Analysis

BATS-Analysis: Set Analysis Parameters

Select dataset file

`cicatiello_et_al.xls`

[Load dataset]

○ **Function type**

- ⦿ Legendre
- ○ Fourier

○ **Smoothness of the profiles**

vi: [ ]

○ **Maximal degree of polynomial**

L: [ ]

Extimation of the noise variance

- ⦿ Standard
- ○ MAD
- ○ Custom

○ **Expected degree of polynomial**

lambda: [ ]

Proportion of DE genes

- ⦿ Universal
- ○ Custom proportion

○ **Tau² interval [Xo, X1]**

Xo: [1E-8]   X1: [80]

Choice of the prior model

- ⦿ Model1 (Delta)
- ○ Model 2 (Inverse gamma)
- ○ Model 3 (Double exponential)

○ **Estimation of the polinomial degree**

- ⦿ Map
- ○ Mean

○ **Test procedure**

- ⦿ Binomial
- ○ Truncated poisson
- ○ Standard odds
- ○ Standard BF
- ○ Full ranked list

○ **Display&Save estimated profiles**

Scale options

- ⦿ Global scale
- ○ Auto scale

Ordered genes profiles to plot

nfirst: [1000]

BATS

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