Package ‘TMB’

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Type Package

Title Template Model Builder: A General Random Effect Tool Inspired by 'ADMB'

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Description With this tool, a user should be able to quickly implement complex random effect models through simple C++ templates. The package combines 'CppAD' (C++ automatic differentiation), 'Eigen' (templated matrix-vector library) and 'CHOLMOD' (sparse matrix routines available from R) to obtain an efficient implementation of the applied Laplace approximation with exact derivatives. Key features are: Automatic sparseness detection, parallelism through 'BLAS' and parallel user templates.

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URL http://tmb-project.org

BugReports https://github.com/kaskr/adcomp/issues

Depends R (>= 3.0.0)

Imports graphics, methods, stats, utils, Matrix (>= 1.0-12)

LinkingTo Matrix, RcppEigen
Convert estimates to original list format.

Get estimated parameters or standard errors in the same shape as the original parameter list.
Usage

## S3 method for class 'sdreport'

as.list(x, what = "", report = FALSE, ...)

Arguments

- **x**
  - Output from `sdreport`.
- **what**
  - Select what to convert (Estimate / Std. Error).
- **report**
  - Get AD reported variables rather than model parameters?
- **...**
  - Passed to `summary.sdreport`.

Details

This function converts the selected column what of `summary(x, select = c("fixed", "random"), ...)` to the same format as the original parameter list (re-ordered as the template parameter order). The argument what is partially matched among the column names of the summary table. The actual match is added as an attribute to the output.

Value

List of same shape as original parameter list.

Examples

## Not run:

```r
example(sdreport)
```

## Estimates as a parameter list:

```r
as.list(rep, "Est")
```

## Std Errors in the same list format:

```r
as.list(rep, "Std")
```

## p-values in the same list format:

```r
as.list(rep, "Pr", p.value=TRUE)
```

## AD reported variables as a list:

```r
as.list(rep, "Estimate", report=TRUE)
```

## Bias corrected AD reported variables as a list:

```r
as.list(rep, "Est. (bias.correct)", report=TRUE)
```

## End(Not run)
benchmark

**Benchmark parallel templates**

### Description
Bethmark parallel templates
Plot result of parallel benchmark

### Usage

```r
benchmark(obj, n = 10, expr = NULL, cores = NULL)
```

```r
## S3 method for class 'parallelBenchmark'
plot(x, type = "b", ..., show = c("speedup", "time"), legendpos = "topleft")
```

### Arguments

- `obj` Object from `makeADFun`
- `n` Number of replicates to obtain reliable results.
- `expr` Optional expression to benchmark instead of default.
- `cores` Optional vector of cores.
- `x` Object to plot
- `type` Plot type
- `...` Further plot arguments
- `show` Plot relative speedup or relative time?
- `legendpos` Position of legend

### Details
By default this function will perform timings of the most critical parts of an AD model, specifically

1. Objective function of evaluated template.
2. Gradient of evaluated template.
4. Cholesky factorization of sparse hessian.

(for pure fixed effect models only the first two). Expressions to time can be overwritten by the user (expr). A plot method is available for Parallel benchmarks.
checkConsistency

Examples

```r
## Not run:
runExample("linreg_parallel",thisR=TRUE)  ## Create obj
ben <- benchmark(obj,n=100,cores=1:4)
plot(ben)
ben <- benchmark(obj,n=100,cores=1:4,expr=expression(do.call("optim",obj)))
plot(ben)

## End(Not run)
```

checkConsistency  
Check consistency and Laplace accuracy

Description

Check consistency of various parts of a TMB implementation. Requires that user has implemented simulation code for the data and optionally random effects. *(Beta version; may change without notice)*

Usage

```r
checkConsistency(obj, par = NULL, hessian = FALSE, n = 100)
```

Arguments

- **obj**: Object from MakeADFun
- **par**: Parameter vector (θ) for simulation. If unspecified use the best encountered parameter of the object.
- **hessian**: Calculate the hessian matrix for each replicate?
- **n**: Number of simulations

Details

This function checks that the simulation code of random effects and data is consistent with the implemented negative log-likelihood function. It also checks whether the approximate marginal score function is central indicating whether the Laplace approximation is suitable for parameter estimation.

