Modelos de Regressão Linear Mistos para dados discretos: Uma abordagem utilizando MCMC através do Stan integrado ao R.

Guilherme Artoni - RA160318   Citzen4 - RAXXXXXX   Student - RAXXXXXX

Malba Tahan - RAXXXXXX

The Stan project develops a probabilistic programming language that implements full Bayesian statistical inference via Markov Chain Monte Carlo, rough Bayesian inference via 'variational' approximation, and (optionally penalized) maximum likelihood estimation via optimization. In all three cases, automatic differentiation is used to quickly and accurately evaluate gradients without burdening the user with the need to derive the partial derivatives.
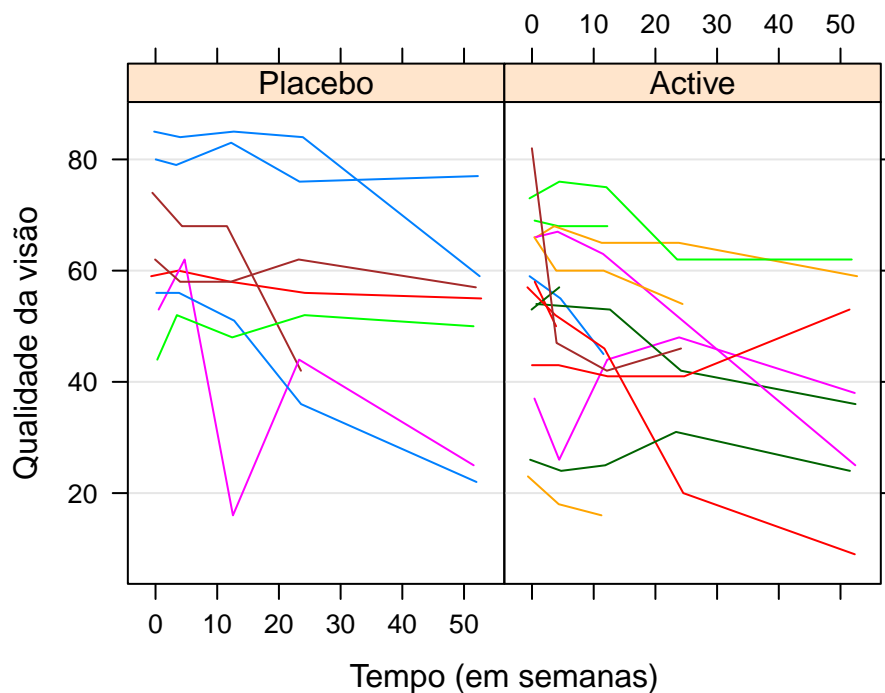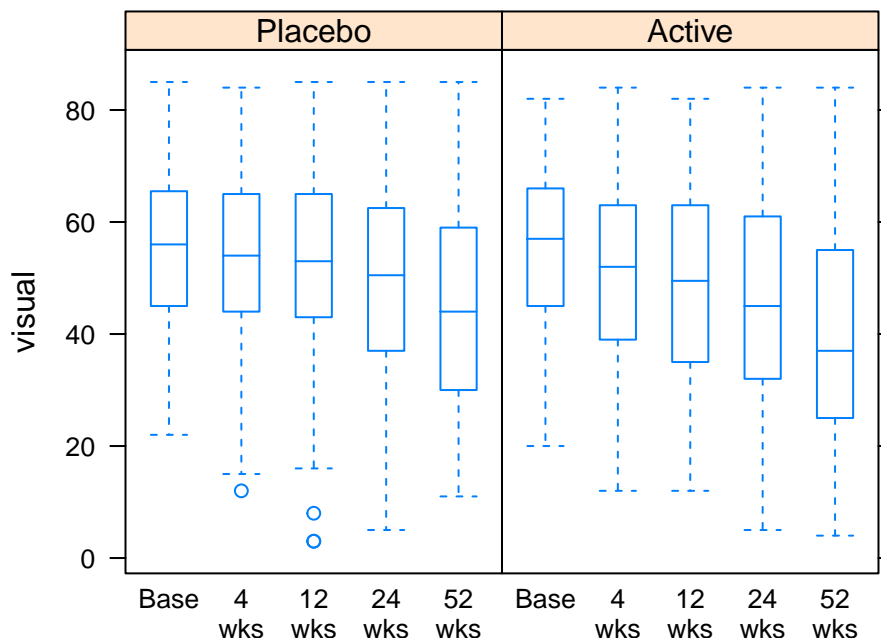


```
##          Placebo Active
## Baseline     119    121
## 4wks         117    114
## 12wks        117    110
## 24wks        112    102
## 52wks        105     90
## [1] "Placebo" "Active"  "Placebo" "Active"  "Placebo" "Active"
##          P:n A:n   P:Mean   A:Mean P:Mdn A:Mdn
## Baseline 119 121 55.33613 54.57851  56.0  57.0
```

