

Variable importances: simulated data.

'Scree plots' or 'importance spectrum':

`ntree = 5000`

`mtry = ncol`

Black: original data sets;

Blue: variables with true signal;

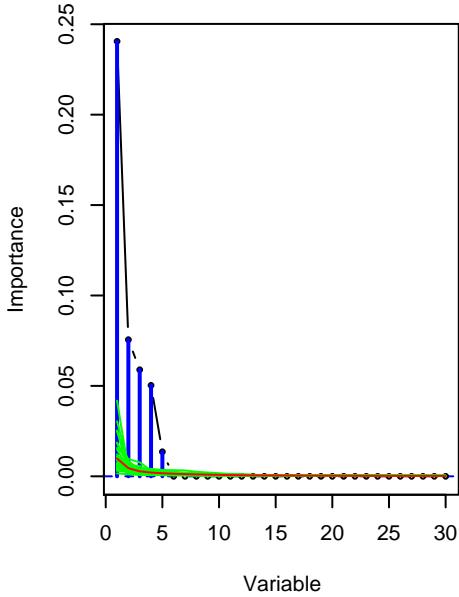
green: permuted class labels data sets;

red: average from permuted class labels data sets.

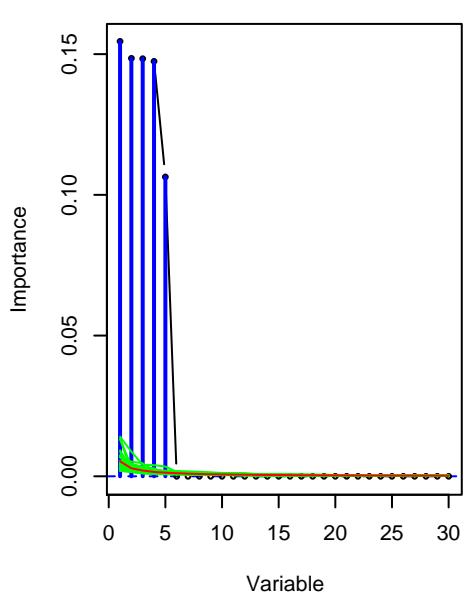
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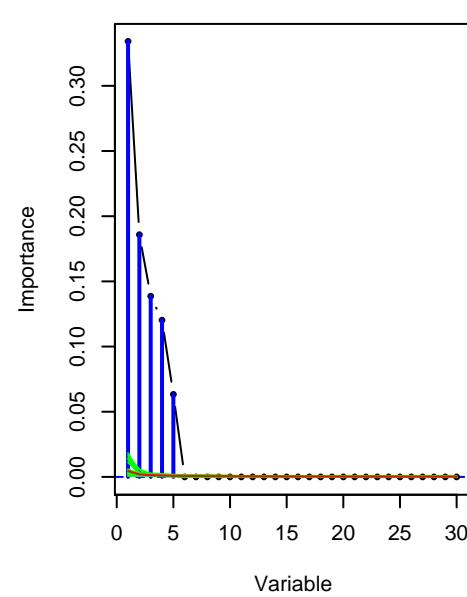
2 classes; 1 comp.; 5 genes/comp.



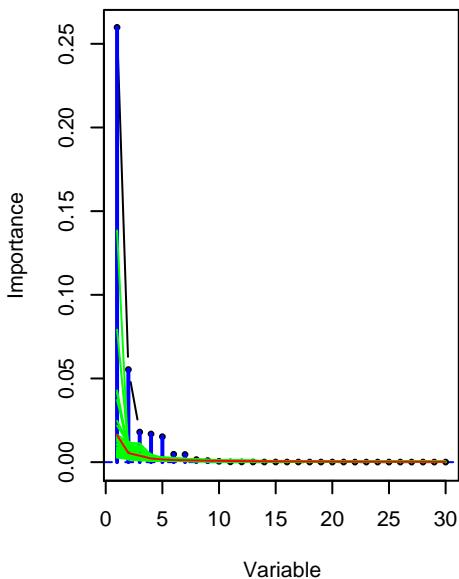
3 classes; 1 comp.; 5 genes/comp.



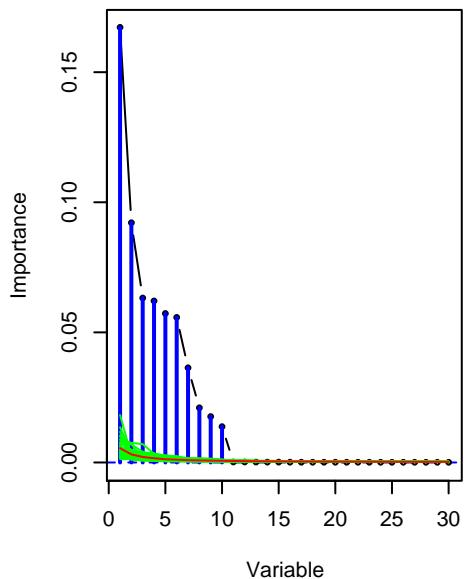
4 classes; 1 comp.; 5 genes/comp.



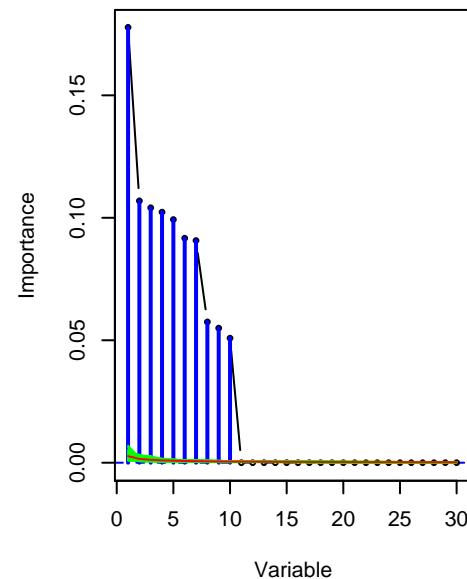
2 classes; 2 comp.; 5 genes/comp.



