

Stan Diagnostic plotting in R

January 3, 2014

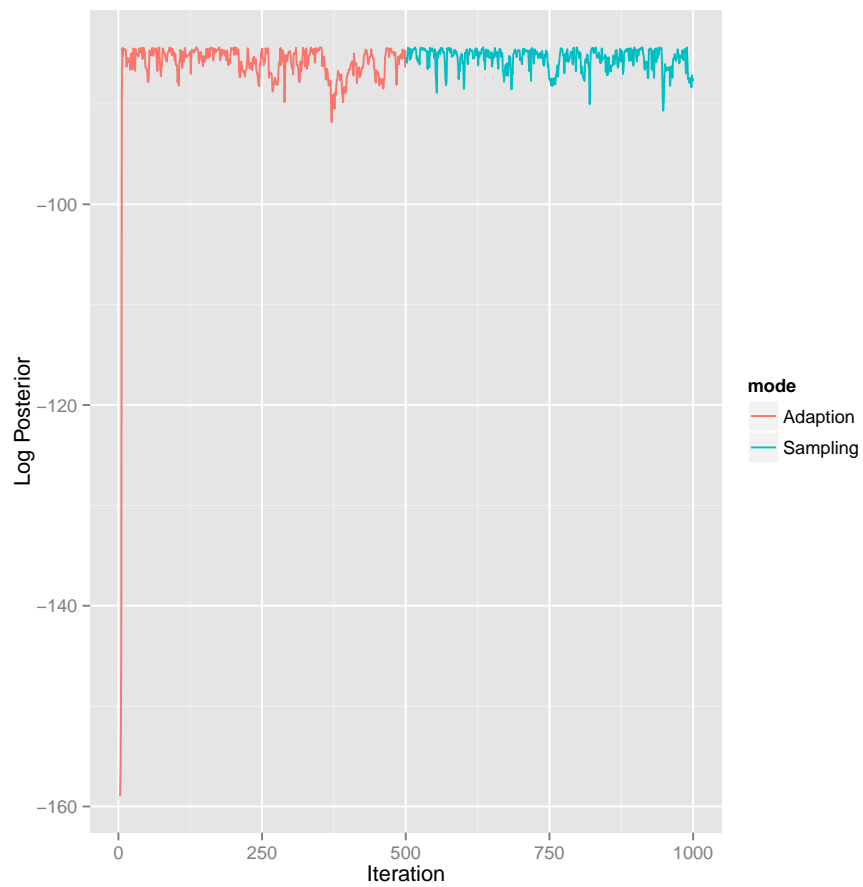
```
source("parsedidiagnostic.R")
tg1 <- parsedidiagnostic("diagnostic_file.dat_1.csv")

## Warning:  NAs introduced by coercion
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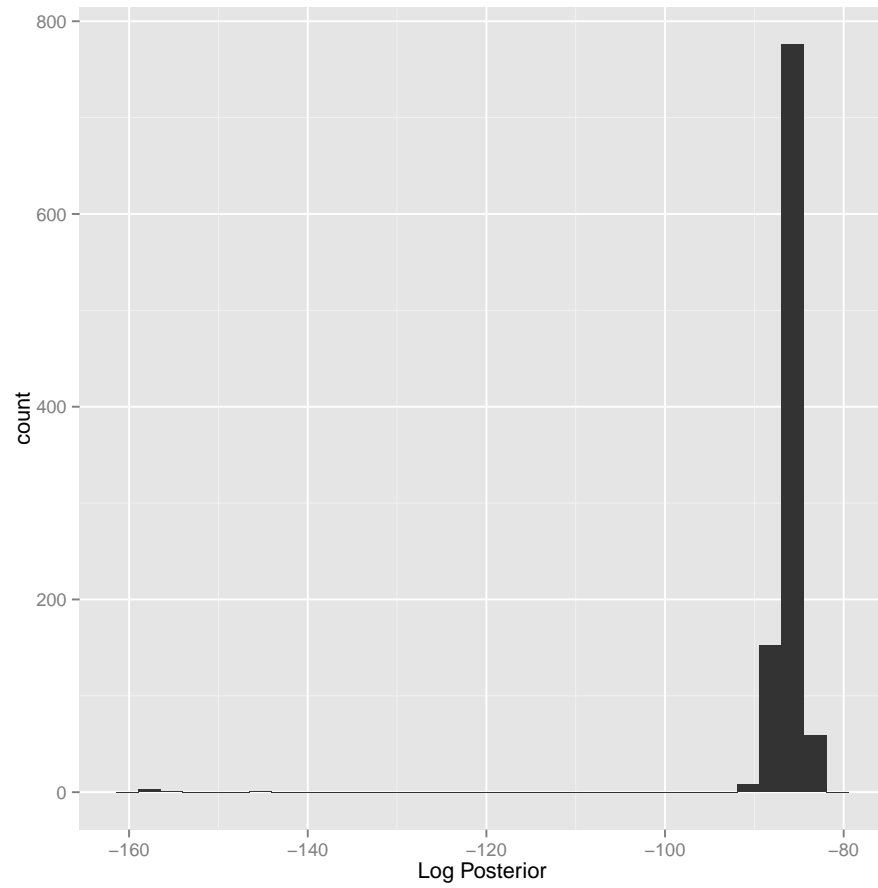
tg1d <- tg1$diags
require(ggplot2)

## Loading required package:  ggplot2

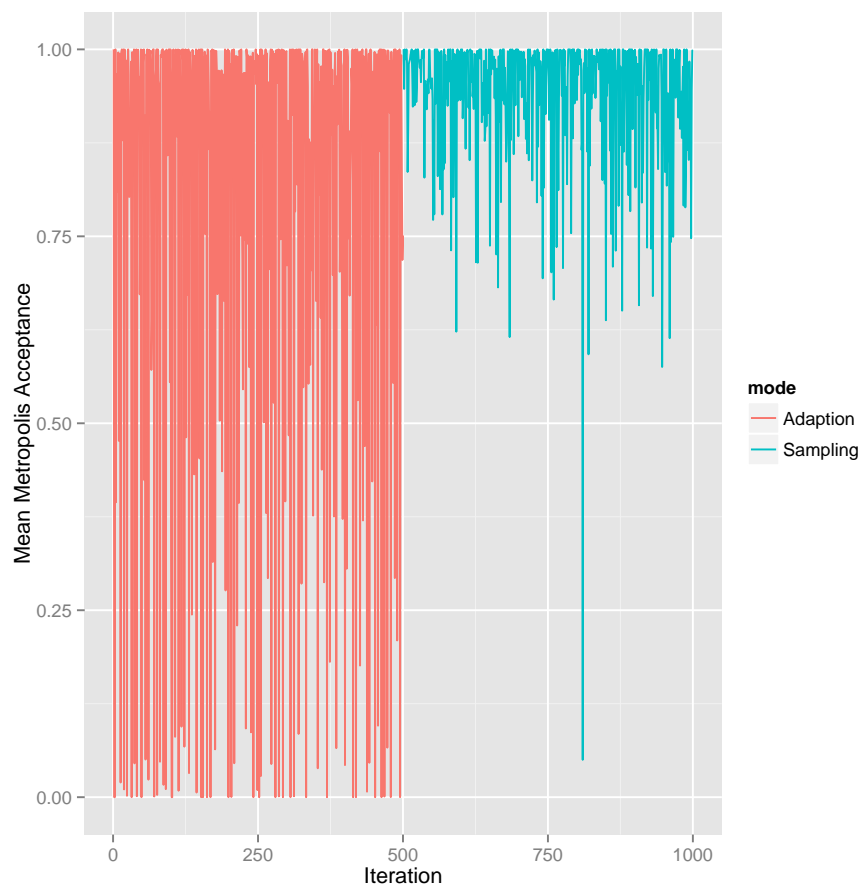
qplot(1:nrow(tg1d), lp__, data = tg1d, xlab = "Iteration", ylab = "Log Posterior",
      geom = "line", colour = mode)
```



