

# Package ‘growcurves’

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**Type** Package

**Title** Bayesian semi and nonparametric growth curve models that additionally include multiple membership random effects.

**Version** 0.2.3.9

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**Description** Employs a non-parametric formulation for by-subject random effect parameters to borrow strength over a constrained number of repeated measurement waves in a fashion that permits multiple effects per subject. One class of models employs a Dirichlet process (DP) prior for the subject random effects and includes an additional set of random effects that utilize a different grouping factor and are mapped back to clients through a multiple membership weight matrix; e.g. treatment(s) exposure or dosage. A second class of models employs a dependent DP (DDP) prior for the subject random effects that directly incorporates the multiple membership pattern.

**License** GPL (>= 2)

**LazyLoad** yes

**Depends** R (>= 3.0.2), Rcpp (>= 0.10.6),

**LinkingTo** Rcpp (>= 0.10.6), RcppArmadillo (>= 0.4.000)

**Imports** RcppArmadillo (>= 0.4.000), reshape2 (>= 1.2.1), scales (>= 0.2.0), ggplot2 (>= 0.9.2), Formula (>= 1.0-0), testthat (>= 0.8)

**Collate** 'getmf.R' 'XZcov.R' 'datbrghtmodterms.R' 'datbrghtterms.R'  
'dateduc.R' 'datsim.R' 'datsimcov.R' 'datsimmult.R'  
'ddpMCMCplots.R' 'ddp\_quantiles.R' 'ddpeffectsplot.R'  
'relabel.R' 'growthCurve.R' 'summary\_quantiles.R' 'mcmcPlots.R'  
'dpgrowmm.R' 'ddpgrow.R' 'dpgrow.R' 'dpgrowmult.R'  
'effectsplot.R' 'growplot.R' 'help.R' 'trtplot.R'

**NeedsCompilation** yes

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growcurves-package	<i>Bayesian semi and nonparametric growth curve models with employment of multiple membership random effects for longitudinal data.</i>
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## Description

Package:	growcurves
Type:	Package
Version:	0.2.3.9
Date:	2014-02-23
License:	GPL (>= 3)
LazyLoad:	yes

## Details

Specifies a non-parametric prior for subject random effects and adds additional sets of dose or exposure random effects that are linked to subjects through a multiple membership construction for application to repeated measures data on subjects. One class of models employs a set of by-subject random effect parameters under a Dirichlet process (DP) prior with the addition of one or more sets of multiple membership (MM) effects that map by-dose effects to subject for data characterized by repeated measures on subject. There may be specified  $q$  random effect parameters per subject, possibly equal to the number of measurement waves,  $T$ , as the DP prior borrows estimation strength across subjects. Another class of models employs a single set of by-subject effects under a dependent DP (DDP) prior for a collection of random distributions that are indexed by MM dose or sequence. Each set of subject random effects under the DDP formulation are now indexed by a full set of MM sequences (for all subjects).

### CORE "ENGINE" FUNCTIONS

`dpgrow` performs Bayesian mixed effects estimation for data characterized by repeated subject measures (typically in time). The user inputs a subject identifier vector, a vector of time measurements, and a `trt` vector for treatment/group assignments. Fixed and random effects are then automatically generated and both subject and treatment level growth curves are constructed.

`dpgrowmm` is very similar to `dpgrow`, but it adds an additional set of exposure random effects which aren't grouped by subject that may be used to inject treatment dosage or attendance patterns that is mapped back to clients via a multiple membership weight matrix. The option `multi = TRUE` specifies each exposure random effect as polynomial in time as is done for the by-subject effects.

`dpgrowmult` is very similar to `dpgrowmm`, but it allows more than one set of multiple membership effects. Each multiple membership effects term (block) may apply to any sub-set of subjects through

specification of the weight matrix and identification of affected subjects for that term.

`ddpgrow` generalizes `dpgrowmm` and `dpgrowmult` by indexing the subject random effects with a set of exposures linked to subjects from an MM weight matrix. This model brings the MM term inside the DP by specifying a set of dose-based (MM) random effects for each subject. The model formally employs a dependent DP (DDP) prior on a set of subject effects with the a single unknown prior distribution now replaced by a collection of unknown distributions indexed by dosage pattern. For example, a dosage or exposure may be characterized by a sequence of cognitive behavior therapy sessions attended.

#### CORE "ACCESSOR" (PLOT) FUNCTIONS

`growplot` uses model outputs from `dpgrow`, `dpgrowmm`, `dpgrowmult` and `ddpgrow` to provide by-subject growth curves in two forms: 1. Growth curves aggregated under specified groupings; 2. Individual growth curves plotted along with data for selected (or random subset of) subjects.

`trtplot` uses model outputs from `dpgrow`, `dpgrowmm`, `dpgrowmult` and `ddpgrow` to plot a distribution for fixed mean effects difference between two selected treatments across a range of chosen models for a one or more chosen time points. Outputs include a set of boxplots for each time point that span 95

`effectsplot` uses model outputs from `dpgrow`, `dpgrowmm` and `dpgrowmult` to overlay plots of multiple membership effects for a given term under use of different prior formulations and/or from distinctly formulated models (e.g. with varying numbers of multiple membership terms).

`ddpEffectsplot` uses model outputs from `ddpgrow` to produce by subject and by clusters of subjects summaries for the  $q \times (S+1)$  multivariate random effects for each subject, where  $S$  denotes the number of unique dosages across all subjects, and  $q$  denotes the polynomial order for each of the  $S+1$  effects. There is also a  $q \times 1$  set of subject intercept effects. This function is analogous to `effectsplot`, only each client now has its own set of MM random effects.

#### SIMULATED DATA SETS

There are 3 simulated data sets available in order to allow exploration of the engine and associated accessor functions.

`datstim` Simulated dataset with two treatment arms (treatment and control) composed from a model with a Dirichlet process (DP) prior on the set of client effects and a single MM term under a "mmcar" formulation. Structured to express similar properties as the case example in both Savitsky and Paddock (2012) references, below.

`datstimcov` Of similar structure to `simdat`, only the data generating model now additionally employs 2 nuisance fixed effects.

`datstimmult` Simulated data under 2 treatment arms generated from a model with now 2 multiple membership terms. The terms are generated under `c("mmi", "mmcar")` prior formulations.

#### BENCHMARK DATA SETS

`datbrghtterms` Data derived from BRIGHT study reviewed in reference and includes BDI-II depressive symptom scores for client experimental units. Associated data objects are included to facilitate runs under engine functions `dpgrow`, `dpgrowmm` and `dpgrowmult`.

`datbrghtmodterms` Data derived from BRIGHT study reviewed in reference and includes BDI-II depressive symptom scores for client experimental units. CBT treatment sessions are collected into higher level modules. All objects are then specified by module, rather than session. These data may be used with any engine function, though were created to facilitate use of `ddpgrow`. Data objects are included, therefore, to enable employment of `ddpgrow`, as well as the other engine functions.

`dateduc` Tests for students tracked for 5 years from grades 1 - 5 for a single school in a large urban school district. Associated data objects are included to facilitate runs under engine functions `dpgrow`, `dpgrowmm`, `ddpgrow`.

### Author(s)

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### References

S. M. Paddock and T. D. Savitsky (2013) Bayesian Hierarchical Semiparametric Modeling of Longitudinal Post-treatment Outcomes from Open-enrollment Therapy Groups., JRSS Series A (Statistics in Society), 2013, Volume 176, Part 2, pp. 797 - 808.

T. D. Savitsky and S. M. Paddock (2013) Bayesian Non-Parametric Hierarchical Modeling for Multiple Membership Data, Annals of Applied Statistics, Volume 7, Number 2, pp. 1074 - 1094.

T. D. Savitsky and S. M. Paddock (2014) Bayesian Semi- and Non-Parametric Models for Longitudinal Data with Multiple Membership Effects in R, Journal of Statistical Software, Volume 57, Number 3, pp. 1 – 35, <http://www.jstatsoft.org/v57/i03/>

### Examples

```
## Not run:
## extract simulated dataset
library(growcurves)
data(datsim)
## attach(datsim)
## run dpgrow mixed effects model, returning object of class "dpgrow"
shape.dp = 4
res = dpgrow(y = datsim$y, subject = datsim$subject,
trt = datsim$trt, time = datsim$time,
n.random = 3, n.fix_degree = 2,
n.iter = 10000, n.burn = 2000,
n.thin = 10, shape.dp = shape.dp,
option = "dp")
## Each plot is a "ggplot2" object saved in
## a list to plot.results
plot.results = plot(res) ## includes subject and
## treatment growth curves
## Extract credible intervals (2.5%, mean, 97.5%).
## Includes fit statistics: Dbar, DIC, pD, lpml.
## Note: DIC is the DIC3 of Celeaux et. al. (2006)
## for option = "dp". Finally, the constructed fixed
## and random effects matrices, X and Z, are returned
## with growth curve covariates appended
## to user submitted nuisance covariates.
summary.results = summary(res)
## View the summary results in the console
print(summary.results)
## Collect posterior sampled values over
## the (n.iter - n.burn) retained iterations
## for each sampled parameter.
```

```

samples.posterior = samples(res)
## model residuals (y - fit)
residuals = resid(res)
## Model with DP on clients effects, but
## now INCLUDE session random effects
## in a multiple membership construction
## communicated with the N x S matrix, W.subj.aff.
## Returns object, res.mm, of class "dpgrowmm".
shape.dp = 4
strength.mm = 0.1
res.mm = dpgrowmm(y = datsim$y, subject = datsim$subject,
                  trt = datsim$trt, time = datsim$time,

n.random = 3,
Omega = datsim$Omega, group = datsim$group,
subj.aff = datsim$subj.aff,
W.subj.aff = datsim$W.subj.aff,
n.iter = 10000, n.burn = 2000, n.thin = 10,
strength.mm = strength.mm,
shape.dp = shape.dp,
option = "mmcar")
plot.results = plot(res.mm)

## End(Not run)

```

---

datbrghtmodterms

*BRIGHT BDI depressive symptom data with (G = 4) module groups  
divided into separate MM terms.*


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## Description

The Beck Depression Inventory - II scores for the set of de-identified clients who participated in the Building Recovery by Improving Goals, Habits and Thoughts (BRIGHT) study, a community-based effectiveness trial of group cognitive behavioral therapy intervention for treating residential substance abuse treatment clients experiencing depressive symptoms. These data include scores for three measurement waves; the first at baseline enrollment to the study, followed by two post-treatment measurements with the aim to test whether clients receiving BRIGHT intervention would experience sustained improvement. There 299 participating clients, divided between 159 assigned to the usual care arm, and 140 assigned to CBT. These data are differentiated from datbrght terms in that sessions are replaced with (coarsened to) modules, each of which contains 4 sessions. Under the open-enrollment protocol, clients could start at the beginning of any module. Each module represents one of four topic areas that collect sessions focused on those topics. The data are configured to support model runs using engine functions (dpgrowmm, dpgrowmult, ddpgrow).

## Usage

```
datbrghtmodterms
```

## Format

A list object for 815 total observations on 299 subjects

## Details

- `y`. Client depressive symptom score responses. There are  $N = 815$  total measures for  $P = 299$  subjects. Each entry contains a composite Beck Depression Inventory-II (BDI-II) score. The BDI-II score is a sum across 21 four-level items (each scored 0 - 3) with a higher score signifying a greater level of depressive symptoms.
- `subject`. BRIGHT study client identifier (1, 2, ..., 299). Note: Participating clients are de-identified in this dataset.
- `trt`. Treatment arm identifier of length  $N$  (e.g. (0, 0, 0, ..., 1, 1, 1, ...)), either {0, 1} with usual care (UC) = 0 and group cognitive behavioral therapy (CBT) = 1. There are 140 clients with CBT = 1 (even though 132 of these actually attend sessions) in order to facilitate an intent-to-treat comparison.
- `time`. Measurement times in months for each repeated subject measure of length  $N$ . There are 3 distinct time points or measurement waves. e.g. (0, 3, 6, 0, 3, 6, 0, 0, 3, , , ,). The first measure is at baseline when clients enrolled to BRIGHT and at two post-treatment follow-ups at 3 and 6 months with response rates of 86 object with each term a vector that indexes  $n[g]$  subjects linked to each of  $g = 1, \dots, (G = 4)$  CBT therapy groups. Each group is specialized to its own multiple membership (MM) term for employment of engine function `dpgrowmmult`. The number of CBT clients for each group are ( $n[1] = 17$ ,  $n[2] = 18$ ,  $n[3] = 19$ ,  $n[4] = 78$ ) for a total of  $P_{aff} = 132$  clients that attended sessions, as compared to the 140 assigned to the CBT arm.
- `subj.aff_mat`. A matrix object that concatenates the client identifiers in `subj.aff` across groups for modeling all groups, together, in a single MM term with engine function `dpgrowmm`.
- `W.subj.aff`. A list object containing  $G$ ,  $n[g] \times S[g]$  multiple membership weight matrices that together map the  $P_{aff} = 132$  affected subjects (in each element of the `subj.aff` list) to their particular sessions attended within their assigned group. There are a total of 61 CBT modules allocated to the  $G$  CBT therapy groups as  $S[1] = 9$ ,  $S[2] = 10$ ,  $S[3] = 10$ ,  $S[4] = 32$ . The study was designed for clients to attend 16 sessions organized into 4 modules of 4 sessions each. The 4 modules were offered on an open enrollment or rotating basis. Additional make-up sessions added within 2 modules resulted in the possibility for some clients to attend up to 20 sessions.
- `W.subj.aff_mat`. An  $n = 132 \times S = 61$  matrix object that concatenates the matrix entries of the list object from `W.subj.aff` into a block-diagonal matrix (with each group of clients and modules disjoint and non-communicating with the others) for modeling in a single MM term under function `dpgrowmm`.
- `dosemat`. An  $n_{tot} = 299 \times (S+1) = 62$  matrix object that maps all clients to modules for use under engine function `ddpgrow`. The first column is an intercept filled with 1's. The rows for column 2:62 sum to 1 for the first 132 clients (who attend CBT modules) in a multiple membership fashion. The rows for non-CBT clients are constructed as (1, 0, 0, ..., 0) such that no attendance is the hold-out category for identification.
- `numdose`. A numeric vector of length equal to  $G=4$  CBT open enrollment groups with each entry capturing the number of modules for that group. This vector is used to allocate modules to the set of base distributions chosen with `option` under the `ddpgrow` engine function; for example, `option = c("car", "mvm", "car", "ind")` assigns the noted distributional choices to the corresponding blocks of modules collected in `numdose`.

- `labt`. A character vector of length equal to  $G=4$  CBT open enrollment groups that provides a label for each module block under a distinct base distribution. These labels will be used in the rendered plots using accessor functions associated to `ddpgrow`.
- `group`. A list object of length equal to the number of MM terms under the "mmcar" or "mmigrp" prior formulations for session effects. Each item contains a vector that specifies sub-group membership for each block of sessions within the  $G=4$  MM terms. A sub-group would collect modules that communicate with each other, but not with the modules of other sub-groups. For these data, the modules within each CBT therapy group all communicate. Then each vector in `group` contains the single value 1 of length equal to the number of sessions in the applicable therapy group. This object is input for engine function `dpgrowmult` in the case it is desired to place all of the  $G = 4$  MM terms under prior "mmcar". One may employ the appropriate subset of list entries for those terms under which it is desired to employ prior "mmcar".
- `group_mat`. A matrix object denotes the group memberships, from  $1 - G = 4$  groups, for the  $S = 61$  CBT modules for modeling under engine function `dpgrowmm`.
- `Omega`. A list object with each element containing an  $S[g] \times S[g]$  CAR adjacency matrix used to model prior association among effects for each MM term under prior "mmcar", where  $S[g]$  are the number of effects for CBT therapy group  $g$ . One may employ the approach subset of adjacency matrices for those terms under which one desires to specify prior "mmcar".
- `Omega_mat`. An  $(S = 61) \times (S = 61)$  matrix object encoding the dependence structure among modules that concatenates the entries of `Omega` into a block diagonal structure for use in `dpgrowmm`.

## References

- K. E. Watkins, S. B. Hunter, K. A. Hepner, S. M. Paddock, E. de la Cruz, A. J. Zhou and J. Gilmore (2011) An effectiveness trial of group cognitive behavioral therapy for patients with persistent depressive symptoms in substance abuse treatment, *Archives of General Psychiatry*, 68(6), 1- 8.
- S. M. Paddock and T. D. Savitsky (2012) Bayesian Hierarchical Semiparametric Modeling of Longitudinal Post-treatment Outcomes from Open-enrollment Therapy Groups, soon to appear in: *JRSS Series A (Statistics in Society)*.

