

Figure 7: Pathological example of non-convergence of the MICE algorithm. Plotted are the means and standard deviations per iteration of the imputed values of `hgt`, `wgt` and `bmi`. The values are locked to the starting imputation.

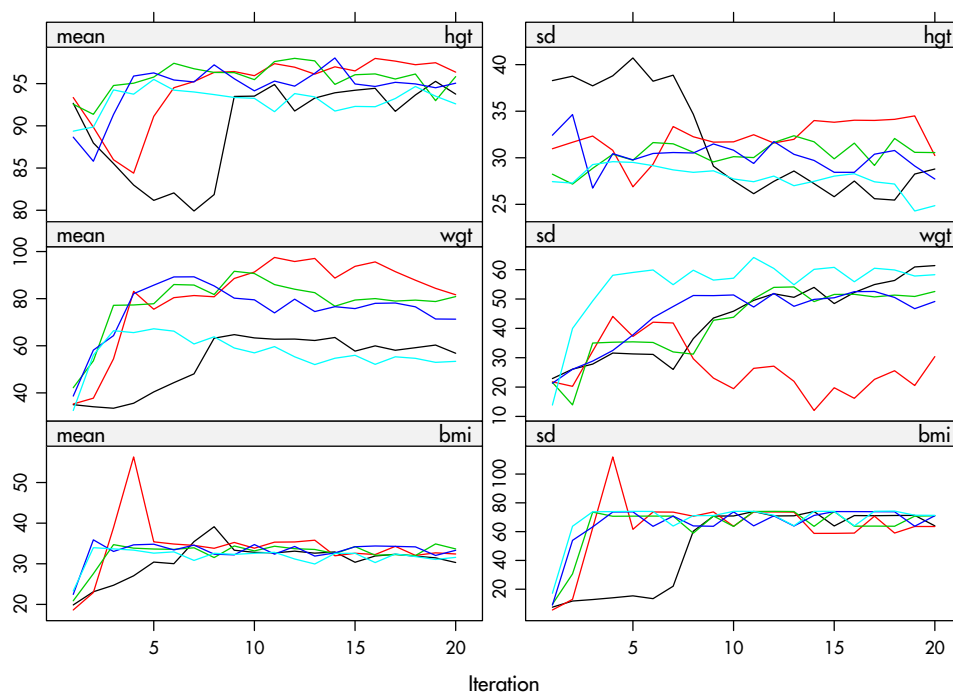


Figure 8: Non-convergence of the MICE algorithm. Imputations for `hgt`, `wgt` and `bmi` hardly mix and resolve into a steady state.

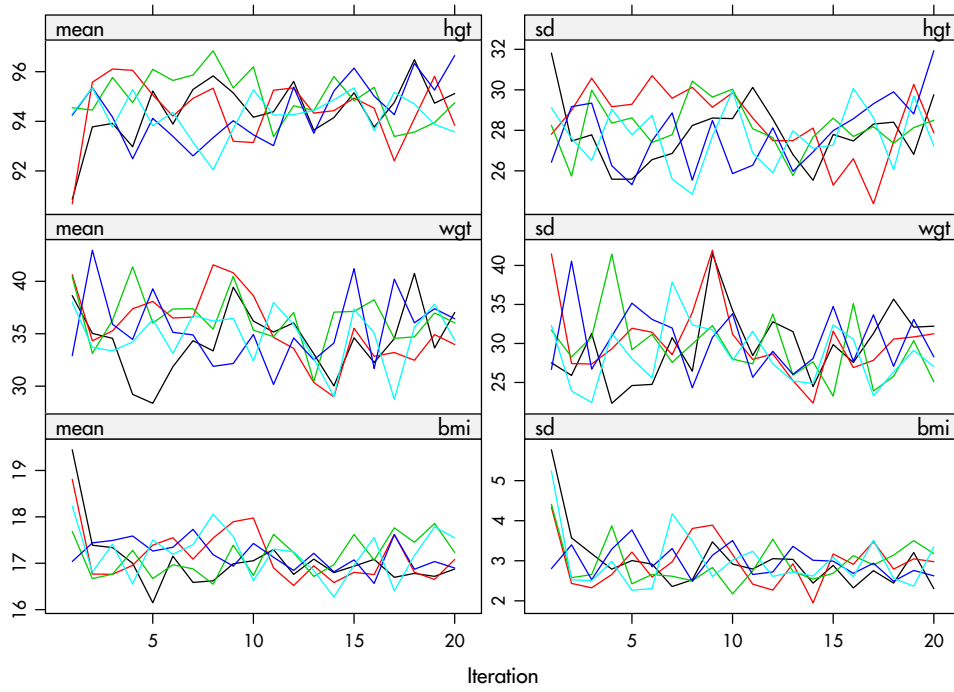


Figure 9: Healthy convergence of the MICE algorithm for `hgt`, `wgt` and `bmi`, where feedback loop of `bmi` into `hgt` and `wgt` is broken (`solution imp.idx`).

