

bild: a
package for
Binary
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bild: a package for Blnary Longitudinal Data

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What is bild?

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- an R package for Binary Longitudinal Data.
- parametric models with exact likelihood MLE.
- allows serial dependence and random effects.
- graphical analysis.
- allows missing data (with some restrictions).
- R code interfaced to some Fortran routines.
- S4 methods.

Marginal Model

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Let y_{it} ($t = 1, \dots, T_i$) $\in \{0, 1\}$ be the response value at time t from subject i ($i = 1, \dots, n$). The parameter of interest is the marginal probability of success, that is related to the covariates via a logistic regression model,

$$\text{logit } P(Y_{it} = 1) = \text{logit}(\theta_{it}) = x_{it}^\top \beta \quad (1)$$

- Y_{it} its generating random variable whose mean values is $\theta_{it} = P(Y_{it} = 1)$.
- x_{it} a set of p covariates associated to each observation time and each subject.
- β is a p vector of unknown parameters.

Structure Dependence

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Taking into account that successive observations from the same individual cannot be assumed to be independent, the model considered for serial dependence is of Markovian type of first order (ψ_1) or of second order (ψ_2).

$$OR(Y_{t-1}, Y_{t-2}) = \psi_1 = OR(Y_{t-1}, Y_t)$$

$$OR(Y_{t-2}, Y_t | Y_{t-1} = 0) = \psi_2 = OR(Y_{t-2}, Y_t | Y_{t-1} = 1)$$

Random intercept model

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This package allows individual random effects by adding the component $b_i \sim N(0, \sigma^2)$ in (1) leading to the logistic model with random intercept

$$\text{logit } P(Y_{it} = 1) = x_{it}^\top \beta + b_i, \quad (2)$$

the b_i 's are assumed to be independent from each other.

- $\omega = \log \sigma^2$ for numerical convenience and to improve accuracy of the asymptotic approximation to the distribution of MLEs.
- Integrals are computed using adaptive Gaussian quadrature.

function bild()

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```
bild(formula=formula(data), data, time, id, subSET, aggregate=  
      FALSE, start=NULL, trace=FALSE, dependence="ind", method=  
      "BFGS", control=bildControl(), integrate=bildIntegrate())
```

bild() takes the following arguments:

- **formula** a description of the model to be fitted of the form response predictors
- **data** a data frame containing the variables in the formula. NA values are allowed.
- **time** a string that matches the name of the time variable in data.
- **id** a string that matches the name of the id variable in data.
- **subSET** an optional expression indicating the subset of the rows of data that should be used in the fit.

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- **aggregate** a string that permits the user identify the factor to be used in the plot-methods.
- **start** a vector of initial values for the nuisance parameters of the likelihood.
- **trace** logical flag: if TRUE, details of the nonlinear optimization are printed.
- **dependence** expression stating which dependence structure should be used in the fit.
- **method** the method to be used in the optimization process for function optim().
- **control** a list of algorithmic constants for the optimizer optim.
- **integrate** a list of algorithmic constants for the computation of a definite integral using a FORTRAN-77 subroutine.

selecting the **dependence** structure

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`bild()` allows the following choices for the serial dependence structure:

- independence (**dependence="ind"**)
- first order Markov Chain (**dependence="MC1"**)
- second order Markov Chain (**dependence="MC2"**)
- first order Markov Chain with random intercept
(**dependence="MC1R"**)
- second order Markov Chain with random intercept
(**dependence="MC2R"**)

controlling bild() fitting

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`bildControl()` and `bildIntegrate()` are two auxiliary function as user interface for `bild()` fitting having the following arguments:

- `bildControl(maxit=100, abstol=1e-006,
reltol=1e-006)`
- `bildIntegrate(li=-4, ls=4,
epsabs=.Machine$double.eps^.25,
epsrel=.Machine$double.eps^.25,
limit=100, key=6, lig=-4, lsg=4)`

Locust data

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Observations on locomotory behaviour of 24 locusts observed at 161 time points: moving vs non-moving.