1

```
## 4wks       117 114 53.96581 50.91228  54.0  52.0
## 12wks      117 110 52.87179 48.67273  53.0  49.5
## 24wks      112 102 49.33036 45.46078  50.5  45.0
## 52wks      105  90 44.43810 39.10000  44.0  37.0
```



```
##              visual0   visual4 visual12 visual24 visual52
## visual0  220.3055 206.7096 196.2439 193.3099 152.7141
## visual4  206.7096 246.2204 224.7933 221.2677 179.2284
## visual12 196.2439 224.7933 286.2072 257.7738 222.6830
## visual24 193.3099 221.2677 257.7738 334.4456 285.2327
## visual52 152.7141 179.2284 222.6830 285.2327 347.4311

##          visual0 visual4 visual12 visual24 visual52
## visual0     1.00    0.89     0.78     0.71     0.55
## visual4     0.89    1.00     0.85     0.77     0.61
## visual12    0.78    0.85     1.00     0.83     0.71
## visual24    0.71    0.77     0.83     1.00     0.84
## visual52    0.55    0.61     0.71     0.84     1.00
```

# 1   MODELO NORMAL INDEPENDENTE HOMOCEDASTICO

```
##
## Call:
## lm(formula = lm.form, data = armd)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -45.210  -6.459   1.532   7.512  33.283
```

```
## 
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## visual0                   0.83037    0.02842  29.213  < 2e-16 ***
## time.f4wks                8.07531    1.94341   4.155 3.58e-05 ***
## time.f12wks               7.08066    1.94066   3.649  0.00028 ***
## time.f24wks               3.63022    1.95316   1.859  0.06342 .
## time.f52wks              -1.74643    1.98952  -0.878  0.38029
## time.f4wks:treat.fActive -2.35278    1.62894  -1.444  0.14900
## time.f12wks:treat.fActive -3.70852   1.64378  -2.256  0.02432 *
## time.f24wks:treat.fActive -3.44915   1.69399  -2.036  0.04205 *
## time.f52wks:treat.fActive -4.47345   1.77811  -2.516  0.01206 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 12.38 