

Variable importances: simulated data.

'Scree plots' or 'importance spectrum':

Black: original data sets;

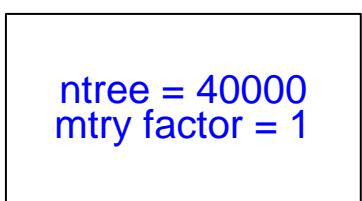
Blue: variables with true signal;

green: permuted class labels data sets;

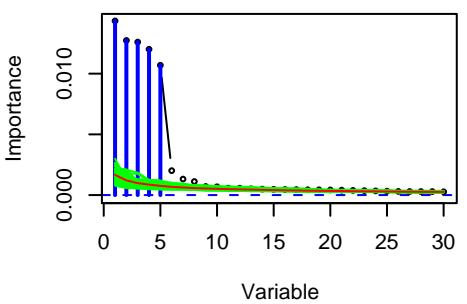
red: average from permuted class labels data sets.

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file= /scree-plots-analyses/simul-data/simul.data.analyses.screePlots.R
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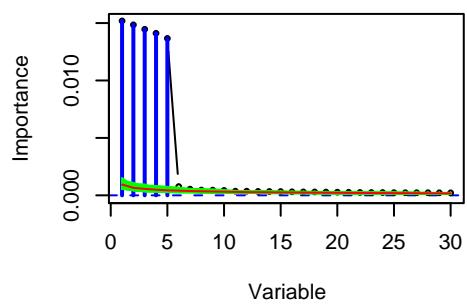
2004-12-29 11:41:00



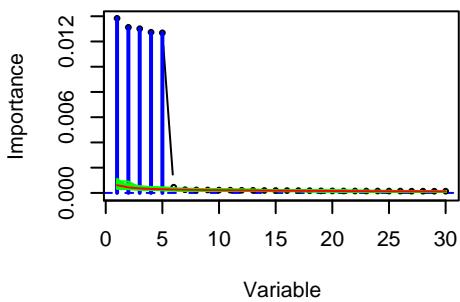
2 classes; 1 comp.; 5 genes/comp.



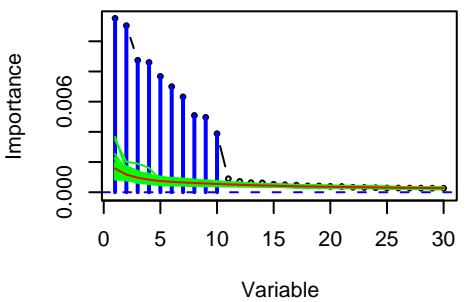
3 classes; 1 comp.; 5 genes/comp.



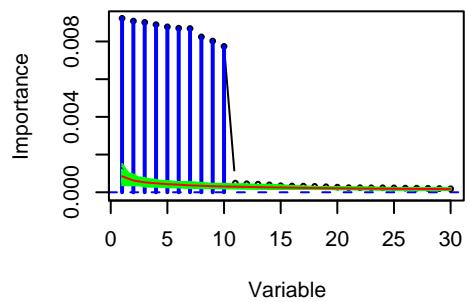
4 classes; 1 comp.; 5 genes/comp.



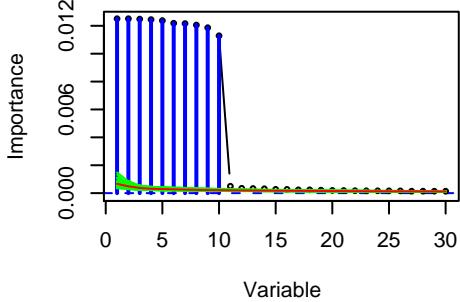
2 classes; 2 comp.; 5 genes/comp.



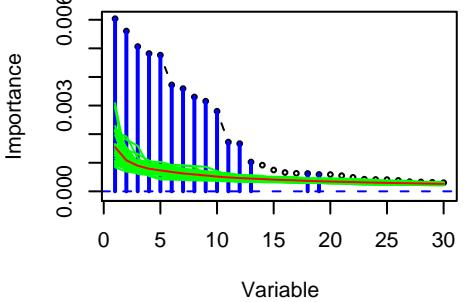
3 classes; 2 comp.; 5 genes/comp.



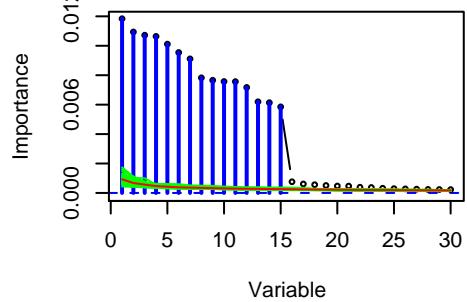
4 classes; 2 comp.; 5 genes/comp.



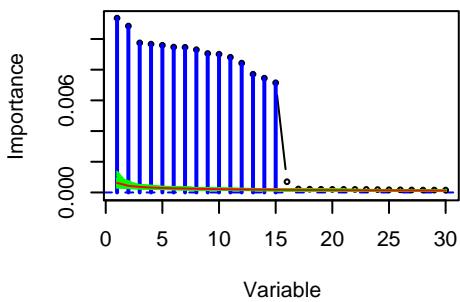
2 classes; 3 comp.; 5 genes/comp.



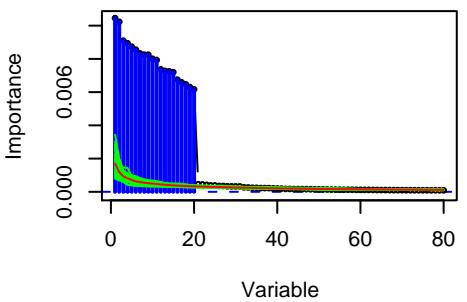
3 classes; 3 comp.; 5 genes/comp.



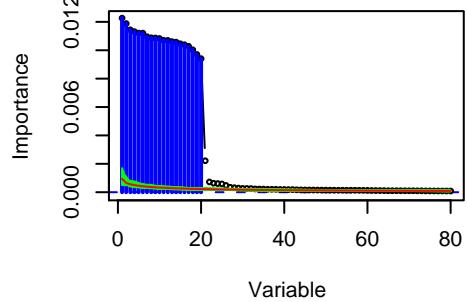
4 classes; 3 comp.; 5 genes/comp.



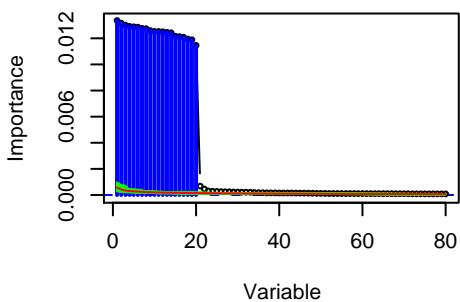
2 classes; 1 comp.; 20 genes/comp.



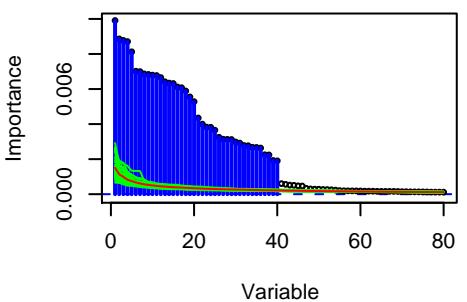
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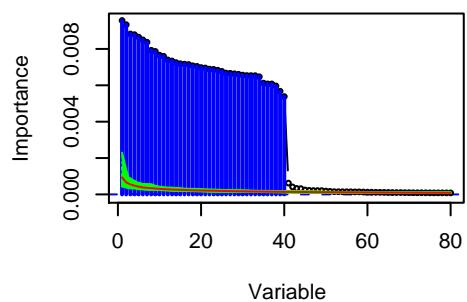
4 classes; 1 comp.; 20 genes/comp.

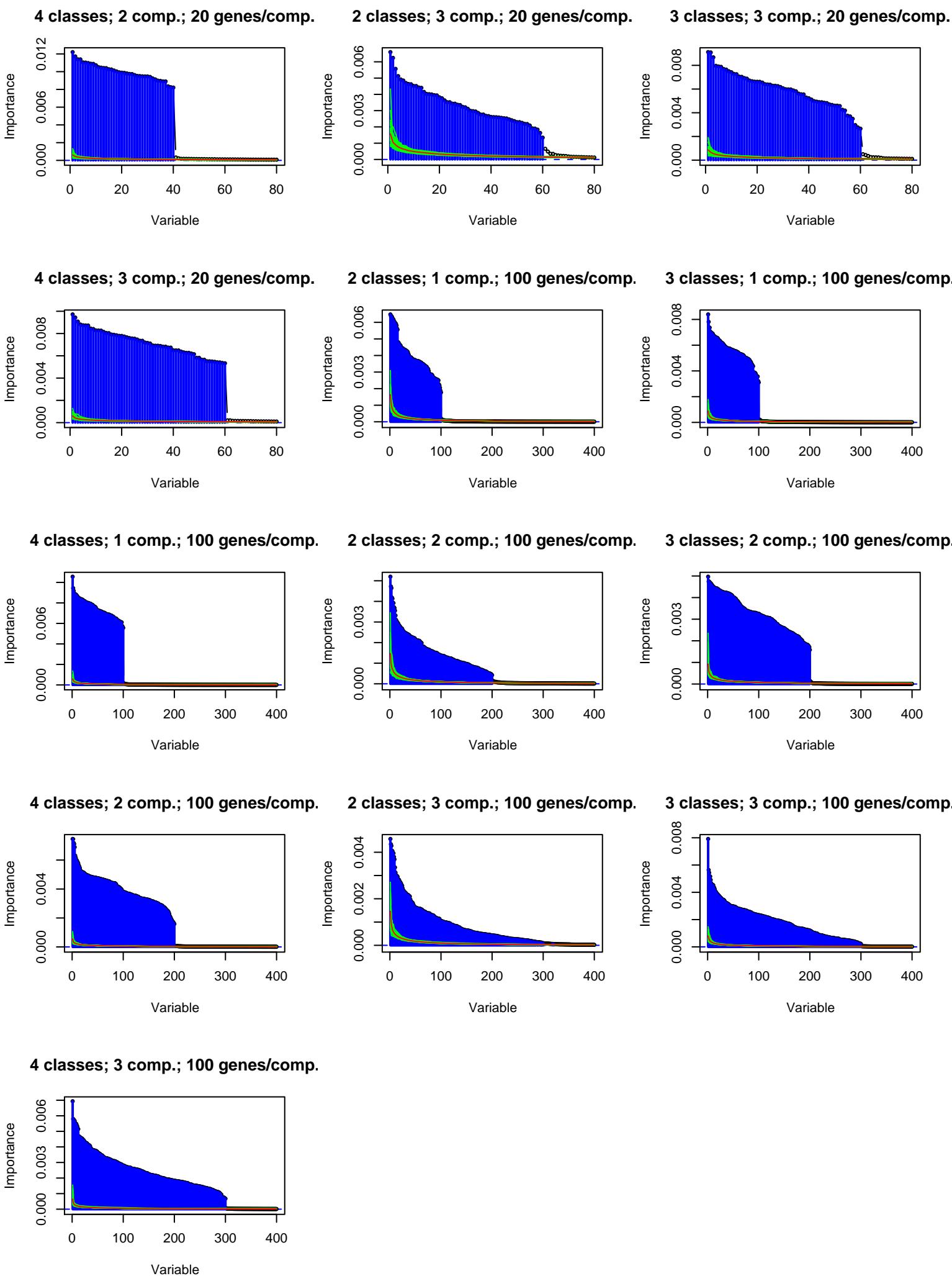


2 classes; 2 comp.; 20 genes/comp.



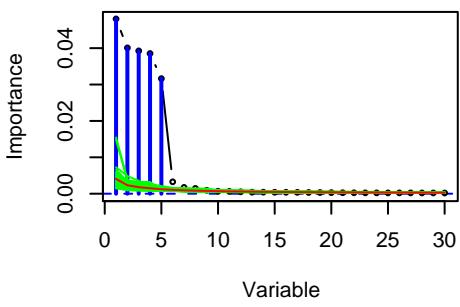
3 classes; 2 comp.; 20 genes/comp.



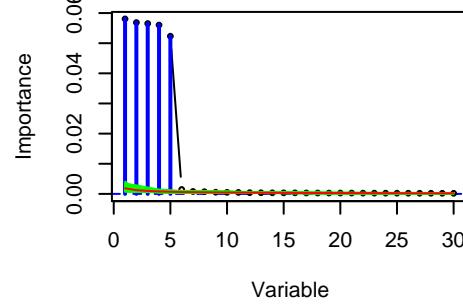


**ntree = 40000
mtry factor = 5**

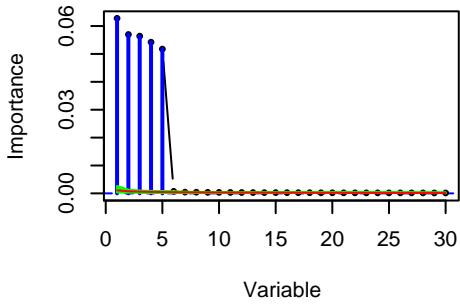
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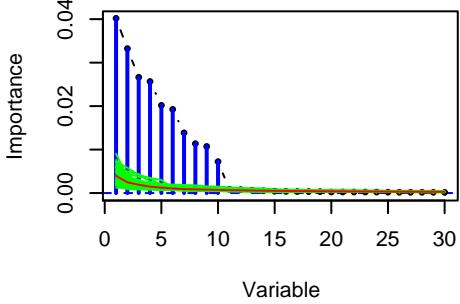
3 classes; 1 comp.; 5 genes/comp.



