

# Package ‘panelPomp’

April 3, 2025

**Type** Package

**Title** Inference for Panel Partially Observed Markov Processes

**Version** 1.6.0.0

**Description** Data analysis based on panel partially-observed Markov process (PanelPOMP) models. To implement such models, simulate them and fit them to panel data, 'panelPomp' extends some of the facilities provided for time series data by the 'pomp' package. Implemented methods include filtering (panel particle filtering) and maximum likelihood estimation (Panel Iterated Filtering) as proposed in Breto, Ionides and King (2020) ``Panel Data Analysis via Mechanistic Models" <doi:10.1080/01621459.2019.1604367>.

**License** GPL-3

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'get\_col\_row.R' 'panel\_loglik.R' 'panel\_logmeanexp.R'  
'panelPomp.R' 'panelPomp\_methods.R' 'params.R' 'pfilter.R'  
'pfilter\_methods.R' 'mif2.R' 'mif2\_methods.R' 'panelGompertz.R'  
'panelGompertzLikelihood.R' 'panelMeasles.R'  
'panelRandomWalk.R' 'panel\_designs.R' 'plot.R' 'simulate.R'  
'twentycities.R' 'uk\_measles.R'

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panelPomp-package	<i>Inference for PanelPOMPs (Panel Partially Observed Markov Processes)</i>
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## Description

The **panelPomp** package provides facilities for inference on panel data using panel partially-observed Markov process (PANELPOMP) models. To do so, it relies on and extends a number of facilities that the **pomp** package provides for inference on time series data using partially-observed Markov process (POMP) models.

The **panelPomp** package extends to panel data some of the capabilities of the **pomp** package to fit nonlinear, non-Gaussian dynamic models. This is done accomodating both fixed and random effects. Currently, the focus is on likelihood-based approaches. In addition to these likelihood-based tools, **panelPomp** also provides a framework under which alternative statistical methods for PANELPOMP models can be developed (very much like **pomp** provides a platform upon which statistical inference methods for POMP models can be implemented).

## Data analysis using panelPomp

The first step in using **panelPomp** is to encode one's model(s) and data in objects of class `panelPomp`. One does this via a call to the `panelPomp` constructor function.

**panelPomp** version 1.6.0.0 provides algorithms for

1. particle filtering of panel data (AKA sequential Monte Carlo or sequential importance sampling), as proposed in Bretó, Ionides and King (2020). This reference provides the fundamental theoretical support for the averaging of Monte Carlo replicates of panel unit likelihoods as implemented in **panelPomp**; see `pfilter`
2. the panel iterated filtering method of Bretó, Ionides and King (2020). This reference provides the fundamental theoretical support for the extensions of the iterated filtering ideas of Ionides et al. (2006, 2011, 2015) to panel data as implemented in **panelPomp**; see `mif2`

The package also provides various tools for handling and extracting information on models and data.

## Extending the pomp platform for developing inference tools

**panelPomp** extends to panel data the general interface to the components of POMP models provided by **pomp**. In doing so, it contributes to the goal of the **pomp** project of facilitating the development of new algorithms in an environment where they can be tested and compared on a growing body of models and datasets.

## Comments, bug reports, and requests

Contributions are welcome, as are suggestions for improvement, feature requests, and bug reports. Please submit these via the [panelPomp issues page](#). We particularly welcome minimal working examples displaying uninformative, misleading or inaccurate error messages. We also welcome suggestions for clarifying obscure passages in the documentation. Help requests are welcome, but please consider before sending requests whether they are regarding the use of **panelPomp** or that of **pomp**. For help with **pomp**, please visit [pomp's FAQ](#).

## Documentation

Examples are provided via the `contacts()`, `panelGompertz()` and `panelRandomWalk()` functions.

## License

**panelPomp** is provided under the GPL-3 License.

## Author(s)

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## References

Bretó, C., Ionides, E. L. and King, A. A. (2020) Panel Data Analysis via Mechanistic Models. *Journal of the American Statistical Association*, **115**(531), 1178–1188. doi:10.1080/01621459.2019.1604367

## See Also

[pomp package](#), [panelPomp](#)

---

.modifyOther *Internal function for modifying pparamArray in Mif2*

---

## Description

Internal function for modifying pparamArray in Mif2

## Usage

```
.modifyOther(x, snames, indices, unit)
```

## Arguments

x	pparamArray in mif2 internal
snames	names of parameters to update
indices	indices that are the output of a mif2 call to pomp
unit	unit in the unit loop

---

.modifySelf *Internal function for modifying pparamArray in Mif2*

---

## Description

Internal function for modifying pparamArray in Mif2

## Usage

```
.modifySelf(x, snames, M, unit)
```

## Arguments

x	pparamArray in mif2 internal
snames	names of parameters to update
M	Matrix of replacement values
unit	unit in the unit loop

as

*Coercing panelPomp objects as list, pompList or data.frame***Description**

When coercing to a `data.frame`, it coerces a `panelPomp` into a `data.frame`, assuming units share common variable names.

