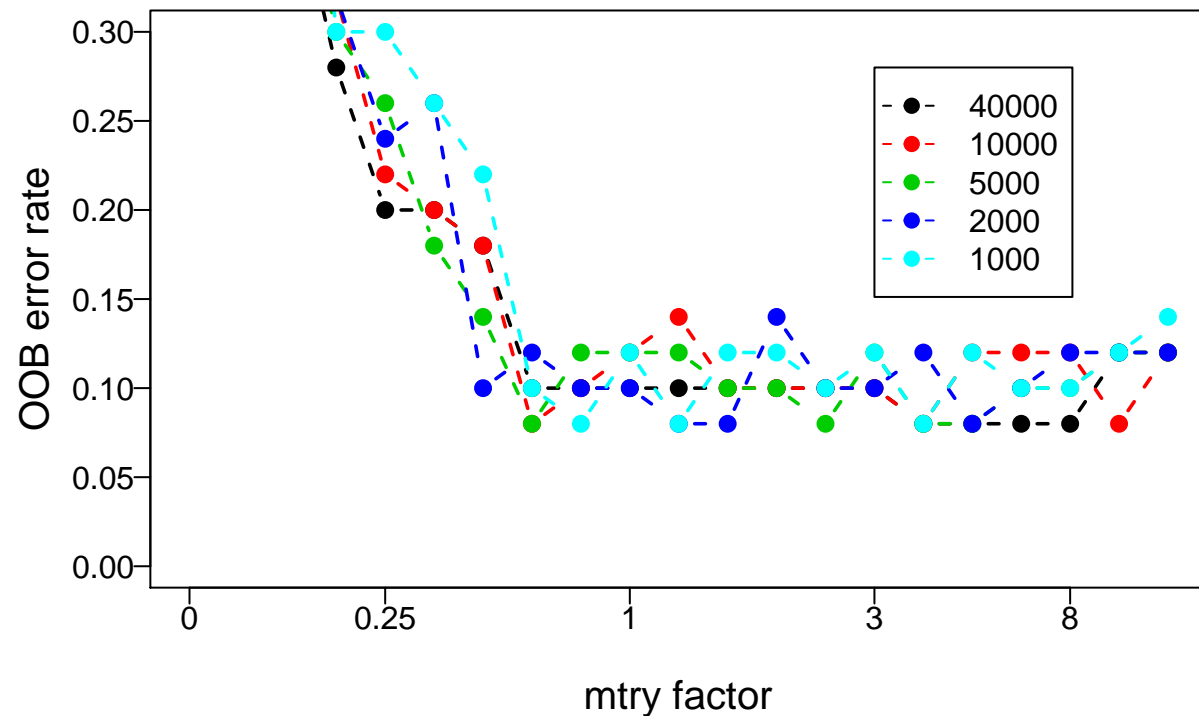
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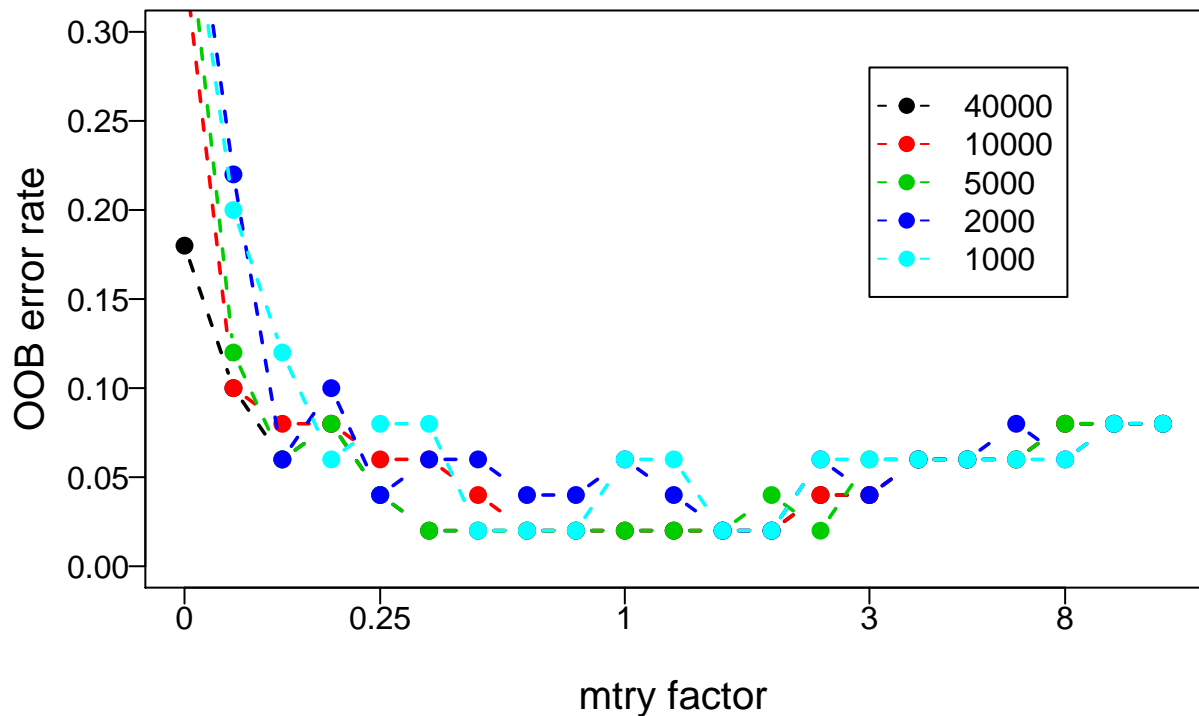
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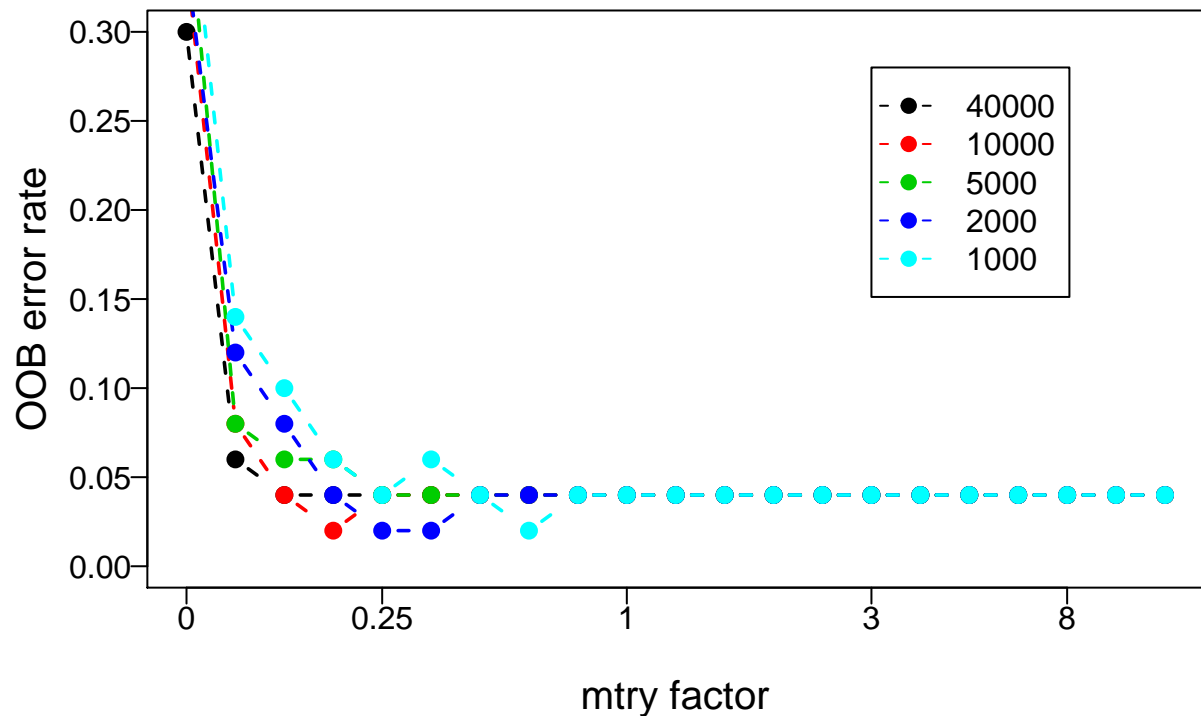
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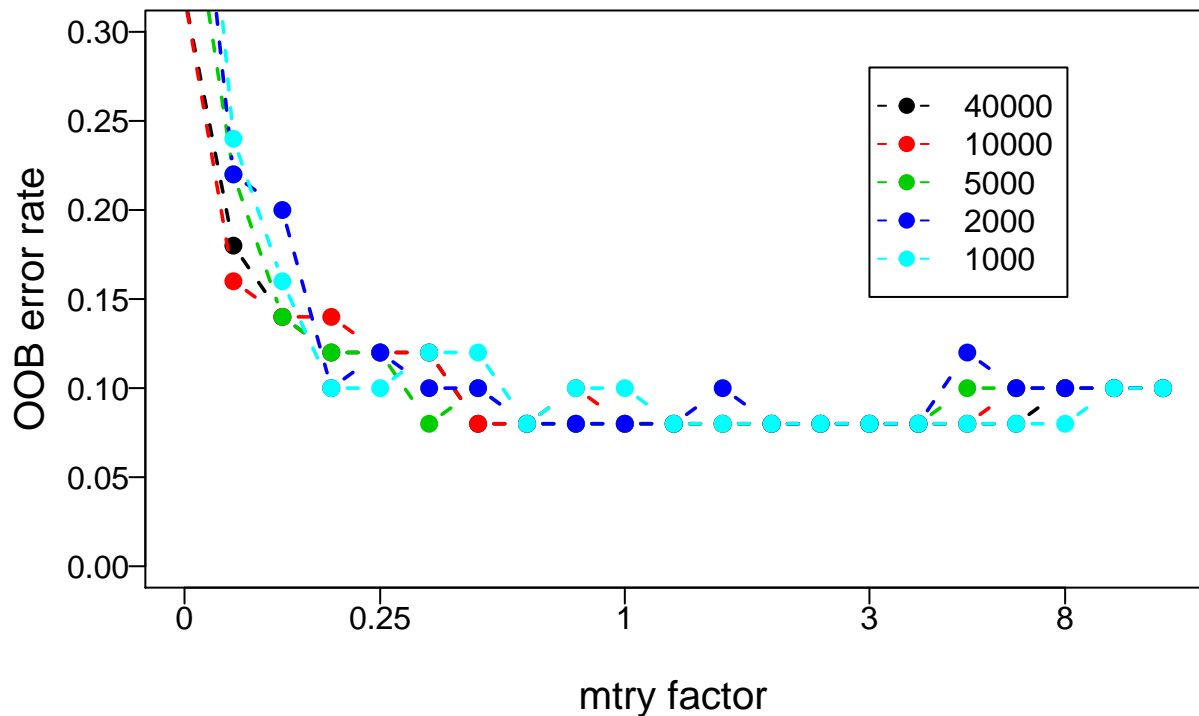
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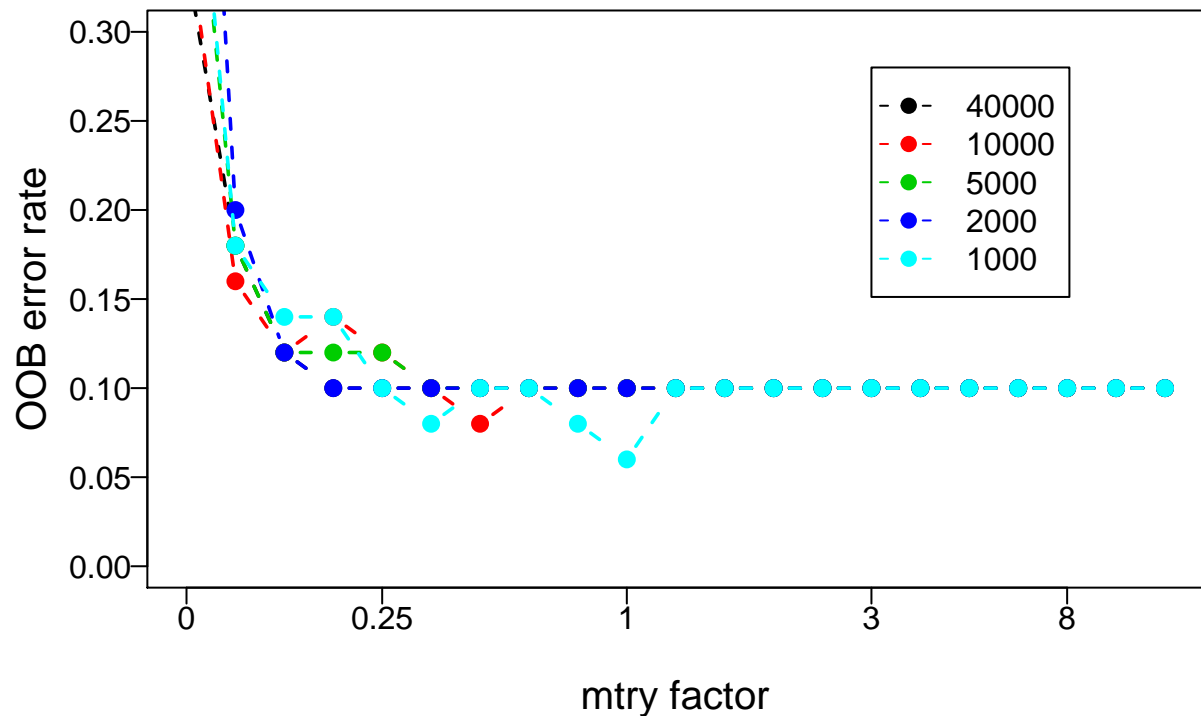
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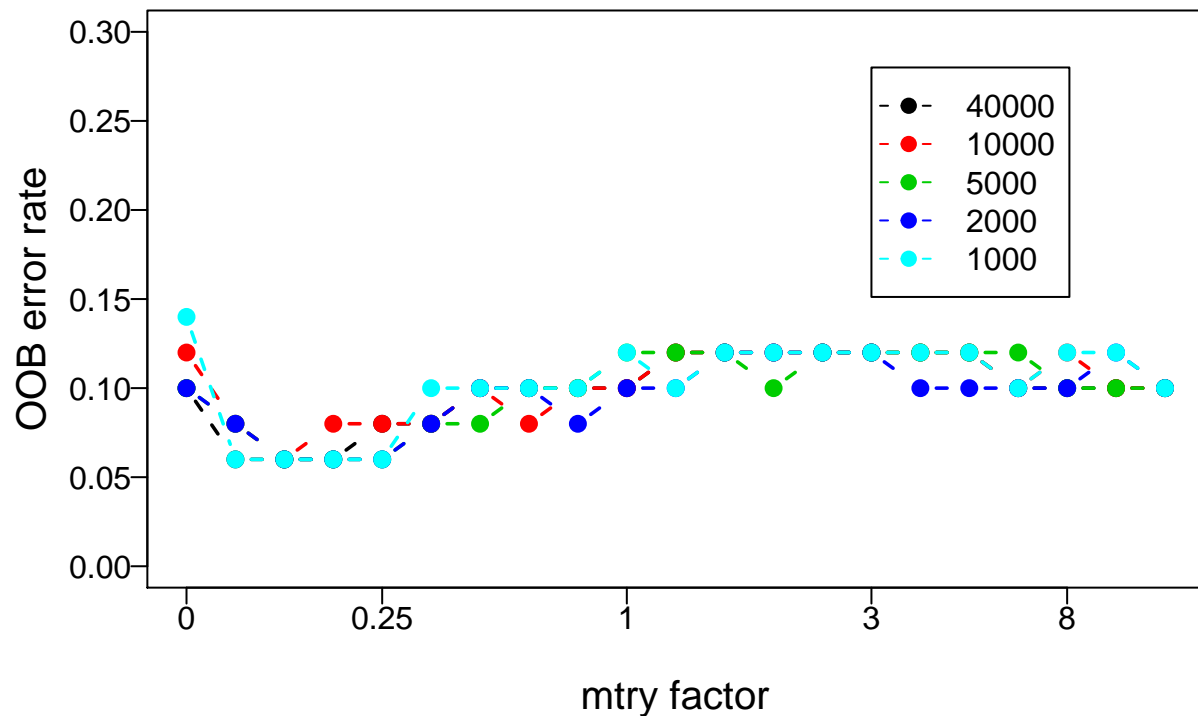
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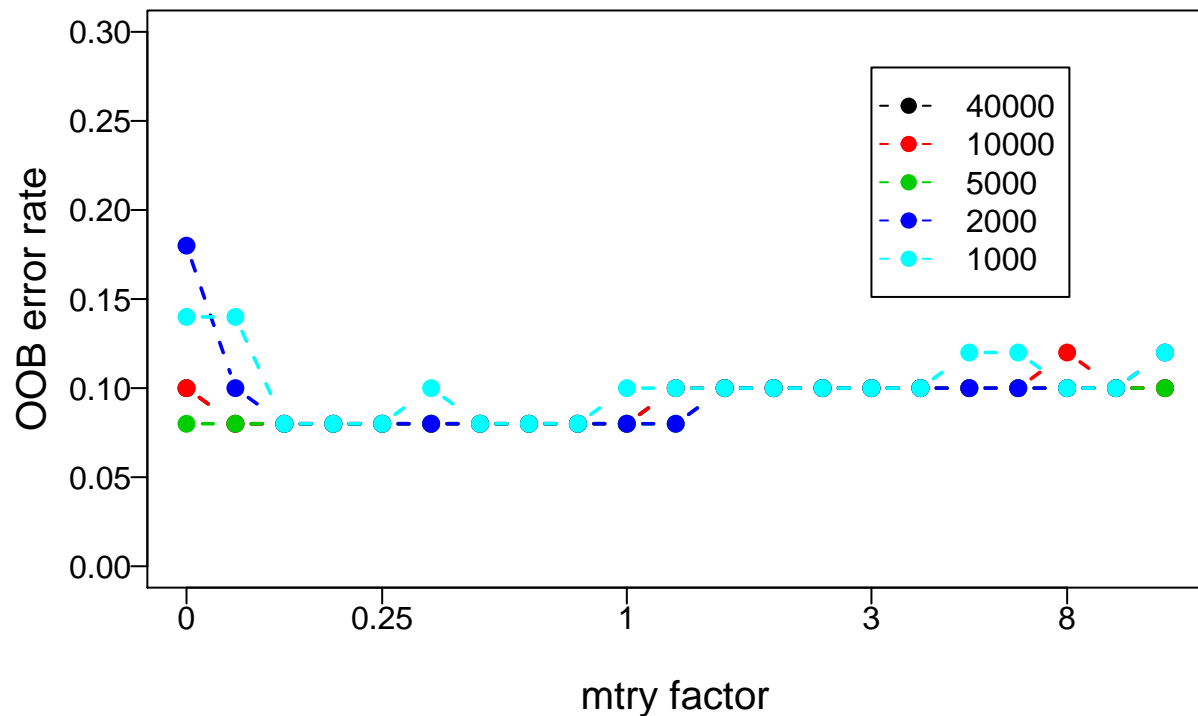
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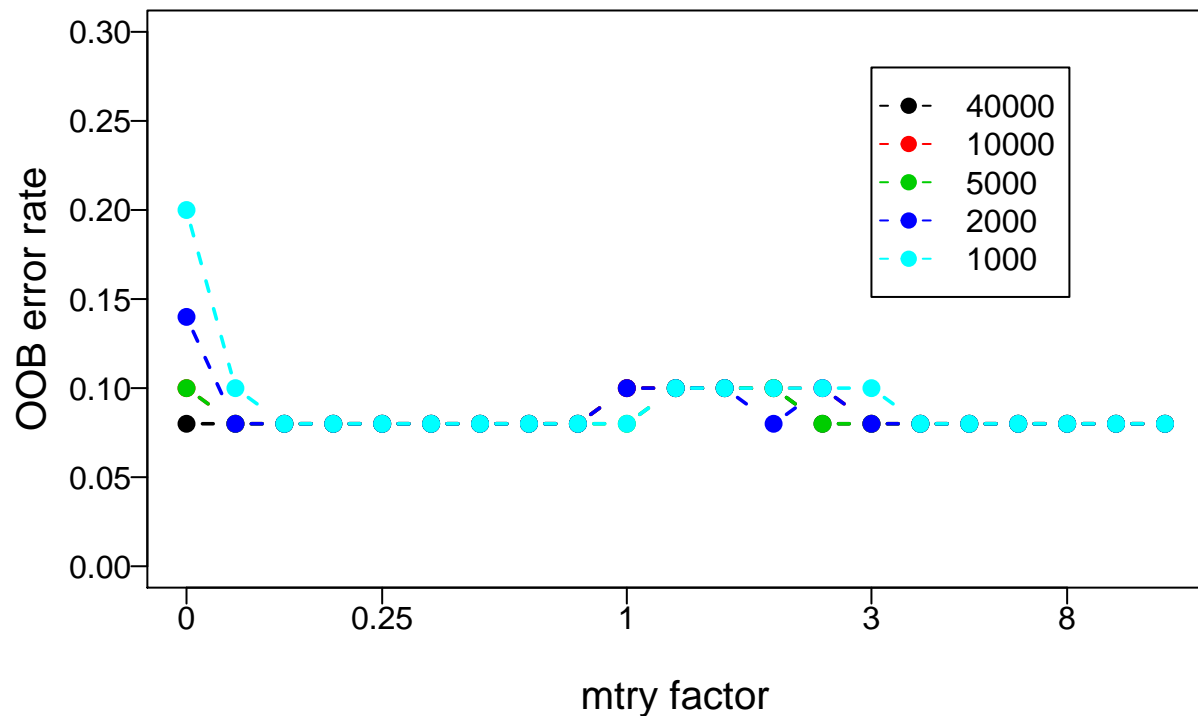
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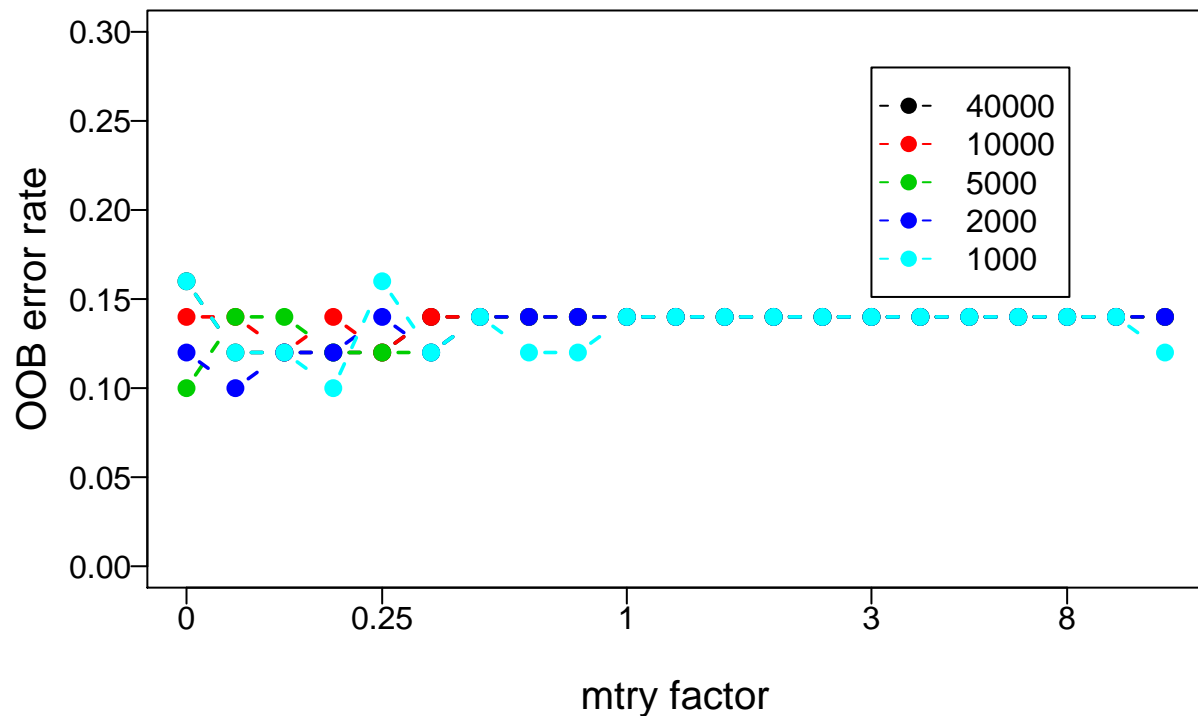
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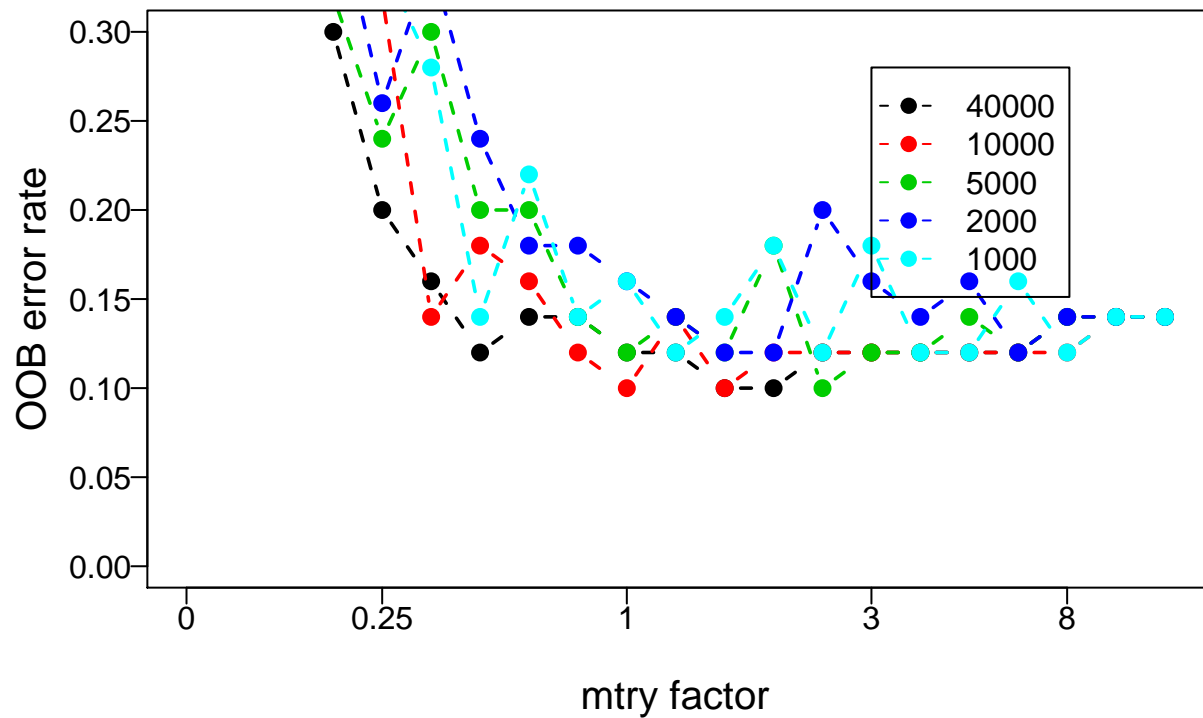
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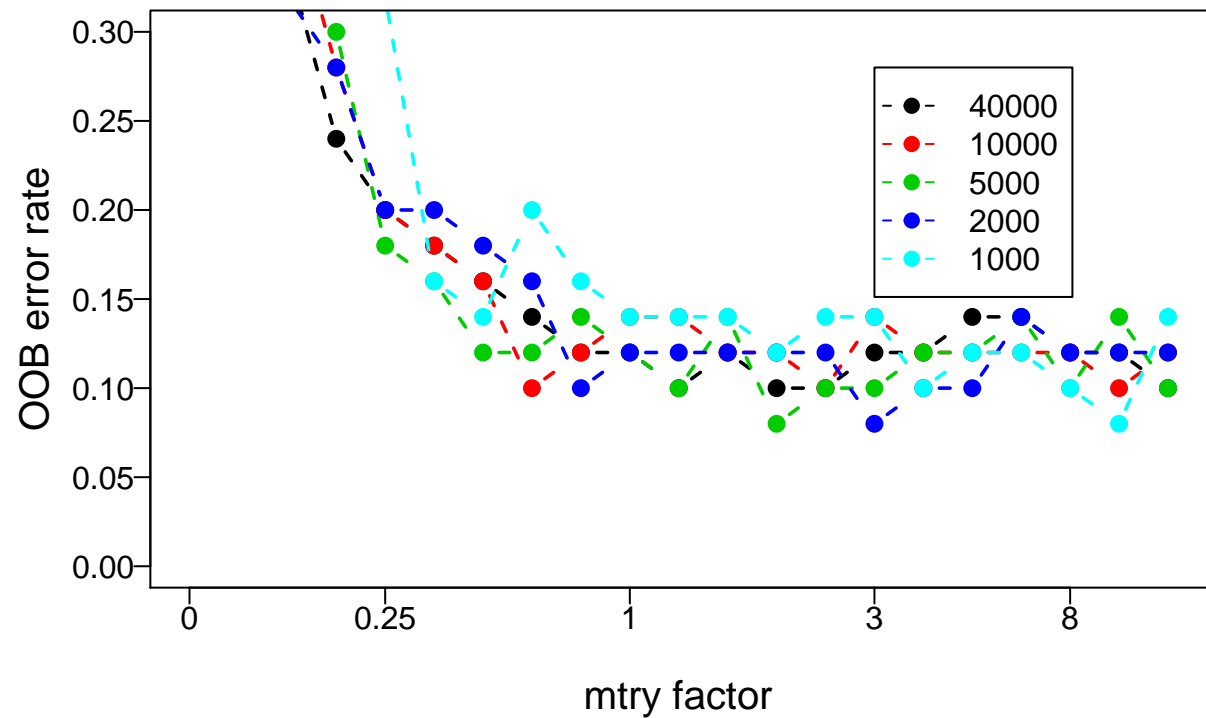
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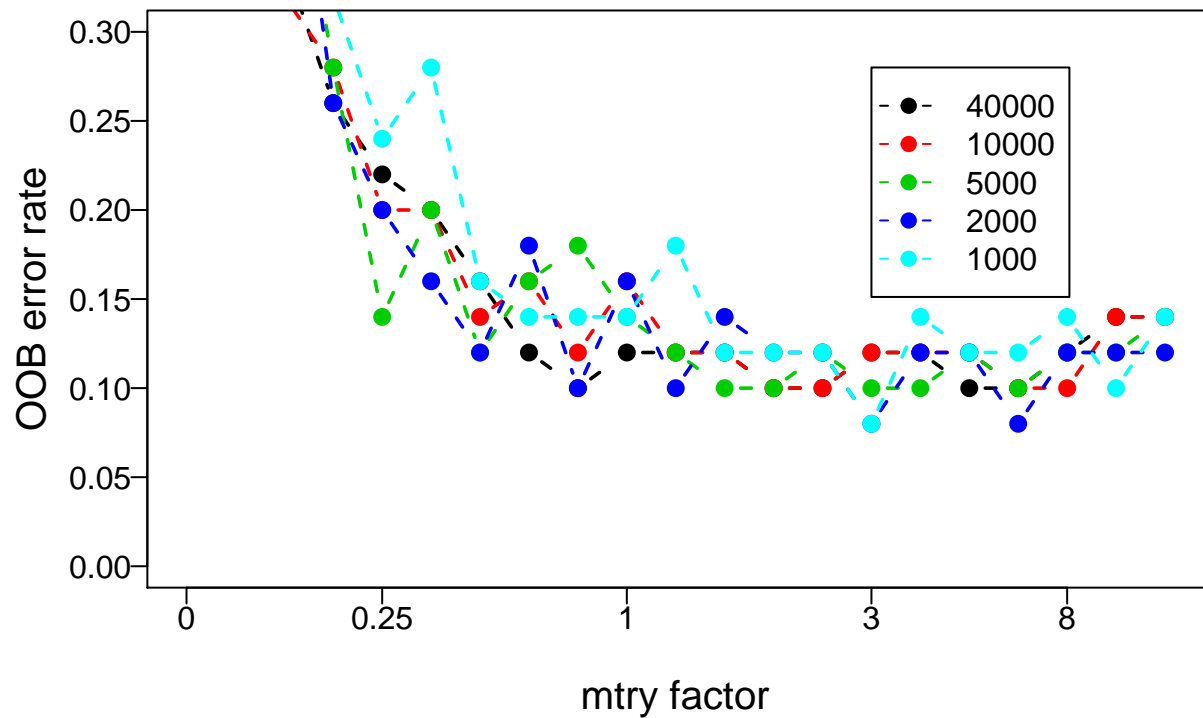
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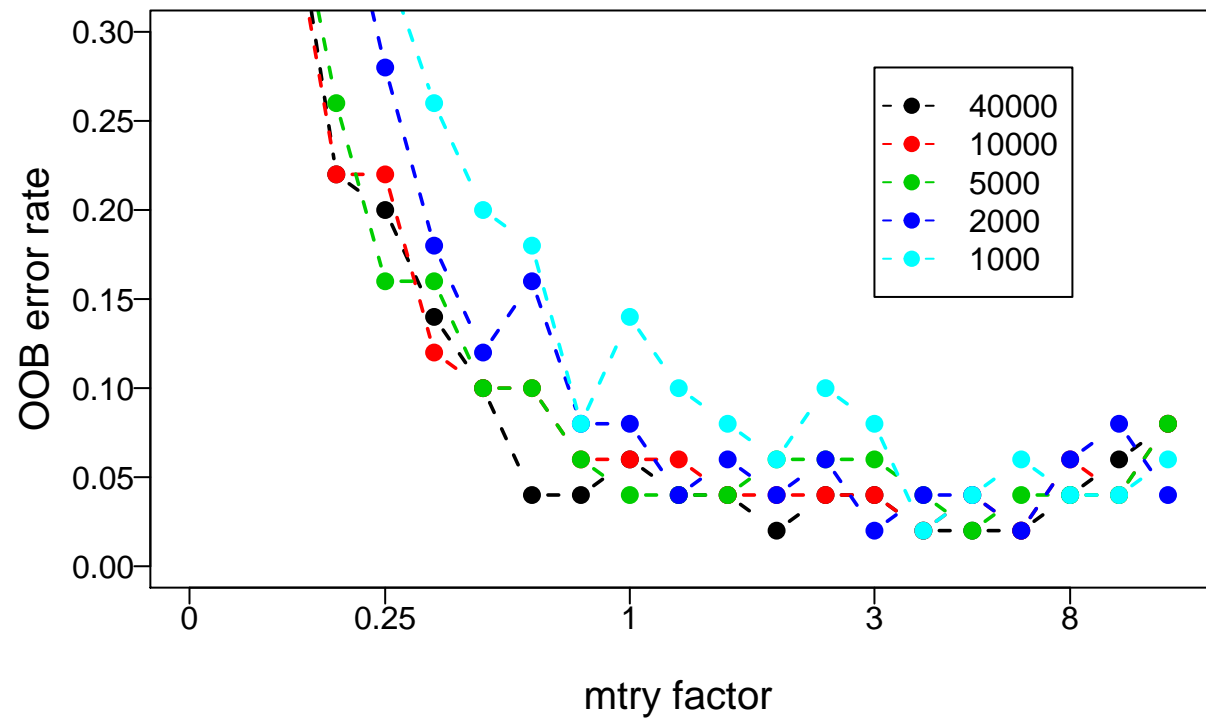
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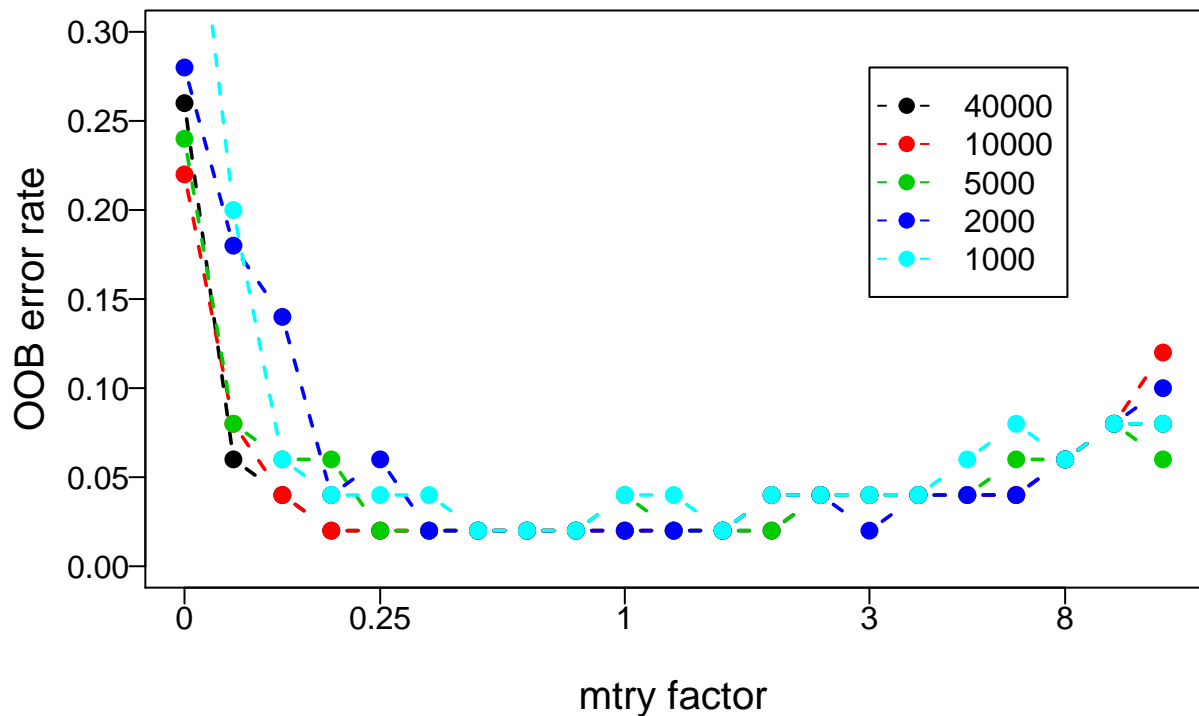
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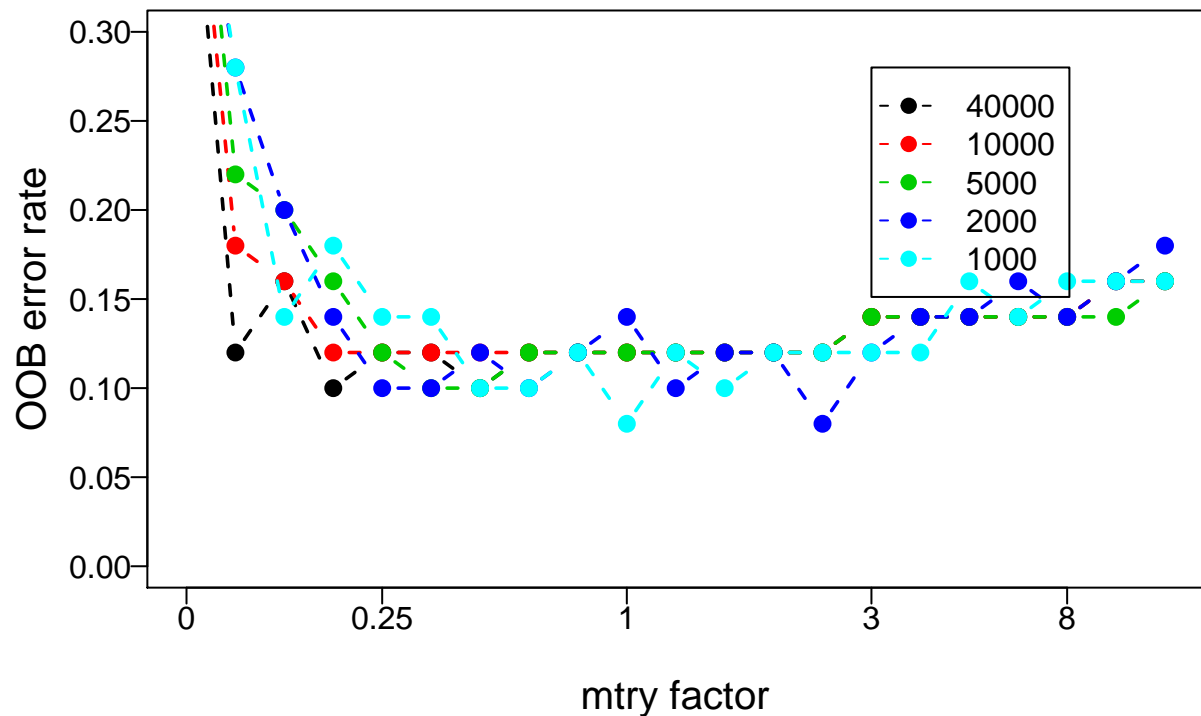
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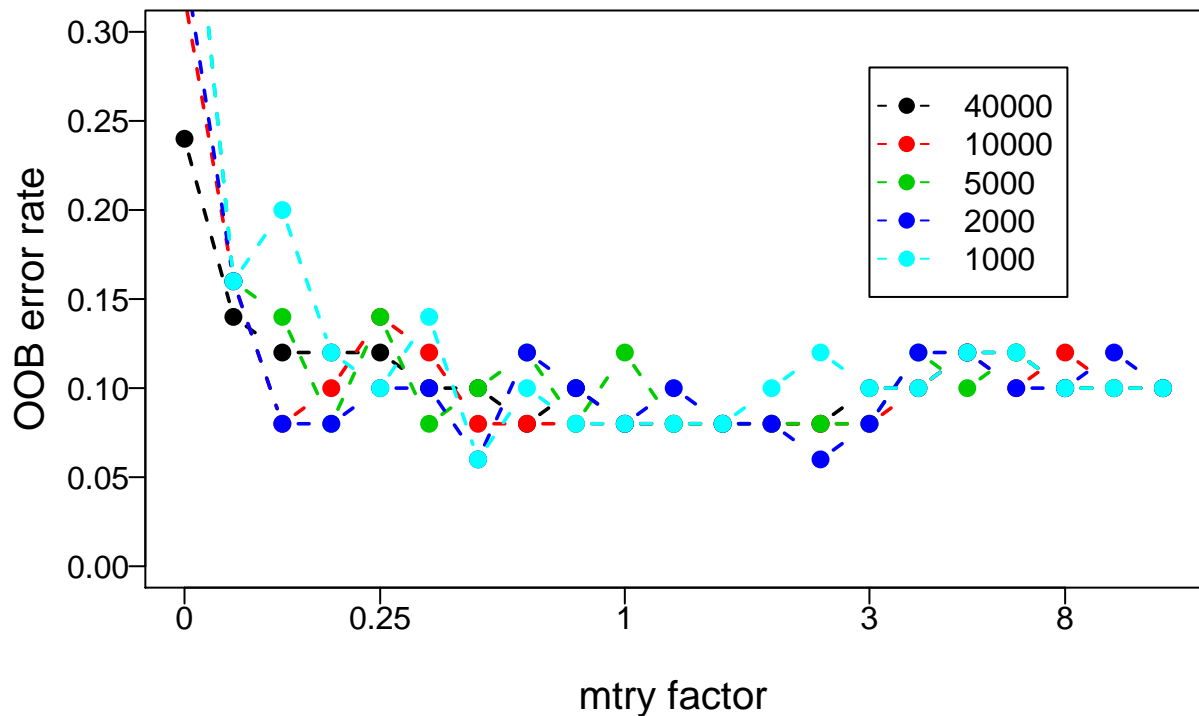
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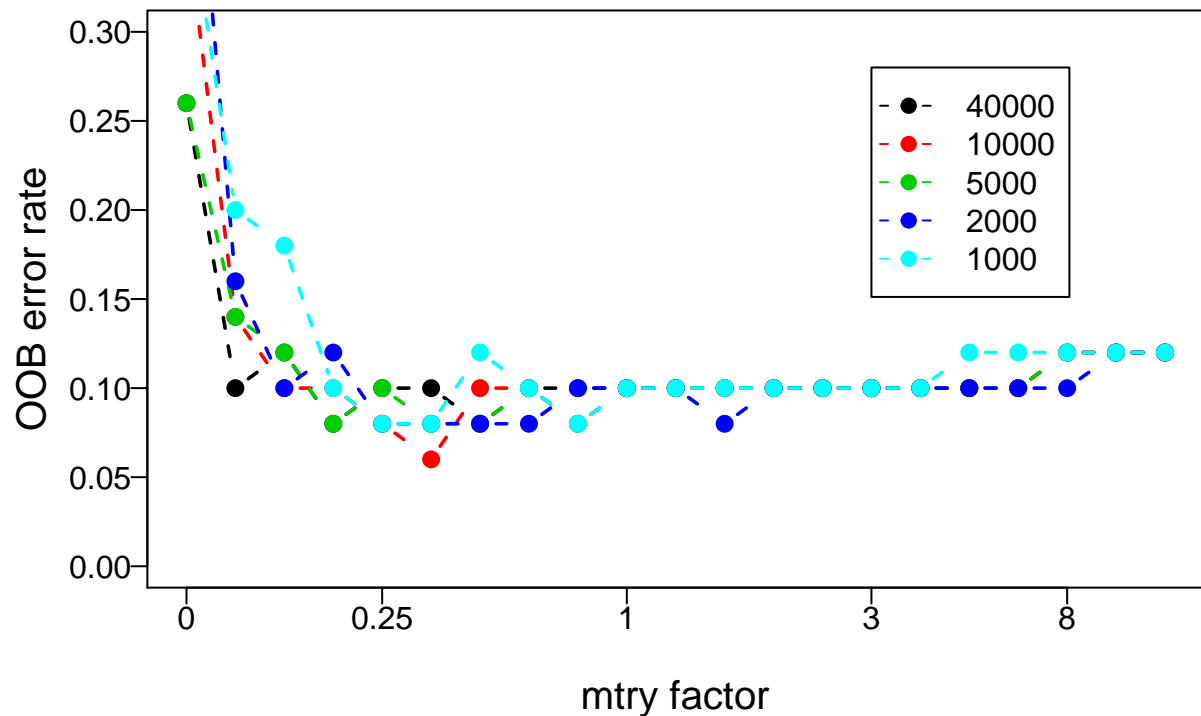
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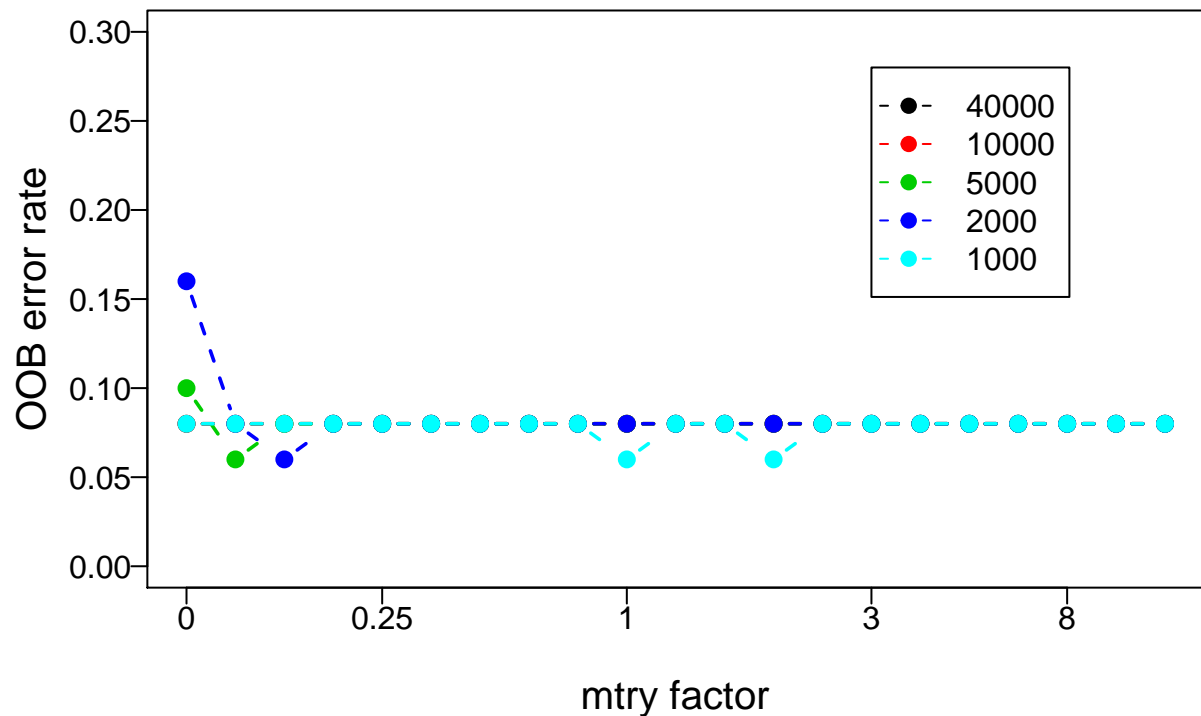
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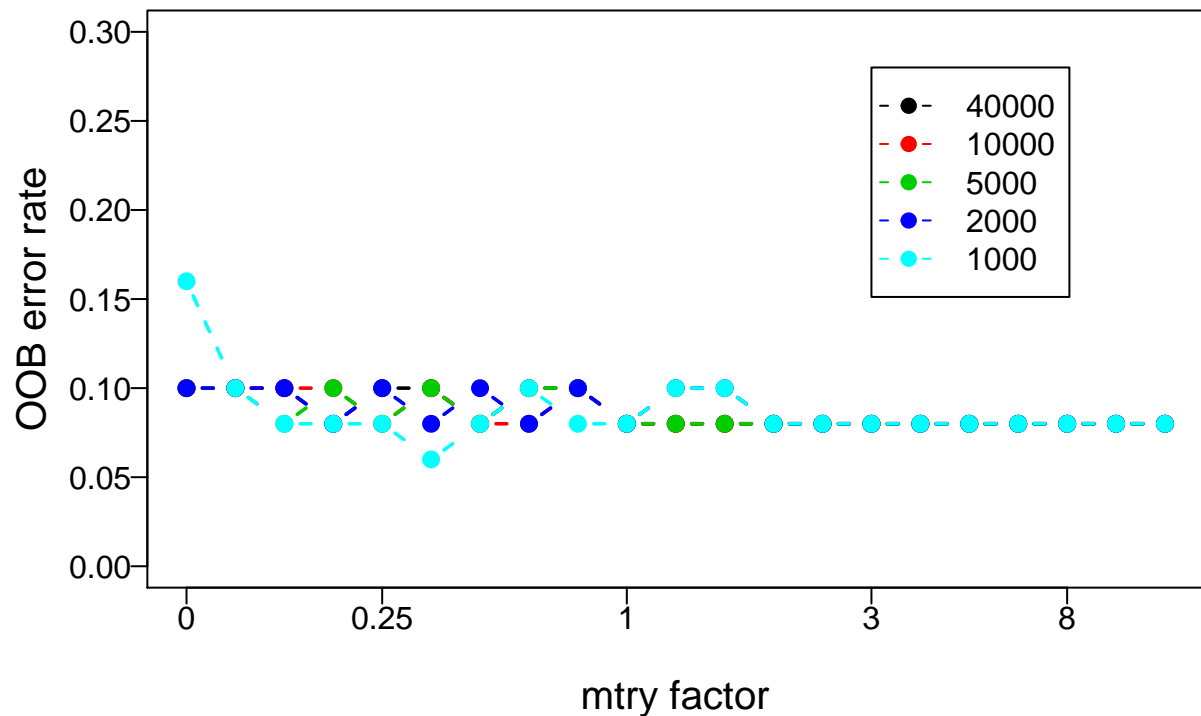
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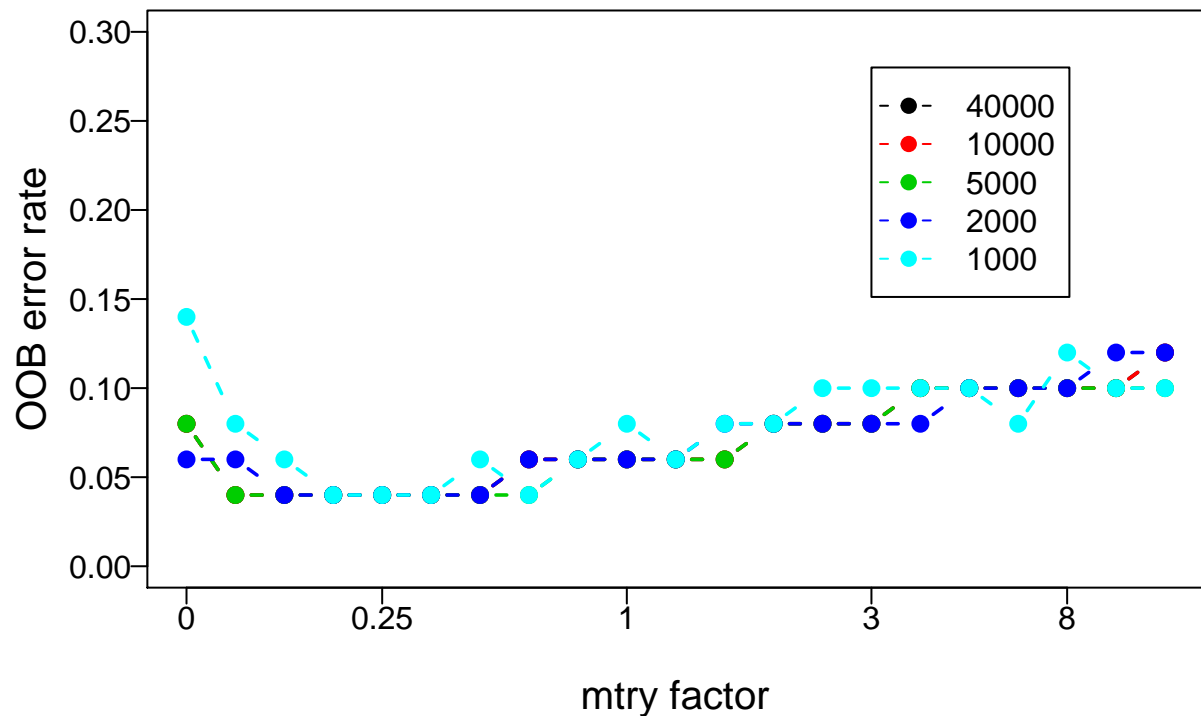
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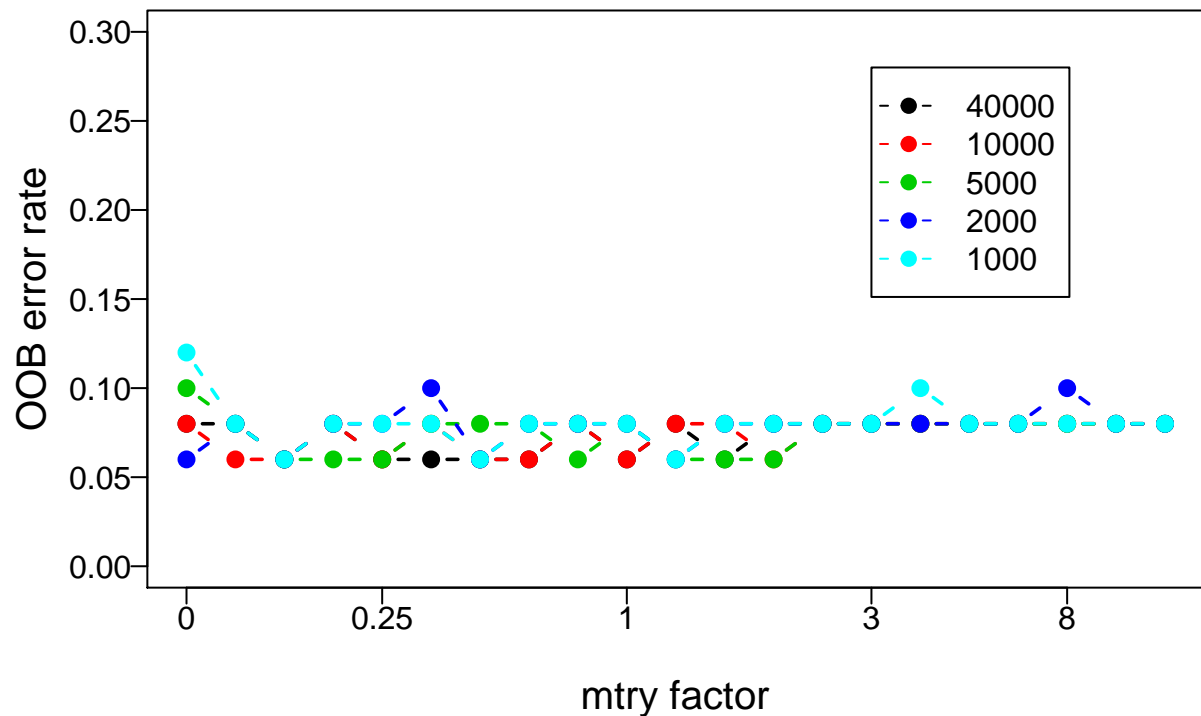
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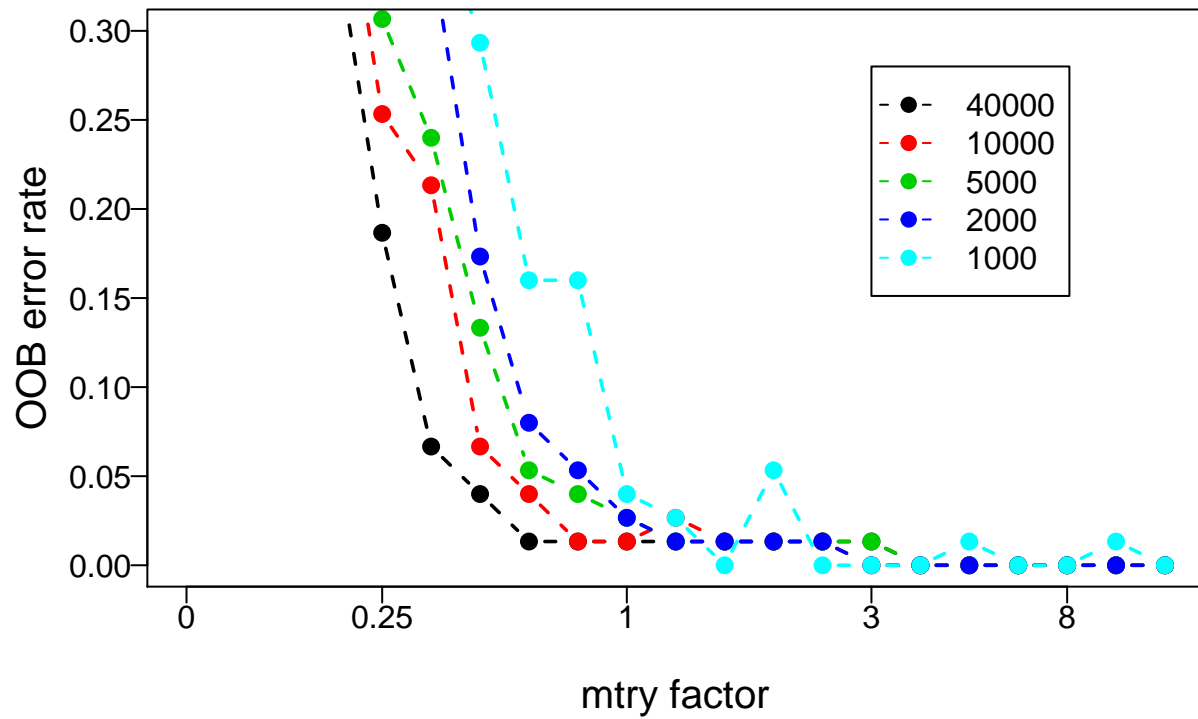
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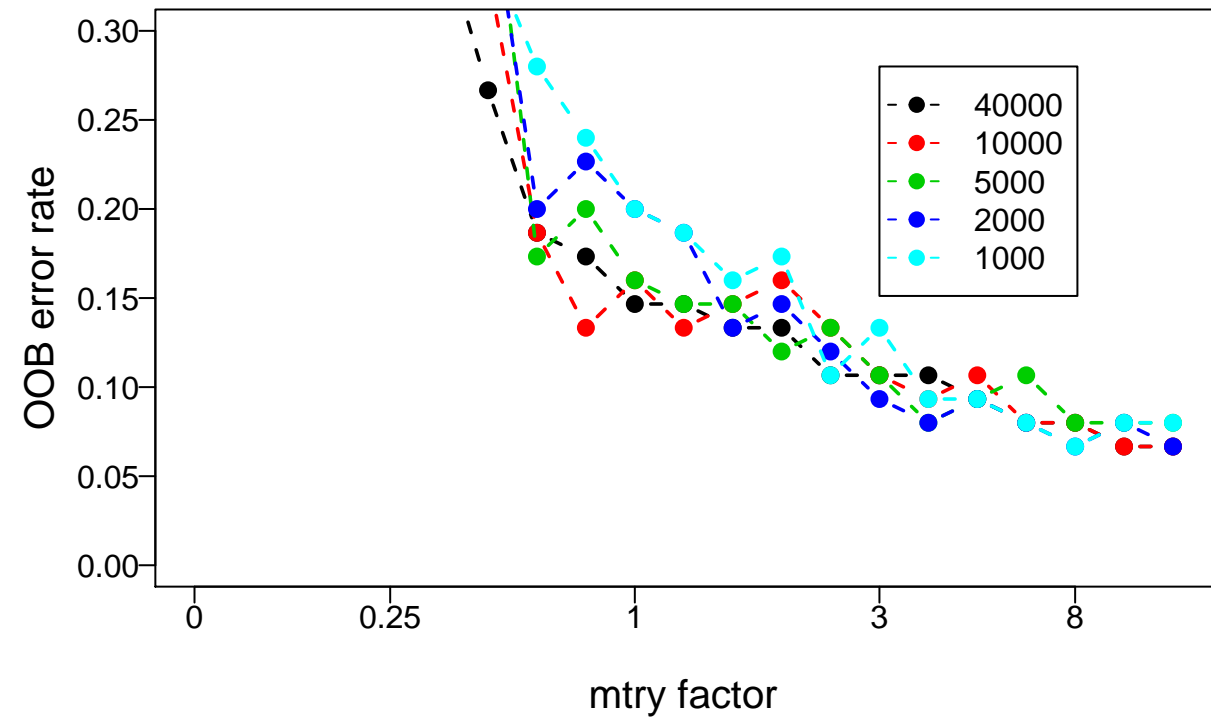
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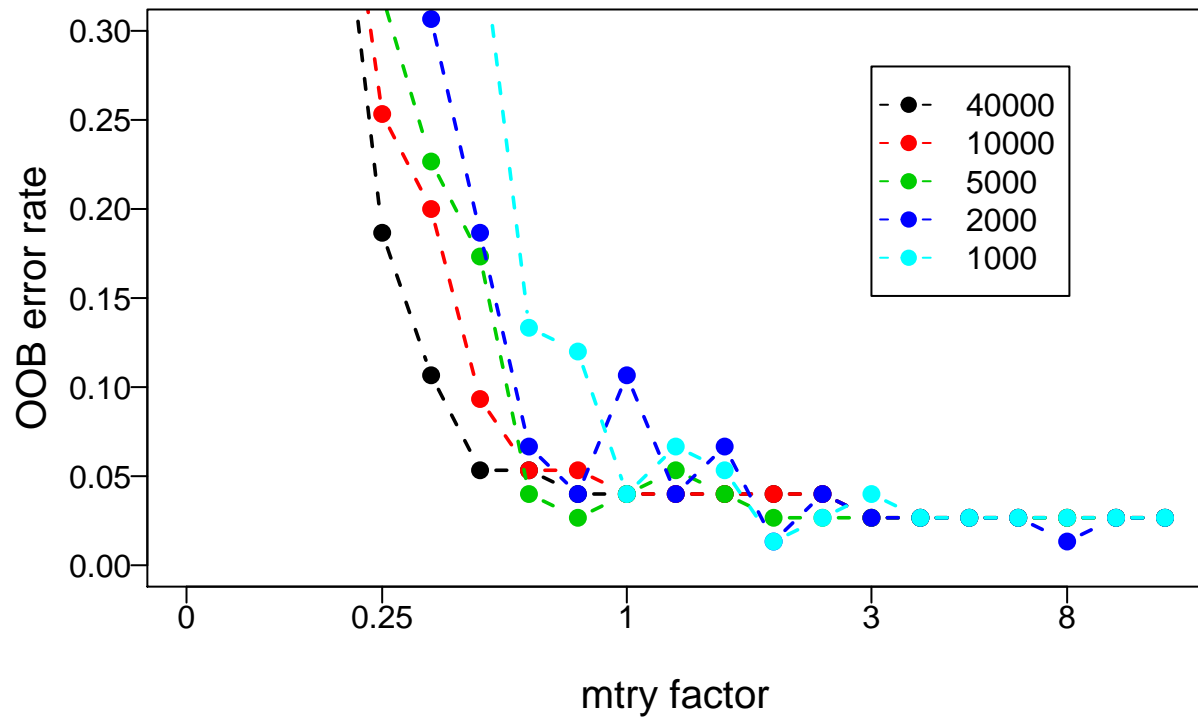
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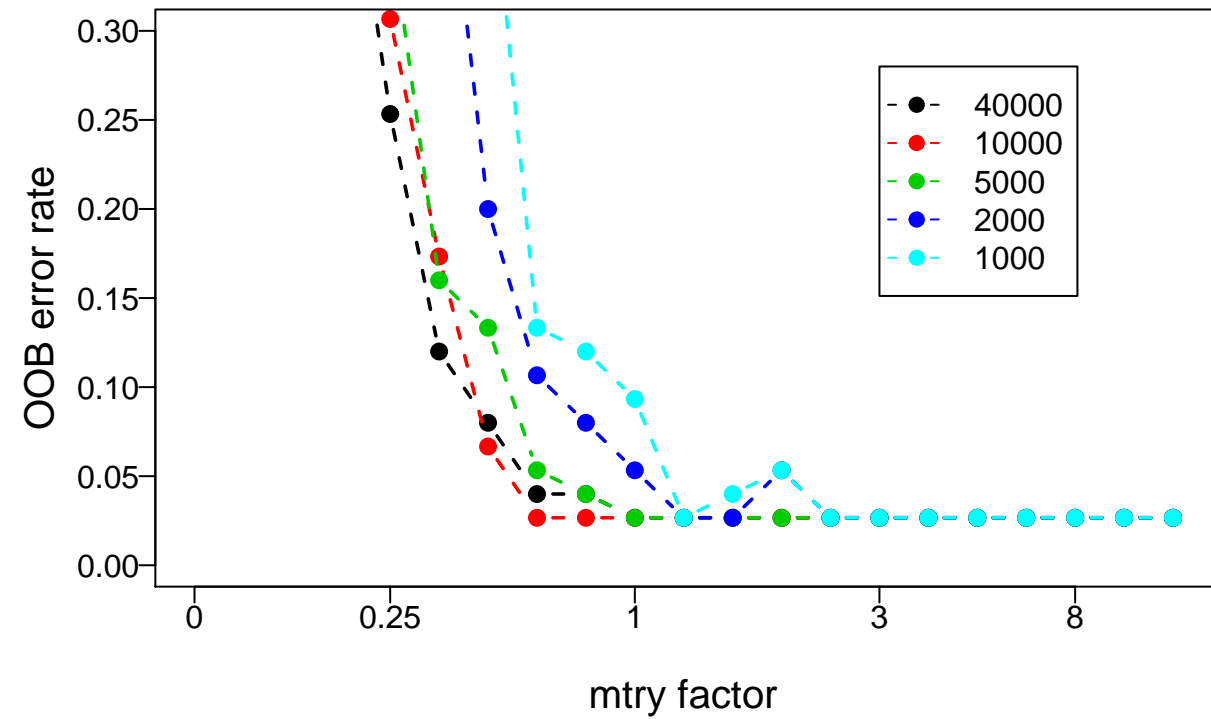
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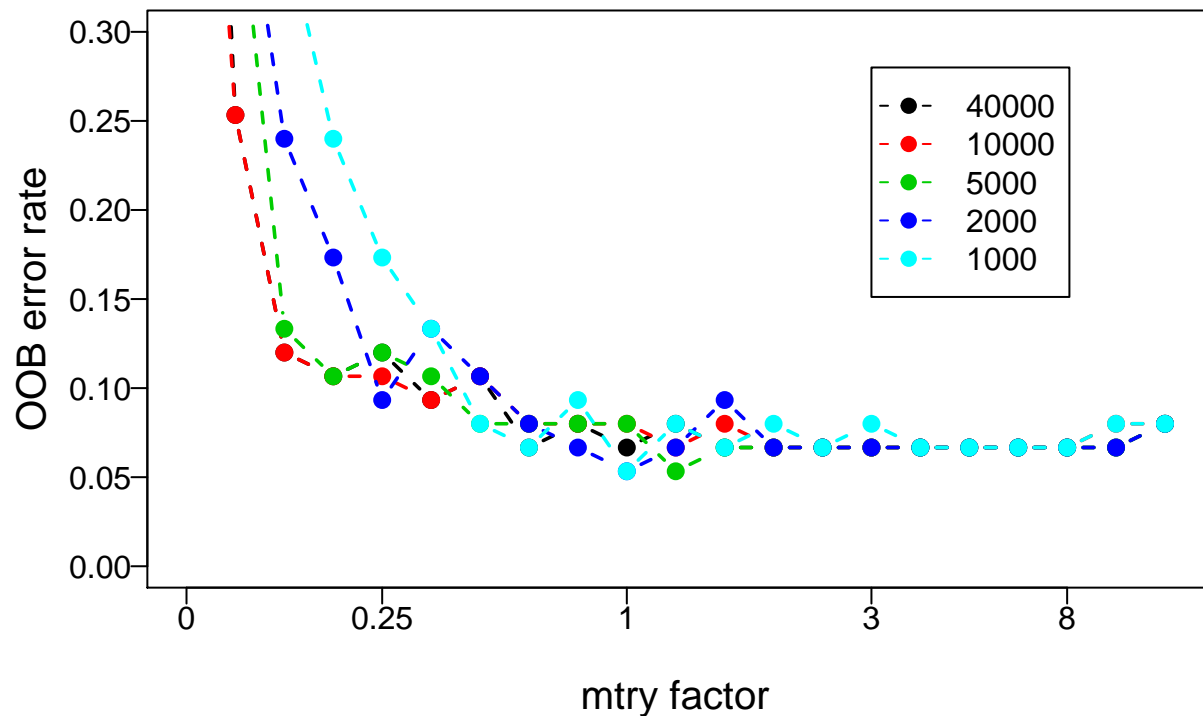
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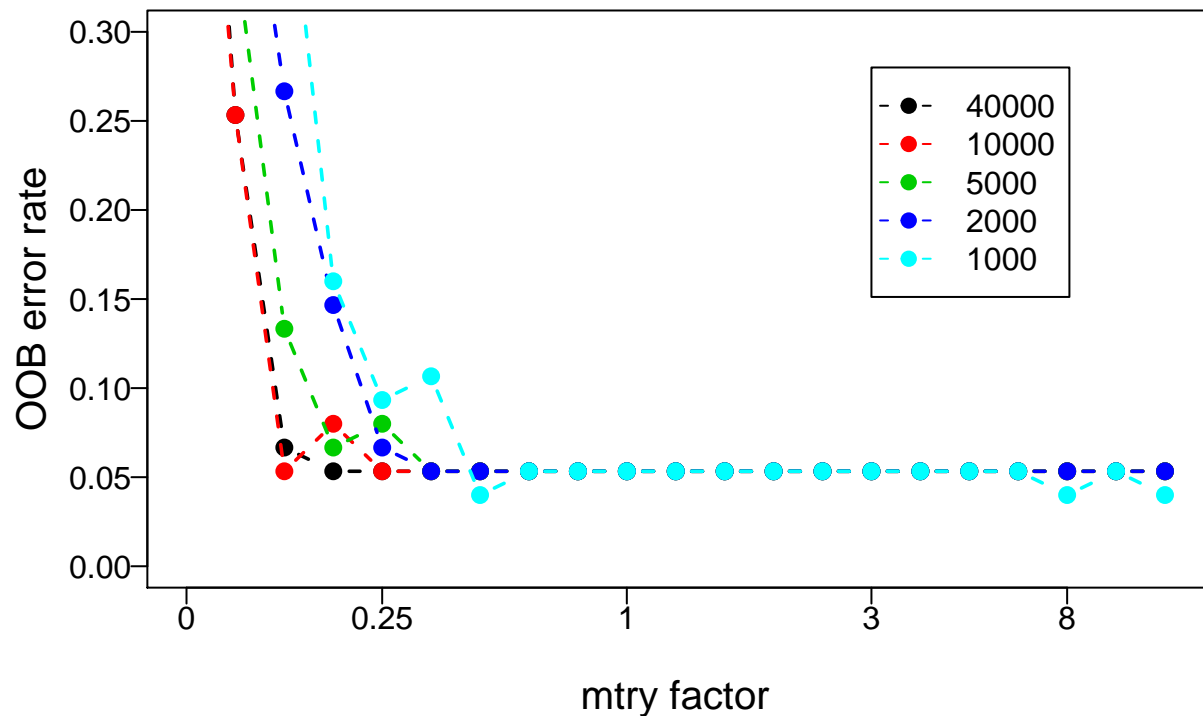
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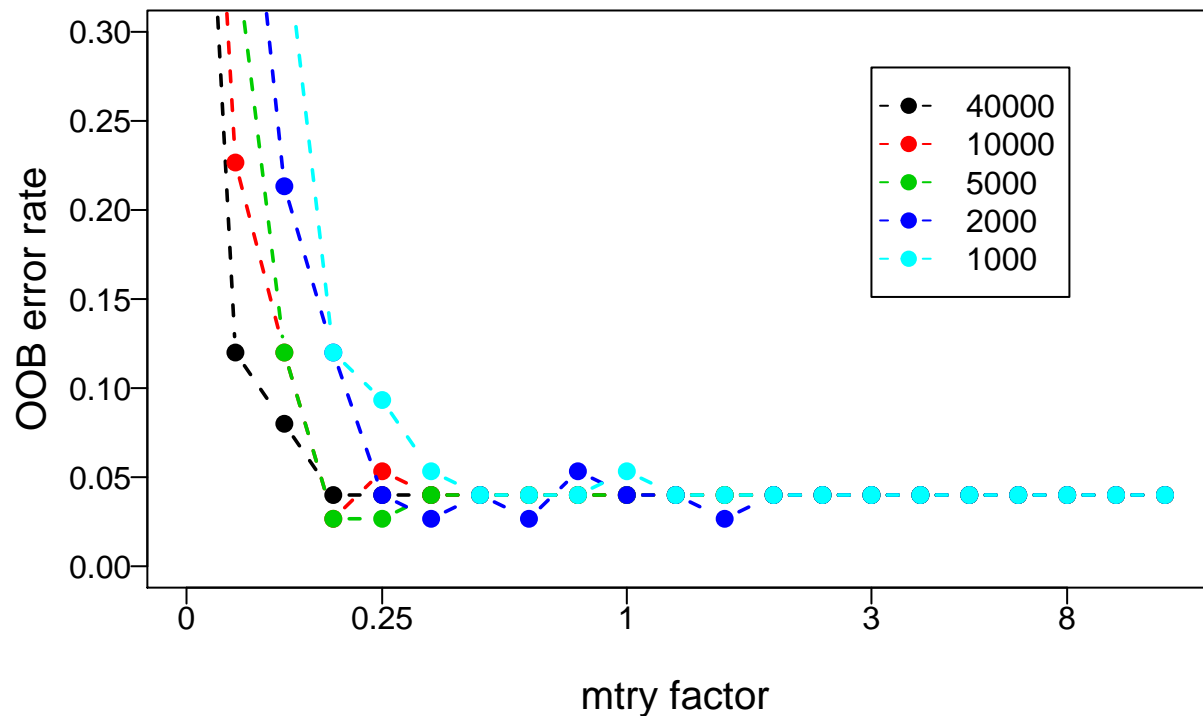
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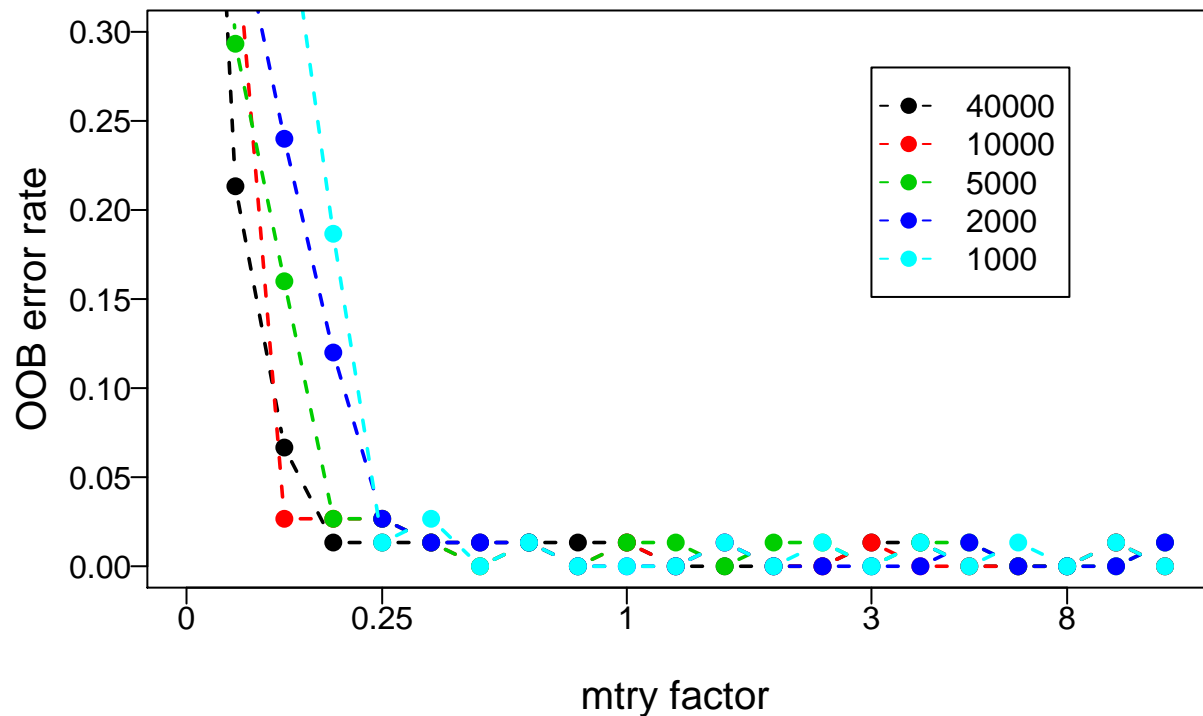
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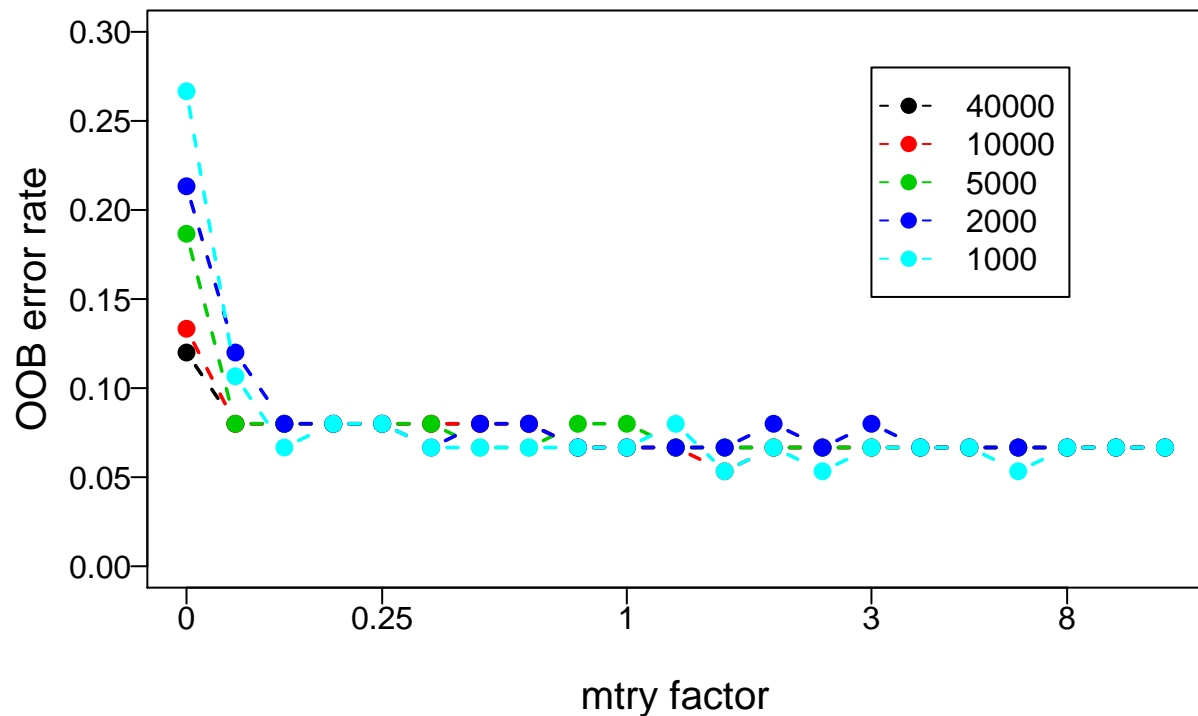
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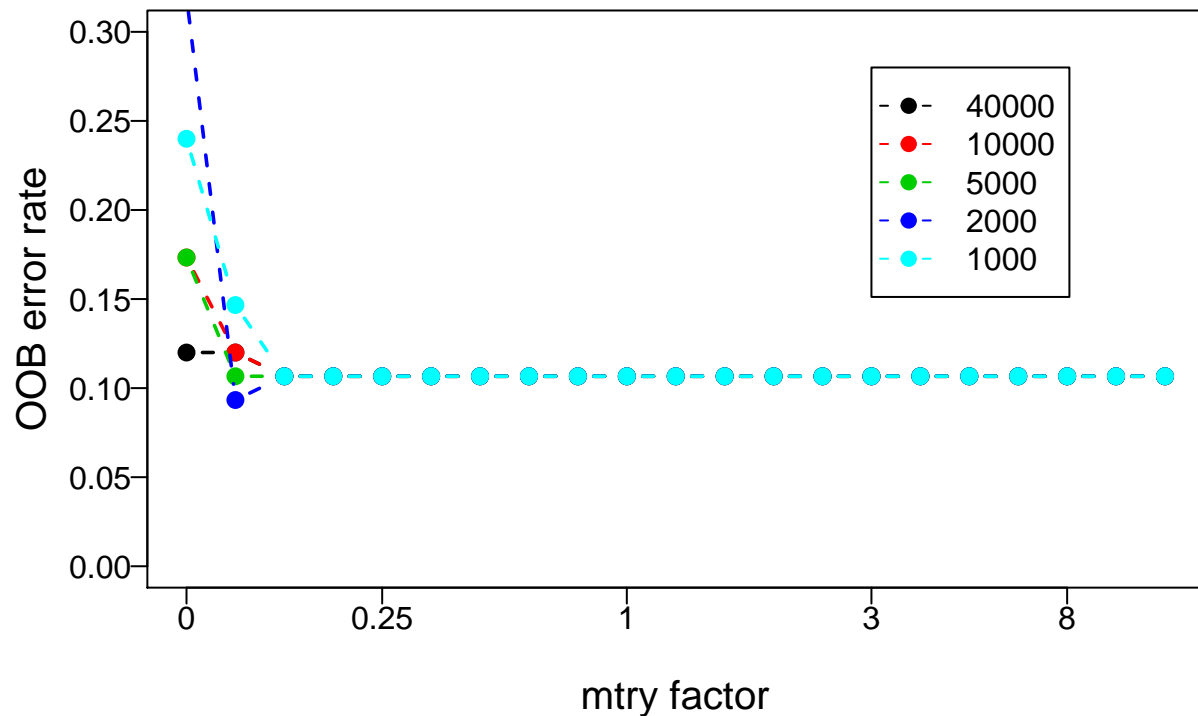
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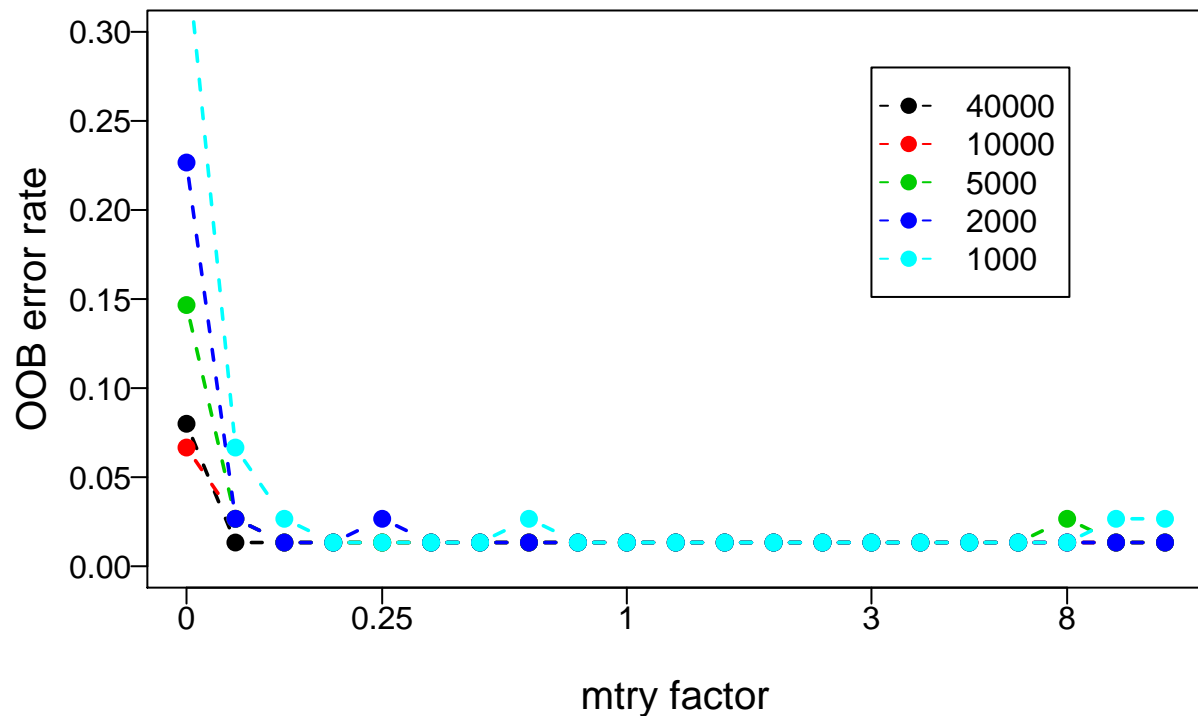
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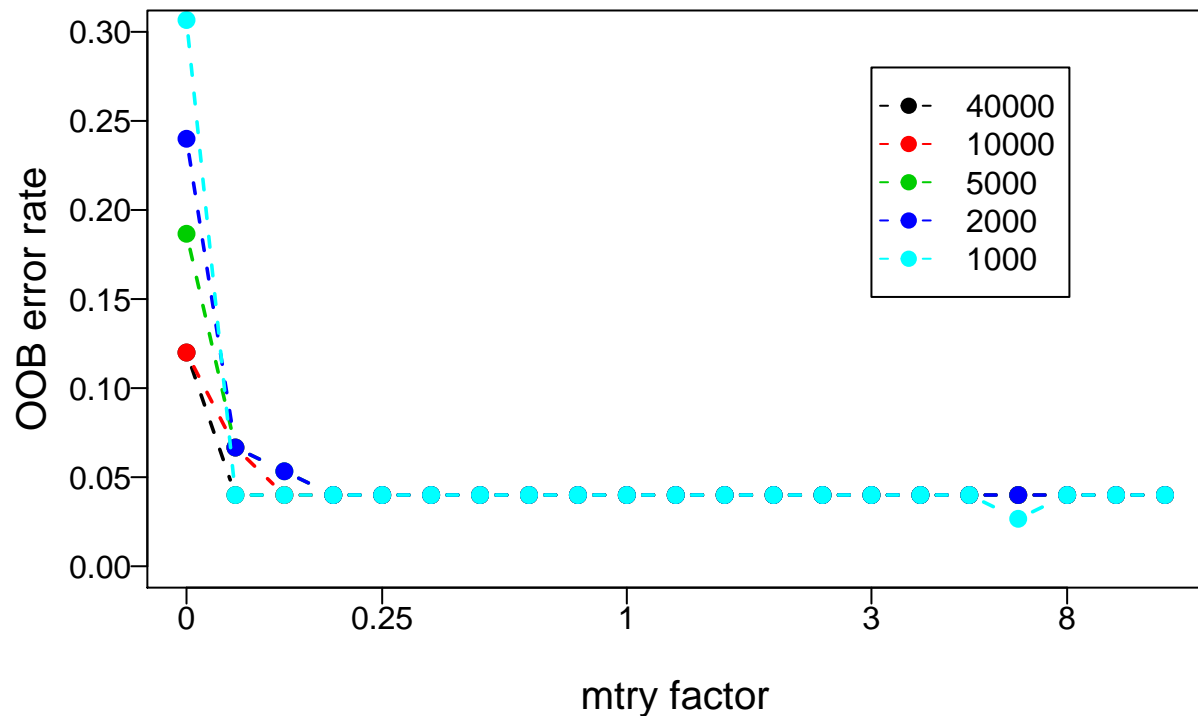
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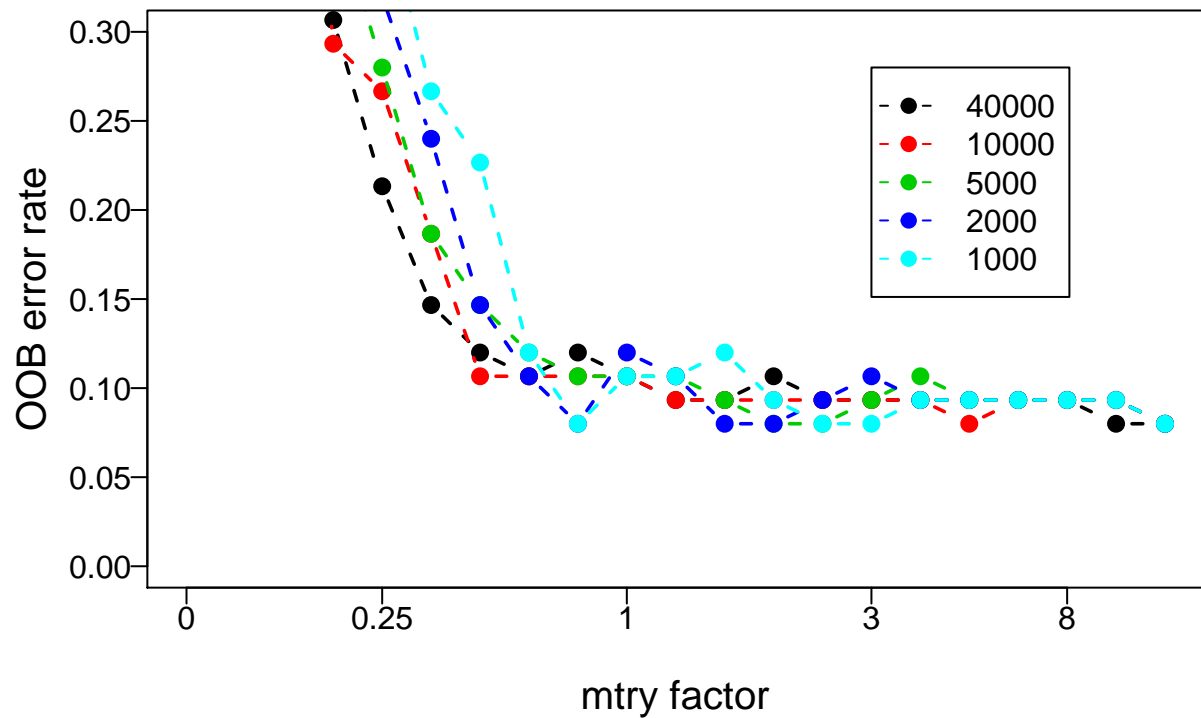
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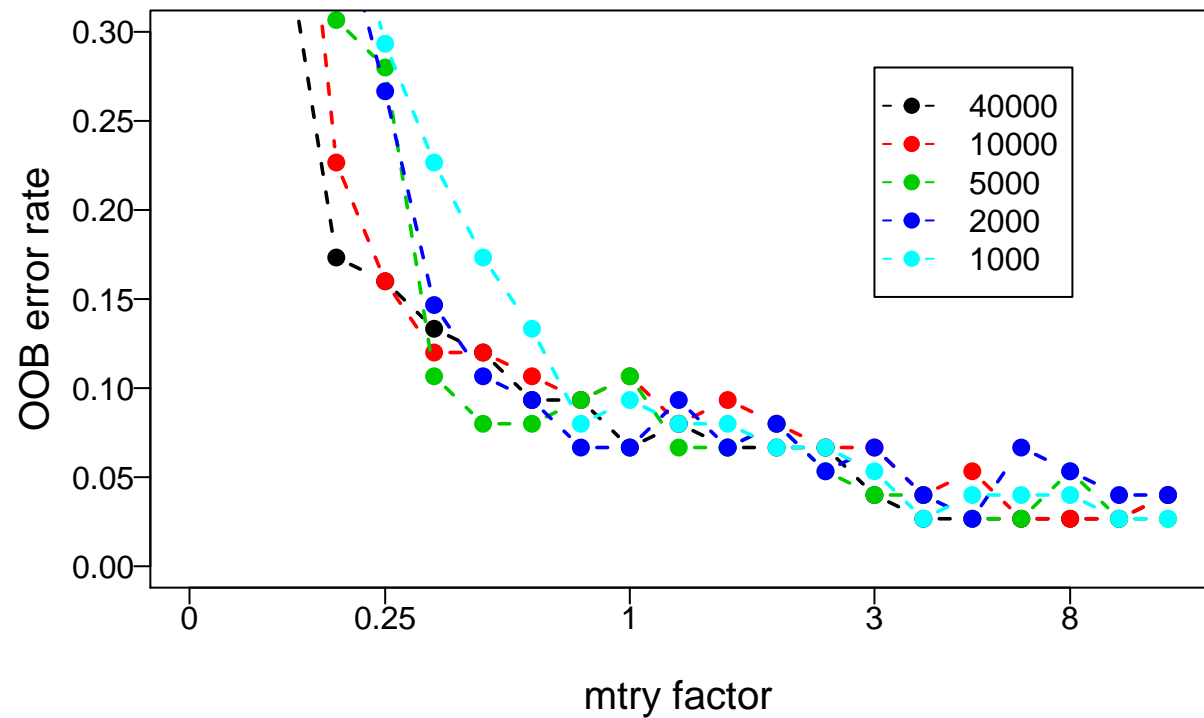
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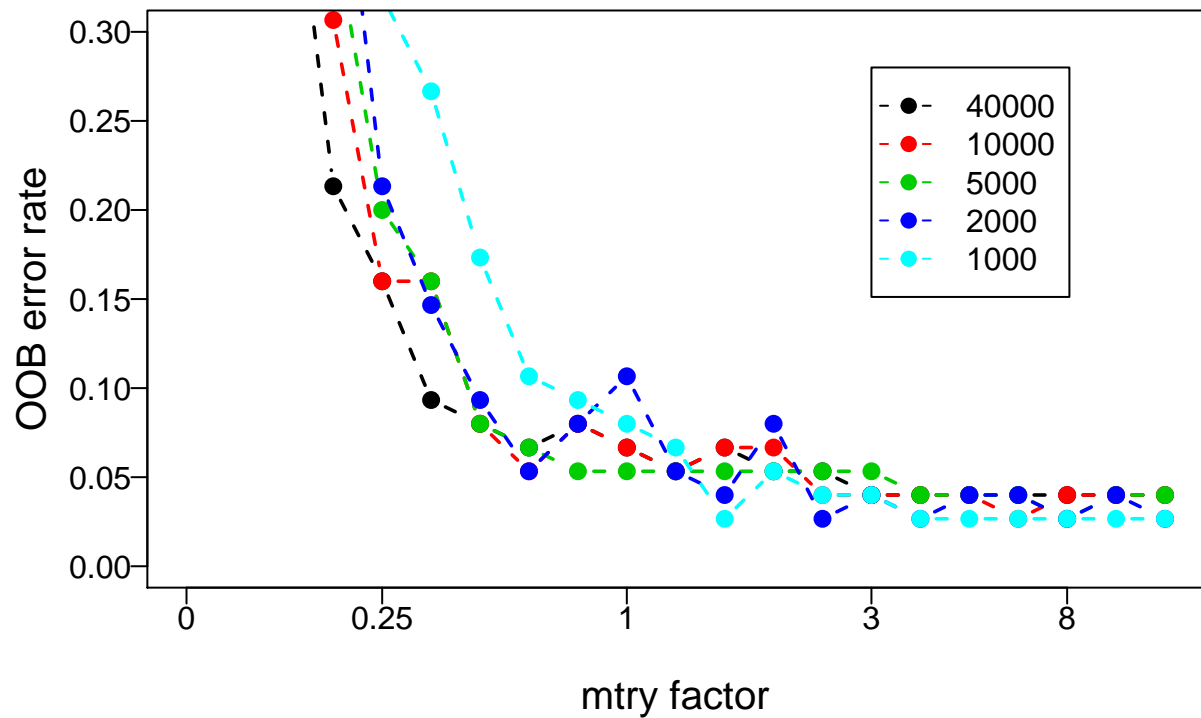
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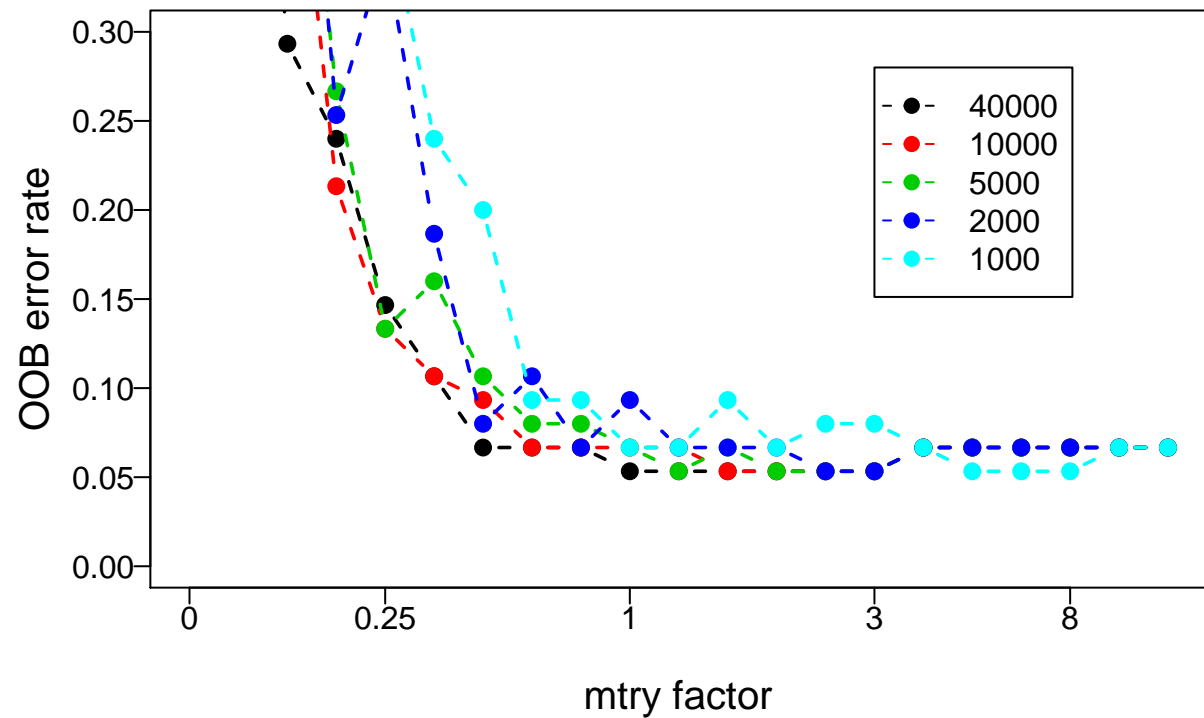
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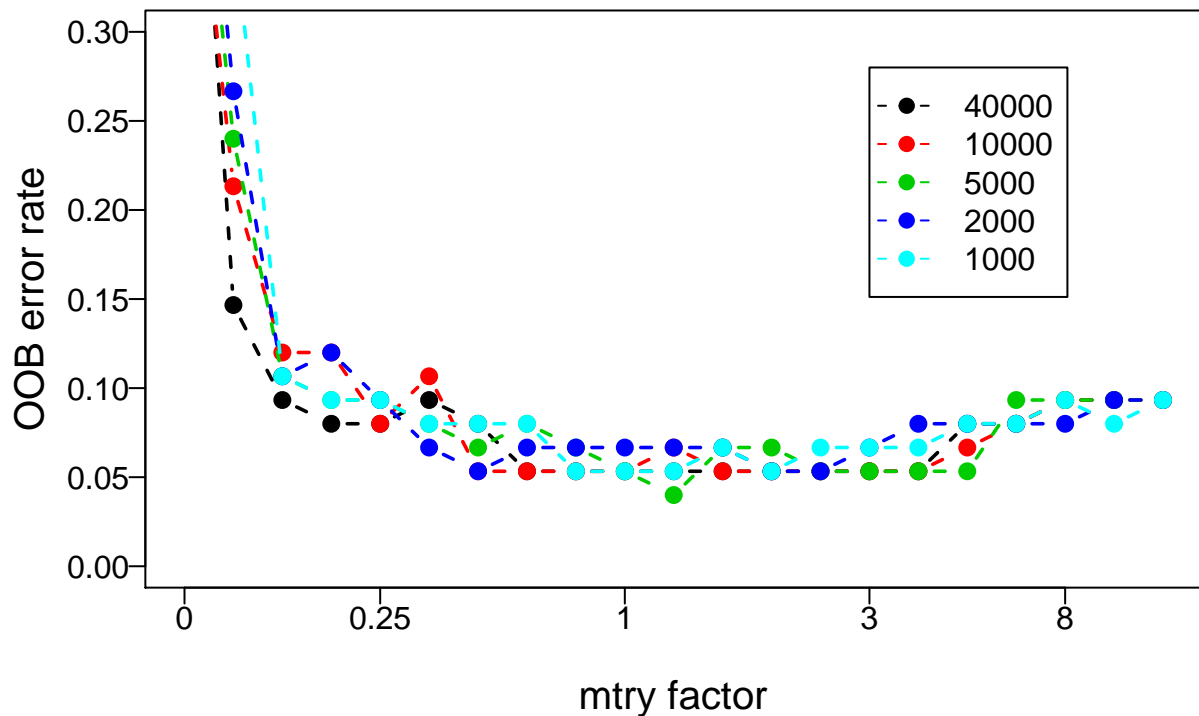
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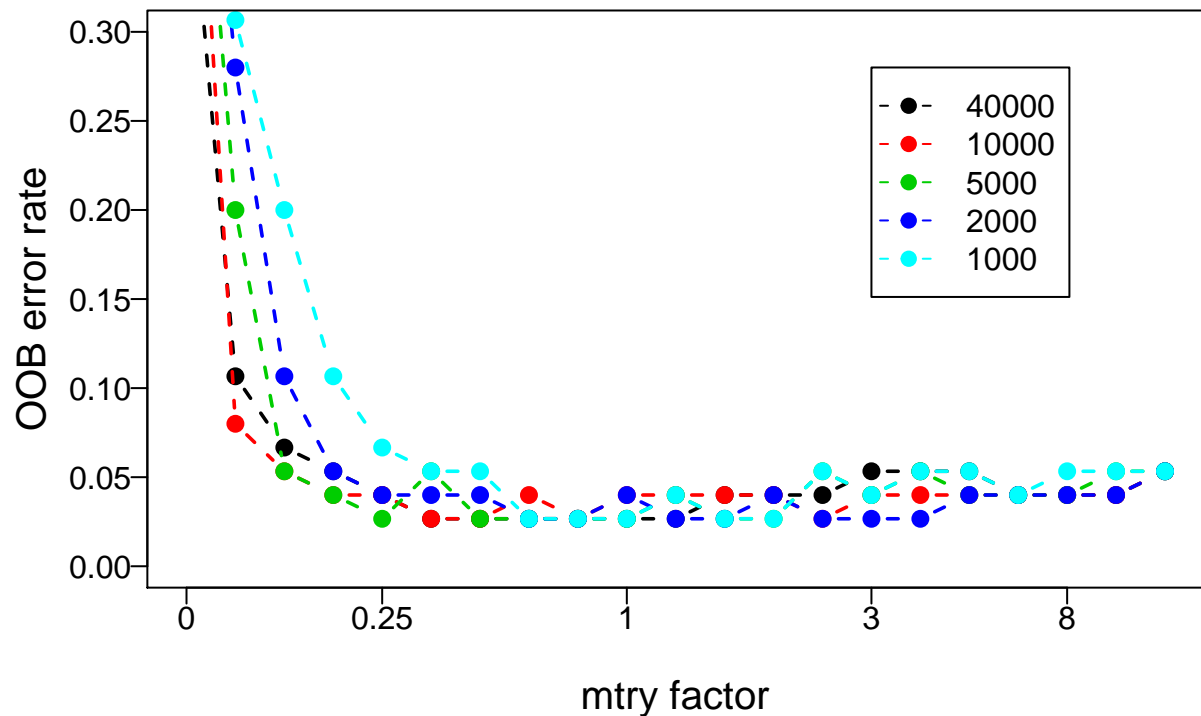
3 classes; 2 dimensions; 5 genes/dimen.; nodesize = 5