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datbrghtterms

*BRIGHT BDI depressive symptom data with (G = 4) session groups divided into separate MM terms.*

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## Description

The Beck Depression Inventory - II scores for the set of de-identified clients who participated in the Building Recovery by Improving Goals, Habits and Thoughts (BRIGHT) study, a community-based effectiveness trial of group cognitive behavioral therapy intervention for treating residential substance abuse treatment clients experiencing depressive symptoms. These data include scores for three measurement waves; the first at baseline enrollment to the study, followed by two post-treatment measurements with the aim to test whether clients receiving BRIGHT intervention would experience sustained improvement. There 299 participating clients, divided between 159 assigned to the usual care arm, and 140 assigned to CBT. The data are configured to support model runs using engine function `dpgrowmm`.



**Usage**

datbrghtterms

**Format**

A list object for 815 total observations on 299 subjects

**Details**

- `y`. Client depressive symptom score responses. There are  $N = 815$  total measures for  $P = 299$  subjects. Each entry contains a composite Beck Depression Inventory-II (BDI-II) score. The BDI-II score is a sum across 21 four-level items (each scored 0 - 3) with a higher score signifying a greater level of depressive symptoms.
- `subject`. BRIGHT study client identifier (1, 2, ..., 299). Note: Participating clients are de-identified in this dataset.
- `trt`. Treatment arm identifier of length  $N$  (e.g. (0, 0, 0, ..., 1, 1, 1, ...)), either {0, 1} with usual care (UC) = 0 and group cognitive behavioral therapy (CBT) = 1. There are 140 clients with CBT = 1 (even though 132 of these actually attend sessions) in order to facilitate an intent-to-treat comparison.
- `time`. Measurement times in months for each repeated subject measure of length  $N$ . There are 3 distinct time points or measurement waves. e.g. (0, 3, 6, 0, 3, 6, 0, 0, 3, , ,). The first measure is at baseline when clients enrolled to BRIGHT and at two post-treatment follow-ups at 3 and 6 months with response rates of 86 object with each term a vector that indexes  $n[g]$  subjects linked to each of  $g = 1, \dots, (G = 4)$  CBT therapy groups. Each group is specialized to its own multiple membership (MM) term for employment of engine function `dpgrowmmult`. The number of CBT clients for each group are ( $n[1] = 17$ ,  $n[2] = 18$ ,  $n[3] = 19$ ,  $n[4] = 78$ ) for a total of  $P_{\text{aff}} = 132$  clients that attended sessions, as compared to the 140 assigned to the CBT arm.
- `subj.aff_mat`. A matrix object that concatenates the client identifiers in `subj.aff` across groups for modeling all groups, together, in a single MM term with engine function `dpgrowmm`.
- `W.subj.aff`. A list object containing  $G$ ,  $n[g] \times S[g]$  multiple membership weight matrices that together map the  $P_{\text{aff}} = 132$  affected subjects (in each element of the `subj.aff` list) to their particular sessions attended within their assigned group. There are a total of 245 CBT sessions allocated to the  $G$  CBT therapy groups as  $S[1] = 36$ ,  $S[2] = 40$ ,  $S[3] = 40$ ,  $S[4] = 129$ . The study was designed for clients to attend 16 sessions organized into 4 modules of 4 sessions each. The 4 modules were offered on an open enrollment or rotating basis. Additional make-up sessions added within 2 modules resulted in the possibility for some clients to attend up to 20 sessions.
- `W.subj.aff_mat`. An  $n = 132 \times S = 245$  matrix object that concatenates the matrix entries of the list object from `W.subj.aff` into a block-diagonal matrix (with each group of clients and sessions disjoint and non-communicating with the others) for modeling in a single MM term under function `dpgrowmm`.
- `group`. A list object of length equal to the number of MM terms under the "mmcar" or "mmigrp" prior formulations for session effects. Each item contains a vector that specifies sub-group membership for each block of sessions within the  $G=4$  MM terms. A sub-group would collect sessions that communicate with each other, but not with the sessions of other

sub-groups. For these data, the sessions within each CBT therapy group all communicate. Then each vector in group contains the single value 1 of length equal to the number of sessions in the applicable therapy group. This object is input for engine function `dpgrowmult` in the case it is desired to place all of the  $G = 4$  MM terms under prior "mmcar". One may employ the appropriate subset of list entries for those terms under which it is desired to employ prior "mmcar".

- `group_mat`. A matrix object denotes the group memberships, from  $1 - G = 4$  groups, for the  $S = 245$  CBT sessions for modeling under engine function `dpgrowmm`.
- `Omega`. A list object with each element containing an  $S[g] \times S[g]$  CAR adjacency matrix used to model prior association among effects for each MM term under prior "mmcar", where  $S[g]$  are the number of effects for CBT therapy group  $g$ . One may employ the approach subset of adjacency matrices for those terms under which one desires to specify prior "mmcar".
- `Omega_mat`. An  $S \times S$  matrix object encoding the dependence structure among sessions that concatenates the entries of `Omega` into a block diagonal structure for use in `dpgrowmm`.

## References

K. E. Watkins, S. B. Hunter, K. A. Hepner, S. M. Paddock, E. de la Cruz, A. J. Zhou and J. Gilmore (2011) An effectiveness trial of group cognitive behavioral therapy for patients with persistent depressive symptoms in substance abuse treatment, *Archives of General Psychiatry*, 68(6), 1- 8.

S. M. Paddock and T. D. Savitsky (2012) Bayesian Hierarchical Semiparametric Modeling of Longitudinal Post-treatment Outcomes from Open-enrollment Therapy Groups, invited re-submission to: *JRSS Series A (Statistics in Society)*.

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dateduc

*Student test scores and associated teachers for a single school in a large urban school district*

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## Description

Response captures vertically linked mathematics and reading scores on a norm-referenced standardized test administered during the spring of the years 1998 to 2002 obtained from a large urban school district. Included student are in grade 1 during the 1997 - 1998 school year and followed successively until grade 5 for the 2001-2002 school year. These data focus on a single school of 227 students and 34 teachers. Teacher links to students did not vary by subject. The data are configured to support model runs using engine functions `dpgrowmm` and `ddpgrow`.

## Usage

dateduc

## Format

A list object for 562 total observations on 227 subjects

## Details

- `y`. Numeric vector of  $N = 562$  student-year test scores.
- `subject`. Numeric vector,  $1, \dots, n = 227$ , student identifiers
- `trt`. A numeric vector of  $N$  0's to indicate there are not separate treatment arms.
- `time`. An  $N \times 1$  numeric vector of associated measurement times in 1-5.
- `subj.aff`. Same as `subject` as all students receive the "school" treatment.
- `W.subj.aff`. An  $n = 227 \times S = 34$  matrix object that links the  $n = 227$  students to the  $S = 34$  teachers. The rows sum to 1. This object is used in engine function `dpgrowmm`.
- `dosemat`. An  $n = 227 \times S = 34$  numeric matrix where the first column is 1's for the intercept and the first teacher is left out for identifiability. This matrix is the same as `W.subj.aff` except that the first column is replaced with an intercept. This object is use for engine function `ddpgrow`.
- `tchr.aff`. A numeric vector with values  $1, \dots, T=34$  encoding the id's for the participating teachers.
- `labt`. A character input providing the label "school" for the treatment delivered to students

## References

J.R. Lockwood, Daniel F. McCaffrey, Louis T. Mariano and Claude Setodji (2007) Bayesian Methods for Scalable Multivariate Value-Added Assessment, *Journal of Educational and Behavioral Statistics*, 32(2), 125 - 150.

S. M. Paddock and T. D. Savitsky (2012) Bayesian Hierarchical Semiparametric Modeling of Longitudinal Post-treatment Outcomes from Open-enrollment Therapy Groups, invited re-submission to: *JRSS Series A (Statistics in Society)*.

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datsim

*Repeated measures for two groups of subjects drawn from mmcar model with no nuisance covariates*

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## Description

A simulation dataset containing repeated subject measures for 2 treatment groups, (control = 0, treatment = 1), constructed from an mmcar model with correlation between adjacent sessions equal to 0.25. Subject effects were randomly drawn from 10 clusters with weights/probabilities drawn from a Dirichlet distribution. Cluster location values were generated from a Gaussian base distribution.

## Usage

datsim

## Format

A list object of 19 variables for 792 total observations on 264 subjects

## Details

- `y`. response. there are  $N = 792$  total measures for  $P = 264$  subjects
- `subject`. subject identifier (1, 2, . . . , 264)
- `trt`. treatment group identifier of length  $N$  (e.g. (0, 0, 0, . . . , 1, 1, 1, . . .) , either {0, 1} for control and treatment.
- `time`. times in months for each repeated subject measure of length  $N$ . There are 3 distinct time points. e.g. (0, 3, 6, 0, 3, 6, 0, 0, 3, . . .)
- `n.random`. number of random effects per subject. Set = 3.
- `n.fix_degree`. order of fixed effects. Set = 2, for quadratic, meaning 3 effects (intercept, slope, quadratic) each, for treatment and control groups.
- `coefs`. true fixed effect coefficient values used to generate data.
- `subj.aff`. indexes subjects receiving treatment.
- `W.subj.aff`. multiple membership weight matrix that maps the  $P_{\text{aff}} = 132$  affected subjects (in `subj.aff`) to any of  $S = 245$  treatment sessions.
- `group`. treatment group membership for each of the  $S$  sessions.
- `Omega`. the  $S \times S$  CAR adjacency matrix used to model prior dependence among sessions
- `gamma`. true session effect values (of length  $S$ ) used to generate model response.
- `s`. true cluster memberships for each of the  $P$  subjects.
- `b.star`. a list object of true cluster location values for each of  $M = 10$  clusters. Each entry contains the `n.random = 3` location values for that cluster.
- `b`. a list object true random effect coefficient values for each of  $P$  subjects. Each entry contains the `n.random = 3` effect values for that subject.
- `tau.b`. true values for the prior precisions of the base Gaussian distribution for each of `n.random = 3` subject effects.
- `tau.e`. true value for overall model error.
- `coefs`. true coefficient values for the time-based quadratic fixed effects generated from the `trt`, and `time` inputs. e.g.  $X = c(1, \text{time}, \text{time}^2, \text{trt}_1, \text{trt}_1 * \text{time}, \text{trt}_1 * \text{time}^2)$ .

---

datsimcov

*Repeated measures for two groups of subjects drawn from mmcar model with 2 nuisance covariates*

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## Description

A simulation dataset containing repeated subject measures for 2 treatment groups, (control = 0, treatment = 1), constructed from an 'mmcar' model with correlation between adjacent sessions equal to 0.25. Subject effects were randomly drawn from 10 clusters with weights/probabilities drawn from a Dirichlet distribution. Cluster location values were generated from a Gaussian base distribution. Two nuisance demographic variables, age and income, are included.

**Usage**

```
datsimcov
```

**Format**

A list object of 19 variables for 792 total observations on 264 subjects

**Details**

- `subject`. subject identifier (1, 2, . . . , 264)
- `trt`. treatment group identifier of length N (e.g. (0, 0, 0, . . . , 1, 1, 1, . . .) , either {0, 1} for control and treatment.
- `time`. times in months for each repeated subject measure of length N. There are 3 distinct time points. e.g. (0, 3, 6, 0, 3, 6, 0, 0, 3, . . . , )
- `n.random`. number of random effects per subject. Set = 3.
- `n.fix_degree`. order of fixed effects. Set = 2, for quadratic, meaning 3 effects (intercept, slope, quadratic) each, for treatment and control groups.
- `coefs`. true fixed effect coefficient values used to generate data.
- `subj.aff`. indexes subjects receiving treatment.
- `W.subj.aff`. multiple membership weight matrix that maps the  $P_{\text{aff}} = 132$  affected subjects (in `subj.aff`) to any of  $S = 245$  treatment sessions.
- `group`. treatment group membership for each of the S sessions.
- `Omega`. the  $S \times S$  CAR adjacency matrix used to model prior dependence among sessions
- `gamma`. true session effect values (of length S) used to generate model response.
- `s`. true cluster memberships for each of the P subjects.
- `b.star`. a list object of true cluster location values for each of  $M = 10$  clusters. Each entry contains the  $n.random = 3$  location values for that cluster.
- `b`. a list object true random effect coefficient values for each of P subjects. Each entry contains the  $n.random = 3$  effect values for that subject.
- `tau.b`. true values for the prior precisions of the base Gaussian distribution for each of  $n.random = 3$  subject effects.
- `tau.e`. true value for overall model error.
- `coefs`. true coefficient values for the time-based quadratic fixed effects generated from the `trt`, and `time` inputs, as well as the 2 nuisance covariates. e.g.  $X = c(1, \text{time}, \text{time}^2, \text{trt}_1, \text{trt}_1 * \text{time}, \text{trt}_1 * \text{time}^2, \text{age}, \text{income})$ .
- `formula`. the additive formula containing the response and nuisance fixed effects. In this case,  $y \sim \text{age} + \text{income}$ .
- `data`. ( $N = 792$ )  $\times$  3 `data.frame` associated to `formula`. Includes model response, `y`, a  $N = 792 \times 1$  numeric vector capturing repeated measures for  $P = 264$  subjects. Also contained in `data` are two nuisance fixed effects, `age` and `income`.

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datsimmult	<i>Repeated measures for two groups of subjects with two multiple membership (MM) terms</i>
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### Description

A simulation dataset containing repeated subject measures for 2 treatment arms, (control = 0, treatment = 1), constructed from a four- MM term multiple membership model. MM terms 1 and 3 employ an 'mmi' prior over the set of treatment groups, which are then linked back to subjects with a weight matrix. MM terms 2 and 4 employ an 'mmcar' prior over the number of treatment sessions attended, with correlations between adjacent number of sessions equal to 0.25. Subject effects were randomly drawn from 10 clusters with assignment weights/probabilities drawn from a Dirichlet distribution. Cluster location values were generated from a Gaussian base distribution.

### Usage

```
datsimmult
```

### Format

A list object of 22 variables for 897 total observations on 299 subjects

### Details

- `y`. response. there are  $N = 897$  total measures for  $P = 299$  subjects
- `subject`. subject identifier (1, 2, ..., 299)
- `trt`. treatment group identifier of length  $N$  (e.g. (0, 0, 0, ..., 1, 1, 1, ...)) , either {0, 1} for control and treatment.
- `time`. times in months for each repeated subject measure of length  $N$ . There are 3 distinct time points. e.g. (0, 3, 6, 0, 3, 6, 0, 0, 3, , , ,)
- `n.random`. number of random effects per subject. Set = 3.
- `n.fix_degree`. order of fixed effects. Set = 2, for quadratic, meaning 3 effects (intercept, slope, quadratic) each, for treatment and control groups.
- `X` The resultant  $N \times n$ . fixed fixed effects design matrix.  $X = c(1, time, time^2, trt_1, trt_1*time, trt_1*time^2)$
- `coefs`. true coefficient values for the time-based quadratic fixed effects generated from the `trt`, and `time` inputs.
- `Z` The resultant  $N \times n$ . random by-subject random effects design matrix.  $Z = c(1, time, time^2, n.random)$
- `Z.b` The  $N \times 1$  matrix  $[Z_1 * b_1, \dots, Z_n * b_n]$ . where  $n$  equals the number of (unique) subjects.
- `subj.aff`. A list object with each term a vector that indexes  $n[g]$  subjects linked to each of  $g = 1, \dots, (G = 4)$  CBT therapy groups. Each group is specialized to its own multiple membership (MM) term for employment of engine function `dpgrowmmult`. The number of treatment arm subjects for each group are ( $n[1] = 17$ ,  $n[2] = 18$ ,  $n[3] = 19$ ,  $n[4] = 78$ ) for a total of  $P_{aff} = 132$  subjects assigned to the treatment arm.