```
> str(locust)
'data.frame': 3864 obs. of 5 variables:
 $ id : int 1 1 1 1 1 1 1 1 1 ...
 $ move: num 0 0 0 0 0 0 0 0 0 ...
 $ sex : Factor w/ 2 levels "0","1": 2 2 2 2 2 2 2 2 2 ...
 $ time: num 0.00833 0.01667 0.025 0.03333 0.04167 ...
 $ feed: Factor w/ 2 levels "0","1": 2 2 2 2 2 2 2 2 2 ...
```

function `bild()` to fit the model

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the function `bild()` is called to fit the model

$$\text{logit}(\theta_{it}^b) = \beta_0 + b_i + \beta_1 \text{time} + \beta_2 \text{time}^2 + \beta_3 \text{feed} + \beta_4 \text{time} \times \text{feed} + \beta_5 \text{time}^2 \times \text{feed}$$

using a dependence structure MC2R

```
> Integ <- bildIntegrate(li=-2.5, ls=2.5, lig=-2.5, lsg=2.5)

> locust2r <- bild(move ~ (time + I(time^2))*feed, data=locust,
+   aggregate=feed, dependence="MC2R", integrate=Integ)
```

summary

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```
> summary(locust2r)
Call: bild(formula=move ~ (time + I(time^2))*feed, data=locust,
           aggregate=feed, dependence="MC2R", integrate=Integ)
```

Number of profiles in the dataset: 24

Number of profiles used in the fit: 24

Log likelihood: -1495.802

AIC: 3009.603

Coefficients:

	Label	Value	Std. Error	t value	p-value
(Intercept)	1	-1.8145720	0.3680344	-4.930	0.000001
time	2	5.3239922	0.7594622	7.010	0.000000
I(time^2)	3	-2.9392803	0.5315684	-5.529	0.000000
feed1	4	-2.3050095	0.6616485	-3.484	0.000494
time:feed1	5	-6.0737691	1.5647952	-3.882	0.000104
I(time^2):feed1	6	5.0664871	1.0435033	4.855	0.000001
log.psi1	7	0.9811151	0.1125461	8.717	0.000000
log.psi2	8	0.5583951	0.1030314	5.420	0.000000

```
Random effect (omega):          Value        Std. Error
                           -0.002794812  0.350137839
```

Message: 0

probability plot

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```
> plot(locust2r, which = 5, ylab = "probability of locomoting")
```

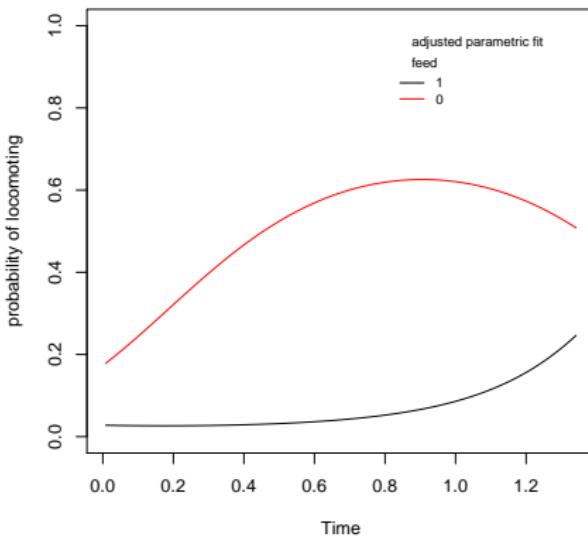


Figure 1: probability of locomoting of locust data for MC2R

residual plots

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The residual analysis can be summarized using `plot-methods` setting `which=1` for Residuals vs Fitted, `which=2` for Residuals vs Time, `which=3` for ACF residuals and `which=4` for PACF residuals