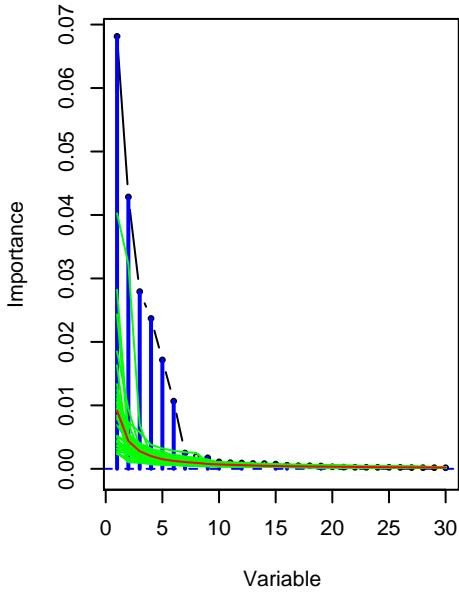
3 classes; 2 comp.; 5 genes/comp.



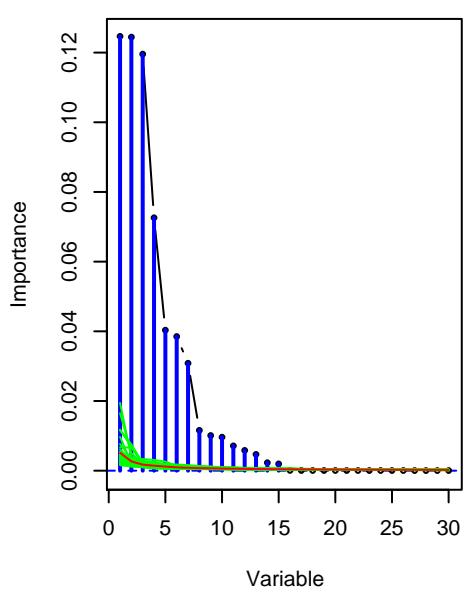
4 classes; 2 comp.; 5 genes/comp.



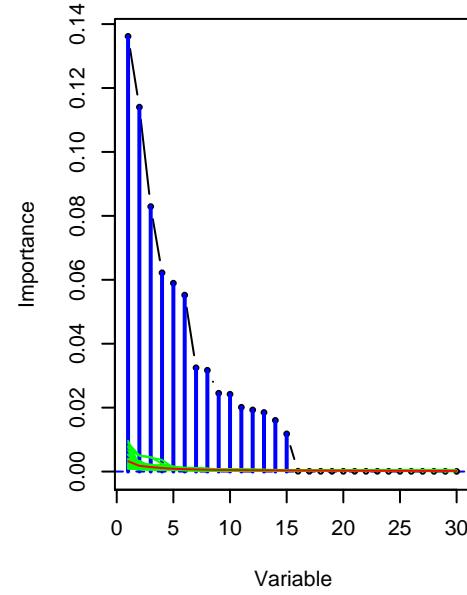
2 classes; 3 comp.; 5 genes/comp.



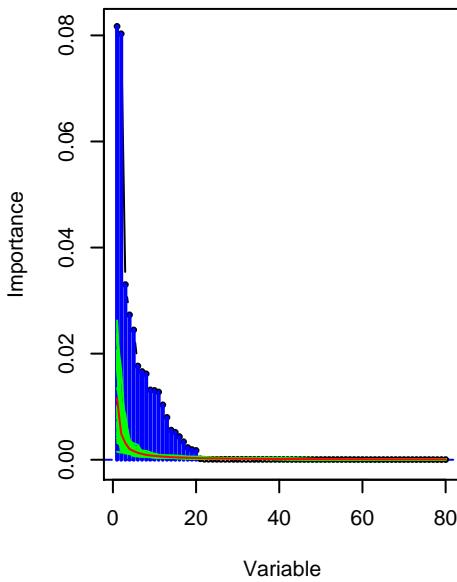
3 classes; 3 comp.; 5 genes/comp.



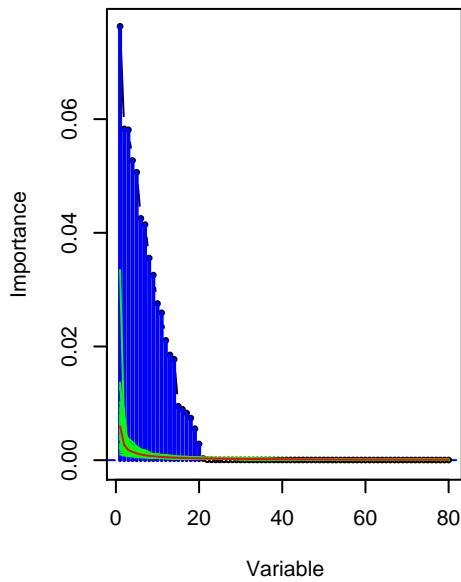
4 classes; 3 comp.; 5 genes/comp.



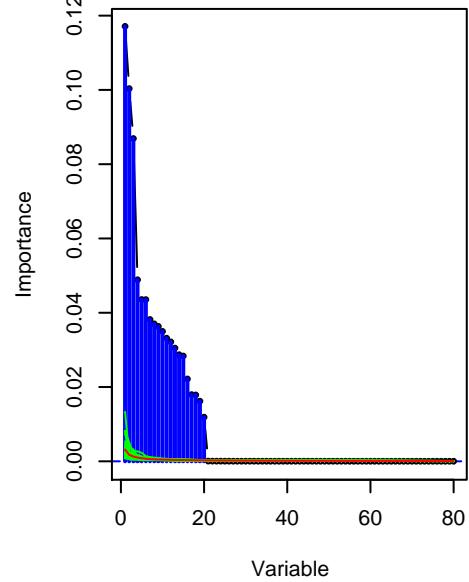
2 classes; 1 comp.; 20 genes/comp.



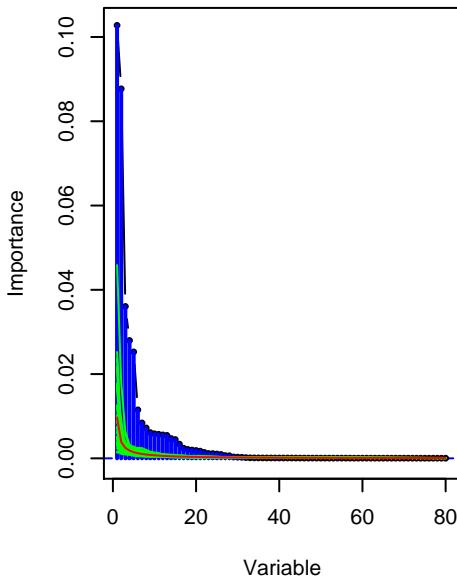
3 classes; 1 comp.; 20 genes/comp.



