Test divergence between chains

Contents

```r
library(blme)
```

```
## Loading required package: lme4
```

```
## Loading required package: Matrix
```

```
##
## Attaching package: 'lme4'
```

```
## The following object is masked from 'package:stats':
##
##     sigma
```

```r
library(party)
```

```
## Loading required package: grid
```

```
## Loading required package: mvtnorm
```

```
## Loading required package: modeltools
```

```
## Loading required package: stats4
```

```
##
## Attaching package: 'modeltools'
```

```
## The following object is masked from 'package:lme4':
##
##     refit
```

```
## Loading required package: strucchange
```

```
## Loading required package: zoo
```

```
##
## Attaching package: 'zoo'
```

```
## The following objects are masked from 'package:base':
##
##     as.Date, as.Date.numeric
```

```
## Loading required package: sandwich
```

```r
library(sjPlot)


setwd("/Library/WebServer/Documents/ILMTurk/stats/R")
load("stabilityAcrossChains.Rdat")


dx = stability.accross.chains[stability.accross.chains$run=="MT" ,]
dx = dx[complete.cases(dx),]

dx$distance.norm = dx$distance - mean(dx$distance)
dx$curvature.norm = dx$curvature - 0.2
```

```r
dx$curvature.norm.q = (dx$curvature.norm + 0.1)^2
dx$curvature.norm.c = (dx$curvature.norm + 0.1)^3
dx$gen = dx$gen - 5

summary(lm(distance~curvature*gen, data=dx))
```

```
##
## Call:
## lm(formula = distance ~ curvature * gen, data = dx)
##
## Residuals:
##     Min     1Q Median     3Q    Max
## -34093  -9352  -3248   6703  75528
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    28611.6     1050.4  27.240  < 2e-16 ***
## curvature      -9995.7     3491.2  -2.863  0.00432 **
## gen             3598.0      378.4   9.509  < 2e-16 ***
## curvature:gen  -3854.9     1239.6  -3.110  0.00195 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 14810 on 677 degrees of freedom
## Multiple R-squared:  0.2096, Adjusted R-squared:  0.2061
## F-statistic: 59.83 on 3 and 677 DF,  p-value: < 2.2e-16
```

```r
m0 = lmer(distance.norm~ 1 + (1|chainA) + (1|chainB),data=dx)
m1 = lmer(distance.norm~ 1 + curvature.norm + (1|chainA) + (1|chainB),data=dx)
m2 = lmer(distance.norm~ 1 + curvature.norm + gen  + (1|chainA) + (1|chainB),data=dx)
m3 = lmer(distance.norm~ 1 + curvature.norm*gen + (1|chainA) + (1|chainB),data=dx)
m4 = lmer(distance.norm~ 1 + curvature.norm* gen  +curvature.norm.q + (1|chainA) + (1|chainB),data=dx)
m5 = lmer(distance.norm~ 1 + curvature.norm* gen  +curvature.norm.q*gen + (1|chainA) + (1|chainB),data=
m6 = lmer(distance.norm~ 1 + curvature.norm* gen  +curvature.norm.q*gen + curvature.norm.c + (1|chainA)
m7 = lmer(distance.norm~ 1 + curvature.norm* gen  +curvature.norm.q*gen +curvature.norm.c*gen + (1|chai

anova(m0,m1,m2,m3,m4,m5,m6,m7)
```

```
## refitting model(s) with ML (instead of REML)
```

```
## Data: dx
## Models:
## m0: distance.norm ~ 1 + (1 | chainA) + (1 | chainB)
## m1: distance.norm ~ 1 + curvature.norm + (1 | chainA) + (1 | chainB)
## m2: distance.norm ~ 1 + curvature.norm + gen + (1 | chainA) + (1 |
## m2:     chainB)
## m3: distance.norm ~ 1 + curvature.norm * gen + (1 | chainA) + (1 |
## m3:     chainB)
## m4: distance.norm ~ 1 + curvature.norm * gen + curvature.norm.q +
## m4:     (1 | chainA) + (1 | chainB)
## m5: distance.norm ~ 1 + curvature.norm * gen + curvature.norm.q *
## m5:     gen + (1 | chainA) + (1 | chainB)
## m6: distance.norm ~ 1 + curvature.norm * gen + curvature.norm.q *
## m6:     gen + curvature.norm.c + (1 | chainA) + (1 | chainB)
## m7: distance.norm ~ 1 + curvature.norm * gen + curvature.norm.q *
```