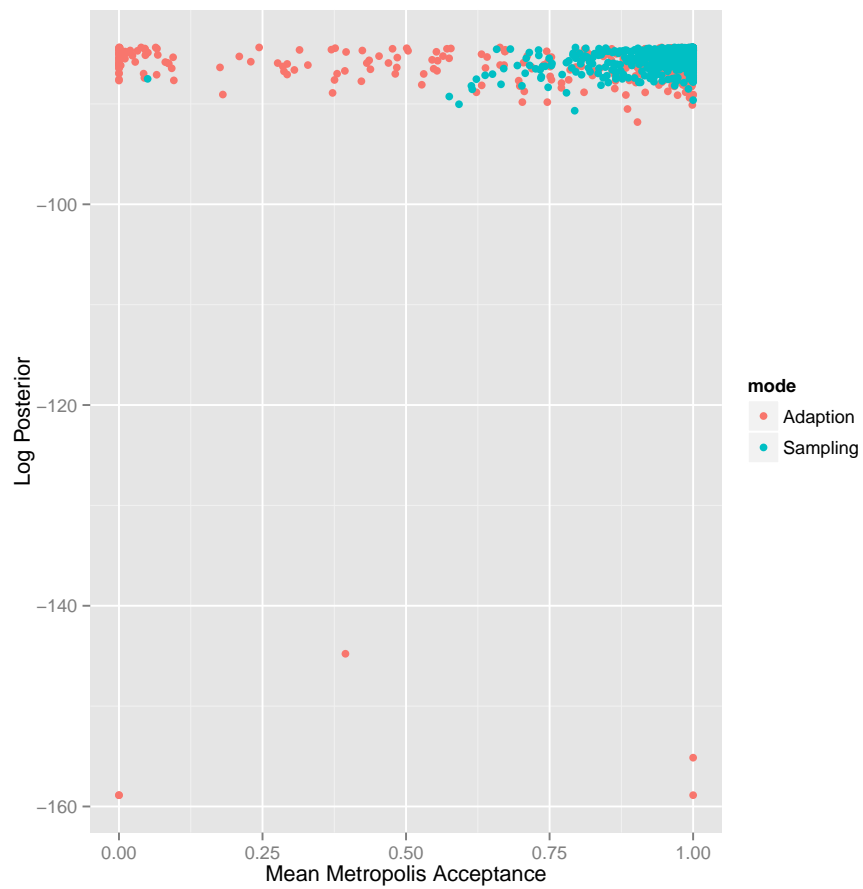
```
qplot(lp__, data = tgid, geom = "histogram", xlab = "Log Posterior")  
  
## stat_bin: binwidth defaulted to range/30. Use 'binwidth = x' to  
adjust this.
```



```
qplot(1:nrow(tg1d), accept_stat__, data = tg1d, xlab = "Iteration", ylab = "Mean Metropolis  
geom = "line", colour = mode)
```