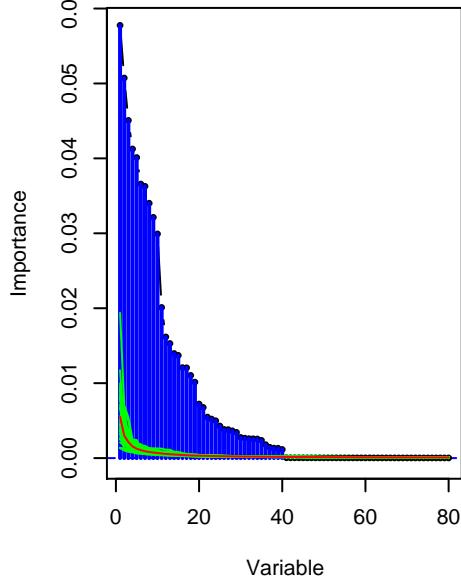
4 classes; 1 comp.; 20 genes/comp.



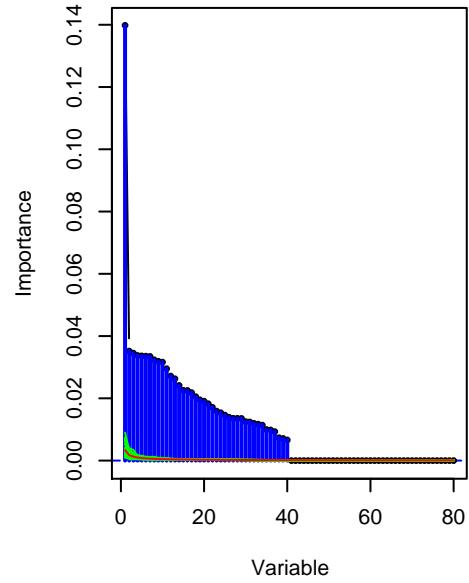
2 classes; 2 comp.; 20 genes/comp.



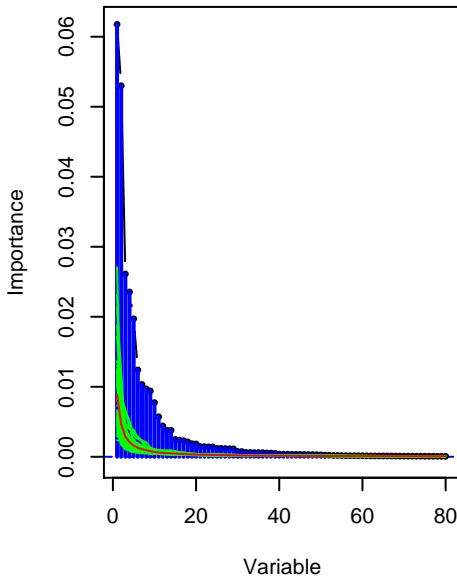
3 classes; 2 comp.; 20 genes/comp.



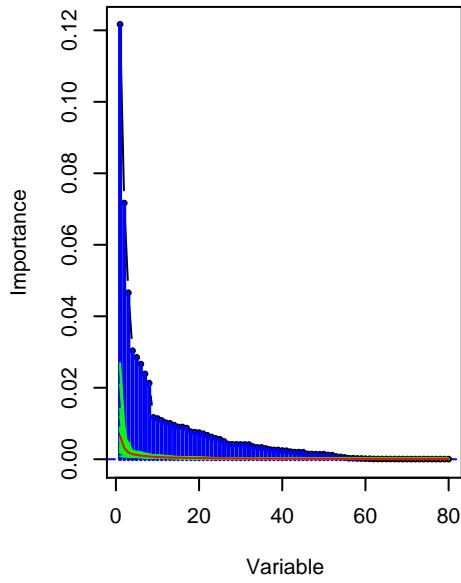
4 classes; 2 comp.; 20 genes/comp.



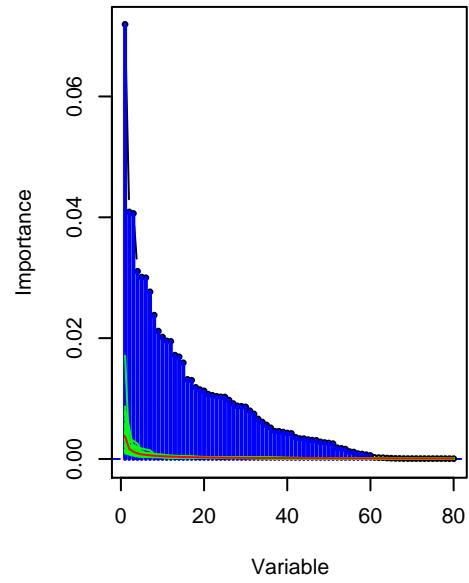
2 classes; 3 comp.; 20 genes/comp.



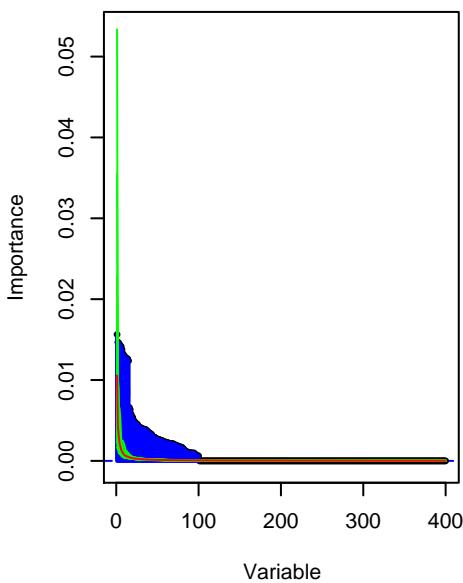
3 classes; 3 comp.; 20 genes/comp.



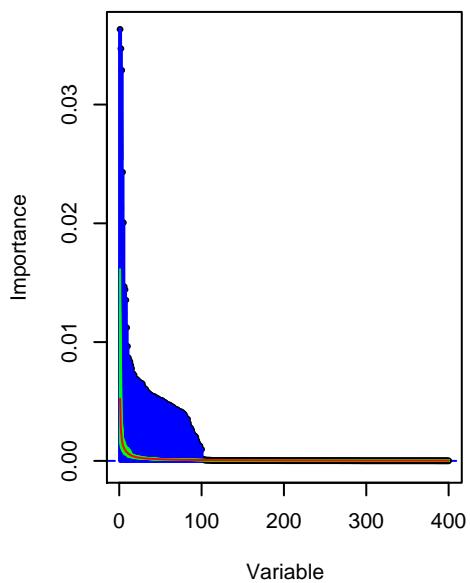
4 classes; 3 comp.; 20 genes/comp.