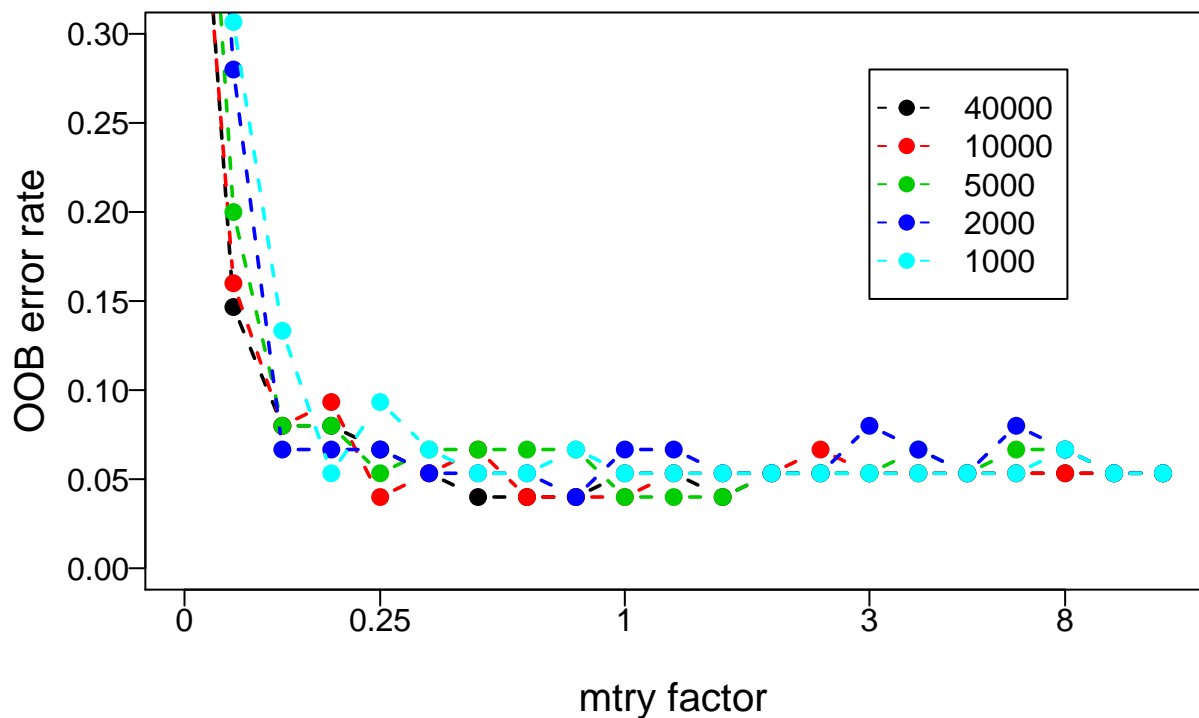
3 classes; 2 dimensions; 20 genes/dimen.; nodesize = 5