on 858 degrees of freedom
## Multiple R-squared:  0.9432, Adjusted R-squared:  0.9426
## F-statistic:  1583 on 9 and 858 DF,  p-value: < 2.2e-16

## [1] 12.37649

##                                2.5 %      97.5 %
## visual0                    0.7745832   0.8861617
## time.f4wks                 4.2609239  11.8897036
## time.f12wks                3.2716615  10.8896534
## time.f24wks               -0.2033236   7.4637556
## time.f52wks               -5.6513208   2.1584611
## time.f4wks:treat.fActive  -5.5499518   0.8443996
## time.f12wks:treat.fActive -6.9348245  -0.4822195
## time.f24wks:treat.fActive -6.7740045  -0.1243018
## time.f52wks:treat.fActive -7.9634126  -0.9834943

## Analysis of Variance Table
## 
## Response: visual
##               Df  Sum Sq Mean Sq     F value     Pr(>F)
## visual0        1 2165776 2165776 14138.9886 < 2.2e-16 ***
## time.f         4   14434    3608    23.5574 < 2.2e-16 ***
## time.f:treat.f 4    2703     676     4.4109  0.001555 **
## Residuals    858  131426     153
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
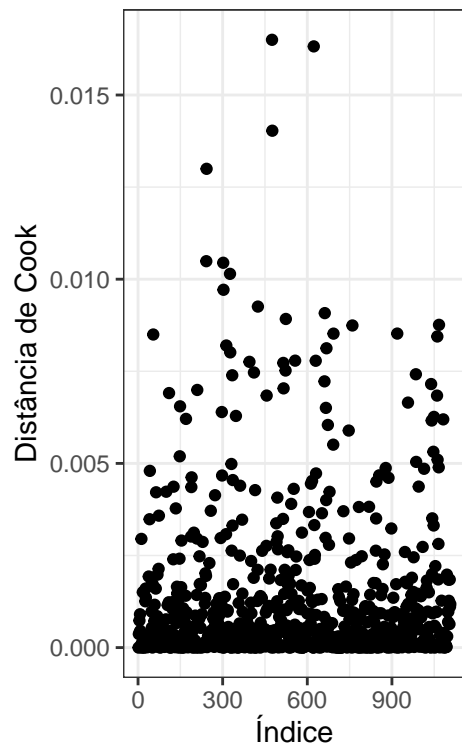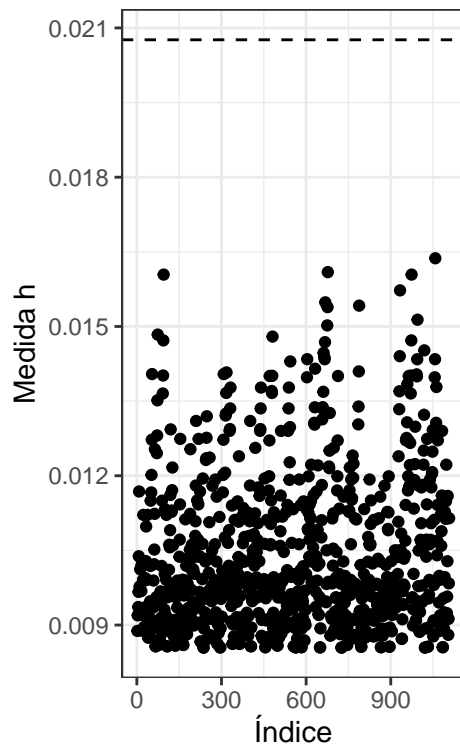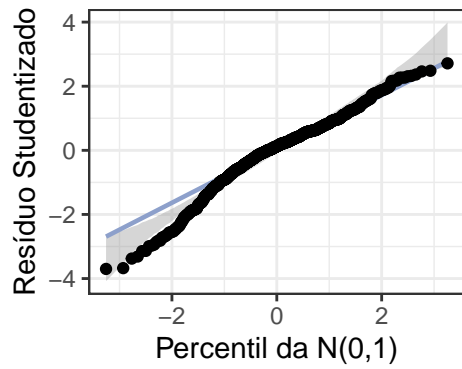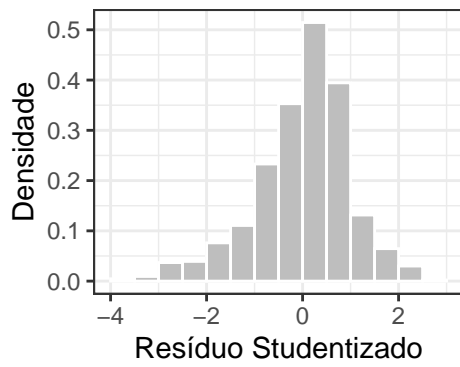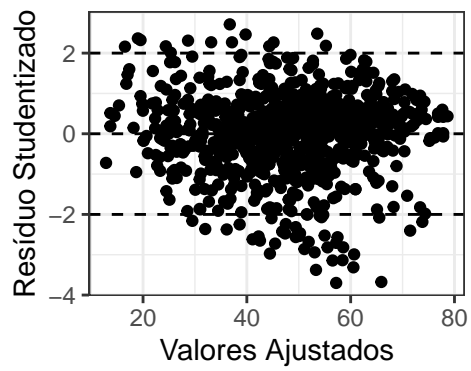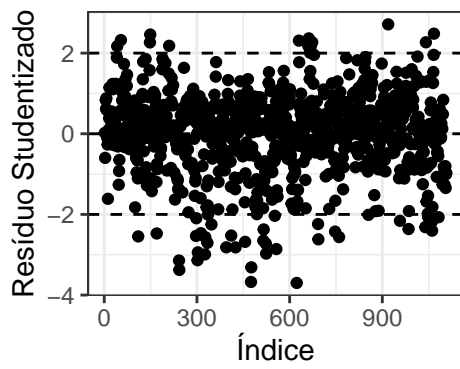
2 MODELO MISTO FREQUENTISTA

```
## Linear mixed-effects model fit by REML
##   Data: armd
##   Log-restricted-likelihood: -3288.986
##   Fixed: lme.form
##        (Intercept)          visual0            time      treat.fActive
##         9.28807837       0.82643987      -0.21221595        -2.42200012
## time:treat.fActive
##        -0.04959058
##
## Random effects:
##  Formula: ~1 | subject
##        (Intercept) Residual
## StdDev:   8.978212 8.627514
##
## Number of Observations: 867
## Number of Groups: 234