When coercing to a `list`, it extracts the `unit_objects` slot of `panelPomp` objects and attaches associated parameters.

When coercing to a `pompList`, it extracts the `unit_objects` slot of `panelPomp` objects and attaches associated parameters, converting the resulting list to a `pompList` to help the assignment of `pomp` methods.

**Value**

An object of class matching that specified in the second argument (`to=`).

**Author(s)**

Carles Bretó

**See Also**

Other `panelPomp` methods: [panelPomp\\_methods](#)

---

`coef<- , pfilterd.ppomp-method`

*Modifying parameters of filtered objects*

---

**Description**

The setter functions for parameters of `pfilterd.ppomp` objects do not allow users to set parameters of `panelPomp` objects that have been filtered. This is done to avoid the possibility of having parameter values in an object that do not match other attributes of a filtered object to be saved together.

The setter functions for parameters of `pfilterd.ppomp` objects do not allow users to set parameters of `panelPomp` objects that have been filtered. This is done to avoid the possibility of having parameter values in an object that do not match other attributes of a filtered object to be saved together.

The setter functions for parameters of `pfilterd.ppomp` objects do not allow users to set parameters of `panelPomp` objects that have been filtered. This is done to avoid the possibility of having parameter values in an object that do not match other attributes of a filtered object to be saved together.

**Usage**

```
## S4 replacement method for signature 'pfilterd.ppomp'
coef(object, ...) <- value

## S4 replacement method for signature 'pfilterd.ppomp'
shared(object) <- value

## S4 replacement method for signature 'pfilterd.ppomp'
specific(object) <- value
```

**Arguments**

object	pfilterd.ppomp object
...	additional arguments.
value	New parameter value. This function does not allow users to set this value.

---

 contacts

---

*Contacts model*


---

**Description**

A panel model for dynamic variation in sexual contacts, with data from Vittinghof et al (1999). The model was developed by Romero-Severson et al (2015) and discussed by Bretó et al (2020).

**Usage**

```
contacts(
  params = c(mu_X = 1.75, sigma_X = 2.67, mu_D = 3.81, sigma_D = 4.42, mu_R = 0.04,
    sigma_R = 0, alpha = 0.9)
)
```

**Arguments**

params	parameter vector.
--------	-------------------

**Value**

A panelPomp object.

**Author(s)**

Edward L. Ionides

## References

- Bretó, C., Ionides, E. L. and King, A. A. (2020) Panel Data Analysis via Mechanistic Models. *Journal of the American Statistical Association*, **115**(531), 1178–1188. doi:10.1080/01621459.2019.1604367
- Romero-Severson, E.O., Volz, E., Koopman, J.S., Leitner, T. and Ionides, E.L. (2015) Dynamic variation in sexual contact rates in a cohort of HIV-negative gay men. *American journal of epidemiology*, **182**(3), 255–262. doi:10.1093/aje/kwv044
- Vittinghoff, E., Douglas, J., Judon, F., McKiman, D., MacQueen, K. and Buchinder, S.P. (1999) Per-contact risk of human immunodeficiency virus transmission between male sexual partners. *American journal of epidemiology*, **150**(3), 306–311. doi:10.1093/oxfordjournals.aje.a010003

## See Also

Other panelPomp examples: [panelGompertz\(\)](#), [panelMeasles\(\)](#), [panelRandomWalk\(\)](#)

## Examples

```
contacts()
```

---

```
get_dim
```

---

*Get single column or row without dropping names*

---

## Description

Subset matrix dropping dimension but without dropping dimname (as done by `[` by default).

## Usage

```
get_col(matrix, rows, col)
```

```
get_row(matrix, row, cols)
```

## Arguments

- |                     |  |
|---------------------|--|
| <code>matrix</code> | matrix.  |
| <code>rows</code>   | numeric; rows to subset; like with `[`, this argument can be left empty to designate all rows.       |
| <code>col</code>    | integer; single column to subset.  |
| <code>row</code>    | integer; single row to subset.   |
| <code>cols</code>   | numeric; columns to subset; like with `[`, this argument can be left empty to designate all columns. |

## Value

A named vector object.

**Author(s)**

Carles Bretó

**Examples**

```
m <- matrix(NA,dimnames=list('r1','c1'))
m[1,1] # = NA; R removes both names
get_col(m,rows=1,col=1) # = c(r1=NA) keeps colname
get_row(m,row=1,cols=1) # = c(c1=NA) keeps rowname
```

---

mif2

*PIF: Panel iterated filtering*


---

**Description**

Tools for applying iterated filtering algorithms to panel data. The panel iterated filtering of Bretó et al. (2020) extends to panel models the improved iterated filtering algorithm (Ionides et al., 2015) for estimating parameters of a partially observed Markov process. Iterated filtering algorithms rely on extending a partially observed Markov process model of interest by introducing random perturbations to the model parameters. The space where the original parameters live is then explored at each iteration by running a particle filter. Convergence to a maximum likelihood estimate has been established for appropriately constructed procedures that iterate this search over the parameter space while diminishing the intensity of perturbations (Ionides et al. 2006, 2011, 2015).