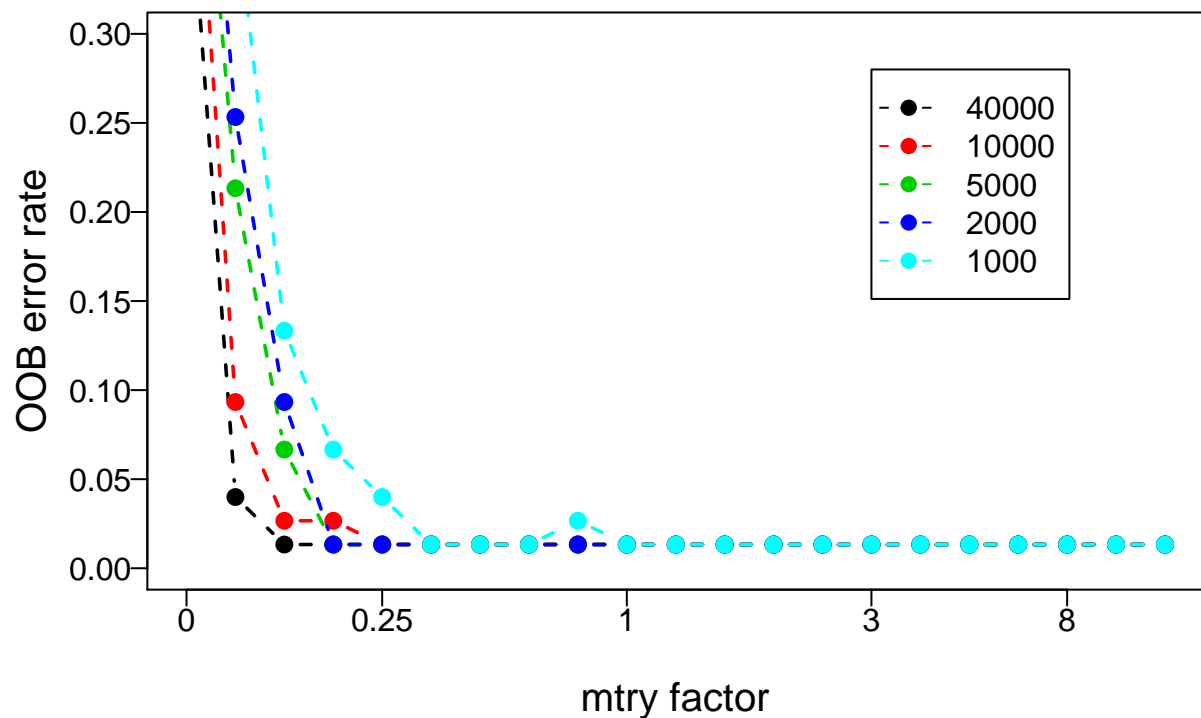
3 classes; 2 dimensions; 20 genes/dimen.; nodesize = 5



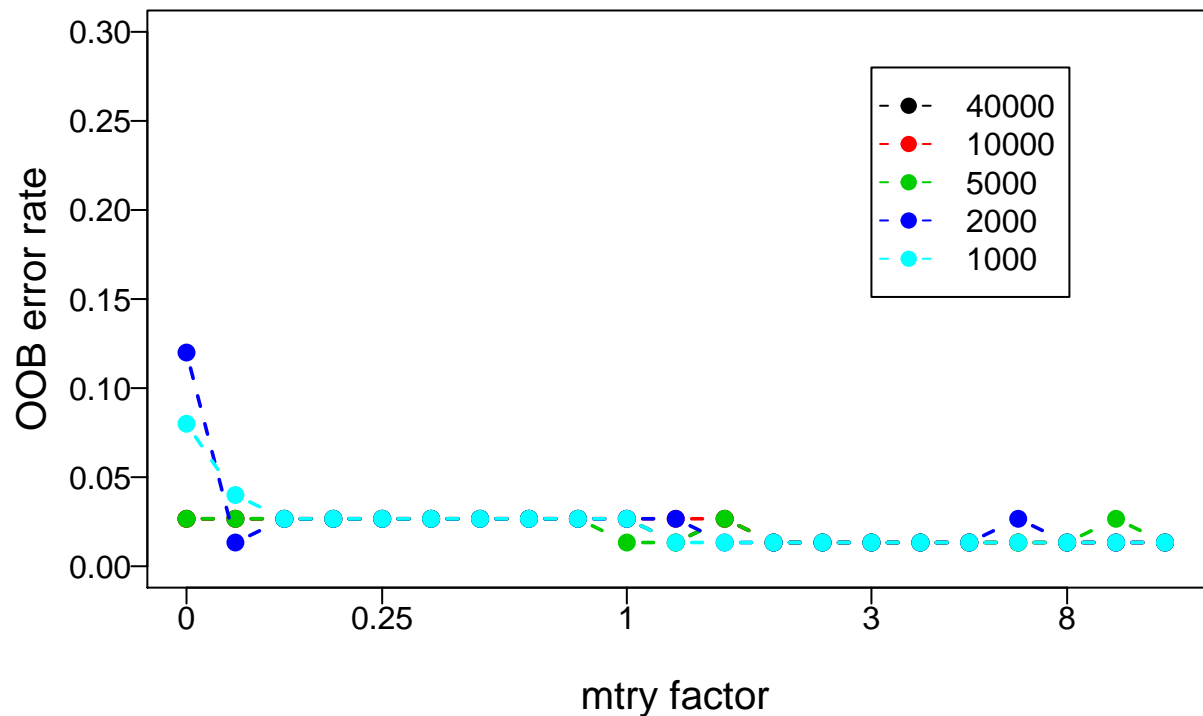
3 classes; 2 dimensions; 20 genes/dimen.; nodesize = 5



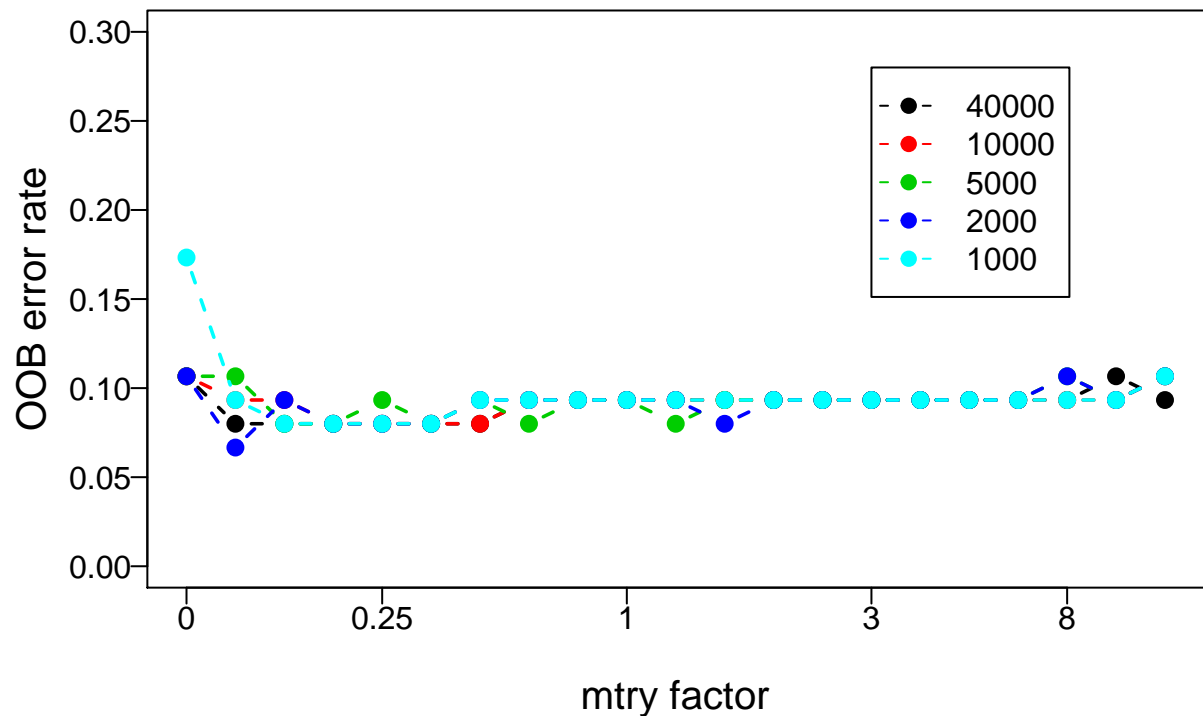
3 classes; 2 dimensions; 20 genes/dimen.; nodesize = 5



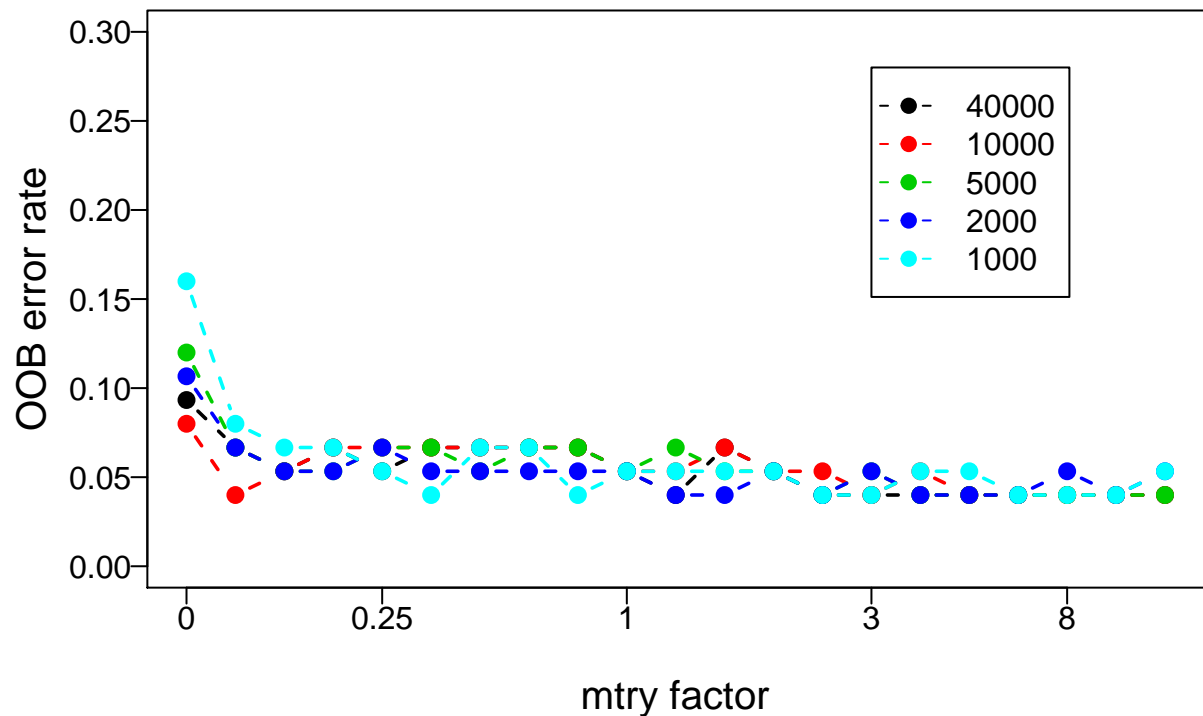
3 classes; 2 dimensions; 100 genes/dimen.; nodesize = 5



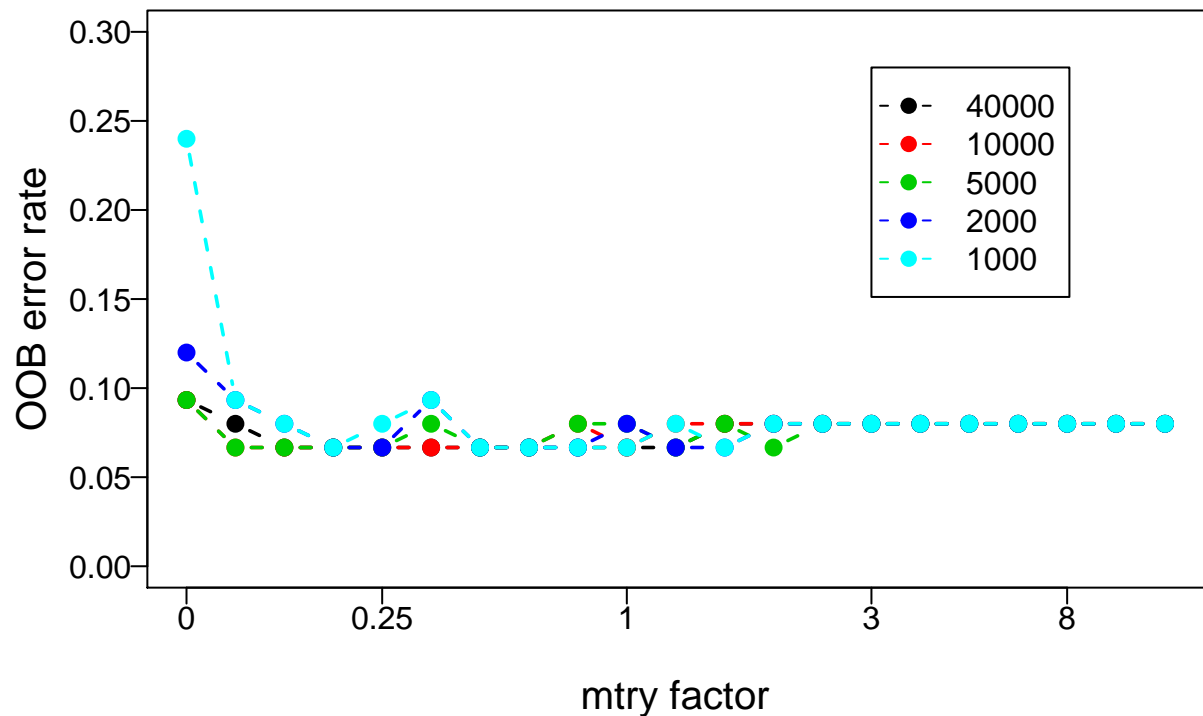
3 classes; 2 dimensions; 100 genes/dimen.; nodesize = 5



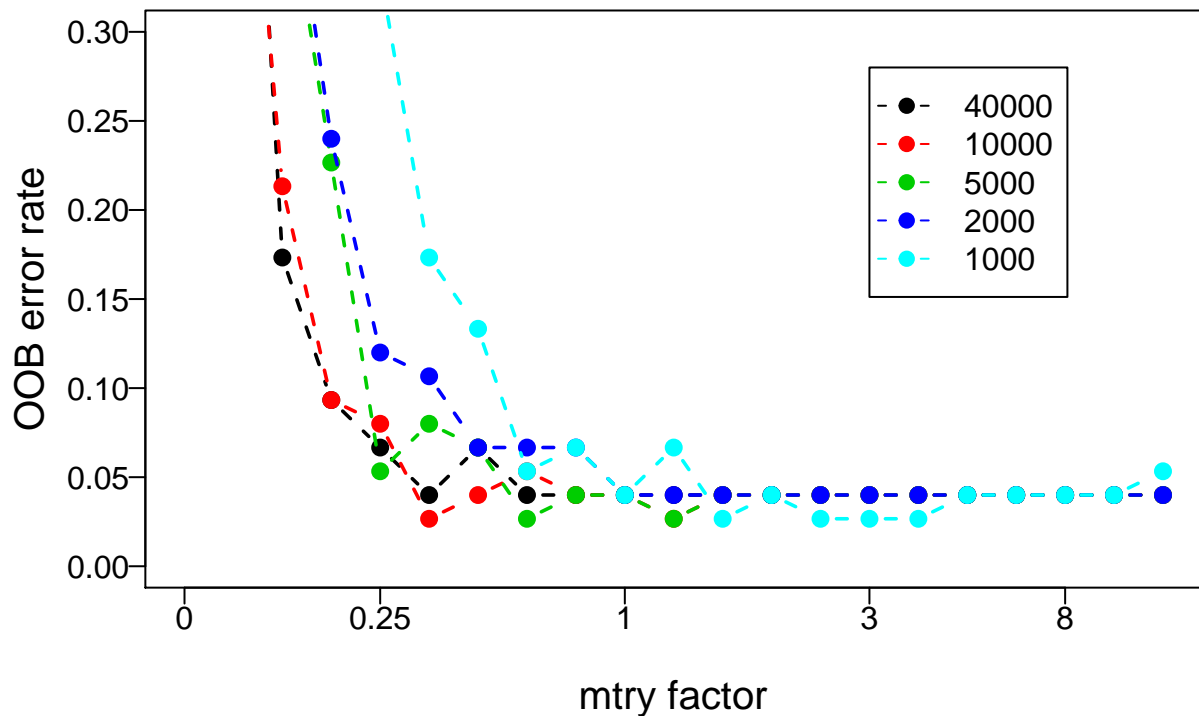
3 classes; 2 dimensions; 100 genes/dimen.; nodesize = 5



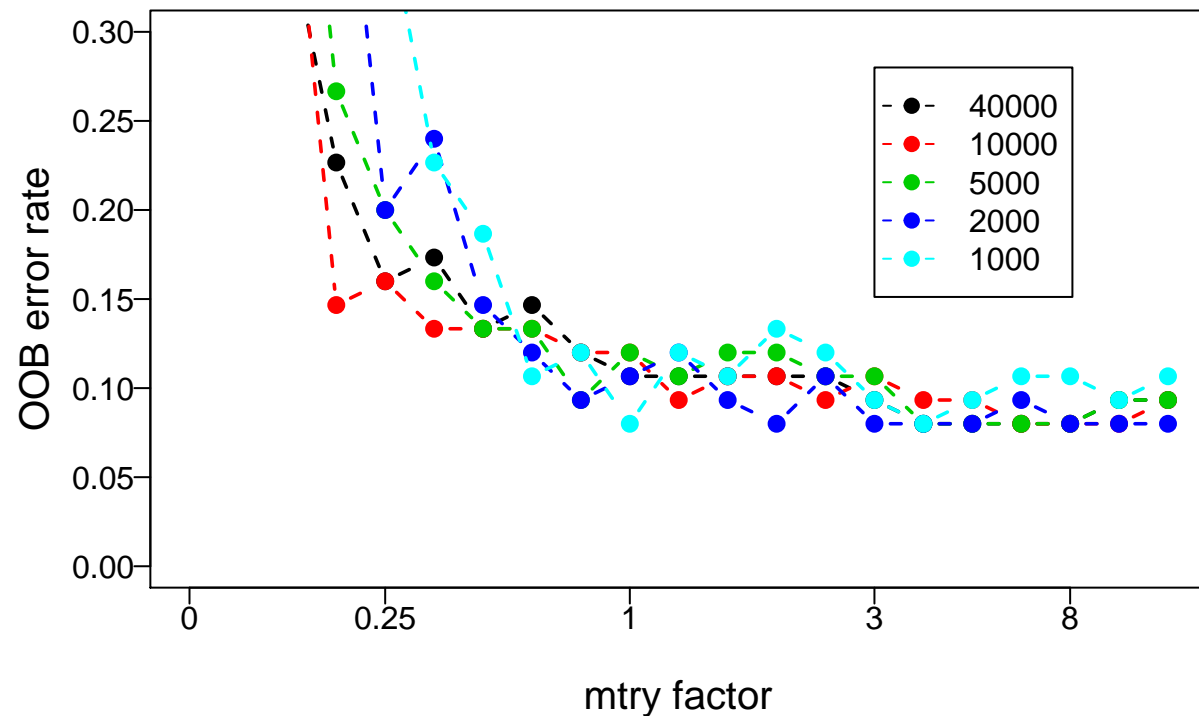
3 classes; 2 dimensions; 100 genes/dimen.; nodesize = 5



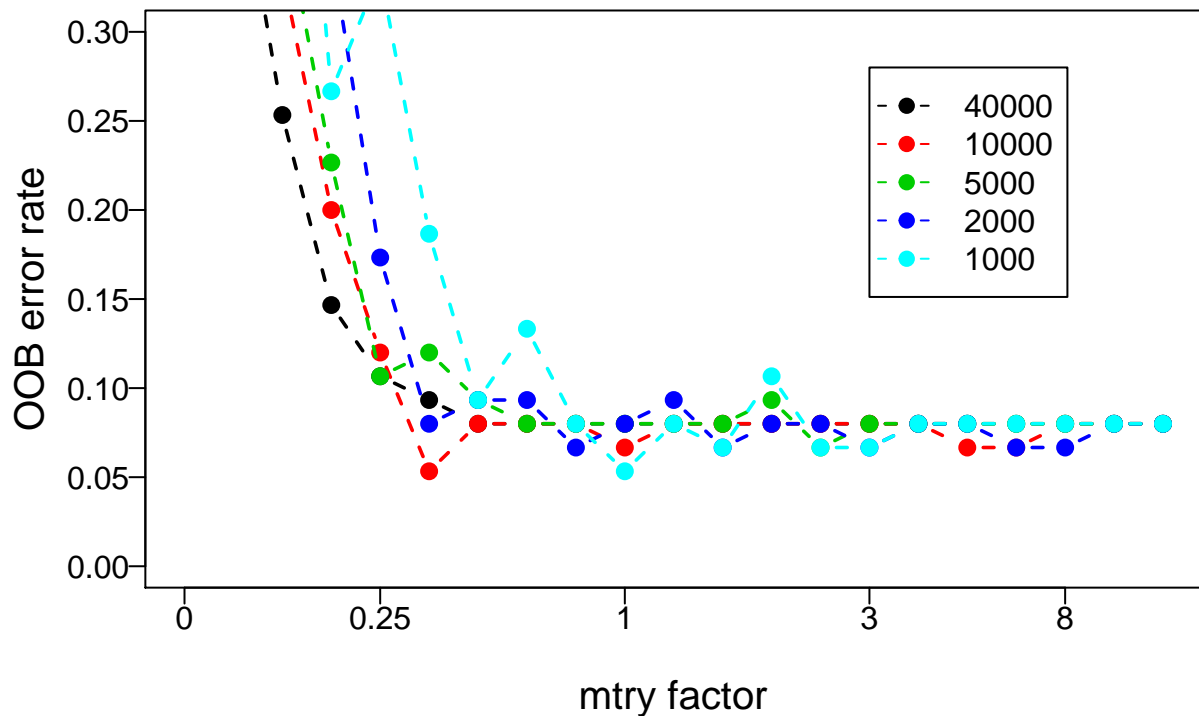
3 classes; 3 dimensions; 5 genes/dimen.; nodelist = 5



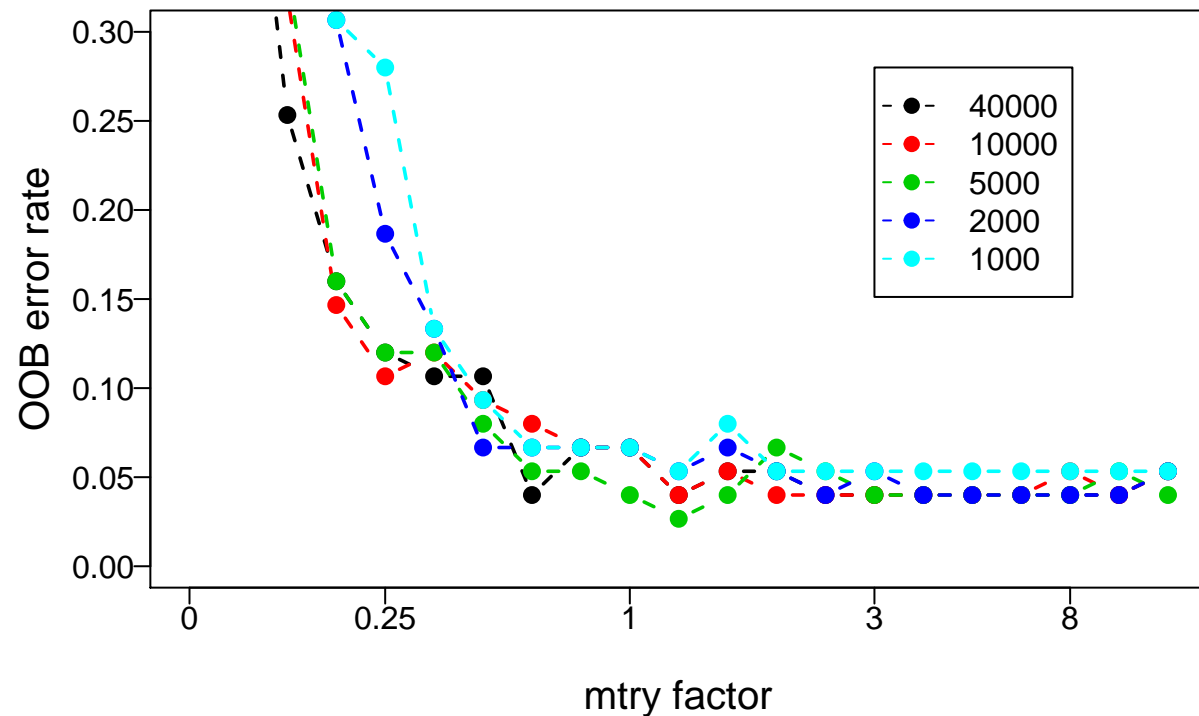
3 classes; 3 dimensions; 5 genes/dimen.; nodelist = 5



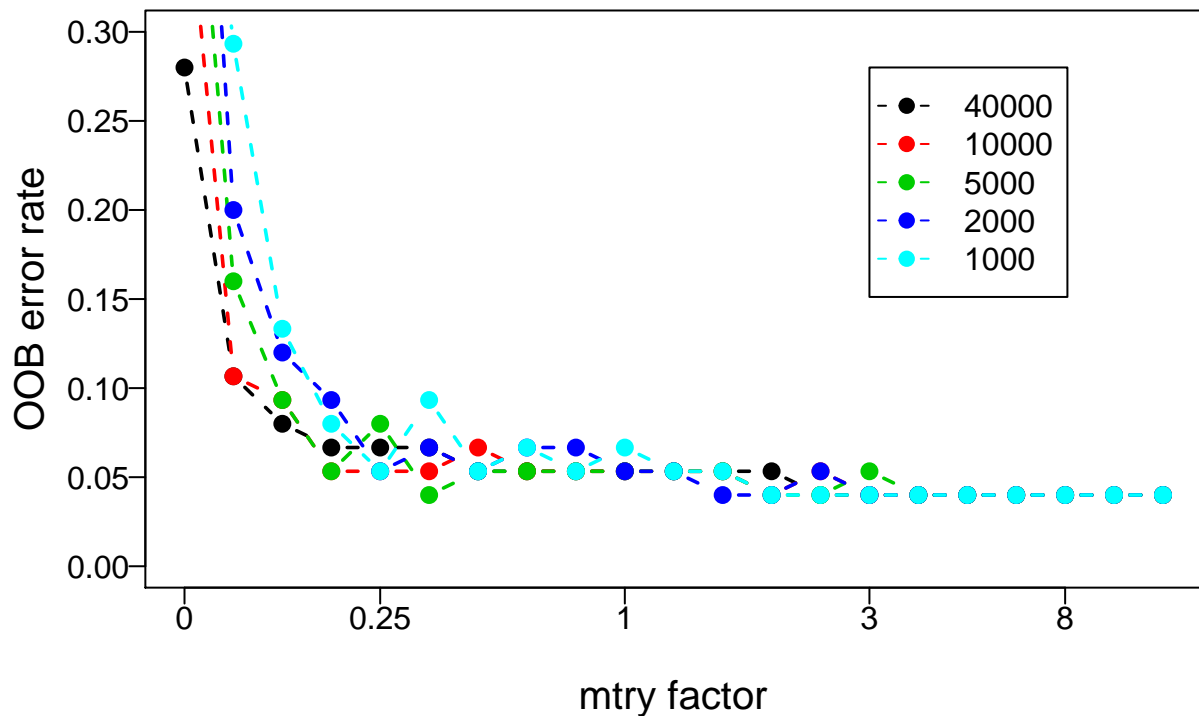
3 classes; 3 dimensions; 5 genes/dimen.; nodelist = 5



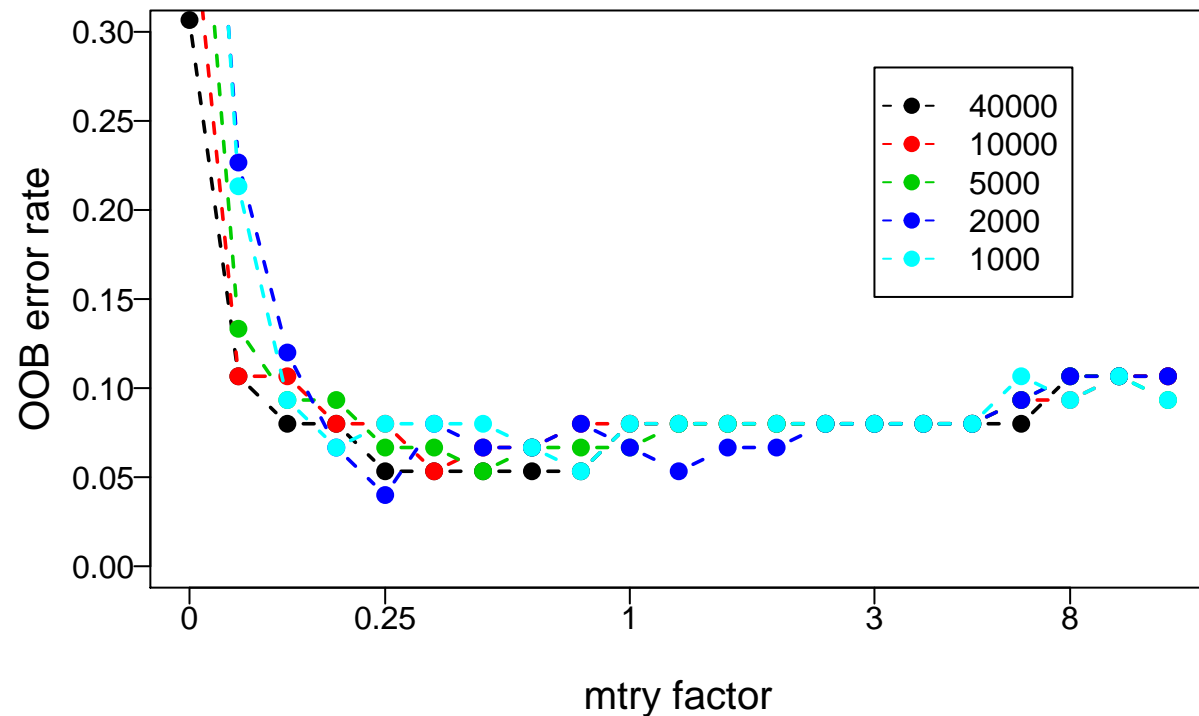
3 classes; 3 dimensions; 5 genes/dimen.; nodelist = 5



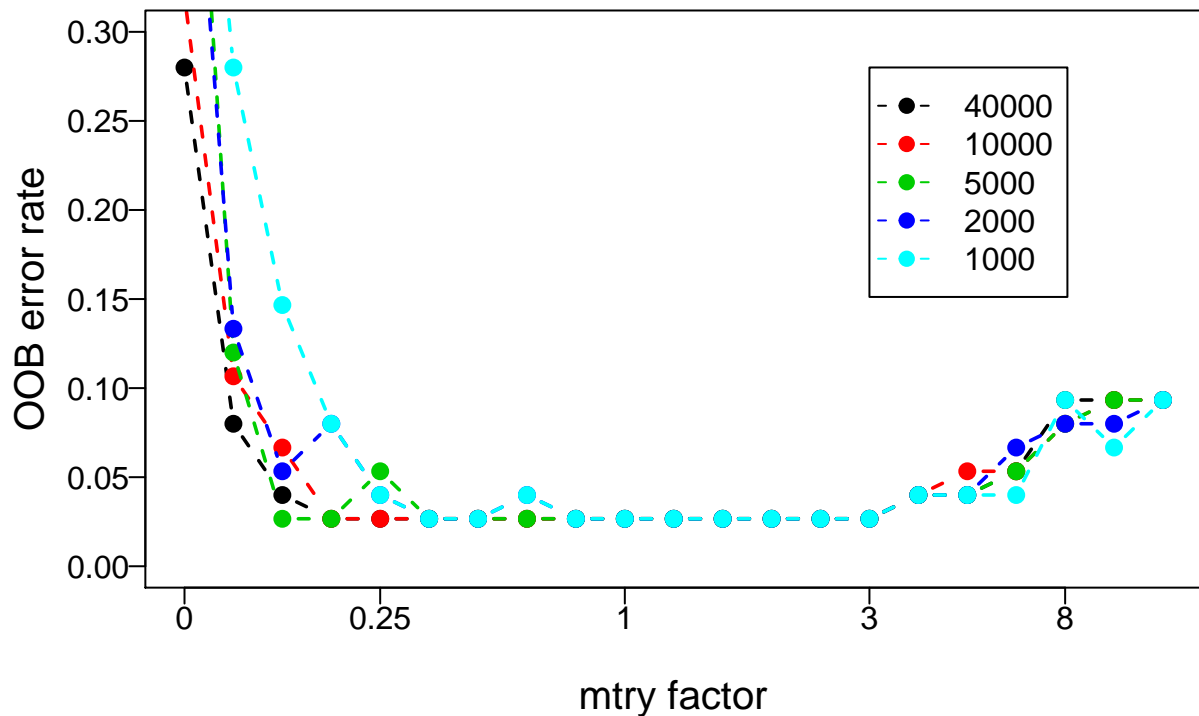
3 classes; 3 dimensions; 20 genes/dimen.; nodesize = 5



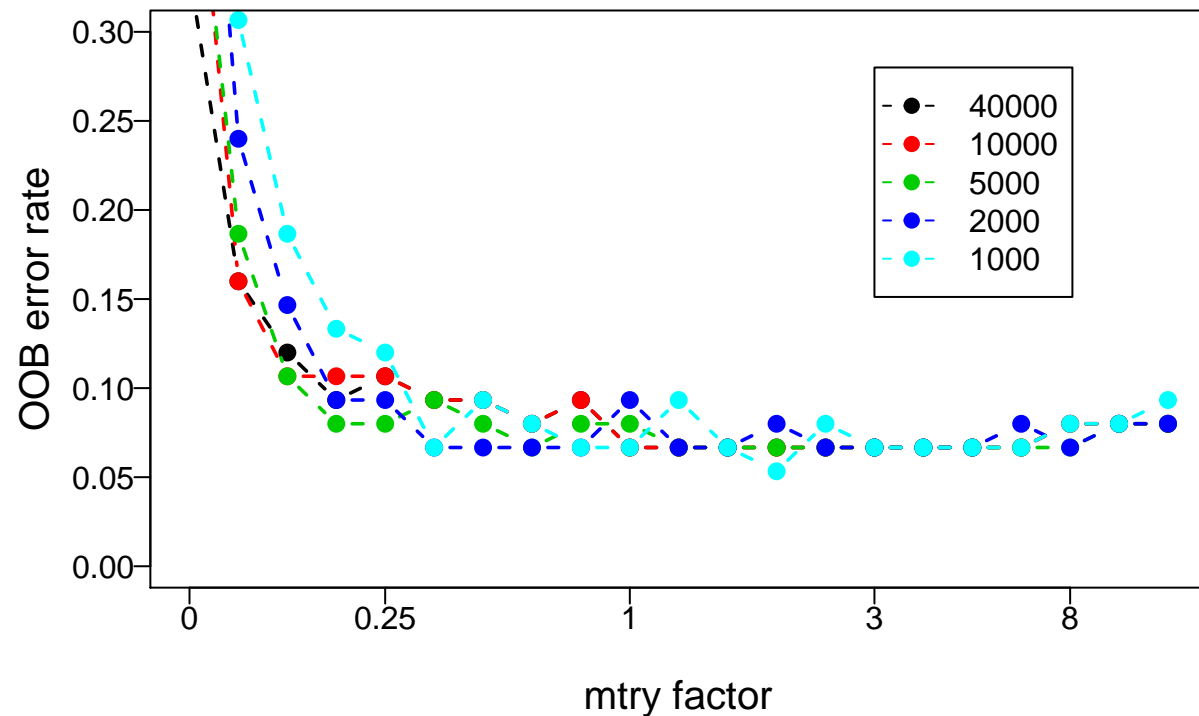
3 classes; 3 dimensions; 20 genes/dimen.; nodesize = 5