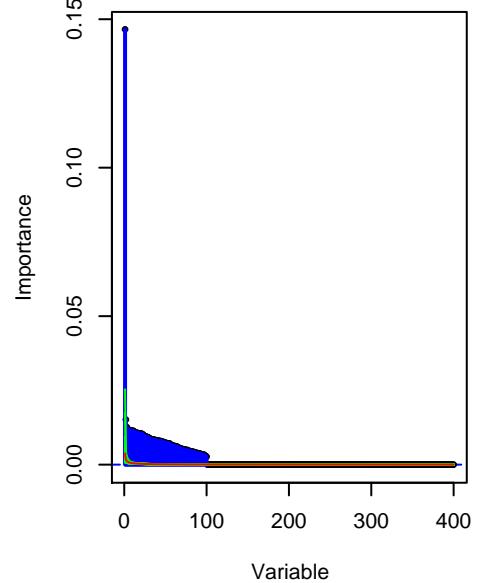
2 classes; 1 comp.; 100 genes/comp.



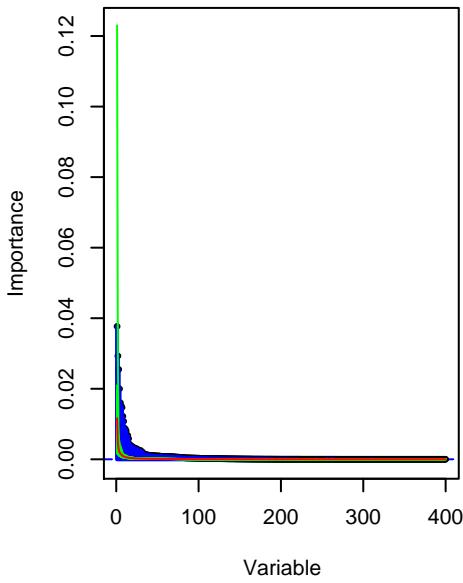
3 classes; 1 comp.; 100 genes/comp.



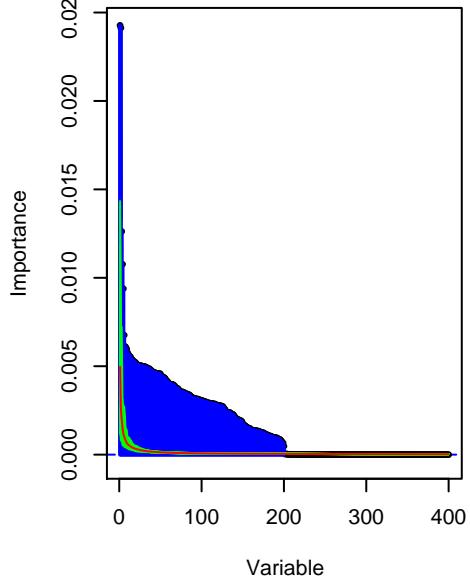
4 classes; 1 comp.; 100 genes/comp.



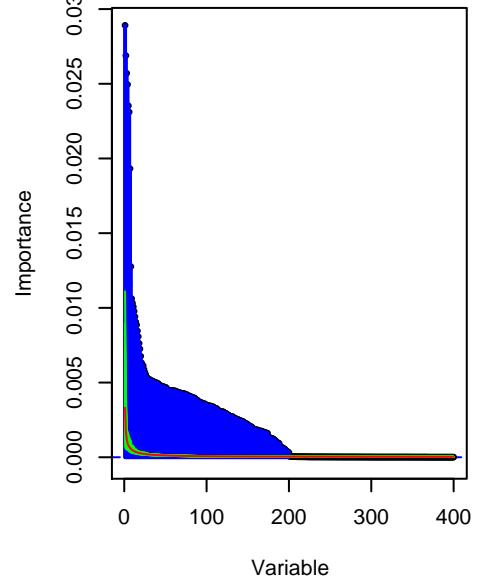
2 classes; 2 comp.; 100 genes/comp.



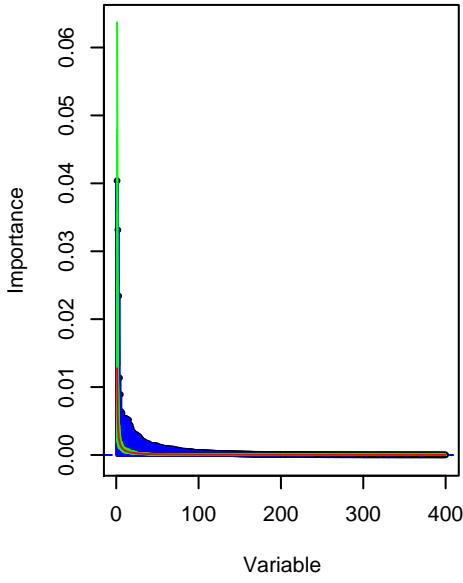
3 classes; 2 comp.; 100 genes/comp.



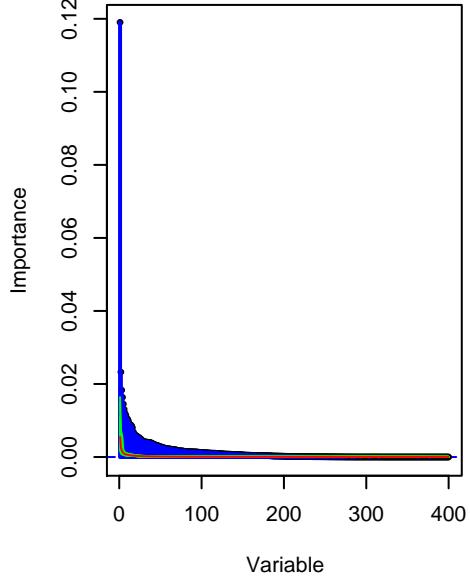
4 classes; 2 comp.; 100 genes/comp.