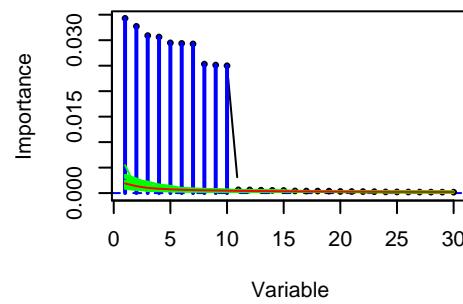
4 classes; 1 comp.; 5 genes/comp.



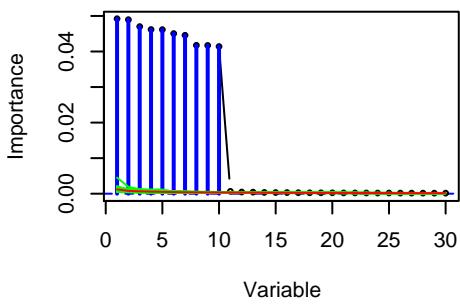
2 classes; 2 comp.; 5 genes/comp.



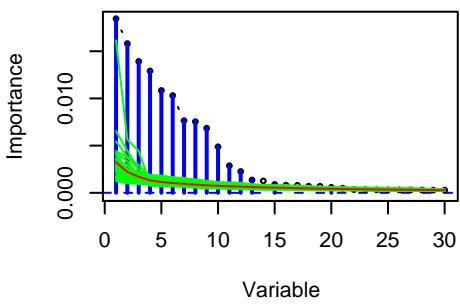
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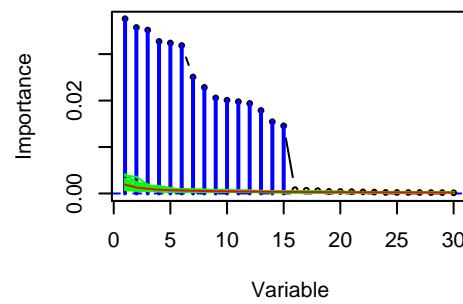
4 classes; 2 comp.; 5 genes/comp.



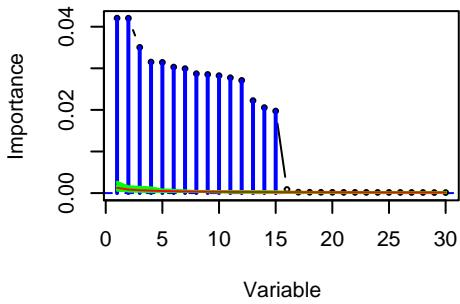
2 classes; 3 comp.; 5 genes/comp.



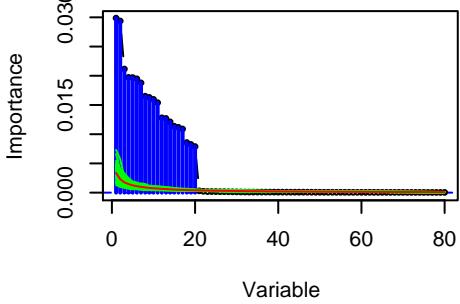
3 classes; 3 comp.; 5 genes/comp.



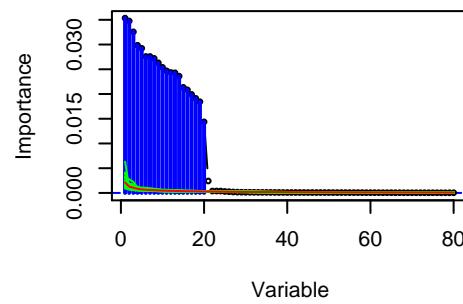
4 classes; 3 comp.; 5 genes/comp.



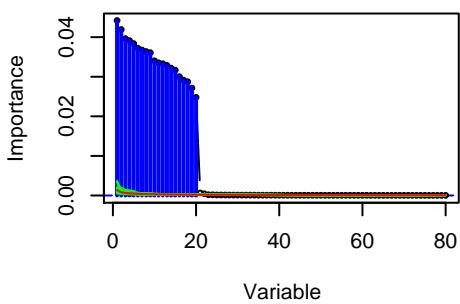
2 classes; 1 comp.; 20 genes/comp.



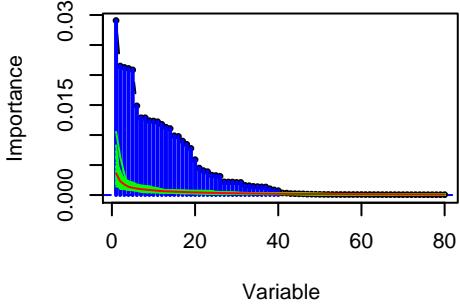
3 classes; 1 comp.; 20 genes/comp.



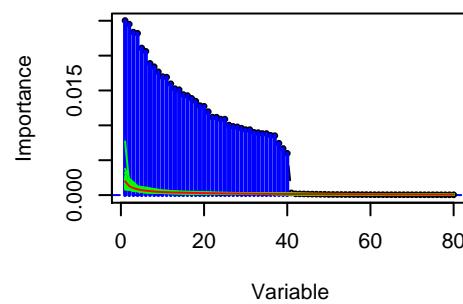
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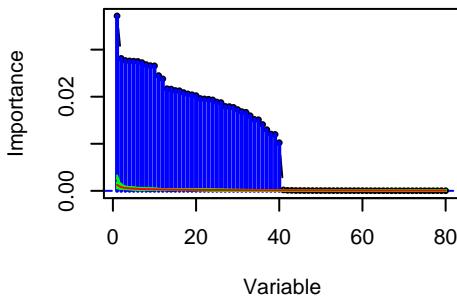
2 classes; 2 comp.; 20 genes/comp.



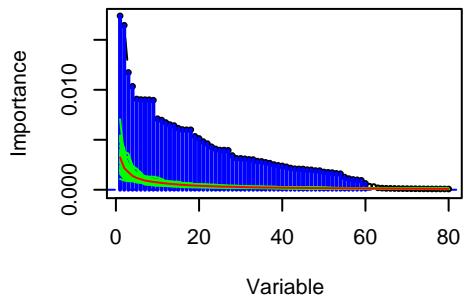
3 classes; 2 comp.; 20 genes/comp.



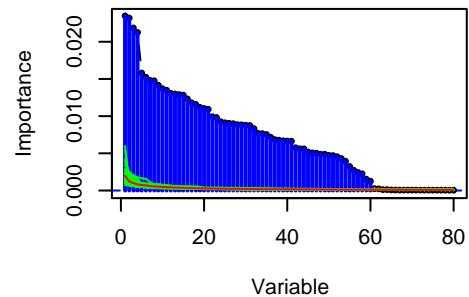
4 classes; 2 comp.; 20 genes/comp.



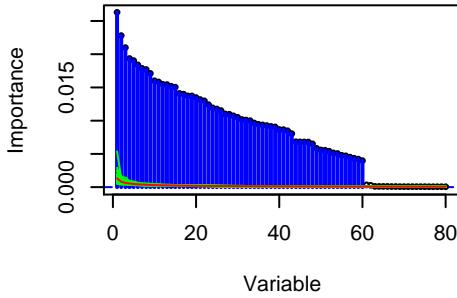
2 classes; 3 comp.; 20 genes/comp.



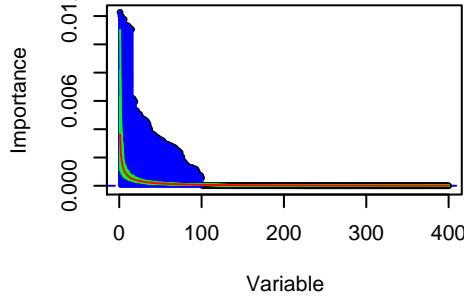
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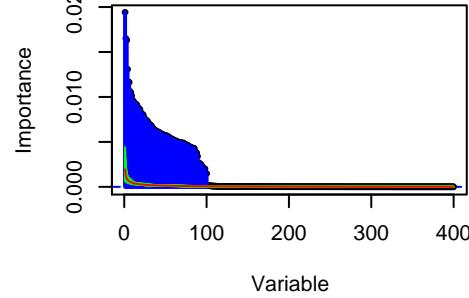
4 classes; 3 comp.; 20 genes/comp.



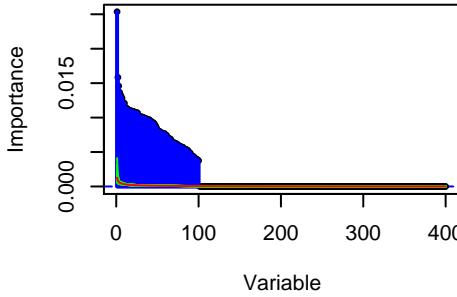
2 classes; 1 comp.; 100 genes/comp.



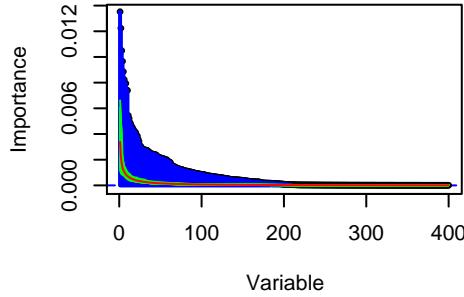
3 classes; 1 comp.; 100 genes/comp



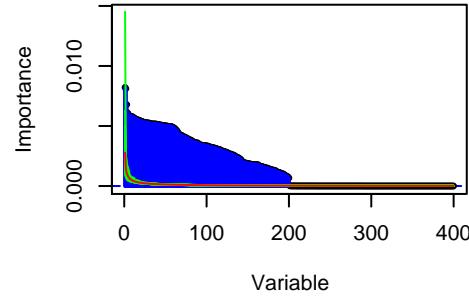
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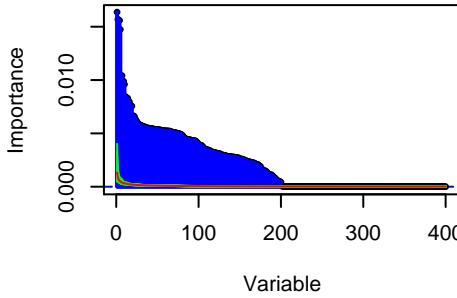
2 classes; 2 comp.; 100 genes/comp.



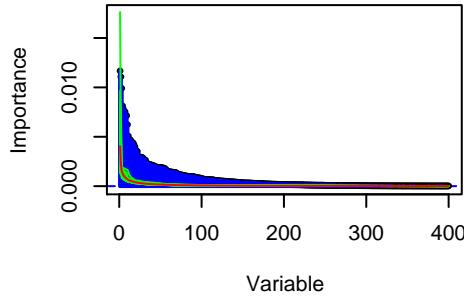
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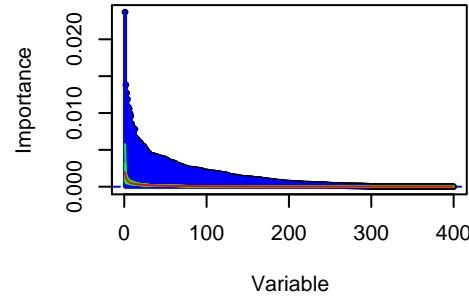
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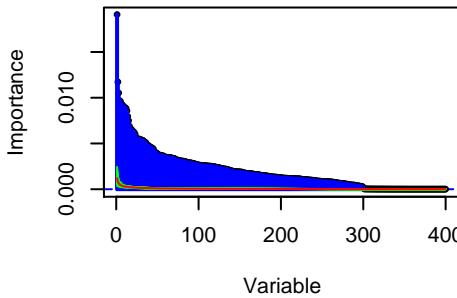
2 classes; 3 comp.; 100 genes/comp.



3 classes; 3 comp.; 100 genes/comp

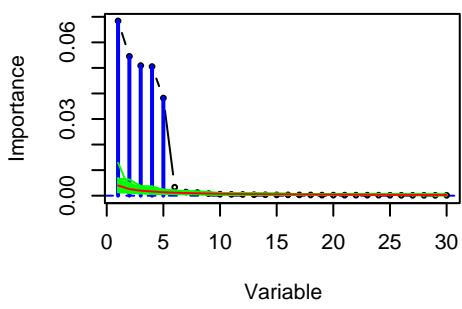


4 classes; 3 comp.; 100 genes/comp.