- `W.subj.aff`. A list object containing  $G$ ,  $n[g] \times S[g]$  multiple membership weight matrices that together map the  $P_{\text{aff}} = 132$  affected subjects (in each element of the `subj.aff` list) to their particular sessions attended within their assigned group. There are a total of 245 sessions allocated to the  $G$  groups as  $S[1] = 36$ ,  $S[2] = 40$ ,  $S[3] = 40$ ,  $S[4] = 129$ .
- `group`. A list object of length equal to the number of MM terms under the 'mmcar' prior - In this case, terms 2 and 4. The elements in this list object contain a vector of labels that align the MM effects in a given term to disjoint, non-communicating groups. For these data, there are no groupings, so the single entry in 'group' associated to the 'mmcar' prior on number of sessions attended is filled with 1's equal to the number of of MM effects in each term.
- `Omega`. A list object containing an  $S[g] \times S[g]$  CAR adjacency matrix used to model prior dependence among effects for each MM term under the 'mmcar' prior, where  $S[g]$  are the number of effects for term  $i$ . Here, there are two terms (2 and 4) under "mmcar", so Omega contains two elements.
- `us`. A list object where each element is a vector of true MM session effect values for a given MM term. There are four MM terms in these data, so there are 4 elements, each of length  $S[g]$ .
- `s`. A vector of true cluster memberships for each of the  $n$  subjects.
- `b.star`. A list object of true cluster location values for each of  $M = 10$  clusters. Each entry contains the  $n.\text{random} = 3$  location values for that cluster.
- `b`. A list object true random effect coefficient values for each of  $n$  subjects. Each entry contains the  $n.\text{random} = 3$  effect values for that subject.
- `coefs`. A numeric vector of length  $n.\text{fixed} + 1$  that contains the true fixed effects coefficient values for the intercept plus the columns in  $X$  (in order).
- `tau.b`. true values for the prior precisions of the base Gaussian distribution for each of  $n.\text{random} = 3$  subject effects.
- `tau.u`. An  $4 \times 1$  vector of precision parameters associated to the Gaussian prior formulations for each MM term (under either 'mmcar' or 'mmi' covariance constructions).
- `tau.e`. true value for overall model error.
- `option`. A character vector equal to `c("mmi", "mmcar", "mmi", "mmcar")` that presents the prior formulations chosen for the 4 MM terms; The "mmi" employs an independent Gaussian prior while the "mmcar" allows for adjacency based dependence.

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 ddpEffectsplot

*Plot by-subject and by-treatment posterior mean values for dosage random effects*


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### Description

Each `ddpgrow` object contains posterior mean estimates for the  $q \times T$  matrix of by-subject random effects that is extracted from the `ddpgrow` object that is input to `ddpEffectsplot`. This function produces a  $q \times T.m$  heat map plot of posterior mean effect values for the dosages in treatment  $m$  faceted on a set of chosen subjects. The resulting plot produces a heatmap for each `trt`-subject combination. Both a `ggplot2` plot object and a `data.frame` object are returned.

**Usage**

```
ddpEffectsplot(object, subjects.plot = NULL, n.plot = 3, trts.plot = NULL,
  x.axis.label = NULL, smoother = TRUE, re.order = TRUE,
  cred.intervals = TRUE, map.group = NULL, n.dose.plot = 5,
  orderto = NULL)
```

**Arguments**

<code>object</code>	A <code>ddpgrow</code> object.
<code>subjects.plot</code>	A vector of subjects for performing plots that is composed of some subset of the subject vector input for modeling. If left blank, a random subset is chosen from subject.
<code>n.plot</code>	An optional scalar input for number of randomly generated subjects to plot (if <code>subjects.plot</code> is left blank).
<code>trts.plot</code>	A vector of focus treatments to use for plotting.
<code>x.axis.label</code>	An optional scalar character entry to label the treatment(s) dosages
<code>smoother</code>	A scalar boolean input indicating whether to co-plot a smoother line with point values.
<code>re.order</code>	A scalar boolean input indicating whether to sort the plots of effects in order of increasing value.
<code>cred.intervals</code>	A boolean scalar indicating whether the by-subject effects plots should include credible intervals.
<code>map.group</code>	A matrix or <code>data.frame</code> object containing a grouping of subjects that will be used to produce an additional set of effect plots that aggregate subjects by the grouping structure. The first column containing subject identifiers for all subjects modeled in <code>object</code> . The second column contains the desired desired group identifiers that may be of type character or numeric.
<code>n.dose.plot</code>	Optional numeric input for number of randomly chosen doses for which to plot effects growth curves.
<code>orderto</code>	A numeric vector of length equal to the total number of dosages across all treatments that conveys an order to be used by-dosage growth curve plots within cluster and treatment.

**Value**

A list object containing a faceted set of heat maps (one per subject), a faceted set of effect point plots, and the associated `data.frame` object.

<code>dat.se</code>	A <code>data.frame</code> object used to generate the trt-subject faceted plots for effect means Fields are titled, <code>c("order", "dose", "trt", "subject", "effects")</code> .
<code>dat.ci</code>	A <code>data.frame</code> object used to generate the trt-subject faceted plots for effect credible intervals Fields are titled, <code>c("order", "dose", "trt", "subject", "quantile", "effects")</code> .
<code>dat.clust</code>	A <code>data.frame</code> object used to generate the trt-group faceted plots for effect means Fields are titled, <code>c("order", "dose", "trt", "cluster", "effects")</code> .



<code>dat.clust.ci</code>	A <code>data.frame</code> object used to generate the trt-group faceted plots for effect credible intervals Fields are titled, <code>c("order", "dose", "trt", "cluster", "quantile", "effects")</code> .
<code>dat.gc</code>	A <code>data.frame</code> object used to generate the by-dose growth curves (for multivariate polynomial effects) Fields are titled, <code>c("fit", "time", "cluster", "trt", "dose")</code> .
<code>p.hm</code>	A <code>ggplot2</code> object of heat maps for mean random effect values, faceted by trt and subject combinations.
<code>p.pp</code>	A <code>ggplot2</code> object of point plots for mean random effect values or credible intervals, faceted by trt and subject combinations.
<code>pc.m</code>	A <code>ggplot2</code> object of point plots for mean random effect values, faceted by trt and group combinations.
<code>pc.ci</code>	A <code>ggplot2</code> object of point plots for credible intervals of random effect values, faceted by trt and cluster combinations.
<code>pc.gc</code>	A <code>ggplot2</code> growth curve plots for each dose where the does effects are multivariate polynomial.

**Author(s)**

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**See Also**

[ddpgrow](#), [dpgrow](#), [dpgrowmm](#), [dpgrowmult](#)

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ddpgrow

*Bayesian semiparametric growth curve models.*

---

**Description**

Employs an anova Dependent Dirichlet Process (DDP) prior on the set of by-subject random effect parameters with dependence indexed by multiple membership effects under repeated waves of measurements to allow the number of random effect parameters specified per subject,  $q$ , to be equal to the number of measurement waves,  $T$ . Random effects are grouped by subject and all  $q$  parameters receive the DP prior. The resulting joint marginal distribution over the data is a DP mixture.

**Usage**

```
ddpgrow(y, subject, trt, time, n.random, n.fix_degree, formula, random.only,
        data, dosemat, numdose, typetreat, labt, Omega, n.iter, n.burn, n.thin,
        shape.dp, rate.dp, M.init, plot.out)
```

**Arguments**

<code>y</code>	A univariate continuous response, specified as an $N \times I$ matrix or vector, where $N$ captures the number of subject-time cases (repeated subject measures). Data may reflect unequal number of measures per subject. Missing occasions are left out as no NA values are allowed.
<code>subject</code>	The objects on which repeated measures are conducted that serves as the random effects grouping factor. Input as an $N \times I$ matrix or vector of subject-measure cases in either integer or character format; e.g. $(1, 1, 1, 2, 2, 3, 3, 3, \dots, n, n, n)$ , where $n$ is the total number of subjects.
<code>trt</code>	An integer or character matrix/vector of length $N$ (number of cases) indicating treatment arm assignments for each case. May also be input as length $n$ vector, where $n$ is the number of unique subjects, indicating subject arm assignment. Multiple treatment arms are allowed and if the vector is entered as numeric, e.g. $(0, 1, 2, 3, \dots)$ , the lowest numbered arm is taken as baseline (captured by global fixed effects). If entered in character format, the first treatment entry is taken as baseline. If there are no treatment (vs. control) arm, then this vector is composed of a single value for all entries.
<code>time</code>	A univariate vector of length $N$ , capturing the time points associated to each by-subject measure.
<code>n.random</code>	The desired number of subject random effect terms, $q$ . May be set equal to the number of measurement waves, $T$ . The <code>y</code> , <code>trt</code> , <code>time</code> vectors will together be used to create both fixed and random effect design matrices. The random effects matrix will be of the form, $(1, \text{time}, \dots, \text{time}^{(n.random - 1)})$ (grouped, by subject). This formulation is a growth curve model that allows assessment of by-treatment effects and by-client growth curves.
<code>n.fix_degree</code>	The desired polynomial order in time to use for generating time-based fix effects. The fixed effects matrix will be constructed as, $(\text{time}, \dots, \text{time}^{(n.fix\_degree)}, \text{trt}_1, \text{time} * \text{trt}_1, \dots, \text{time}^{(n.fix\_degree)} * \text{trt}_L, \text{trt}_L, \dots, \text{time}^{(n.fix\_degree)} * \text{trt}_L)$ .
<code>formula</code>	Nuisance fixed and random effects may be entered in <code>formula</code> with the following format, $y \sim x_1 + x_2 * x_3 \mid z_1 * z_2$ . The bar, <code> </code> , separates fixed and random effects. If it is only desired to enter either fixed or random effects, but not both then the <code> </code> may be omitted. Note: the nuisance random effects are assumed to be grouped by subject. The fixed and random effects values may change with each repeated measure; however, within subject growth curves will keep constant $z$ and $x$ values between measurement waves. It is possible to bypass the growth curve construction by leaving <code>y</code> , <code>trt</code> , <code>time</code> , <code>n.random</code> blank and entering only <code>formula</code> , instead. The model output plots, will, however exclude growth curves in that event. If a formula is input and a response, <code>y</code> , is included, then the parameter input <code>y</code> may be omitted. If the <code>y</code> input is included, it will be over-written by that from <code>formula</code> .
<code>random.only</code>	A Boolean variable indicating whether the input <code>formula</code> contains random (for fixed) effects in the case that only one set are entered. If excluded and <code>formula</code> is entered without a <code> </code> , <code>random.only</code> defaults to FALSE.
<code>data</code>	A data frame containing the variables named in <code>formula</code> .
<code>dosemat</code>	An $n \times (\text{sum}(\text{numdose}) + 1)$ matrix object that maps subjects to treatment dosages. The first column should be an intercept column (filled with 1's). If

there is only a single treatment arm, then the number of columns in `dosemat` should be `sum(numdose)`. There is always a leave-one-out dosage for `dosemat`. For multiple treatment arms, the null (0) treatment is the one left out.

<code>numdose</code>	A vector object containing the number of dosages for each treatment. So the length should be the same as <code>typetreat</code> .
<code>typetreat</code>	A vector object specifying the prior formulation for each treatment. The choices for prior formulations are <code>c("car", "mvn", "ind")</code> .
<code>labt</code>	An optional vector object (of the same length as <code>typetreat</code> ) providing user names for each treatment. The names are used in plot objects. If <code>NULL</code> , then the numerical order of treatment entries are used.
<code>Omega</code>	A list object of length equal to the number of treatments chosen with the <code>"car"</code> <code>%in%</code> <code>typetreat</code> . List element <code>m</code> contains an <code>numdose[m] x numdose[m]</code> numeric matrix to encode the CAR adjacency matrix, where <code>numdose[m]</code> is the number of dosages receiving the multivariate CAR prior. This input is required only under <code>"car"</code> <code>%in%</code> <code>typetreat</code> .
<code>n.iter</code>	Total number of MCMC iterations.
<code>n.burn</code>	Number of MCMC iterations to discard. <code>ddpgrow</code> will return <code>(n.iter - n.burn)</code> posterior samples.
<code>n.thin</code>	Gap between successive sampling iterations to save.
<code>shape.dp</code>	Shape parameter under a $c \sim G(\text{shape.dp}, \text{rate.dp})$ prior on the concentration parameter of the DP (prior on the set of random effects parameters, $b_1, \dots, b_n \sim DP(c, G_0)$ where $n$ is the total number of subjects).
<code>rate.dp</code>	Rate parameter under a $c \sim G(\text{shape.dp}, \text{rate.dp})$ prior on the concentration parameter of the DP.
<code>M.init</code>	Scalar value capturing number of initial subject clusters to kick-off MCMC chain.
<code>plot.out</code>	A boolean variable indicating whether user wants to return plots with output results. Defaults to <code>TRUE</code> .

## Value

S3 `dpgrow` object, for which many methods are available to return and view results. Generic functions applied to an object, `res` of class `dpgrow`, includes:

`summary(res)` returns `call`, the function call made to `dpgrow` and `summary.results`, which contains a list of objects that include 95% credible intervals for each set of sampled parameters, specified as (2.5%, mean, 97.5%, including fixed and random effects. Also contains model fit statistics, including DIC (and associated `Dbar`, `Dhat`, `pD`, `pV`), as well as the log pseudo marginal likelihood (LPML), a leave-one-out fit statistic. Note that DIC is constructed as DIC3 (see Celeaux et. al. 2006), where the conditional likelihood evaluated at the posterior mode is replaced by the marginal predictive density. Lastly, the random and fixed effects design matrices,  $X$ ,  $Z$ , are returned that include both the user input nuisance covariates appended to the time and treatment-based covariates constructed by `dpgrow`.

```
print(summary(res))
```

prints contents of summary to console.

```
plot(res)
```

returns results plots, including the set of subject random effects values and credible intervals, a sample of by-subject growth curves, mean growth curves split by each treatment and control, as well as selected trace plots for number of clusters and for precision parameters for the likelihood and random effects. Lastly, a trace plot for the deviance statistic is also included.

```
samples(res)
```

contains (n.iter - n.burn) posterior sampling iterations for every model parameter, including fixed and random effects.

```
resid(res)
```

contains the model residuals.

### Note

The intended focus for this package are data where both number of subjects and number of repeated measures are limited. This function places a DDP prior on the set of subject effects. This means that the unknown (random) prior on subject effects is indexed by the subject dosage patterns across one or more treatments.

### Author(s)

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### References

T. D. Savitsky and S. M. Paddock (2011) Bayesian Hierarchical Semiparametric Modeling of Longitudinal Post-treatment Outcomes from Open-enrollment Therapy Groups, submitted to: JRSS Series A (Statistics in Society).

T. D. Savitsky and S. M. Paddock (2011) Visual Sufficient Statistics for Repeated Measures data with growcurves for R, submitted to: Journal of Statistical Software.

### See Also

[dpgrowmult](#), [dpgrowmm](#), [dpgrow](#)

### Examples

```
## Not run:
## extract simulated dataset
library(growcurves)
data(datddpsim)
## attach(datddpsim)
## run dpgrow mixed effects model; returns object of class "ddpgrow"
shape.dp = 4
res = ddpgrow(y = dat$y, subject = dat$subject,
trt = dat$trt, time = dat$time,
typetreat = c("mvn", "car", "ind", "car"),
numdose = dat$numdose,
labt = dat$labt, dosemat = dat$dosemat,
Omega = dat$Omega, n.random = dat$n.random,
n.fix_degree = 2, n.iter = 10000, n.burn = 2000,
```

```

n.thin = 10, shape.dp = 1)
plot.results = plot(res) ## ggplot2 plot objects, including growth curves
summary.results = summary(res) ## parameter credible intervals, fit statistics
samples.posterior = samples(res) ## posterior sampled values

## End(Not run)

```

---

ddpMCMCplots

*generate plots of posterior samples under ddpgrow model*


---

## Description

Constructs plots for subject effects, theta, with credible intervals as well as selected trace plots. Returns a list of objects of class ggplot.

## Usage

```

ddpMCMCplots(subjecti.u, labt = NULL, typet, numt, theta.summary, lambda.mean,
  pmvn.mean = NULL, taucar.summary = NULL, alphacar.summary = NULL,
  Taucar = NULL, Alphacar = NULL, tauind.summary = NULL, Tauind = NULL,
  M, Taue, Deviance)

```

## Arguments

subjecti.u	A vector of length P, number of unique subjects, containing unique set of user input values for subject.
labt	An vector object (of the same length as typet) providing user names for each treatment. The names are used in plot objects.
typet	A numeric vector of length equal to the number of treatments that specifies prior option for each treatment. Options must be one of: 1 = "car", 2 = "mvn", 3 = "ind".
numt	A numeric vector with same length as typet where each entry counts the number of doses for that treatment.
theta.summary	A list object of q elements, each containing an $P \times 3$ matrix of c(2.5%,50%,97.5%) quantile summaries for each subject of the applicable subject random effect parameter. P = number of subjects, q = number of random effect parameters, per subject.
lambda.mean	A $q \times q$ matrix of mean values of the polyomial order covariance matrix, Lambda, returned from ddpgrow.
pmvn.mean	A list object of length equal to the number of treatments with "mvn" %in% typetreat. Each list object contains an $numt[m] \times numt[m]$ matrix of mean elements of the "mvn" treatments covariance matrices, Pmvn, returned from ddpgrow.
taucar.summary	A $numcar \times 3$ numeric matrix of c(2.5%,50%,97.5%) quantile summaries for the scale parameter for numcar treatments where "car" %in% typetreat.