**Usage**

```
## S4 method for signature 'panelPomp'
mif2(
  data,
  Nmif = 1,
  shared.start,
  specific.start,
  start,
  Np,
  rw.sd,
  cooling.type = c("geometric", "hyperbolic"),
  cooling.fraction.50,
  block = FALSE,
  verbose = getOption("verbose"),
  ...
)

## S4 method for signature 'mif2d.ppomp'
mif2(
  data,
  Nmif,
  shared.start,
```



```

    specific.start,
    start,
    Np,
    rw.sd,
    cooling.type,
    cooling.fraction.50,
    block,
    ...
)

## S4 method for signature 'mif2d.pmpomp'
traces(object, pars, ...)

```

### Arguments

<code>data</code>	An object of class <code>panelPomp</code> or inheriting class.
<code>Nmif</code>	The number of filtering iterations to perform.
<code>shared.start</code>	named numerical vector; the starting guess of the shared parameters.
<code>specific.start</code>	matrix with row parameter names and column unit names; the starting guess of the specific parameters.
<code>start</code>	A named numeric vector of parameters at which to start the IF2 procedure.
<code>Np</code>	the number of particles to use. This may be specified as a single positive integer, in which case the same number of particles will be used at each timestep. Alternatively, if one wishes the number of particles to vary across timesteps, one may specify <code>Np</code> either as a vector of positive integers of length <code>length(time(object, t0=TRUE))</code> or as a function taking a positive integer argument. In the latter case, <code>Np(k)</code> must be a single positive integer, representing the number of particles to be used at the $k$ -th timestep: <code>Np(0)</code> is the number of particles to use going from <code>timezero(object)</code> to <code>time(object)[1]</code> , <code>Np(1)</code> , from <code>timezero(object)</code> to <code>time(object)[1]</code> , and so on, while when <code>T=length(time(object))</code> , <code>Np(T)</code> is the number of particles to sample at the end of the time-series.
<code>rw.sd</code>	An unevaluated expression of the form <code>quote(rw.sd())</code> to be used for all panel units. If a list of such expressions of the same length as the <code>object</code> argument is provided, each list element will be used for the corresponding panel unit.
<code>cooling.type, cooling.fraction.50</code>	specifications for the cooling schedule, i.e., the manner and rate with which the intensity of the parameter perturbations is reduced with successive filtering iterations. <code>cooling.type</code> specifies the nature of the cooling schedule. See below (under “Specifying the perturbations”) for more detail.
<code>block</code>	A logical variable determining whether to carry out block resampling of unit-specific parameters.
<code>verbose</code>	logical; if TRUE, diagnostic messages will be printed to the console.
<code>...</code>	....
<code>object</code>	an object resulting from the application of IF2 (i.e., of class <code>mif2d.pmpomp</code> )
<code>pars</code>	names of parameters

**Value**

`mif2()` returns an object of class `mif2d.ppomp`.

`traces()` returns a matrix with estimated parameter values at different iterations of the IF2 algorithm in the natural scale. The default is to return values for all parameters but a subset of parameters can be passed via the optional argument `pars`.

**Author(s)**

Carles Bretó

**References**

Bretó, C., Ionides, E. L. and King, A. A. (2020) Panel Data Analysis via Mechanistic Models. *Journal of the American Statistical Association*, **115**(531), 1178–1188. doi:10.1080/01621459.2019.1604367

Ionides, E. L., Bretó, C. and King, A. A. (2006) Inference for nonlinear dynamical systems. *Proceedings of the National Academy of Sciences*, **103**(49), 18438–18443. doi:10.1073/pnas.0603181103

Ionides, E. L., Bhadra, A., Atchadé, Y. and King, A. A. (2011) Iterated filtering. *Annals of Statistics*, **39**(3), 1776–1802. doi:10.1214/11AOS886

Ionides, E. L., Nguyen, D., Atchadé, Y., Stoev, S. and King, A. A. (2015) Inference via iterated, perturbed Bayes maps. *Proceedings of the National Academy of Sciences*, **112**(3), 719–724. doi:10.1073/pnas.1410597112

King, A. A., Nguyen, D. and Ionides, E. L. (2016) Statistical inference for partially observed Markov processes via the package **pomp**. *Journal of Statistical Software* **69**(12), 1–43. DOI: 10.18637/jss.v069.i12. An updated version of this paper is available on the [package website](#).

**See Also**

**pomp**'s `mif2` at [mif2](#), [panel\\_loglik](#)

Other panelPomp workhorse functions: [panelPomp](#), [panel\\_loglik](#), [pfilter\(\)](#)

**Examples**

```
## start with a panelPomp object
p <- panelRandomWalk()
## specify which parameters to estimate via rw_sd() and how fast to cool
mp <- mif2(p, Np=10, rw.sd=rw_sd(X.0=0.2), cooling.fraction.50=0.5, cooling.type="geometric")
mp
## the object resulting from an initial estimation can be used as a new starting point
mmp <- mif2(mp, Np=10, rw.sd=rw_sd(X.0=0.2), cooling.fraction.50=0.5, cooling.type="geometric")
mmp
## convergence can be partly diagnosed by checking estimates and likelihoods at different iterations
traces(mmp)
```

---

```
panel-designs      #' Create design matrix for panelPomp calculations
```

---

## Description

These functions are useful for generating design matrices for the exploration of parameter space.