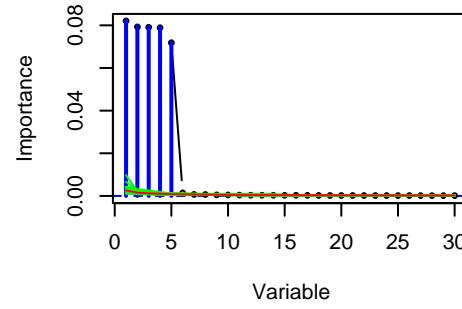


**ntree = 40000
mtry factor = 8**

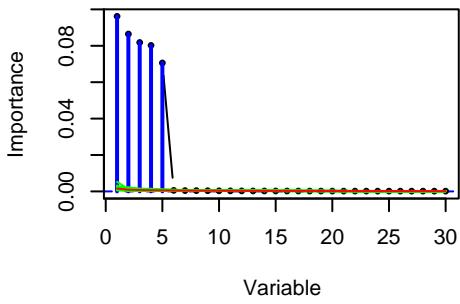
2 classes; 1 comp.; 5 genes/comp.



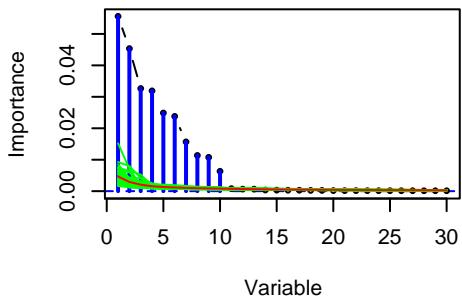
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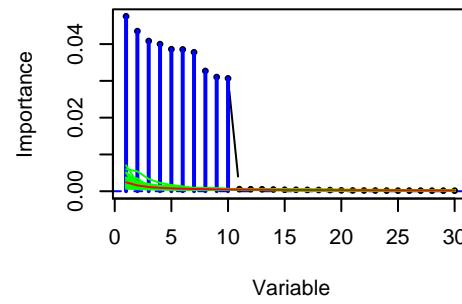
4 classes; 1 comp.; 5 genes/comp.



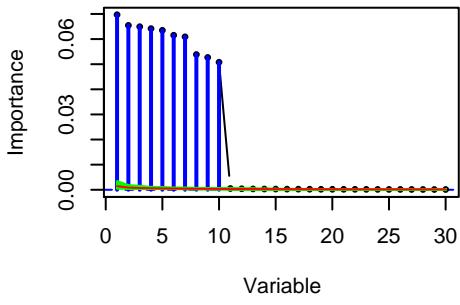
2 classes; 2 comp.; 5 genes/comp.



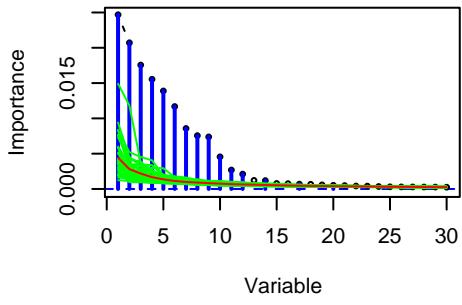
3 classes; 2 comp.; 5 genes/comp.



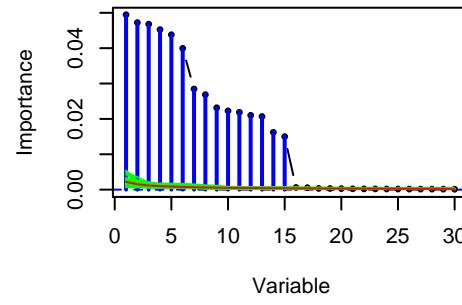
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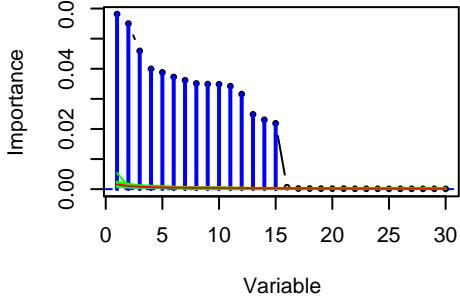
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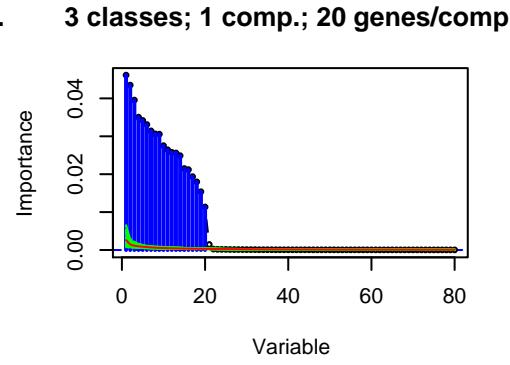
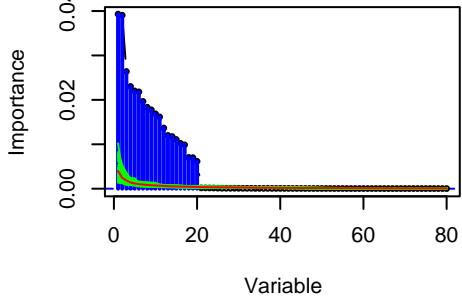
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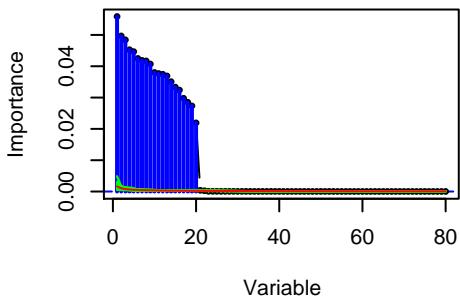
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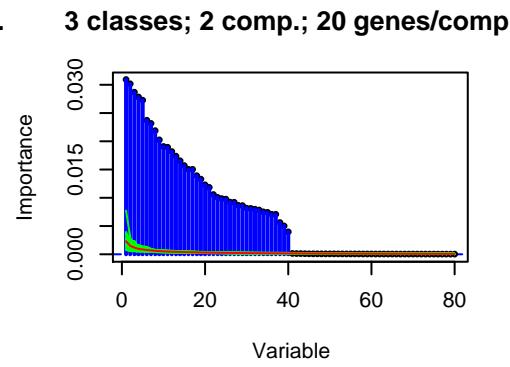
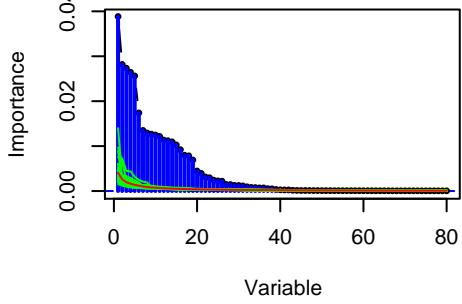
2 classes; 1 comp.; 20 genes/comp.



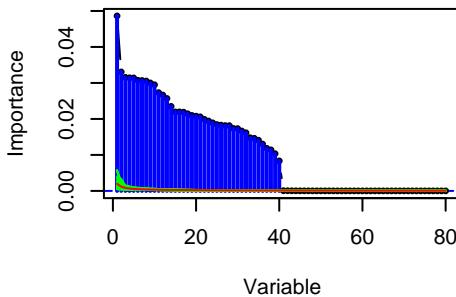
4 classes; 1 comp.; 20 genes/comp.



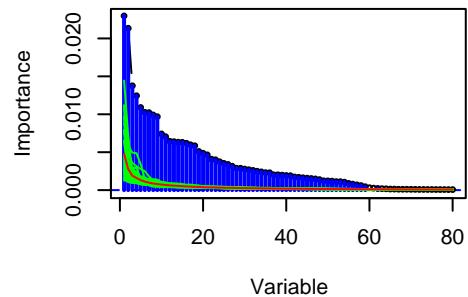
2 classes; 2 comp.; 20 genes/comp.



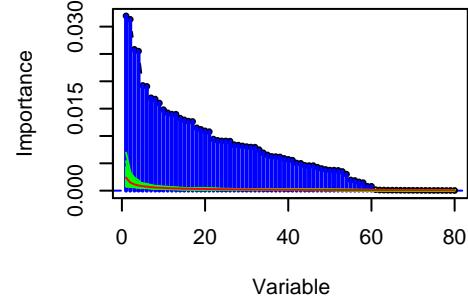
4 classes; 2 comp.; 20 genes/comp.



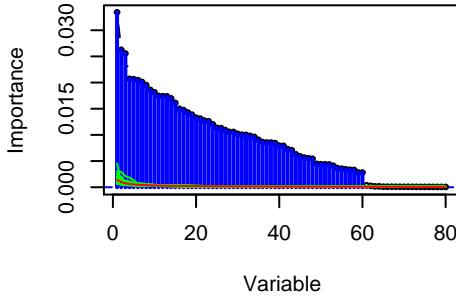
2 classes; 3 comp.; 20 genes/comp.



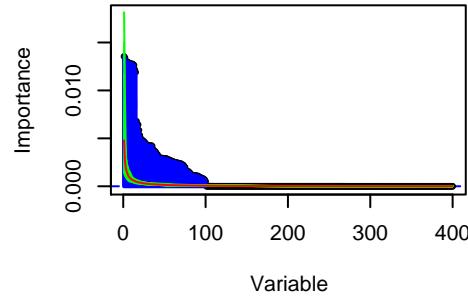
3 classes; 3 comp.; 20 genes/comp.



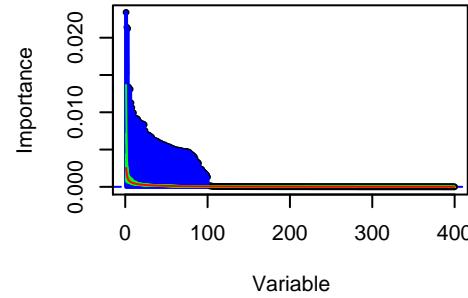
4 classes; 3 comp.; 20 genes/comp.



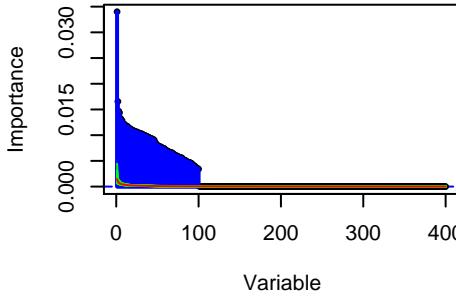
2 classes; 1 comp.; 100 genes/comp



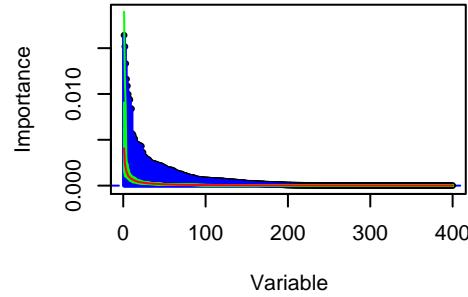
3 classes; 1 comp.; 100 genes/comp



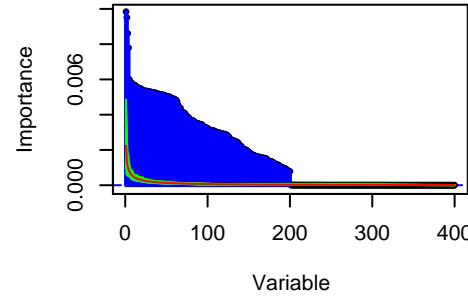
4 classes; 1 comp.; 100 genes/comp.



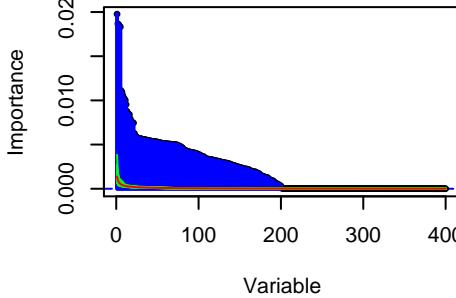
2 classes; 2 comp.; 100 genes/comp



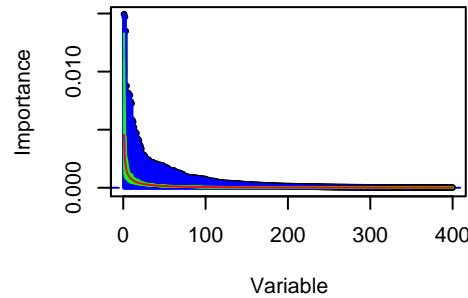
3 classes; 2 comp.; 100 genes/comp



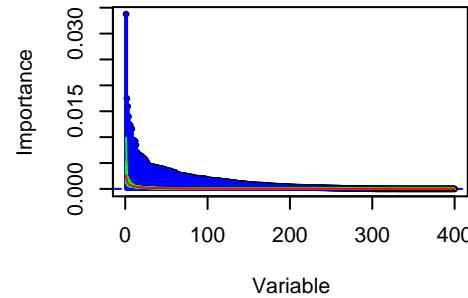
4 classes; 2 comp.; 100 genes/comp.