<code>alphacar.summary</code>	A <code>numcar</code> x 3 numeric matrix of <code>c(2.5%,50%,97.5%)</code> quantile summaries for the strength parameter for <code>numcar</code> treatments where " <code>car</code> " <code>%in%</code> <code>typetreat</code> .
<code>Taucar</code>	An <code>iter.keep</code> x <code>numcar</code> matrix of posterior samples capturing the CAR precision parameter for each treatment where " <code>car</code> " <code>%in%</code> <code>typetreat</code> .
<code>Alphacar</code>	An <code>iter.keep</code> x <code>numcar</code> matrix of posterior samples capturing the CAR strength parameter for each treatment where " <code>car</code> " <code>%in%</code> <code>typetreat</code> .
<code>tauind.summary</code>	A list object of length equal to <code>numcar</code> , the number of treatment with " <code>in</code> " <code>%in%</code> <code>typetreat</code> . Each list element contains an <code>numt[m]</code> x 3 matrix of <code>c(2.5%,50%,97.5%)</code> quantile summaries for the dosage scale parameters associated to that treatment <code>m</code> .
<code>Tauind</code>	A list object of length <code>numind</code> , the number treatments where " <code>car</code> " <code>%in%</code> <code>typetreat</code> with each element holding an <code>nkeep</code> x <code>numt[m]</code> matrix of sampled by-dose precision parameters for treatment <code>m</code> .
<code>M</code>	The <code>iter.keep</code> x 1 matrix of posterior samples for the parameter capturing the number of clusters formed under the DP prior on the client effects.
<code>Tau</code>	<code>iter.keep</code> x 1 matrix of posterior samples capturing the precision parameter for the model error term.
<code>Deviance</code>	<code>iter.keep</code> x 1 matrix of posterior samples for the model deviance.

### Value

A list of plot objects of class `ggplot2` including:

<code>p.theta</code>	stacked plots of <code>b0,...,b(q-1)</code> - vertical lines for each client span 2.5 noted.
<code>p.M</code>	MCMC trace plot of <code>M</code> , number of clusters.
<code>p.acar</code>	MCMC trace plots of <code>alphacar</code> , the CAR strength parameter. Plot is faceted for more than one set of treatments under " <code>car</code> ".
<code>p.tcar</code>	MCMC trace plots of <code>alphacar</code> , the CAR precision parameter. Plot is faceted for more than one set of treatments under " <code>car</code> ".
<code>p.taue</code>	MCMC trace plots of <code>tau.e</code> .
<code>p.dev</code>	MCMC trace plots of deviance.
<code>p.lam</code>	Heatmap (tiled) plot of posterior mean covariance, <code>Lambda</code> , of polynomial orders of random effects, <code>Delta_i</code> .
<code>p.mvn</code>	Heatmap plots of posterior mean covariance, <code>Pmvn</code> , of treatment dosages under " <code>mvn</code> " base distribution. Plots are faceted by treatment.
<code>p.aband</code>	95% credible bands for <code>alphacar</code> CAR strength parameters associated to treatments under " <code>car</code> " base distribution.
<code>p.tband</code>	95% credible bands for <code>taucar</code> CAR precision parameters associated to treatments under " <code>car</code> " base distribution.
<code>p.iband</code>	95% credible bands for <code>tauind</code> dose precision parameters for " <code>ind</code> " base distribution, faceted by treatment (if more than one).

**Note**

Intended as an internal function for [ddpgrow](#)

**Author(s)**

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**See Also**

[ddpgrow](#), [dpgrowmm](#), [dpgrow](#), [dpgrowmult](#)

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ddpPost	<i>Run a Bayesian mixed effects model for by-subject random effects with DDP prior</i>
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**Description**

An internal function to [ddpgrow](#)

**Usage**

```
ddpPost(y, X, Z, subject, dosemat, numt, typet, Omega, omegaplus, n.iter,
        n.burn, n.thin, shapealph, ratebeta, M.init)
```

**Arguments**

y	An $N \times I$ response (of subject-measure cases)
X	Fixed effects design matrix
Z	Random effects design matrix. Assumed grouped by subjects
subject	An $N \times I$ set of subject identifiers
dosemat	An $P \times T$ Anova or Multiple Membership design matrix linking treatment dosages to subjects where $T$ is the total number dosages across all treatments + 1 for an intercept. This formulation assumes there is a hold-out dose for each treatment. e.g. the null dosage.
numt	A numeric vector of length equal to the number of treatments that contains the number of dosages for each treatment.
typet	A numeric vector of length equal to the number of treatments that contains the base distribution for each treatment. 1 = "car", 2 = "mvn", 3 = "ind"
Omega	A list object of length equal to the number of treatments with "car" selected for base distribution. Each entry is an $\text{numt}[m] \times \text{numt}[m]$ numeric CAR adjacency matrix for the dosages of treatment $m$ .
omegaplus	A list object of length equal to the number of treatments under "car" containing numeric vectors that are rowSums of the corresponding matrix element in Omega.
n.iter	The number of MCMC iterations

n.burn	The number of MCMC burn-in iterations to discard
n.thin	The step increment of MCMC samples to return
shapealph	The shape parameter for the $\Gamma$ prior on the DP concentration parameter.
ratebeta	The rate parameter for the $\Gamma$ prior on the DP concentration parameter.
M.init	Initial MCMC chain scalar value for number of by-subject clusters. If excluded defaults to <code>length(unique(subject))</code> .

**Value**

res A list object containing MCMC runs for all model parameters.

**Note**

Intended as an internal function for [ddpgrow](#)

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**See Also**

[dpgrow](#)

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ddp_quantiles	<i>Produce quantile summaries of model posterior samples</i>
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**Description**

Inputs MCMC samples for model parameters and constructs `c(2.5%,50%,97.5%)` quantile summaries.

**Usage**

```
ddp_quantiles(model.output, dosemat, Nfixed, Nrandom, Nsubject, typet)
```

**Arguments**

model.output	A list vector of objects returned by MCMC sampling functions. e.g. <code>mmCplusDpPost</code> for option = "mmcar".
dosemat	An $P \times (T+1)$ matrix object that maps subjects to treatment dosages. The first column should be an intercept column (filled with 1's).
Nfixed	Number of total fixed effects, both time-based and nuisance.
Nrandom	Number of total random effects, both time-based and nuisance, all grouped by subject.
Nsubject	Number of unique subjects (on which repeated measures are observed).
typet	A numeric vector of length equal to the number of treatments that contains the base distribution for each treatment. 1 = "car", 2 = "mvn", 3 = "ind".



**Value**

A list object containing quantile summaries for all sampled model parameters.

deviance.summary	vector of length 3 summarizing quantiles for model deviance.
beta.summary	$N_{\text{fixed}} \times 3$ quantile summaries of model fixed effects.
alpha.summary	quantile summary of model global intercept parameter.
theta.summary	list object of length $N_{\text{random}}$ , each cell containing a $n \times 3$ matrix of by-subject random effect parameter quantile summaries.
lambda.summary	$N_{\text{random}}^2 \times 3$ quantile summaries of by-polynomial order precision parameters used in base distributions.
lambda.mean	$N_{\text{random}} \times N_{\text{random}}$ posterior means of by-polynomial order precision parameters used in base distributions.
alphacar.summary	$\text{numcar} \times 3$ quantile summaries of proper CAR strength of correlation parameters for CAR base distribution on subject-dose random effects, where $\text{numcar} \leq \text{nty}$ treatments.
taucar.summary	$\text{numcar} \times 3$ quantile summaries of proper CAR precision parameters for CAR base distribution on subject-dose random effects, where $\text{numcar} \leq \text{nty}$ treatments.
dosetrt.summary	list object of length $\text{nty}$ , each cell containing a $N_{\text{subject}} \times (N_{\text{random}} \times \text{numt}[m]) \times 3$ matrix of quantile summaries for subject-dose random effects.
dosetrt.mean	list object of length $\text{nty}$ , each cell containing a $N_{\text{subject}} \times (N_{\text{random}} \times \text{numt}[m])$ matrix of posterior mean values for subject-dose random effects.
pind.summary	list object of length $\text{numind}$ , each cell contains a $\text{numt}[m] \times 3$ matrix of quantile summaries for precision values under IND base distribution, where $\text{numind} \leq \text{nty}$ treatments.
pmvn.summary	list object of length $\text{nummvn}$ , each cell containing quantile summaries for precision parameters used for MVN base distribution on subject-dose random effects, where $\text{nummvn} \leq \text{nty}$ treatments.
pmvn.summary	list object of length $\text{nummvn}$ , each cell containing posterior mean for $\text{numt}[m] \times \text{numt}[m]$ matrix of precision parameters used for MVN base distribution on subject-dose random effects, where $\text{nummvn} \leq \text{nty}$ treatments.
doseint.summary	list object of length $N_{\text{random}}$ , each cell containing a $N_{\text{subject}} \times 3$ matrix of quantile summaries for the intercept parameter in the subject-dose random effects.
taue.summary	quantile summary for model error precision parameter.
M.summary	quantile summary for number of DP posterior clusters formed.
Dbar	Model fit statistics.
pD	Model fit statistics.
pV	Model fit statistics.
DIC	Model fit statistics.
lpml	Model fit statistics.

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**See Also**

[dpgrowmm](#), [dpgrow](#)

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dpgrow

*Bayesian semiparametric growth curve models.*

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**Description**

Employs a Dirichlet Process (DP) prior on the set of by-subject random effect parameters under repeated waves of measurements to allow the number of random effect parameters specified per subject,  $q$ , to be equal to the number of measurement waves,  $T$ . Random effects are grouped by subject and all  $q$  parameters receive the DP prior. The resulting joint marginal distribution over the data is a DP mixture.

**Usage**

```
dpgrow(y, subject, trt, time, n.random, n.fix_degree, formula, random.only,
       data, n.iter, n.burn, n.thin, shape.dp, rate.dp, plot.out, option)
```

**Arguments**

<code>y</code>	A univariate continuous response, specified as an $N \times I$ matrix or vector, where $N$ captures the number of subject-time cases (repeated subject measures). Data may reflect unequal number of measures per subject. Missing occasions are left out as no NA values are allowed.
<code>subject</code>	The objects on which repeated measures are conducted that serves as the random effects grouping factor. Input as an $N \times I$ matrix or vector of subject-measure cases in either integer or character format; e.g. $(1, 1, 1, 2, 2, 3, 3, 3, \dots, n, n, n)$ , where $n$ is the total number of subjects.
<code>trt</code>	An integer or character matrix/vector of length $N$ (number of cases) indicating treatment group assignments for each case. May also be input as length $P$ vector, where $P$ is the number of unique subjects, indicating subject group assignment. Multiple treatment groups are allowed and if the vector is entered as numeric, e.g. $(0, 1, 2, 3, \dots)$ , the lowest numbered group is taken as baseline (captured by global fixed effects). If entered in character format, the first treatment entry is taken as baseline. If there are no treatment (vs. control) groups, then this input may be excluded (set to NULL).
<code>time</code>	A univariate vector of length $N$ , capturing the time points associated to each by-subject measure. May leave blank if only one time point (no repeated measures).

n.random	The desired number of subject random effect terms, $q$ . Under option = "dp" may be set equal to the number of measurement waves, $T$ . The $y$ , $trt$ , $time$ vectors will together be used to create both fixed and random effect design matrices. The random effects matrix will be of the form, $(1, time, \dots, time^{(n.random - 1)})$ (grouped, by subject). This formulation is a growth curve model that allows assessment of by-treatment effects and by-client growth curves.
n.fix_degree	The desired polynomial order in time to use for generating time-based fix effects. The fixed effects matrix will be constructed as, $(time, \dots, time^{(n.fix\_degree)}, trt_1, time*trt_1, \dots, time^{(n.fix\_degree)}*trt_1, trt_L, \dots, time^{(n.fix\_degree)}*trt_L)$ . If $is.null(n.fix\_degree)   n.fix\_degree == 0 \& is.null(trt)$ time-by-treatment fixed effects and growth curves are not generated.
formula	Nuisance fixed and random effects may be entered in formula with the following format, $y \sim x_1 + x_2*x_3   z_1*z_2$ as an object of class formula. The bar,  , separates fixed and random effects. If it is only desired to enter either fixed or random effects, but not both then the   may be omitted. Note: the nuisance random effects are assumed to be grouped by subject. The fixed and random effects values may change with each repeated measure; however, within subject growth curves will keep constant $z$ and $x$ values between measurement waves. It is possible to bypass the growth curve construction by leaving $y$ , $trt$ , $time$ , $n.random$ , $n.fix\_degree$ blank and entering only formula, instead. The model output plots, will, however exclude growth curves in that event. If a formula is input (which requires response, $y$ ) then the separate entry of $y$ may be omitted. If the parameter $y$ is input, it will be over-written by that from formula.
random.only	A Boolean variable indicating whether the input formula contains random (for fixed) effects in the case that only one set are entered. If excluded and formula is entered without a  , random.only defaults to FALSE.
data	a data.frame containing the variables with names as specified in formula, including the response, $y$ .
n.iter	Total number of MCMC iterations.
n.burn	Number of MCMC iterations to discard. dpgrow will return $(n.iter - n.burn)$ posterior samples.
n.thin	Gap between successive sampling iterations to save.
shape.dp	Shape parameter under a $c \sim G(shape.dp, 1)$ prior on the concentration parameter of the DP (prior on the set of random effects parameters, $b_1, \dots, b_n \sim DP(c, G_0)$ where $n$ is the total number of subjects.
rate.dp	Rate parameter under a $c \sim G(shape.dp, rate.dp)$ prior on the concentration parameter of the DP.
plot.out	A boolean variable indicating whether user wants to return plots with output results. Defaults to TRUE.
option	Modeling option, of which there are two: 1. dp places a DP prior on the set of subject random effects; 2. lgm places the usual independent Gaussian priors on the set of random effects.

**Value**

S3 dpgrow object, for which many methods are available to return and view results. Generic functions applied to an object, `res` of class `dpgrow`, includes:

<code>summary(res)</code>	returns <code>call</code> , the function call made to <code>dpgrow</code> and <code>summary.results</code> , which contains a list of objects that include 95% credible intervals for each set of sampled parameters, specified as (2.5%, mean, 97.5%, including fixed and random effects. Also contains model fit statistics, including DIC (and associated <code>Dbar</code> , <code>Dhat</code> , <code>pD</code> , <code>pV</code> ), as well as the log pseudo marginal likelihood (LPML), a leave-one-out fit statistic. Note that for <code>option = "dp"</code> , DIC is constructed as DIC3 (see Celeaux et. al. 2006), where the conditional likelihood evaluated at the posterior mode is replaced by the marginal predictive density. Lastly, the random and fixed effects design matrices, <code>X</code> , <code>Z</code> , are returned that include both the user input nuisance covariates appended to the time and treatment-based covariates constructed by <code>dpgrow</code> .
<code>print(summary(res))</code>	prints contents of <code>summary</code> to console.
<code>plot(res)</code>	returns results plots, including the set of subject random effects values and credible intervals, a sample of by-subject growth curves, mean growth curves split by each treatment and control, as well as selected trace plots for number of clusters and for precision parameters for the likelihood and random effects. Lastly, a trace plot for the deviance statistic is also included.
<code>samples(res)</code>	contains ( <code>n.iter - n.burn</code> ) posterior sampling iterations for every model parameter, including fixed and random effects.
<code>resid(res)</code>	contains the model residuals.

**Note**

The intended focus for this package are data where both number of subjects and number of repeated measures are limited. A DP prior is placed on the by-subject random effects to borrow strength across subjects for each estimation of each subject's growth curve. The imposition of the DP prior also allows the resulting posterior distributions over the subject random effects to be non-Gaussian. The `dpgrow` function is very similar to `dpgrowmm`; only the latter includes a separate set of random effects not grouped by subject (e.g. for treatment dosages allocated to subjects) mapped back to subject-time cases through a multiple membership design matrix. The `dpgrowmult` function generalizes `dpgrowmm` by allowing more than one multiple membership effects term. See Savitsky and Paddock (2011) for detailed model constructions.

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**References**

S. M. Paddock and T. D. Savitsky (2012) Bayesian Hierarchical Semiparametric Modeling of Longitudinal Post-treatment Outcomes from Open-enrollment Therapy Groups, submitted to: JRSS Series A (Statistics in Society).