Denote by \( u \) the random effects, \( \theta \) the parameters and by \( x \) the data. The main assumption is that the user has implemented the joint negative log likelihood \( f_\theta(u, x) \) satisfying

\[
\int \int \exp(-f_\theta(u, x)) \, du \, dx = 1
\]

It follows that the joint and marginal score functions are central:

1. \( E_{u,x} [\nabla_\theta f_\theta(u, x)] = 0 \)
2. \( E_x [\nabla_\theta - \log (\int \exp(-f_\theta(u, x)) \, du)] = 0 \)
For each replicate of $u$ and $x$ joint and marginal gradients are calculated. Appropriate centrality tests are carried out by `summary.checkConsistency`. An asymptotic $\chi^2$ test is used to verify the first identity. Power of this test increases with the number of simulations $n$. The second identity holds *approximately* when replacing the marginal likelihood with its Laplace approximation. A formal test would thus fail eventually for large $n$. Rather, the gradient bias is transformed to parameter scale (using the estimated information matrix) to provide an estimate of parameter bias caused by the Laplace approximation.

### Value

List with gradient simulations (joint and marginal)

### See Also

`summary.checkConsistency`, `print.checkConsistency`

### Examples

```r
## Not run:
runExample("simple")
chk <- checkConsistency(obj)
chk
## Get more details
s <- summary(chk)
s$margin$dp.value ## Laplace exact for Gaussian models
## End(Not run)
```

---

### `compile`

*Compile a C++ template to DLL suitable for MakeADFun.*

#### Description

Compile a C++ template into a shared object file. OpenMP flag is set if the template is detected to be parallel.

#### Usage

```r
compile(file, flags = "", safebounds = TRUE, safeunload = TRUE,
         openmp = isParallelTemplate(file[[1]]), libtmb = TRUE, libinit = TRUE,
         tracesweep = FALSE, ...)
```

#### Arguments

- `file` C++ file.
- `flags` Character with compile flags.
- `safebounds` Turn on preprocessor flag for bound checking?
- `safeunload` Turn on preprocessor flag for safe DLL unloading?
openmp  Turn on openmp flag? Auto detected for parallel templates.
libtmb  Use precompiled TMB library if available (to speed up compilation)?
libinit  Turn on preprocessor flag to register native routines?
tracesweep  Turn on preprocessor flag to trace AD sweeps? (Silently disables libtmb)
...  Passed as Makeconf variables.

Details
TMB relies on R’s built in functionality to create shared libraries independent of the platform. A template is compiled by `compile("template.cpp"), which will call R’s makefile with appropriate preprocessor flags. Compiler and compiler flags can be stored in a configuration file. In order of precedence either via the file pointed at by R_MAKEVARS_USER or the file ~/.R/Makevars if it exists. Additional configuration variables can be set with the `flags` and ... arguments, which will override any previous selections.

See Also
precompile

Description
Get or set internal configuration variables of user’s DLL.

Usage
`config(..., DLL = getUserDLL())`

Arguments
... Variables to set
DLL Name of user’s DLL. Auto-detected if missing.

Details
A model compiled with the TMB C++ library has several configuration variables set by default. The variables can be read and modified using this function. The meaning of the variables can be found in the Doxygen documentation.

Value
List with current configuration
Examples

```r
## Not run:
## Load library
dyn.load(dynlib("mymodel"))
## Read the current settings
cfg(DLL="mymodel")
## Reduce memory peak of a parallel model by creating tapes in serial
cfg(tape.parallel=0, DLL="mymodel")
obj <- MakeADFun(..., DLL="mymodel")

## End(Not run)
```

confint.tmbprofile  Profile based confidence intervals.