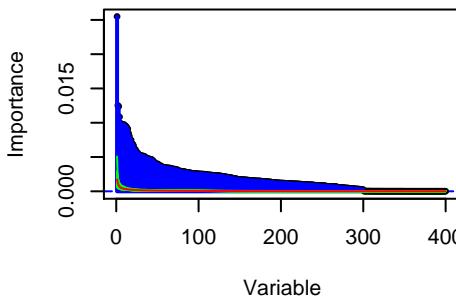
2 classes; 3 comp.; 100 genes/comp



3 classes; 3 comp.; 100 genes/comp

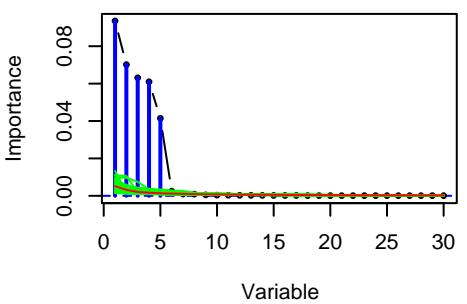


4 classes; 3 comp.; 100 genes/comp.

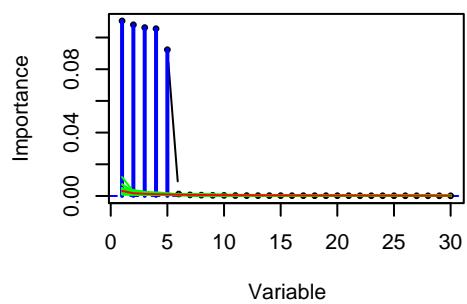


**ntree = 40000
mtry factor = 13**

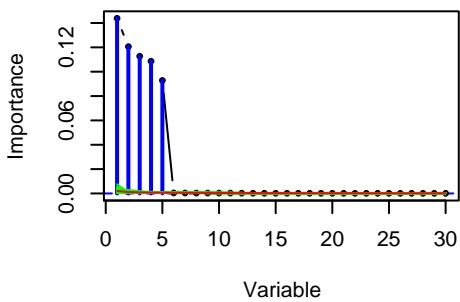
2 classes; 1 comp.; 5 genes/comp.



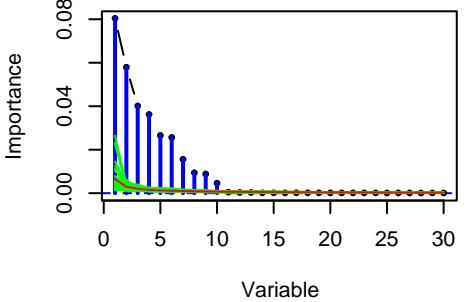
3 classes; 1 comp.; 5 genes/comp.



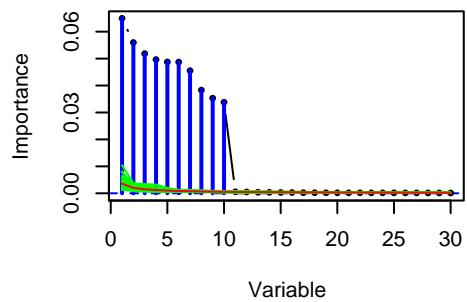
4 classes; 1 comp.; 5 genes/comp.



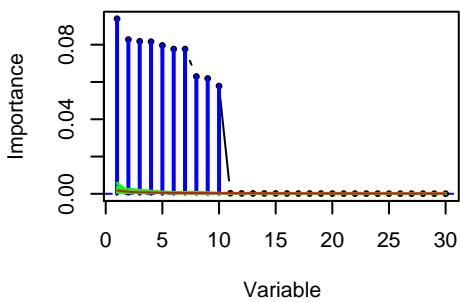
2 classes; 2 comp.; 5 genes/comp.



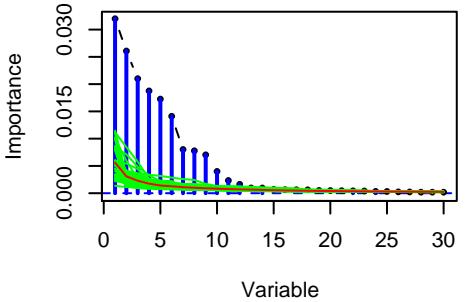
3 classes; 2 comp.; 5 genes/comp.



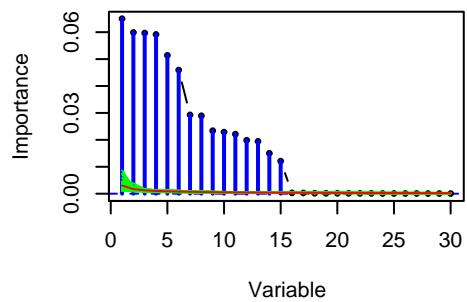
4 classes; 2 comp.; 5 genes/comp.



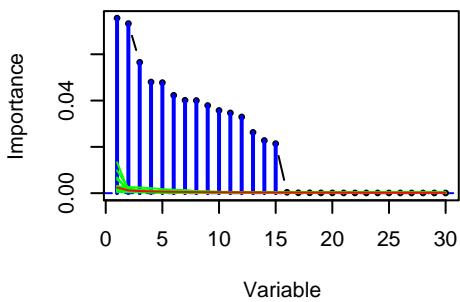
2 classes; 3 comp.; 5 genes/comp.



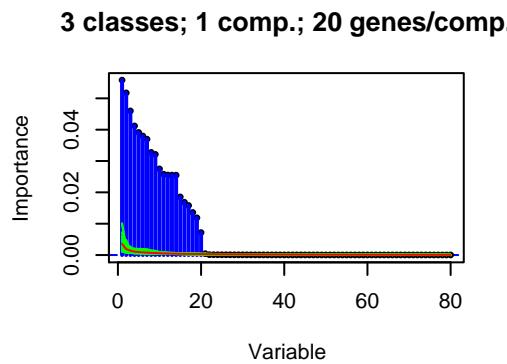
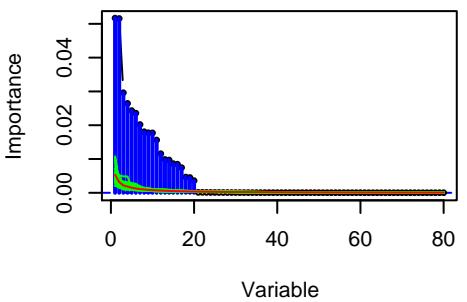
3 classes; 3 comp.; 5 genes/comp.



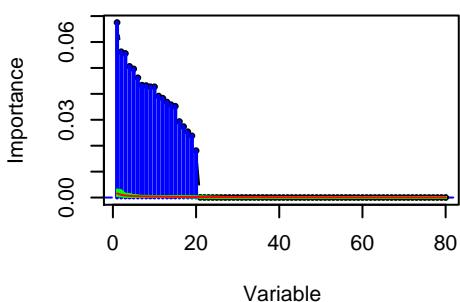
4 classes; 3 comp.; 5 genes/comp.



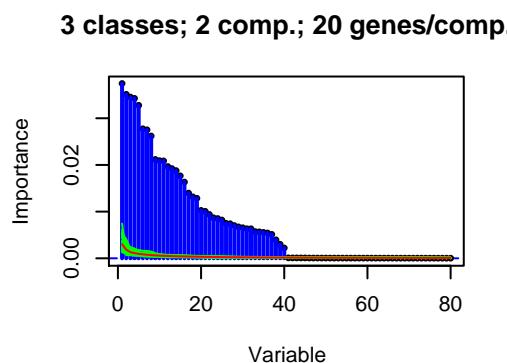
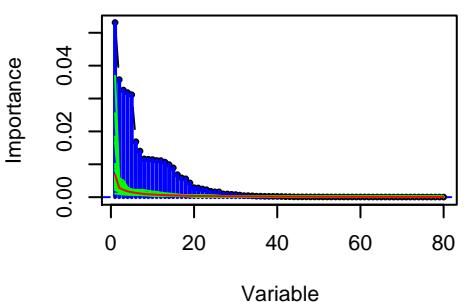
2 classes; 1 comp.; 20 genes/comp.



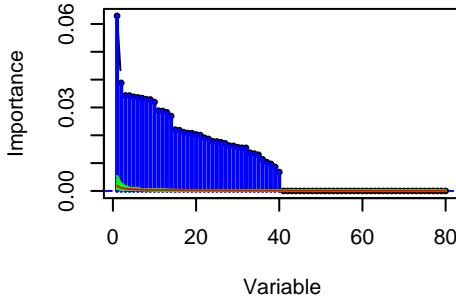
4 classes; 1 comp.; 20 genes/comp.



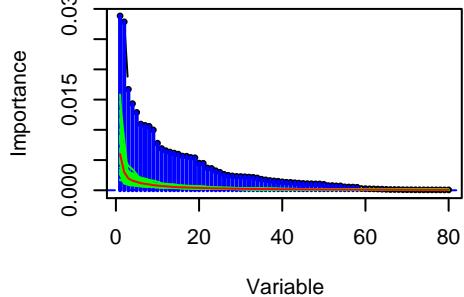
2 classes; 2 comp.; 20 genes/comp.



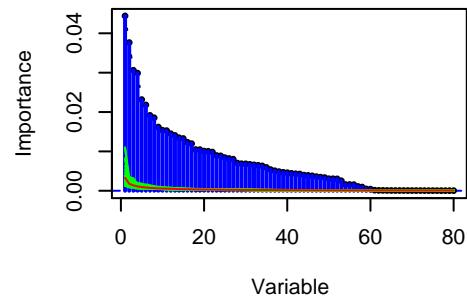
4 classes; 2 comp.; 20 genes/comp.



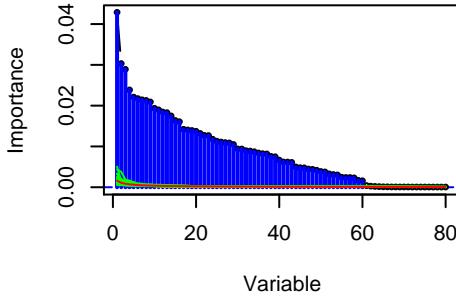
2 classes; 3 comp.; 20 genes/comp.



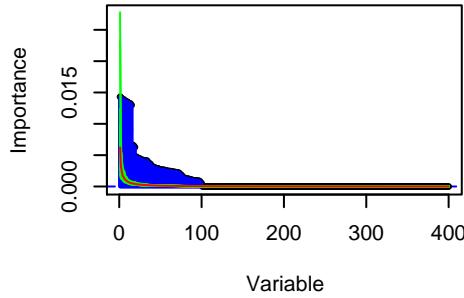
3 classes; 3 comp.; 20 genes/comp.



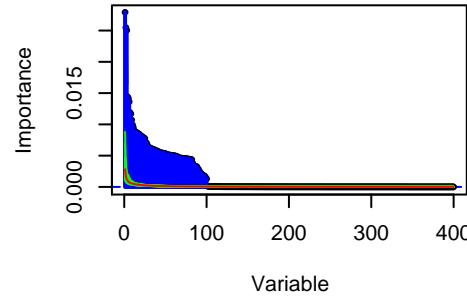
4 classes; 3 comp.; 20 genes/comp.



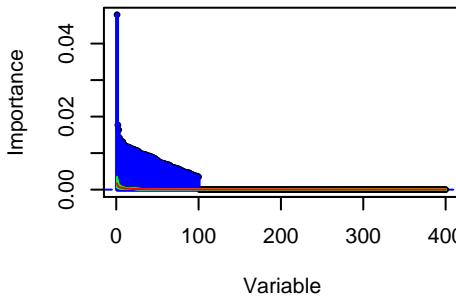
2 classes; 1 comp.; 100 genes/comp



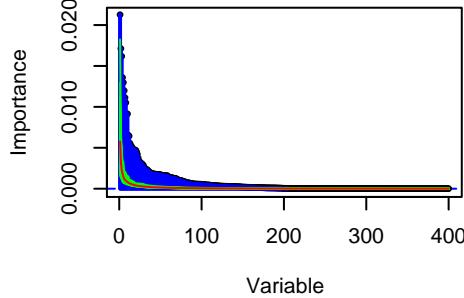
3 classes; 1 comp.; 100 genes/comp



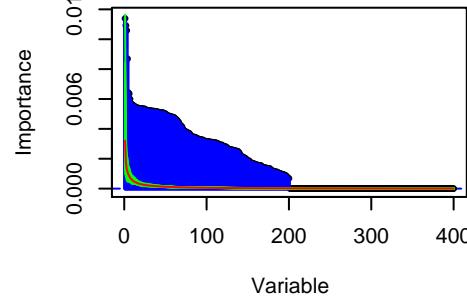
4 classes; 1 comp.; 100 genes/comp.