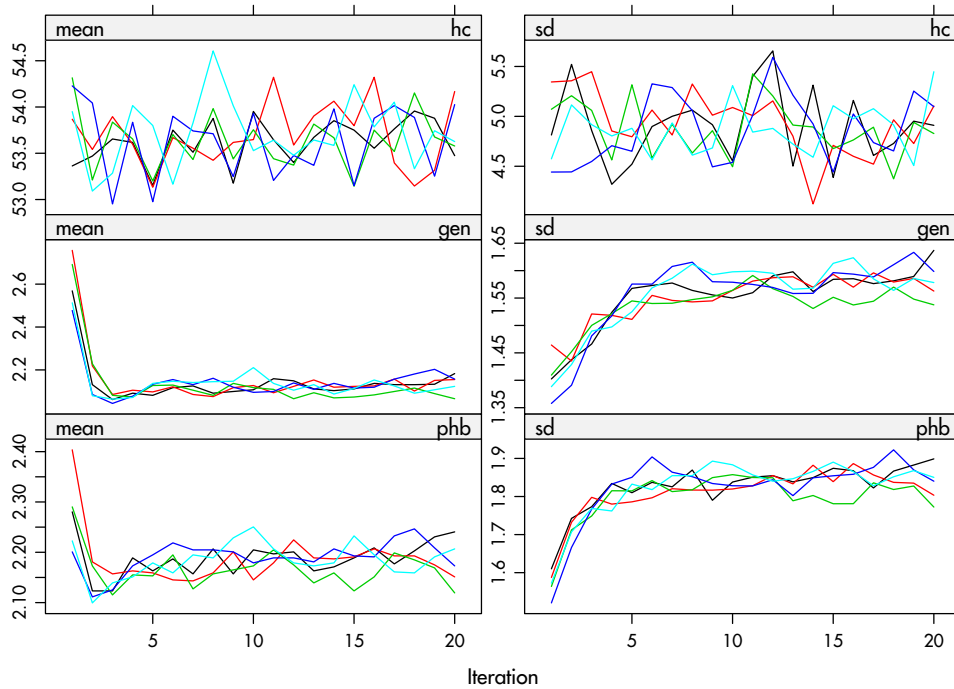


Figure 10: Healthy convergence of the MICE algorithm for `hc`, `gen` and `phb` showing a strong initial trend for the latter two (`solution imp.idx`).

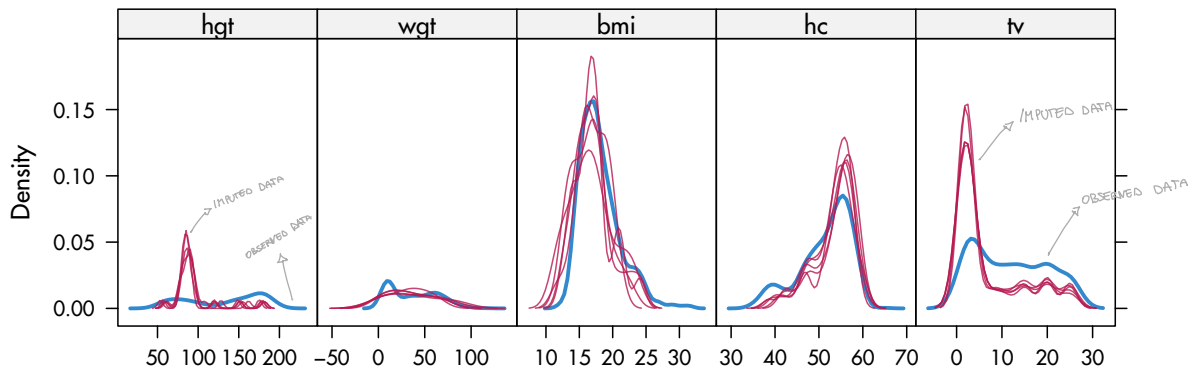


Figure 12: Kernel density estimates for the marginal distributions of the observed data (blue) and the  $m = 5$  densities per variable calculated from the imputed data (thin red lines).

plot densities of both the observed and imputed values of all variables to see whether the imputations are reasonable. Differences in the densities between the observed and imputed values may suggest a problem that needs to be further checked. The `densityplot()` function from the **lattice** package can be used on `mids` objects to produce Figure 12 as

```
R> densityplot(imp.kendall, scales = list(x = list(relation = "free")),
+   layout = c(5, 1))
```

Figure 12 shows that the imputed values can be quite different from the observed data. For example, the imputed heights are around 90 cm, which is due to the fact the some of the values of the two-year olds were missing. The same holds for testicular volume (`tv`), which was not measured below the age of 8 years. Reversely, the imputed values for head circumference (`hc`) are higher since `hc` was not measured in the older boys. In general, plots like this are useful to detect interesting differences between the observed and imputed data.

code  
producing  
plot