Description

Calculate confidence interval from a likelihood profile.

Usage

```r
## S3 method for class 'tmbprofile'
confint(object, parm, level = 0.95, ...)
```

Arguments

- **object**: Output from `tmbprofile`.
- **parm**: Not used
- **level**: Confidence level.
- **...**: Not used

Value

Lower and upper limit as a matrix.

dynlib  Add dynlib extension

Description

Add the platform dependent dynlib extension. In order for examples to work across platforms DLLs should be loaded by `dyn.load(dynlib("name"))`.

Usage

dynlib(name)
gdbsource

Arguments

name  Library name without extension

Value

Character

gdbsource  Source R-script through gdb to get backtrace.

Description

Source R-script through gdb to get backtrace.

If gdbsource is run non-interactively (the default) only the relevant information will be printed. Note that this will only work if the cpp file and the R file share the same base name.

Usage

gdbsource(file, interactive = FALSE)

## S3 method for class 'backtrace'
print(x, ...)

Arguments

file  Your R script
interactive  Run interactive gdb session?
x  Backtrace from gdbsource
...  Not used

Details

This function is useful for debugging templates. If a script aborts e.g. due to an out-of-bound index operation it should be fast to locate the line that caused the problem by running gdbsource(file). Alternatively, If more detailed debugging is required, then gdbsource(file, TRUE) will provide the full backtrace followed by an interactive gdb session where the individual frames can be inspected. Note that templates should be compiled without optimization and with debug information in order to provide correct line numbers:

- On Linux/OS X use compile(cppfile,"-00 -g").
- On Windows use compile(cppfile,"-01 -g",DLLFLAGS="") (lower optimization level will cause errors).

Value

Object of class backtrace
MakeADFun

Construct objective functions with derivatives based on a compiled C++ template.

Description

Construct objective functions with derivatives based on the users C++ template.

Usage

MakeADFun(data, parameters, map = list(), type = c("ADFun", "Fun", "ADGrad"[!is.null(random) || !is.null(profile)]), random = NULL, profile = NULL, random.start = expression(last.par.best[random]), hessian = FALSE, method = "BFGS", inner.method = "newton", inner.control = list(maxit = 1000), MCcontrol = list(doMC = FALSE, seed = 123, n = 100), ADreport = FALSE, atomic = TRUE, LaplaceNonZeroGradient = FALSE, DLL = getUserDLL(), checkParameterOrder = TRUE, regexp = FALSE, silent = FALSE, ...)

Arguments

data List of data objects (vectors, matrices, arrays, factors, sparse matrices) required by the user template (order does not matter and un-used components are allowed).

parameters List of all parameter objects required by the user template (both random and fixed effects).

map List defining how to optionally collect and fix parameters - see details.

type Character vector defining which operation stacks are generated from the users template - see details.

random Character vector defining the random effect parameters. See also regexp.

profile Parameters to profile out of the likelihood (this subset will be appended to random with Laplace approximation disabled).

random.start Expression defining the strategy for choosing random effect initial values as function of previous function evaluations - see details.

hessian Calculate Hessian at optimum?

method Outer optimization method.

inner.method Inner optimization method (see function "newton").

inner.control List controlling inner optimization.

MCcontrol List controlling importance sampler (turned off by default).

ADreport Calculate derivatives of macro ADREPORT(vector) instead of objective_function return value?

atomic Allow tape to contain atomic functions?

LaplaceNonZeroGradient Allow Taylor expansion around non-stationary point?
Details

A call to `MakeADFUn` will return an object that, based on the users DLL code (specified through `dll`), contains functions to calculate the objective function and its gradient. The object contains the following components:

- `par` A default parameter.
- `fn` The likelihood function.
- `gr` The gradient function.
- `report` A function to report all variables reported with the `REPORT()` macro in the user template.
- `env` Environment with access to all parts of the structure.

and is thus ready for a call to an R optimizer, such as `nlminb` or `optim`. Data (`data`) and parameters (`parameters`) are directly read by the user template via the macros beginning with `DATA_` and `PARAMETER_`. The order of the `PARAMETER_` macros defines the order of parameters in the final objective function. There are no restrictions on the order of random parameters, fixed parameters or data in the template.