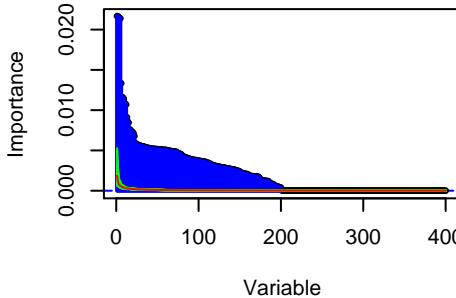
2 classes; 2 comp.; 100 genes/comp



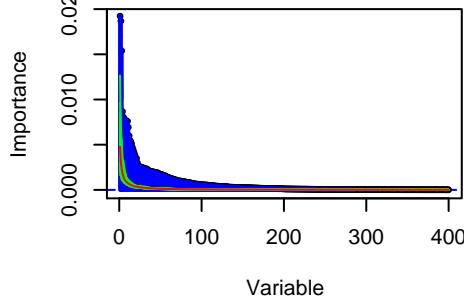
3 classes; 2 comp.; 100 genes/comp



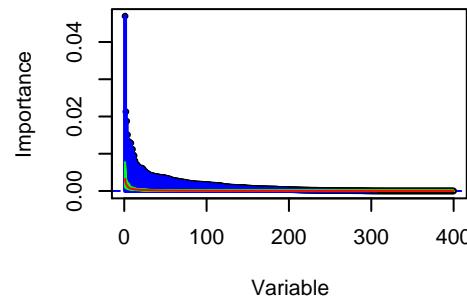
4 classes; 2 comp.; 100 genes/comp.



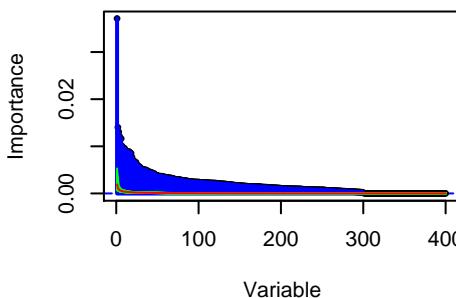
2 classes; 3 comp.; 100 genes/comp



3 classes; 3 comp.; 100 genes/comp

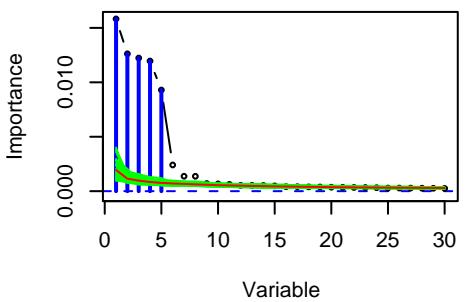


4 classes; 3 comp.; 100 genes/comp.

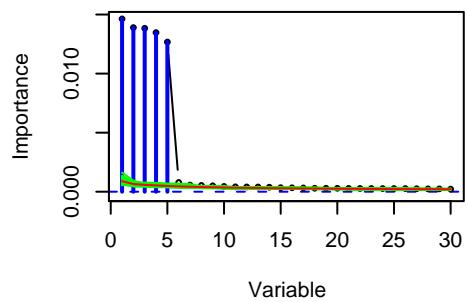


**ntree = 5000
mtry factor = 1**

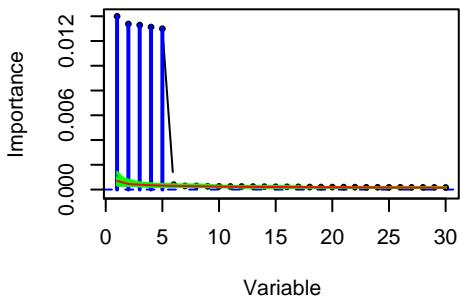
2 classes; 1 comp.; 5 genes/comp.



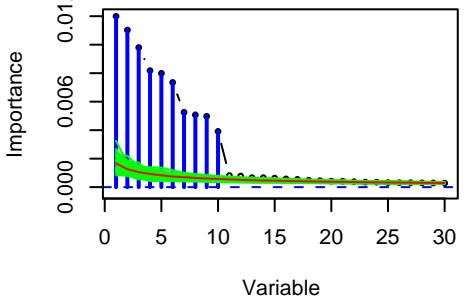
3 classes; 1 comp.; 5 genes/comp.



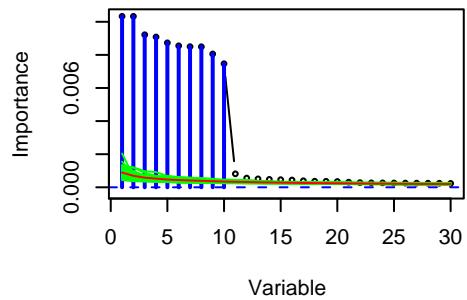
4 classes; 1 comp.; 5 genes/comp.



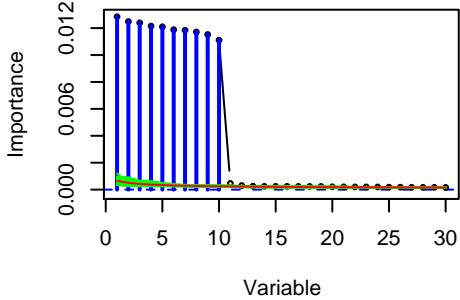
2 classes; 2 comp.; 5 genes/comp.



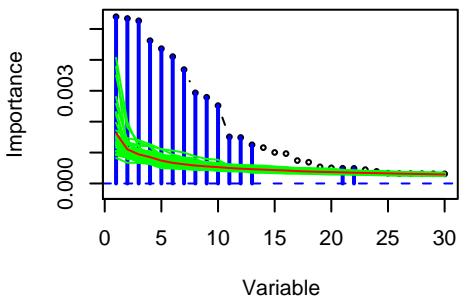
3 classes; 2 comp.; 5 genes/comp.



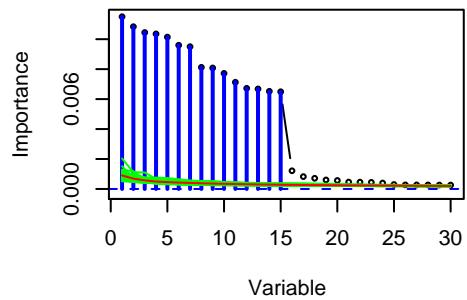
4 classes; 2 comp.; 5 genes/comp.



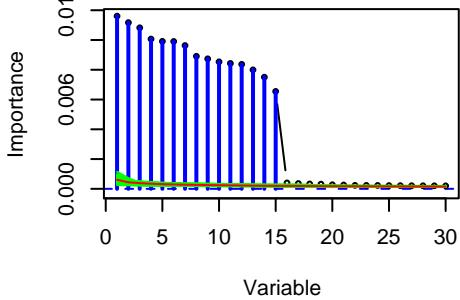
2 classes; 3 comp.; 5 genes/comp.



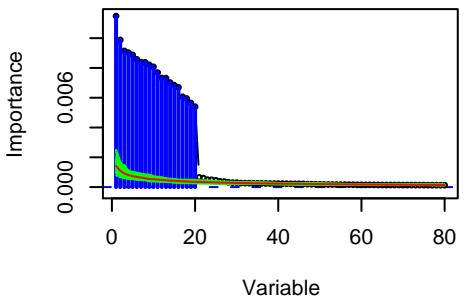
3 classes; 3 comp.; 5 genes/comp.



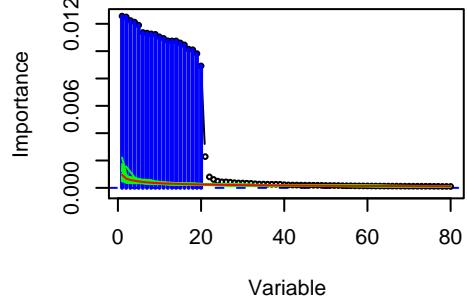
4 classes; 3 comp.; 5 genes/comp.



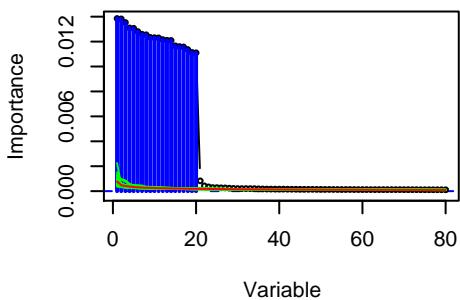
2 classes; 1 comp.; 20 genes/comp.



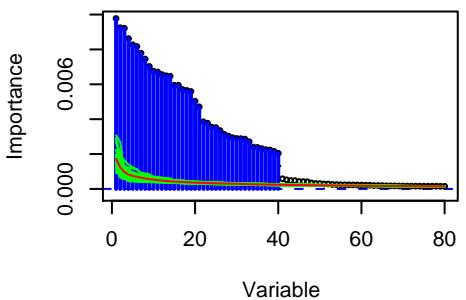
3 classes; 1 comp.; 20 genes/comp.



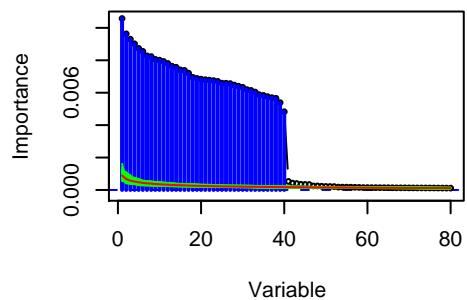
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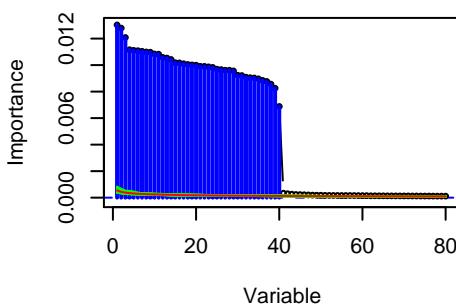
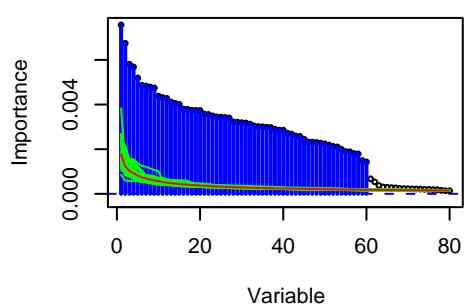
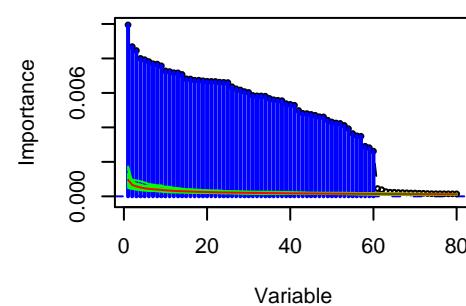
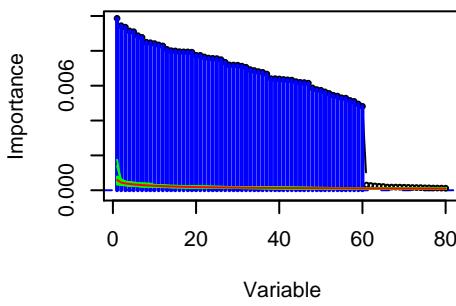
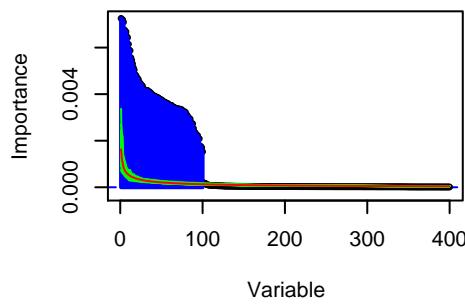
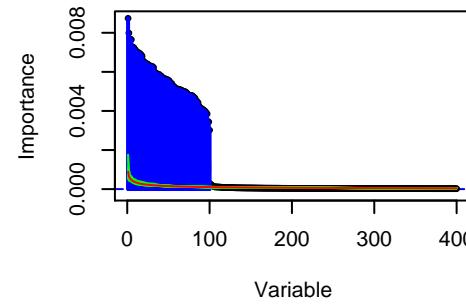
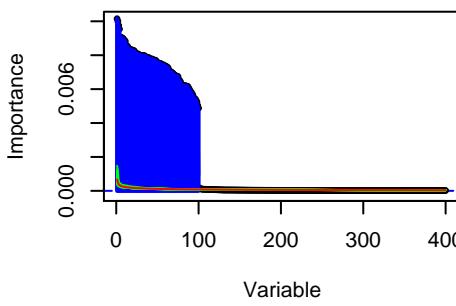
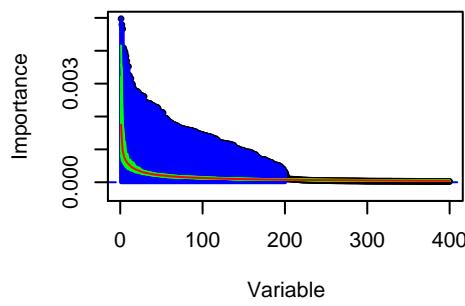
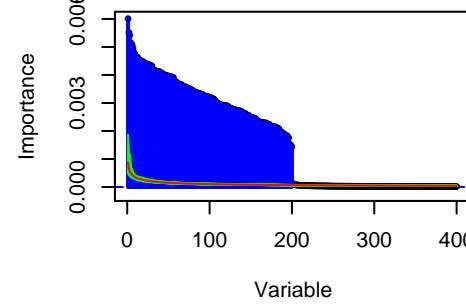
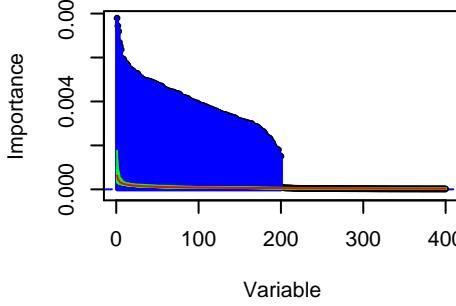
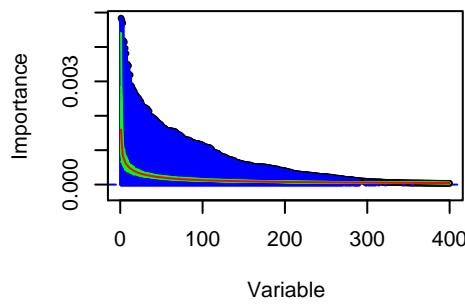
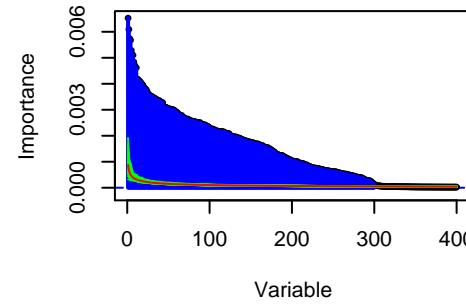
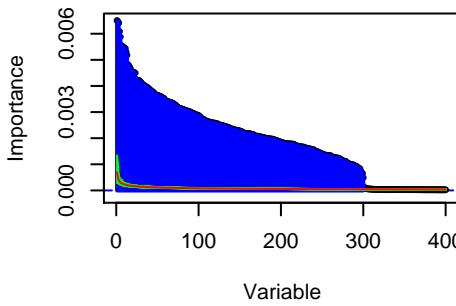