## Usage

```
runif_panel_design(  
  lower = numeric(0),  
  upper = numeric(0),  
  nseq,  
  specific_names,  
  unit_names  
)
```

## Arguments

lower, upper	named numeric vectors giving the lower and upper bounds of the ranges, respectively.
nseq	Total number of points requested
specific_names	Character vector containing the names of unit-specific parameters. This argument must be used in conjunction with the argument unit_names; it is used if the search bounds for all unspecified unit-specific parameters are the same.
unit_names	Character vector containing the names of the units of the panel. If not used in conjunction with unit_names this argument is ignored.

## Value

runif\_panel\_design returns a data.frame object with nseq rows. Each row corresponds to a parameter set drawn randomly from a multivariate uniform distribution specified by the lower, upper, specific\_names and unit\_names arguments.

## Author(s)

Jesse Wheeler, Aaron A. King

## Examples

```
runif_panel_design(  
  lower = c('a' = 0, 'b' = 10, 'a[u2]' = 0.5),  
  upper = c('a' = 1, 'b' = 15, 'a[u2]' = 0.75),  
  specific_names = c('a'),  
  unit_names = paste0(rep('u', 5), 1:5),  
  nseq = 10  
)
```

---

panelGompertz	<i>Panel Gompertz model</i>
---------------	-----------------------------

---

### Description

Builds a collection of independent realizations from the Gompertz model.

### Usage

```
panelGompertz(  
  N = 100,  
  U = 50,  
  params = c(K = 1, r = 0.1, sigma = 0.1, tau = 0.1, X.0 = 1),  
  seed = 12345678  
)
```

### Arguments

N	number of observations for each unit.
U	number of units.
params	parameter vector, assuming all units have the same parameters.
seed	passed to the random number generator for simulation.

### Value

A panelPomp object.

### Author(s)

Edward L. Ionides, Carles Bretó

### References

Bretó, C., Ionides, E. L. and King, A. A. (2020) Panel Data Analysis via Mechanistic Models. *Journal of the American Statistical Association*, **115**(531), 1178–1188. doi:10.1080/01621459.2019.1604367

King, A. A., Nguyen, D. and Ionides, E. L. (2016) Statistical inference for partially observed Markov processes via the package **pomp**. *Journal of Statistical Software* **69**(12), 1–43. DOI: 10.18637/jss.v069.i12. An updated version of this paper is available on the [package website](#).

### See Also

Other panelPomp examples: [contacts\(\)](#), [panelMeasles\(\)](#), [panelRandomWalk\(\)](#)

### Examples

```
panelGompertz()
```

---

 panelGompertzLikelihood

*Likelihood for a panel Gompertz model via a Kalman filter*


---

### Description

Evaluates the likelihood function for a panel Gompertz model, using a format convenient for maximization by `optim()` to obtain a maximum likelihood estimate. Specifically, estimated and fixed parameters are supplied by two different arguments.

### Usage

```
panelGompertzLikelihood(x, panelPompObject, params)
```

### Arguments

<code>x</code>	named vector for a subset of parameters, corresponding to those being estimated.
<code>panelPompObject</code>	a panel Gompertz model.
<code>params</code>	named vector containing all the parameters of the panel Gompertz model. Estimated parameters are overwritten by <code>x</code> .

### Value

A numeric value.

### Author(s)

Edward L. Ionides

### Examples

```
pg <- panelGompertz(N=2,U=2)
panelGompertzLikelihood(coef(pg),pg,coef(pg))
```

---

 panelMeasles

*Make a panelPomp model using UK measles data.*


---

### Description

The model is a modified [panelPomp](#) version of the model of He et al. 2010. The model is a stochastic SEIR model that accounts for population demographics in the form of births and deaths. Because of the increased transmission that results from school-aged children entering the susceptible pool once they begin attending classes for the first time, the model includes a birth-cohort effect, which moves a specified fraction of the cohort into the susceptible pool all at once. The model also includes a seasonality in transmission rate that is larger during school terms than it is during holidays.

**Usage**

```
panelMeasles(
  units = c("Bedwellty", "Birmingham", "Bradford", "Bristol", "Cardiff", "Consett",
            "Dalton.in.Furness", "Halesworth", "Hastings", "Hull", "Leeds", "Lees", "Liverpool",
            "London", "Manchester", "Mold", "Northwich", "Nottingham", "Oswestry", "Sheffield"),
  starting_pparams = NULL,
  interp_method = c("shifted_splines", "linear"),
  first_year = 1950,
  last_year = 1963,
  dt = 1/365.25
)
```

**Arguments**

units	Character vector of units in <a href="#">uk_measles</a> to be used in the panel model.
starting_pparams	Parameters in the list format, having shared and specific components. Set to NULL to assign NA values.
interp_method	Method used to interpolate population and births. Possible options are "shifted_splines" and "linear".
first_year	Integer for the first full year of data desired.
last_year	Integer for the last full year of data desired.
dt	Size of the time step.