Optionally, a simple mechanism for collecting and fixing parameters from R is available through the `map` argument. A map is a named list of factors with the following properties:

- `names(map)` is a subset of `names(parameters)`.
- For a parameter "p" `length(map$p)` equals `length(parameters$p)`.
- Parameter entries with NAs in the factor are fixed.
- Parameter entries with equal factor level are collected to a common value.

More advanced parameter mapping, such as collecting parameters between different vectors etc., must be implemented from the template.

Random effects are specified via the argument `random`: A component of the parameter list is marked as random if its name is matched by any of the characters of the vector `random` (Regular expression match is performed if `regexp`=`TRUE`). If some parameters are specified as random effects, these will be integrated out of the objective function via the Laplace approximation. In this situation the functions `fn` and `gr` automatically perform an optimization of random effects for each function evaluation. This is referred to as the 'inner optimization'. Strategies for choosing initial values of the inner optimization can be controlled via the argument `random.start`. The default is `expression(last.par.best[random])` where `last.par.best` is an internal full parameter vector corresponding to the currently best likelihood. An alternative choice could be `expression(last.par[random])` i.e. the random effect optimum of the most recent - not necessarily best - likelihood evaluation. Further control of the inner optimization can be obtained by
the argument `inner.control` which is a list of control parameters for the inner optimizer `newton`. Depending of the inner optimization problem type the following settings are recommended:

1. Quasi-convex: `smartsearch=TRUE` (the default).
3. Quadratic: `smartsearch=FALSE` and `maxit=1`.

Technically, the user template is processed several times by inserting different types as template parameter, selected by argument type:

- "ADFun" Run through the template with AD-types and produce a stack of operations representing the objective function.
- "Fun" Run through the template with ordinary double-types.
- "ADGrad" Run through the template with nested AD-types and produce a stack of operations representing the objective function gradient.

Each of these are represented by external pointers to C++ structures available in the environment `env`.

Further objects in the environment `env`:

- `validpar` Function defining the valid parameter region (by default no restrictions). If an invalid parameter is inserted `fn` immediately return NaN.
- `parList` Function to get the full parameter vector of random and fixed effects in a convenient list format.
- `random` An index vector of random effect positions in the full parameter vector.
- `last.par` Full parameter of the latest likelihood evaluation.
- `last.par.best` Full parameter of the best likelihood evaluation.
- `tracepar` Trace every likelihood evaluation?
- `tracemgc` Trace maximum gradient component of every gradient evaluation?
- `silent` Pass ‘silent=TRUE’ to all try-calls?

A high level of tracing information will be output by default when evaluating the objective function and gradient. This is useful while developing a model, but may eventually become annoying. Disable all tracing by passing `silent=TRUE` to the `MakeADFun` call.

**Value**

List with components (`fn`, `gr`, etc) suitable for calling an R optimizer, such as `nlminb` or `optim`.

**Note**

Do not rely upon the default arguments of any of the functions in the model object `obj$fn`, `obj$gr`, `obj$he`, `obj$report`. I.e. always use the explicit form `obj$fn(obj$par)` rather than `obj$fn()`.
**Generalized newton optimizer.**

**Description**

Generalized newton optimizer used for the inner optimization problem.

