Documentation: banisterModel.R

Function	`banisterModel()`
File version	1.0
Last updated	6 December 2020
Associated source code file	www.github.com/bsh2/Fitness-Fatigue-Models/tree/docs-and-utilities/software/utilities/banisterModel.R
Dependencies (packages required)	`caret, GA, parallel, foreach, iterators, doParallel, doRNG, deSolve`
Functionality	Simultaneously solve and fit a first-order system of independent differential equations for a set of experimental data. Includes estimation of initial model conditions. Optimisation performed by tuneable genetic algorithm with stochastic local search.
Underlying model: A system of linear first-order differential equations	$$\hat{p}(t) = p^* + k_g g(t) - k_h h(t),$$ $$g'(t) = \omega(t) - \frac{1}{\tau_g} g(t)$$ $$h'(t) = \omega(t) - \frac{1}{\tau_h} h(t)$$ Where: $$g(t) \geq 0, h(t) \geq 0, k_h \geq k_g > 0$$

1. Usage

```
banisterModel(inputData, constraints, doTrace = FALSE, initialWindow = NULL, testHorizon= NULL, expandRate = NULL, doParallel = FALSE, maxIt = 1000, popSize = 120, gaSelection = “gareal_tourSelection”, gaCrossover = “gareal_blxCrossover”, gaMutation = “gareal_rsMutation”, gaElitism = 7.5)
```

2. Arguments

Argument	Required	Category	Default	Details
`inputData`	Yes	Core arg.	`No default`	Data frame. Contains time-series data in sequential order. Three columns in order from left to right: “days”, “performances”, “loads”. Data ordered in equal time steps, controlled by the “days” column (i.e. 1 day). Example dataset available in repository. 0 values used in loads column to represent no training on a given day. `NA` values in performance column to represent no observed measure on a given day.

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Argument	Required	Category	Default	Details
`constraints`	Yes	Core arg.	`No default`	Box constraints for the parameter values. Supplied as a data frame with two columns ("lower", "upper"), each containing non-named numeric values in a specific order. `data.frame("lower" = c(), "upper" = c())` Where order of the values in the lower and upper bound vectors comprising the data frame are as follows: $k_g, k_h, \tau_g, \tau_h, p(0), g(0), h(0)$
`doTrace`	No	Optimisation	`TRUE`	`TRUE/FALSE` argument. Controls whether optimisation output is printed to the console
`initialWindow`	No	Cross-validation	`NULL`	Initial model training window size for out-of-sample walk forward method (expanding window). Supplied as a percentage value (without the % sign). If `NULL`, default will be set to 60% of the data (i.e. `initialWindow = 60`)
`testHorizon`	No	Cross-validation	`NULL`	Walk forward testing size. Supplied as percentage value (without % sign). If `NULL`, default will be set to 20% (i.e. `testHorizon = 20`)
`expandRate`	No	Cross-validation	`NULL`	Walk forward increment rate. Supplied as percentage value (without % sign). If `NULL`, default will be set to 4% (i.e. `expandRate = 4`)
`doParallel`	No	Optimisation	`FALSE`	`TRUE/FALSE` argument. Controls whether the optimisation will be split across available logical nodes.
`maxIt`	No	Optimisation	`1000`	The maximum number of iterations to run before the GA search is halted
`popSize`	No	Optimisation	`120`	The population size

Argument	Required	Category	Default	Details
`gaSelection`	No	Optimisation	`"gareal_tourSelection"`	The selection function (i.e. function that generates a new population of individuals from the current population probablistically according to individual fitness). See GA package documentation for other options
`gaCrossover`	No	Optimisation	`"gareal_blxCrossover"`	The crossover function (i.e. a function which forms offsprings by combining part of the genetic information from their parents). See GA package documentation for other options
`gaMutation`	No	Optimisation	`"gareal_rsMutation"`	The mutation function (i.e. a function which randomly alters the values of some genes in a parent chromosome). See GA package documentation for other options
`gaElitism`	No	Optimisation	`7.5`	The number of best fitness individuals to survive at each generation. By default top 7.5% will survive at each iteration.

3. Value (output)

Returns an object of class list, with the following slots

Slot	Name	Type	Relates to	Contains
1	`mainSet`	List	Primary fitted model	**Further objects:** Summary information (`summary`), parameters found (`parameters`), model fit metrics (`metrics`), model prediction series (`predictions`), raw optimisation data (`optim`)
2	`crossValidation`	List	Cross validation slice data	**Further objects**: Summary information (`summary`), model fit metrics across the CV slices (`metrics`), parameter values across slices (`parameters`), prediction series across slices (`predictions`), raw slice data (`raw`)