**Value**

A panelPomp object.

**References**

D. He, E.L. Ionides, and A.A. King. Plug-and-play inference for disease dynamics: measles in large and small populations as a case study. *Journal of the Royal Society Interface* **7**, 271–283, 2010.

**See Also**

Other panelPomp examples: [contacts\(\)](#), [panelGompertz\(\)](#), [panelRandomWalk\(\)](#)

**Examples**

```
panelMeasles(units = "London")
```

---

panelPomp	<i>Constructing panelPomp objects</i>
-----------	---------------------------------------

---

### Description

This function constructs panelPomp objects, representing PanelPOMP models (as defined in Bretó et al., 2020). PanelPOMP models involve multiple units, each of which can in turn be modeled by a POMP model. Such POMP models can be encoded as a list of pomp objects, a cornerstone that the panelPomp function can use to construct the corresponding panelPomp object.

### Usage

```
panelPomp(object, shared, specific, params)
```

### Arguments

object	<p>required; either (i) a list of pomp objects; or (ii) an object of class panelPomp or inheriting class panelPomp.</p> <p>If object is a list of pomps, the list must be named. All these pomps must either have no parameters or have the same parameter names. (This is just a format requirement. pomp codes can ignore any parameter that is irrelevant to any given panel unit.)</p> <p>If object is a panelPomp object, the function allows modifying the shared and unit-specific configuration of object.</p>
shared, specific	<p>optional; these arguments depend on the type of object.</p> <p>If object is a list of pomps, shared must be a numeric vector specifying parameter values shared among panel units. specific must be a matrix with parameter values that are unit-specific with rows naming parameters and columns naming units (these names must match those of object). If no values are specified and object has parameter values, these are set to be all unit-specific.</p> <p>If object is a panelPomp object, these arguments can still be used as described above to modify the parameters of object. Alternatively, the parameter configuration of object can be modified providing only a character shared naming parameters of object that should be shared (with values for parameters not originally shared taken from the unit-specific parameters of the first panel unit of object). shared=NULL sets all parameters as unit-specific.</p>
params	<p>optional; a named numeric vector. In this case, the nature of parameters is determined via a naming convention: names ending in “[unit_name]” are assumed to denote unit-specific parameters; all other names specify shared parameters.</p>

### Value

A panelPomp object.

**Author(s)**

Carles Bretó

**References**

Bretó, C., Ionides, E. L. and King, A. A. (2020) Panel Data Analysis via Mechanistic Models. *Journal of the American Statistical Association*, **115**(531), 1178–1188. doi:10.1080/01621459.2019.1604367

King, A. A., Nguyen, D. and Ionides, E. L. (2016) Statistical inference for partially observed Markov processes via the package **pomp**. *Journal of Statistical Software* **69**(12), 1–43. DOI: 10.18637/jss.v069.i12. An updated version of this paper is available on the [package website](#).

**See Also**

**pomp**'s constructor at [pomp](#)

Other panelPomp workhorse functions: [mif2\(\)](#), [panel\\_loglik](#), [pfilter\(\)](#)

**Examples**

```
## recreate the 'panelRandomWalk()' example
prw <- panelRandomWalk()
prw2 <- panelPomp(unit_objects(prw), params = coef(prw))
identical(prw, prw2) # TRUE
```

---

panelPomp\_methods      *Manipulating panelPomp objects*

---

**Description**

Tools for manipulating panelPomp objects.

**Usage**

```
## S4 method for signature 'panelPomp'
coef(object, format = c("vector", "list"))

## S4 replacement method for signature 'panelPomp'
coef(object, ...) <- value

## S4 method for signature 'panelPomp'
length(x)

## S4 method for signature 'panelPomp'
names(x)

toParamList(value)

## S4 method for signature 'panelPomp'
```



```

print(x, ...)

## S4 method for signature 'panelPomp'
show(object)

## S4 method for signature 'panelPomp'
unit_objects(object)

## S4 method for signature 'panelPomp'
window(x, start, end)

## S4 method for signature 'panelPomp'
x[i]

## S4 method for signature 'panelPomp'
x[[i]]

## S4 method for signature 'panelPomp'
specific(object, ..., format = c("matrix", "vector"))

## S4 replacement method for signature 'panelPomp'
specific(object) <- value

## S4 method for signature 'panelPomp'
shared(object)

## S4 replacement method for signature 'panelPomp'
shared(object) <- value

```

### Arguments

object, x	An object of class panelPomp or inheriting class panelPomp.
format	the format (data type) of the return value.
...	....
value	value to be assigned.
start, end	position in original times(pomp) at which to start.
i	unit index (indices) or name (names).

### Value

coef() returns a numeric vector.  
length() returns an integer.  
names() returns a character vector.  
toParamList() returns a list with the model parameters in list form.  
When given objects of class panelPomp, unit\_objects() returns a list of pomp objects.  
window() returns a panelPomp object with adjusted times.