T. D. Savitsky and S. M. Paddock (2011) Visual Sufficient Statistics for Repeated Measures data with growcurves for R, submitted to: Journal of Statistical Software.

### See Also

[dpgrowmm](#)

### Examples

```
## Not run:
## extract simulated dataset
library(growcurves)
data(datsim)
## attach(datsim)
## run dpgrow mixed effects model; returns object of class "dpgrow"
shape.dp = 4
res = dpgrow(y = datsim$y, subject = datsim$subject,
trt = datsim$trt, time = datsim$time,
n.random = datsim$n.random,
n.fix_degree = 2, n.iter = 10000,
n.burn = 2000, n.thin = 10,
shape.dp = shape.dp, option = "dp")
plot.results = plot(res) ## ggplot2 plot objects, including growth curves
summary.results = summary(res) ## parameter credible intervals, fit statistics
samples.posterior = samples(res) ## posterior sampled values

## End(Not run)
```

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dpgrowmm

*Bayesian semiparametric growth curve models with employment of multiple membership random effects.*

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### Description

Employs a Dirichlet Process (DP) prior on the set of by-subject random effect parameters under repeated waves of measurements to allow the number of random effect parameters specified per subject,  $q$ , to be equal to the number of measurement waves,  $T$ . Random effects are grouped by subject and all  $q$  parameters receive the DP prior. An additional set of random effects are included that utilize a different grouping factor; e.g. treatment(s) exposure or dosage. These additional random effects are mapped back to subjects through a multiple membership weight matrix.

### Usage

```
dpgrowmm(y, subject, trt, time, n.random, n.fix_degree, formula, random.only,
data, Omega, group, subj.aff, W.subj.aff, multi, n.iter, n.burn, n.thin,
strength.mm, shape.dp, rate.dp, plot.out, option)
```

**Arguments**

<code>y</code>	A univariate continuous response, specified as an $N \times I$ matrix or vector, where $N$ captures the number of subject-time cases (repeated subject measures). Data may reflect unequal number of measures per subject. Missing occasions are left out as no NA values are allowed.
<code>subject</code>	The objects on which repeated measures are conducted that serves as the random effects grouping factor. Input as an $N \times I$ matrix or vector of subject-measure cases in either integer or character format; e.g. $(1, 1, 1, 2, 2, 3, 3, 3, \dots, n, n, n)$ , where $n$ is the total number of subjects.
<code>trt</code>	An integer or character matrix/vector of length $N$ (number of cases) indicating treatment group assignments for each case. May also be input as length $P$ vector, where $P$ is the number of unique subjects, indicating subject group assignment. Multiple treatment groups are allowed and if the vector is entered as numeric, e.g. $(0, 1, 2, 3, \dots)$ , the lowest numbered group is taken as baseline (captured by global fixed effects). If entered in character format, the first treatment entry is taken as baseline. If there are no treatment (vs. control) groups, then this vector may be excluded (set to NULL).
<code>time</code>	A univariate vector of length $N$ , capturing the time points associated to each by-subject measure. May leave blank if only one time point (no repeated measures).
<code>n.random</code>	The desired number of time-indexed subject random effect terms, $q$ . Since a DP prior is used on subject effects, may be set equal to the number of measurement waves, $T$ . The <code>y</code> , <code>trt</code> , <code>time</code> vectors will together be used to create both fixed and random effect design matrices. The random effects matrix will be of the form, $(1, \text{time}, \dots, \text{time}^{(n.random - 1)})$ (grouped, by subject). This formulation is a growth curve model that allows assessment of by-treatment effects and by-client growth curves.
<code>n.fix_degree</code>	The desired polynomial order in time to use for generating time-based fix effects. The fixed effects matrix will be constructed as, $(\text{time}, \dots, \text{time}^{(n.fix\_degree)}, \text{trt}_1, \text{time} * \text{trt}_1, \dots, \text{time}^{(n.fix\_degree)} * \text{trt}_1, \text{trt}_L, \dots, \text{time}^{(n.fix\_degree)} * \text{trt}_L)$ . This formulation is a growth curve model that allows assessment of by-treatment effects and by-client growth curves. If <code>is.null(n.fix_degree)   n.fix_degree == 0 &amp; is.null(trt)</code> time-by-treatment fixed effects and growth curves are not generated.
<code>formula</code>	Nuisance fixed and random effects may be entered in formula with the following format, $y \sim x_1 + x_2 * x_3 \mid z_1 * z_2$ as an object of class formula. The bar, <code> </code> , separates fixed and random effects. If it is only desired to enter either fixed or random effects, but not both then the <code> </code> may be omitted. Note: the nuisance random effects are assumed to be grouped by subject. The fixed and random effects values may change with each repeated measure; however, within subject growth curves will keep constant $z$ and $x$ values between measurement waves. It is possible to bypass the growth curve construction by leaving <code>y</code> , <code>trt</code> , <code>time</code> , <code>n.random</code> , <code>n.fix_degree</code> blank and entering only formula, instead. The model output plots, will, however exclude growth curves in that event. If a formula is input (which requires response, <code>y</code> ) then the separate entry of <code>y</code> may be omitted. If the parameter <code>y</code> is input, it will be over-written by that from formula.

random.only	A Boolean variable indicating whether the input formula contains random (for fixed) effects in the case that only one set are entered. If excluded and formula is entered without a  , random.only defaults to FALSE.
data	a data.frame containing the variables with names as specified in formula, including the response, y.
Omega	An $S \times S$ numerical matrix object to encode the CAR adjacency matrix for random effects mapped through multiple membership, where $S$ is the number of effects mapped to subjects through the multiple membership construction. This input applies only to option = "mmcar".
group	A numeric or character vector of length $S$ , providing group identifiers for each of $S$ multiple membership effects (e.g. (1,1,1,2,2,...)). If excluded, it is assumed there is a single group.
subj.aff	A $n.aff \times 1$ vector subset of subject composed with unique subject identifiers that are linked to the multiple membership effects; e.g. one or more treatment cohorts. If all subjects are to receive the mapping of multiple membership effects, subj.aff may be left blank.
W.subj.aff	An $n.aff \times S$ numeric matrix that maps a set of random effects to affected subjects, where $P.aff$ is the length of the unique subjects to whom the multiple membership random effects applies. It is assumed that the row order is the same as the order of subj.aff (or unique(subject) if subj.aff is not input). If W.subj.aff is a multiple membership weight matrix, then the rows will sum to 1. The form and therefore, interpretation of output is dependent on form of input; for example, the rows of W.subj.aff may include indicators for whether each of $S$ treatment dosages are linked to a given subject.
multi	A boolean scalar input that when set to TRUE indicates the each of the $S$ MM effects is multivariate. Leave blank if univariate multiple membership effects are desired. It is assumed that the associated design matrix is equal to the number of time-indexed random effects. For example, the time-indexed (non-nuisance) random effects design matrix, $Z = (1, time, time^n.random - 1)$ is also used to compose an inner product with each row of the $N \times n$ . random MM product, $W * U$ , where $W$ is case-expanded MM design matrix and $U$ is the $S \times n$ . random set of multivariate MM effects.
n.iter	Total number of MCMC iterations.
n.burn	Number of MCMC iterations to discard. dpgrow will return (n.iter - n.burn) posterior samples.
n.thin	Gap between successive sampling iterations to save.
strength.mm	Sets both the shape and rate parameter for a $\tau_{\{\gamma\}} \sim G(strength.mm, strength.mm)$ prior on the precision parameter of either a CAR ( $\gamma \sim CAR(\tau_{\gamma})$ ) or independent ( $\gamma \sim N(0, \tau^{-1})I_S$ ) prior on the set of $S$ multiple membership effects.
shape.dp	Shape parameter under a $c \sim G(shape.dp, 1)$ prior on the concentration parameter of the DP (prior on the set of random effects parameters, $b_1, \dots, b_n \sim DP(c, G_0)$ where $n$ is the total number of subjects.
rate.dp	Rate parameter under a $c \sim G(shape.dp, rate.dp)$ prior on the concentration parameter of the DP.

<code>plot.out</code>	A boolean variable indicating whether user wants to return plots with output results. Defaults to TRUE.
<code>option</code>	Modeling option, of which there are three: 1. <code>mmcar</code> places a CAR prior on the set of multiple membership effects; 2. <code>mmi</code> places the usual independent Gaussian priors on the set of multiple membership effects. 3. <code>mmigrp</code> employs a set of independent Gaussian priors, but with a common mean parameter for each sub-group of multiple membership effects sharing a common group identifier. (e.g. treatment groups that disjointly divide therapy sessions from Savitsky and Paddock (2011))

### Value

S3 `dpgrowmm` object, for which many methods are available to return and view results. Generic functions applied to an object, `res` of class `dpgrow`, includes:

<code>summary(res)</code>	returns <code>call</code> , the function call made to <code>dpgrowmm</code> and <code>summary.results</code> , which contains a list of objects that include 95% credible intervals for each set of sampled parameters, specified as (2.5%, mean, 97.5%, including fixed and random effects. Also contains model fit statistics, including DIC (and associated <code>Dbar</code> , <code>Dhat</code> , <code>pD</code> , <code>pV</code> ), as well as the log pseudo marginal likelihood (LPML), a leave-one-out fit statistic. Note that DIC is constructed as DIC3 (see Celeaux et. al. 2006), where the conditional likelihood evaluated at the posterior mode is replaced by the marginal predictive density. Lastly, the random and fixed effects design matrices, $X$ , $Z$ , are returned that include both the user input nuisance covariates appended to the time and treatment-based covariates constructed by <code>dpgrowmm</code> .
<code>print(summary(res))</code>	prints contents of <code>summary</code> to console.
<code>plot(res)</code>	returns results plots, including the set of subject random effects values and credible intervals, a sample of by-subject growth curves, mean growth curves split by each treatment and control, as well as selected trace plots for number of clusters and for precision parameters for the likelihood and random effects. Lastly, a trace plot for the deviance statistic is also included.
<code>samples(res)</code>	contains ( <code>n.iter - n.burn</code> ) posterior sampling iterations for every model parameter, including fixed and random effects.
<code>resid(res)</code>	contains the model residuals.

### Note

The intended focus for this package are data where both number of subjects and number of repeated measures are limited. A DP prior is placed on the by-subject random effects to borrow strength across subjects for each estimation of each subject's growth curve. The imposition of the DP prior also allows the resulting posterior distributions over the subject random effects to be non-Gaussian. The `dpgrow` function is very similar to `dpgrowmm`; only the latter includes a separate set of random effects not grouped by subject (e.g. for treatment dosages allocated to subjects) mapped back to subject-time cases through a multiple membership design matrix. The `dpgrowmult` function generalizes `dpgrowmm` by allowing more than one multiple membership effects term. See Savitsky and Paddock (2011) for detailed model constructions.



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**References**

S. M. Paddock and T. D. Savitsky (2012) Bayesian Hierarchical Semiparametric Modeling of Longitudinal Post-treatment Outcomes from Open-enrollment Therapy Groups, submitted to: JRSS Series A (Statistics in Society).

T. D. Savitsky and S. M. Paddock (2012) Visual Sufficient Statistics for Repeated Measures data with growcurves for R, submitted to: Journal of Statistical Software.

**See Also**

[dpgrow](#), [dpgrowmult](#)

**Examples**

```
## Not run:
## extract simulated dataset
library(growcurves)
data(datsim)
## attach(datsim)
## Model with DP on clients effects, but now INCLUDE session random effects
## in a multiple membership construction communicated with the N x S matrix, W.subj.aff.
## Returns object, res.mm, of class "dpgrowmm".
shape.dp = 3
strength.mm = 0.001
res.mm = dpgrowmm(y = datsim$y, subject = datsim$subject,
trt = datsim$trt, time = datsim$time,
n.random = datsim$n.random,
n.fix_degree = 2, Omega = datsim$Omega,
group = datsim$group,
subj.aff = datsim$subj.aff,
W.subj.aff = datsim$W.subj.aff,
n.iter = 10000, n.burn = 2000, n.thin = 10,
shape.dp = shape.dp, rate.dp = rate.dp,
strength.mm = strength.mm, option = "mmcar")
plot.results = plot(res.mm) ## ggplot2 plot objects,
summary.results = summary(res.mm) ## credible intervals and fit statistics
samples.posterior = samples(res.mm) ## posterior sampled values

## End(Not run)
```

## Description

Employs a Dirichlet Process (DP) prior on the set of by-subject random effect parameters under repeated waves of measurements to allow the number of random effect parameters specified per subject,  $q$ , to be equal to the number of measurement waves,  $T$ . Random effects are grouped by subject and all  $q$  parameters receive the DP prior. Additional sets of possibly more than 1 multiple membership effect terms are included, each with a separate weight/design matrix that maps the effects back to clients. A variety of prior formulations are available for the effects in each multiple membership term.

## Usage

```
dpgrowthmult(y, subject, trt, time, n.random, n.fix_degree, formula, random.only,
  data, Omega, group, subj.aff, W.subj.aff, n.iter, n.burn, n.thin, strength.mm,
  shape.dp, rate.dp, plot.out, option, ulabs)
```

## Arguments

<code>y</code>	A univariate continuous response, specified as an $N \times I$ matrix or vector, where $N$ captures the number of subject-time cases (repeated subject measures). Data may reflect unequal number of measures per subject. Missing occasions are left out as no NA values are allowed.
<code>subject</code>	The objects on which repeated measures are conducted that serves as the random effects grouping factor. Input as an $N \times I$ matrix or vector of subject-measure cases in either integer or character format; e.g. $(1, 1, 1, 2, 2, 3, 3, 3, \dots, n, n, n)$ , where $n$ is the total number of subjects.
<code>trt</code>	An integer or character vector of length $N$ (number of cases) indicating treatment group assignments for each case. May also be input as length $P$ vector, where $P$ is the number of unique subjects, indicating subject group assignment. Multiple treatment groups are allowed and if the vector is entered as numeric, e.g. $(0, 1, 2, 3, \dots)$ , the lowest numbered group is taken as baseline (captured by global fixed effects). If entered in character format, the first treatment entry is taken as baseline. If there are no treatment (vs. control) groups, then this vector may be excluded (set to NULL).
<code>time</code>	A univariate vector of length $N$ , capturing the time points associated to each by-subject measure. May leave blank if only one time point (no repeated measures).
<code>n.random</code>	The desired number of subject random effect terms, $q$ . Since a DP prior is used on client effects, may be set equal to the number of measurement waves, $T$ . The <code>y</code> , <code>trt</code> , <code>time</code> vectors will together be used to create both fixed and random effect design matrices. The random effects matrix will be of the form, $(1, \text{time}, \dots, \text{time}^{(n.random - 1)})$ (grouped, by subject). This formulation is a growth curve model that allows assessment of by-treatment effects and by-client growth curves.
<code>n.fix_degree</code>	The desired polynomial order in time to use for generating time-based fix effects. The fixed effects matrix will be constructed as, $(\text{time}, \dots, \text{time}^{(n.fix\_degree)}, \text{trt}_1, \text{time} * \text{trt}_1, \dots, \text{time}^{(n.fix\_degree)} * \text{trt}_1, \text{trt}_L, \dots, \text{time}^{(n.fix\_degree)} * \text{trt}_L)$ . This formulation is a growth curve model that allows assessment of by-treatment effects and by-client growth curves. If <code>is.null(n.fix_degree)   n.fix_degree == 0</code> &