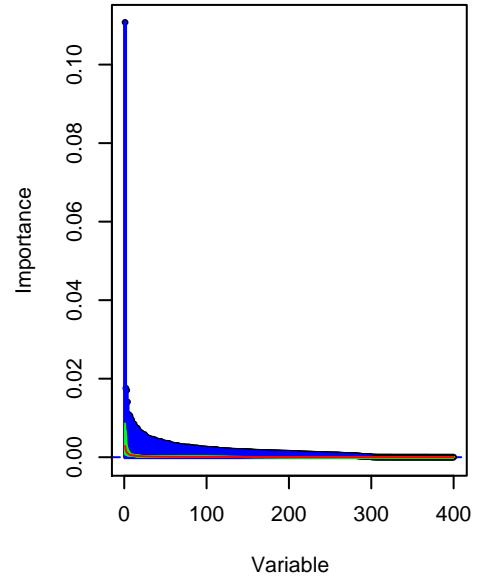
2 classes; 3 comp.; 100 genes/comp.



3 classes; 3 comp.; 100 genes/comp.



4 classes; 3 comp.; 100 genes/comp.



Variable importances: simulated data.

'Scree plots' or 'importance spectrum':

`ntree = 5000`

`mtry = 0.5 * ncol`

Black: original data sets;

Blue: variables with true signal;

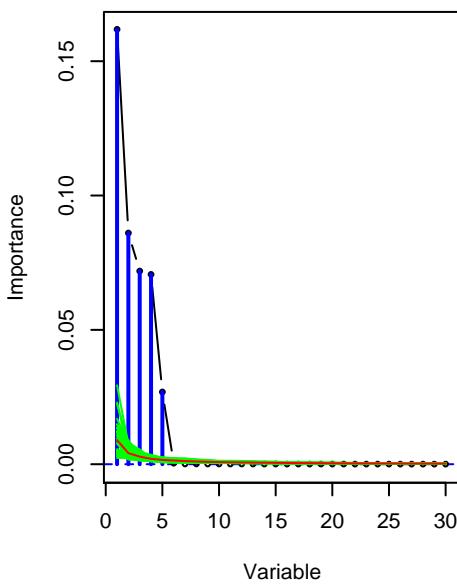
green: permuted class labels data sets;

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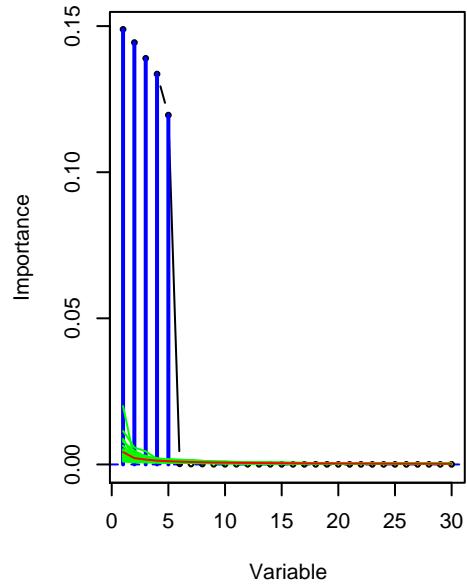
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file= /scree-plots-analyses/simul-data/huge-mtry/simul.data.analyses.screePlots.R
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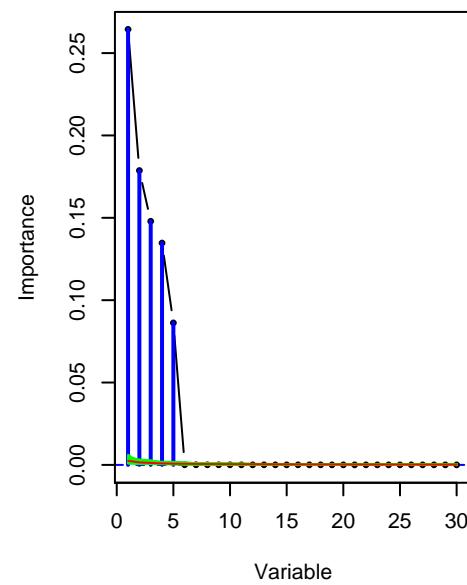
2 classes; 1 comp.; 5 genes/comp.



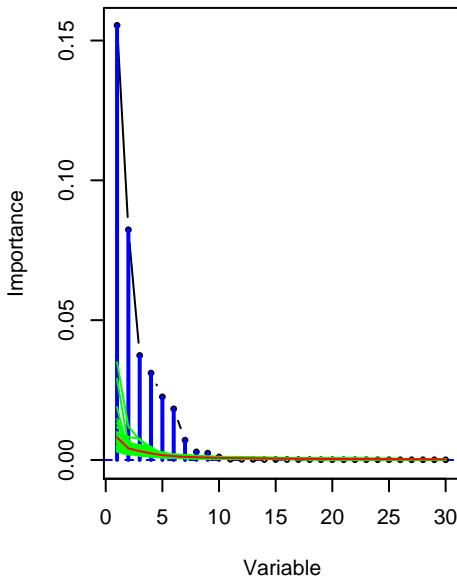
3 classes; 1 comp.; 5 genes/comp.



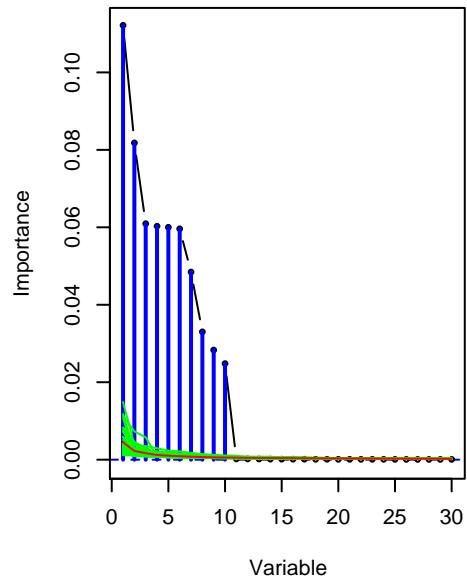
4 classes; 1 comp.; 5 genes/comp.



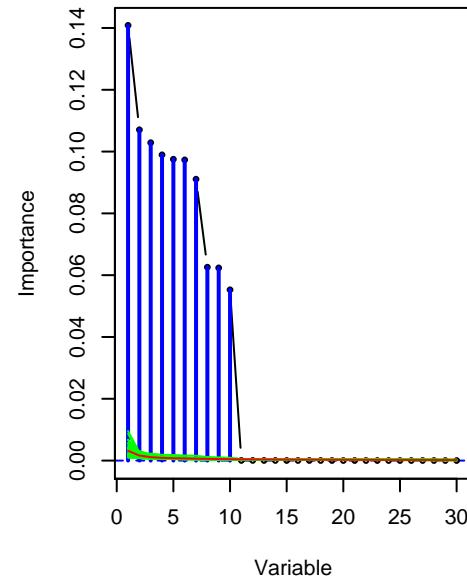
2 classes; 2 comp.; 5 genes/comp.