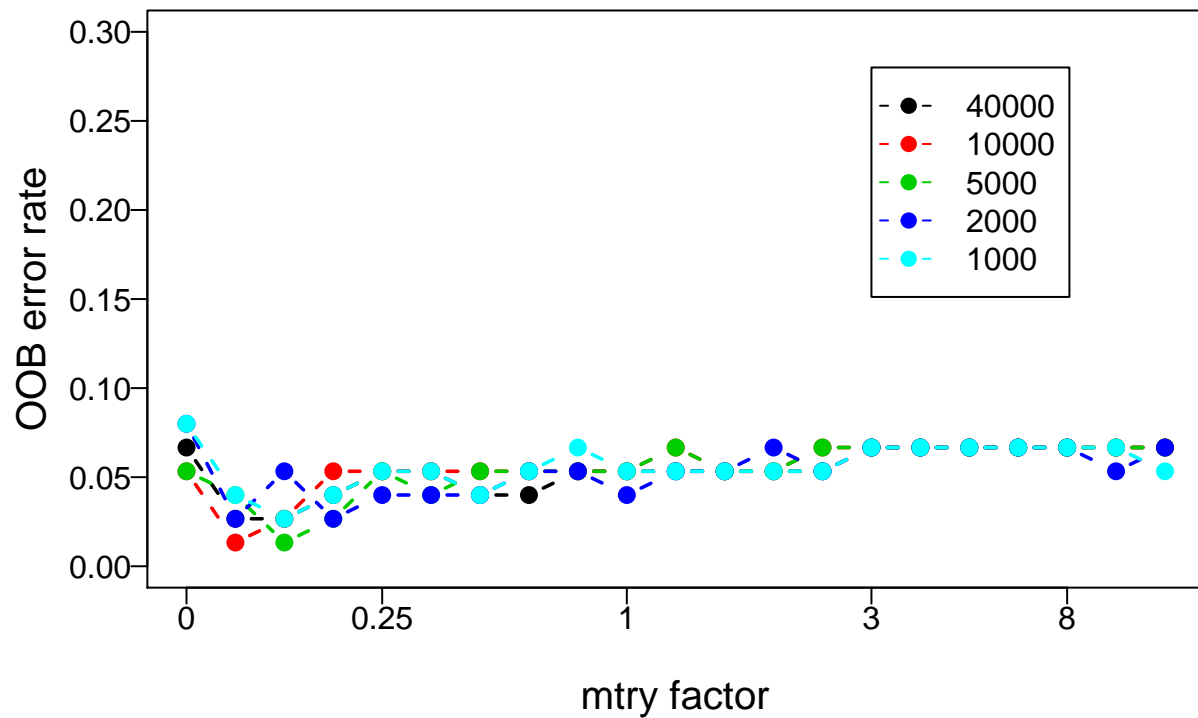
3 classes; 3 dimensions; 20 genes/dimen.; nodesize = 5



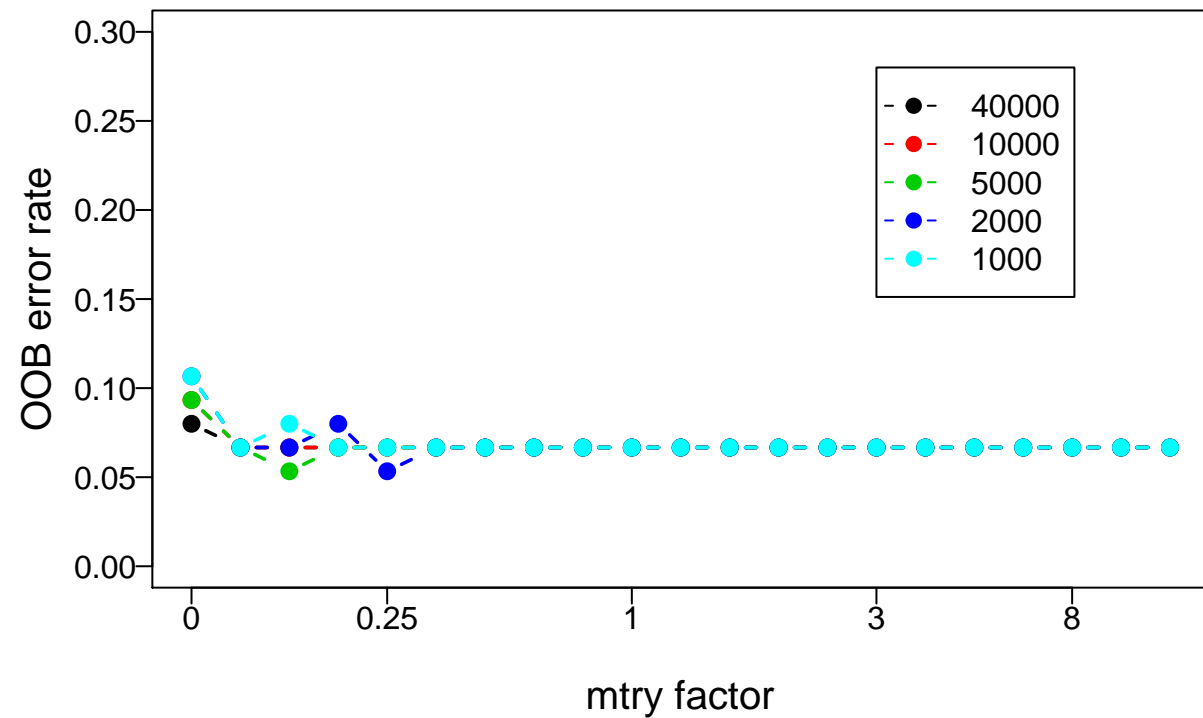
3 classes; 3 dimensions; 20 genes/dimen.; nodesize = 5



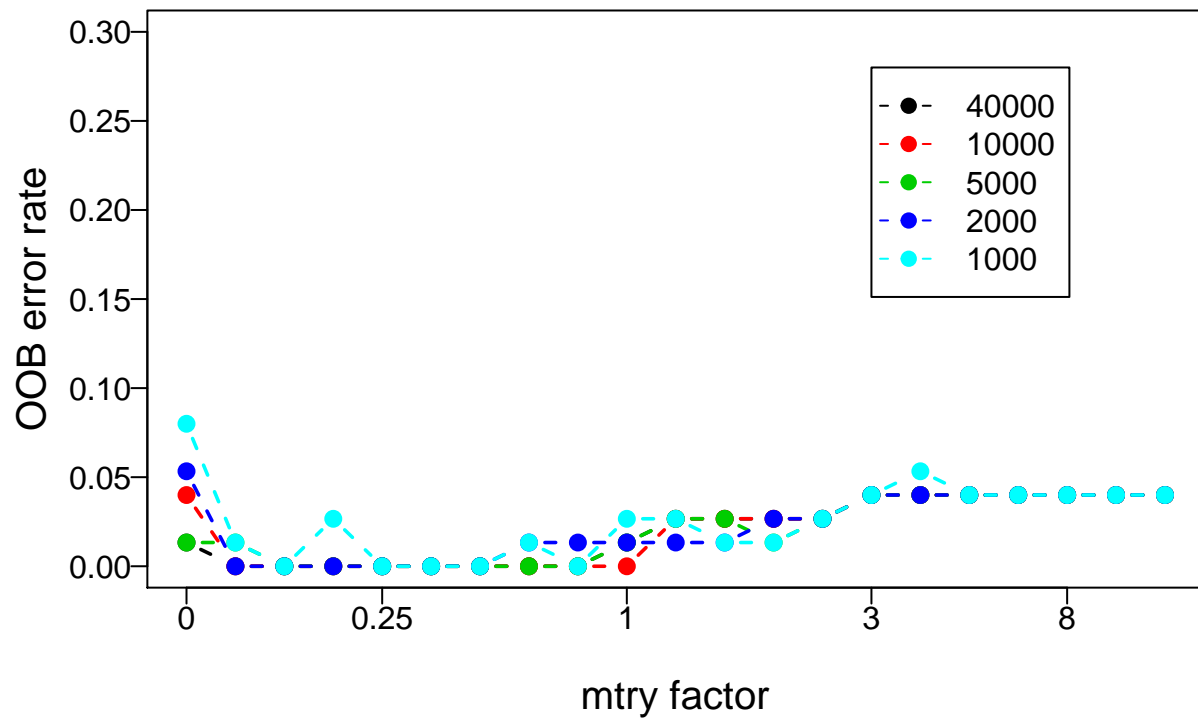
3 classes; 3 dimensions; 100 genes/dimen.; nodesize = 5



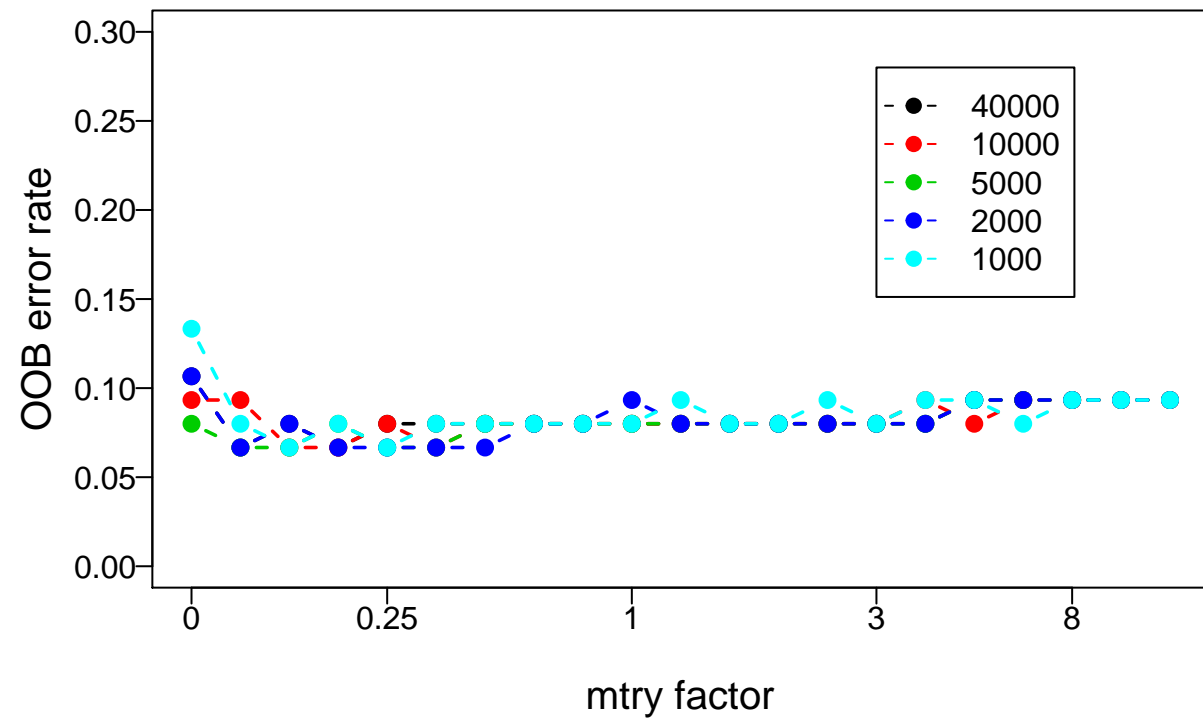
3 classes; 3 dimensions; 100 genes/dimen.; nodesize = 5



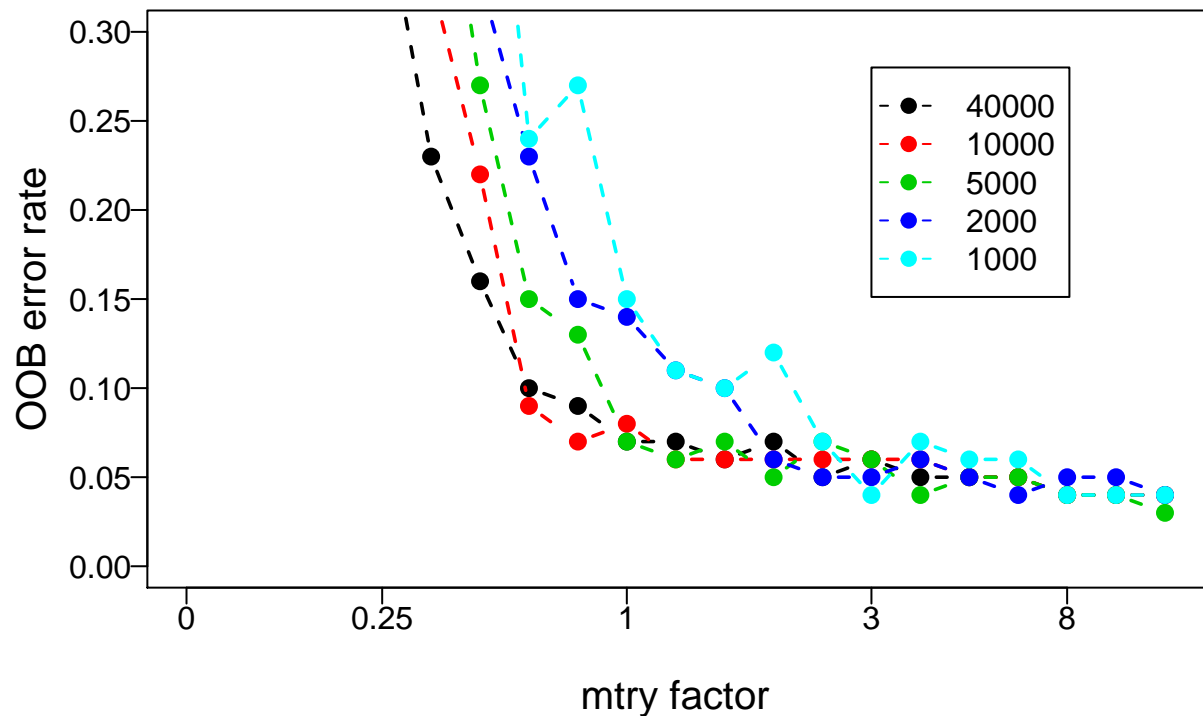
3 classes; 3 dimensions; 100 genes/dimen.; nodesize = 5



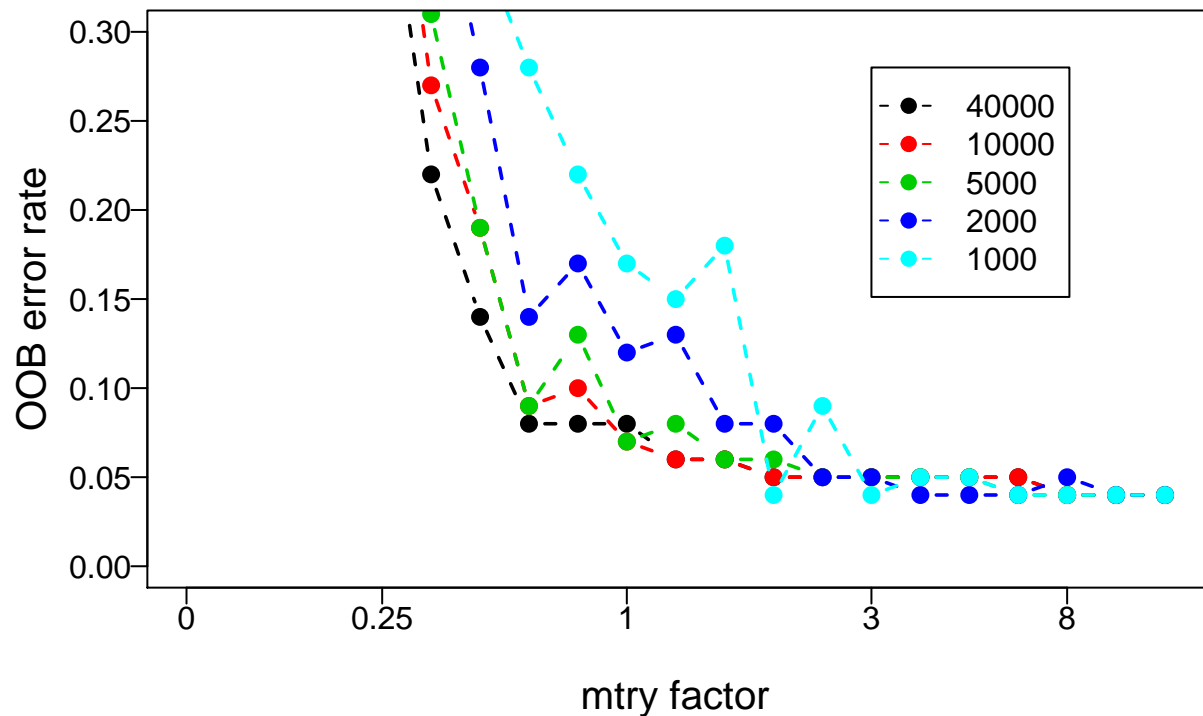
3 classes; 3 dimensions; 100 genes/dimen.; nodesize = 5



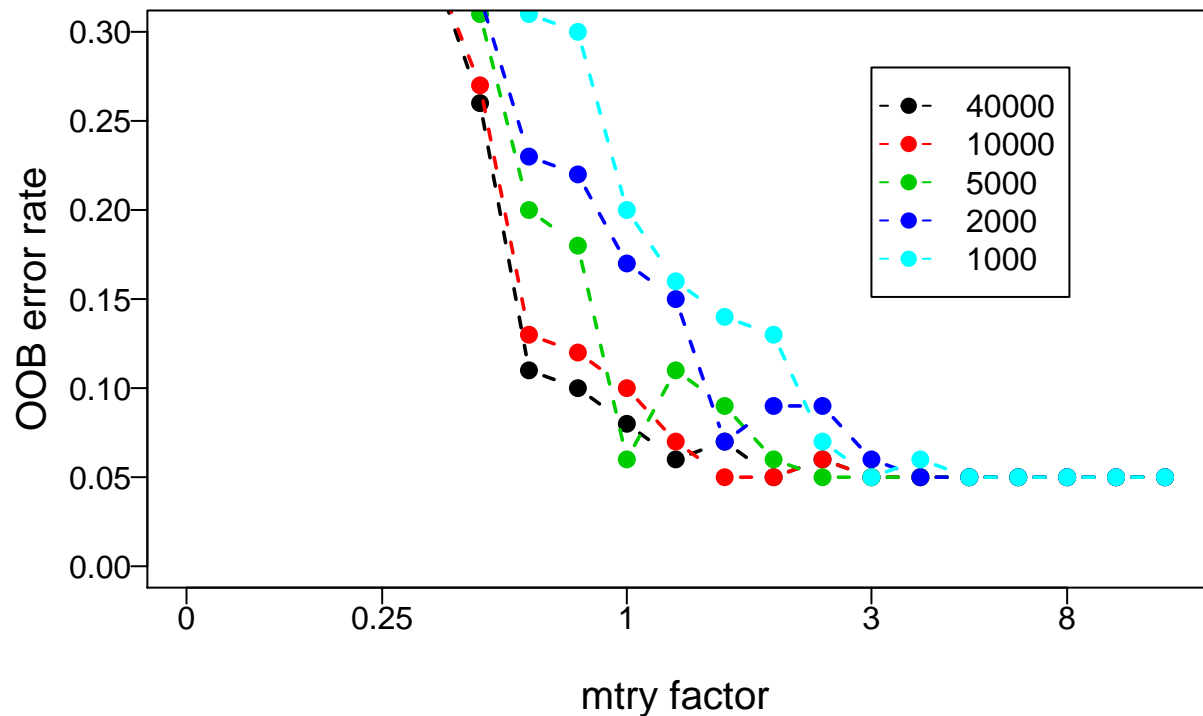
4 classes; 1 dimensions; 5 genes/dimen.; nodesize = 5



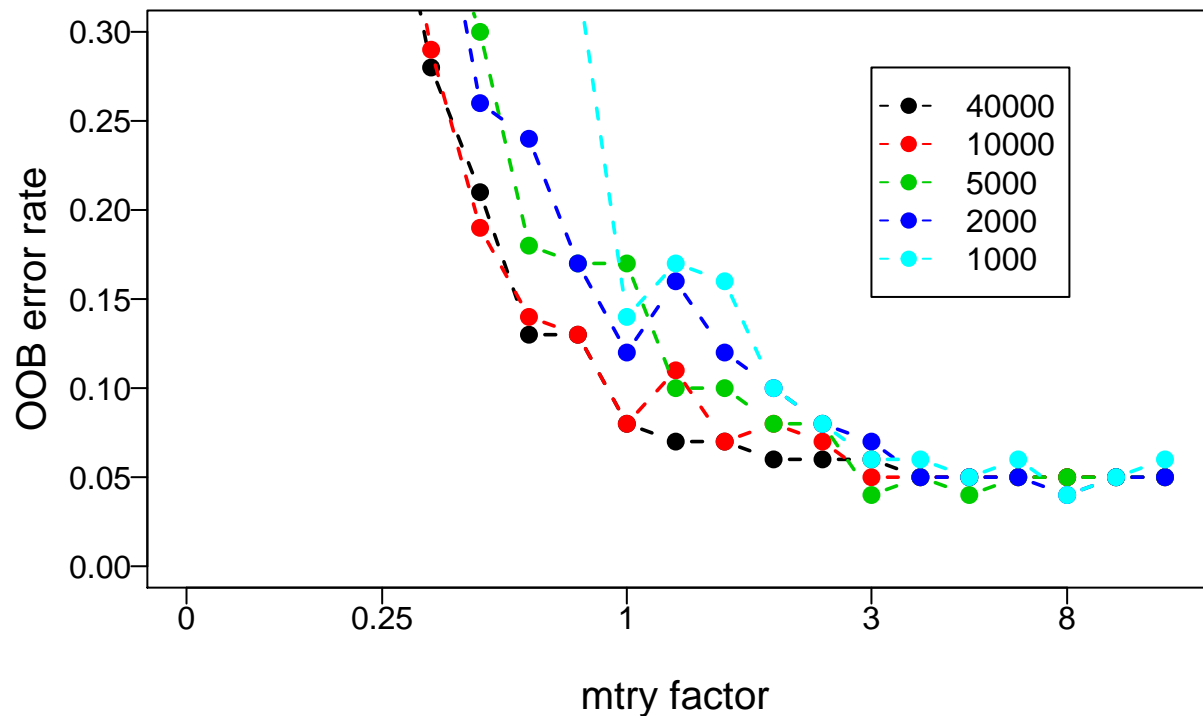
4 classes; 1 dimensions; 5 genes/dimen.; nodesize = 5



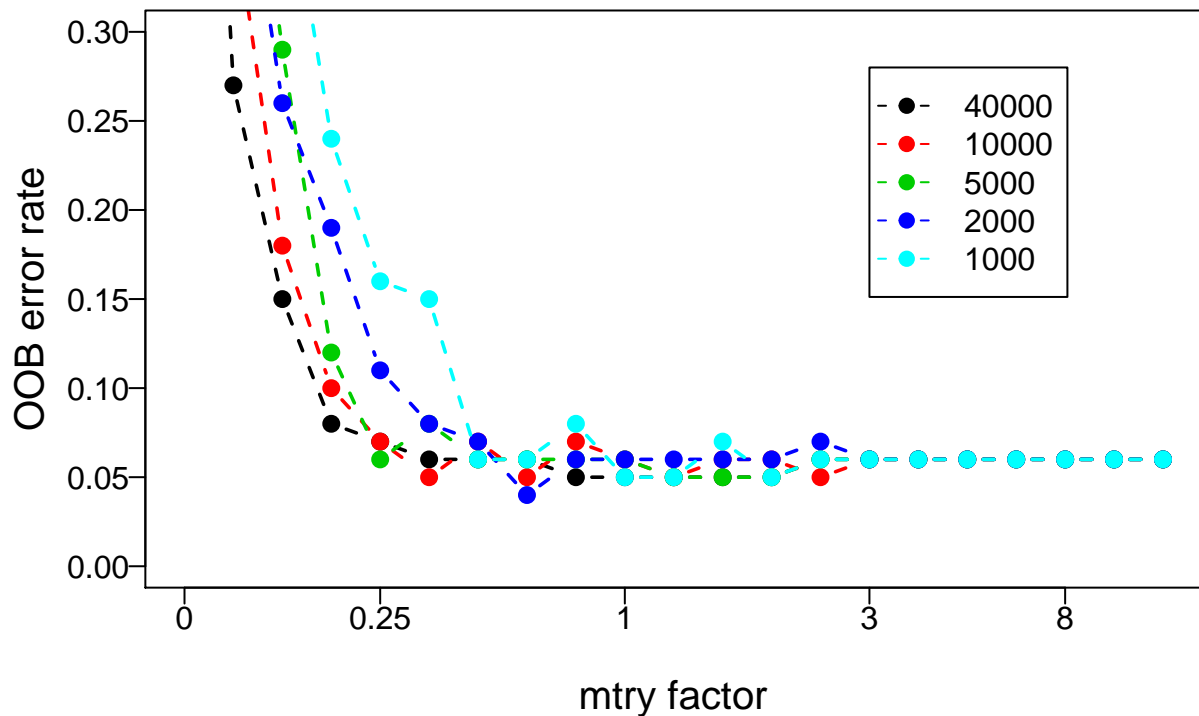
4 classes; 1 dimensions; 5 genes/dimen.; nodesize = 5



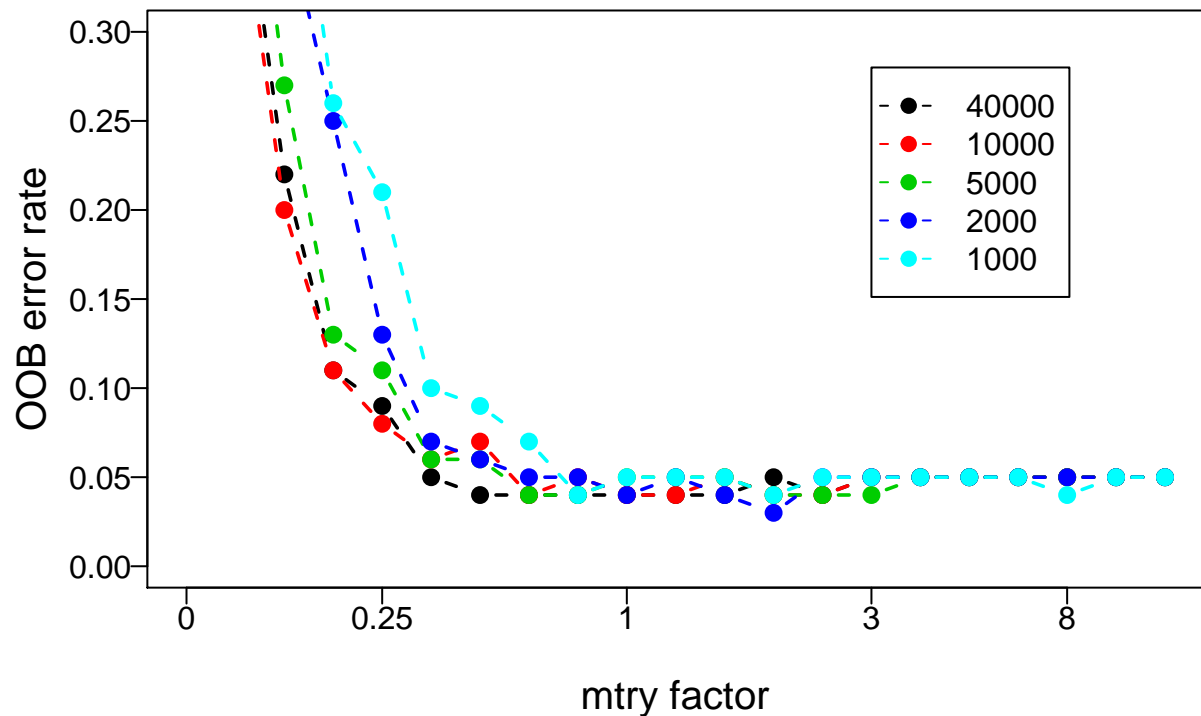
4 classes; 1 dimensions; 5 genes/dimen.; nodesize = 5



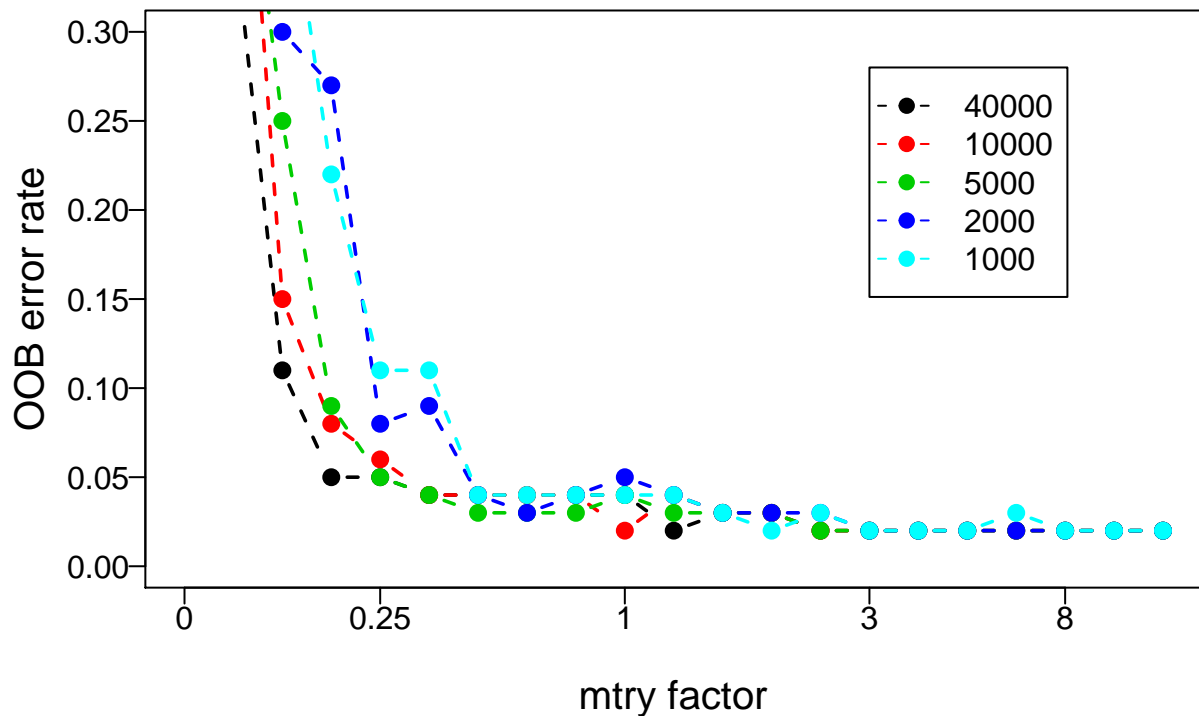
4 classes; 1 dimensions; 20 genes/dimen.; nodesize = 5



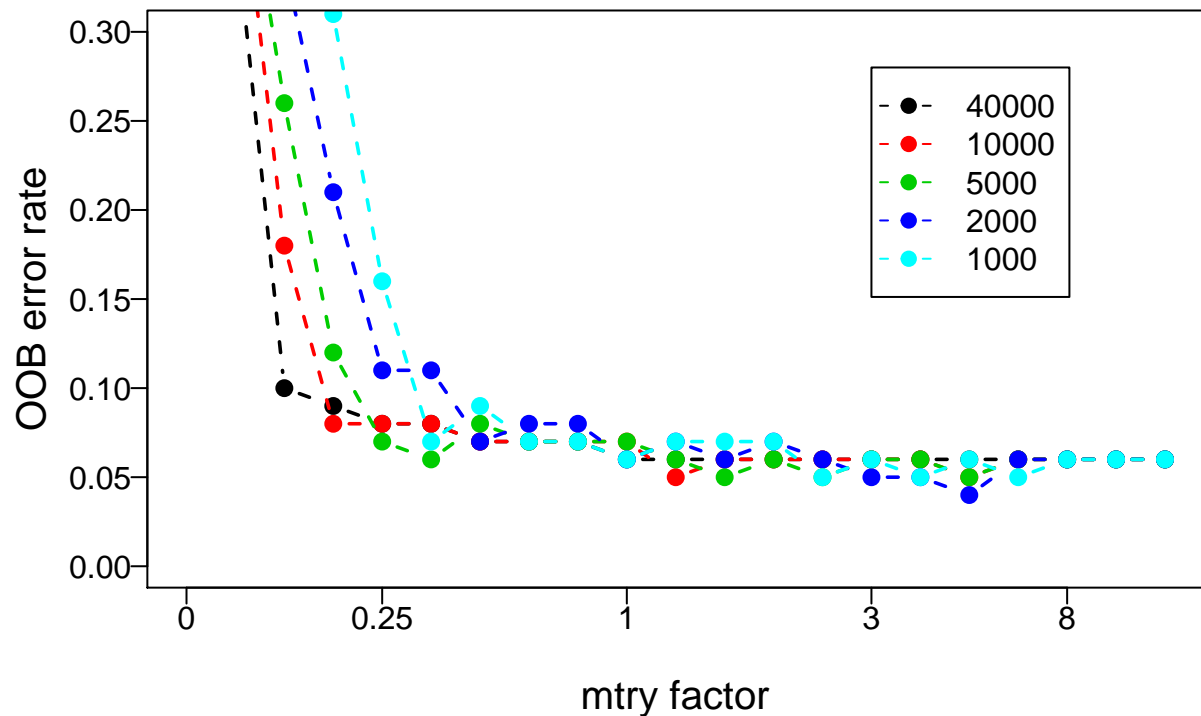
4 classes; 1 dimensions; 20 genes/dimen.; nodesize = 5



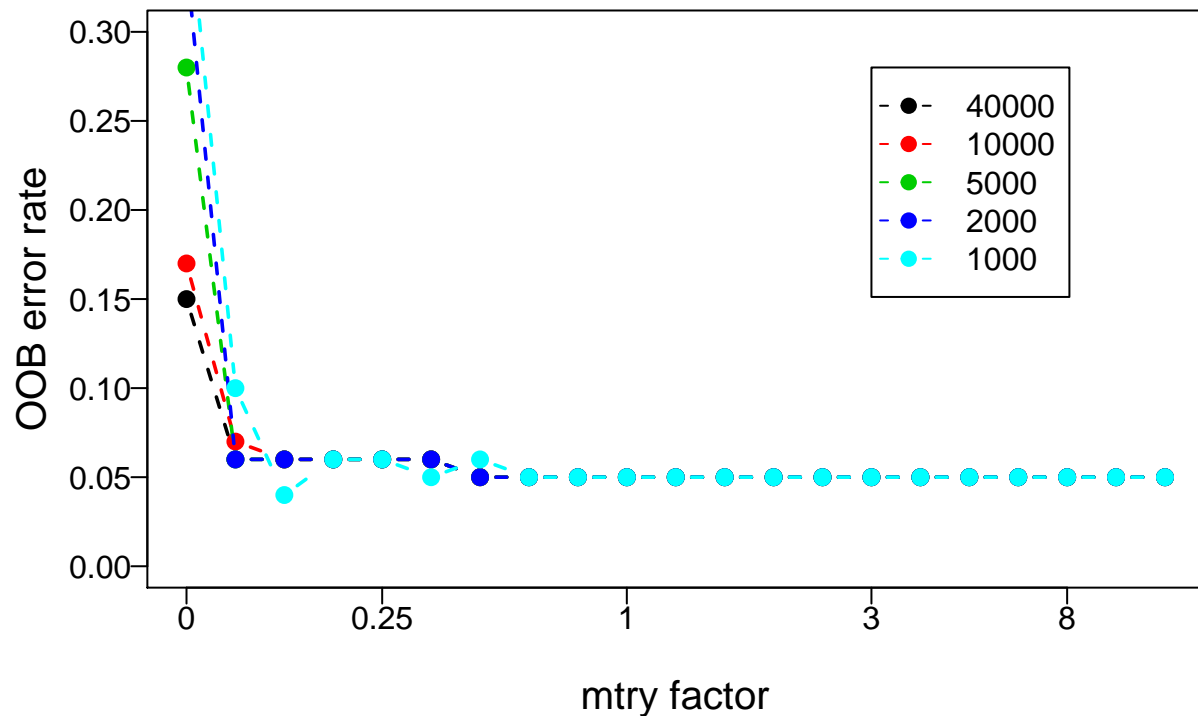
4 classes; 1 dimensions; 20 genes/dimen.; nodesize = 5



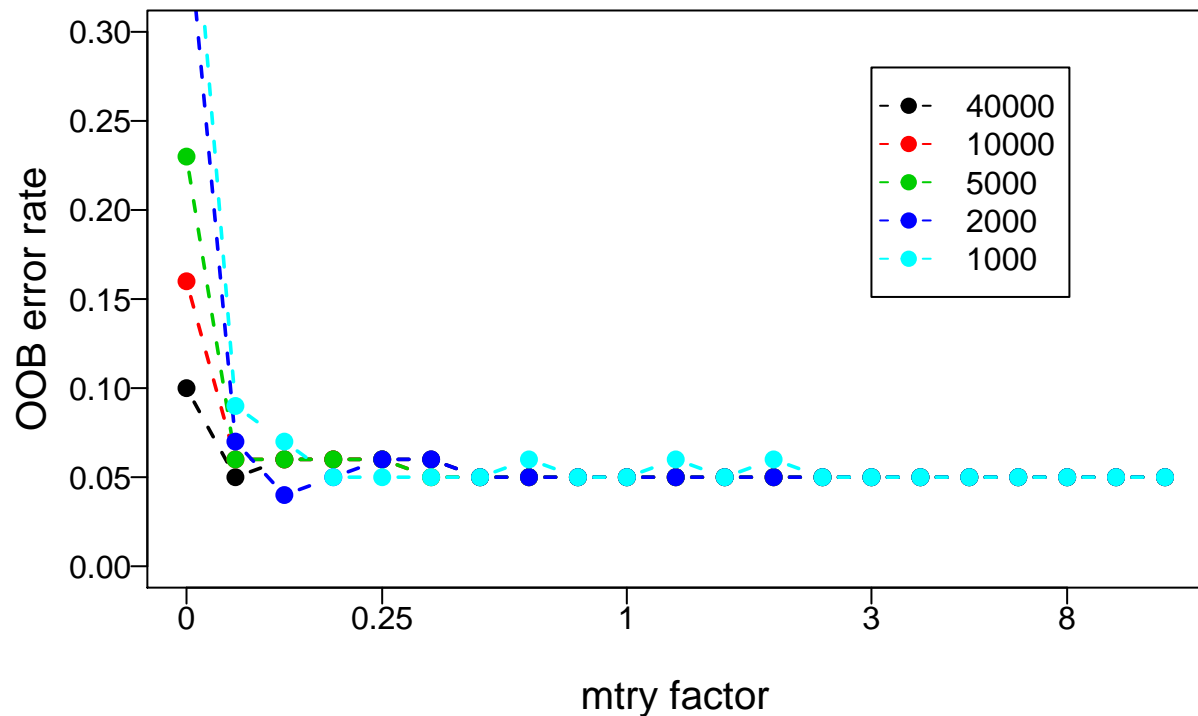
4 classes; 1 dimensions; 20 genes/dimen.; nodesize = 5



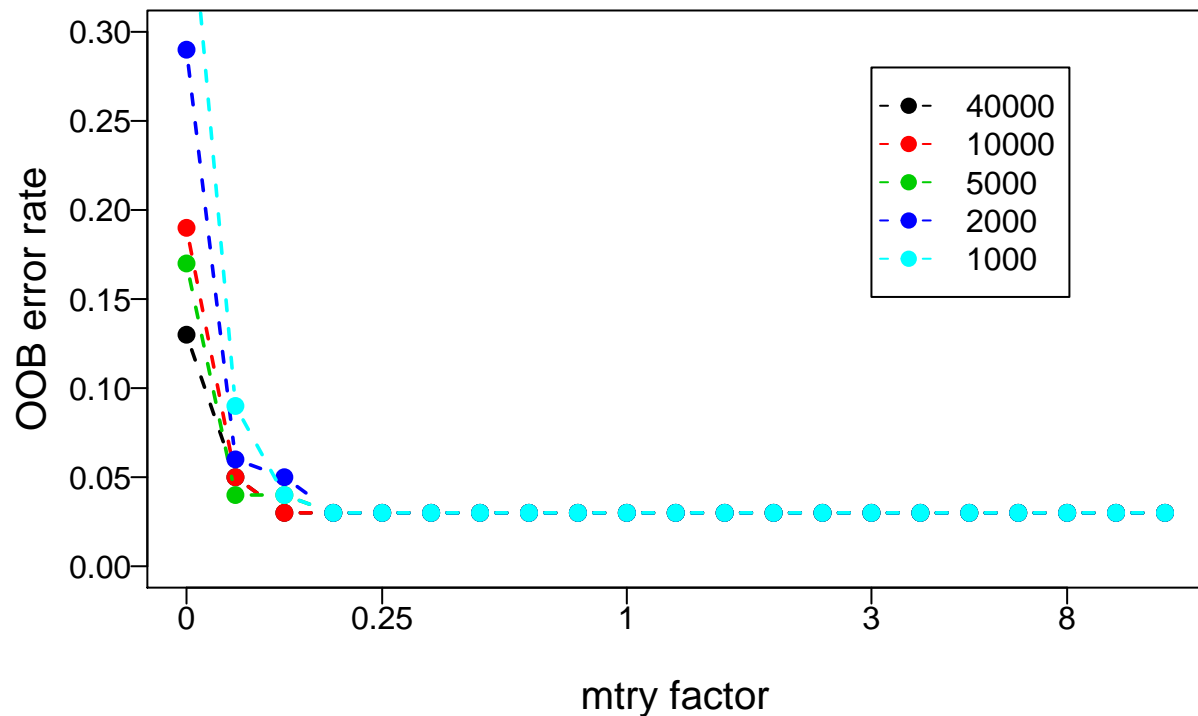
4 classes; 1 dimensions; 100 genes/dimen.; nodesize = 5



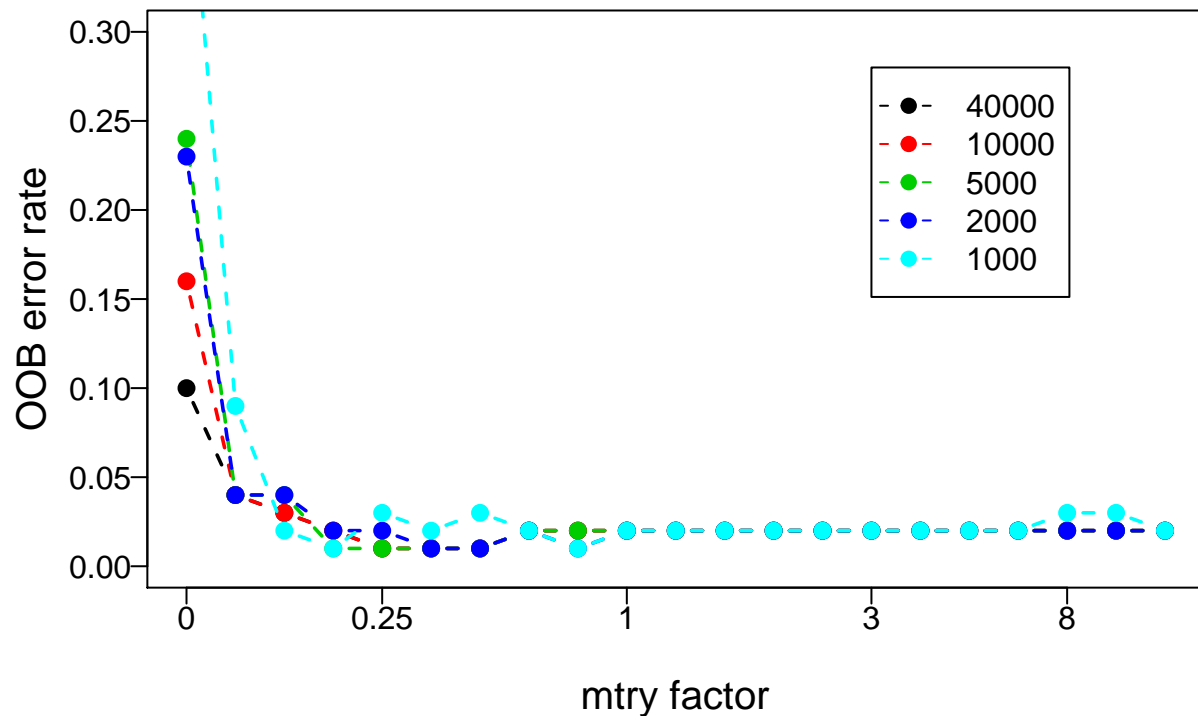
4 classes; 1 dimensions; 100 genes/dimen.; nodesize = 5



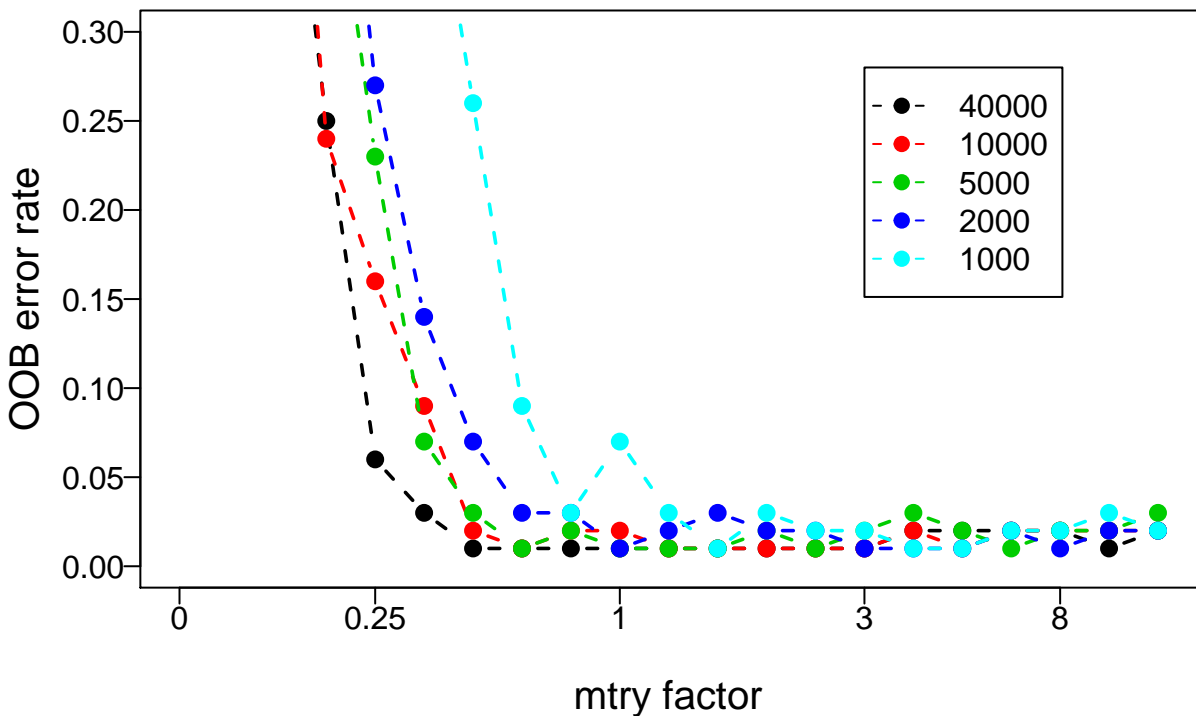
4 classes; 1 dimensions; 100 genes/dimen.; nodesize = 5



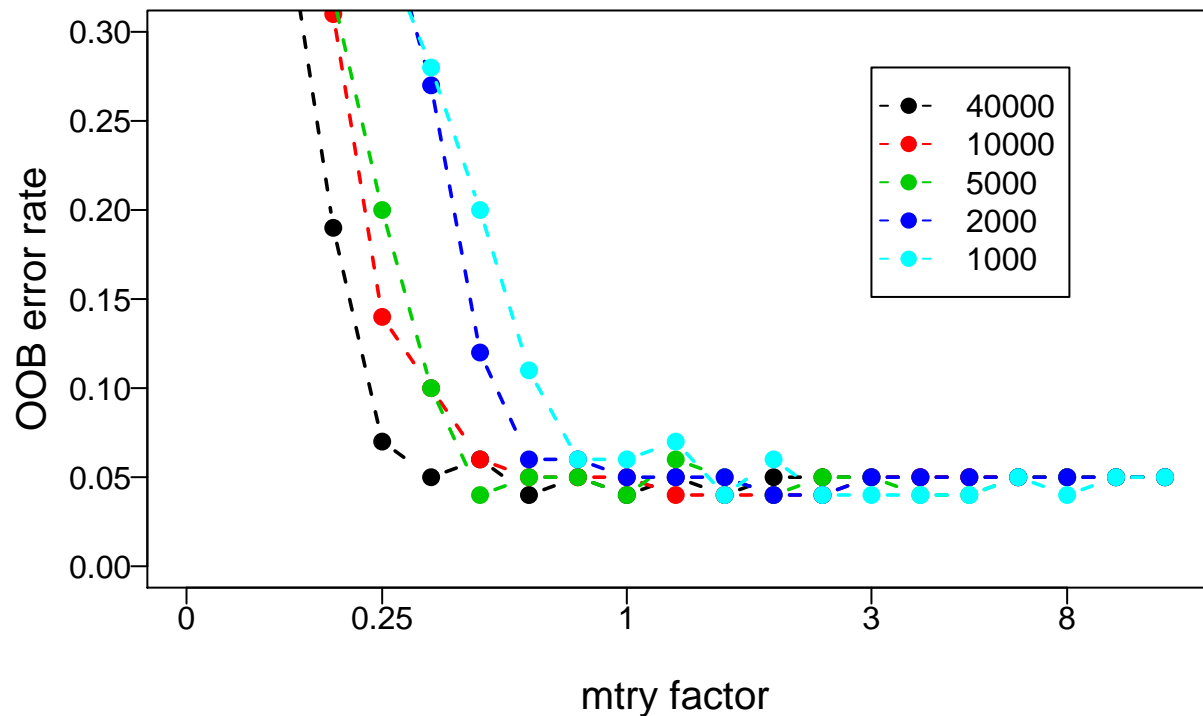
4 classes; 1 dimensions; 100 genes/dimen.; nodesize = 5