``[`` returns a panelPomp object.

``[[`` returns a pomp object.

`specific()` returns unit-specific parameters as a numeric matrix or vector

`shared()` returns shared parameters from a panelPomp object

## Methods

**coef** Extracts coefficients of panelPomp objects.

**coef<-** Assign coefficients to panelPomp objects.

**length** Count the number of units in panelPomp objects.

**names** Get the unit names of panelPomp objects.

**toParamList** Converts panel coefficients from vector form to list form.

**window** Subset panelPomp objects by changing start time and end time.

`[]` Take a subset of units.

`[[[]]` Select the pomp object for a single unit.

**specific** Extracts the specific coefficients.

**specific<-** Assigns the specific coefficients.

**shared** Extracts the shared coefficients.

**shared<-** Assigns the shared coefficients.

## Author(s)

Carles Bretó, Aaron A. King, Edward L. Ionides, Jesse Wheeler

## See Also

Other panelPomp methods: [as\(\)](#)

## Examples

```
## access and manipulate model parameters and other features
prw <- panelRandomWalk()
coef(prw)
# replace coefficients
coef(prw) <- c(sigmaX=2,coef(prw)[-1])
coef(prw)
length(prw)
names(prw)
# convert vector-form parameters to list-form parameters
toParamList(coef(prw))
## summaries of objects
print(prw)
show(prw)
## access underlying pomp objects
unit_objects(prw)
## select windows of time
```

```
window(prw,start=2,end=4)
## subsetting panelPomp objects
prw[1] # panelPomp of 1 unit (first unit of prw)
prw[[2]] # pomp object corresponding to unit 2 of prw
# access and manipulate model parameters and other features
specific(prw)
# replace unit-specific coefficients
specific(prw) <- c("sigmaX[rw1]"=2)
specific(prw)
# access and manipulate model parameters and other features
shared(prw)
# replace unit-specific coefficients
shared(prw) <- c('sigmaY'=2)
shared(prw)
```

---

panelRandomWalk	<i>Panel random walk model</i>
-----------------	--------------------------------

---

## Description

Builds a collection of independent realizations from a random walk model.

## Usage

```
panelRandomWalk(
  N = 5,
  U = 2,
  params = c(sigmaY = 1, sigmaX = 1, X.0 = 1),
  seed = 3141592
)
```

## Arguments

N	number of observations for each unit.
U	number of units.
params	parameter vector, assuming all units have the same parameters.
seed	passed to the random number generator for simulation.

## Value

A panelPomp object.

## Author(s)

Edward L. Ionides, Carles Bretó

## See Also

Other panelPomp examples: [contacts\(\)](#), [panelGompertz\(\)](#), [panelMeasles\(\)](#)

**Examples**

```
panelRandomWalk()
```

---

panel_loglik	<i>Handling of loglikelihood replicates</i>
--------------	---

---

**Description**

Handling of loglikelihood replicates.

**Usage**

```
## S4 method for signature 'matrix'
logLik(object, repMargin, first = "aver", aver = "logmeanexp", se = FALSE)
```

**Arguments**

object	Matrix with the same number of replicated estimates for each panel unit loglikelihood.
repMargin	The margin of the matrix having the replicates (1 for rows, 2 for columns).
first	Whether to "aver"(age replicates) or "aggr"(egate units) before performing the other action.
aver	How to average: 'logmeanexp' to average on the likelihood scale before taking logs or 'mean' to average after taking logs (in which case, which action is performed first does not change the result).
se	logical; whether to give standard errors.

**Details**

When se = TRUE, the jackknife se's from `pomp::logmeanexp` are squared, summed and the squared root is taken.

**Value**

numeric vector with the average panel log likelihood and, when se = TRUE, the corresponding standard error.

**Author(s)**

Carles Bretó

**See Also**

Other panelPomp workhorse functions: [mif2\(\)](#), [panelPomp](#), [pfilter\(\)](#)

**Examples**

```

ulls <- matrix(c(1,1.1,10.1,10),nr=2)
# when combining log likelihood estimates, the order in which aggregation and
# averaging are done can make a difference: panel_logmeanexp() implements the best
logLik(ulls,repMargin=1,first="aver",aver="logmeanexp")
logLik(ulls,repMargin=1,first="aggr",aver="mean",se=TRUE)

```

---

panel\_logmeanexp      *Log-mean-exp for panels*

---

**Description**

This function computes the [logmeanexp](#) for each column or row of a numeric matrix and sums the result. Because the loglikelihood of a panelPomp object is the sum of the loglikelihoods of its units, this function can be used to summarize replicated estimates of the panelPomp model likelihood. If `se = TRUE`, the jackknife SE estimates from [logmeanexp](#) are squared, summed and the squared root is taken.

