AHELP for CIAO 3.4 **monte−powell** Context: sherpa

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Synopsis

A Monte Carlo search utilizing the Powell method at each selected point.

Syntax

```
monte-powell  [nloop] [iseed]
```

Description

The MONTE−POWELL method randomly samples the parameter space bounded by the lower and upper limits for each thawed parameter. At each grid point, the POWELL optimization method is used to determine the local fit−statistic minimum. The smallest of all observed minima is then adopted as the global fit−statistic minimum. The advantage of MONTE−POWELL is that it can provide a good sampling of parameter space. This is good for situations where the best−fit parameter values are not easily guessed a priori, and where there is a high probability that false minima would be found if one−shot techniques such as POWELL are used instead. Its disadvantage is that it can be very slow.

Note that MONTE−POWELL is similar in nature to GRID−POWELL; in the latter method, the initial parameter values in each cycle are determined from a grid, rather than being chosen randomly.

The MONTE−POWELL method parameters are a superset of those listed for the POWELL method and the ones listed below.

If the number of thawed parameters is larger than 2, one should increase the value of nloop from its default value. Otherwise the sampling may be too sparse to estimate the global fit−statistic minimum well.

Parameters

name	type	def	min	max
nloop	integer	128	1	16384
iseed	integer	14391	−1.e+20	1.e+20

Detailed Parameter Descriptions

Parameter=nloop `(integer default=128 min=1 max=16384)`

Number of parameter space samples.

Parameter=iseed `(integer default=14391 min=-1.e+20 max=1.e+20)`

Seed for random number generator.

Bugs

See the Sherpa bug pages online for an up−to−date listing of known bugs.

See Also

sherpa

get_method_expr, grid, grid−powell, levenberg−marquardt, method, monte−lm, montecarlo, powell, sigma−rejection, simplex, simul−ann−1, simul−ann−2, simul−pow−1, simul−pow−2, usermethod

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