**Usage**

```
newton(par, fn, gr, he, trace = 1, maxit = 100, tol = 1e-08, alpha = 1,
        smartsearch = TRUE, mgcmax = 1e+60, super = TRUE, silent = TRUE,
        ustep = 1, power = 0.5, u0 = 1e-04, grad.tol = tol, step.tol = tol,
        to10 = 0.001, env = environment(), ...)```

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>par</td>
<td>Initial parameter.</td>
</tr>
<tr>
<td>fn</td>
<td>Objective function.</td>
</tr>
<tr>
<td>gr</td>
<td>Gradient function.</td>
</tr>
<tr>
<td>he</td>
<td>Sparse hessian function.</td>
</tr>
<tr>
<td>trace</td>
<td>Print tracing information?</td>
</tr>
<tr>
<td>maxit</td>
<td>Maximum number of iterations.</td>
</tr>
<tr>
<td>tol</td>
<td>Convergence tolerance.</td>
</tr>
<tr>
<td>alpha</td>
<td>Newton stepsize in the fixed stepsize case.</td>
</tr>
<tr>
<td>smartsearch</td>
<td>Turn on adaptive stepsize algorithm for non-convex problems?</td>
</tr>
<tr>
<td>mgcmax</td>
<td>Refuse to optimize if the maximum gradient component is too steep.</td>
</tr>
<tr>
<td>super</td>
<td>Supernodal Cholesky?</td>
</tr>
<tr>
<td>silent</td>
<td>Be silent?</td>
</tr>
<tr>
<td>ustep</td>
<td>Adaptive stepsize initial guess between 0 and 1.</td>
</tr>
<tr>
<td>power</td>
<td>Parameter controlling adaptive stepsize.</td>
</tr>
<tr>
<td>u0</td>
<td>Parameter controlling adaptive stepsize.</td>
</tr>
<tr>
<td>grad.tol</td>
<td>Gradient convergence tolerance.</td>
</tr>
<tr>
<td>step.tol</td>
<td>Stepsize convergence tolerance.</td>
</tr>
<tr>
<td>to10</td>
<td>Try to exit if last 10 iterations not improved more than this.</td>
</tr>
<tr>
<td>env</td>
<td>Environment for cached Cholesky factor.</td>
</tr>
<tr>
<td>...</td>
<td>Currently unused.</td>
</tr>
</tbody>
</table>
Details

If `smartsearch`=FALSE this function performs an ordinary newton optimization on the function \( fn \) using an exact sparse hessian function. A fixed stepsize may be controlled by \( \alpha \) so that the iterations are given by:

\[
u_{n+1} = u_n - \alpha f''(u_n)^{-1} f'(u_n)\]

If `smartsearch`=TRUE the hessian is allowed to become negative definite preventing ordinary newton iterations. In this situation the newton iterations are performed on a modified objective function defined by adding a quadratic penalty around the expansion point \( u_0 \):

\[
f_t(u) = f(u) + \frac{t}{2} \| u - u_0 \|^2\]

This function’s hessian \( f''(u) + tI \) is positive definite for \( t \) sufficiently large. The value \( t \) is updated at every iteration: If the hessian is positive definite \( t \) is decreased, otherwise increased. Detailed control of the update process can be obtained with the arguments `ustep`, `power` and `u0`.

Value

List with solution similar to `optim` output.

See Also

`newtonOption`

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**newtonOption**

Set newton options for a model object.

---

**Description**

Inner-problem options can be set for a model object using this function.

**Usage**

`newtonOption(obj, ...)`

**Arguments**

- `obj` Object from `MakeADFUn` for which to change settings.
- `...` Parameters for the `newton` optimizer to set.

**Value**

List of updated parameters.
**normalize**

Normalize process likelihood using the Laplace approximation.

**Description**

If the random effect likelihood contribution of a model has been implemented without proper normalization (i.e., lacks the normalizing constant), then this function can perform the adjustment automatically. In order for this to work, the model must include a flag that disables the data term so that the un-normalized random effect (negative log) density is returned from the model template. Automatic process normalization may be useful if either the normalizing constant is difficult to implement, or if its calculation involves so many operations that it becomes infeasible to include in the AD machinery.

**Usage**

