

Customizing the `rpart` library for multivariate gaussian outcomes: the `longRPart` library

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Abdoell et al. (2001)¹ implemented a binary partitioning algorithm for the case of continuous repeated measures outcomes, using Mahalanobis distance as a deviance measure to evaluate goodness-of-split. The algorithm was implemented only for a single split at the root node of the tree with the single purpose of dichotomising prognostic variables. The binary partitioning algorithm was implemented in SAS using the PROC MIXED procedure, along with a permutation test to evaluate the p-value of the associated binary split and a bootstrap method to calculate a confidence interval.

This project extends the binary partitioning algorithm of Abdoell et. al to a binary recursive partitioning algorithm² which is implemented in R. We utilize the `nlme` library to extend the `rpart` library³, producing the `longRPart` library for binary recursive partitioning in the case of MVN outcomes, and extends the algorithm to split on unordered categorical variables. A tree plotting function is developed for annotated plots that are applied to terminal nodes of the tree to display the longitudinal profiles of the outcome variable.

A detailed discussion will be presented of how the `rpart` library was extended to accommodate the longitudinal outcome with its associated deviance measure, and how to apply these same principles to the case of other non-standard outcomes using custom R functions.

References

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<http://mayoresearch.mayo.edu/mayo/research/biostat/splusfunctions.cfm>