2 classes; 2 comp.; 20 genes/comp.



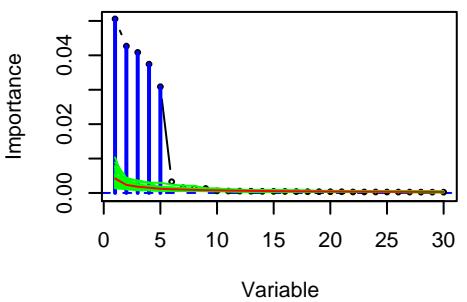
3 classes; 2 comp.; 20 genes/comp.



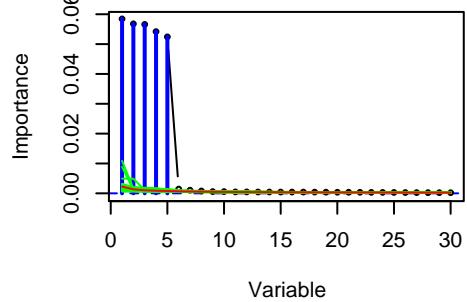
4 classes; 2 comp.; 20 genes/comp.**2 classes; 3 comp.; 20 genes/comp.****3 classes; 3 comp.; 20 genes/comp.****4 classes; 3 comp.; 20 genes/comp.****2 classes; 1 comp.; 100 genes/comp.****3 classes; 1 comp.; 100 genes/comp.****4 classes; 1 comp.; 100 genes/comp.****2 classes; 2 comp.; 100 genes/comp.****3 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.**

**ntree = 5000
mtry factor = 5**

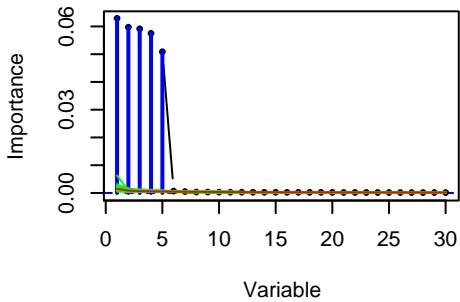
2 classes; 1 comp.; 5 genes/comp.



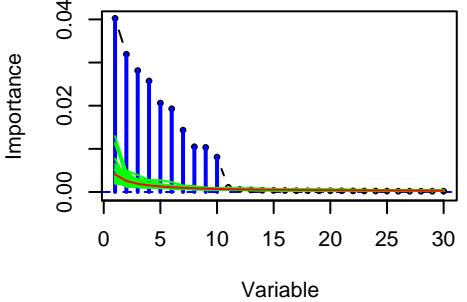
3 classes; 1 comp.; 5 genes/comp.



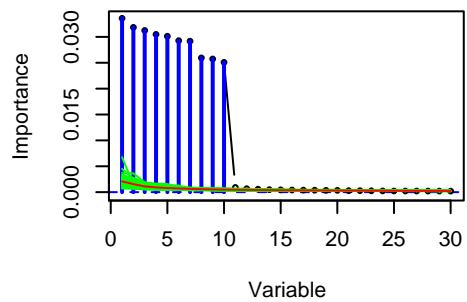
4 classes; 1 comp.; 5 genes/comp.



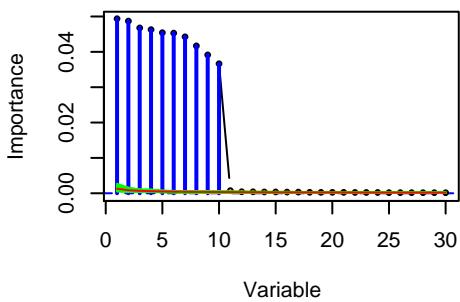
2 classes; 2 comp.; 5 genes/comp.



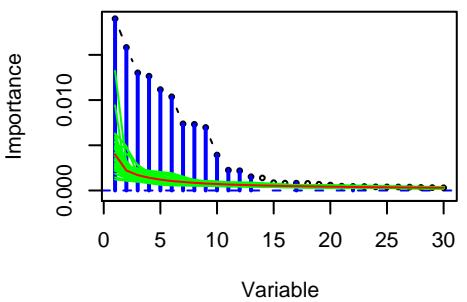
3 classes; 2 comp.; 5 genes/comp.



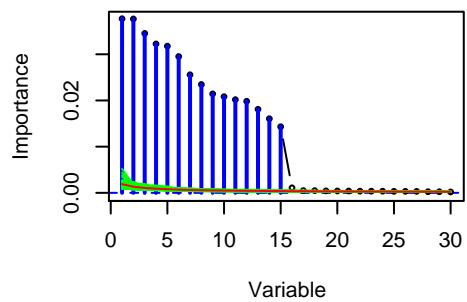
4 classes; 2 comp.; 5 genes/comp.



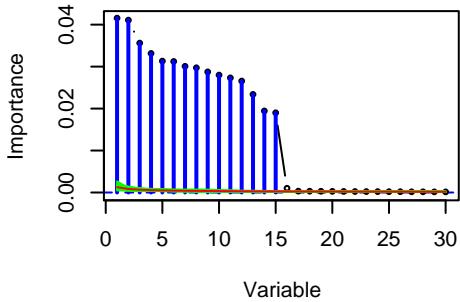
2 classes; 3 comp.; 5 genes/comp.



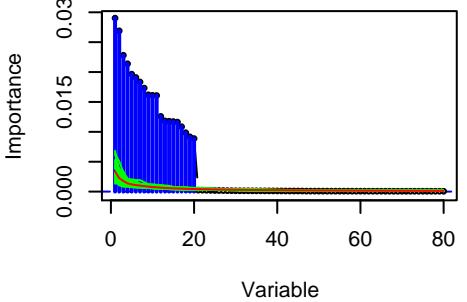
3 classes; 3 comp.; 5 genes/comp.



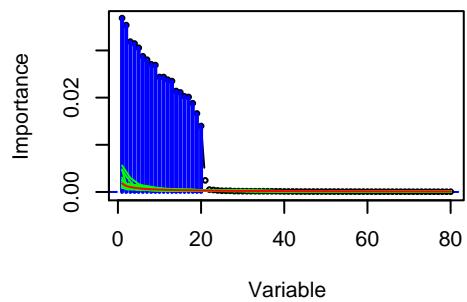
4 classes; 3 comp.; 5 genes/comp.



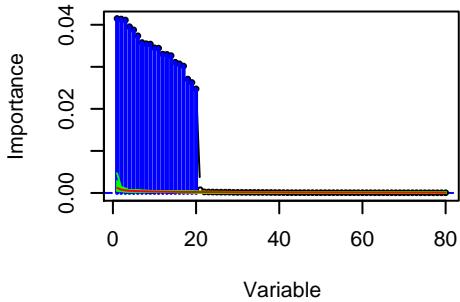
2 classes; 1 comp.; 20 genes/comp.



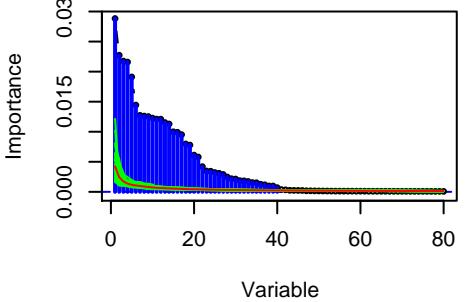
3 classes; 1 comp.; 20 genes/comp.



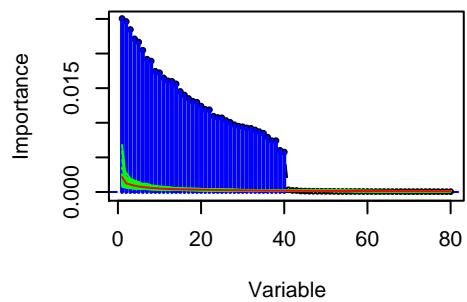
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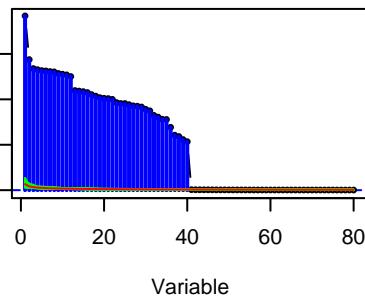
2 classes; 2 comp.; 20 genes/comp.



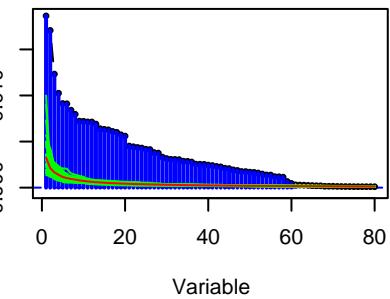
3 classes; 2 comp.; 20 genes/comp.



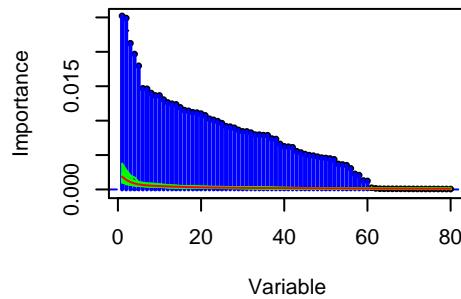
4 classes; 2 comp.; 20 genes/comp.



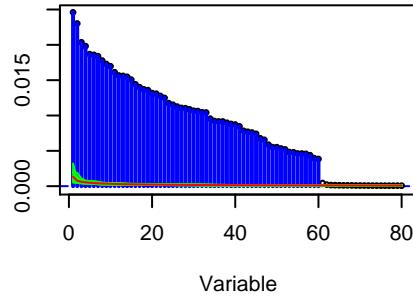
2 classes; 3 comp.; 20 genes/comp.



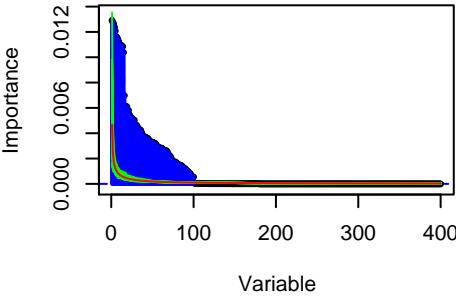
3 classes; 3 comp.; 20 genes/comp.



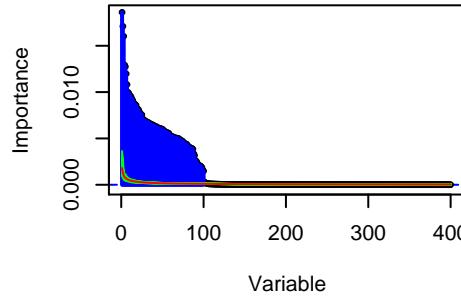
4 classes; 3 comp.; 20 genes/comp.