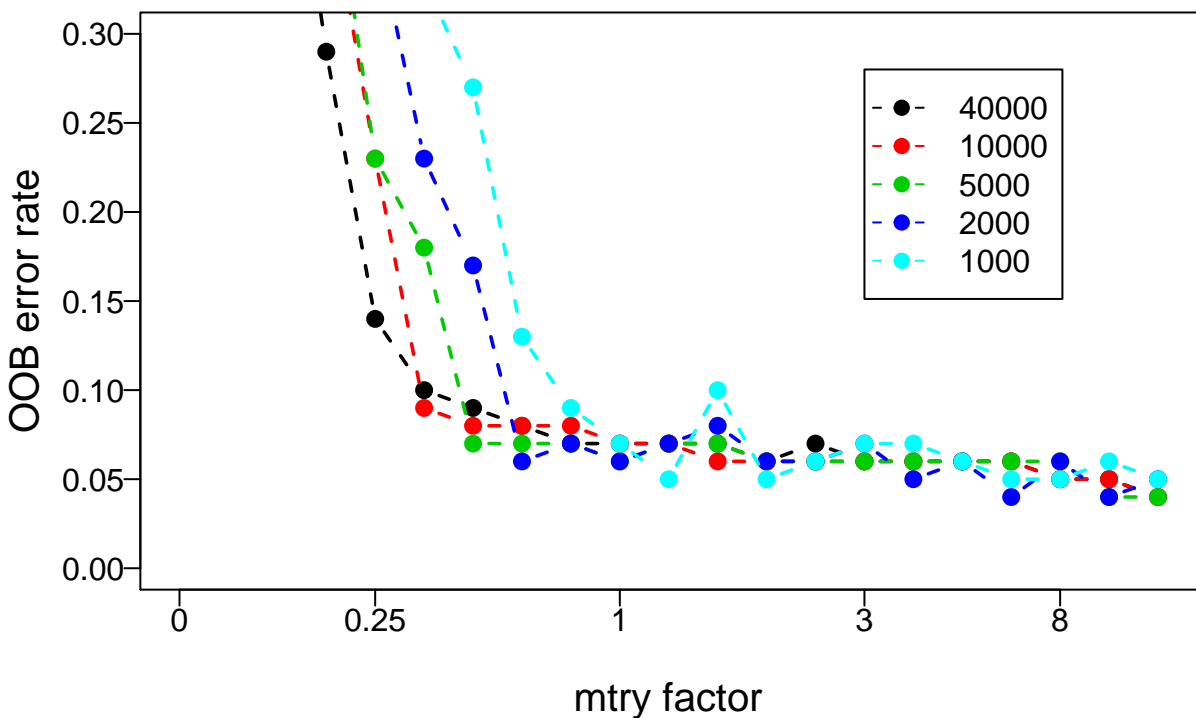
4 classes; 2 dimensions; 5 genes/dimen.; nodesize = 5



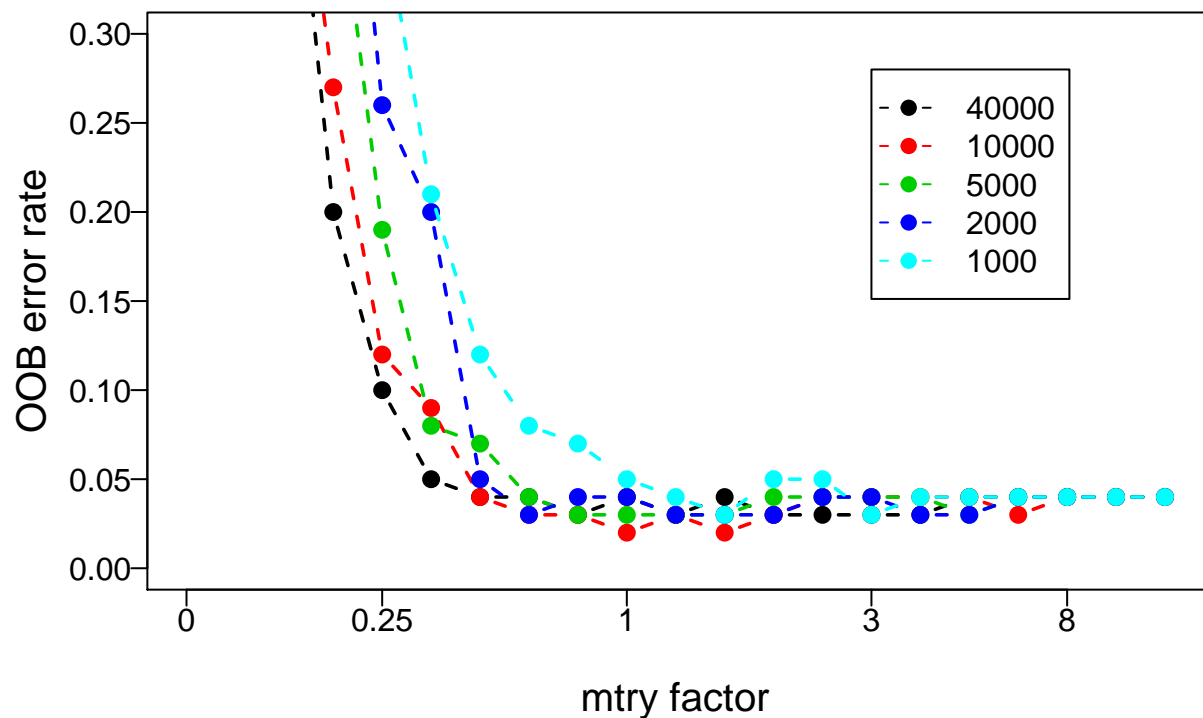
4 classes; 2 dimensions; 5 genes/dimen.; nodesize = 5



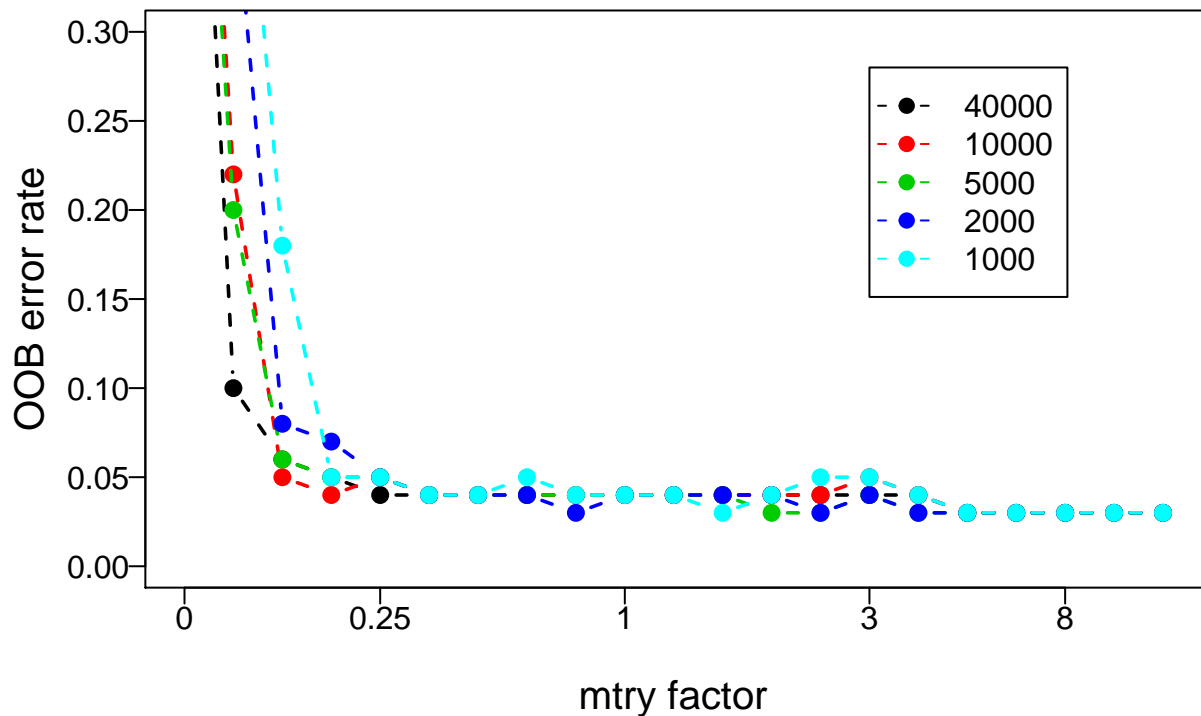
4 classes; 2 dimensions; 5 genes/dimen.; nodesize = 5



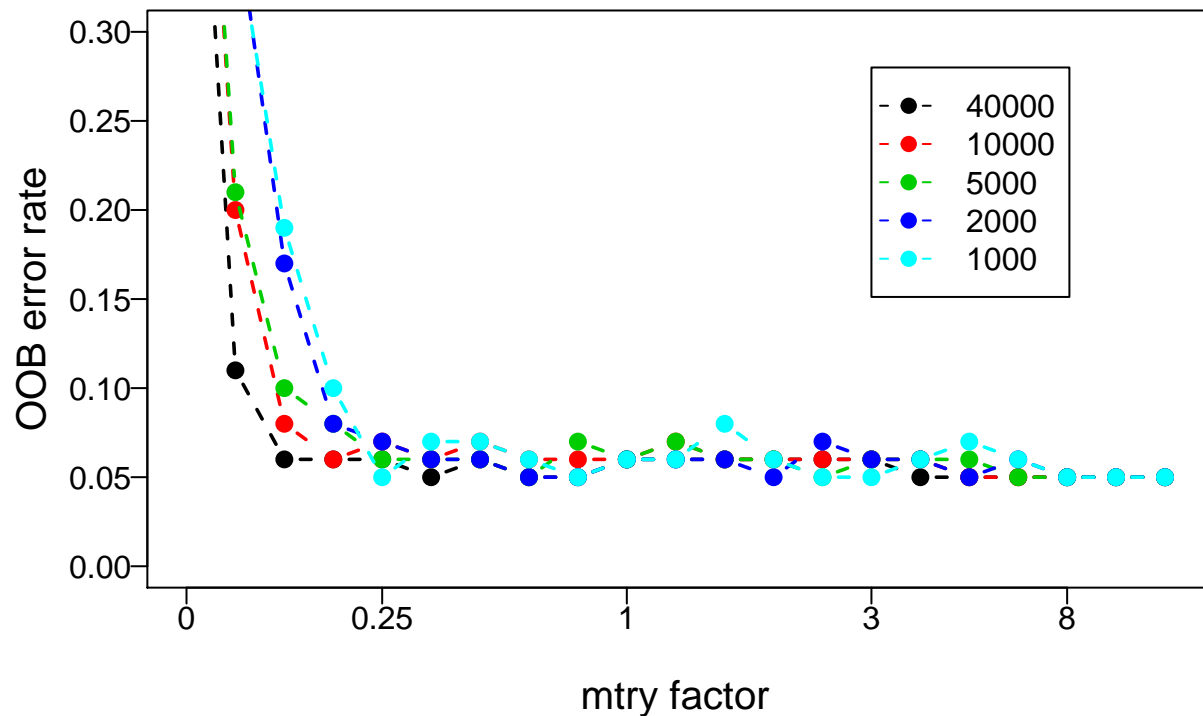
4 classes; 2 dimensions; 5 genes/dimen.; nodesize = 5



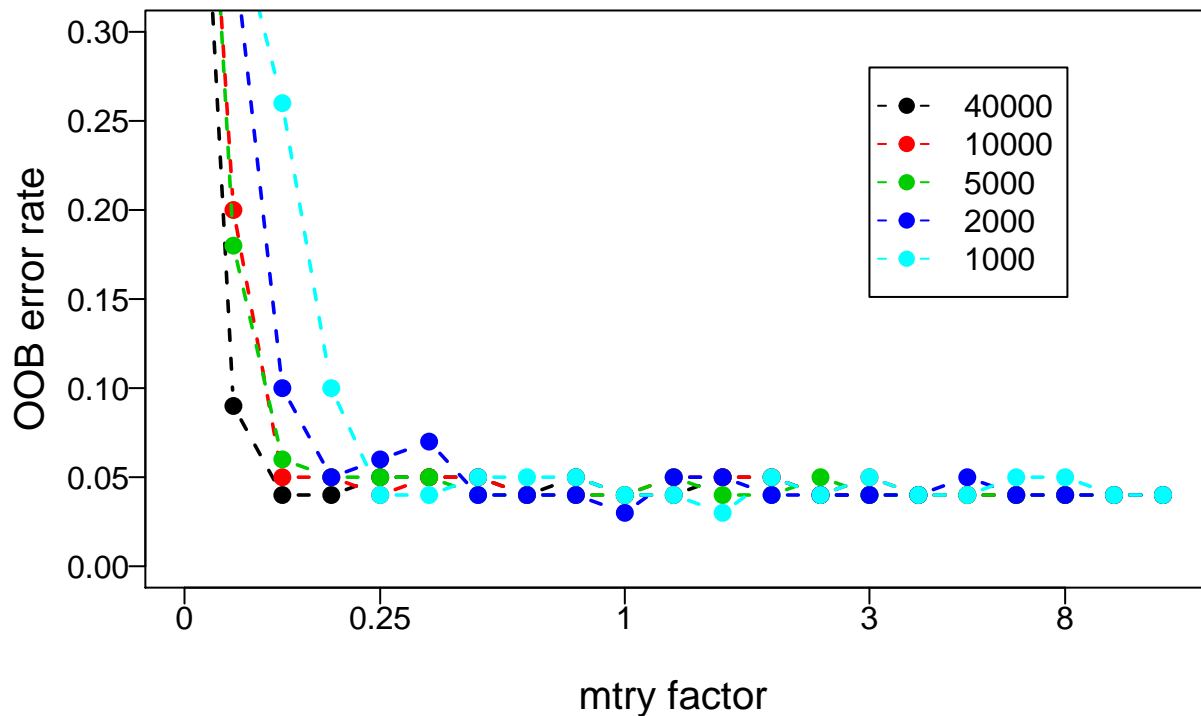
4 classes; 2 dimensions; 20 genes/dimen.; nodesize = 5



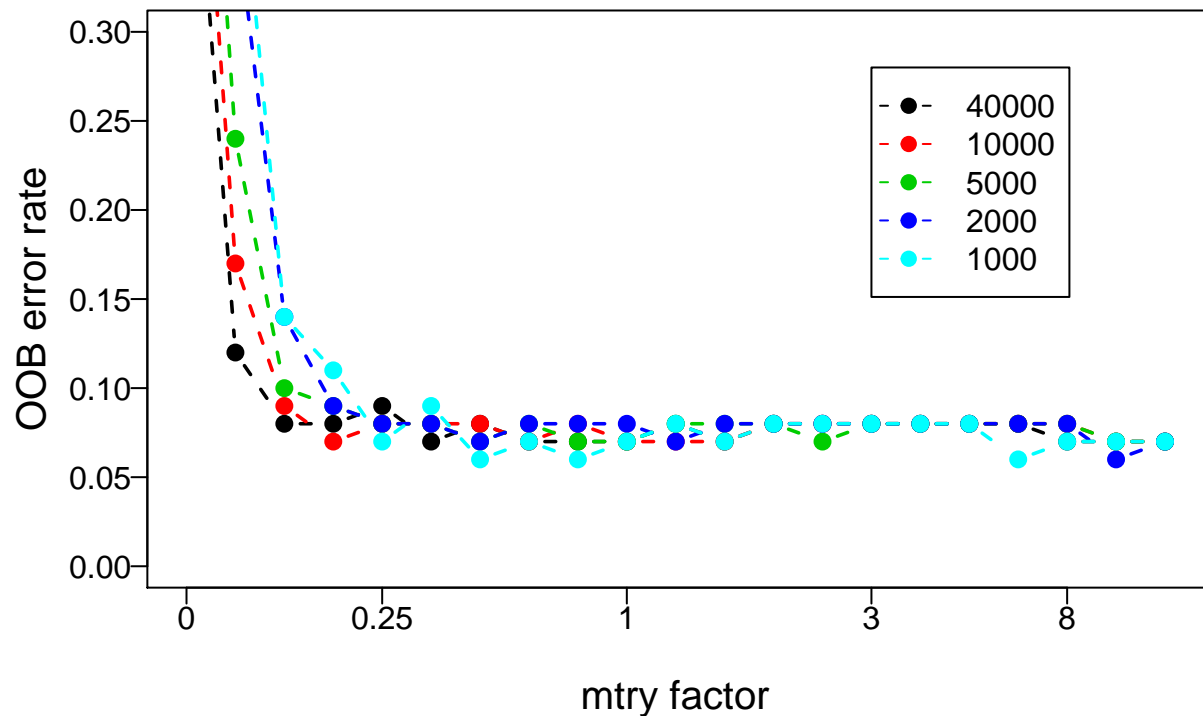
4 classes; 2 dimensions; 20 genes/dimen.; nodesize = 5



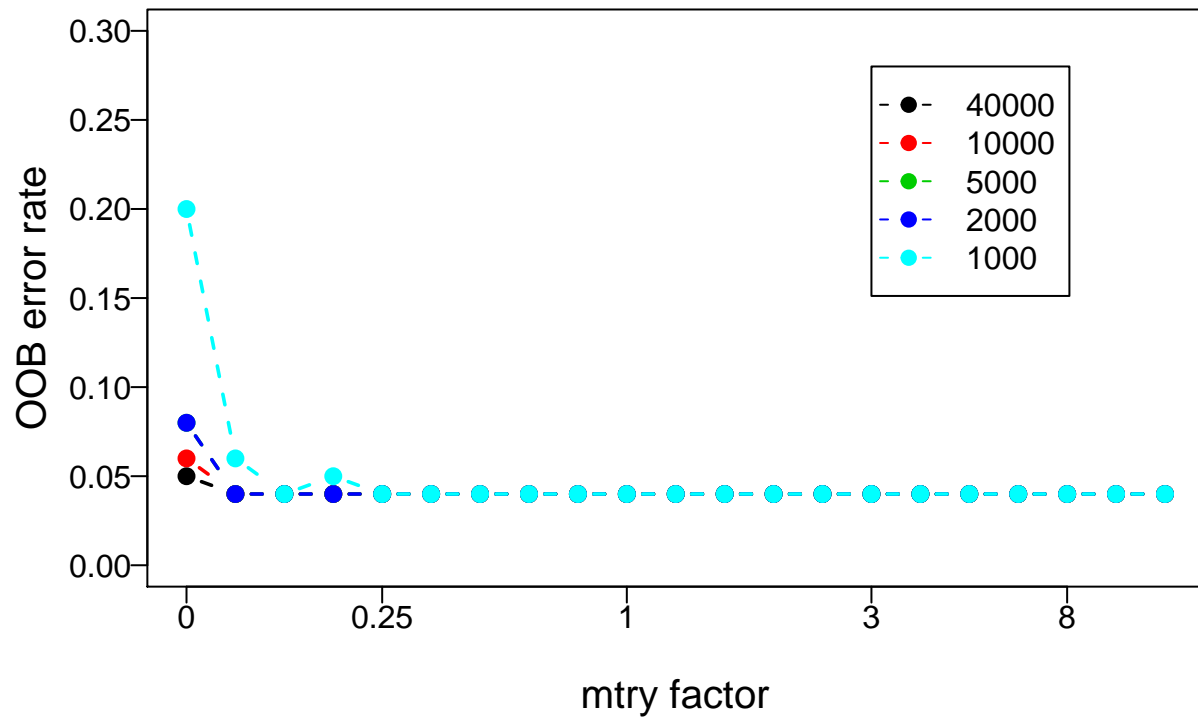
4 classes; 2 dimensions; 20 genes/dimen.; nodesize = 5



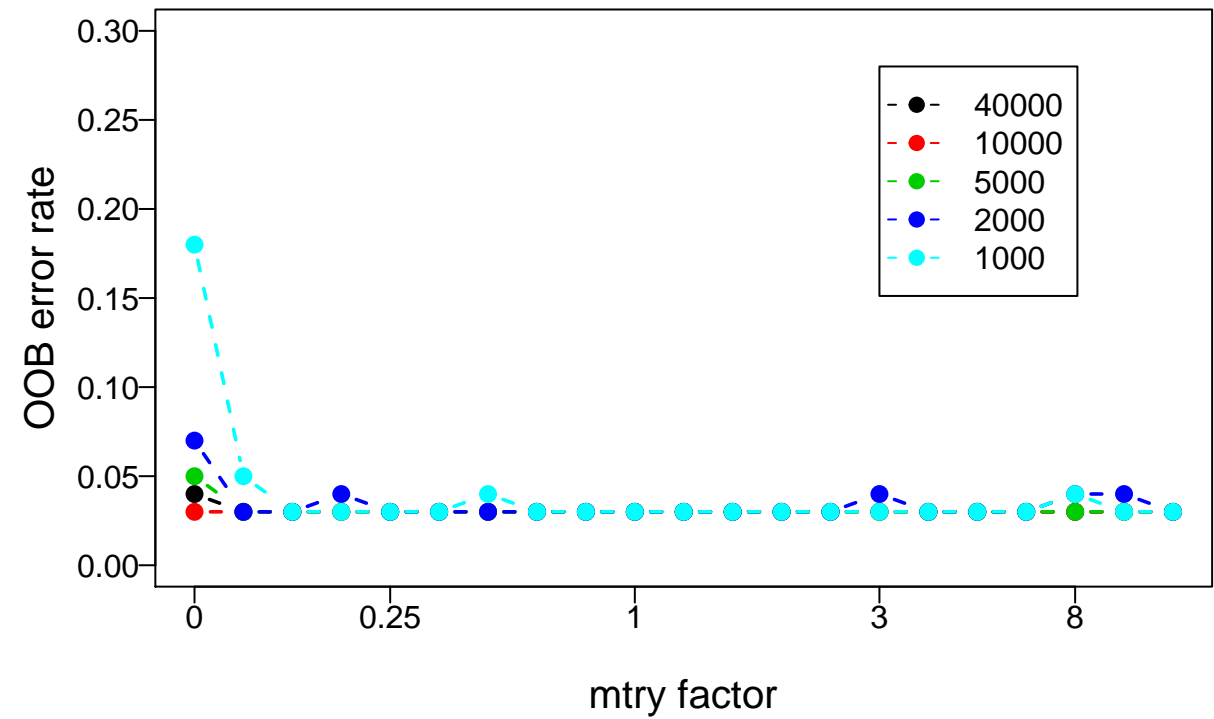
4 classes; 2 dimensions; 20 genes/dimen.; nodesize = 5



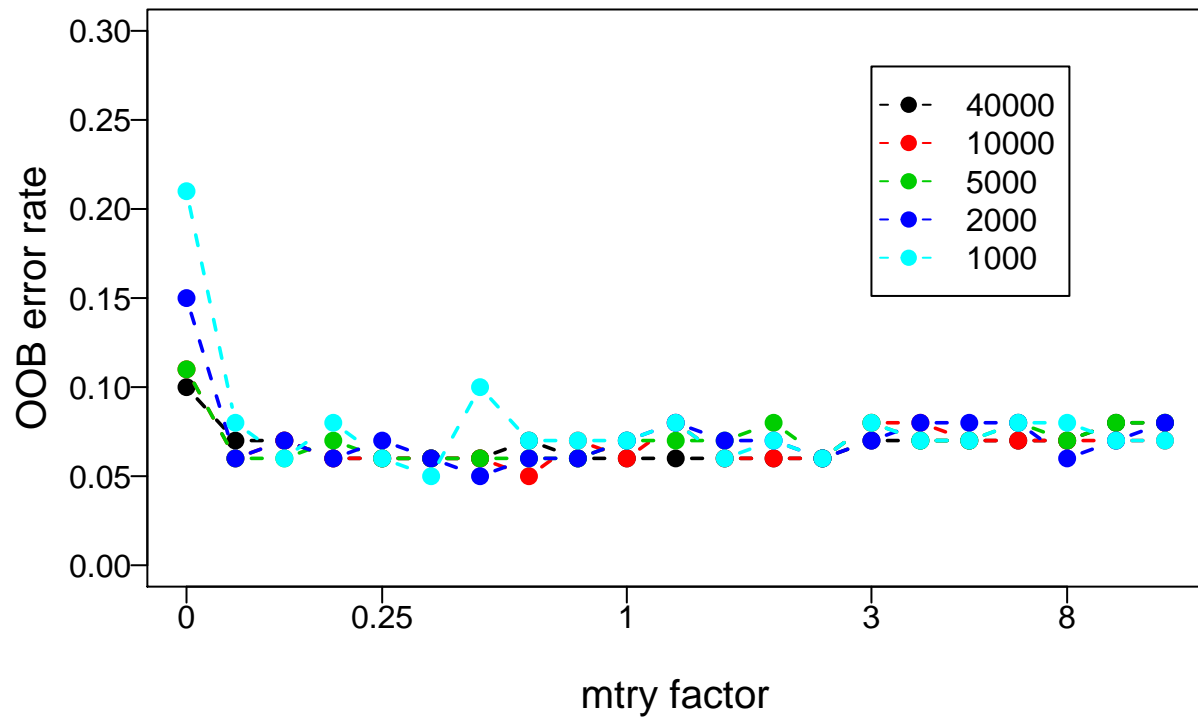
4 classes; 2 dimensions; 100 genes/dimen.; nodesize = 5



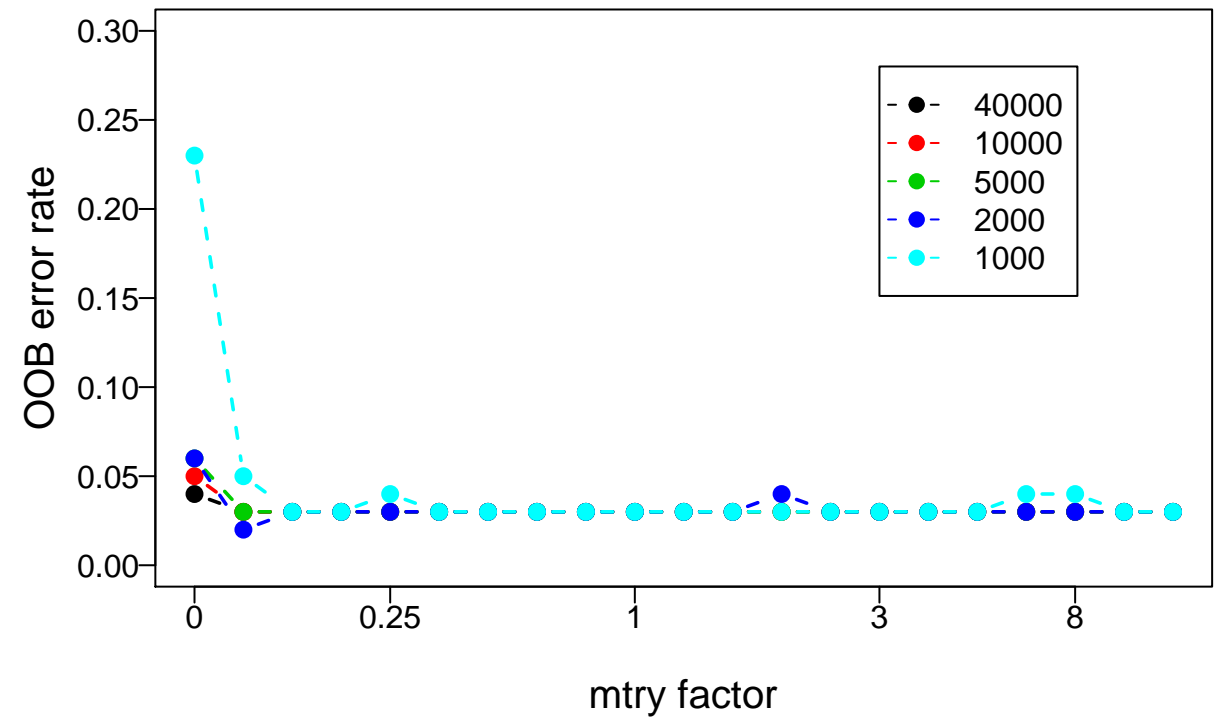
4 classes; 2 dimensions; 100 genes/dimen.; nodesize = 5



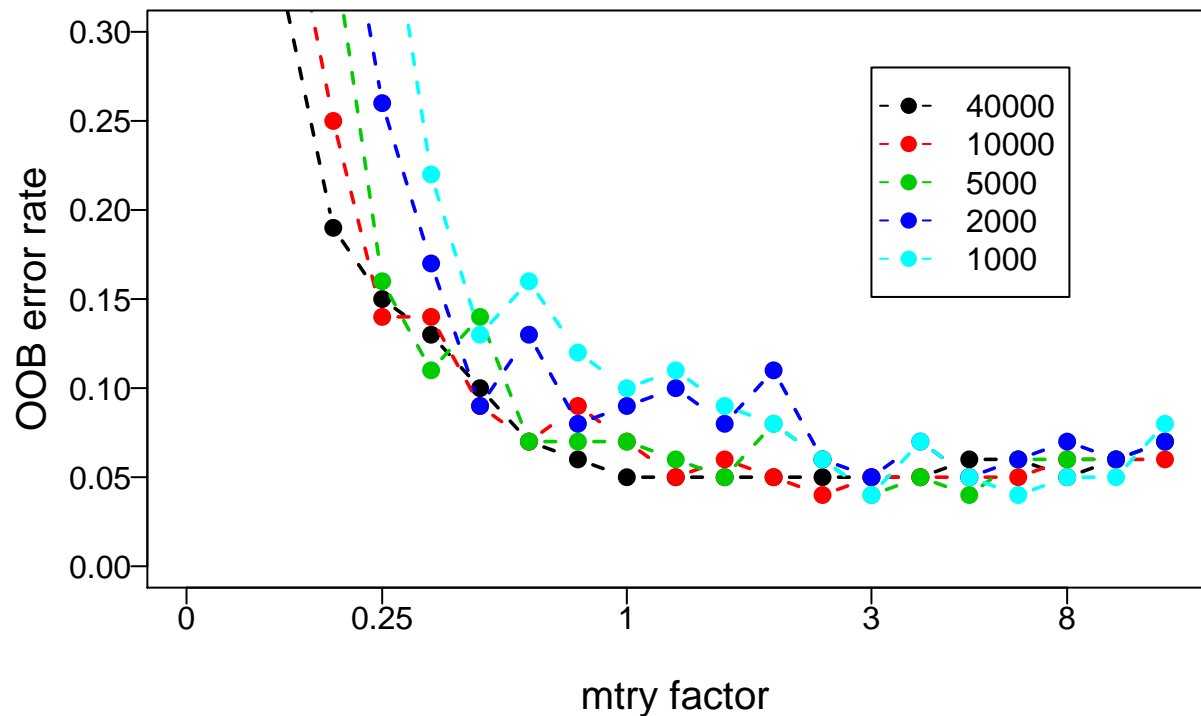
4 classes; 2 dimensions; 100 genes/dimen.; nodesize = 5



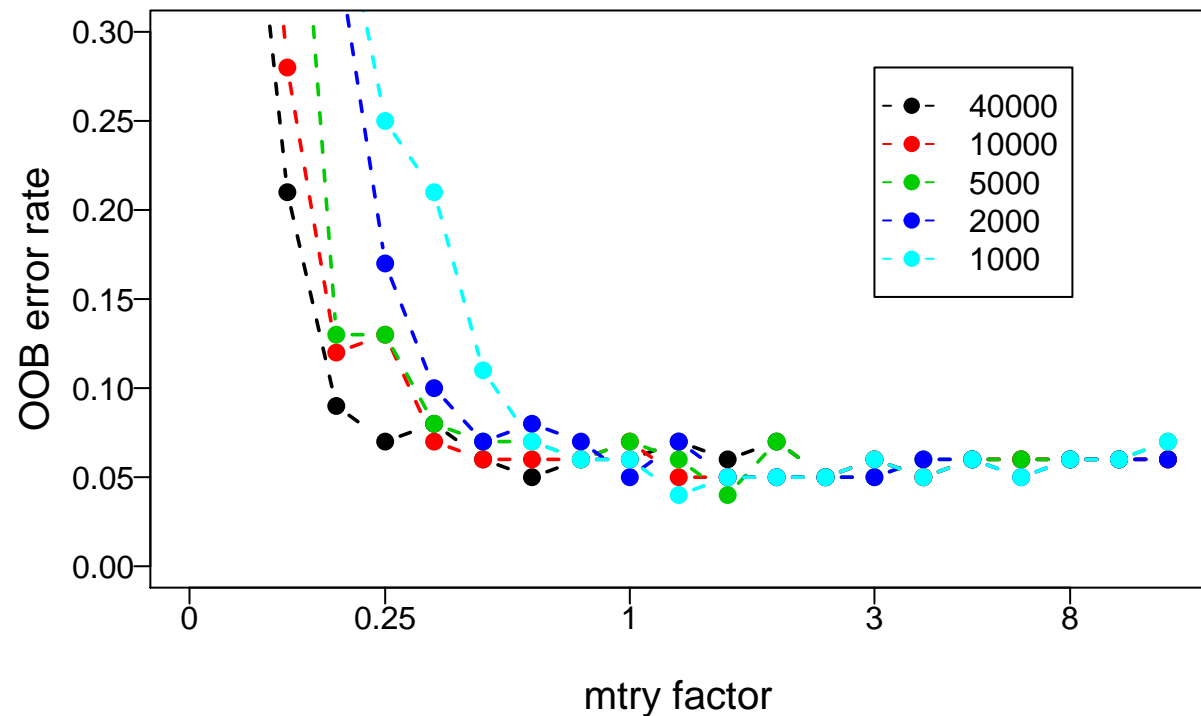
4 classes; 2 dimensions; 100 genes/dimen.; nodesize = 5



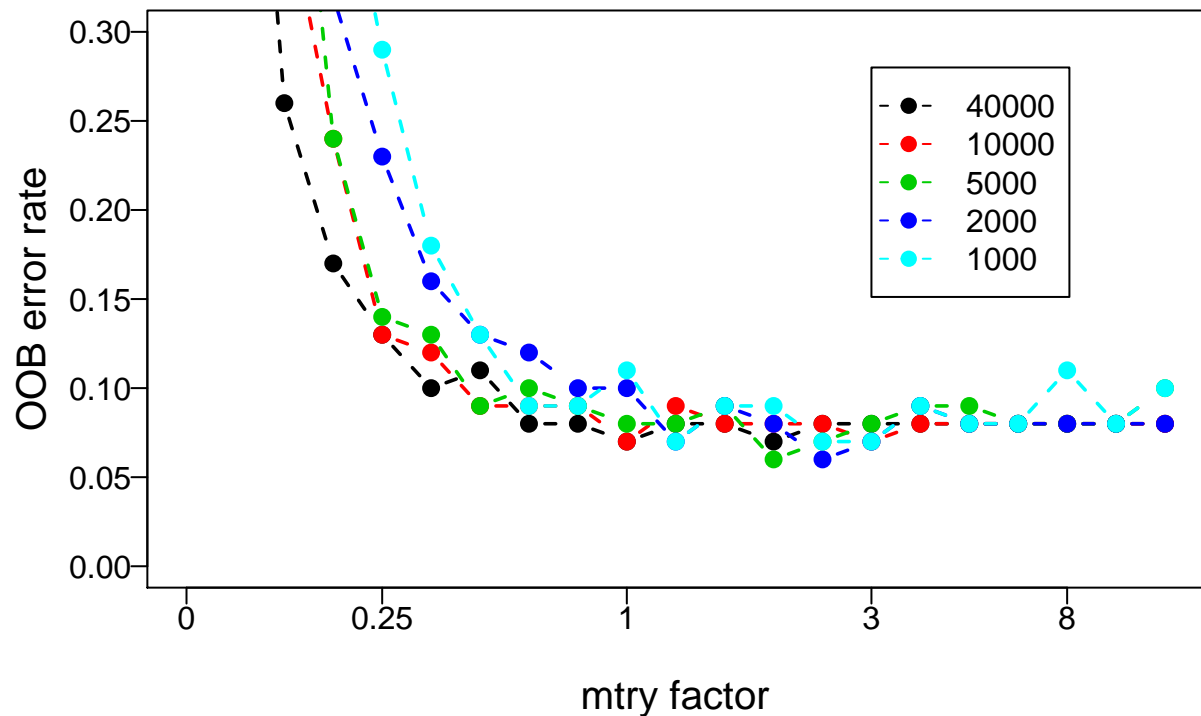
4 classes; 3 dimensions; 5 genes/dimen.; nodesize = 5



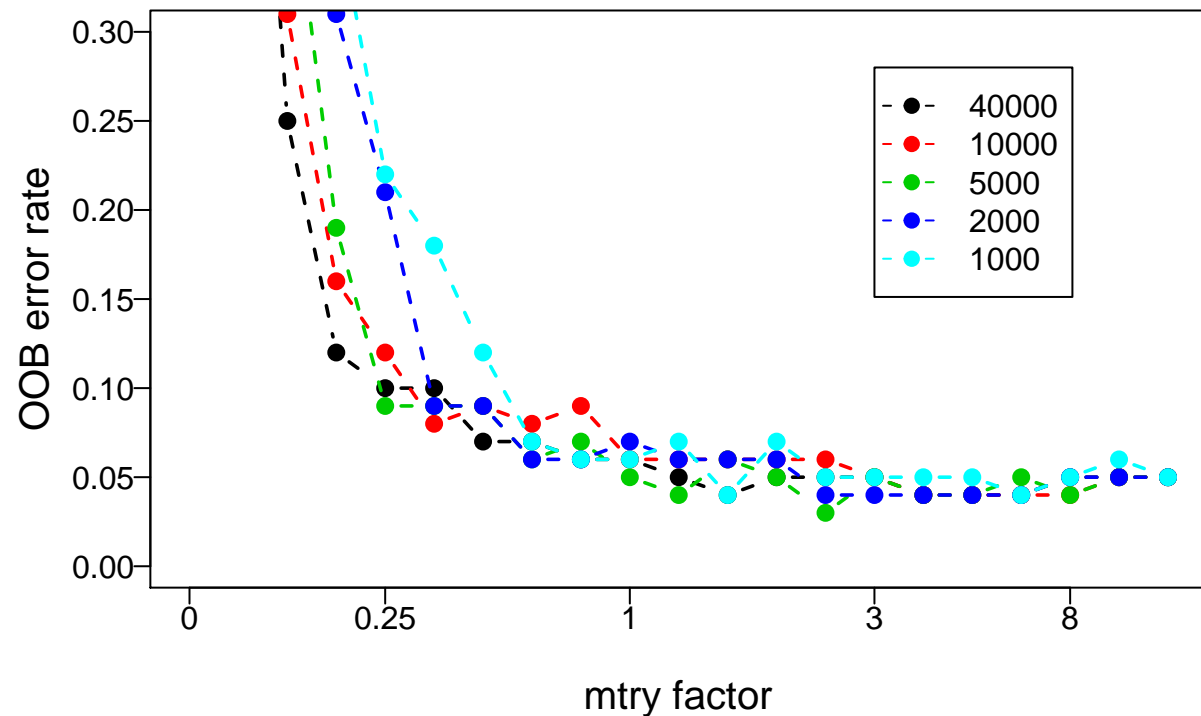
4 classes; 3 dimensions; 5 genes/dimen.; nodesize = 5



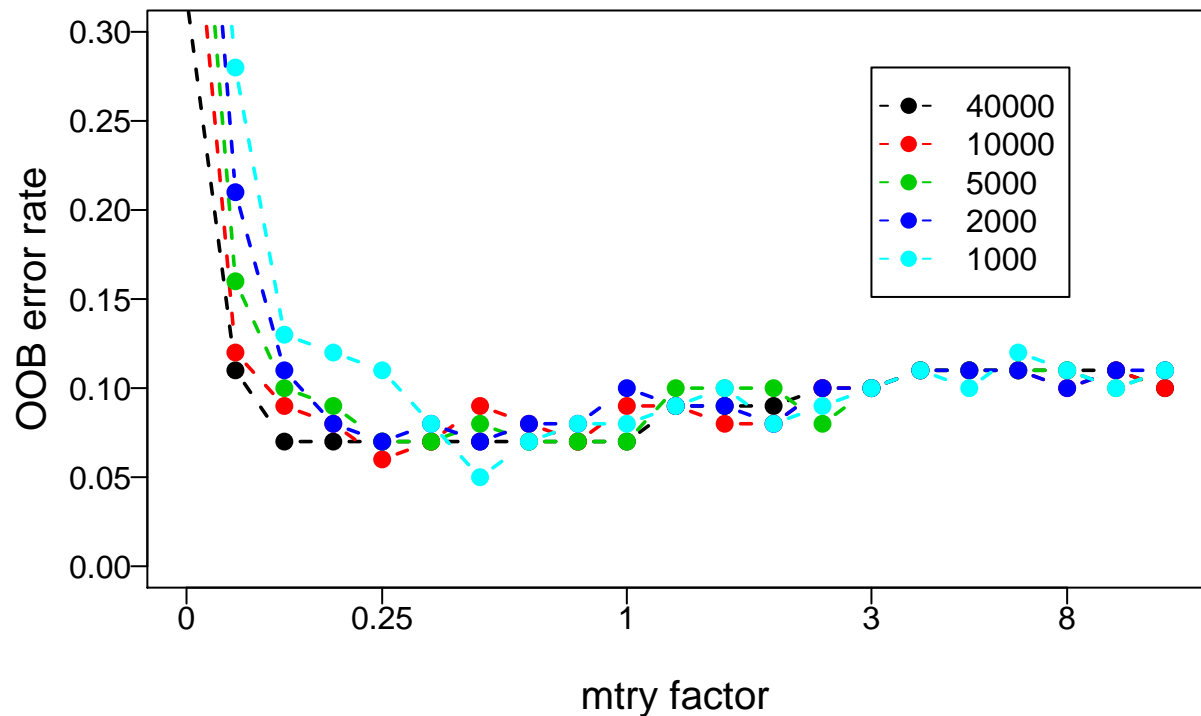
4 classes; 3 dimensions; 5 genes/dimen.; nodesize = 5



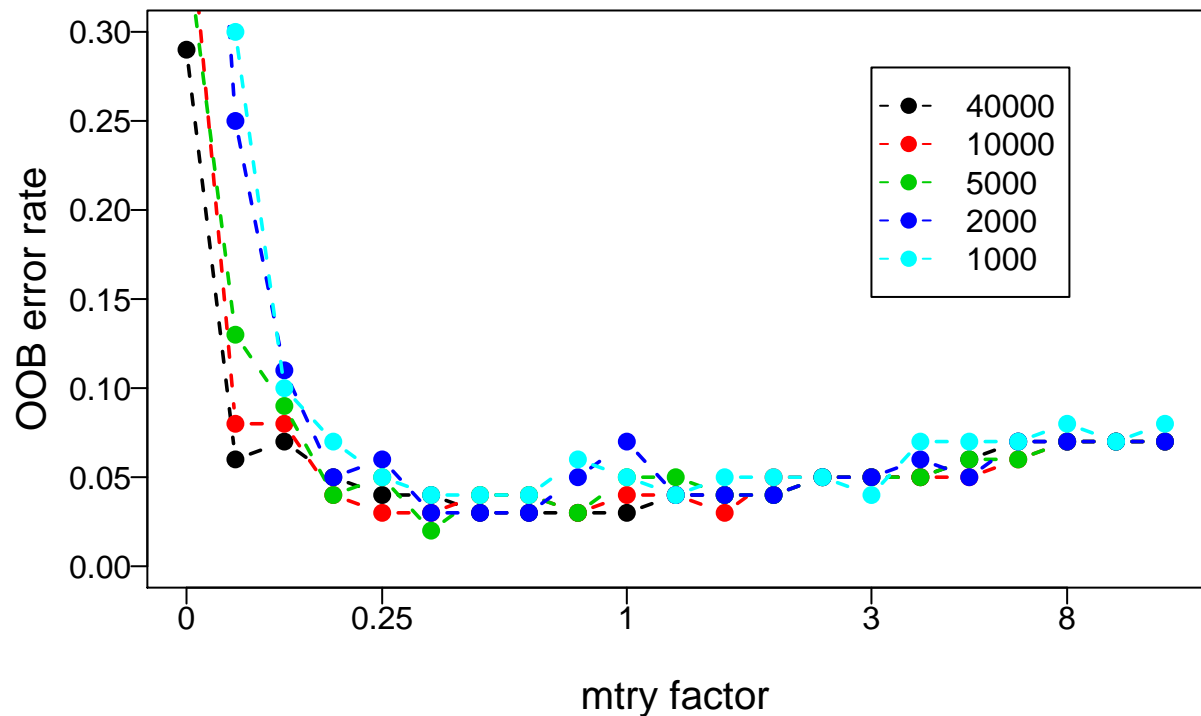
4 classes; 3 dimensions; 5 genes/dimen.; nodesize = 5



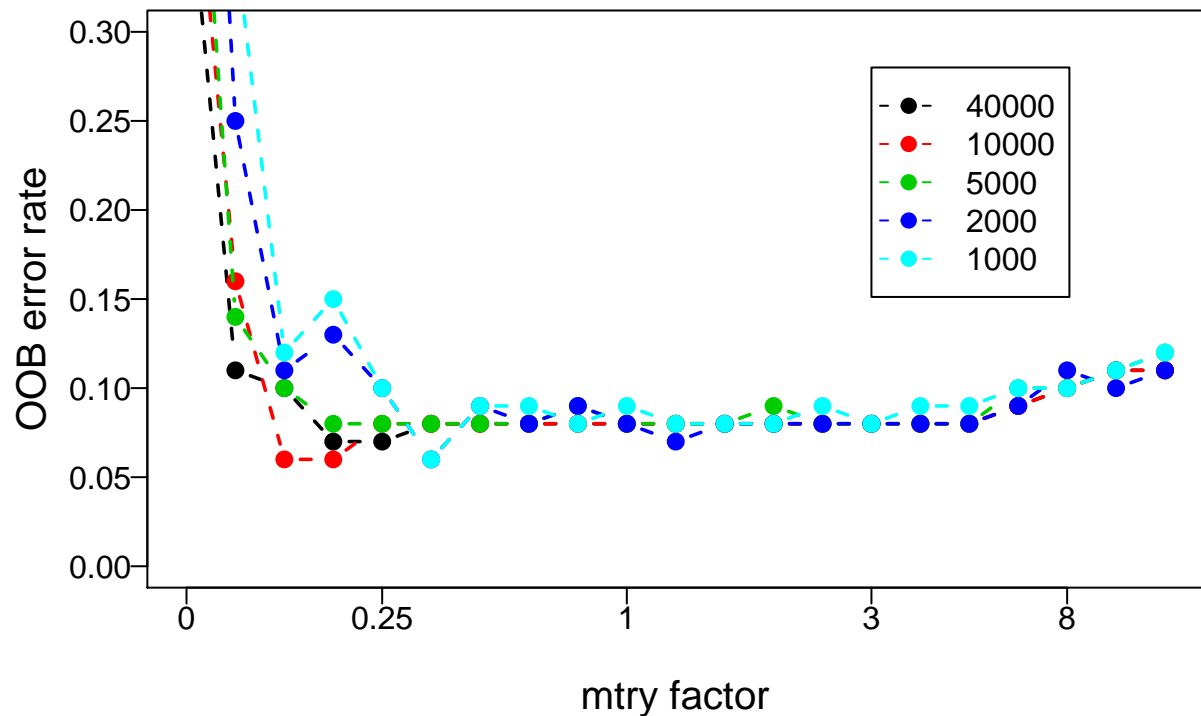
4 classes; 3 dimensions; 20 genes/dimen.; nodesize = 5