```r
normalize(obj, flag, value = 0)
```

**Arguments**

- `obj`: Model object from `makeADFun` without proper normalization of the random effect likelihood.
- `flag`: Flag to disable the data term from the model.
- `value`: Value of 'flag' that signifies to not include the data term.

**Value**

Modified model object that can be passed to an optimizer.

**oneStepPredict**

Calculate one-step-ahead (OSA) residuals for a latent variable model.

**Description**

Calculate one-step-ahead (OSA) residuals for a latent variable model. *(Beta version; may change without notice)*

**Usage**

```r
oneStepPredict(obj, observation.name = NULL, data.term.indicator = NULL, method = c("oneStepGaussianOffMode", "fullGaussian", "oneStepGeneric", "oneStepGaussian", "cdf"), subset = NULL, conditional = NULL, discrete = NULL, discreteSupport = NULL, range = c(-Inf, Inf), seed = 123, parallel = FALSE, trace = TRUE, ...)
```
Arguments

obj
Output from MakeADFun.

observation.name
Character naming the observation in the template.

data.term.indicator
Character naming an indicator data variable in the template (not required by all methods - see details).

method
Method to calculate OSA (see details).

subset
Index vector of observations that will be added one by one during OSA. By default 1:length(observations) (with conditional subtracted).

conditional
Index vector of observations that are fixed during OSA. By default the empty set.

discrete
Are observations discrete? (assumed FALSE by default)

discreteSupport
Possible outcomes of discrete distribution (method="oneStepGeneric" only).

range
Possible range of the observations.

seed
Randomization seed (discrete case only). If NULL the RNG seed is untouched by this routine.

parallel
Run in parallel using the parallel package?

trace
Trace progress?

... Control parameters for OSA method

Details

Given a TMB latent variable model this function calculates OSA standardized residuals that can be used for goodness-of-fit assessment. The approach is based on a factorization of the joint distribution of the observations $X_1, \ldots, X_n$ into successive conditional distributions. Denote by

$$ F_n(x_n) = P(X_n \leq x_n | X_1 = x_1, \ldots, X_{n-1} = x_{n-1}) $$

the one-step-ahead CDF, and by

$$ p_n(x_n) = P(X_n = x_n | X_1 = x_1, \ldots, X_{n-1} = x_{n-1}) $$

the corresponding point probabilities (zero for continuous distributions). In case of continuous observations the sequence

$$ \Phi^{-1}(F_1(X_1)), \ldots, \Phi^{-1}(F_n(X_n)) $$

will be iid standard normal. These are referred to as the OSA residuals. In case of discrete observations draw (unit) uniform variables $U_1, \ldots, U_n$ and construct the randomized OSA residuals

$$ \Phi^{-1}(F_1(X_1) - U_1 p_1(X_1)), \ldots, \Phi^{-1}(F_n(X_n) - U_n p_n(X_n)) $$

These are also iid standard normal.

The user must specify one of the following methods to calculate the residuals:
**method="fullGaussian"**  This method assumes that the joint distribution of data and random effects is Gaussian (or well approximated by a Gaussian). It does not require any changes to the user template. However, if used in conjunction with subset and/or conditional a data.term.indicator is required - see the next method.

**method="oneStepGeneric"**  This method calculates the one-step conditional probability density as a ratio of Laplace approximations. The approximation is integrated (and re-normalized for improved accuracy) using 1D numerical quadrature to obtain the one-step CDF evaluated at each data point. The method works in the continuous case as well as the discrete case (discrete=TRUE).

It requires a specification of a data.term.indicator explained in the following. Suppose the template for the observations given the random effects \( u \) looks like

```r
DATA_VECTOR(x);
... 
lll = dnorm(x(i), u(i), sd(i), true);
... 
```

Then this template can be augmented with a data.term.indicator = "keep" by changing the template to