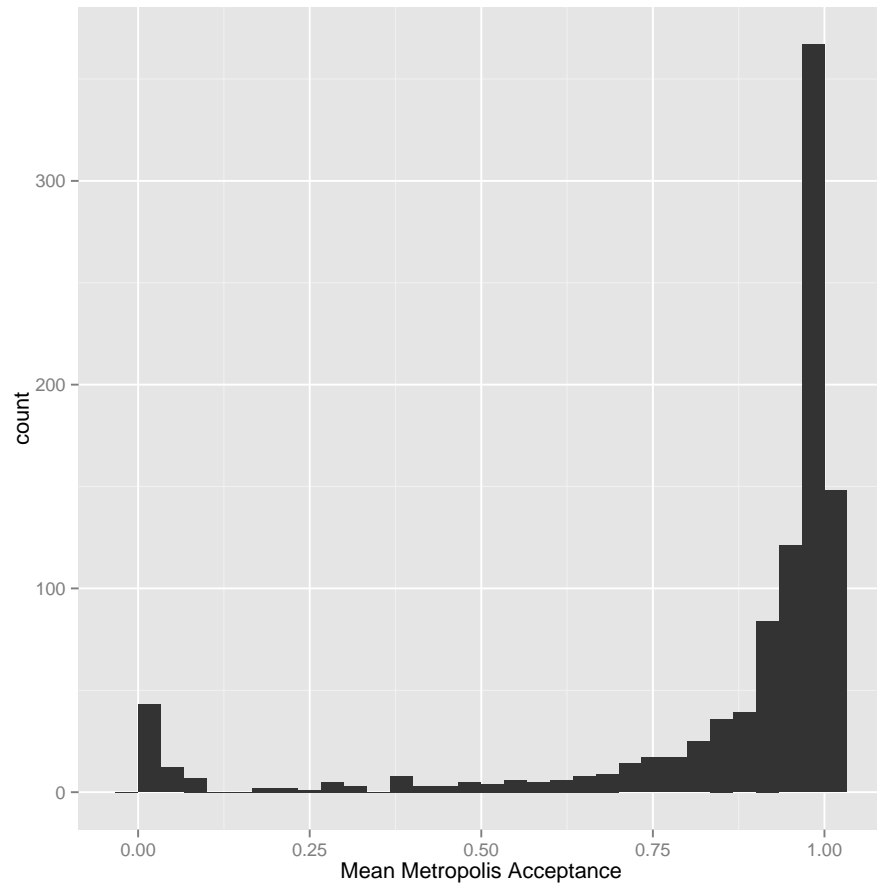


```
qplot(accept_stat__, lp__, data = tg1d, colour = mode, xlab = "Mean Metropolis Acceptance",
      ylab = "Log Posterior")
```



```
qplot(accept_stat_., data = tg1d, geom = "histogram", xlab = "Mean Metropolis Acceptance")

## stat_bin: binwidth defaulted to range/30. Use 'binwidth = x' to
adjust this.
```



```
qplot(1:nrow(tg1d), treedepth__, data = tg1d, xlab = "Iteration", ylab = "Tree depth",  
      geom = "line", colour = mode)
```