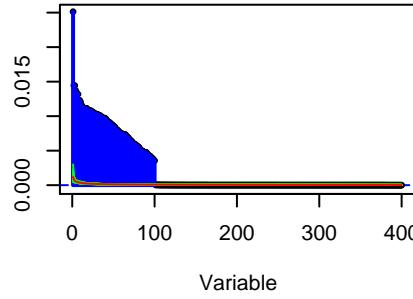
2 classes; 1 comp.; 100 genes/comp.



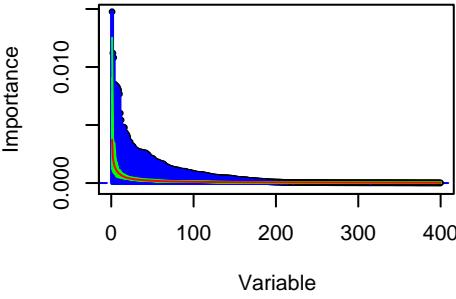
3 classes; 1 comp.; 100 genes/comp



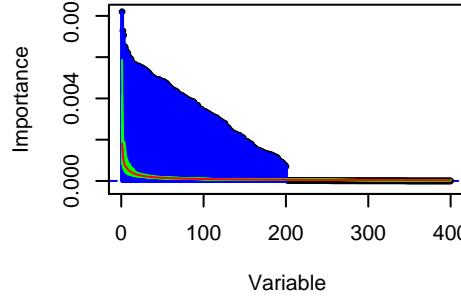
4 classes; 1 comp.; 100 genes/comp.



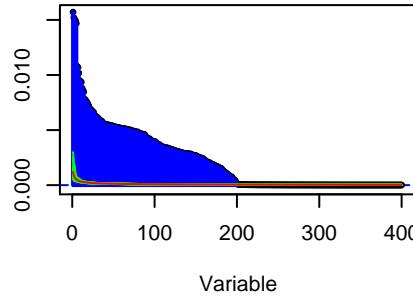
2 classes; 2 comp.; 100 genes/comp.



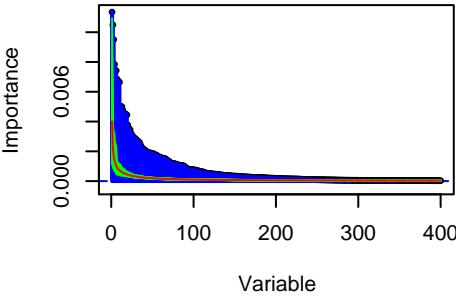
3 classes; 2 comp.; 100 genes/comp



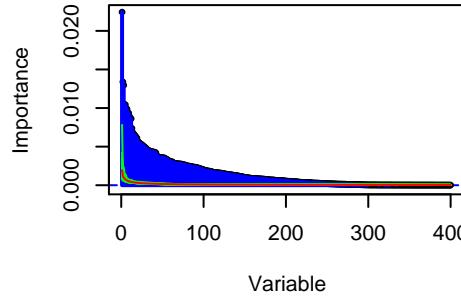
4 classes; 2 comp.; 100 genes/comp.



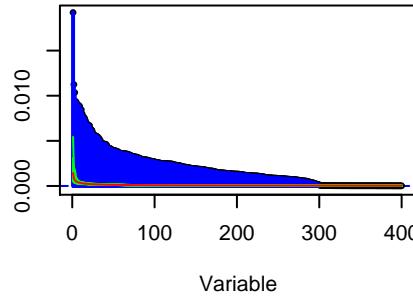
2 classes; 3 comp.; 100 genes/comp.



3 classes; 3 comp.; 100 genes/comp

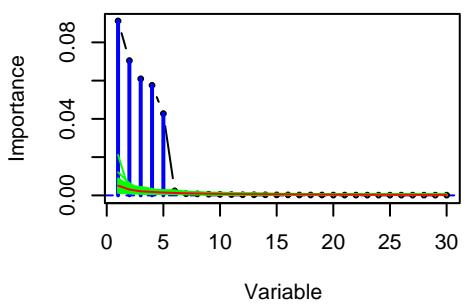


4 classes; 3 comp.; 100 genes/comp.

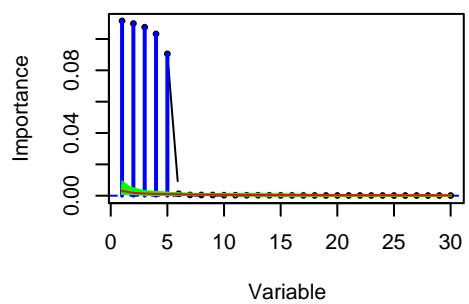


**ntree = 5000
mtry factor = 8**

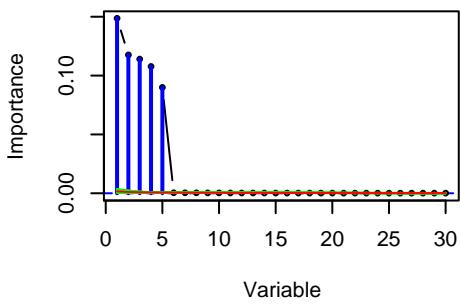
2 classes; 1 comp.; 5 genes/comp.



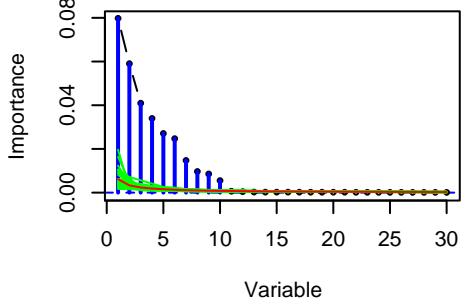
3 classes; 1 comp.; 5 genes/comp.



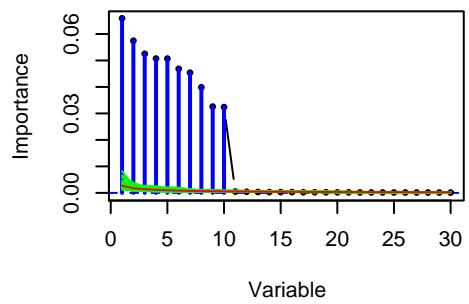
4 classes; 1 comp.; 5 genes/comp.



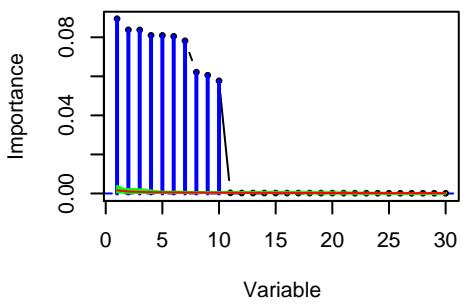
2 classes; 2 comp.; 5 genes/comp.



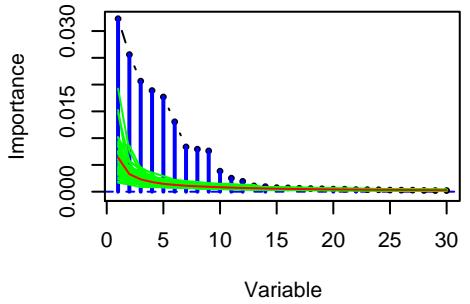
3 classes; 2 comp.; 5 genes/comp.



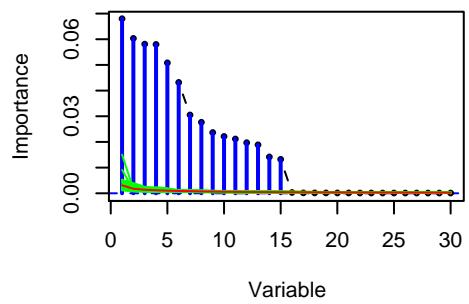
4 classes; 2 comp.; 5 genes/comp.



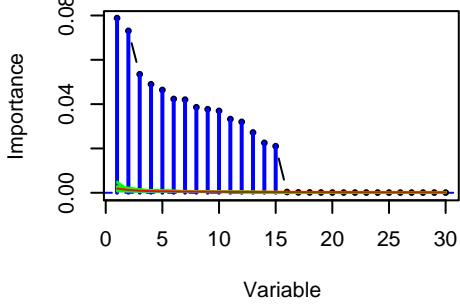
2 classes; 3 comp.; 5 genes/comp.



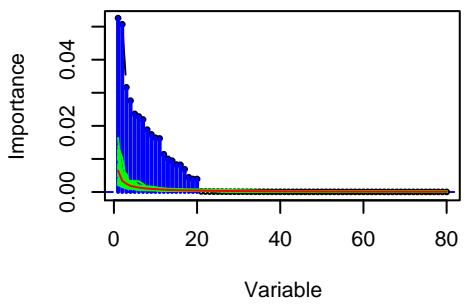
3 classes; 3 comp.; 5 genes/comp.



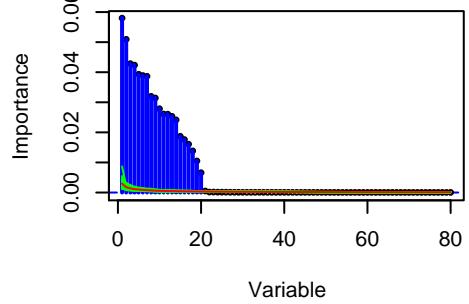
4 classes; 3 comp.; 5 genes/comp.



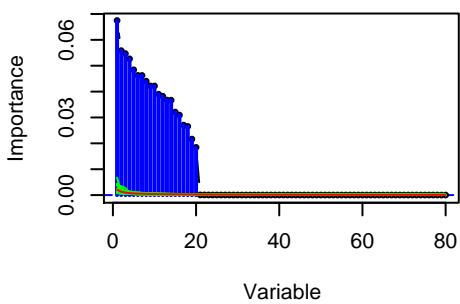
2 classes; 1 comp.; 20 genes/comp.



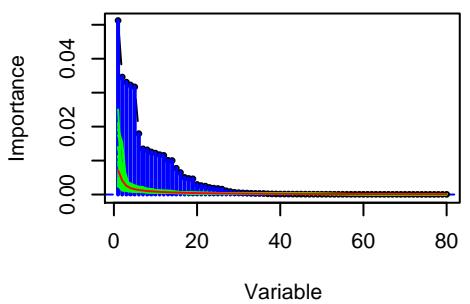
3 classes; 1 comp.; 20 genes/comp.



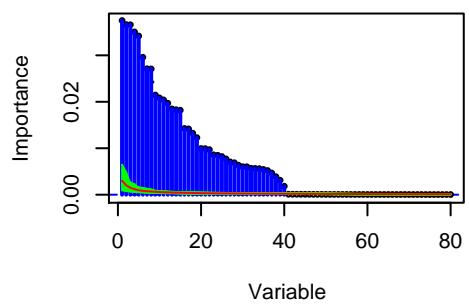
4 classes; 1 comp.; 20 genes/comp.