	<p><code>is.null(trt)</code> time-by-treatment fixed effects and growth curves are not generated.</p>
formula	<p>Nuisance fixed and random effects may be entered in formula with the following format, <math>y \sim x_1 + x_2 * x_3 \mid z_1 * z_2</math> as an object of class formula. The bar,  , separates fixed and random effects. If it is only desired to enter either fixed or random effects, but not both then the   may be omitted. Note: the nuisance random effects are assumed to be grouped by subject. The fixed and random effects values may change with each repeated measure; however, within subject growth curves will keep constant z and x values between measurement waves. It is possible to bypass the growth curve construction by leaving y, trt, time, n.random, n.fix_degree blank and entering only formula, instead. The model output plots, will, however exclude growth curves in that event. If a formula is input (which requires response, y) then the separate entry of y may be omitted. If the parameter y is input, it will be over-written by that from formula.</p>
random.only	<p>A Boolean variable indicating whether the input formula contains random (for fixed) effects in the case that only one set are entered. If excluded and formula is entered without a  , random.only defaults to FALSE.</p>
data	<p>a data.frame containing the variables with names as specified in formula, including the response, y.</p>
Omega	<p>A list object of length equal to the number of multiple membership (MM) effect terms chosen with the "mmcar" option. List element i contains an <math>S[i] \times S[i]</math> numeric matrix to encode the CAR adjacency matrix, where <math>S[i]</math> is the number of effects mapped to subjects for list component i. This input is required only under option = "mmcar".</p>
group	<p>A list object of length equal to the number of MM terms chosen with prior formulation options "mmcar" or "mmigrp". List element i contains a numeric or character vector of length <math>S[i]</math>, providing group identifiers for each of <math>S[i]</math> effects in term i. (e.g. (1,1,1,2,2,...)). If there is only a single group for term [i], this element should be loaded with an <math>S[i] \times 1</math> vector of a single value.</p>
subj.aff	<p>A list object of length equal to the number of total MM terms. List element i contains a <math>P.aff[i] \times 1</math> vector subset of subject composed with unique subject identifiers that are linked to the effects in term i; e.g. one or more treatment cohorts. <math>P.aff[i]</math> is the length of the unique subjects linked to the effects in MM term i. If all subjects are to receive the mapping of multiple membership effects then <math>P.aff[i]</math> should contain a list of the unique subjects in subject.</p>
W.subj.aff	<p>A list object of length equal to the number of MM terms. List element i contains a <math>P.aff[i] \times S[i]</math> numeric matrix that maps a set of random effects to affected subjects (<code>subj.aff[[i]]</code>). It is assumed that the row order is the same as the order of <code>subj.aff[[i]]</code>. If <code>W.subj.aff[[i]]</code> is a multiple membership weight matrix, then the rows will sum to 1, though this is not required. The rows of <code>W.subj.aff</code> may alternatively be formulated with indicators for whether each of S treatment dosages are linked to a given subject.</p>
n.iter	<p>Total number of MCMC iterations.</p>
n.burn	<p>Number of MCMC iterations to discard. dpgrow will return (<code>n.iter - n.burn</code>) posterior samples.</p>

n.thin	Gap between successive sampling iterations to save.
strength.mm	Sets both the shape and rate parameter for a $\tau_{\{\gamma\}} \sim G(\text{strength.mm}, \text{strength.mm})$ prior on the precision parameter of either a CAR ( $\gamma \sim \text{CAR}(\tau_{\gamma})$ ) or independent ( $\gamma \sim N(0, \tau_{\gamma}^{-1} I_S)$ ) prior on the set of S multiple membership effects. Defaults to $\text{strength.mm} = 0.01$ .
shape.dp	Shape parameter under a $c \sim G(\text{shape.dp}, 1)$ prior on the concentration parameter of the DP (prior on the set of random effects parameters, $b_1, \dots, b_n \sim \text{DP}(c, G_0)$ where n is the total number of subjects).
rate.dp	Rate parameter under a $c \sim G(\text{shape.dp}, \text{rate.dp})$ prior on the concentration parameter of the DP.
plot.out	A boolean variable indicating whether user wants to return plots with output results. Defaults to TRUE.
option	A character vector of length equal to the total number of multiple membership terms that supplies the prior formulation choice for each term. The elements of option are confined to choose from among <code>c("mmcar", "mmi", "mmigrp", "mmdp")</code> . Any element of this choice set may be selected multiple times as desired. For example, to add 3 multiple membership terms with effects in the first term under a DP prior, the second term under a CAR prior and the third also under a CAR prior, the entry would be, <code>option = c("mmdp", "mmcar", "mmcar")</code> . The corresponding list entries should conform this choice for option. The order of sampled effect values returned conforms to this order of input in option (and the corresponding <code>subj.aff</code> and <code>W.subj.aff</code> ).
ulabs	A vector of the same length as option containing desired labels for each multiple membership term. These label values are employed in returned plot objects. If left blank, ulabs is set to a sequential number vector starting at 1.

## Value

S3 `dpgrowthmult` object, for which many methods are available to return and view results. Generic functions applied to an object, `res` of class `dpgrowth`, includes:

<code>summary(res)</code>	returns <code>call</code> , the function call made to <code>dpgrowthmult</code> and <code>summary.results</code> , which contains a list of objects that include 95% credible intervals for each set of sampled parameters, specified as (2.5%, mean, 97.5%, including fixed and random effects. Also contains model fit statistics, including DIC (and associated <code>Dbar</code> , <code>Dhat</code> , <code>pD</code> , <code>pV</code> ), as well as the log pseudo marginal likelihood (LPML), a leave-one-out fit statistic. Note that DIC is constructed as DIC3 (see Celeaux et al. 2006), where the conditional likelihood evaluated at the posterior mode is replaced by the marginal predictive density. Lastly, the random and fixed effects design matrices, <code>X</code> , <code>Z</code> , are returned that include both the user input nuisance covariates appended to the time and treatment-based covariates constructed by <code>dpgrowthmult</code> .
<code>print(summary(res))</code>	prints contents of summary to console.
<code>plot(res)</code>	returns results plots, including the set of subject random effects values and credible intervals, a sample of by-subject growth curves, mean growth curves split

by each treatment and control, as well as selected trace plots for number of clusters and for precision parameters for the likelihood and random effects. Lastly, a trace plot for the deviance statistic is also included.

`samples(res)` contains  $(n.iter - n.burn)$  posterior sampling iterations for every model parameter, including fixed and random effects.

`resid(res)` contains the model residuals.

### Note

The intended focus for this package are data where both number of subjects and number of repeated measures are limited. A DP prior is placed on the by-subject random effects to borrow strength across subjects for each estimation of each subject's growth curve. The imposition of the DP prior also allows the resulting posterior distributions over the subject random effects to be non-Gaussian. The `dpgrowmult` function generalizes `dpgrowmm` by allowing more than one multiple membership effects term.

### Author(s)

Terrance Savitsky <tds151@gmail.com> Susan Paddock <paddock@rand.org>

### References

S. M. Paddock and T. D. Savitsky (2012) Bayesian Hierarchical Semiparametric Modeling of Longitudinal Post-treatment Outcomes from Open-enrollment Therapy Groups, invited re-submission to: JRSS Series A (Statistics in Society).

T. D. Savitsky and S. M. Paddock (2012) Visual Sufficient Statistics for Repeated Measures data with growcurves for R, submitted to: Journal of Statistical Software.

### See Also

[dpgrowmm](#)

### Examples

```
## Not run:
## extract simulated dataset
library(growcurves)
data(datsimmult)
## Model with DP on clients effects, but now INCLUDE session random effects
## in a multiple membership construction communicated with the N x S matrix, W.subj.aff.
## Returns object, res.mm, of class "dpgrowmm".
shape.dp = 3
res.mult = dpgrowmult(y = datsimmult$y, subject = datsimmult$subject,
trt = datsimmult$str, time = datsimmult$time,
n.random = datsimmult$n.random, Omega = datsimmult$Omega,
group = datsimmult$group,
subj.aff = datsimmult$subj.aff,
W.subj.aff = datsimmult$W.subj.aff, n.iter = 10000,
n.burn = 2000, n.thin = 10, shape.dp = shape.dp,
option = c("mmi", "mmcar"))
```

```

plot.results = plot(res.mult) ## ggplot2 plot objects, including growth curves
summary.results = summary(res.mult) ## parameter credible intervals, fit statistics
samples.posterior = samples(res.mult) ## posterior sampled values

## End(Not run)

```

---

dpPost	<i>Run a Bayesian mixed effects model for by-subject random effects with DP prior</i>
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---

## Description

An internal function to [dpgrow](#)

## Usage

```
dpPost(y, X, Z, subjects, niter, nburn, nthin, shapealph, ratebeta)
```

## Arguments

y	An $N \times I$ response (of subject-measure cases)
X	Fixed effects design matrix
Z	Random effects design matrix. Assumed grouped by subjects
subjects	An $N \times I$ set of subject identifiers
niter	The number of MCMC iterations
nburn	The number of MCMC burn-in iterations to discard
nthin	The step increment of MCMC samples to return
shapealph	The shape parameter for the $\Gamma$ prior on the DP concentration parameter. The rate parameter is set of 1.
ratebeta	The rate parameter for the $\Gamma$ prior on the DP concentration parameter. Default value is 1.

## Value

res A list object containing MCMC runs for all model parameters.

## Note

Intended as an internal function for [dpgrow](#)

## Author(s)

Terrance Savitsky <tds151@gmail.com>

## See Also

[dpgrow](#)

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effectsplot	<i>Plot comparison of Effect parameters of a Multiple membership (MM) term under varied prior formulations</i>
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---

### Description

Produces an overlaid plot of multiple membership effect values under chosen prior formulations. The effect values for a focus (or all) multiple membership term(s) or group(s) may be compared under different model formulations (one vs. multiple terms, or multivariate vs. univariate) for differing prior formulations (e.g. "mmcar" vs. "mmi").

### Usage

```
effectsplot(objects, mm.terms = NULL, prior.labs = NULL, center = TRUE,
            axis.labs = NULL, group.plot = NULL, smoother = FALSE, order = FALSE,
            orderto = NULL, label.mm = NULL)
```

### Arguments

objects	A list object where each entry is an object with class within any of either <code>dpgrowmm</code> or <code>dgrowmult</code> . returned from a model run. The list length is equal to the number of models on which a comparison of multiple membership term effects is desired.
mm.terms	An optional character vector of MM term names or numeric vector of MM term positions targeted for plotting. The entries a term name for each <code>dpgrowmult</code> object and group name for each <code>dpgrowmm</code> object. If a character vector is used, names must correspond to those used in package engine functions that generated each object. Length is equal to number of objects.
prior.labs	An optional character vector providing names for the prior formulations under comparison. Length is equal to number of objects.
center	A scalar boolean input to indicate whether effect values in all objects should be centered. Defaults to TRUE.
axis.labs	An optional vector input of length 2 corresponding to <code>x.axis</code> and <code>y.axis</code> labels, respectively.
group.plot	An optional numeric vector that groups or re-groups the MM effects in each term selected in <code>mm.terms</code> .
smoother	A scalar boolean input indicating whether to co-plot a smoother line with point values.
order	A scalar boolean input indicating whether to sort the plots of effects in order of increasing (mean) value.
orderto	A list object of length equal to number of MM terms (for <code>dpgrowmult</code> objects), or groups (for <code>dpgrowmm</code> objects), each holding a vector of length <code>S[n]</code> , the number of MM effects for object <code>n</code> that conveys a desired order for the MM effects under option <code>order = TRUE</code> as an alternative to ordering by increasing mean value.

`label.mm` An optional list object, each containing a vector of labels for the MM random effects in each term (`dpgrowmult`) or each group (`dpgrowmm`). Used for plotting all terms or groups for input objects. The length of `label.mm` is equal to the number of terms or groups per object.

### Value

A list object containing a plot objects and associated plot data.frames

`dat.term` A data.frame object used to generate a plot comparing a specific term or group from an MM object with field titles, `c("session", "group", "low", "mean", "high", "prior")`, where `session` denotes the MM effect labels, `group` the sub-group labels within the focus MM terms, and `prior`, the model identifiers.

`p.term` A `ggplot2` object of effect plots for chosen object terms.

`p.all` A `ggplot2` plots effects, by term and/or compatible group, for each object. Only renders if the number of effects in terms and/or groups are compatible between objects.

`dat.all` A data.frame object used to generate `p.all` with field titles, `c("prior", "session", "block", "low", "high", "mean")`, where `block` denotes labels for MM terms or groups included.

### Author(s)

Terrance Savitsky <tds151@gmail.com>

### See Also

[dpgrowmm](#), [dpgrowmult](#), [ddpgrow](#)

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<code>getmf</code>	<i>Produce fixed and random effects design matrices from single formula input</i>
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### Description

An internal function to [dpgrow](#) and [dpgrowmm](#)

### Usage

```
getmf(formula, random.only, data, na.action)
```

### Arguments

`formula` A formula of format `y ~ x_1 + x_2*x_3 | z_1*z_2` where `|` separates fixed (to the left of `|`) and random effects.

`random.only` A boolean scalar used in the case that either fixed or random effects are entered in `formula`, but not both, which case the `|` is not entered (e.g. `y ~ x_1 + x_2*x_3`). Then, if `random.only == TRUE` the variables on the right-hand side are interpreted to be random effects; otherwise fixed for use in [dpgrow](#) and [dpgrowmm](#).



data	Associated data.frame containing names variables in formula
na.action	Should be left blank for use in <a href="#">dpgrow</a> and <a href="#">dpgrowmm</a> , where is automatically set to na.fail.

**Value**

res A list object containing `list(y = y, x = x, z = z, m = m, mf = mf)`.

**Note**

Intended as an internal function for [dpgrow](#) and [dpgrowmm](#)

**Author(s)**

Terrance Savitsky <tds151@gmail.com>

**See Also**

[dpgrow](#) [dpgrowmm](#)

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growplot

*Plot by-subject and by-group growth curves*

---

**Description**

Produces a by-subject plot of predicted growth curves with associated data values and an aggregated by-group plot of growth curves along with a smoother line for each group based on user input. Facilitates inference for different growth curve patterns based on subsets of subjects and various subject groupings.

**Usage**

```
growplot(object, compare.objects = NULL, subjects.plot = NULL,
         groups.plot = NULL, subjects.subset = NULL, subjects.random = TRUE,
         x.lab = "Time", y.lab = "Fit", main.label = "Main_Model",
         title.lab = NULL)
```

**Arguments**

object	A <code>dpgrow</code> , <code>dgrowmm</code> or <code>dpgrowmult</code> object obtained from running the appropriate modeling function.
compare.objects	An optional list of <code>dpgrow</code> , <code>dgrowmm</code> or <code>dpgrowmm</code> objects to employ as comparison models for by-subject plotting
subjects.plot	A vector of subjects to use for by-group plot that is composed of some subset of subject. Defaults to all subjects modeled in object.

<code>groups.plot</code>	A vector with associated group identifiers for <code>subjects.plot</code> if the grouping is different from <code>trt</code> used to run the <code>dpgrow</code> or <code>dpgrowmm</code> model. The entered grouping does not have to relate to that used for modeling. Defaults to use of treatment groups modeled in <code>object</code> (if not entered).
<code>subjects.subset</code>	A vector of a subset of <code>subjects.plot</code> to use for by-subject plotting for readability. The full <code>subjects.plot</code> set is used for by group plotting. If left blank, the full <code>subjects.plot</code> vector is used for by-subject plotting.
<code>subjects.random</code>	A boolean scalar. If <code>TRUE</code> a random subset (of 10) is selected from <code>subjects.plot</code> for by-subject plotting. Leave blank if enter <code>subjects.subset</code> . Defaults to <code>TRUE</code> .
<code>x.lab</code>	Optional title for x-axis. Default = "Time"
<code>y.lab</code>	Optional title for y-axis. Default = "Fit"
<code>main.label</code>	An optional character model label for <code>object</code> to use in by-subject plots for comparison with models from <code>compare.objects</code>
<code>title.lab</code>	option plot title. A vector of 2 character entries is allowed. The first entry is the title for the group aggregated plot. The second entry is the title for the plot of selected subject growth curves. If <code>title.lab</code> contains a single entry, then it is used as the title for both plots. Otherwise, defaults to <code>NULL</code> .

### Value

A list object containing a plot objects, data.frame object from which it is constructed, and data.frame with actual data values co-plotted.

<code>dat.gc</code>	A data.frame object used to generate the within subject predicted growth curves for <code>object</code> . Used for aggregated plot of growth curves by group returned in <code>p.gctr</code> . Fields are titled, <code>c("fit", "time", "subject", "trt")</code> .
<code>dat.igc</code>	A data.frame object containing within subject predicted growth curves under models in <code>object</code> and <code>compare.objects</code> . Used for by-subject growth curves plot returned in <code>p.gcs</code> .
<code>dat.data</code>	A data.frame object containing the actual data observations for plotted subjects. Field titles are the same as for <code>dat.gc</code> .
<code>p.gctr</code>	A ggplot2 object of subjects aggregated by group.
<code>p.gcs</code>	A ggplot2 object of subjects.

### Author(s)

Terrance Savitsky <tds151@gmail.com>

### See Also

[dpgrowmm](#), [dpgrow](#), [dpgrowmult](#), [growthCurve](#)

growthCurve

*Within subject model-predicted growth curve***Description**

Produces a set of predicted response values, by subject, at T time points. The response values are predicted by employing the posterior samples of model parameters where the resultant response values for each subject are composed by averaging over all posterior samples in a Rao-Blackwellizing fashion.