```
## m7:     gen + curvature.norm.c * gen + (1 | chainA) + (1 | chainB)
##    Df   AIC   BIC  logLik deviance    Chisq Chi Df Pr(>Chisq)
## m0  4 15088 15106 -7539.9    15080
## m1  5 15089 15112 -7539.5    15079   0.7319      1    0.39227
## m2  6 14921 14948 -7454.6    14909 169.8085      1  < 2.2e-16 ***
## m3  7 14904 14936 -7444.9    14890  19.3478      1  1.089e-05 ***
## m4  8 14903 14940 -7443.6    14887   2.5468      1    0.11052
## m5  9 14888 14929 -7435.0    14870  17.3289      1  3.144e-05 ***
## m6 10 14887 14932 -7433.4    14867   3.0544      1    0.08052 .
## m7 11 14889 14939 -7433.4    14867   0.0203      1    0.88664
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
sjp.lmer(m5, 'pred', c("gen","curvature.norm"), facet.grid = F)
```
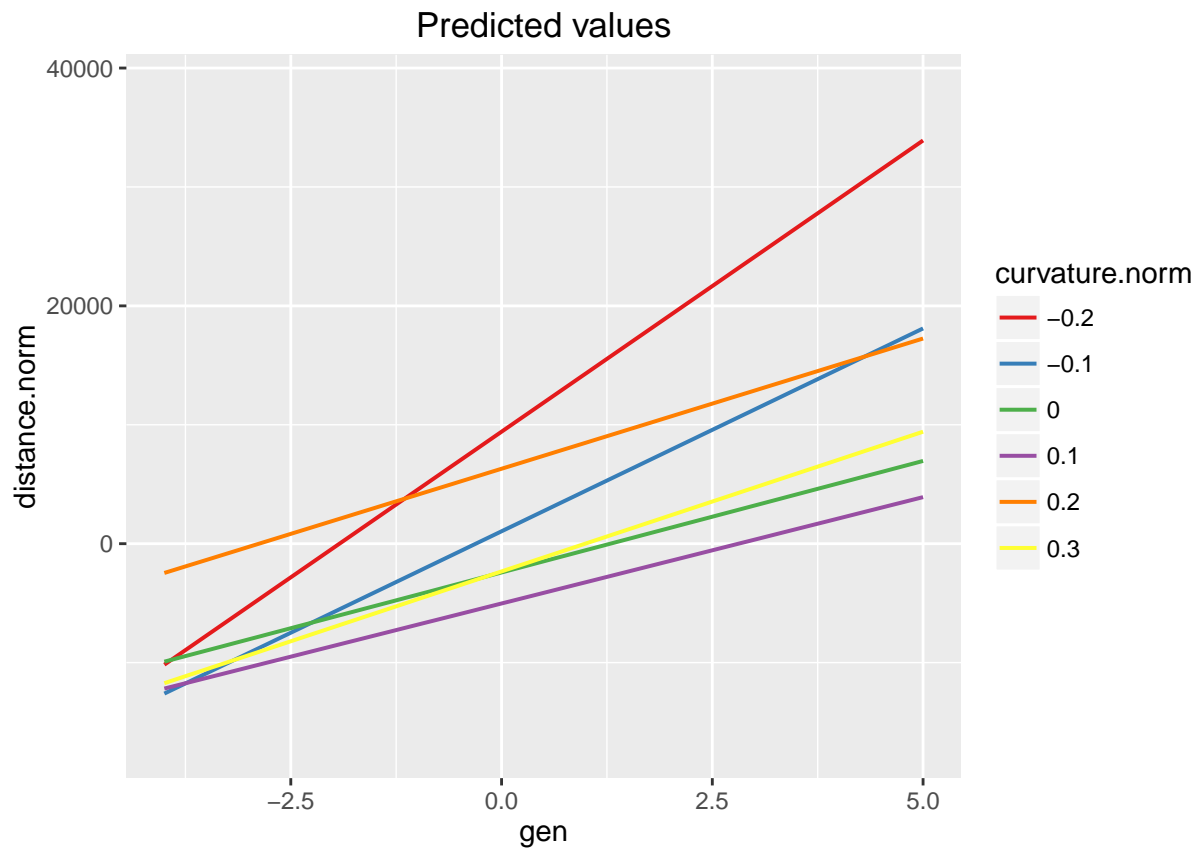

Decision tree:

```
dx = stability.accross.chains[stability.accross.chains$run=="MT" ,]
stree = ctree(distance~gen+curvature,data=dx)
plot(stree)
```