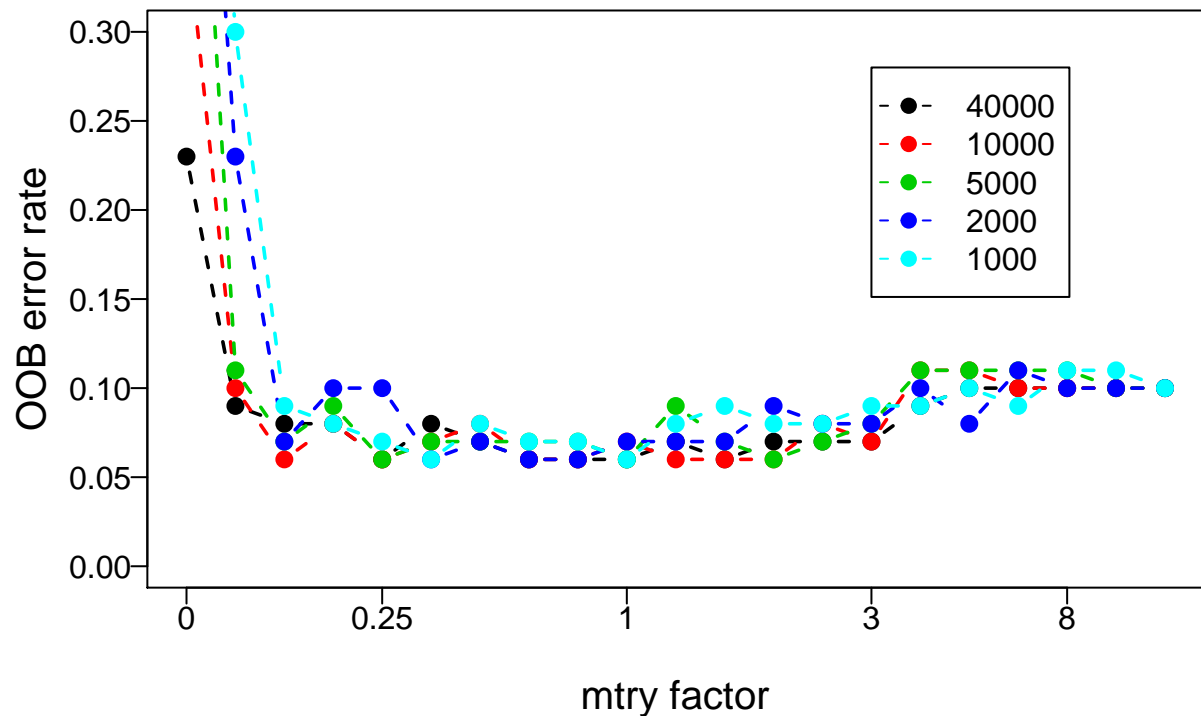
4 classes; 3 dimensions; 20 genes/dimen.; nodesize = 5



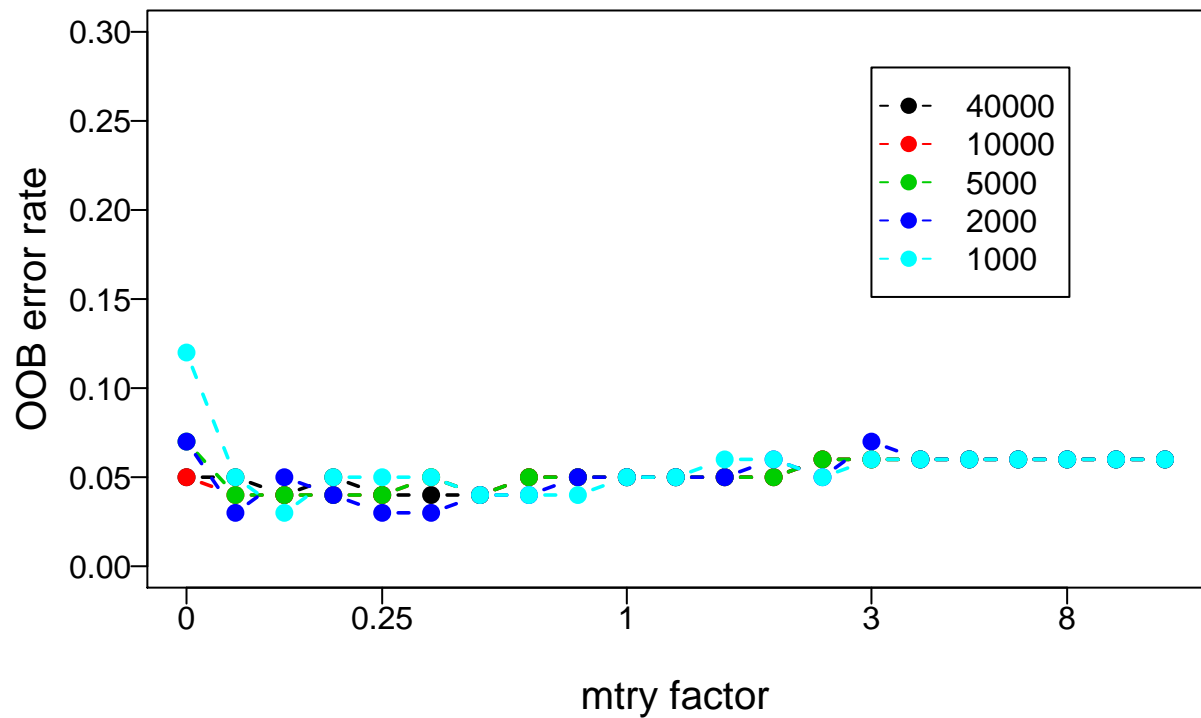
4 classes; 3 dimensions; 20 genes/dimen.; nodesize = 5



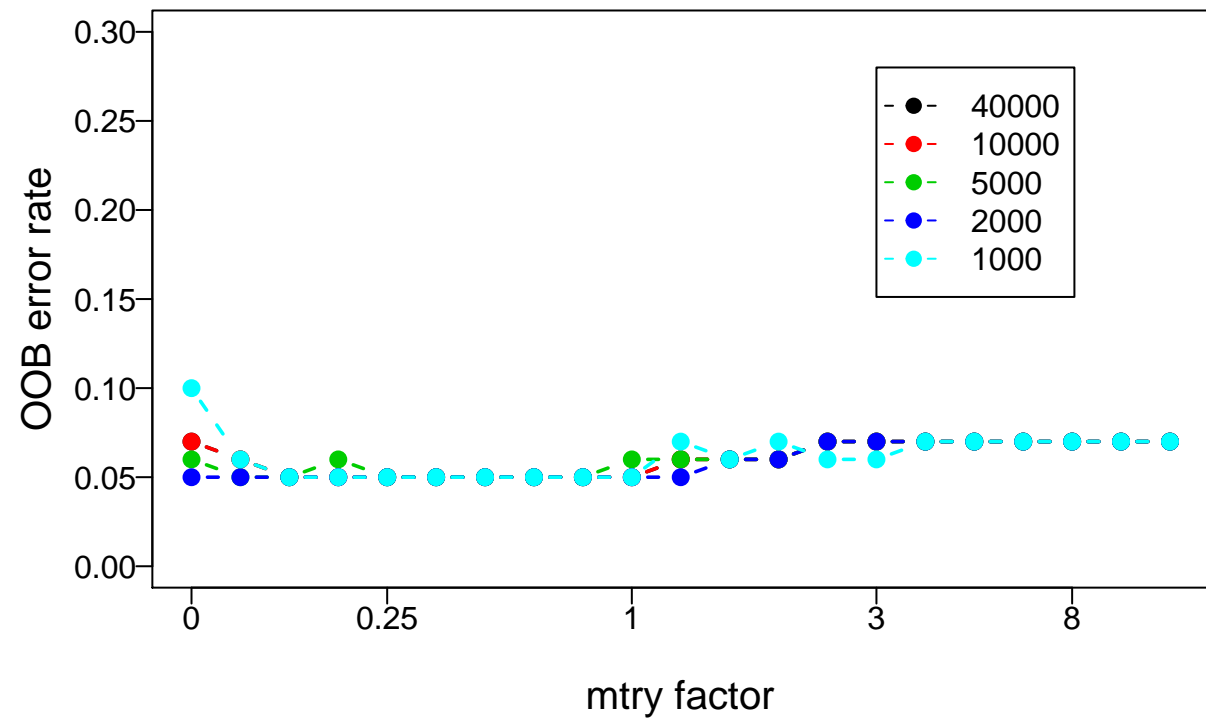
4 classes; 3 dimensions; 20 genes/dimen.; nodesize = 5



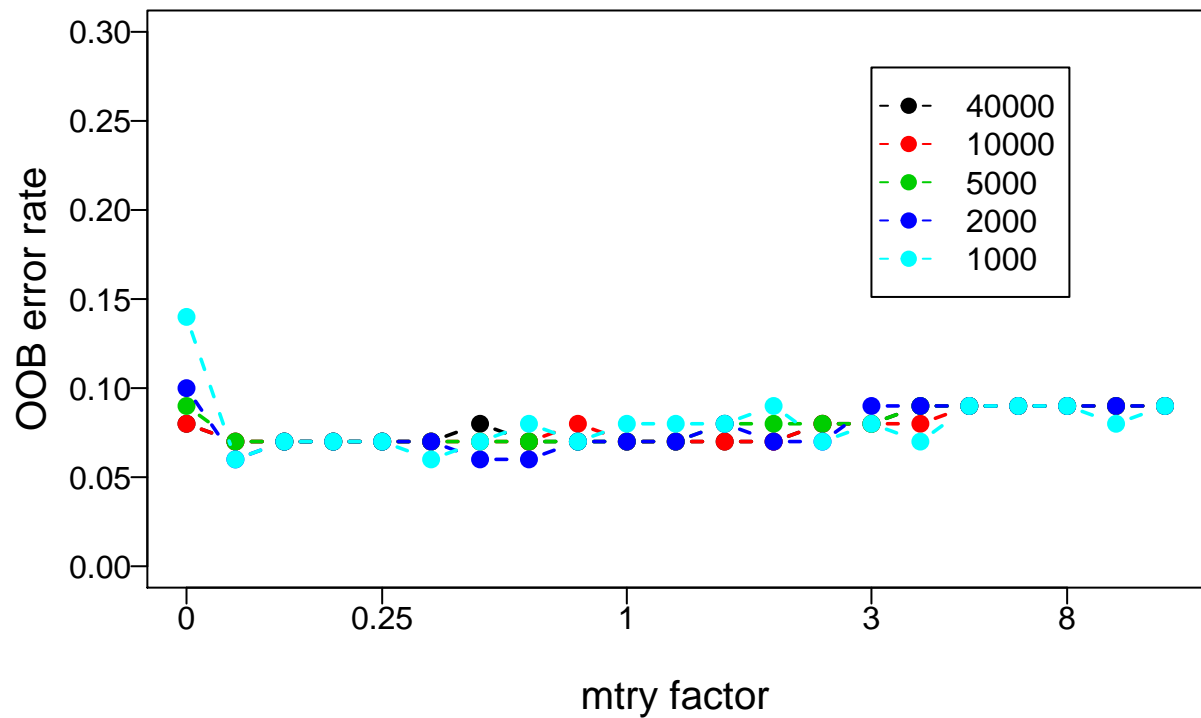
4 classes; 3 dimensions; 100 genes/dimen.; nodesize = 5



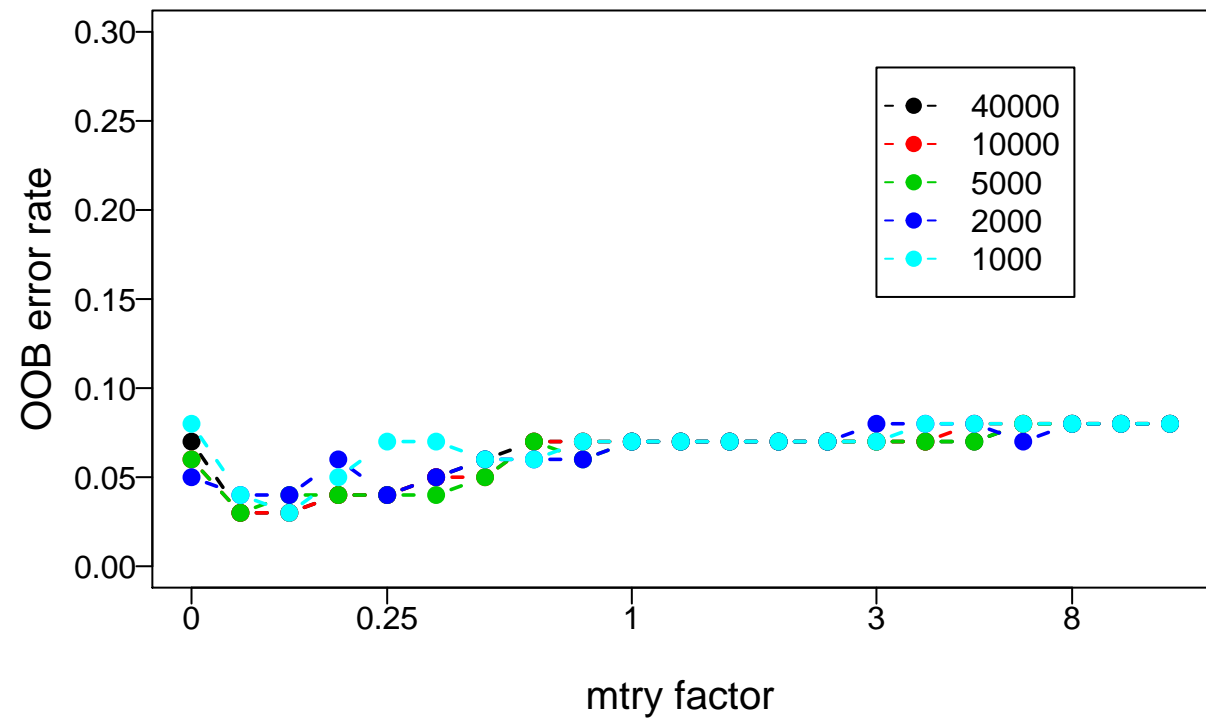
4 classes; 3 dimensions; 100 genes/dimen.; nodesize = 5



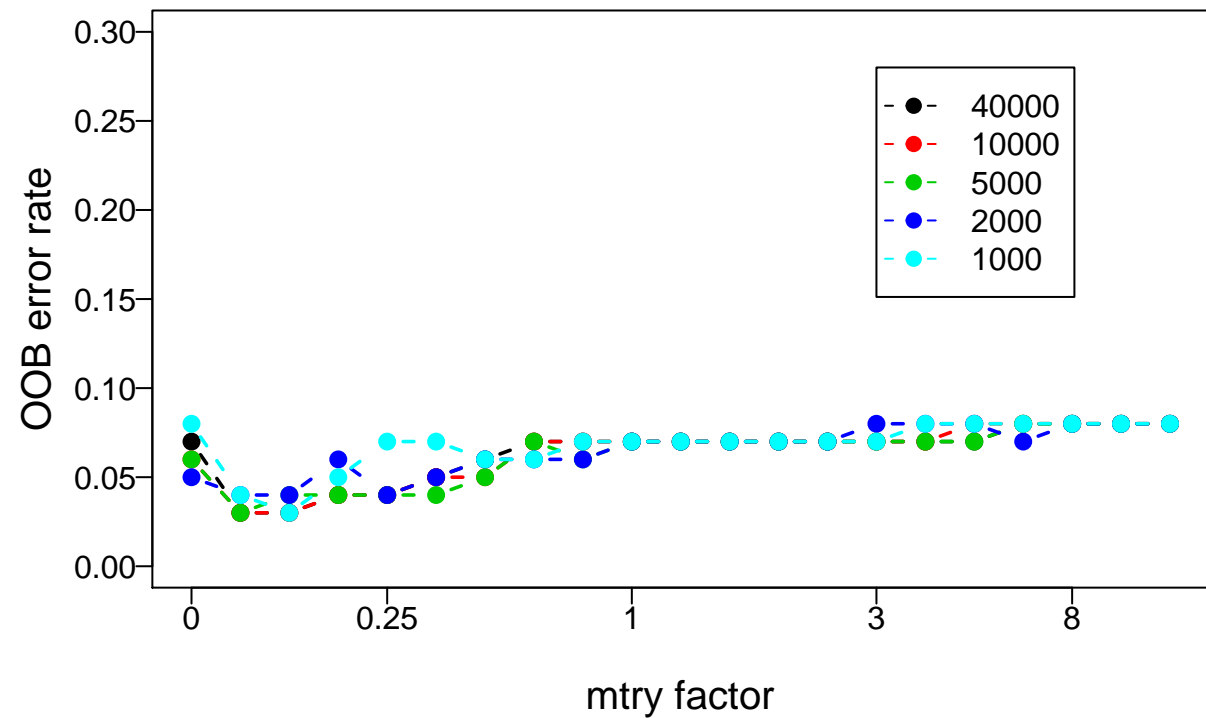
4 classes; 3 dimensions; 100 genes/dimen.; nodesize = 5



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



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

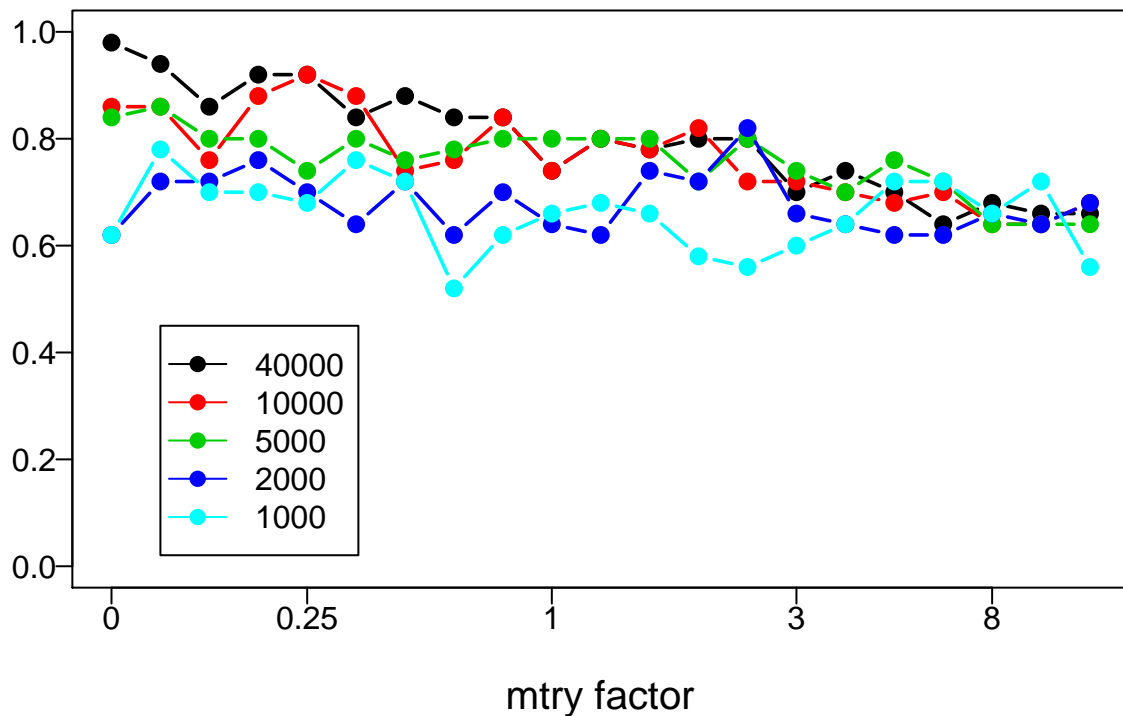


II: Simulated data sets:

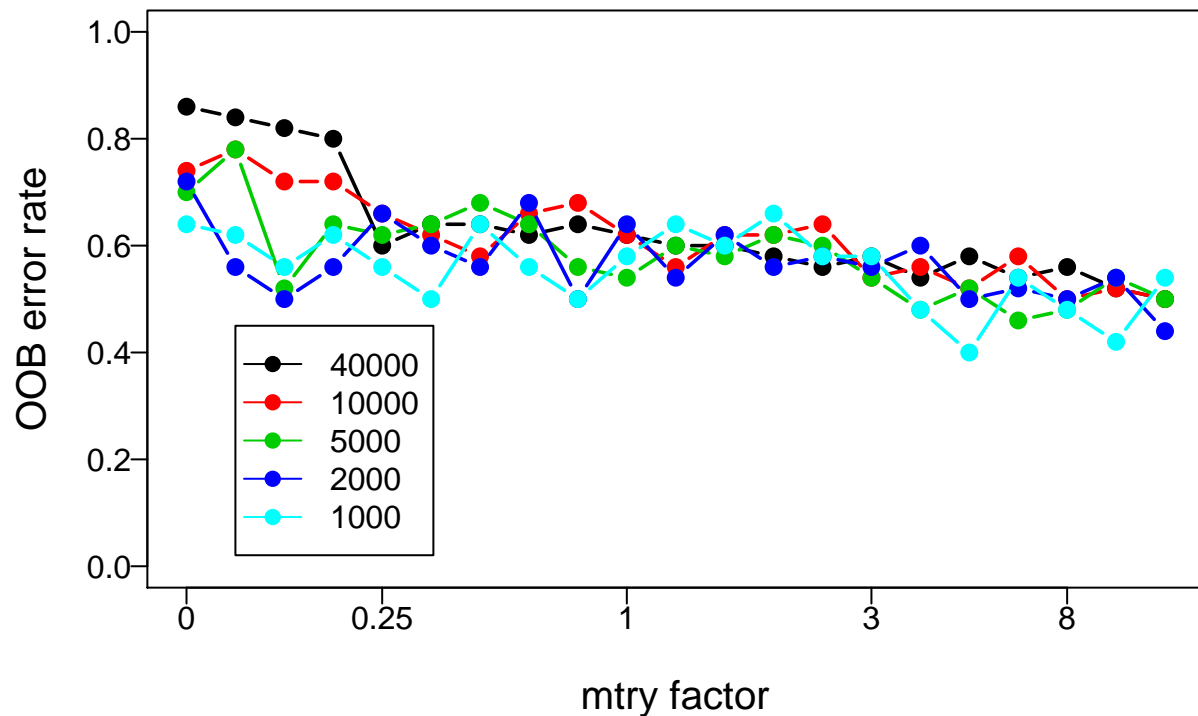
No signal: 4000 noise random variables

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

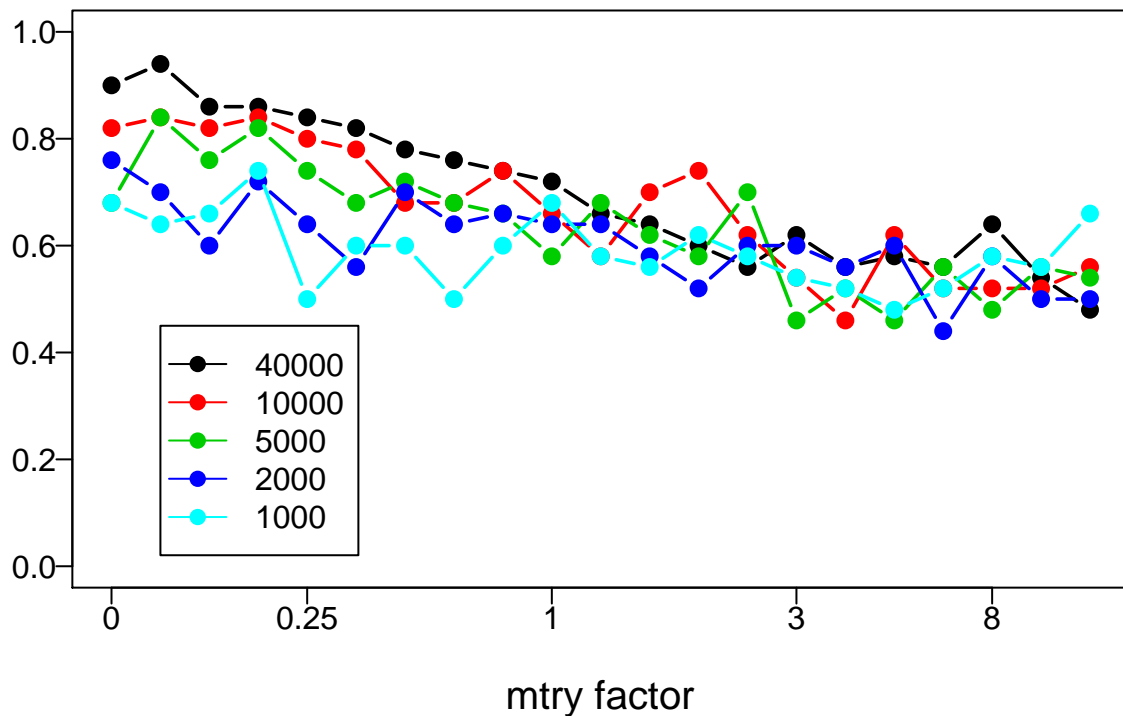
No signal: Classes 2 ; nodesize = 1



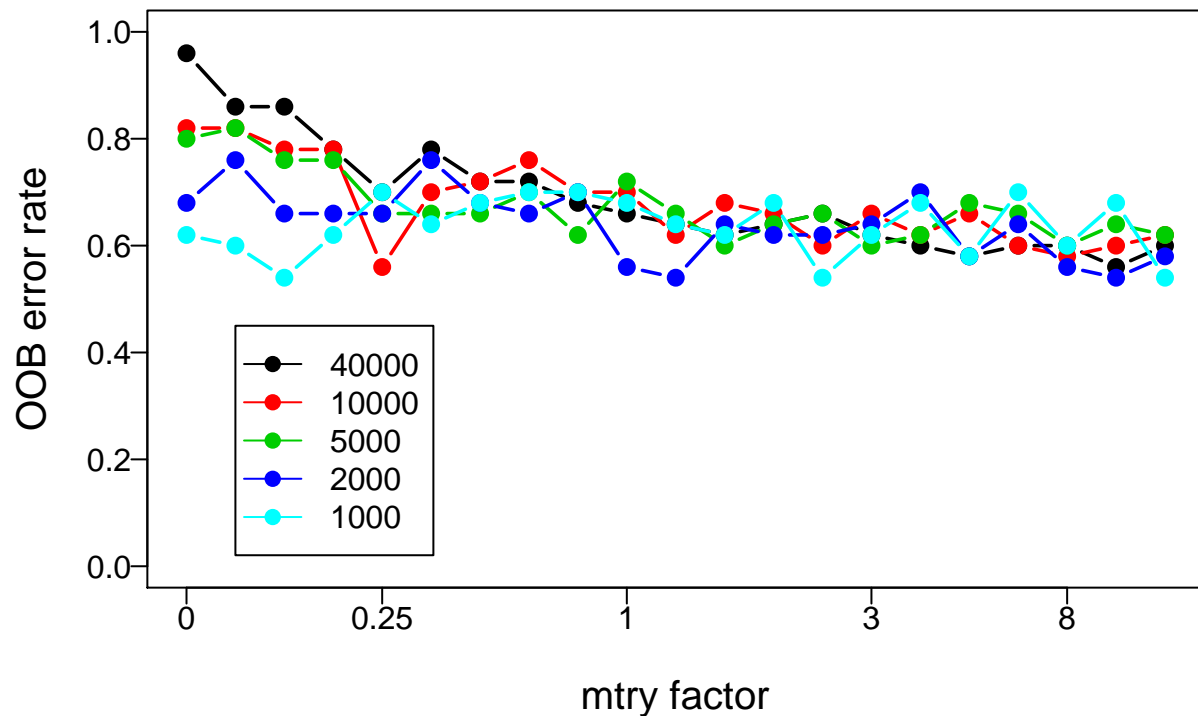
No signal: Classes 2 ; nodesize = 1



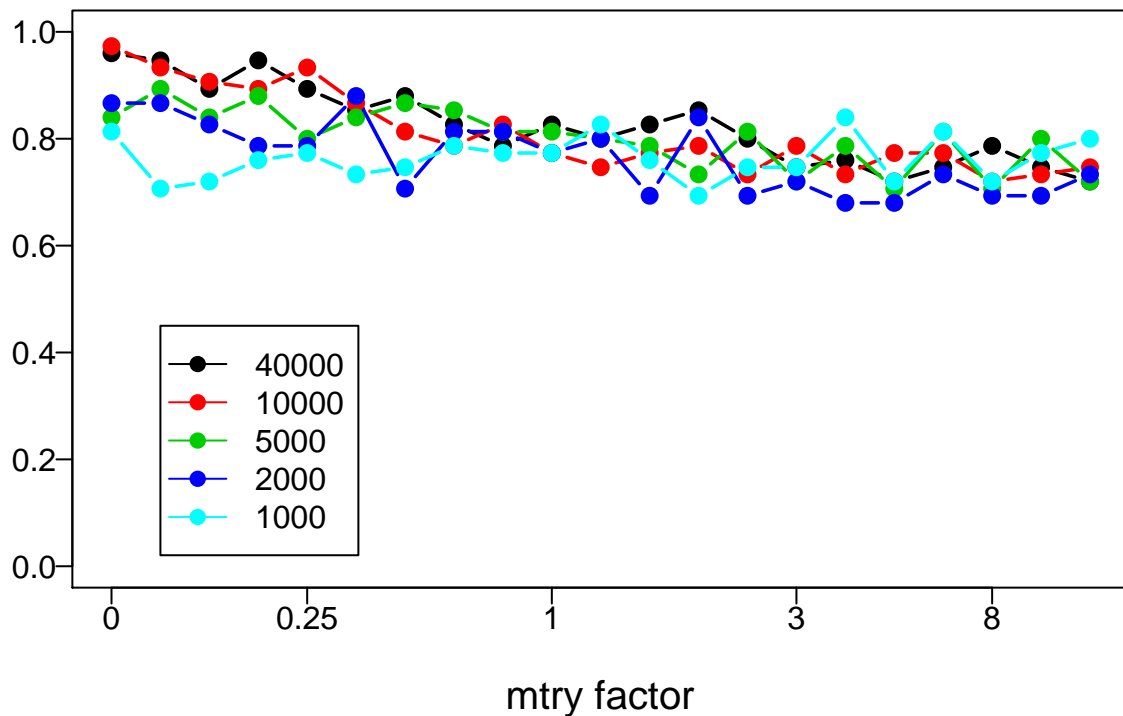
No signal: Classes 2 ; nodesize = 1



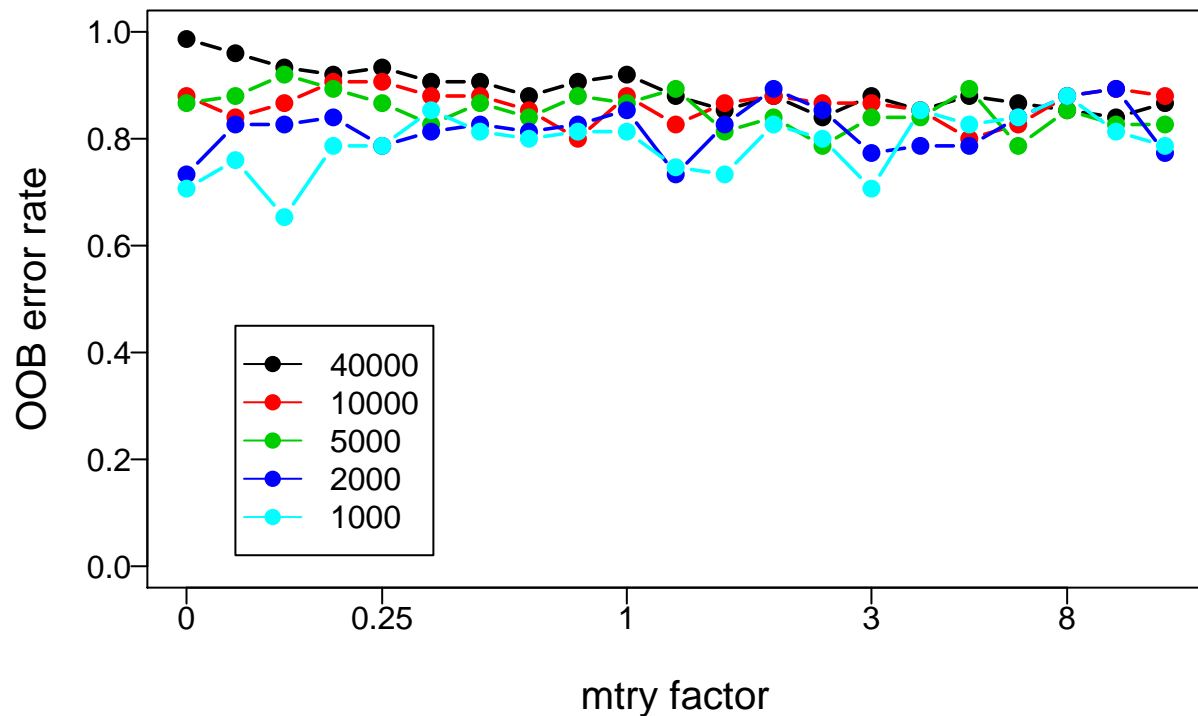
No signal: Classes 2 ; nodesize = 1



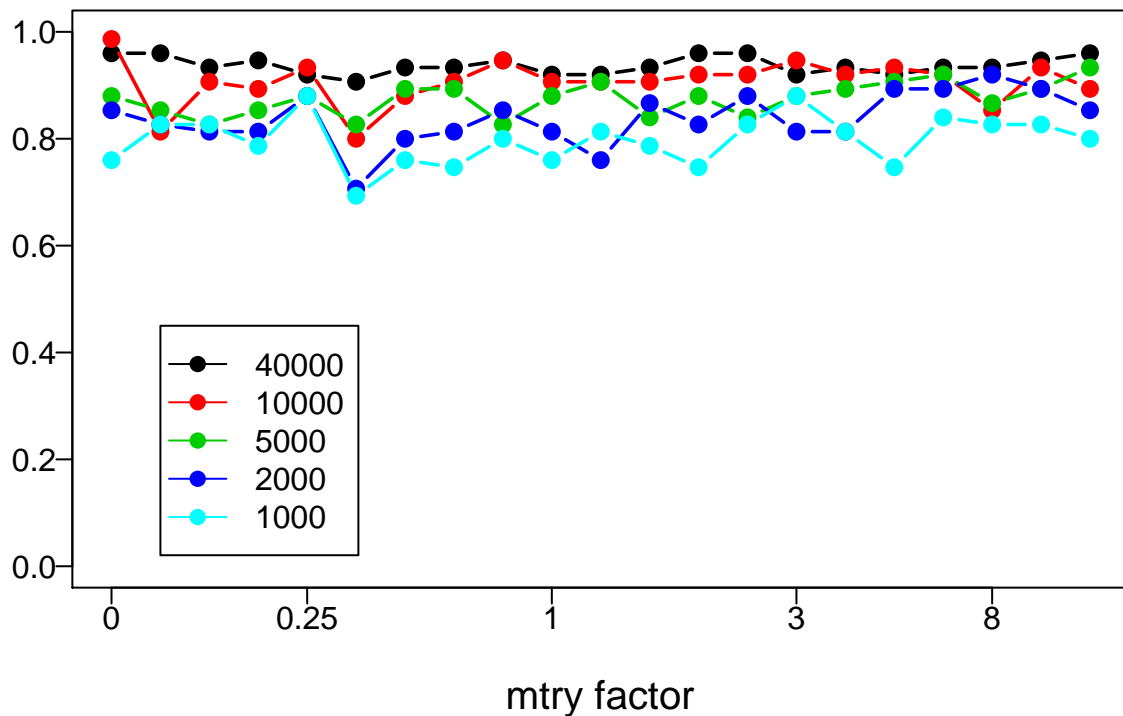
No signal: Classes 3 ; nodesize = 1



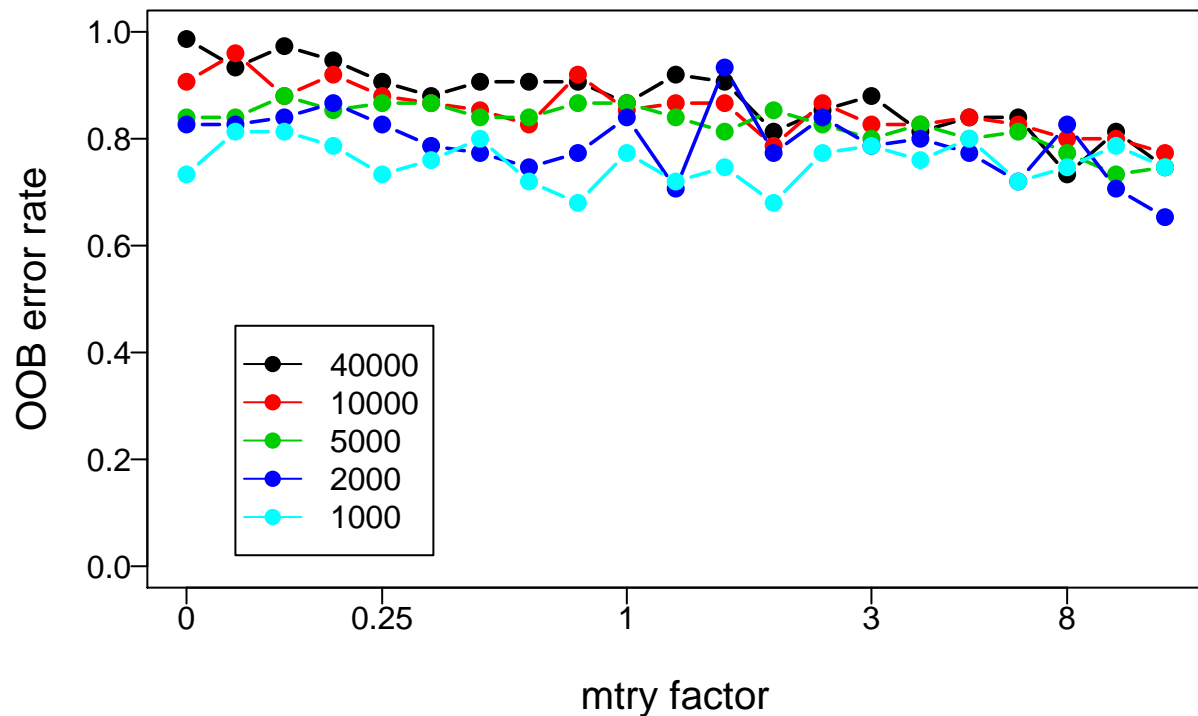
No signal: Classes 3 ; nodesize = 1



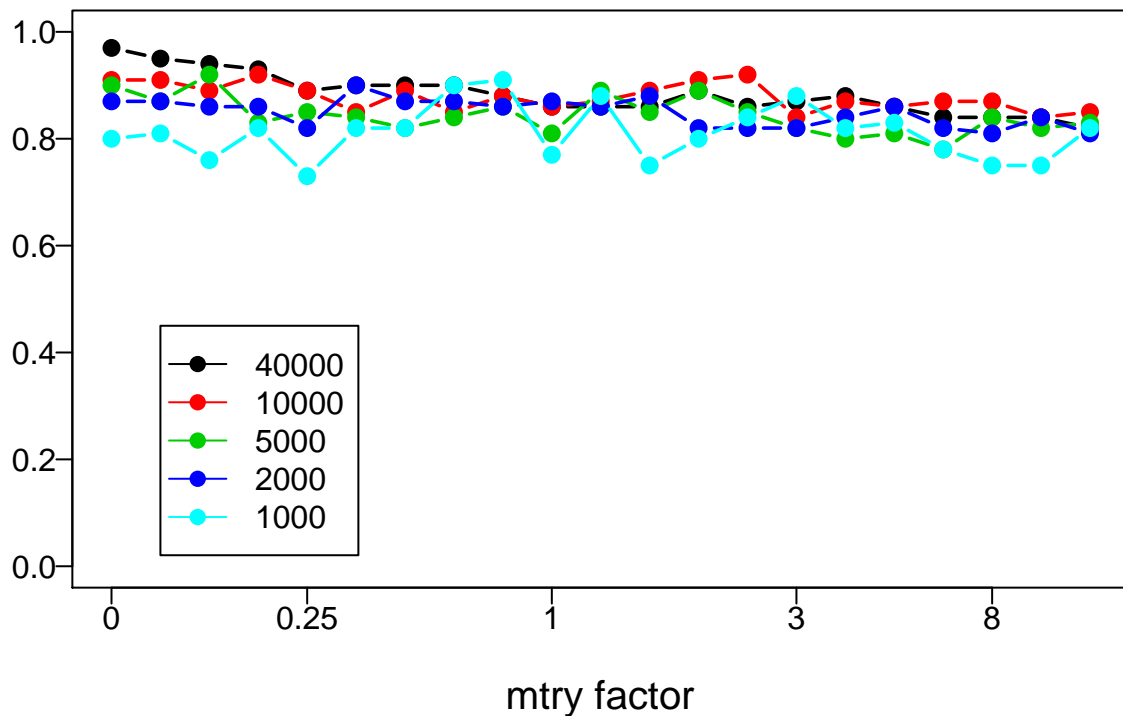
No signal: Classes 3 ; nodesize = 1



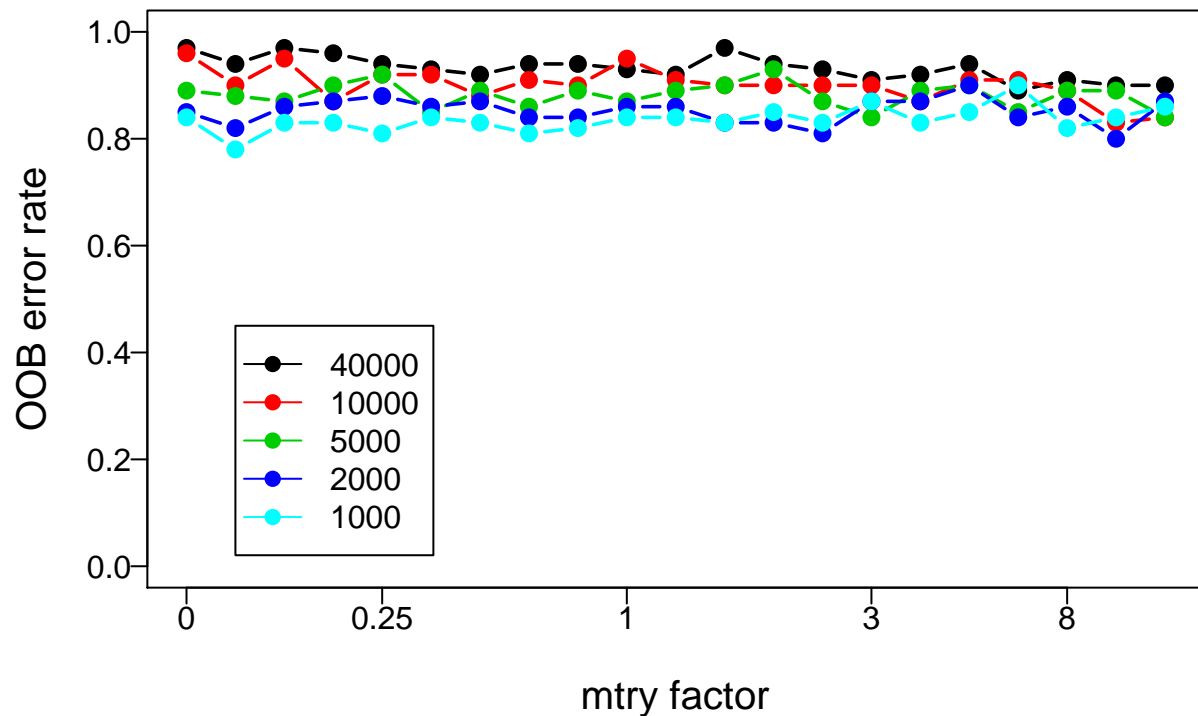
No signal: Classes 3 ; nodesize = 1



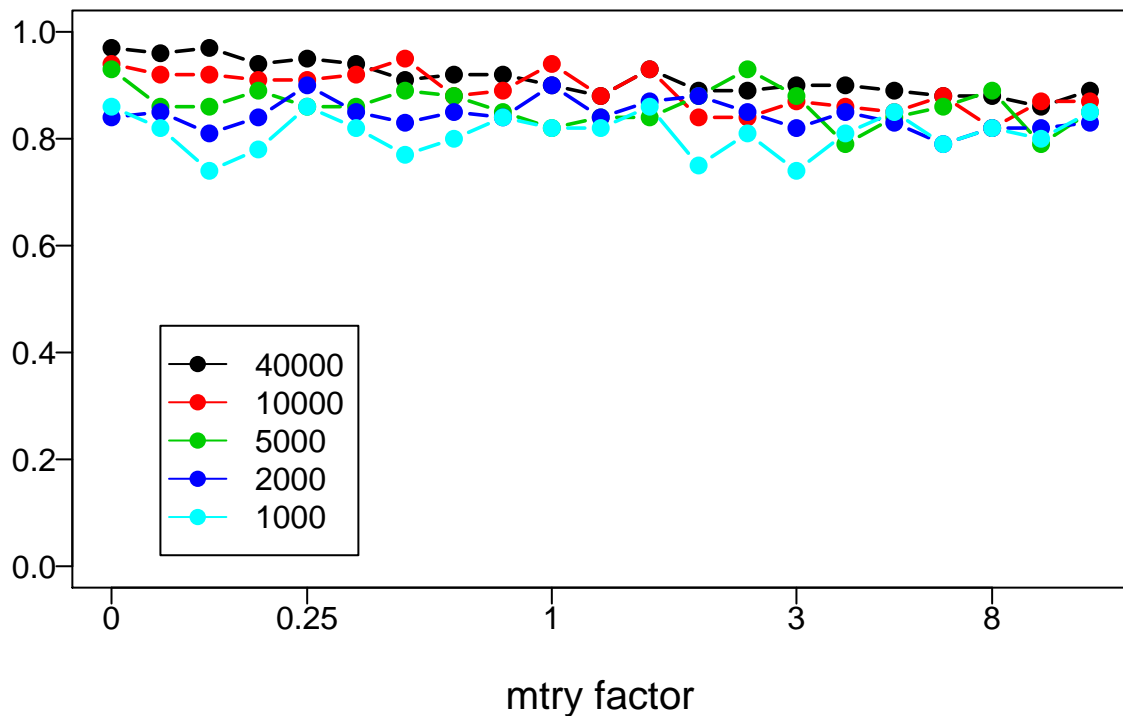
No signal: Classes 4 ; nodesize = 1



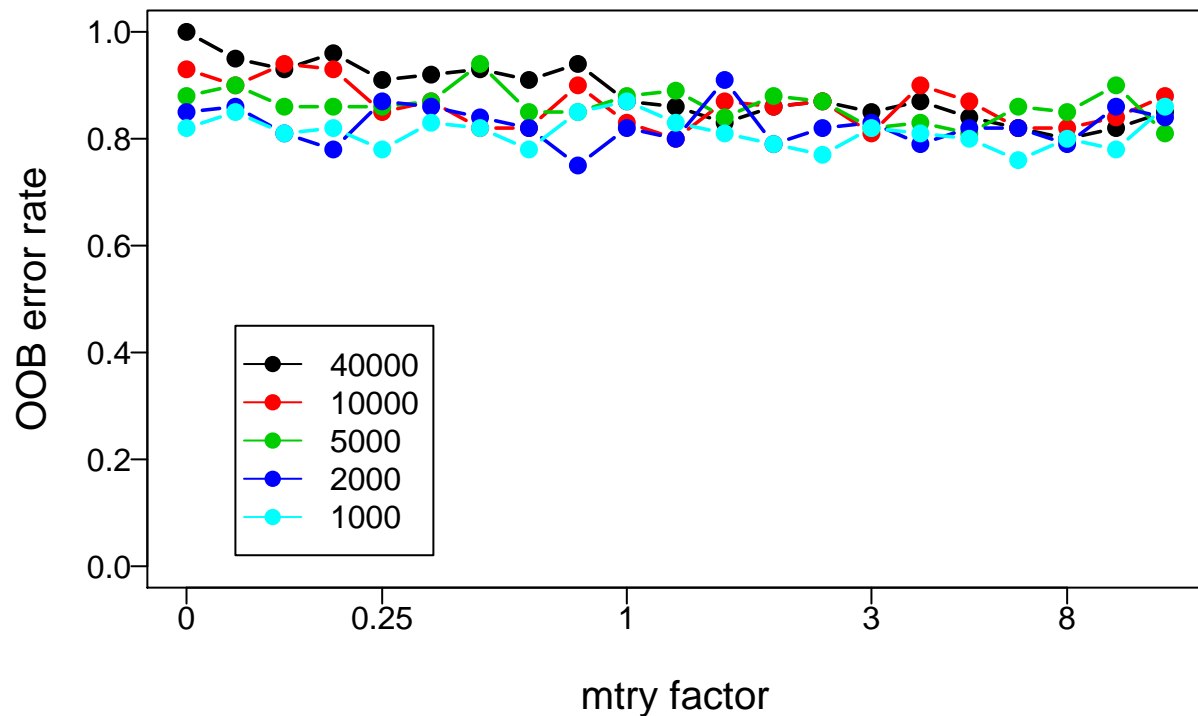
No signal: Classes 4 ; nodesize = 1



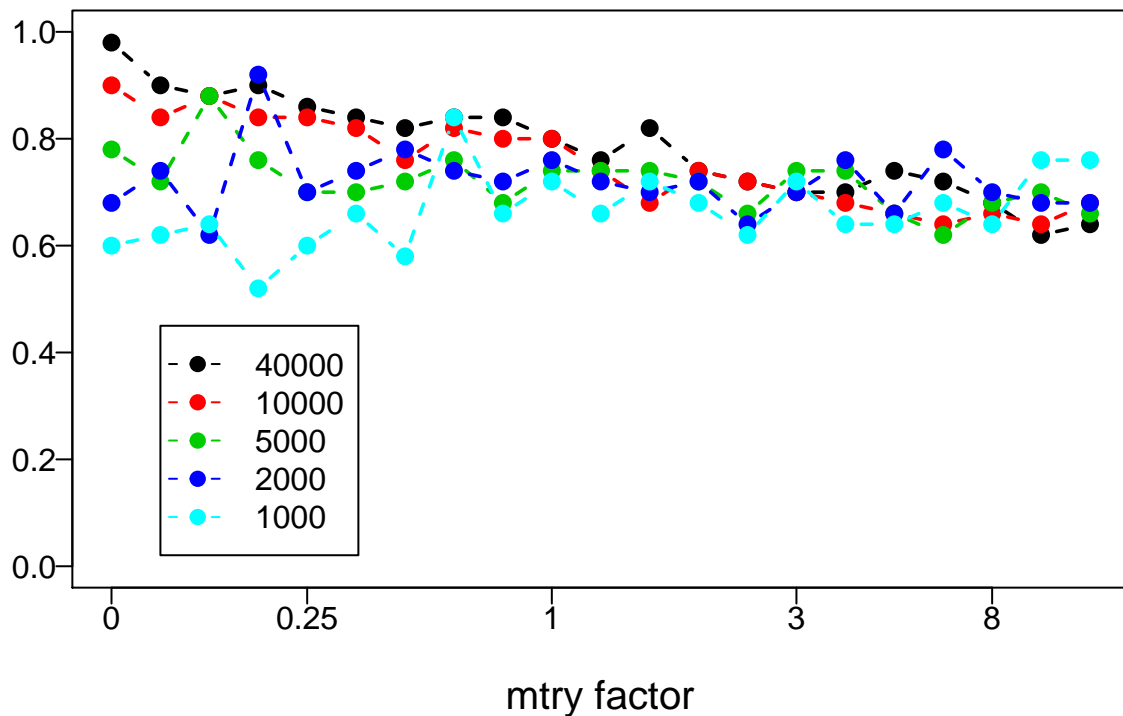
No signal: Classes 4 ; nodesize = 1



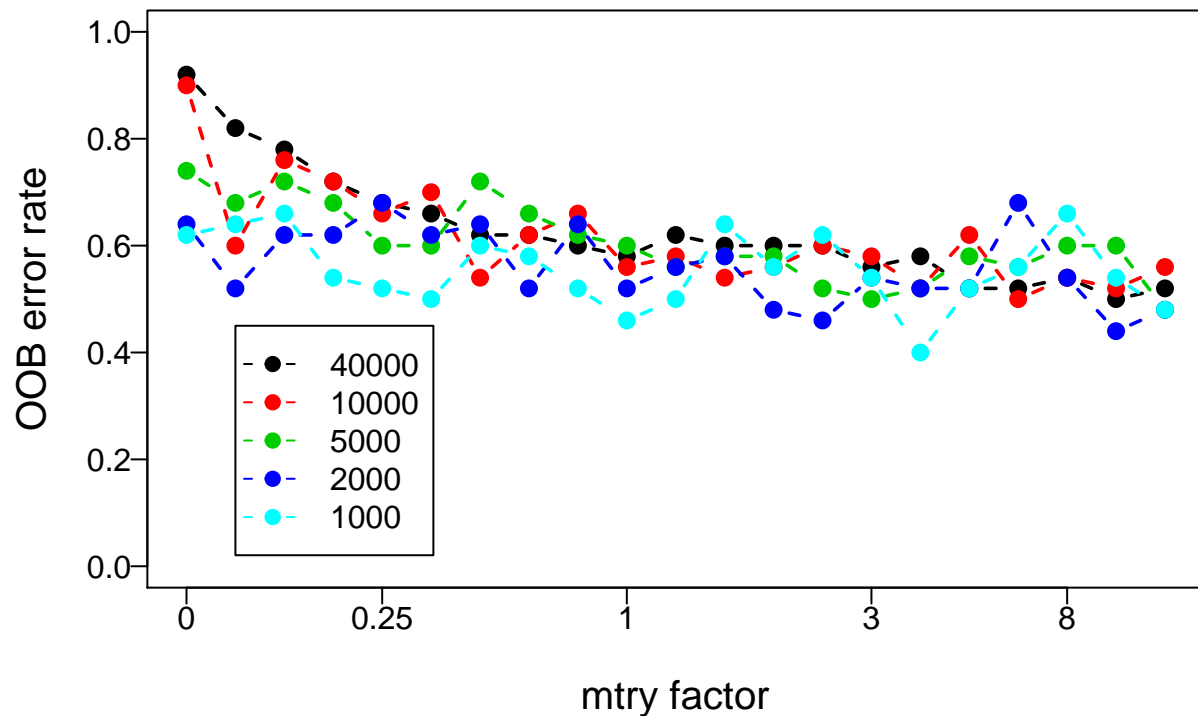
No signal: Classes 4 ; nodesize = 1



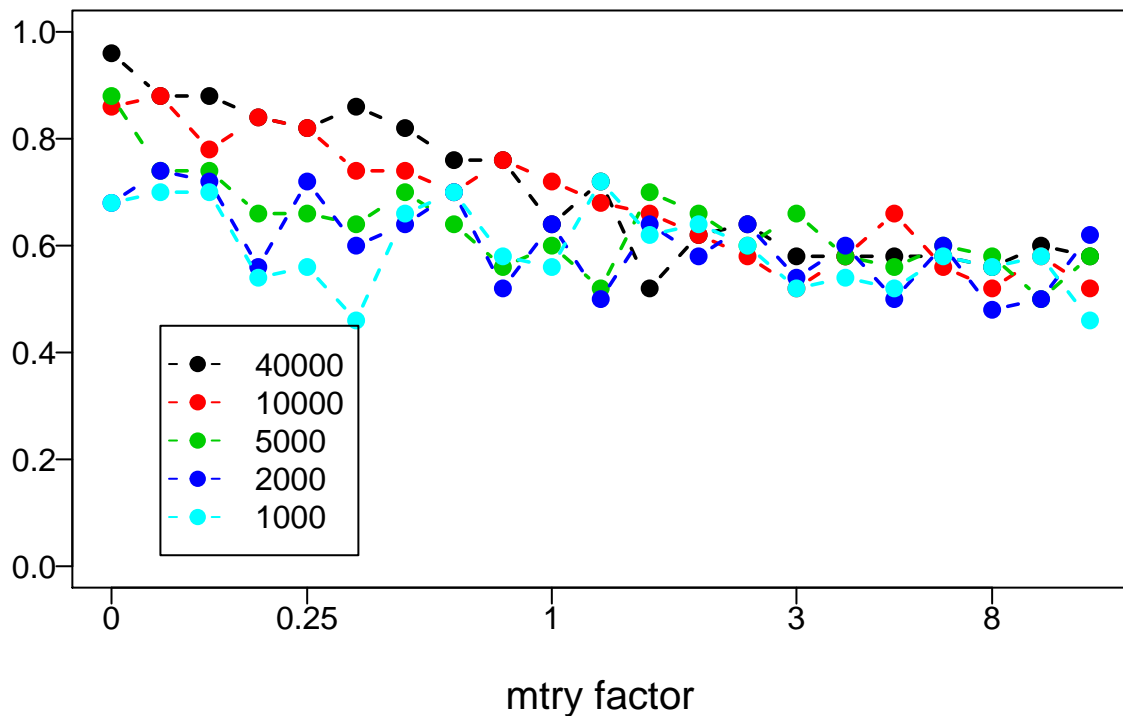
No signal: Classes 2 ; nodesize = 5



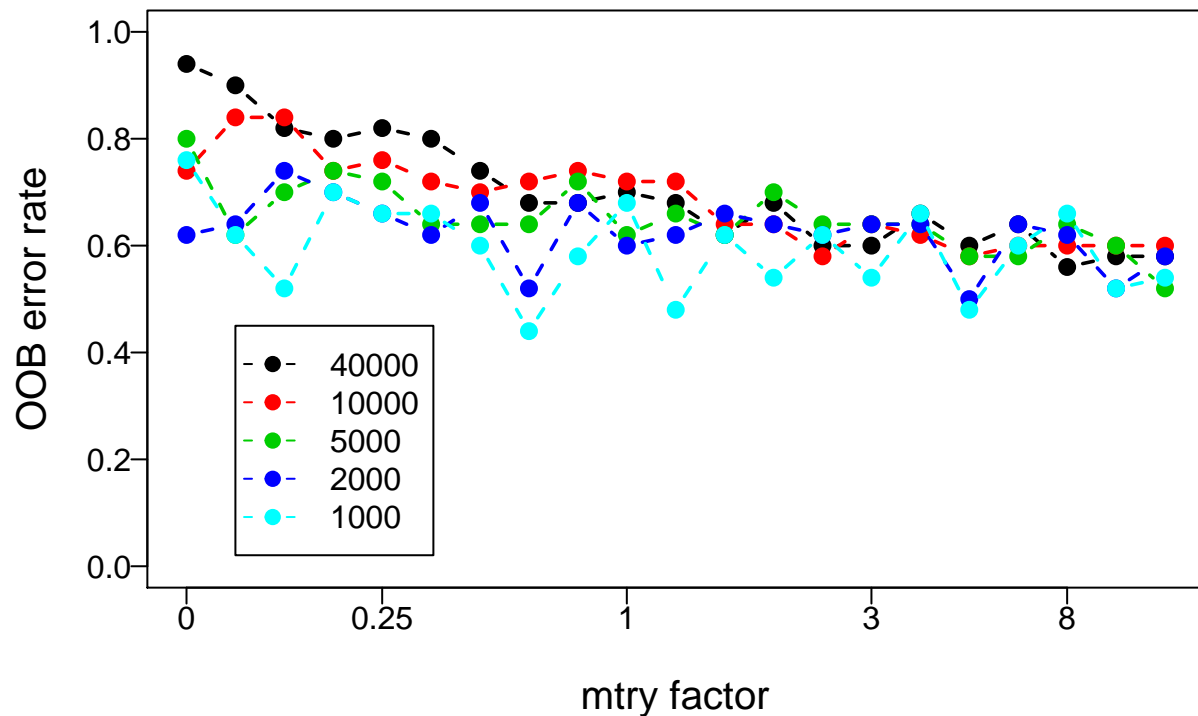
No signal: Classes 2 ; nodesize = 5



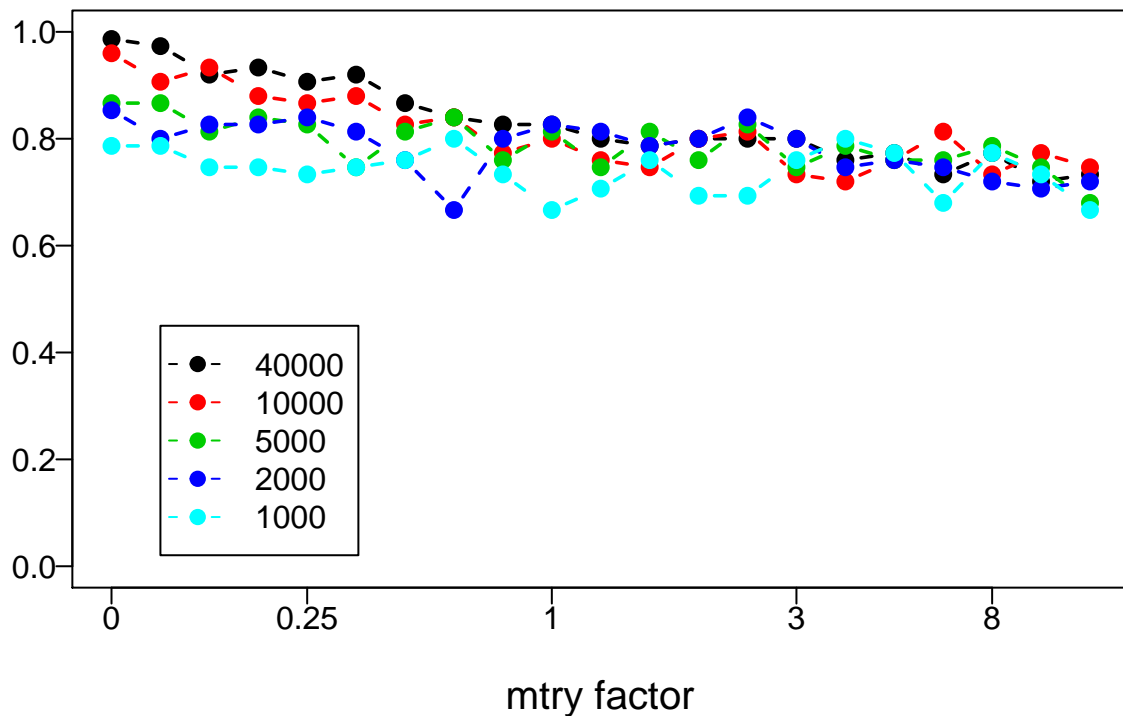
No signal: Classes 2 ; nodesize = 5



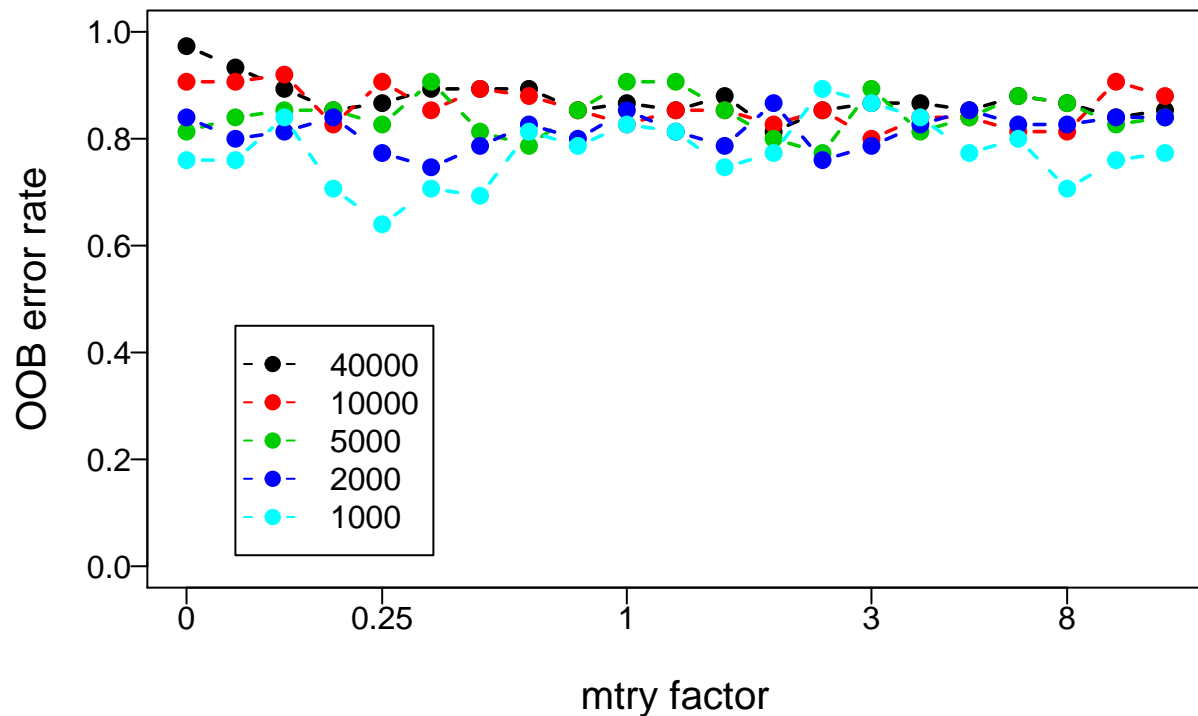
No signal: Classes 2 ; nodesize = 5



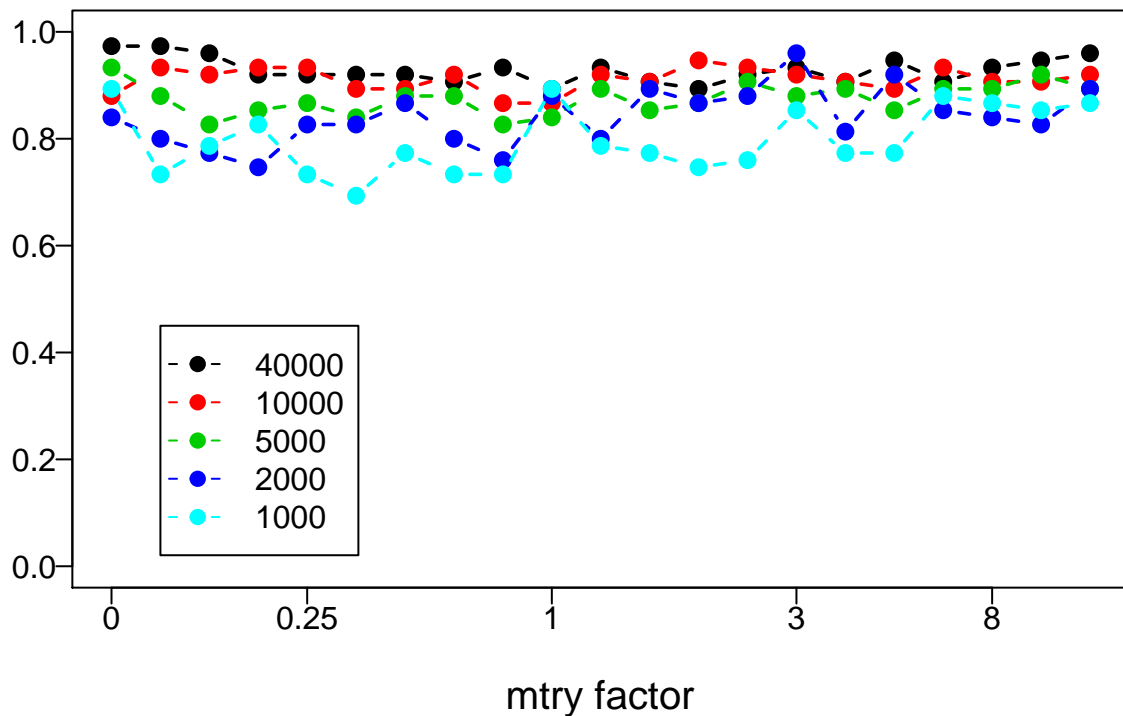
No signal: Classes 3 ; nodesize = 5



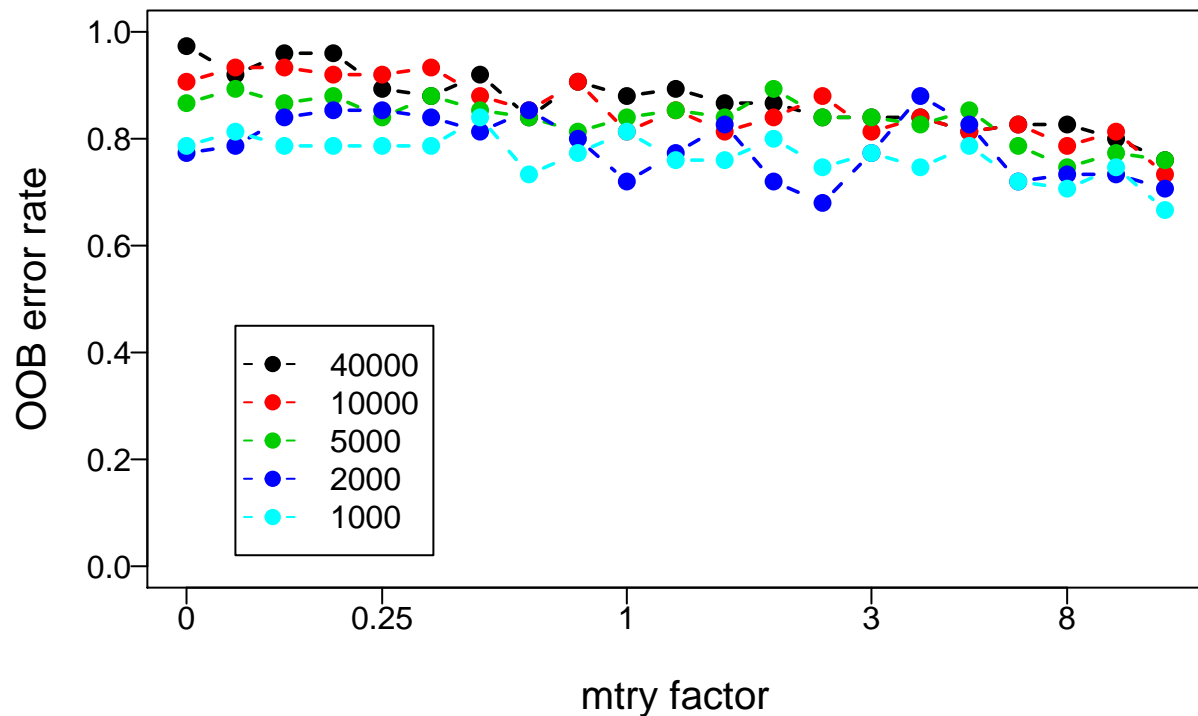
No signal: Classes 3 ; nodesize = 5



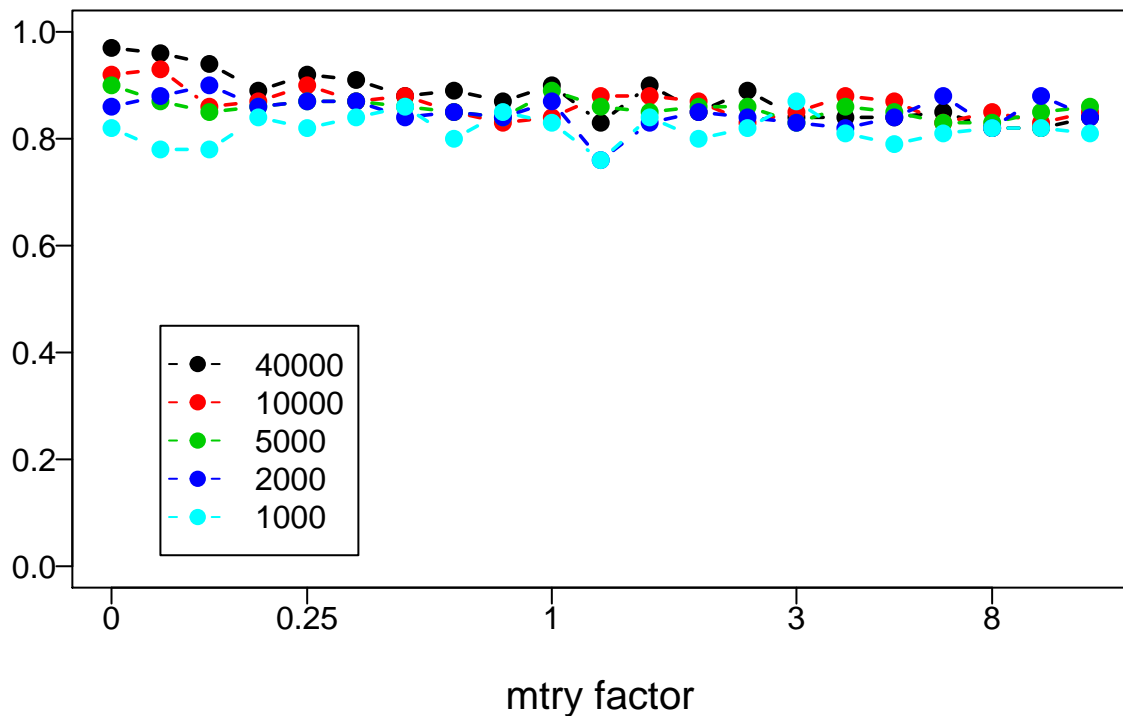
No signal: Classes 3 ; nodesize = 5



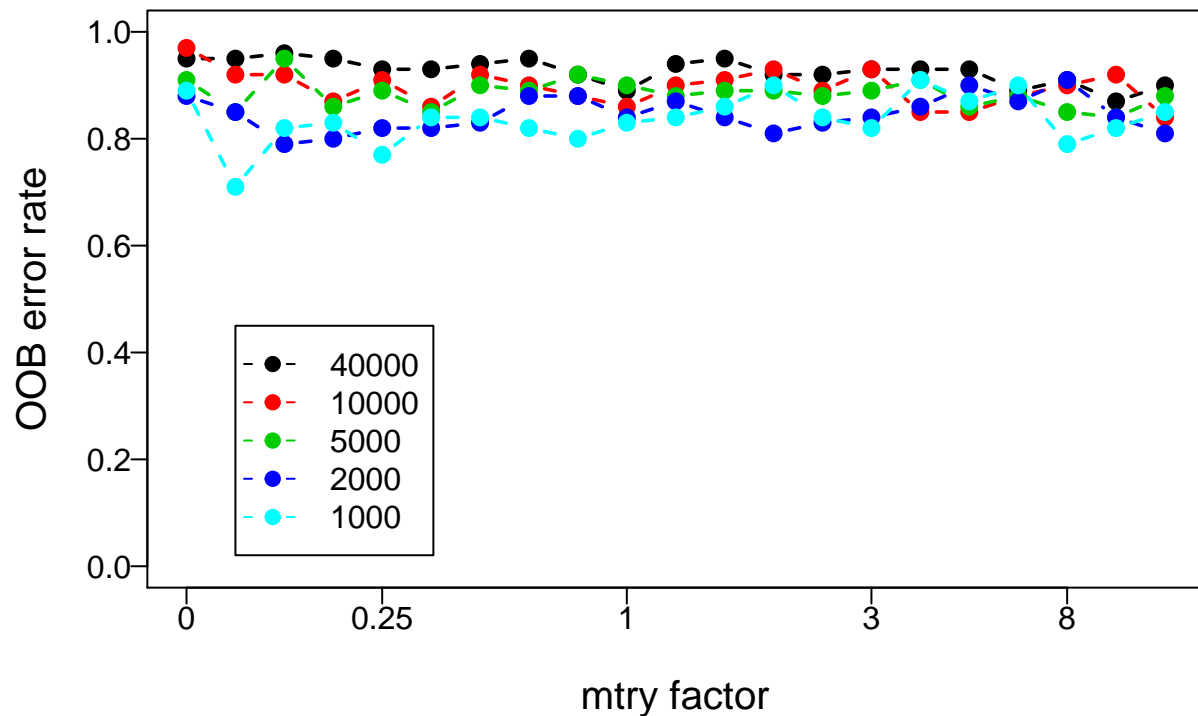
No signal: Classes 3 ; nodesize = 5



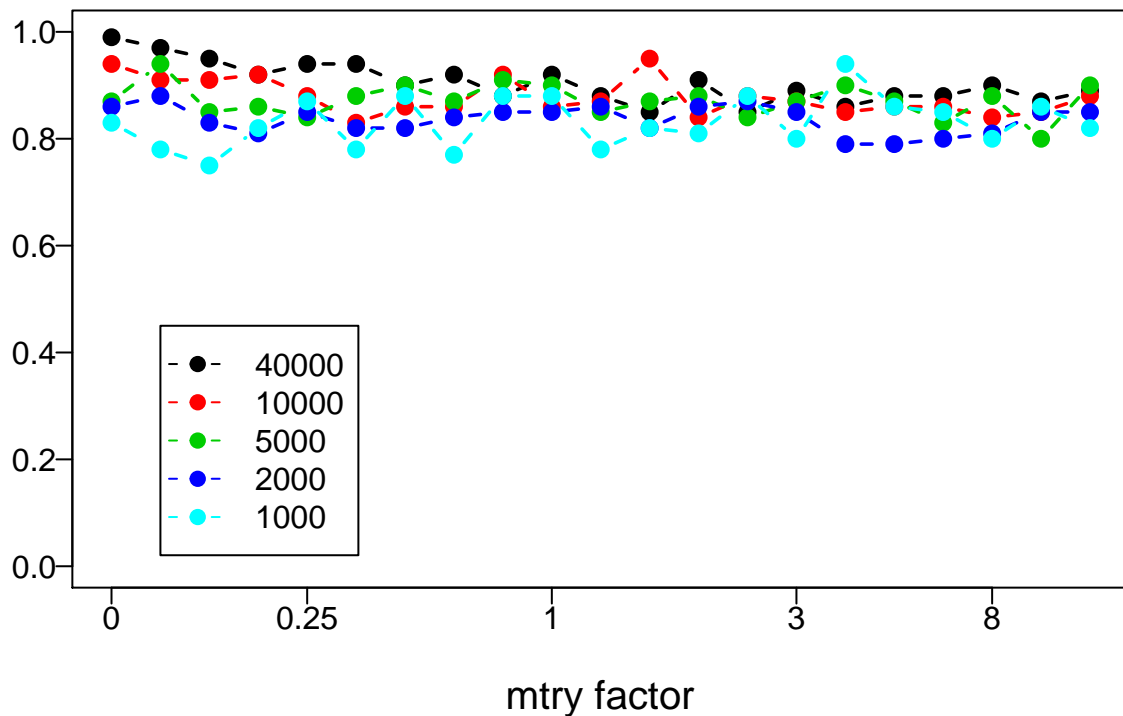
No signal: Classes 4 ; nodesize = 5



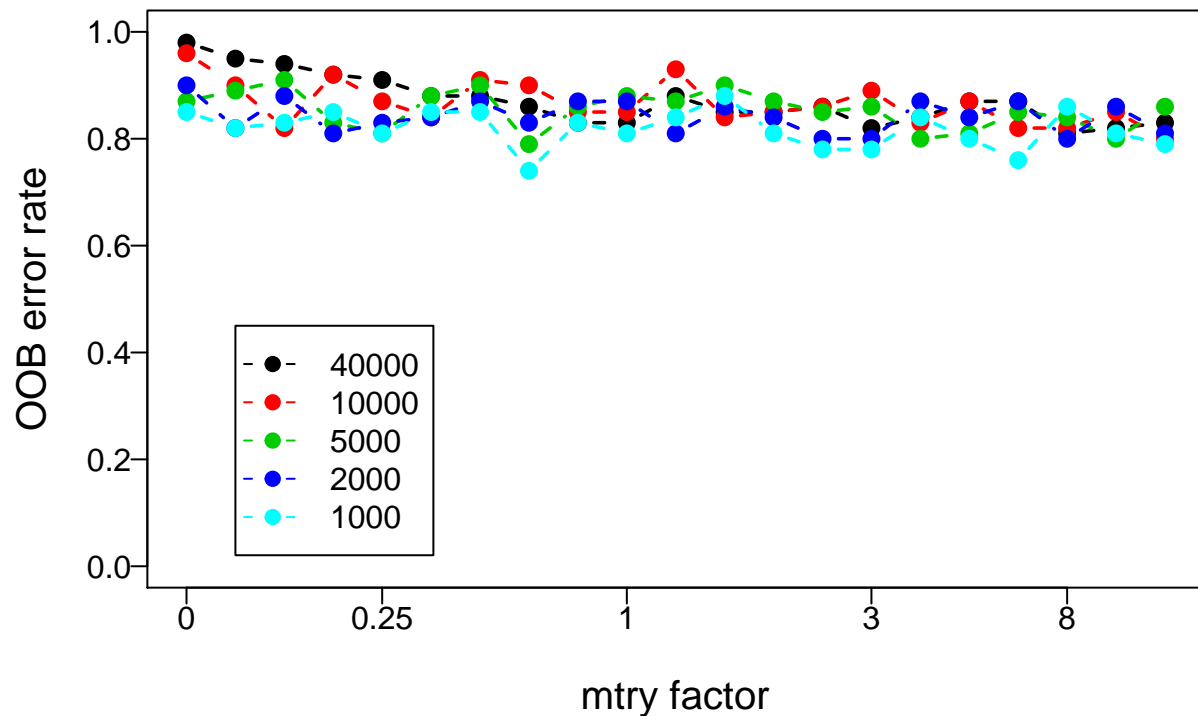
No signal: Classes 4 ; nodesize = 5



No signal: Classes 4 ; nodesize = 5



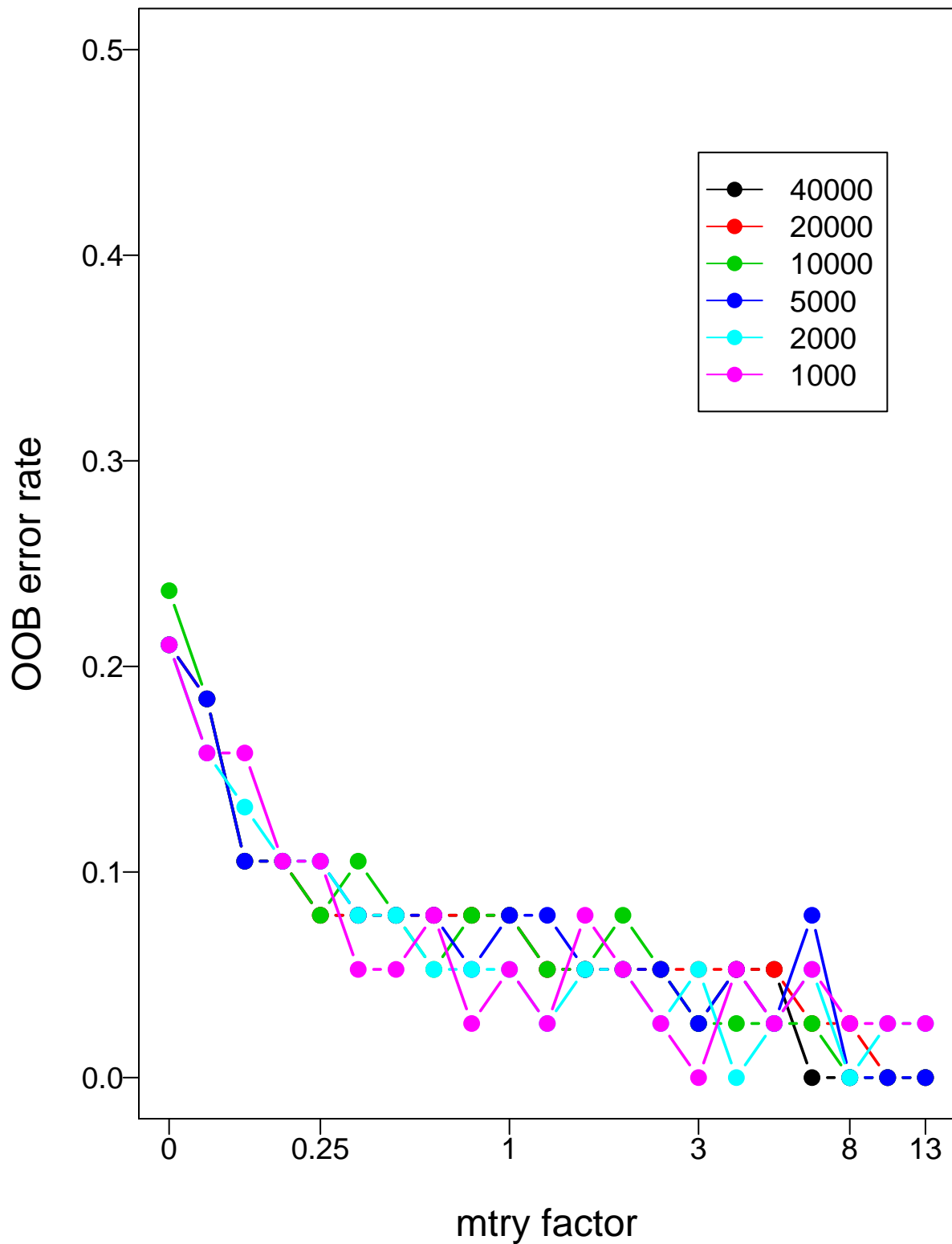
No signal: Classes 4 ; nodesize = 5



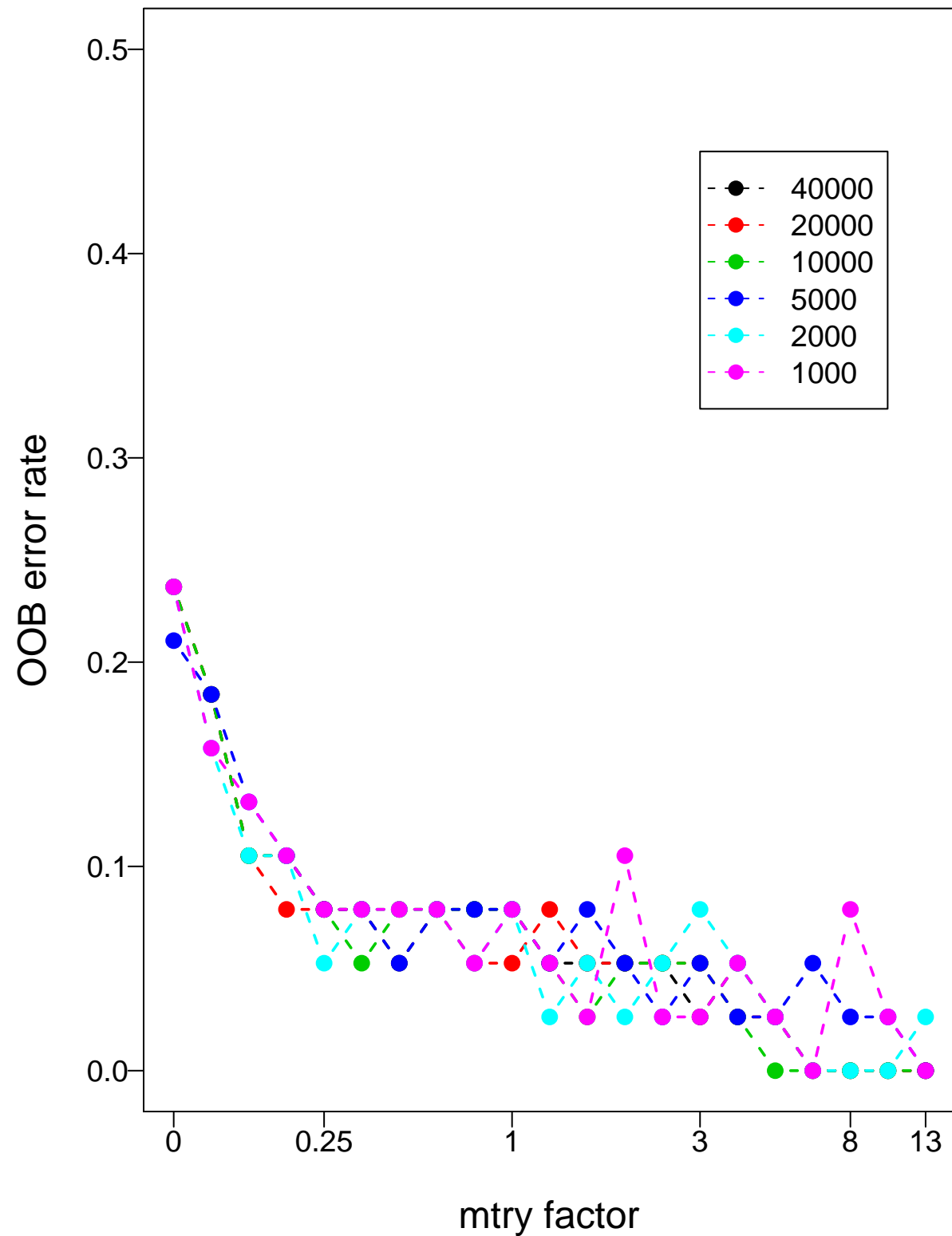
III: Real microarray data sets:

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

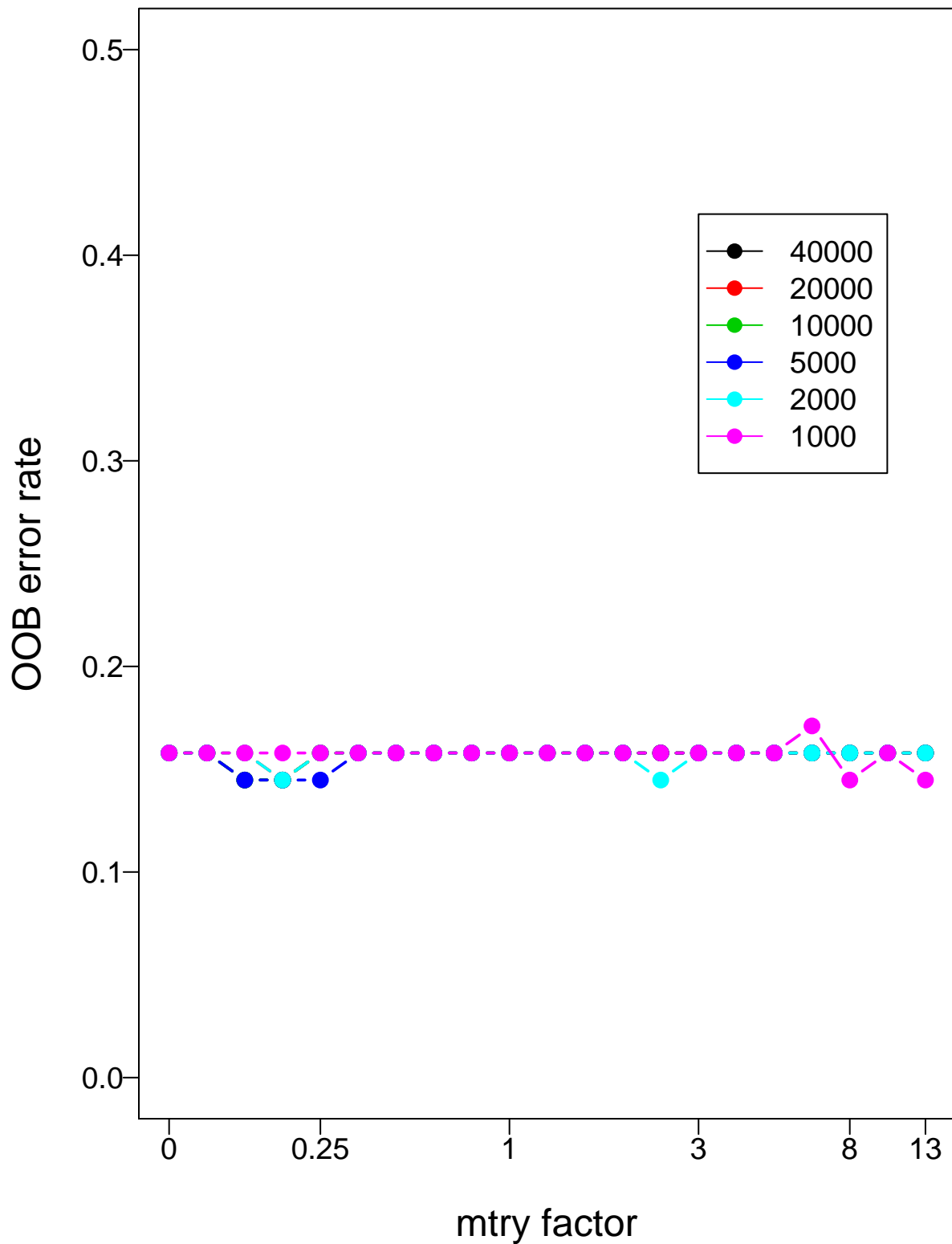
Leukemia; nodesize = 1



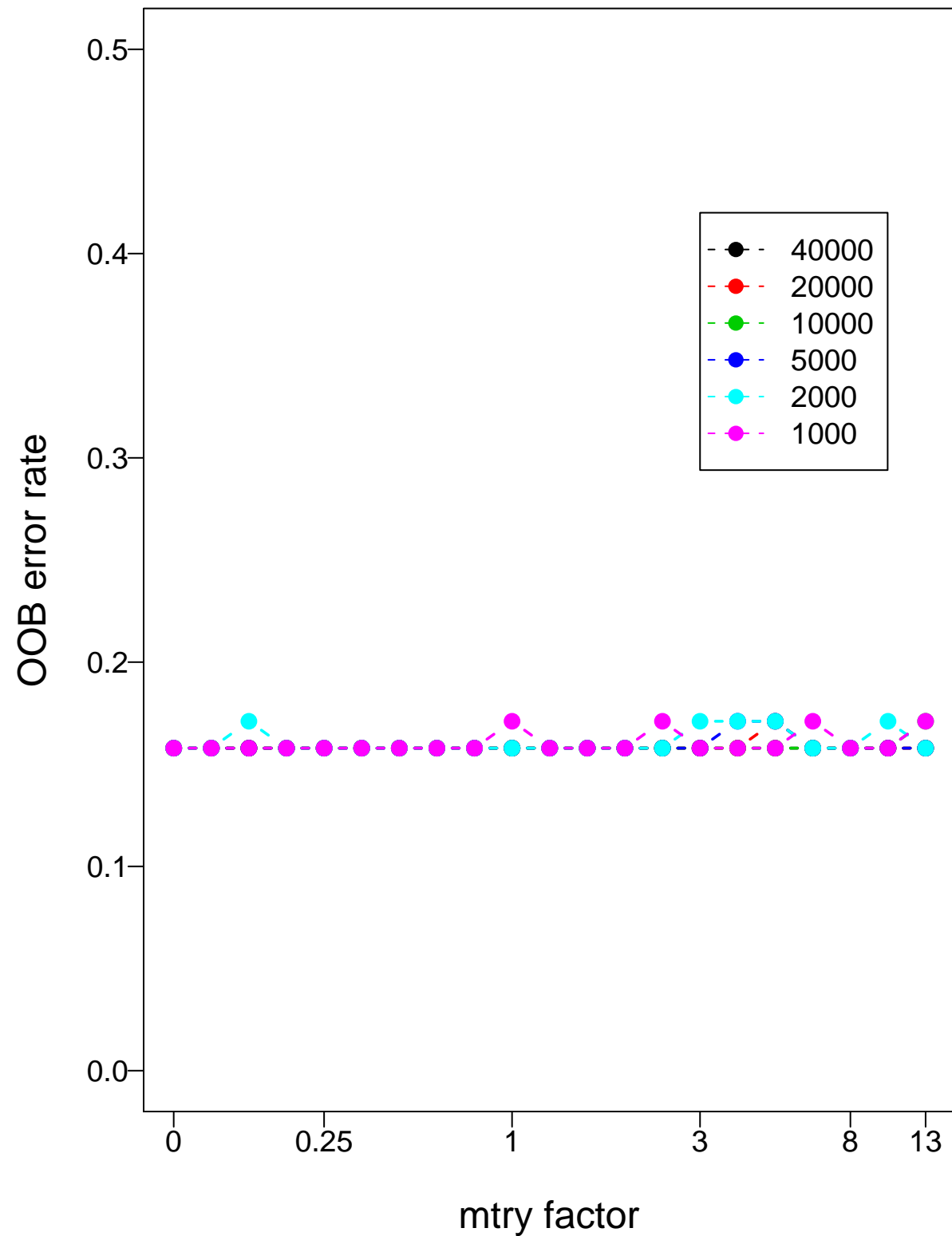
Leukemia; nodesize = 5



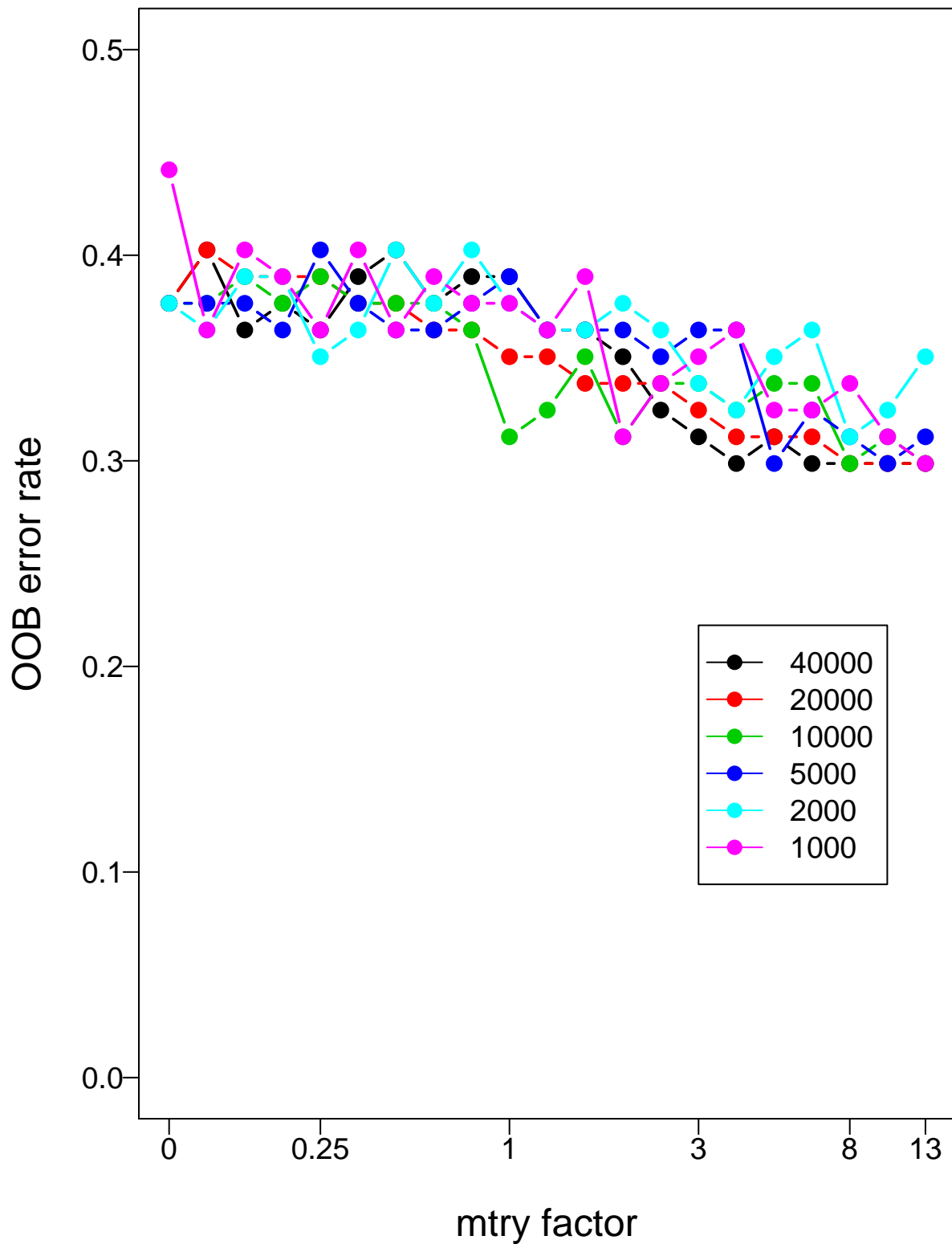
Adenoc.; nodesize = 1



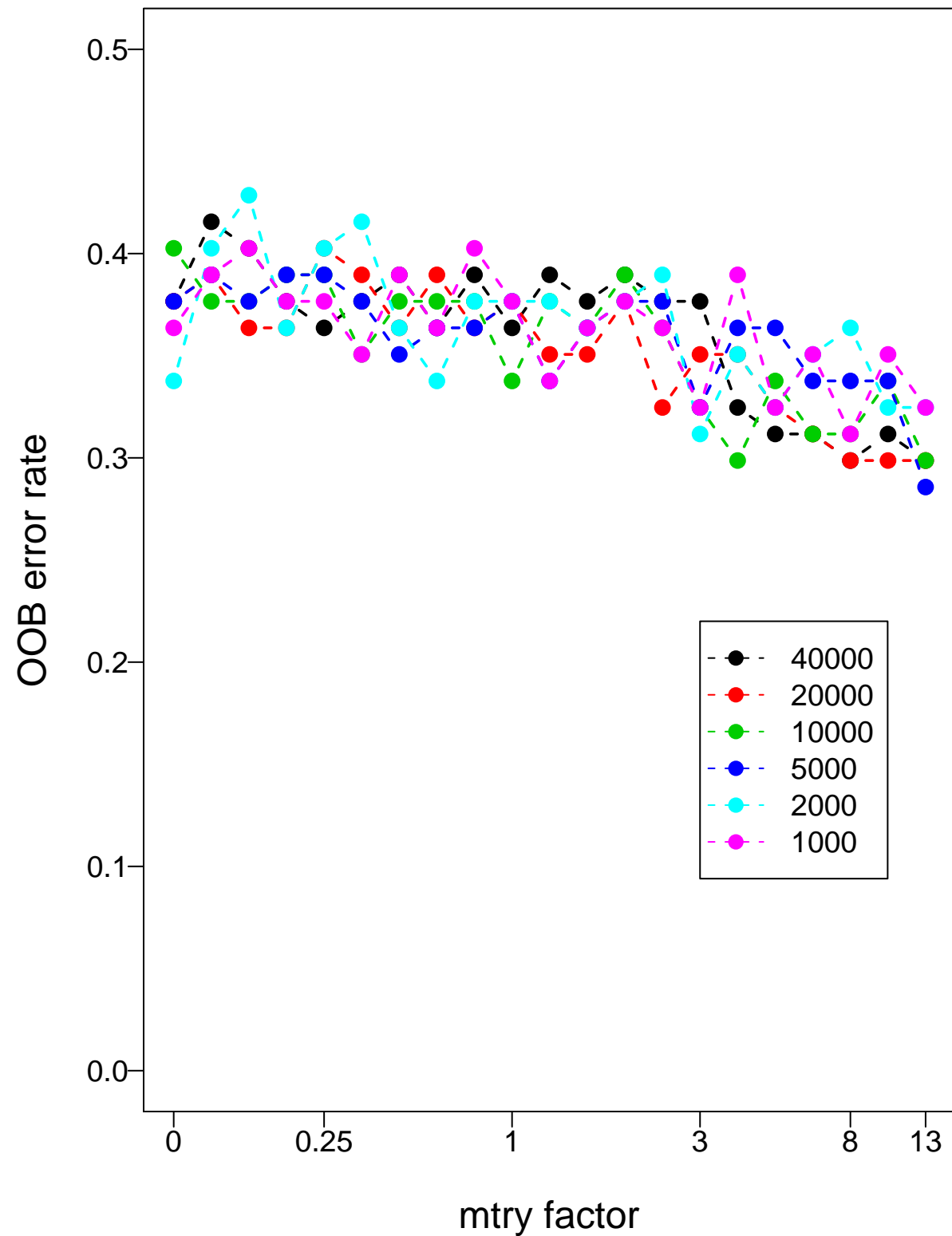
Adenoc.; nodesize = 5



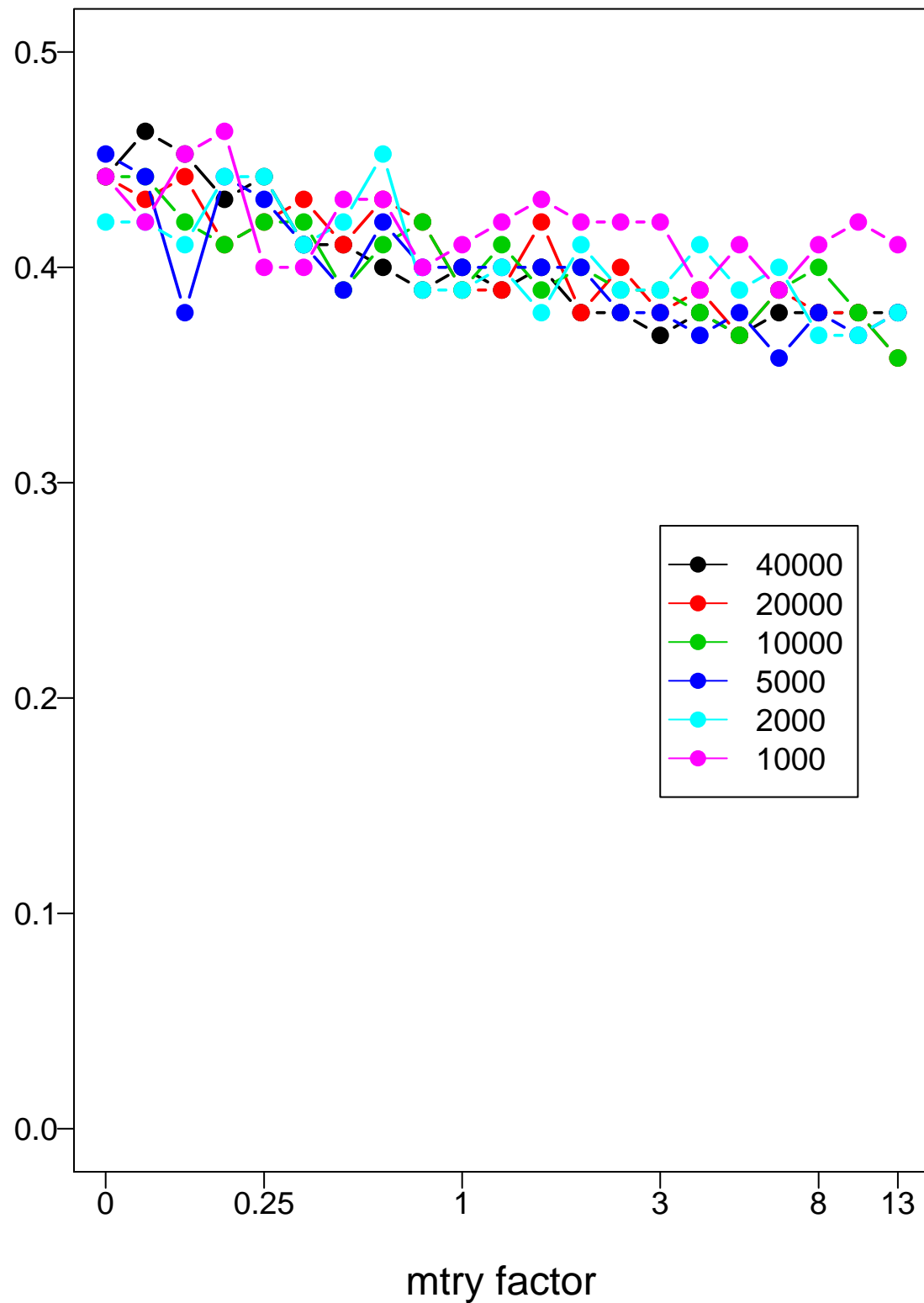
Breast, 2 cl.; nodesize = 1



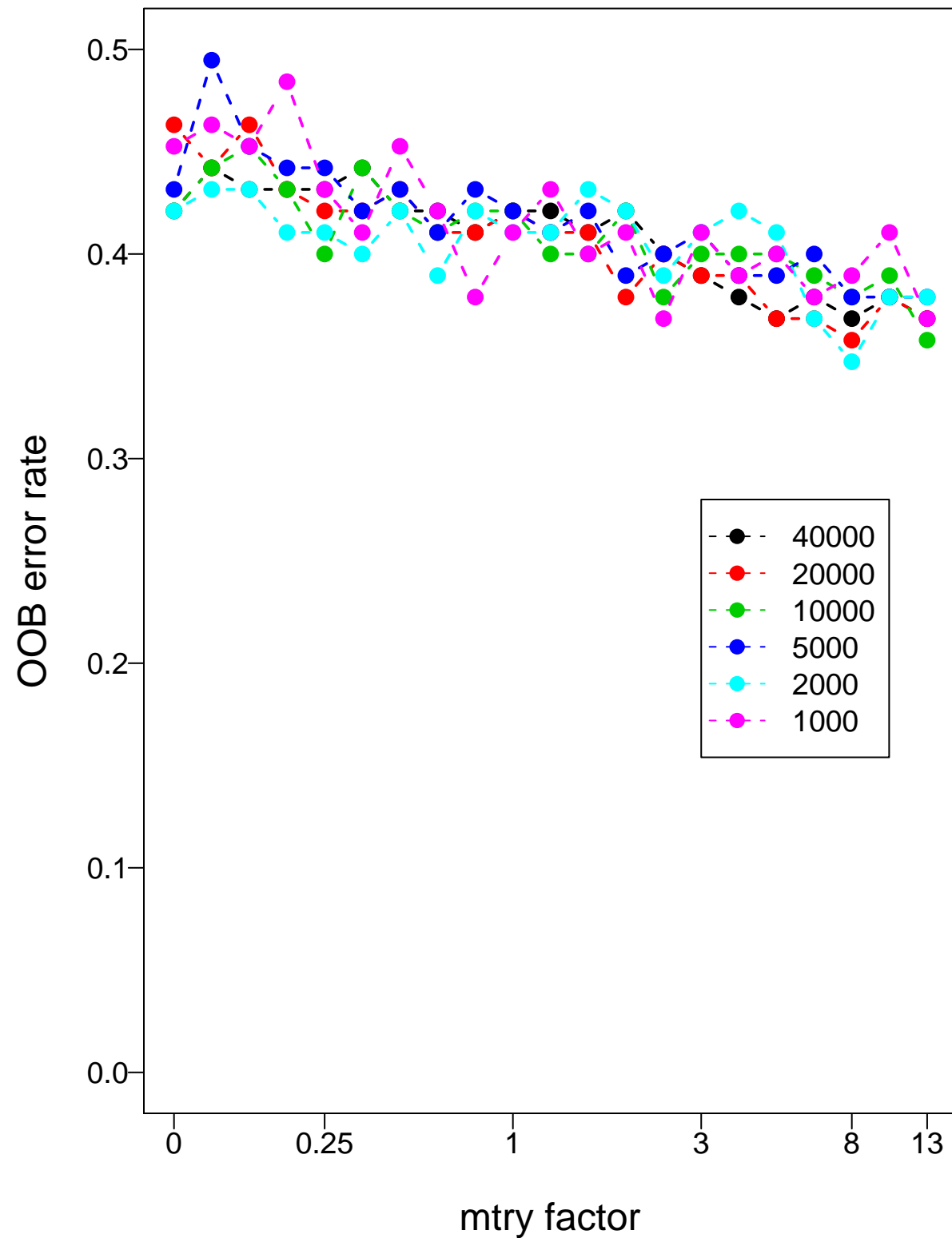
Breast, 2 cl.; nodesize = 5



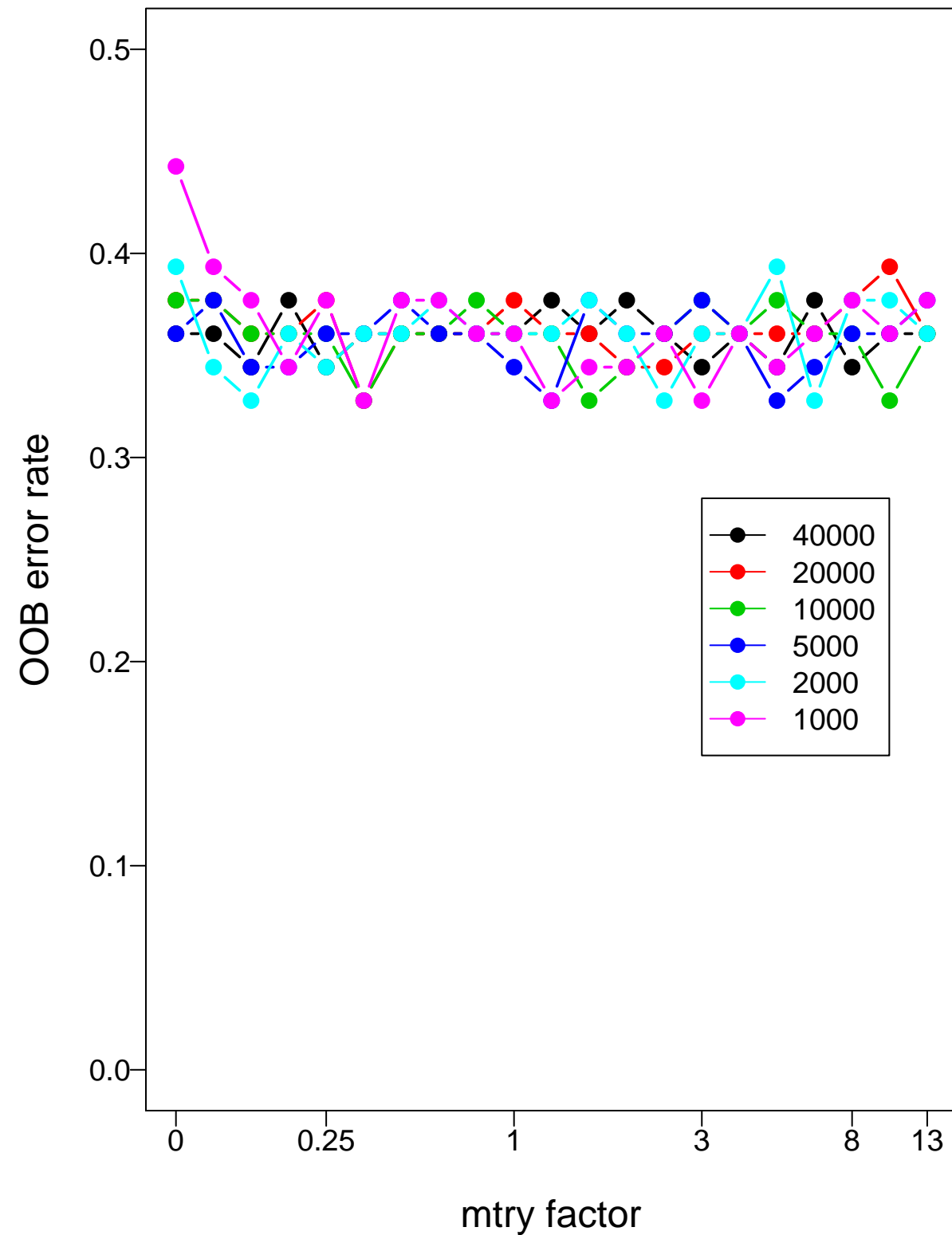
Breast, 3 cl.; nodesize = 1



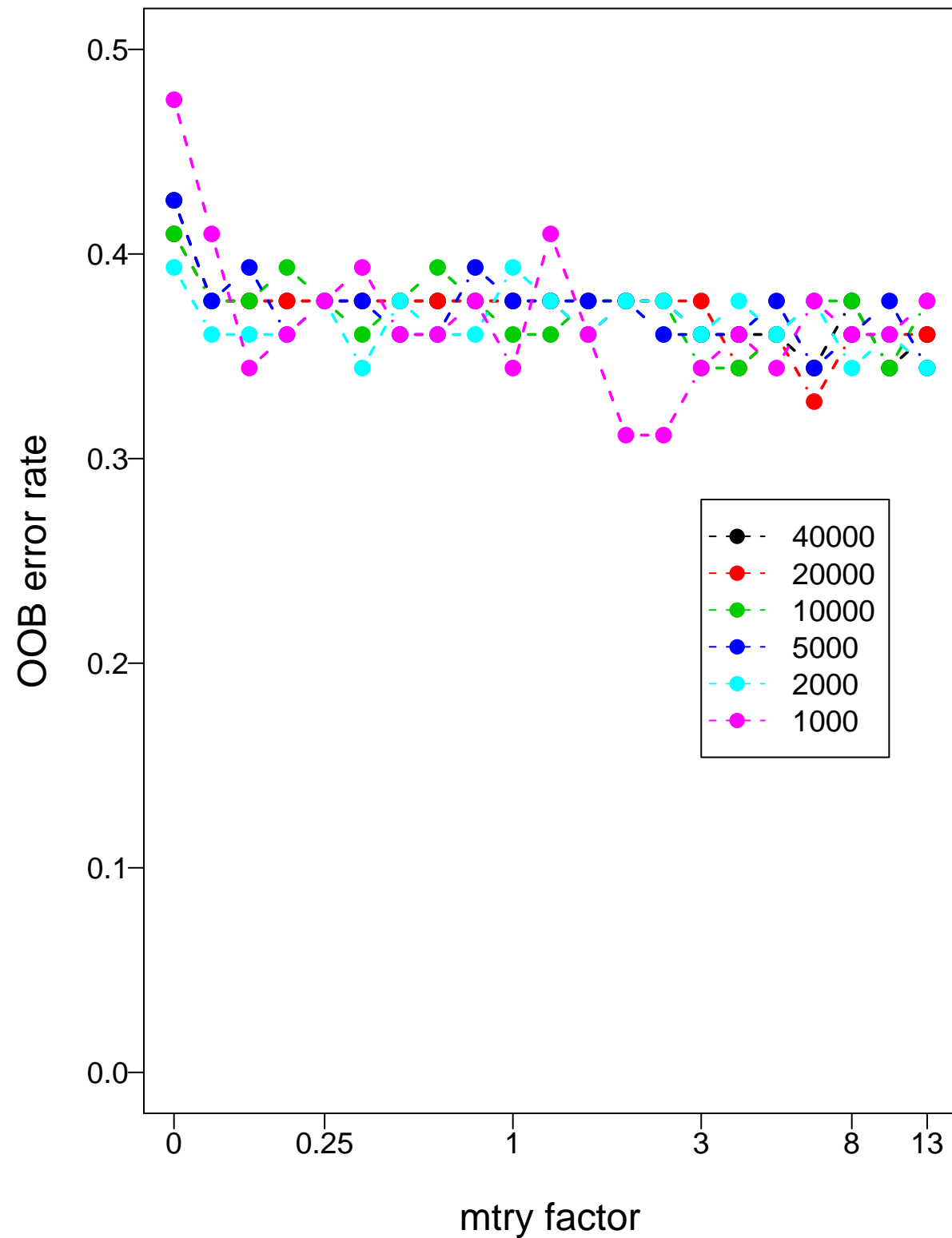
Breast, 3 cl.; nodesize = 5



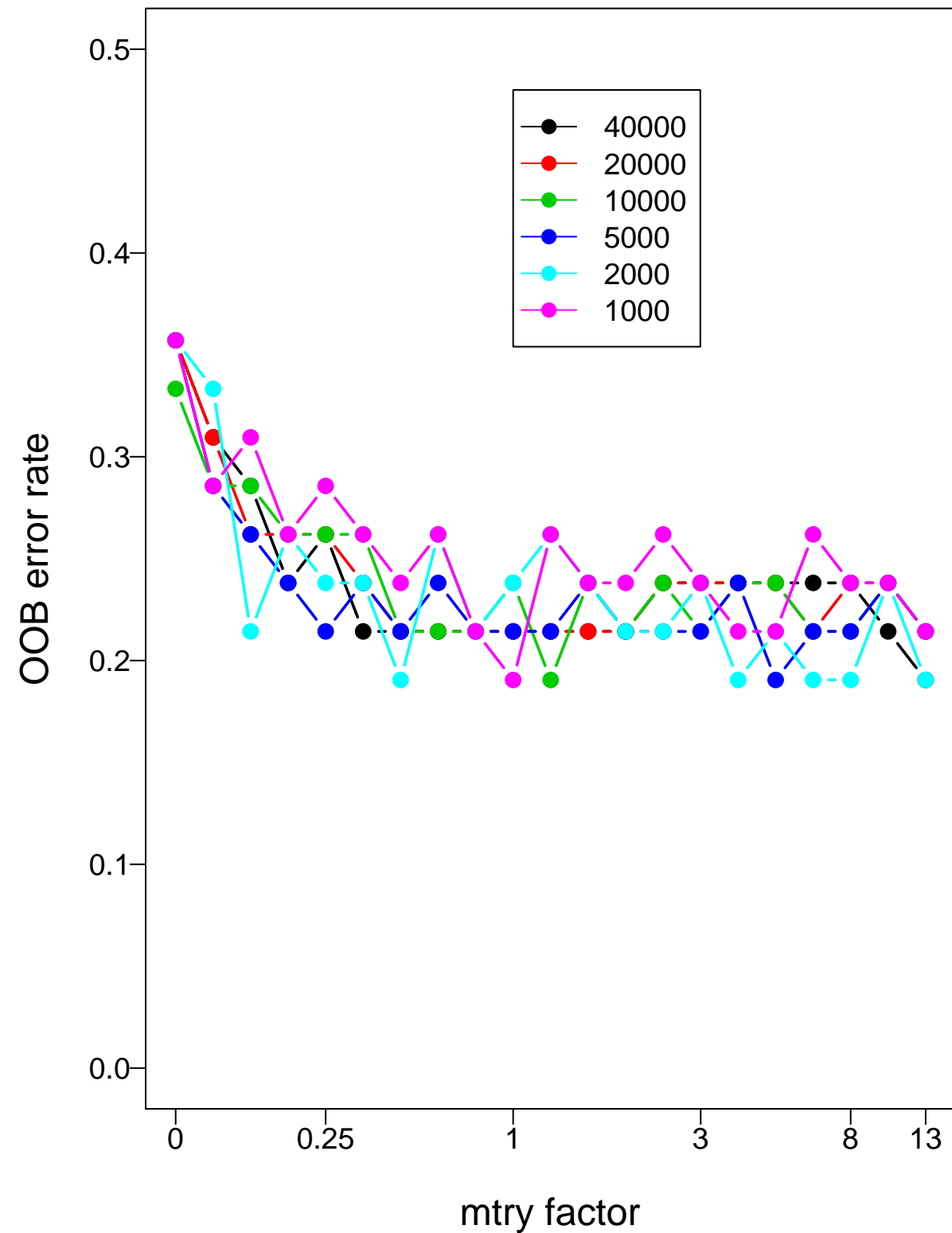
NCI 60; nodesize = 1



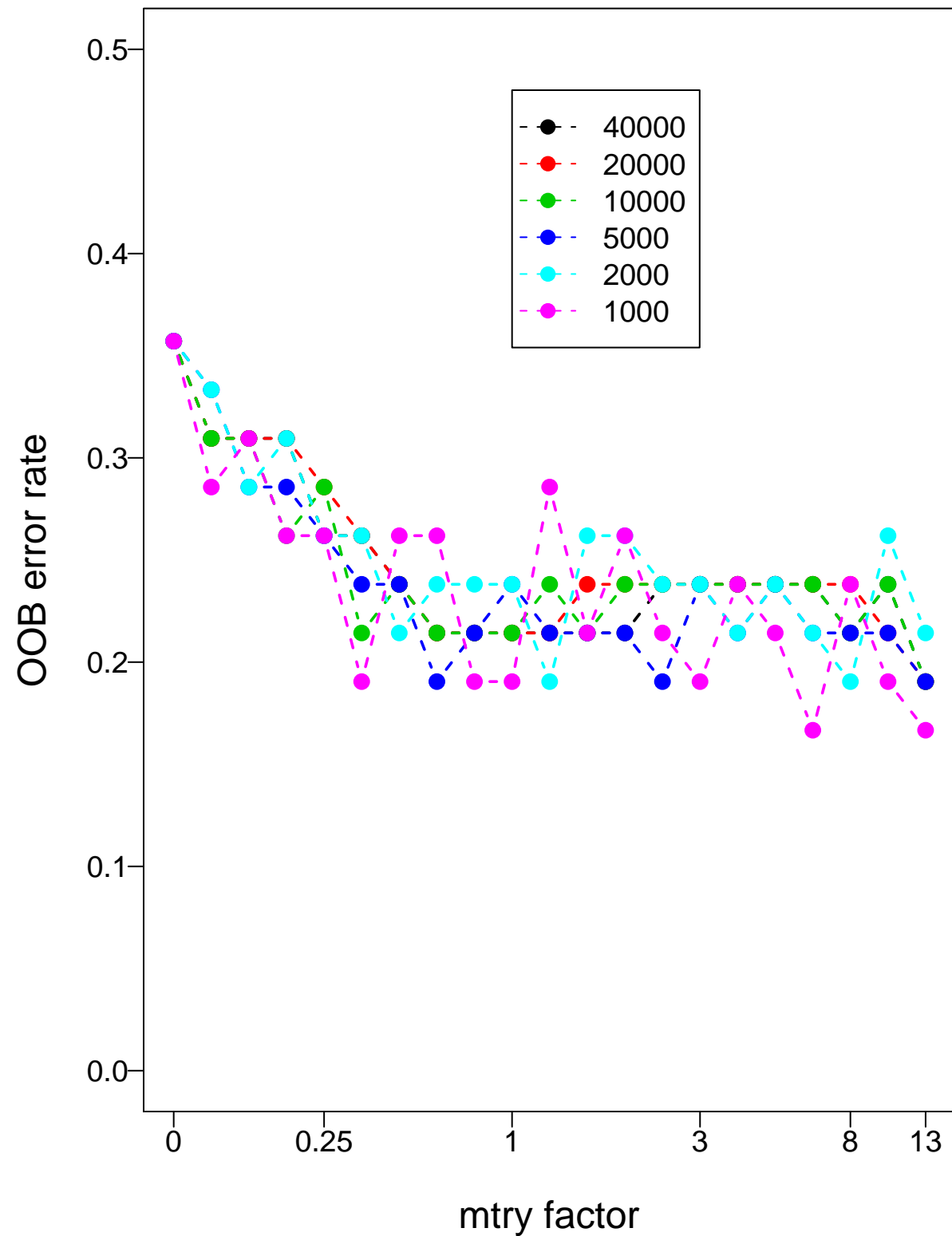
NCI 60; nodesize = 5



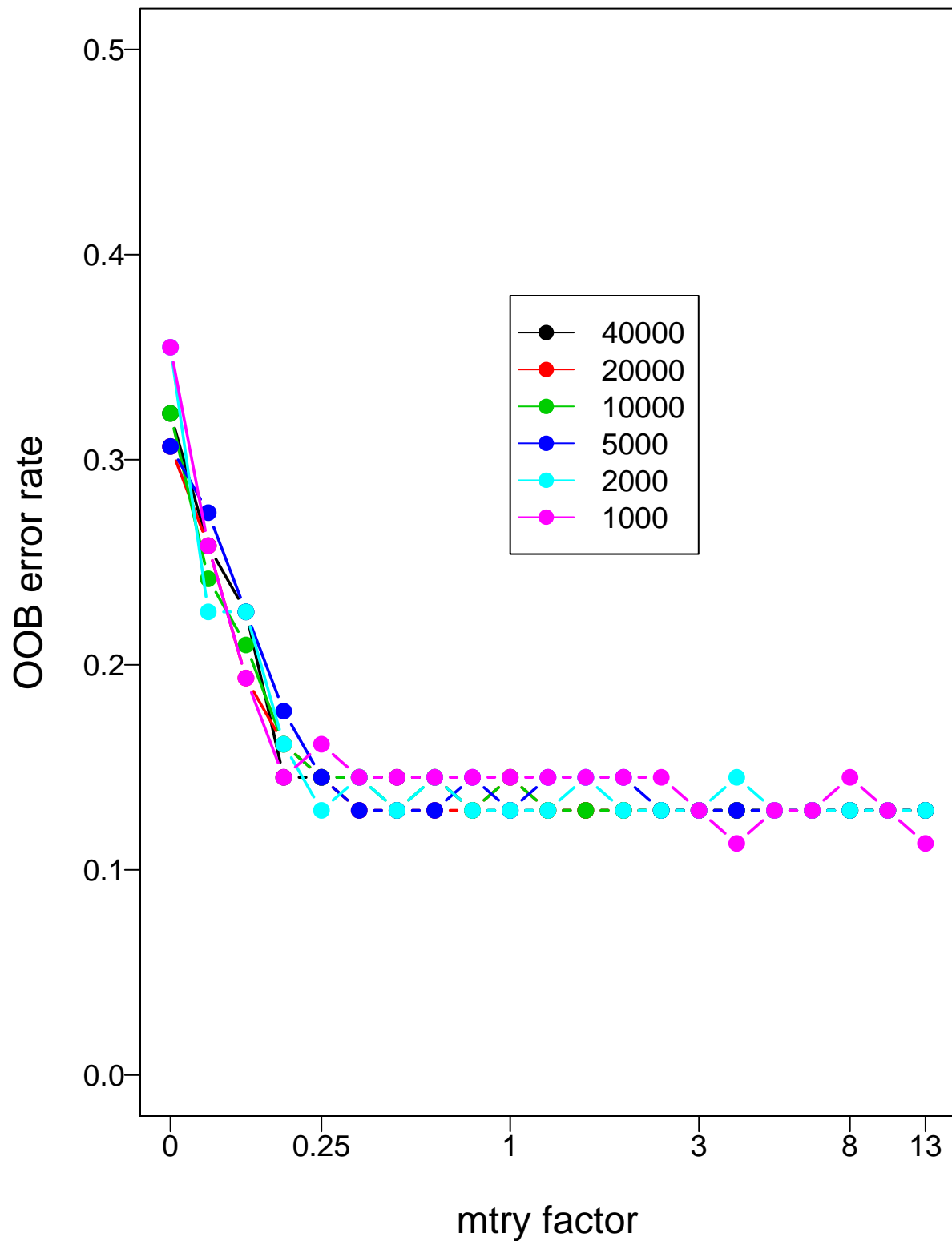
Brain; nodesize = 1



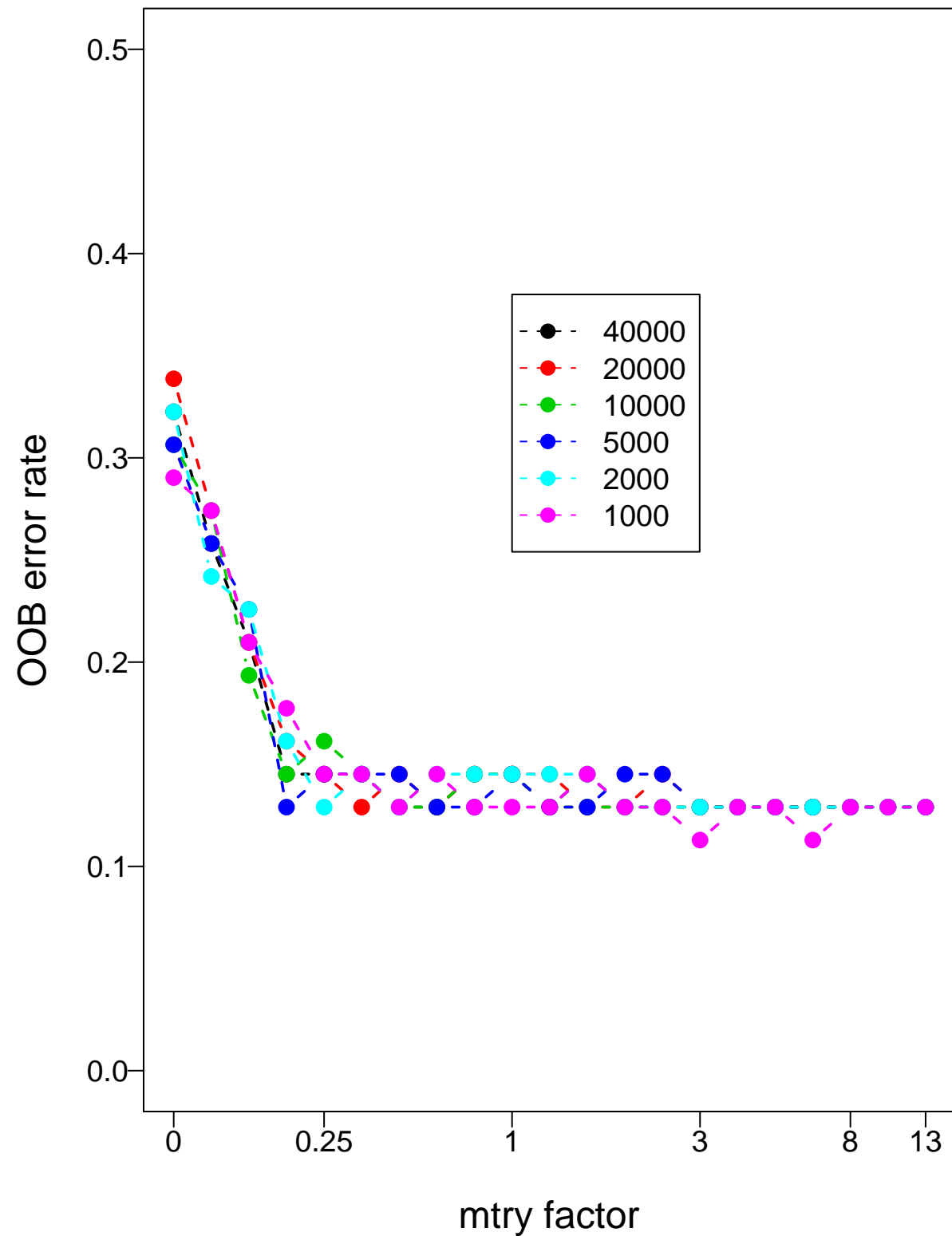
Brain; nodesize = 5



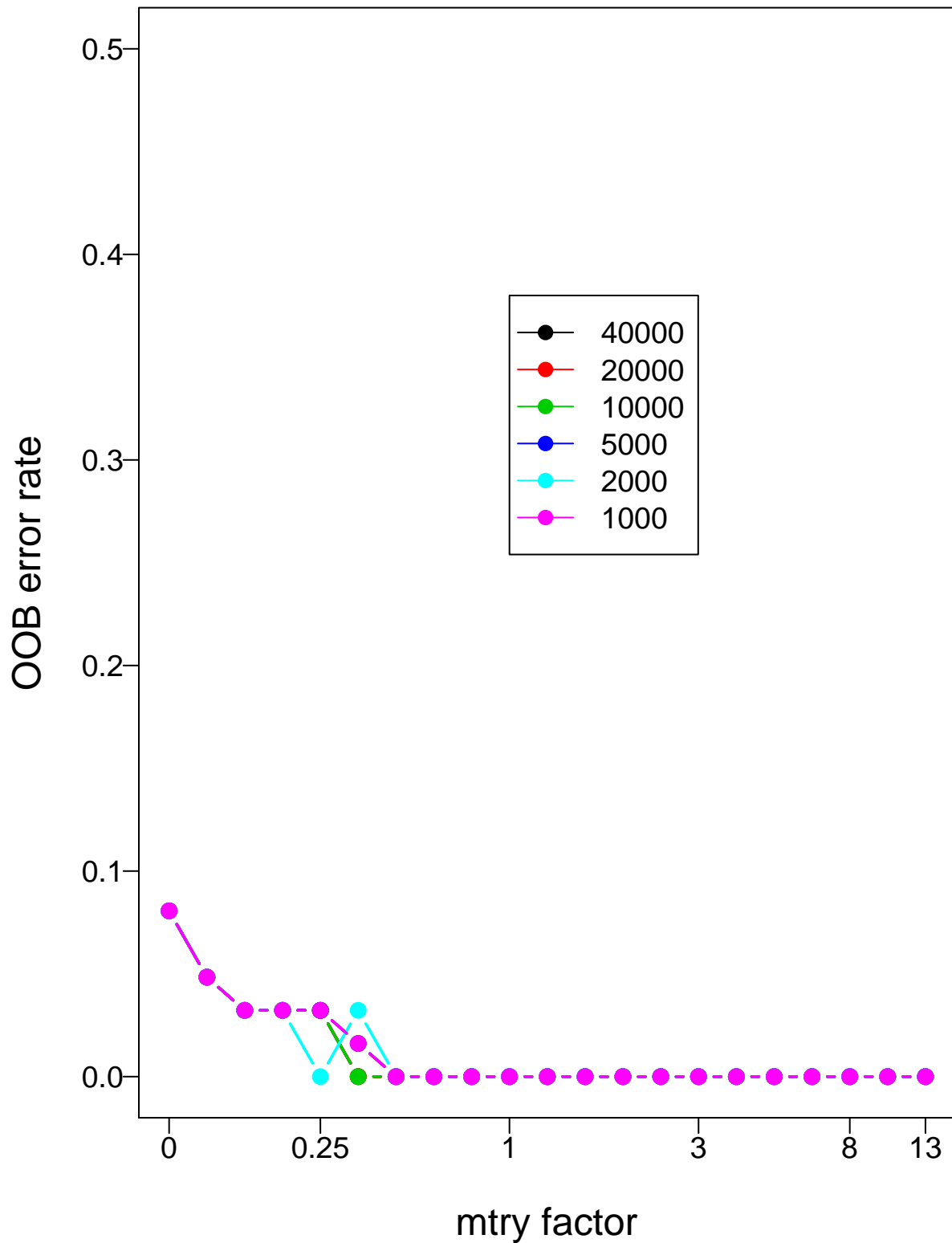
Colon.; nodesize = 1



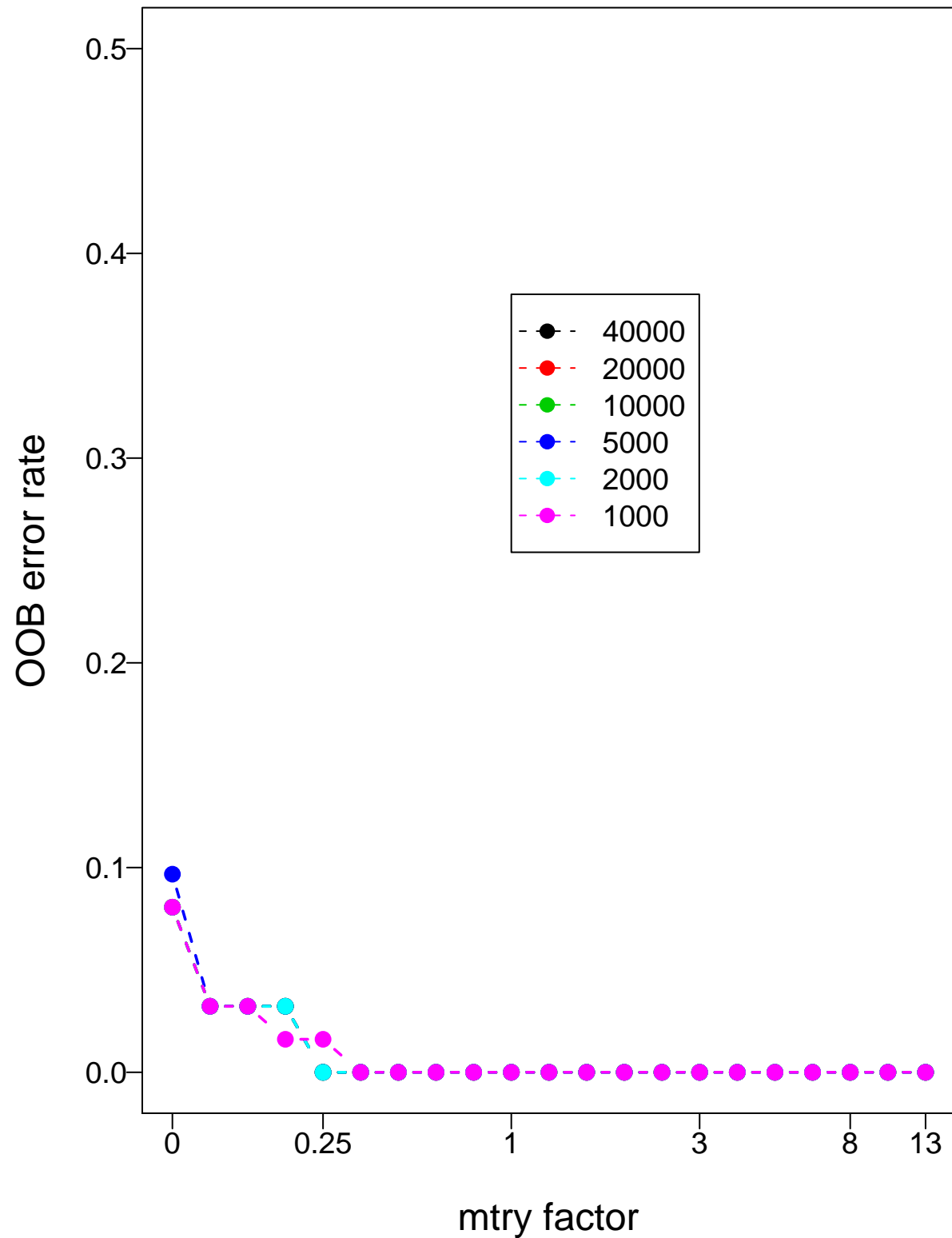
Colon.; nodesize = 5



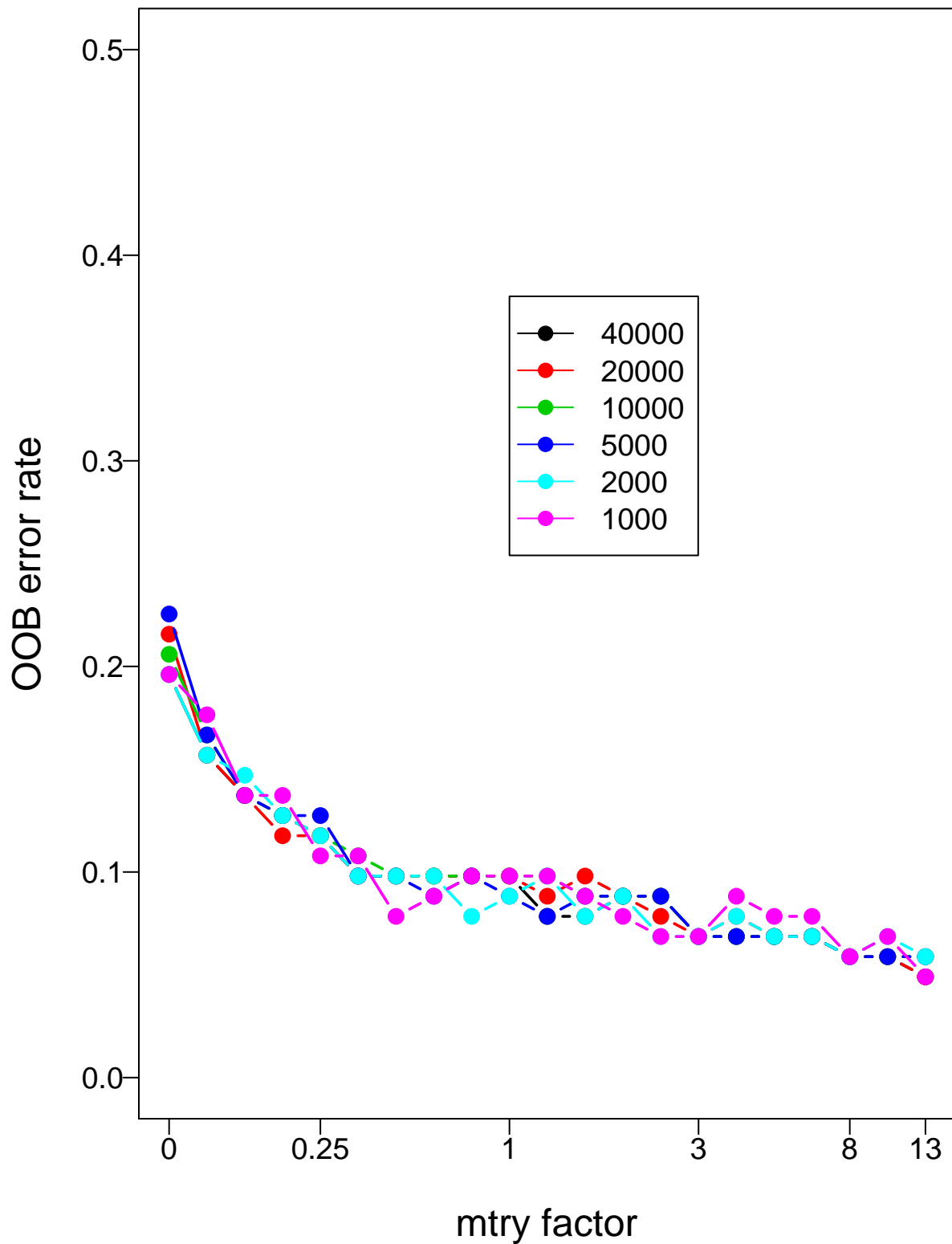
Lymphoma; nodesize = 1



Lymphoma; nodesize = 5



Prostate; nodesize = 1



Prostate; nodesize = 5