**Usage**

```
panel_logmeanexp(x, MARGIN, se = FALSE)
```

**Arguments**

<code>x</code>	Matrix with the same number of replicated estimates for each panel unit loglikelihood.
<code>MARGIN</code>	The dimension of the matrix that corresponds to a panel unit and over which averaging occurs (1 indicates rows, 2 indicates columns).
<code>se</code>	logical; whether to give standard errors.

**Value**

A numeric value with the average panel log likelihood or, when `se = TRUE`, a numeric vector adding the corresponding standard error.

**Author(s)**

Carles Bretó

**See Also**

[panel\\_loglik](#)

**Examples**

```

ulls <- matrix(c(1,1,10,10),nr=2)
panel_logmeanexp(ulls,MARGIN=2,se=TRUE)

```

params

*Manipulating panelPomp object parameter formats*

---

**Description**

These facilitate keeping a record of evaluated log likelihoods.

**Usage**

```
toParamVec(pParams)
```

```
toMatrixPparams(listPparams)
```

**Arguments**

pParams            A list with both shared (vector) and unit-specific (matrix) parameters.

listPparams        PanelPomp parameters in list format

**Value**

toParamVec() returns model parameters in vector form. This function is the inverse of [toParamList](#)

toMatrixPparams() returns an object of class `matrix` with the model parameters in matrix form.

**Author(s)**

Carles Bretó

**Examples**

```
prw <- panelRandomWalk()
toParamVec(coef(prw, format = 'list'))
toMatrixPparams(coef(prw, format = 'list'))
```

---

pfilter*Particle filtering for panel data*

---

**Description**

Tools for applying particle filtering algorithms to panel data.

**Usage**

```
## S4 method for signature 'panelPomp'
pfilter(
  data,
  shared,
  specific,
  params,
  Np,
  verbose = getOption("verbose"),
  ...
)

## S4 method for signature 'pfilterd.ppomp'
logLik(object, ...)

## S4 method for signature 'pfilterd.ppomp'
unitLogLik(object, ...)
```

**Arguments**

<code>data</code>	An object of class <code>panelPomp</code> or inheriting class <code>panelPomp</code> .
<code>shared, specific</code>	optional; these arguments depend on the type of object. If object is a list of poms, <code>shared</code> must be a numeric vector specifying parameter values shared among panel units. <code>specific</code> must be a matrix with parameter values that are unit-specific with rows naming parameters and columns naming units (these names must match those of object). If no values are specified and object has parameter values, these are set to be all unit-specific. If object is a <code>panelPomp</code> object, these arguments can still be used as described above to modify the parameters of object. Alternatively, the parameter configuration of object can be modified providing only a character <code>shared</code> naming parameters of object that should be shared (with values for parameters not originally shared taken from the unit-specific parameters of the first panel unit of object). <code>shared=NULL</code> sets all parameters as unit-specific.
<code>params</code>	optional; a named numeric vector. In this case, the nature of parameters is determined via a naming convention: names ending in “[unit_name]” are assumed to denote unit-specific parameters; all other names specify shared parameters.
<code>Np</code>	the number of particles to use. This may be specified as a single positive integer, in which case the same number of particles will be used at each timestep. Alternatively, if one wishes the number of particles to vary across timesteps, one may specify <code>Np</code> either as a vector of positive integers of length <code>length(time(object, t0=TRUE))</code>  or as a function taking a positive integer argument. In the latter case, <code>Np(k)</code> must be a single positive integer, representing the number of particles to be used at the k-th timestep: <code>Np(0)</code> is the number of particles to use going from <code>timezero(object)</code> to <code>time(object)[1]</code> , <code>Np(1)</code> , from <code>timezero(object)</code> to

	time(object)[1], and so on, while when $T = \text{length}(\text{time}(\text{object}))$ , $Np(T)$ is the number of particles to sample at the end of the time-series.
verbose	logical; if TRUE, diagnostic messages will be printed to the console.
...	additional arguments, passed to the pfilter method of <b>pomp</b> .
object	required; either (i) a list of pomp objects; or (ii) an object of class panelPomp or inheriting class panelPomp.  If object is a list of pomps, the list must be named. All these pomps must either have no parameters or have the same parameter names. (This is just a format requirement. pomp codes can ignore any parameter that is irrelevant to any given panel unit.)  If object is a panelPomp object, the function allows modifying the shared and unit-specific configuration of object.

### Value

pfilter() returns an object of class pfilterd.ppomp that is also a panelPomp object (with the additional filtering details).

When applied to an object of class pfilterd.ppomp, logLik() returns a numeric value.

When given objects of class pfilterd.ppomp, unitLoglik() returns a numeric vector.