```r
DATA_VECTOR(x);
DATA_VECTOR_INDICATOR(keep, x);
... 
lll = keep(i) * dnorm(x(i), u(i), sd(i), true);
... 
```

The new data vector (keep) need not be passed from R. It automatically becomes a copy of \( x \) filled with ones.

**method="oneStepGaussian"**  This is a special case of the generic method where the one step conditional distribution is approximated by a Gaussian (and can therefore be handled more efficiently).

**method="oneStepGaussianOffMode"**  This is an approximation of the "oneStepGaussian" method that avoids locating the mode of the one-step conditional density.

**method="cdf"**  The generic method can be slow due to the many function evaluations used during the 1D integration (or summation in the discrete case). The present method can speed up this process but requires more changes to the user template. The above template must be expanded with information about how to calculate the negative log of the lower and upper CDF:

```r
DATA_VECTOR(x);
DATA_VECTOR_INDICATOR(keep, x);
... 
lll = keep(i) * dnorm(x(i), u(i), 0.0, true);
lll = keep.cdf_lower(i) * log( pnorm(x(i), u(i), 0.0) );
lll = keep.cdf_upper(i) * log( 1.0 - pnorm(x(i), u(i), 0.0) );
... 
```

The specialized members `keep.cdf_lower` and `keep.cdf_upper` automatically become copies of \( x \) filled with zeros.
Value

data.frame with OSA standardized residuals in column residual. Depending on the method the output may also include OSA expected observation in column mean.

Examples

#### Gaussian case
runExample("simple")
osa.simple <- oneStepPredict(obj, observation.name = "x", method="fullGaussian")
qqnorm(osa.simple$residual); abline(0,1)

## Not run:
#### Poisson case (First 100 observations)
runExample("ar1xar1")
osa.ar1xar1 <- oneStepPredict(obj, "N", "keep", method="cdf", discrete=TRUE, subset=1:100)
qqnorm(osa.ar1xar1$residual); abline(0,1)

## End(Not run)

---

openmp

Control number of openmp threads.

Description

Control number of openmp threads.

Usage

openmp(n = NULL)

Arguments

n Requested number of threads, or NULL to just read the current value.

Value

Number of threads.
plot.tmbprofile

Plot likelihood profile.

Description
Plot (negative log) likelihood profile with confidence interval added.

Usage
```r
## S3 method for class 'tmbprofile'
plot(x, type = "l", level = 0.95, ...)
```

Arguments
- `x`: Output from `tmbprofile`.
- `type`: Plot type.
- `level`: Add horizontal and vertical lines depicting this confidence level (NULL disables the lines).
- `...`: Additional plot arguments.

precompile

Precompile the TMB library in order to speed up compilation of templates.

Description
Precompile the TMB library

Usage
```r
precompile(all = TRUE, clean = FALSE, trace = TRUE, ...)
```

Arguments
- `all`: Precompile all or just the core parts of TMB?
- `clean`: Remove precompiled libraries?
- `trace`: Trace precompilation process?
- `...`: Not used.
Details

Precompilation can be used to speed up compilation of templates. It is only necessary to run `precompile()` once, typically right after installation of TMB. The function `precompile()` prepares TMB for precompilation, while the actual pre-compilation takes place the first time you compile a model after running `precompile()`.

Note that the precompilation requires write access to the TMB package folder. Three versions of the library will be prepared: Normal, parallel and a debugable version.

Precompilation works the same way on all platforms. The only known side-effect of precompilation is that it increases the file size of the generated binaries.

Examples

```r
## Not run:
## Prepare precompilation
precompile()
## Perform precompilation by running a model
runExample(all = TRUE)

## End(Not run)
```

print.checkConsistency

Print output from `checkConsistency`

Description

Print diagnostics output from `checkConsistency`

Usage

```r
## S3 method for class 'checkConsistency'
print(x, ...)
```

Arguments

- `x` Output from `checkConsistency`
- `...` Not used
**print.sdreport**

*Print brief model summary*

**Description**

Print parameter estimates and give convergence diagnostic based on gradient and Hessian.

**Usage**