**Usage**

```
growthCurve(y.case, B, Alpha, Beta, U = NULL, aff.clients = NULL,
            W.subj = NULL, X.n = NULL, Z.n = NULL, trt.case, trt.lab, subject.case,
            subject.lab, T, min.T, max.T, n.thin, n.waves = NULL, time.case,
            n.fix_degree, Nrandom = NULL)
```

**Arguments**

y.case	The $N \times 1$ (subject-time case) vector of data response values.
B	The $M \times P \times q$ matrix of subject random effect posterior samples. $M$ = number of MCMC samples, $P$ = number of subjects, $q$ = number of random effect parameters, per subject.
Alpha	The $M \times 1$ vector for the model intercept parameter.
Beta	The $M \times F$ matrix of model fixed effects parameters, where $F$ = number of fixed effects
U	The $M \times S$ matrix of univariate multiple membership random effects, where $S$ = number of random effects. $U$ is multivariate, then the input is of dimension $M \times N_{mv} \times S$ , where $N_{mv}$ is the multivariate dimension. Leave NULL is don't require the multiple membership effects. Input as list of $M \times S$ matrices if have more than one multiple membership term.
aff.clients	Vector of length $P$ . aff that identifies subjects affected by $U$ . Identical to <code>subj.aff</code> from <a href="#">dpgrowmm</a> . Input as list of vectors, each comprised of affected subjects attached to the equivalent multiple membership term if have more than one term.
W.subj	A $P \times S$ multiple membership weight matrix for $U$ that expands <code>W.subj.aff</code> of <a href="#">dpgrowmm</a> from affected subjects, $P_{aff}$ to all subjects, $P$ . Input as list of $P[i] \times S[i]$ matrices, where $i$ indexes an MM term, if have more than one multiple membership term.
X.n	A design matrix with $N$ rows (for subject-measure) cases providing nuisance fixed effects. Will be expanded to the $T$ within sample predictions, but held constant between successive observed values (for generating expanded predictions).
Z.n	A design matrix with $N$ rows providing nuisance random effects. Grouping is assumed to be by-subject.
trt.case	The treatment group membership vector of length $N$ (subject-time cases). Assumed numeric with lowest group level == 0; .e.g. $(0, 0, 0, 1, 1, 2, 2, 2, 2, )$ .

<code>trt.lab</code>	Associated labels for the numeric treatment groups. Each distinct treatment group assumed to have a unique label.
<code>subject.case</code>	Vector of length N providing subject-measure cases. Must be in numerical format with unique subjects sequential starting at 1.
<code>subject.lab</code>	N x 1 case length vector with user desired labels that map 1:1 to <code>subject.case</code> .
<code>T</code>	Number of time points to build each subject curve. $T = 10$ is typically sufficient.
<code>min.T</code>	The minimum time value that T will take.
<code>max.T</code>	The maximum time value that T will take.
<code>n.thin</code>	The gap between each MCMC sample used for the growth curve.
<code>n.waves</code>	The maximum number of observed measurement waves, per subject.
<code>time.case</code>	A vector of length N providing times for associated subject-measure observations. Identical to <code>time</code> from <a href="#">dpgrowmm</a> .
<code>n.fix_degree</code>	The highest polynomial degree to employ for constructing time-based fixed effects covariates.
<code>Nrandom</code>	A scalar input providing the number of by-subject time-based random effect parameters. Only need to input if employ nuisance random effects.

**Value**

A list object containing the following `data.frames` and plots:

<code>plot.dat</code>	A <code>data.frame</code> object containing the within-subjects predicted growth curves. Fields are titled, <code>c("fit", "time", "subject", "trt")</code> .
<code>dat.data</code>	A <code>data.frame</code> object containing actual by-subject data for each measurement occasion. Fields are titled, <code>c("fit", "time", "subject", "trt")</code> .
<code>p.gcall</code>	A <code>ggplot2</code> object that aggregates growth curves by treatment type.
<code>p.gtsel</code>	A <code>ggplot2</code> object that plots growth curves with associated data points for 10 randomly selected subjects.

**Note**

Intended as an internal function for [dpgrow](#), [dpgrowmm](#), and [dpgrowmult](#)

**Author(s)**

Terrance Savitsky <tds151@gmail.com>

**See Also**

[dpgrowmm](#), [dpgrow](#), [dpgrowmult](#)

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lgmPost	<i>Run a Bayesian mixed effects model for by-subject random effects with an independent Gaussian prior</i>
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---

**Description**

An internal function to [dpgrow](#)

**Usage**

```
lgmPost(y, X, Z, subjects, niter, nburn, nthin)
```

**Arguments**

y	An $N \times I$ response (of subject-measure cases)
X	Fixed effects design matrix
Z	Random effects design matrix. Assumed grouped by subjects
subjects	An $N \times I$ set of subject identifiers
niter	The number of MCMC iterations
nburn	The number of MCMC burn-in iterations to discard
nthin	The step increment of MCMC samples to return The rate parameter is set of 1.

**Value**

res A list object containing MCMC runs for all model parameters.

**Note**

Intended as an internal function for [dpgrow](#)

**Author(s)**

Terrance Savitsky <tds151@gmail.com>

**See Also**

[dpgrow](#)

mcmcPlots

*generate plots of model(s) posterior results***Description**

Constructs plots of subject and multiple membership effects, as well as traceplots for model precision and clustering parameters. Returns a list of objects of class `ggplot`.

**Usage**

```
mcmcPlots(subjecti.u, subj.aff = NULL, subjaff.input = NULL, bmat.summary,
  group = NULL, groupi.u = NULL, u.summary = NULL, Nmv = 1,
  ulabs = NULL, mm.summary = NULL, M = NULL, Tauu = NULL, Taub, Taue,
  Deviance)
```

**Arguments**

<code>subjecti.u</code>	A vector of length $P$ , number of unique subjects, containing unique set of user input values for subject.
<code>subj.aff</code>	A vector of length $P$ . <code>aff</code> identifying the unique subjects (which are a subset of variable, <code>subject</code> ) receiving multiple membership random effects. Applies only to case of a single set of multiple membership random effects.
<code>subjaff.input</code>	User input version of <code>subj.aff</code> that may be character or numeric format. (Again, this is a strict subset of <code>subjecti.u</code> ). Applies only to case of a single set of multiple membership random effects.
<code>bmat.summary</code>	A list object of $q$ elements, each containing an $P \times 3$ matrix of $c(2.5\%, 50\%, 97.5\%)$ quantile summaries for each subject of the applicable subject random effect parameter. $P$ = number of subjects, $q$ = number of random effect parameters, per subject.
<code>group</code>	An $S \times 1$ vector of group identifiers for the multiple membership random effects, where $S$ is the number of multiple membership random effects. The format is sequential numeric, starting at 1. Applies only to case of a single set of multiple membership effects.
<code>groupi.u</code>	A vector of user input unique values for the multiple membership effect group identifiers where employ 1 multiple membership term. Input as a list of $S \times 1$ vectors in the case of more than one set of multiple membership effects.
<code>u.summary</code>	An $S \times 3$ matrix of of quantile summaries for each multiple membership session effect where employ 1 multiple membership term. Input as list of $S \times 3$ quantiles in the case of more than one set of multiple membership effects.
<code>Nmv</code>	The order for the multiple membership effects. Defaults to $Nmv = 1$ for univariate effects. Otherwise, $Nmv > 1$ indicates that <code>u.summary</code> is dimensioned as $Nmv \times S \times 3$ .
<code>ulabs</code>	An <code>nty</code> vector of labels for each term (block) in the case of more than one set of multiple membership effects.

mm.summary	A $P.aff \times 3$ matrix of quantile summaries. mm was created by multiple the set of $S$ multiple membership effects, $u$ , on each MCMC iteration by the multiple membership design matrix, $W.subj.aff$ .
M	The $iter.keep \times 1$ matrix of posterior samples for the parameter capturing the number of clusters formed under the DP prior on the client effects.
Tauu	$iter.keep \times 1$ matrix of posterior samples capturing the precision parameter for "mmcar", "mmi" and "mmigrp". Input as $iter.keep \times nty$ matrix in the case of $nty$ multiple membership effect terms.
Taub	$iter.keep \times Nrandom$ matrix of posterior samples capturing the precision parameter for each of the sets of subject random effects.
Tau e	$iter.keep \times 1$ matrix of posterior samples capturing the precision parameter for the model error term.
Deviance	$iter.keep \times 1$ matrix of posterior samples for the model deviance.

### Value

A list of plot objects of class ggplot2 including:

p.U	by group plot of session effects, $u[1:Nsession]$ . Plot is faceted for more than one set of effect terms.
p.Umm	plot of " $mm = W.subj.aff$ clients attending assessions.
p.Ub0	plot of " $mm + b0$ ", the total random intercept, for those clients attending sessions.
p.Ub	plot of " $mm + b$ " for multivariate MM effects with order equal to " $Nrandom$ ".
p.b	stacked plots of $b0, \dots, b(q-1)$ - vertical lines for each client span 2.5% - 97.5% values with mean noted.
p.M	MCMC trace plot of $M$ , number of clusters.
p.tauu	MCMC trace plots of $\tau.u$ . Plot is faceted for more than one set of effect terms.
p.tau e	MCMC trace plots of $\tau.e$ .
p.taub	MCMC faceted trace plot for each of the $q$ components of $\tau.b$ .
p.dev	MCMC trace plots of deviance.

### Note

Intended as an internal function for [dpgrow](#), [dpgrowmm](#), and [dpgrowmult](#)

### Author(s)

Terrance Savitsky <tds151@gmail.com>

### See Also

[dpgrowmm](#), [dpgrow](#)

---

mmCmvplusDpPost	<i>Bayesian mixed effects model with a DP prior on by-subject effects and CAR prior on a multivariate set of multiple membership effects</i>
-----------------	--

---

## Description

An internal function to [dpgrowmm](#)

## Usage

```
mmCmvplusDpPost(y, X, Z, H, Wcase, Wsubject, Omega, omegaplus, groups, subjects,
  niter, nburn, nthin, strength.mm, corsess, shapealph, ratebeta, typemm)
```

## Arguments

y	An $N \times I$ response (of subject-measure cases)
X	Fixed effects design matrix
Z	Random effects design matrix. Assumed grouped by subjects
H	Multivariate MM effects design matrix.
Wcase	An $N \times I$ multiple membership weight matrix to map supplemental random effects
Wsubject	An $P \times S$ multiple membership weight matrix with rows equal to number of unique affected subjects
Omega	An $S \times S$ unnormalized adjacency matrix with entries equal to 1 where two effects communicate and 0, otherwise. Diagonal elements are zero
omegaplus	$S \times I$ vector of row sums of Omega
groups	$S \times I$ vector of group identifiers for each effect. Effects within each group communicate. Effects don't communicate across groups. Not used under "mmi" prior (though input is required).
subjects	An $N \times I$ set of subject identifiers
niter	The number of MCMC iterations
nburn	The number of MCMC burn-in iterations to discard
nthin	The step increment of MCMC samples to return
strength.mm	The shape and rate parameters for the $\Gamma$ prior on the CAR precision parameter, $\tau_\gamma$ .
corsess	A single value to set the prior correlations among the multivariate $q = \text{ncol}(H)$ orders for the MM effects. where $\tau_\gamma$ is replaced by the $q \times q, \Lambda$ .
shapealph	The shape parameter for the $\Gamma$ prior on the DP concentration parameter. The rate parameter is set of 1.
ratebeta	The rate parameter for the $\Gamma$ prior on the DP concentration parameter. Default value is 1.
typemm	An indicator the prior formulation specified for the multivariate MM effects term. Set <code>typemm = 0</code> for "mmi" and <code>typemm = 1</code> for "mmcar".



**Value**

res A list object containing MCMC runs for all model parameters.

**Note**

Intended as an internal function for [dpgrowmm](#)

**Author(s)**

Terrance Savitsky <tds151@gmail.com>

**See Also**

[dpgrow](#)

---

mmCplusDpPost	<i>Bayesian mixed effects model with a DP prior on by-subject effects and CAR prior on a set of multiple membership effects</i>
---------------	---

---

**Description**

An internal function to [dpgrowmm](#)

**Usage**

```
mmCplusDpPost(y, X, Z, Wcase, Wsubject, Omega, omegaplus, groups, subjects,
  niter, nburn, nthin, strength.mm, shapealph, ratebeta)
```

**Arguments**

y	An $N \times I$ response (of subject-measure cases)
X	Fixed effects design matrix
Z	Random effects design matrix. Assumed grouped by subjects
Wcase	An $N \times I$ multiple membership weight matrix to map supplemental random effects
Wsubject	An $P \times S$ multiple membership weight matrix with rows equal to number of unique affected subjects
Omega	An $S \times S$ unnormalized adjacency matrix with entries equal to 1 where two effects communicate and 0, otherwise. Diagonal elements are zero
omegaplus	$S \times I$ vector of row sums of Omega
groups	$S \times I$ vector of group identifiers for each effect. Effects within each group communicate. Effects don't communicate across groups.
subjects	An $N \times I$ set of subject identifiers
niter	The number of MCMC iterations

nburn	The number of MCMC burn-in iterations to discard
nthin	The step increment of MCMC samples to return
strength.mm	The shape and rate parameters for the $\Gamma$ prior on the CAR precision parameter, $\tau_\gamma$
shapealph	The shape parameter for the $\Gamma$ prior on the DP concentration parameter. The rate parameter is set of 1.
ratebeta	The rate parameter for the $\Gamma$ prior on the DP concentration parameter. Default value is 1.

**Value**

res A list object containing MCMC runs for all model parameters.

**Note**

Intended as an internal function for [dpgrowmm](#)

**Author(s)**

Terrance Savitsky <tds151@gmail.com>

**See Also**

[dpgrow](#)

---

mmIgroupDpPost	<i>Bayesian mixed effects model with a DP prior on by-subject effects and use of group means for multiple membership effects</i>
----------------	--

---

**Description**

An internal function to [dpgrowmm](#)

**Usage**

```
mmIgroupDpPost(y, X, Z, Wcase, Wsubject, M, subjects, niter, nburn, nthin,
  strength.mm, shapealph, ratebeta)
```

**Arguments**

y	An $N \times I$ response (of subject-measure cases)
X	Fixed effects design matrix
Z	Random effects design matrix. Assumed grouped by subjects
Wcase	An $N \times I$ multiple membership weight matrix to map supplemental random effects

Wsubject	An $P \times S$ multiple membership weight matrix with rows equal to number of unique affected subjects
M	An $S \times G$ design matrix mapping (G) group means to the multiple membership effects. Posterior samples are centered on each iteration to identify the global mean parameter.
subjects	An $N \times I$ set of subject identifiers
niter	The number of MCMC iterations
nburn	The number of MCMC burn-in iterations to discard
nthin	The step increment of MCMC samples to return
strength.mm	The shape and rate parameters for the $\Gamma$ prior on the CAR precision parameter, $\tau_\gamma$
shapealph	The shape parameter for the $\Gamma$ prior on the DP concentration parameter. The rate parameter is set of 1.
ratebeta	The rate parameter for the $\Gamma$ prior on the DP concentration parameter. Default value is 1.

**Value**

res A list object containing MCMC runs for all model parameters.

**Note**

Intended as an internal function for [dpgrowmm](#)

**Author(s)**

Terrance Savitsky <tds151@gmail.com>

**See Also**

[dpgrowmm](#)

---

mmIplusDpPost	<i>Bayesian mixed effects model with a DP prior on by-subject effects and zero mean independent Gaussian priors on multiple membership effects</i>
---------------	--

---

**Description**

An internal function to [dpgrowmm](#)

**Usage**

```
mmIplusDpPost(y, X, Z, Wcase, Wsubject, subjects, niter, nburn, nthin,
  strength.mm, shapealph, ratebeta)
```

**Arguments**

y	An $N \times I$ response (of subject-measure cases)
X	Fixed effects design matrix
Z	Random effects design matrix. Assumed grouped by subjects
Wcase	An $N \times I$ multiple membership weight matrix to map supplemental random effects
Wsubject	An $P.aff \times S$ multiple membership weight matrix with rows equal to number of unique affected subjects
subjects	An $N \times I$ set of subject identifiers
niter	The number of MCMC iterations
nburn	The number of MCMC burn-in iterations to discard
nthin	The step increment of MCMC samples to return
strength.mm	The shape and rate parameters for the $\Gamma$ prior on the CAR precision parameter, $\tau_\gamma$
shapealph	The shape parameter for the $\Gamma$ prior on the DP concentration parameter. The rate parameter is set of 1.
ratebeta	The rate parameter for the $\Gamma$ prior on the DP concentration parameter. Default value is 1.

**Value**

res A list object containing MCMC runs for all model parameters.