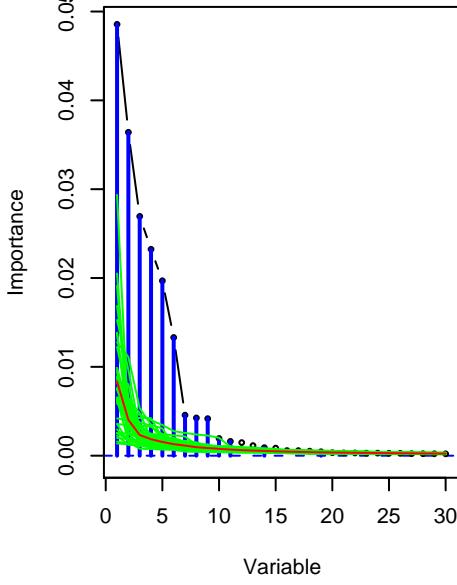
3 classes; 2 comp.; 5 genes/comp.



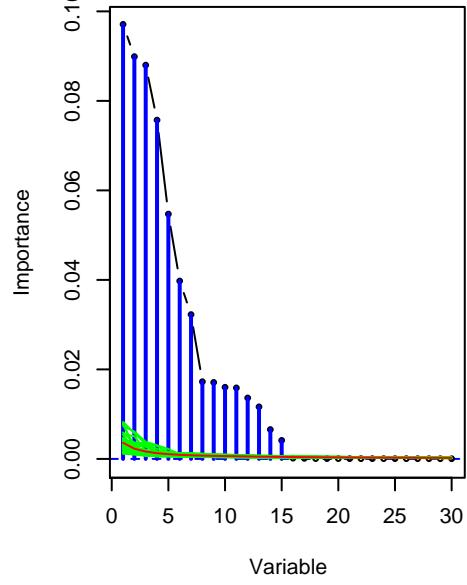
4 classes; 2 comp.; 5 genes/comp.



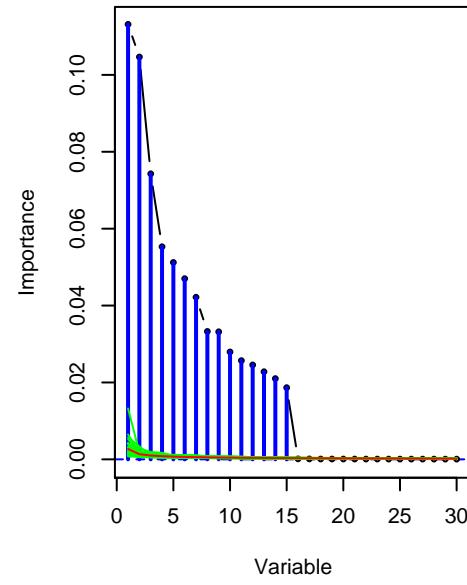
2 classes; 3 comp.; 5 genes/comp.



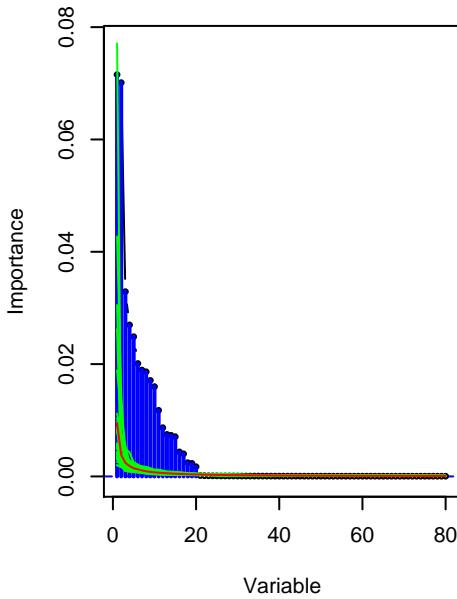
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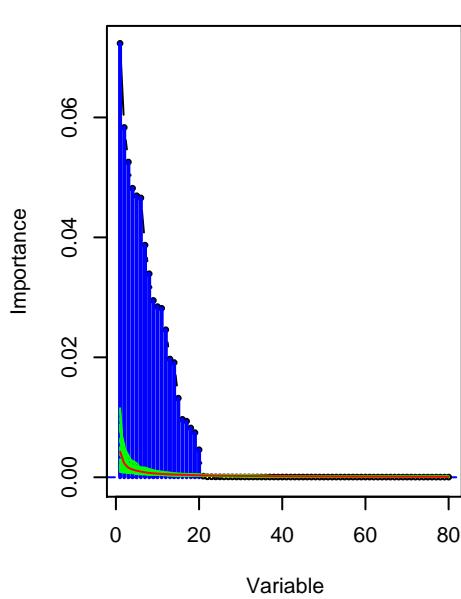
4 classes; 3 comp.; 5 genes/comp.



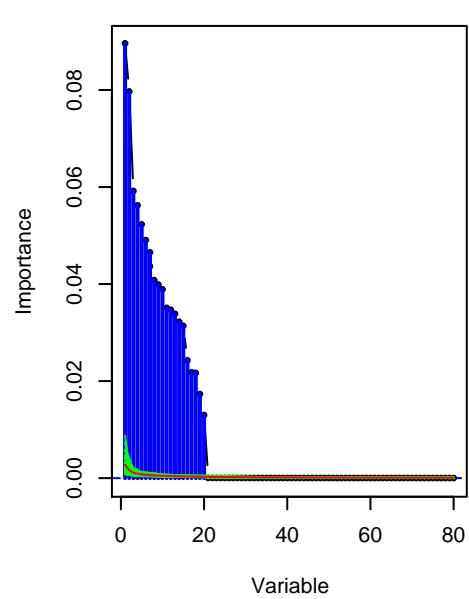
2 classes; 1 comp.; 20 genes/comp.