##                          Value  Std.Error        DF t-value   p-value
## (Intercept)           9.288078   2.681889 631.000000  3.4633 0.0005698 ***
## visual0               0.826440   0.044667 231.000000 18.5022 < 2.2e-16 ***
## time                 -0.212216   0.022929 631.000000 -9.2552 < 2.2e-16 ***
## treat.fActive        -2.422000   1.499967 231.000000 -1.6147 0.1077402
## time:treat.fActive   -0.049591   0.033562 631.000000 -1.4776 0.1400155
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## subject 2
## Conditional variance covariance matrix
##        1      2      3      4
## 1 74.434  0.000  0.000  0.000
## 2  0.000 74.434  0.000  0.000
## 3  0.000  0.000 74.434  0.000
## 4  0.000  0.000  0.000 74.434
##   Standard Deviations: 8.6275 8.6275 8.6275 8.6275

##           1         2         3         4
## 1 1.0000000 0.5199116 0.5199116 0.5199116
## 2 0.5199116 1.0000000 0.5199116 0.5199116
## 3 0.5199116 0.5199116 1.0000000 0.5199116
## 4 0.5199116 0.5199116 0.5199116 1.0000000

##      AIC      BIC     AICc    SABIC    HQCIC -2log.lik
## 6833.788 6881.438 6833.998 6846.091 6848.200 6813.788

##      AIC      BIC     AICc    SABIC    HQCIC -2log.lik
## 6591.971 6625.286 6592.026 6597.137 6597.444 6577.971
```

3 MODELO MISTO BAYESIANO

Segundo Manly (1997) a ideia básica por trás da Inferência Bayesiana é mudar as probabilidades para os parâmetros tomando valores númericos particulares para novas probabilidades como um resultado da coleta de mais dados, com essa mudança sendo alcançada através do Teorema de Bayes. Como um exemplo da abordagem Bayesiana, suponha que temos interesse no valor de um parâmetro θ de uma determinada população, e que antes de qualquer informação ser observada é de alguma forma possível afirmar que θ deve assumir um dos valores entre θ_1, θ_1, ..., θ_n e que a probabilidade de o valor ser θ_i é $\pi(\theta_i)$. Suponha também que alguns dados novos são coletados e a probabilidade de observar estes dados é $\pi(dados|\theta_i)$ se de fato $\theta = \theta_i$. Então o Teorema de Bayes afirma que a probabilidade de θ ser igual a θ_i, dado novas observações, é

$$\pi(\theta_i|dados) = \frac{\pi(dados|\theta_i)p(\theta_i)}{\sum_{j=1}^{n}\pi(data|\theta_j)\pi(\theta_j)}, \quad (??)$$

```
##
## SAMPLING FOR MODEL 'matrixModel' NOW (CHAIN 1).
## Chain 1:
## Chain 1: Gradient evaluation took 0.00149 seconds
## Chain 1: 1000 transitions using 10 leapfrog steps per transition would take 14.9 seconds.
## Chain 1: Adjust your expectations accordingly!
## Chain 1:
## Chain 1:
## Chain 1: Iteration:    1 / 2000 [  0%]  (Warmup)
## Chain 1: Iteration:  200 / 2000 [ 10%]  (Warmup)
## Chain 1: Iteration:  400 / 2000 [ 20%]  (Warmup)
## Chain 1: Iteration:  600 / 2000 [ 30%]  (Warmup)
## Chain 1: Iteration:  800 / 2000 [ 40%]  (Warmup)
## Chain 1: Iteration: 1000 / 2000 [ 50%]  (Warmup)
## Chain 1: Iteration: 1001 / 2000 [ 50%]  (Sampling)
## Chain 1: Iteration: 1200 / 2000 [ 60%]  (Sampling)
## Chain 1: Iteration: 1400 / 2000 [ 70%]  (Sampling)
## Chain 1: Iteration: 1600 / 2000 [ 80%]  (Sampling)
## Chain 1: Iteration: 1800 / 2000 [ 90%]  (Sampling)
## Chain 1: Iteration: 2000 / 2000 [100%]  (Sampling)
## Chain 1:
## Chain 1:  Elapsed Time: 28.9122 seconds (Warm-up)
## Chain 1:                16.8265 seconds (Sampling)
## Chain 1:                45.7386 seconds (Total)
## Chain 1:
##
## SAMPLING FOR MODEL 'matrixModel' NOW (CHAIN 2).
## Chain 2:
## Chain 2: Gradient evaluation took 0.000298 seconds
## Chain 2: 1000 transitions using 10 leapfrog steps per transition would take 2.98 seconds.
## Chain 2: Adjust your expectations accordingly!
## Chain 2:
## Chain 2:
## Chain 2: Iteration:    1 / 2000 [  0%]  (Warmup)
## Chain 2: Iteration:  200 / 2000 [ 10%]  (Warmup)
## Chain 2: Iteration:  400 / 2000 [ 20%]  (Warmup)
## Chain 2: Iteration:  600 / 2000 [ 30%]  (Warmup)
```

