

Example_CVlm.R

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log-transformation makes
more like 

```
library(DAAG)
```

```
## Loading required package: lattice
```

```
CVlm(data=nihills, form.lm = formula(log(time) ~ log(climb) + log(dist)),  
      plotit="Observed")
```

```
## Analysis of Variance Table
```

```
##
```

```
## Response: log(time)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
log(climb)	1	5.94	5.94	1013	< 2e-16 ***
log(dist)	1	0.89	0.89	152	8.2e-11 ***
Residuals	20	0.12	0.01		

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## Warning in CVlm(data = nihills, form.lm = formula(log(time) ~ log(climb) + :
```

```
##
```

```
## As there is >1 explanatory variable, cross-validation  
## predicted values for a fold are not a linear function  
## of corresponding overall predicted values. Lines that  
## are shown for the different folds are approximate
```

transformed variables
(log-transformed)

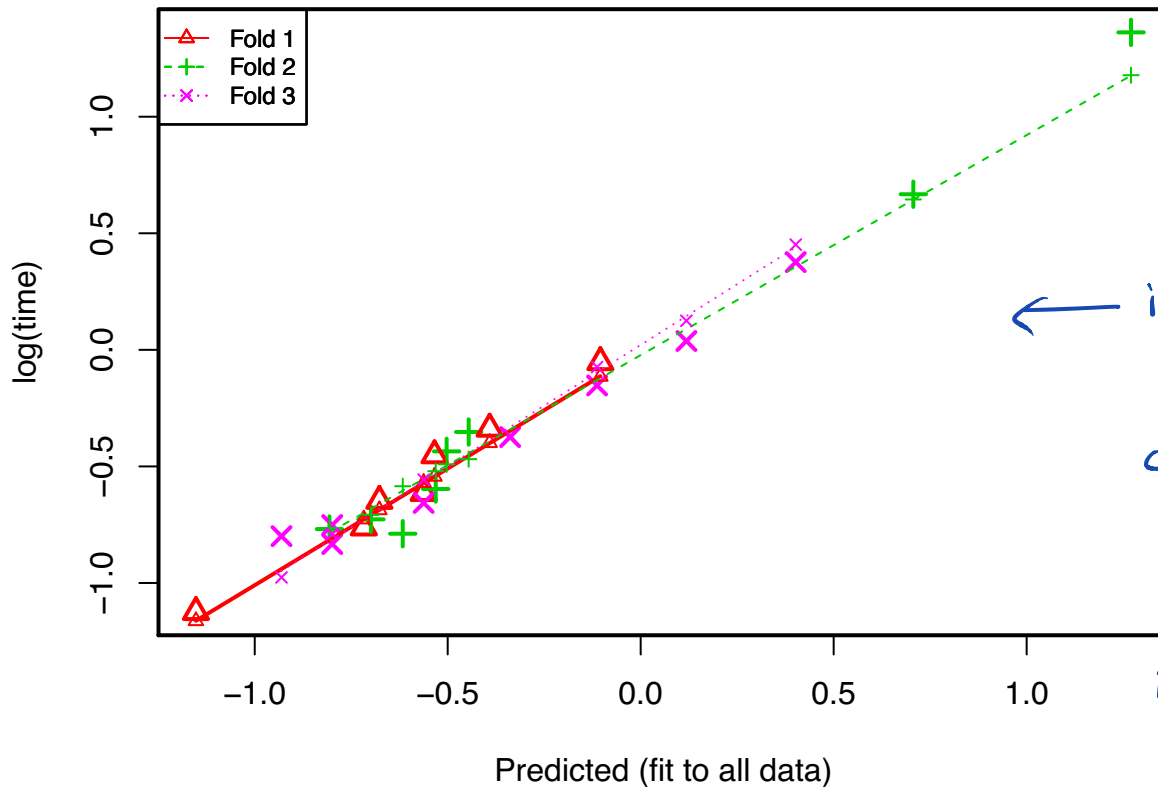
example from the CVlm() function

standard ANOVA table

residual variance for complete data $\rightarrow \frac{\text{Sum Sq}}{\text{Df}}$

just a warning that
you have more than
one predictor and that
the resulting crossvalidation
is thus based on a set of
additive effects.

Small symbols show cross-validation predicted values



inspection:
Lines seem very similar

conclusion:
no important visual difference between the three folds

implication:
the model

seems to fit more-or-less equally to the three folds.
Here, evidence for a useful model

```
##
## fold 1
## Observations in test set: 7
##      Slieve Gullion McVeigh Classic   Rocky Slieve Donard
## Predicted      -0.7174      -0.5623 -0.6770      -0.1044
## cvpred         -0.7264      -0.5702 -0.6870      -0.1147
## log(time)      -0.7621      -0.6141 -0.6481      -0.0530
## CV residual    -0.0358      -0.0439  0.0389      0.0616
##
##      Scrabo Hill Race Slieve Gullion BARF Turkey Trot
## Predicted      -1.1523      -0.534      -0.3913
## cvpred         -1.1627      -0.543      -0.3989
## log(time)      -1.1248      -0.452      -0.3382
## CV residual     0.0379      0.091      0.0607
##
## Sum of squares = 0.02   Mean square = 0   n = 7
##
## fold 2
## Observations in test set: 8
##      Glenariff Mountain Tollymore Mountain Slieve Martin
## Predicted      -0.446      -0.6989      -0.5310
## cvpred         -0.469      -0.7078      -0.5204
## log(time)      -0.352      -0.7270      -0.5968
## CV residual     0.117      -0.0192      -0.0764
##
##      Moughanmore Annalong Horseshoe Loughshannagh Horseshoe
## Predicted      -0.80639      0.7063      -0.5028
## cvpred         -0.76424      0.6451      -0.4910
## log(time)      -0.76871      0.6674      -0.4355
```

residual variance for fold # 1

```

## CV residual      -0.00447          0.0223          0.0555
##               Meelbeg Meelmore Seven Sevens
## Predicted        -0.616          1.270
## cvpred           -0.585          1.178
## log(time)        -0.789          1.362
## CV residual      -0.204          0.184
##
## Sum of squares = 0.1    Mean square = 0.01    n = 8
##
## fold 3
## Observations in test set: 8
##               Binevenagh Donard & Commedagh Hen & Cock Monument Race
## Predicted        -0.1129          0.1184          -0.931          -0.799
## cvpred           -0.0738          0.1249          -0.976          -0.790
## log(time)        -0.1528          0.0379          -0.799          -0.751
## CV residual      -0.0789          -0.0870          0.177          0.039
##
##               Donard Forest Flagstaff to Carling Slieve Bearnagh
## Predicted        -0.5623          0.402          -0.33834
## cvpred           -0.5568          0.451          -0.36764
## log(time)        -0.6566          0.376          -0.37429
## CV residual      -0.0998          -0.075          -0.00665
##
##               Lurig Challenge
## Predicted        -0.7992
## cvpred           -0.7905
## log(time)        -0.8330
## CV residual      -0.0426
##
## Sum of squares = 0.06    Mean square = 0.01    n = 8
##
## Overall (Sum over all 8 folds)
##               ms
## 0.00803

```

residual variance for fold #2

residual variance for fold #3

overall residual variance for cross validation

observed data	fold 1	fold 2	fold 3	fold overall
0.01	0	0.01	0.01	0.00803
	very similar			
	average (not rounded)			

very similar!

Here more evidence for a useful, well-fitted model that can be generalized to the population