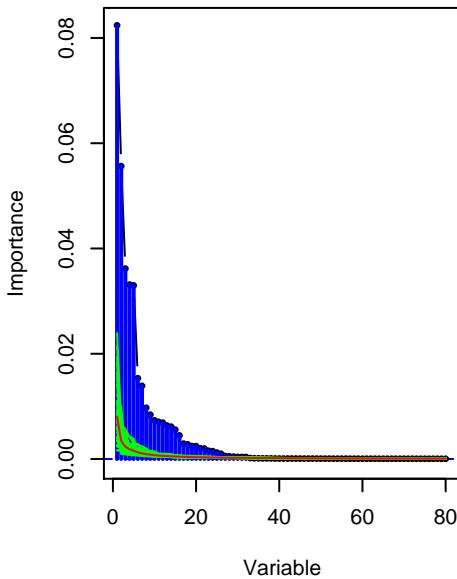
3 classes; 1 comp.; 20 genes/comp.



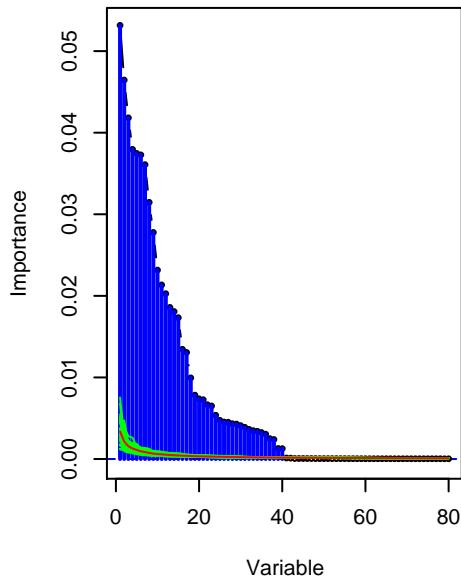
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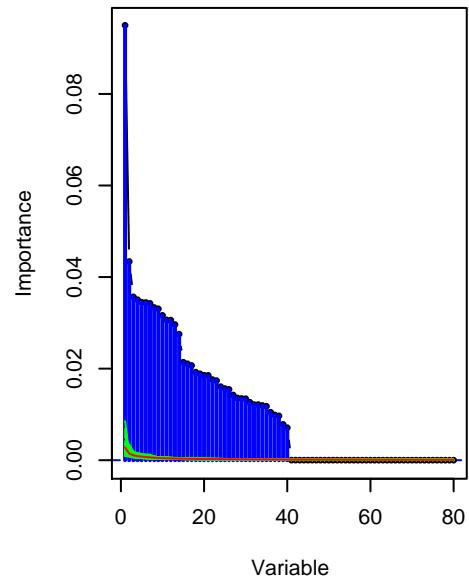
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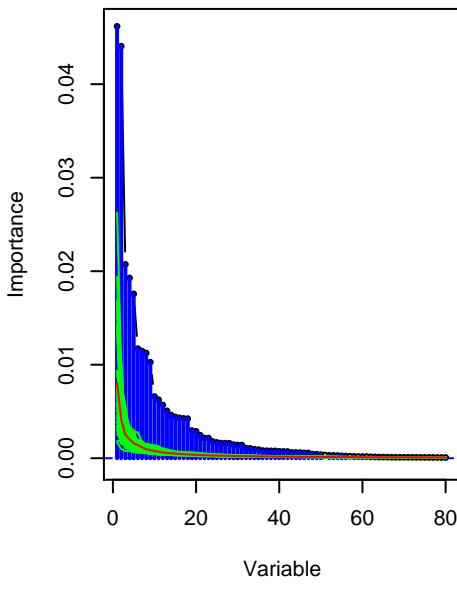
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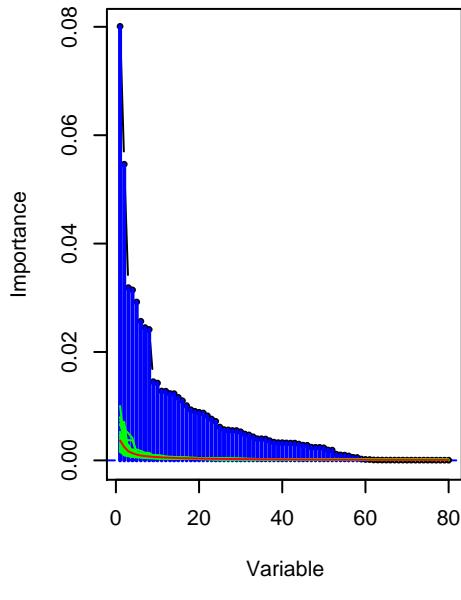
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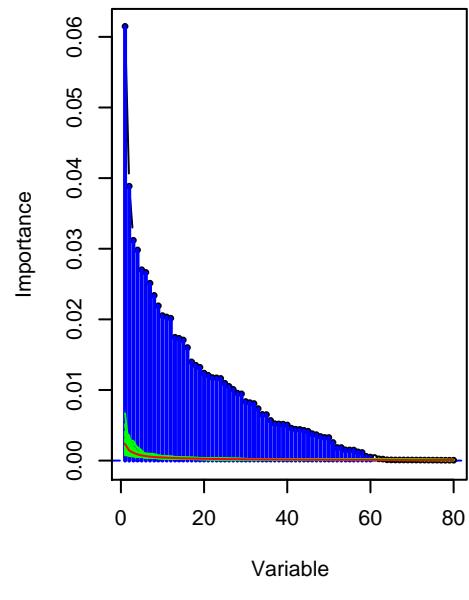
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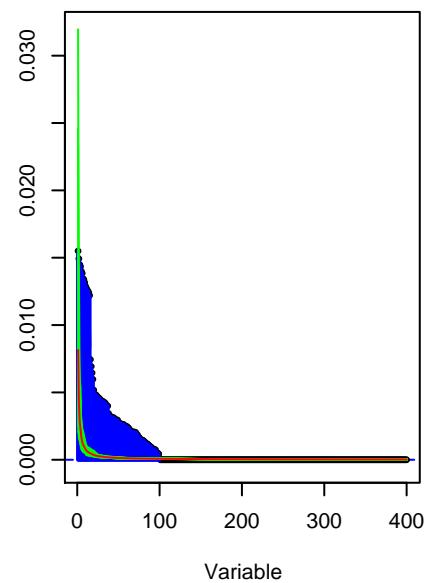
3 classes; 3 comp.; 20 genes/comp.