```
## Chain 2: Iteration:  800 / 2000 [ 40%]  (Warmup)
## Chain 2: Iteration: 1000 / 2000 [ 50%]  (Warmup)
## Chain 2: Iteration: 1001 / 2000 [ 50%]  (Sampling)
## Chain 2: Iteration: 1200 / 2000 [ 60%]  (Sampling)
## Chain 2: Iteration: 1400 / 2000 [ 70%]  (Sampling)
## Chain 2: Iteration: 1600 / 2000 [ 80%]  (Sampling)
## Chain 2: Iteration: 1800 / 2000 [ 90%]  (Sampling)
## Chain 2: Iteration: 2000 / 2000 [100%]  (Sampling)
## Chain 2:
## Chain 2:   Elapsed Time: 31.6098 seconds (Warm-up)
## Chain 2:                 17.1195 seconds (Sampling)
## Chain 2:                 48.7293 seconds (Total)
## Chain 2:
##
## SAMPLING FOR MODEL 'matrixModel' NOW (CHAIN 3).
## Chain 3:
## Chain 3: Gradient evaluation took 0.000365 seconds
## Chain 3: 1000 transitions using 10 leapfrog steps per transition would take 3.65 seconds.
## Chain 3: Adjust your expectations accordingly!
## Chain 3:
## Chain 3:
## Chain 3: Iteration:    1 / 2000 [  0%]  (Warmup)
## Chain 3: Iteration:  200 / 2000 [ 10%]  (Warmup)
## Chain 3: Iteration:  400 / 2000 [ 20%]  (Warmup)
## Chain 3: Iteration:  600 / 2000 [ 30%]  (Warmup)
## Chain 3: Iteration:  800 / 2000 [ 40%]  (Warmup)
## Chain 3: Iteration: 1000 / 2000 [ 50%]  (Warmup)
## Chain 3: Iteration: 1001 / 2000 [ 50%]  (Sampling)
## Chain 3: Iteration: 1200 / 2000 [ 60%]  (Sampling)
## Chain 3: Iteration: 1400 / 2000 [ 70%]  (Sampling)
## Chain 3: Iteration: 1600 / 2000 [ 80%]  (Sampling)
## Chain 3: Iteration: 1800 / 2000 [ 90%]  (Sampling)
## Chain 3: Iteration: 2000 / 2000 [100%]  (Sampling)
## Chain 3:
## Chain 3:   Elapsed Time: 29.797 seconds (Warm-up)
## Chain 3:                 17.972 seconds (Sampling)
## Chain 3:                 47.769 seconds (Total)
## Chain 3:
##
## SAMPLING FOR MODEL 'matrixModel' NOW (CHAIN 4).
## Chain 4:
## Chain 4: Gradient evaluation took 0.000276 seconds
## Chain 4: 1000 transitions using 10 leapfrog steps per transition would take 2.76 seconds.
## Chain 4: Adjust your expectations accordingly!
## Chain 4:
## Chain 4:
## Chain 4: Iteration:    1 / 2000 [  0%]  (Warmup)
## Chain 4: Iteration:  200 / 2000 [ 10%]  (Warmup)
## Chain 4: Iteration:  400 / 2000 [ 20%]  (Warmup)
```

```
## Chain 4: Iteration:  600 / 2000 [ 30%]  (Warmup)
## Chain 4: Iteration:  800 / 2000 [ 40%]  (Warmup)
## Chain 4: Iteration: 1000 / 2000 [ 50%]  (Warmup)
## Chain 4: Iteration: 1001 / 2000 [ 50%]  (Sampling)
## Chain 4: Iteration: 1200 / 2000 [ 60%]  (Sampling)
## Chain 4: Iteration: 1400 / 2000 [ 70%]  (Sampling)
## Chain 4: Iteration: 1600 / 2000 [ 80%]  (Sampling)
## Chain 4: Iteration: 1800 / 2000 [ 90%]  (Sampling)
## Chain 4: Iteration: 2000 / 2000 [100%]  (Sampling)
## Chain 4:
## Chain 4:  Elapsed Time: 34.9958 seconds (Warm-up)
## Chain 4:                16.8582 seconds (Sampling)
## Chain 4:                51.854 seconds (Total)
## Chain 4:
```

Manly, Bryan F. J. 1997. *Randomization, Bootstrap and Monte Carlo Methods in Biology*. Chapman & Hall.