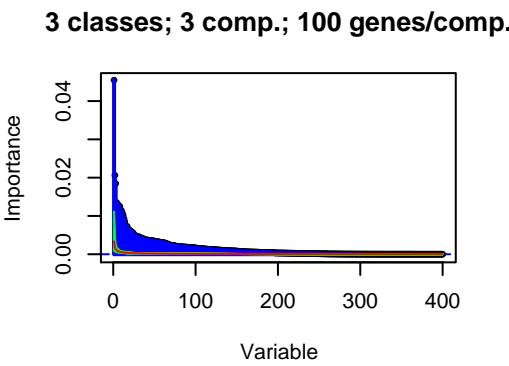
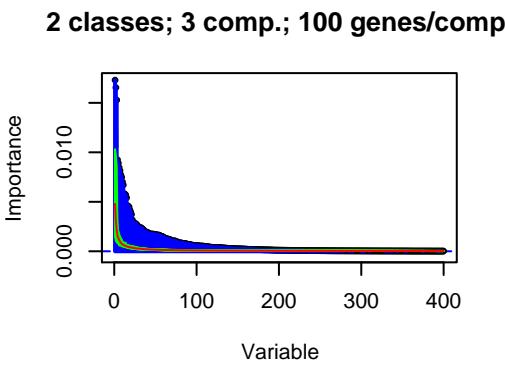
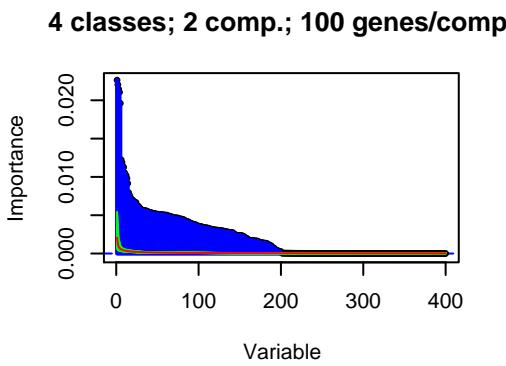
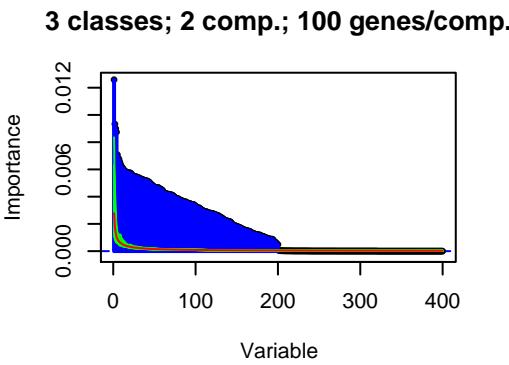
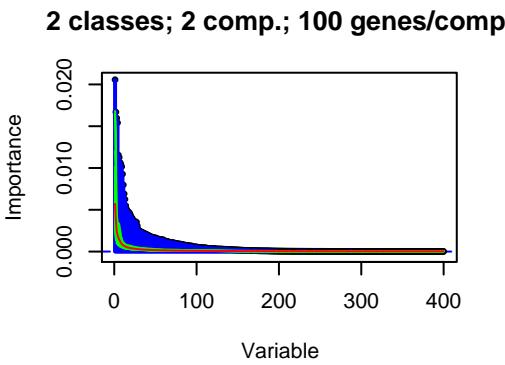
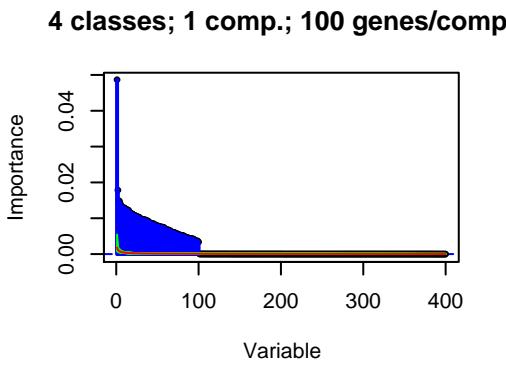
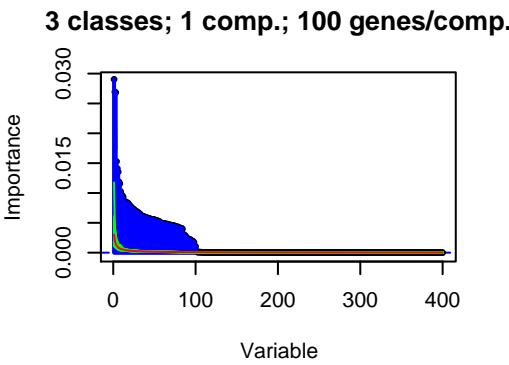
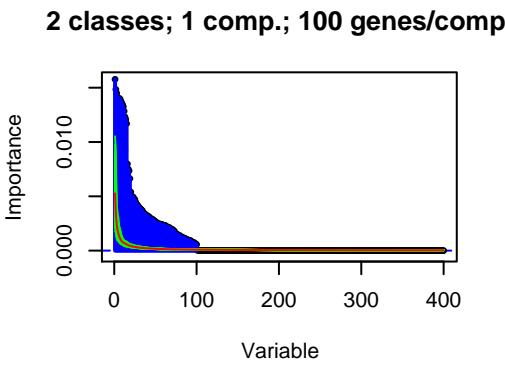
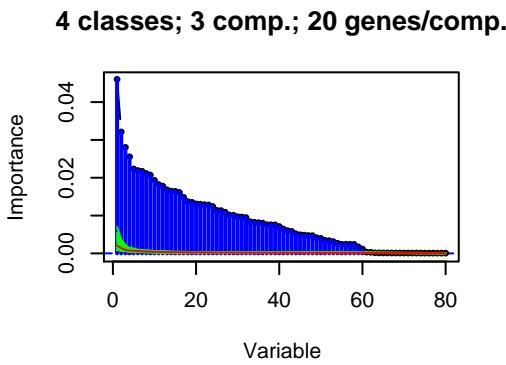
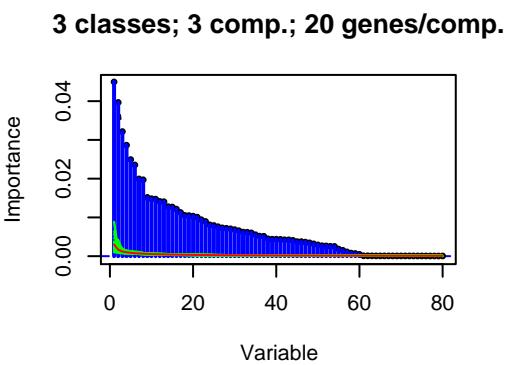
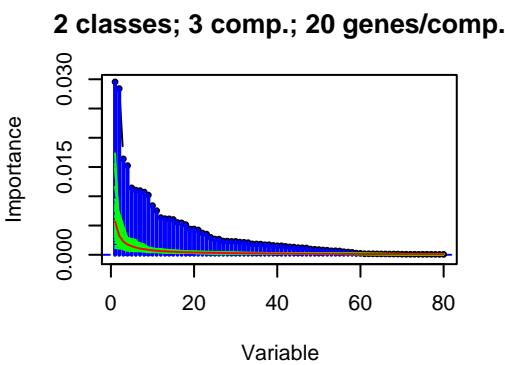
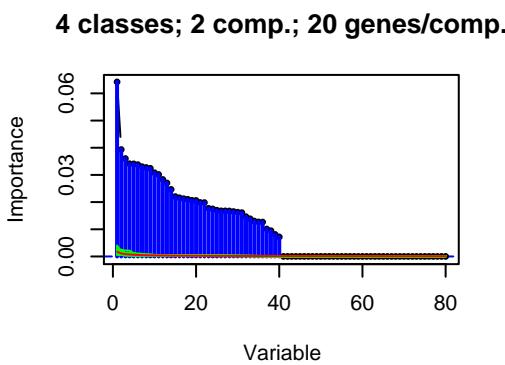


2 classes; 2 comp.; 20 genes/comp.

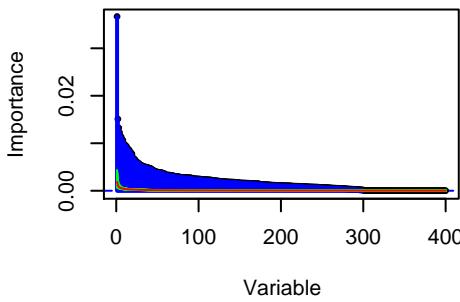


3 classes; 2 comp.; 20 genes/comp.



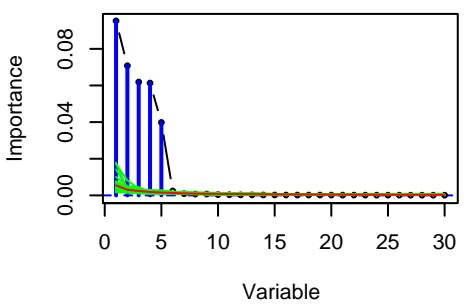


4 classes; 3 comp.; 100 genes/comp.

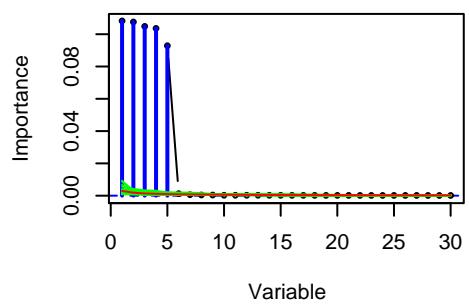


**ntree = 5000
mtry factor = 13**

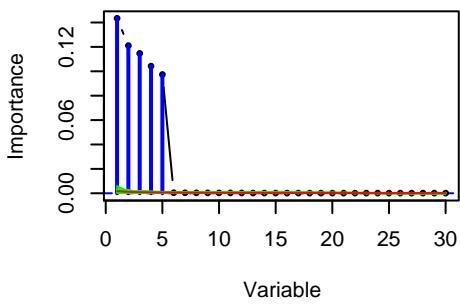
2 classes; 1 comp.; 5 genes/comp.



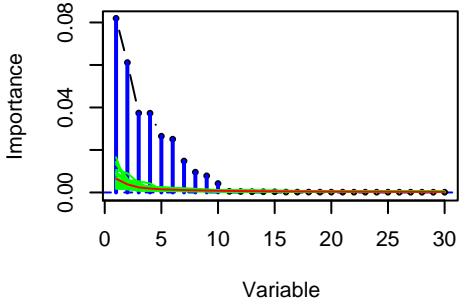
3 classes; 1 comp.; 5 genes/comp.



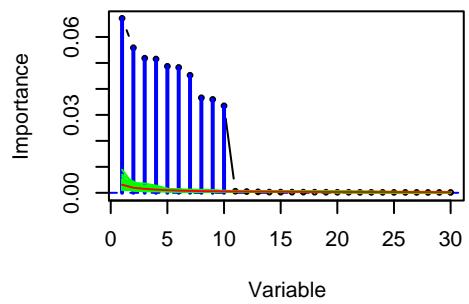
4 classes; 1 comp.; 5 genes/comp.



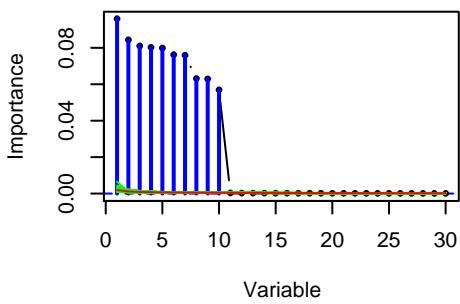
2 classes; 2 comp.; 5 genes/comp.



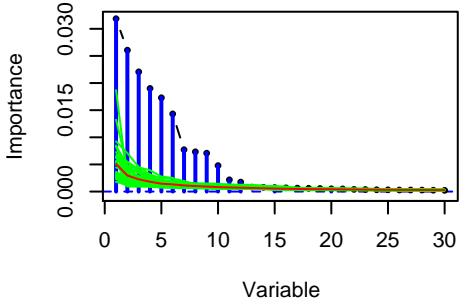
3 classes; 2 comp.; 5 genes/comp.



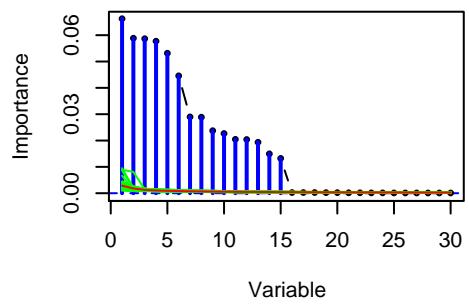
4 classes; 2 comp.; 5 genes/comp.



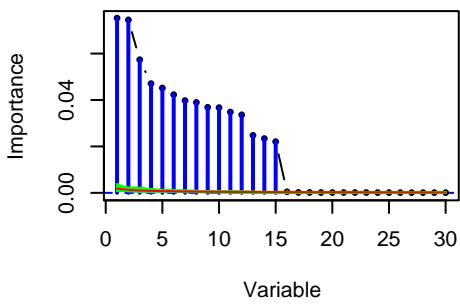
2 classes; 3 comp.; 5 genes/comp.



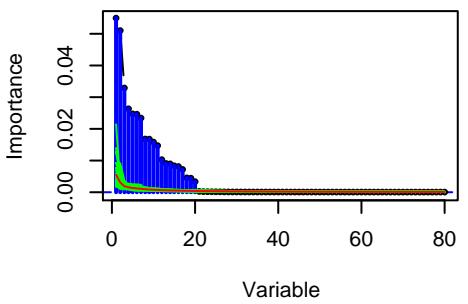
3 classes; 3 comp.; 5 genes/comp.



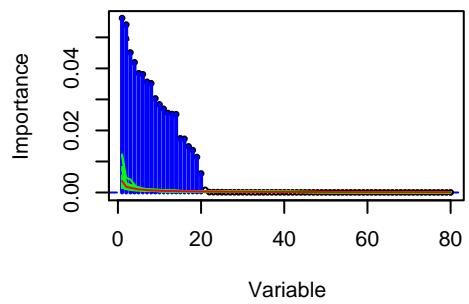
4 classes; 3 comp.; 5 genes/comp.



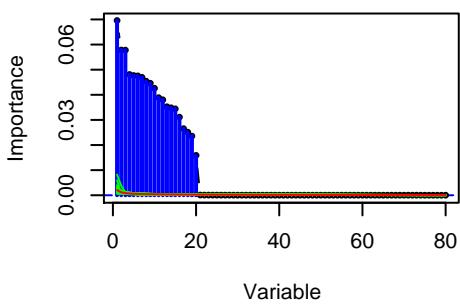
2 classes; 1 comp.; 20 genes/comp.



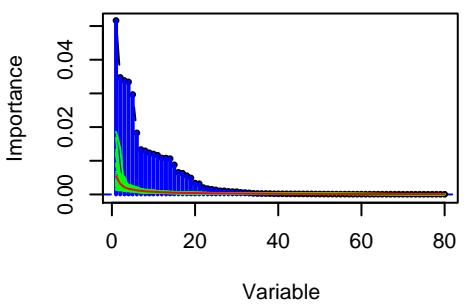
3 classes; 1 comp.; 20 genes/comp.



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



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



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