### Methods

**logLik** Extracts the estimated log likelihood for the entire panel.

**unitLogLik** Extracts the estimated log likelihood for each panel unit.

### Author(s)

Carles Bretó

### References

Arulampalam, M. S., Maskell, S., Gordon, N. and Clapp, T. (2002) A Tutorial on Particle Filters for Online Nonlinear/Non-Gaussian Bayesian Tracking. *IEEE Trans. Sig. Proc.*, **50**(2), 174–188. [doi:10.1109/78.978374](https://doi.org/10.1109/78.978374)

Bretó, C., Ionides, E. L. and King, A. A. (2020) Panel Data Analysis via Mechanistic Models. *Journal of the American Statistical Association*, **115**(531), 1178–1188. [doi:10.1080/01621459.2019.1604367](https://doi.org/10.1080/01621459.2019.1604367)

### See Also

**pomp**'s pfilter at [pfilter](#), [panel\\_loglik](#)

Other panelPomp workhorse functions: [mif2\(\)](#), [panelPomp](#), [panel\\_loglik](#)



**Examples**

```
# filter, which generates log likelihoods
pfrw <- pfilter(panelRandomWalk(),Np=10)
class(pfrw) # "pfilterd.ppomp"
is(pfrw,"panelPomp") # TRUE
pfrw
# extract single log likelihood for the entire panel
logLik(pfrw)
# extract log likelihood for each panel unit
unitLogLik(pfrw)
```

---

plot

*panelPomp plotting facilities*


---

**Description**

Diagnostic plots for each unit in a panelPomp

**Usage**

```
## S4 method for signature 'panelPomp_plottable'
plot(
  x,
  variables,
  panel = lines,
  nc = NULL,
  yax.flip = FALSE,
  mar = c(0, 5.1, 0, if (yax.flip) 5.1 else 2.1),
  oma = c(6, 0, 5, 0),
  axes = TRUE,
  ...
)
```

**Arguments**

x	the object to plot
variables	optional character; names of variables to be displayed
panel	function of prototype panel(x, col, bg, pch, type, ...) which gives the action to be carried out in each panel of the display.
nc	the number of columns to use. Defaults to 1 for up to 4 series, otherwise to 2.
yax.flip	logical; if TRUE, the y-axis (ticks and numbering) should flip from side 2 (left) to 4 (right) from series to series.
mar, oma	the <code>par</code> mar and oma settings. Modify with care!
axes	logical; indicates if x- and y- axes should be drawn
...	ignored or passed to low-level plotting functions

**Value**

No return value (the function returns NULL).

**Author(s)**

Edward L. Ionides

**Examples**

```
plot(panelRandomWalk())
```

---

simulate

*Simulations of a panel of partially observed Markov process*

---

**Description**

simulate generates simulations of the state and measurement processes.

**Usage**

```
## S4 method for signature 'panelPomp'
simulate(object, nsim = 1, shared, specific)
```

**Arguments**

object	a panelPomp object.
nsim	The number of simulations to perform. Unlike the pomp simulate method, all simulations share the same parameters.
shared	Named vector of the shared parameters.
specific	Matrix of unit-specific parameters, with a column for each unit.

**Value**

A single panelPomp object (if nsim=1) or a list of panelPomp objects (if nsim>1).

**Author(s)**

Edward L. Ionides

**Examples**

```
simulate(panelRandomWalk())
```

---

`twentycities`*He et al. 2010 twenty UK cities weekly reported measles data*

---

**Description**

He et al. 2010 twenty UK cities weekly reported measles data

**Usage**

```
twentycities
```

**Format**

```
twentycities:
```

A list of 3 data frames.

```
twentycities$measles::
```

**unit** City name

**data** Date of observation

**cases** Number of measles cases reported during the week

```
twentycities$demog::
```

**unit** City name

**year** Year that demography was recorded

**pop** Population

**births** Births

```
twentycities$coord::
```

**unit** City name

**long** Longitude of city

**lat** Latitude of city

**Source**

<https://kingaa.github.io/pomp/vignettes/twentycities.rda>

**References**

D. He, E.L. Ionides, and A.A. King. Plug-and-play inference for disease dynamics: measles in large and small populations as a case study. *Journal of the Royal Society Interface* **7**, 271–283, 2010.

---

`uk_measles`*Weekly reported measles data for 362 locations in the UK*

---

**Description**

Weekly reported measles data for 362 locations in the UK

**Usage**`uk_measles`**Format**`uk_measles:`

A list of 3 data frames Unit names ending in .RD are for rural areas; other unit names are for urban areas. NOTE: not all units have coordinates.

`uk_measles$measles::`**unit** City name**data** Date of observation**cases** Number of measles cases reported during the week`uk_measles$demog::`**unit** City name**year** Year that demography was recorded**pop** Population**births** Births`uk_measles$coord::`**unit** City name**long** Longitude of city**lat** Latitude of city**Source**

[https://rs.figshare.com/collections/Supplementary\\_material\\_from\\_Structure\\_space\\_and\\_size\\_competing\\_drivers\\_of\\_variation\\_in\\_urban\\_and\\_rural\\_measles\\_transmission\\_/5036567/1](https://rs.figshare.com/collections/Supplementary_material_from_Structure_space_and_size_competing_drivers_of_variation_in_urban_and_rural_measles_transmission_/5036567/1)

**References**

Korevaar H, Metcalf CJ, Grenfell BT. 2020 Structure, space and size: competing drivers of variation in urban and rural measles transmission. *J. R. Soc. Interface* 17: 20200010. <http://dx.doi.org/10.1098/rsif.2020.0010>

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