



Programa nIFIT - Ajuste não linear

José Maurício Schneedorf Ferreira da Silva
Depto. de Bioquímica, Instituto de Ciências Biomédicas
Universidade Federal de Alfenas - UNIFAL-MG
Alfenas, MG, Brasil

[Link para acesso](#) no portal hpcalc.org:

```
« → x1 y1 w1 ↓↑f ↓↑p ↓↑v it
« 1. it
  FOR k k 1. DISP x1 SIZE → n
    « ↓↑f ↓↑p ↓↑v ↓↑s 4. →LIST DUP 'fields' STO EVAL DROP DUP SIZE → m
    « 3. →LIST { ↓↑f ↓↑p ↓↑v } STO ↓↑v ↓↑p STO ↓↑p 1.
      « ↓↑f SWAP -3. CF DUP → x ↑↓
      «
        IF DUP TYPE 9. ==
        THEN x SHOW
        END x { ↑↓ } + ↓MATCH DROP '↑↓' DUP STO ↑↓ ♂ x '↑↓' STO EVAL
      »
    » DOLIST 'da' STO y1 x1 2.
    « 'x' STO ↓↑f EVAL -
    » DOLIST OBJ→ 1. 2. →LIST →ARRY 1. n
    FOR i x1 i GET 'x' STO 1. m
      FOR j da j GET EVAL
      NEXT
    NEXT { n m } →ARRY w1 DUP SIZE SWAP OBJ→ →ARRY SWAP DIAG→
    IF w1 ELIST NOT
    THEN 1. SF
    END → ym xm wm
    « xm TRN wm * xm * INV DUP xm TRN * wm * ym * DUP m 1. →LIST RDM 3.
    ROLLD ym xm ROT * - DUP TRN SWAP * 1. GET n m - /
    IF 1. FS?C
    THEN SWAP OVER * SWAP
    END √ 'x' PURGE ROT OBJ→ 1. GET →LIST ↓↑v ADD '↓↑v' STO '↓↑s' STO
    DUP →DIAG OBJ→ 1. GET →LIST √ 'sig' STO 'cm' STO ↓↑v ↓↑p STO
  »
»
»
NEXT cm 'cov' →TAG ↓↑p 'pars' →TAG ↓↑v 'vals' →TAG sig 'sd' →TAG ↓↑s SQ x1
SIZE 2. - * 'chiSQ' →TAG ERASE SCATTER x1
« MIN
» STREAM ABS NEG 1.1 * x1
« MAX
» STREAM ABS 1.1 * XRNG 'x' INDEP y1
« MIN
» STREAM y1
« MAX
» STREAM DUP2 - ABS 1.2 * DUP .05 * ROT + ABS 3. ROLLD .15 * - ABS NEG SWAP
YRNG 0. RES DRAX 1. x1 SIZE
FOR q x1 y1 q GET SWAP q GET SWAP R→C PIXON
NEXT ↓↑f STEQ FUNCTION DRAW PICTURE
» { ↓↑s sig cm fields x da ΣDAT ΣPAR PPAR EQ Vm Km } PURGE 1000. 3. BEEP
»
```