**Note**

Intended as an internal function for [dpgrowmm](#)

**Author(s)**

Terrance Savitsky <tds151@gmail.com>

**See Also**

[dpgrowmm](#)

---

mmmultPost	<i>Bayesian mixed effects model with a DP prior on by-subject effects and more than one multiple membership random effects term</i>
------------	---

---

## Description

An internal function to [dpgrowmult](#)

## Usage

```
mmmultPost(y, X, Z, Wcases, Mmats, Omegas, omegapluses, ngs, subjects, typet,
           niter, nburn, nthin, shapealph, ratebeta, strength.mm)
```

## Arguments

y	An $N \times I$ response (of subject-measure cases)
X	Fixed effects design matrix
Z	Random effects design matrix. Assumed grouped by subjects
Wcases	A list object containing $N \times 1$ multiple membership (MM) weight matrices; one for each MM term.
Mmats	A list object containing $S[i] \times G[i]$ matrices, where $S[i]$ are the number of effects for MM term $i$ and $G[i]$ is the number of (unique) groups for the $S[i]$ effects. The length of this list is equal to the number of terms under prior option set to "mmigrp"
Omegas	A list object containing $S[i] \times S[i]$ unnormalized adjacency matrices for MM term $i$ , each with entries equal to 1 where two effects communicate and 0, otherwise. Diagonal elements are zero. The length of this list is equal to the number terms with prior option set to "mmcar"
omegapluses	A list object containing $S \times 1$ vector of row sums of $\text{Omega}[[i]]$ . The length of <code>omegaplus</code> should equal <code>Omega</code> .
ngs	A numeric vector containing the number of total groups for each MM term under prior option "mmcar".
subjects	An $N \times I$ set of subject identifiers.
typet	A numeric vector of length equal to the number of MM terms, where each entry specifies the prior formulation for that effect term (block). Prior formulation options are 1 = "mmcar", 2 = "mmi", 3 = "mmigrp", 4 = "mmdp".
niter	The number of MCMC iterations
nburn	The number of MCMC burn-in iterations to discard
nthin	The step increment of MCMC samples to return
shapealph	The shape parameter for the $\Gamma$ prior on the DP concentration parameter. The rate parameter is set of 1.
ratebeta	The rate parameter for the $\Gamma$ prior on the DP concentration parameter. Default value is 1.
strength.mm	The shape and rate parameters for the $\Gamma$ prior on the CAR precision parameter, $\tau_\gamma$

**Value**

res A list object containing MCMC runs for all model parameters.

**Note**

Intended as an internal function for [dpgrowmult](#)

**Author(s)**

Terrance Savitsky <tds151@gmail.com>

**See Also**

[dpgrowmm](#)

---

plot.ddpgrow

*Produce model plots*

---

**Description**

Builds model plots, including MCMC trace plots, analysis of subject effects and subject growth curves

**Usage**

```
## S3 method for class 'ddpgrow'
plot(x, plot.out = TRUE, ...)
```

**Arguments**

x	A dpgrow object
plot.out	A boolean object. If TRUE, plots are rendered. In either case, plots are stored
...	Ignored

**Value**

res a list object of class `plot.ddpgrow` of two items:

plot.results	ggplot2 plot objects. See <a href="#">ddpMCMCplots</a> .
dat.growcurve	A data.frame containing fields <code>c("fit", "time", "subject", "trt")</code> with $P \times T$ rows, where $P$ is the length of subject and $T = 10$ are the number of in-subject predictions for each subject. This object may be used to construct additional growth curves using - see <a href="#">growplot</a> .
dat.gcdata	A data.frame containing fields <code>c("fit", "time", "subject", "trt")</code> with $N$ rows, where $N$ are the number of subject-time cases. This object contains the actual data for all subjects used to co-plot with predicted growth curves.

---

plot.dpgrow	<i>Produce model plots</i>
-------------	----------------------------

---

**Description**

Builds model plots, including MCMC trace plots, analysis of subject effects and subject growth curves

**Usage**

```
## S3 method for class 'dpgrow'
plot(x, plot.out = TRUE, ...)
```

**Arguments**

x	A dpgrow object
plot.out	A boolean object. If TRUE, plots are rendered. In either case, plots are stored
...	Ignored

**Value**

res a list object of class plot.dpgrow of two items:

plot.results	ggplot2 plot objects. See <a href="#">mcmcPlots</a> .
dat.growcurve	A data.frame containing fields c("fit", "time", "subject", "trt") with P*T rows, where P is the length of subject and T = 10 are the number of in-subject predictions for each subject. This object may be used to construct additional growth curves using - see <a href="#">growplot</a> .
dat.gcdata	A data.frame containing fields c("fit", "time", "subject", "trt") with N rows, where N are the number of subject-time cases. This object contains the actual data for all subjects used to co-plot with predicted growth curves.

---

plot.dpgrowmm	<i>Produce model plots</i>
---------------	----------------------------

---

**Description**

Builds model plots, including MCMC trace plots, analysis of session effects and subject growth curves

**Usage**

```
## S3 method for class 'dpgrowmm'
plot(x, plot.out = TRUE, ...)
```

**Arguments**

x	A dpgrowmm object
plot.out	A boolean object. If TRUE, plots are rendered. In either case, plots are stored
...	Ignored

**Value**

res a list object of class `plot.dpgrowmm` of 3 items:

plot.results	ggplot2 plot objects; see <a href="#">mcmcPlots</a> .
dat.growcurve	A data.frame containing fields <code>c("fit", "time", "subject", "trt")</code> with $P \times T$ rows, where $P$ is the length of subject and $T = 10$ are the number of in-subject predictions for each subject. This object may be used to construct additional growth curves using - see <a href="#">growplot</a> .
dat.gpdata	A data.frame containing fields <code>c("fit", "time", "subject", "trt")</code> with $N$ rows, where $N$ are the number of subject-time cases. This object contains the actual data for all subjects used to co-plot with predicted growth curves.

---

plot.dpgrowmult	<i>Produce model plots</i>
-----------------	----------------------------

---

**Description**

Builds model plots, including MCMC trace plots, analysis of session effects and subject growth curves

**Usage**

```
## S3 method for class 'dpgrowmult'
plot(x, plot.out = TRUE, ...)
```

**Arguments**

x	A dpgrowmult object
plot.out	A boolean object. If TRUE, plots are rendered. In either case, plots are stored
...	Ignored

**Value**

res a list object of class `plot.dpgrowmm` of 3 items:

plot.results	ggplot2 plot objects; see <a href="#">mcmcPlots</a> .
dat.growcurve	A data.frame containing fields <code>c("fit", "time", "subject", "trt")</code> with $P \times T$ rows, where $P$ is the length of subject and $T = 10$ are the number of in-subject predictions for each subject. This object may be used to construct additional growth curves using - see <a href="#">growplot</a> .



`dat.gcdata` A data.frame containing fields `c("fit", "time", "subject", "trt")` with N rows, where N are the number of subject-time cases. This object contains the actual data for all subjects used to co-plot with predicted growth curves.

---

`relabel` *Relabel user vector input to sequential numerical*

---

### Description

Takes user input for vector in either character or numerical format and converts it to sequential numeric format. For use in functions requiring sequential numerical format. Returns new sequential numerical vector and vector of unique values inputted by user. The latter is used to label plot variables returned to the user.

### Usage

```
relabel(label.input, start)
```

### Arguments

`label.input` A vector in numerical or character format that the user desires to convert to sequential numeric.

`start` An integer representing the starting value of the sequential sequence for the new label vector.

### Value

A list object containing the new sequential vector, `label.new`, and a vector of unique input values, `labeli.u`.

### Author(s)

Terrance Savitsky <tds151@gmail.com>

### See Also

[dpgrowmm](#), [dpgrow](#)

---

samples	<i>Produce MCMC samples for model parameters</i>
---------	--

---

**Description**

provides posterior sampled values for every model parameter of a dpgrowmm object

**Usage**

```
## S3 method for class 'dpgrowmm'
samples(object, ...)
```

**Arguments**

object	A dpgrowmm object
...	Ignored

**Value**

res list object of class samples.dpgrowmm, samples.dpgrowmult, or samples.dpgrow

---

samples.ddpgrow	<i>Produce samples of MCMC output</i>
-----------------	---------------------------------------

---

**Description**

provides posterior sampled values for every model parameter of a ddpgrow object

**Usage**

```
## S3 method for class 'ddpgrow'
samples(object, ...)
```

**Arguments**

object	A ddpgrow object
...	Ignored

---

samples.dpgrow	<i>Produce samples of MCMC output</i>
----------------	---------------------------------------

---

**Description**

provides posterior sampled values for every model parameter of a dpgrow object

**Usage**

```
## S3 method for class 'dpgrow'  
samples(object, ...)
```

**Arguments**

object	A dpgrow object
...	Ignored

---

samples.dpgrowmult	<i>Produce samples of MCMC output</i>
--------------------	---------------------------------------

---

**Description**

provides posterior sampled values for every model parameter of a dpgrowmult object

**Usage**

```
## S3 method for class 'dpgrowmult'  
samples(object, ...)
```

**Arguments**

object	A dpgrowmult object
...	Ignored

summary.ddpgrow      *S3 functions of dpgrow*

---

**Description**

produces quantile summaries for model parameters

**Usage**

```
## S3 method for class 'ddpgrow'  
summary(object, ...)
```

**Arguments**

object	A ddpgrow object
...	Ignored

---

summary.dpgrow      *S3 functions of dpgrow*

---

**Description**

produces quantile summaries for model parameters

**Usage**

```
## S3 method for class 'dpgrow'  
summary(object, ...)
```

**Arguments**

object	A dpgrow object
...	Ignored

---

summary.dpgrowmm	<i>S3 functions of dpgrowmm</i>
------------------	---------------------------------

---

**Description**

produces quantile summaries for model parameters for an dpgrowmm object.

**Usage**

```
## S3 method for class 'dpgrowmm'  
summary(object, ...)
```

**Arguments**

object	A dpgrowmm object
...	Ignored

---

summary.dpgrowmult	<i>S3 functions of dpgrowmult</i>
--------------------	-----------------------------------

---

**Description**

produces quantile summaries for model parameters for an dpgrowmult object.

**Usage**

```
## S3 method for class 'dpgrowmult'  
summary(object, ...)
```

**Arguments**

object	A dpgrowmult object
...	Ignored

---

summary\_quantiles      *Produce quantile summaries of model posterior samples*

---

### Description

Inputs MCMC samples for model parameters and constructs  $c(2.5\%, 50\%, 97.5\%)$  quantile summaries.

### Usage

```
summary_quantiles(model.output, Nfixed, Nrandom, Nsubject, Nsubj.aff = NULL,
  Nmv = 1, Nsession = NULL)
```

### Arguments

model.output	An output object of class within $c("dpgrow", "dpgrowmm")$
Nfixed	Number of total fixed effects, both time-based and nuisance.
Nrandom	Number of total random effects, both time-based and nuisance, all grouped by subject.
Nsubject	Number of unique subjects (on which repeated measures are observed).
Nsubj.aff	Number of subjects, $P.aff$ , receiving multiple membership effects
Nmv	Number of multivariate MM effects. Defaults to 1 for univariate MM if left blank.
Nsession	Number of multiple membership effects for each entry in "Nmv". May be left blank for univariate MM.

### Value

A list object containing quantile summaries for all sampled model parameters.

deviance.summary	vector of length 3 summarizing quantiles for model deviance.
beta.summary	$Nfixed \times 3$ quantile summaries of model fixed effects.
alpha.summary	quantile summary of model global intercept parameter.
bmat.summary	list object of length $Nrandom$ , each cell containing a $Nsubject \times 3$ matrix of by-subject parameter quantile summaries.
tauu.summary	$Nmv \times 3$ quantile summary for prior precision parameters employed for multiple membership random effects. An $nty \times 3$ matrix in the case of $nty$ multiple membership effect terms.
taue.summary	quantile summary for model error precision parameter.
taub	$Nrandom \times 3$ quantile summaries for subject effect precision parameters.
u.summary	$S \times Nmv \times 3$ quantile summaries for multiple membership random effect parameters. A list of such matrices in the case of $nty$ multiple membership effect terms.

mm.summary	Nsubj.aff x 3 quantile summaries derived from multiplying the affected subject weight matrix by the multiple membership random effects.
M.summary	quantile summary for number of DP posterior clusters formed.
Dbar	Model fit statistics.
pD	Model fit statistics.
pV	Model fit statistics.
DIC	Model fit statistics.
lpml	Model fit statistics.

**Author(s)**

Terrance Savitsky <tds151@gmail.com>

**See Also**

[dpgrowmm](#), [dpgrow](#)

---

trtplot

*Plot comparison of Mean Effects for Any Two Treatments*


---

**Description**

Produces a set of box plots of the posterior distributions of the fixed effects mean difference between any 2 chosen treatments across a chosen subset models (priors) at each of a selection of time points. Each box plot spans the 95 credible interval.

**Usage**

```
trtplot(run.objects, run.models, trt.labs, time.points, y.label = NULL,
        time.labels = NULL, n.thin = 10)
```

**Arguments**

run.objects	A list object where each entry is either a <code>dpgrow</code> , <code>dgrowmm</code> or <code>dpgrowmult</code> object returned from a model run. The list length is equal to the number of models on which a treatment comparison is desired.
run.models	A character vector supplying the names of models to compare of the same length as the number of elements in <code>run.objects</code> .
trt.labs	A vector of exactly 2-elements that contains the labels (used in modeling) for the two treatments desired to compare.
time.points	A numeric vector of data time points on which to compare the fixed effects treatment means.
y.label	An optional character scalar for label for the y axis.
time.labels	An optional character vector of labels for <code>time.points</code> to use in plotting.
n.thin	Gap between successive MCMC sampling iterations on fixed effects parameters to use for generating distribution for each treatment-time. Defaults to <code>n.thin = 10</code> . Higher values produces faster plot generation.

**Value**

A list object containing quantile summaries for all sampled model parameters.

`dat.trt` A `data.frame` object used to generate the fixed effects mean comparison for two chosen treatments. Fields are titled, `c("Mu_diff", "models", "time")`.

`p.trt` A `ggplot2` object of box plots split by time point.

**Author(s)**

Terrance Savitsky <tds151@gmail.com>

**See Also**

[dpgrowmm](#), [dpgrow](#), [dpgrowmult](#)

---

XZcov

*generate fixed and random design matrices, X and Z*

---

**Description**

Constructs fixed and random design matrices comprised of either or both growth curve (time-based) components and user-defined nuisance fixed or random effects (input via a formula). Used to conduct Bayesian mixed effects modeling and to produce growth curve output.

**Usage**

```
XZcov(time = NULL, trt = NULL, trt.lab = NULL, subject = NULL,
       n.random = NULL, n.fix_degree = NULL, formula = NULL,
       random.only = NULL, data = NULL)
```

**Arguments**

`time` A vector of length  $N$  (number of subject-time cases) providing times for associated subject-measure observations. Identical to `time` from [dpgrowmm](#).

`trt` The treatment group membership vector of length  $N$ . Assumed numeric and sequential. (e.g.  $(0, 0, 1, 1, 1, 2, 2, \dots)$ ).

`trt.lab` Associated labels for the numeric treatment groups. Each distinct treatment group assumed to have a unique label.

`subject` Vector of length  $N$  providing subject-measure cases. Identical to `subject` from [dpgrowmm](#).  $P$  = number of subjects,  $q$  = number of random effect parameters, per subject.

`n.random` A scalar input providing the number of by-subject time-based random effect parameters.

`n.fix_degree` The highest polynomial degree to employ for constructing time-based fixed effects covariates.



formula	A formula of format $y \sim x_1 + x_2*x_3 \mid z_1*z_2$ where $\mid$ separates fixed (to the left of $\mid$ ) and random effects.
random.only	A boolean scalar used in the case that either fixed or random effects are entered in formula, but not both, which case the $\mid$ is not entered (e.g. $y \sim x_1 + x_2*x_3$ . Then, if <code>random.only == TRUE</code> the variables on the right-hand side are interpreted to be random effects; otherwise fixed for use in <a href="#">dpgrow</a> and <a href="#">dpgrowmm</a> .
data	Associated data.frame containing names variables in formula

**Value**

A list object containing composed fixed and random effect design matrices, X and Z, with column names and subsets: `c(X.n, Z.n)` nuisance and `c(X.c, Z.c)` growth curve design matrices. Also returns data output, `y`, if included with formula; otherwise returns `y = NULL`.

**Author(s)**

Terrance Savitsky <[tds151@gmail.com](mailto:tds151@gmail.com)>

**See Also**

[dpgrowmm](#), [dpgrow](#)

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