```
> par(mfrow = c(2, 2))
> plot(locust2r, which = 1)
> plot(locust2r, which = 2)
> plot(locust2r, which = 3)
> plot(locust2r, which = 4)
> par(mfrow = c(1, 1))
```

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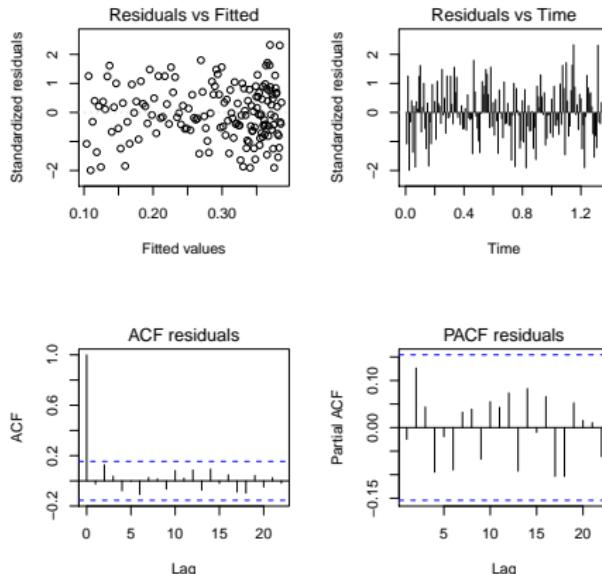


Figure 2: residual plots of locust data for MC2R

individual mean profiles

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The individual mean profile to all subjects (by default) or to a subset (`subSET=`) is obtained choosing `which=6` in `plot-methods`. The identification of the subjects is also allowed by setting `ident=TRUE`. These options are only available for random intercept models.

```
> par(mfrow = c(1, 2))
> plot(locust2r, which = 6, ylab = "probability of locomoting",
       main = "Feed & Unfeed groups")
> plot(locust2r, which = 6, ident = TRUE, subSET = feed == "0",
       ylab = "probability of locomoting", main = "Unfeed group")
> par(mfrow = c(1, 1))
```

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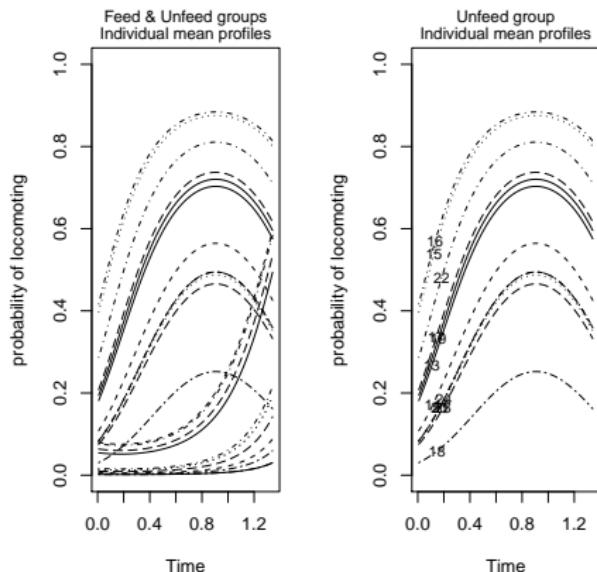


Figure 3: individual mean profiles of locust data for MC2R

References

-  Azzalini, A. (1994). Logistic Regression for Autocorrelated Data with Application to Repeated Measures. *Biometrika*, 81, 767-775. Amendment: vol. 84 (1997), 989.
-  Gonçalves, M. H. and Azzalini, A. (2008). Using Markov chains for marginal modelling of binary longitudinal data in an exact likelihood approach. *Metron*, LXVI, n.2, 157-181.
-  Gonçalves, M. H., Cabral, M. S., and Azzalini, A. (2010). *bild: a package for Blnary Longitudinal Data*, Version 1.0. URL: <http://CRAN.R-project.org/package=bild>

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