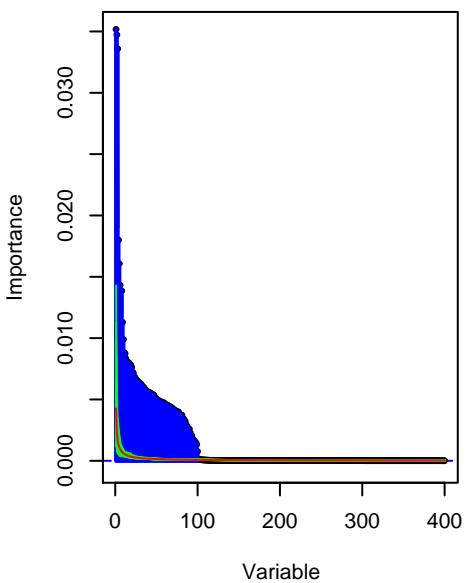
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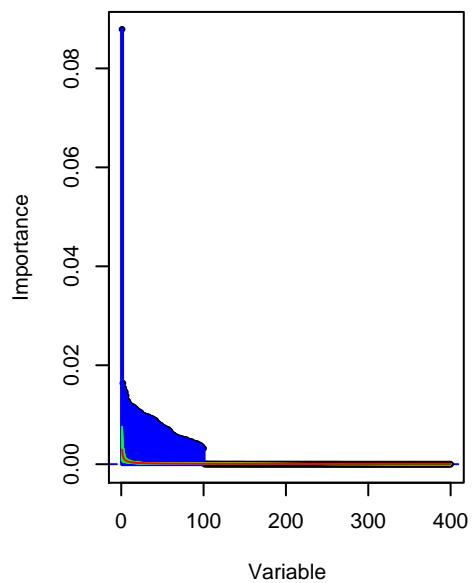
2 classes; 1 comp.; 100 genes/comp.



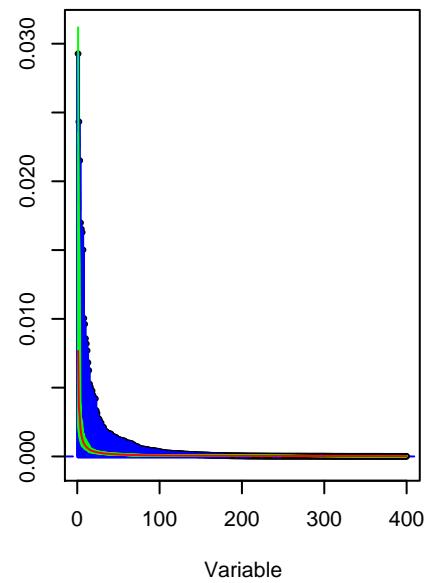
3 classes; 1 comp.; 100 genes/comp.



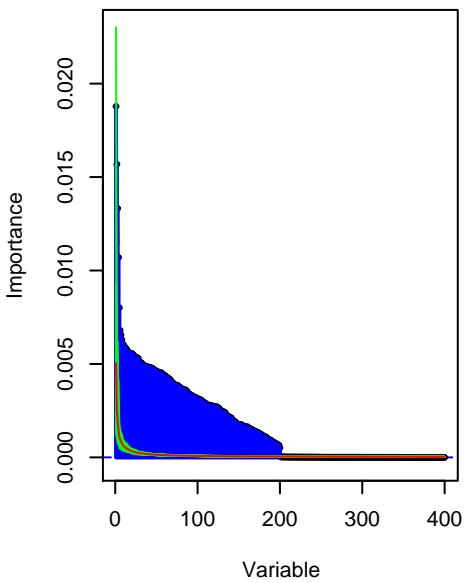
4 classes; 1 comp.; 100 genes/comp.



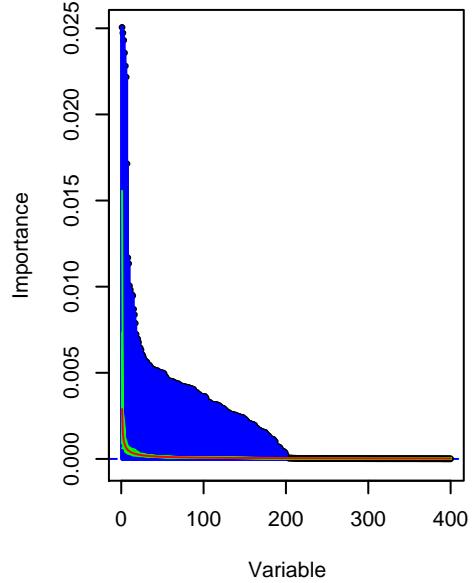
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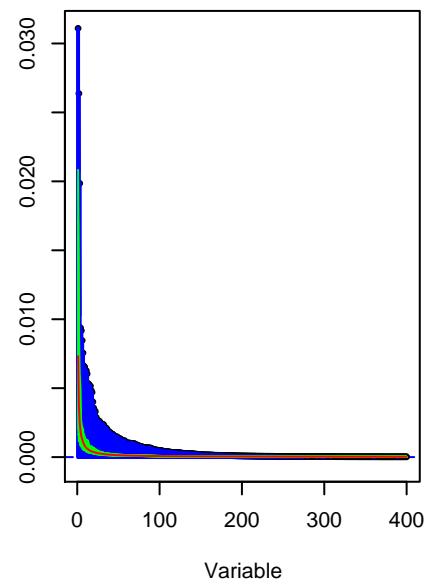
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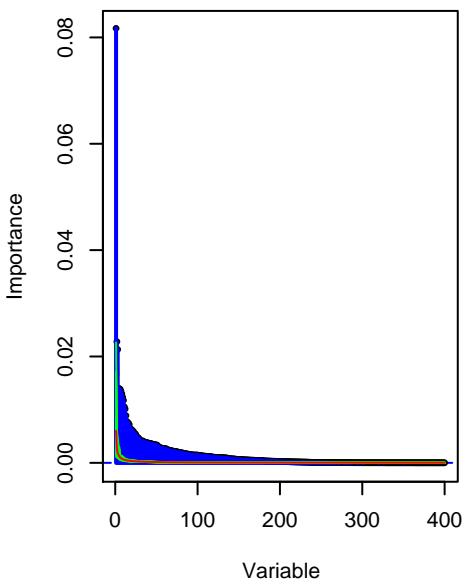
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2 classes; 3 comp.; 100 genes/comp.



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