```r
# S3 method for class 'sdreport'
print(x, ...)  
```

**Arguments**

- `x` Output from `sdreport`
- `...` Not used

---

**Rinterface**

*Create minimal R-code corresponding to a cpp template.*

**Description**

Create a skeleton of required R-code once the cpp template is ready.

**Usage**

```r
Rinterface(file)
```

**Arguments**

- `file` cpp template file.

**Examples**

```r
file <- system.file("examples/simple.cpp", package = "TMB")
Rinterface(file)
```
runExample

Run one of the test examples.

**Description**
Compile and run a test example (runExample() shows all available examples).

**Usage**
runExample(name = NULL, all = FALSE, thisR = TRUE, clean = FALSE, exfolder = NULL, dontrun = FALSE, subarch = TRUE, ...)

**Arguments**
- **name** Character name of example.
- **all** Run all the test examples?
- **thisR** Run inside this R?
- **clean** Cleanup before compile?
- **exfolder** Alternative folder with examples.
- **dontrun** Build only (don’t run) and remove temporary object files?
- **subarch** Build in sub-architecture specific folder?
- **...** Passed to compile.

runSymbolicAnalysis

Run symbolic analysis on sparse Hessian

**Description**
Aggressively tries to reduce fill-in of sparse Cholesky factor by running a full suite of ordering algorithms. NOTE: requires a specialized installation of the package. More information is available at the package URL.

**Usage**
runSymbolicAnalysis(obj)

**Arguments**
- **obj** Output from MakeADFun
sdreport

General sdreport function.

Description

After optimization of an AD model, sdreport is used to calculate standard deviations of all model parameters, including non linear functions of random effects and parameters specified through the ADREPORT() macro from the user template.

Usage

sdreport(obj, par.fixed = NULL, hessian.fixed = NULL, getJointPrecision = FALSE, bias.correct = FALSE, bias.correct.control = list(sd = FALSE, split = NULL, nsplit = NULL), ignore.parm.uncertainty = FALSE, getReportCovariance = TRUE, skip.delta.method = FALSE)

Arguments

obj Object returned by MakeADFun
par.fixed Optional. Parameter estimate (will be known to obj when an optimization has been carried out).
hessian.fixed Optional. Hessian wrt. parameters (will be calculated from obj if missing).
getJointPrecision Optional. Return full joint precision matrix of random effects and parameters?
bias.correct logical indicating if bias correction should be applied
bias.correct.control a list of bias correction options; currently sd, split and nsplit are used - see details.
ignore.parm.uncertainty Optional. Ignore estimation variance of parameters?
getReportCovariance Get full covariance matrix of ADREPORTed variables?
skip.delta.method Skip the delta method? (FALSE by default)

Details

First, the Hessian wrt. the parameter vector ($\theta$) is calculated. The parameter covariance matrix is approximated by

$$ V(\hat{\theta}) = -\nabla^2 l(\hat{\theta})^{-1} $$

where $l$ denotes the log likelihood function (i.e. -obj$fn). If ignore.parm.uncertainty=TRUE then the Hessian calculation is omitted and a zero-matrix is used in place of $V(\hat{\theta})$. 
For non-random effect models the standard delta-method is used to calculate the covariance matrix of transformed parameters. Let $\phi(\theta)$ denote some non-linear function of $\theta$. Then

$$V(\phi(\hat{\theta})) \approx \nabla \phi V(\hat{\theta}) \nabla \phi'$$

The covariance matrix of reported variables $V(\phi(\hat{\theta}))$ is returned by default. This can cause high memory usage if many variables are ADREPORTed. Use getReportCovariance=FALSE to only return standard errors. In case standard deviations are not required one can completely skip the delta method using skip.delta.method=TRUE.

For random effect models a generalized delta-method is used. First the joint covariance of random effects and parameters is estimated by

$$V(\hat{u}, \hat{\theta}) \approx \left( H_{uu}^{-1} \begin{pmatrix} 0 \\ 0 \\
0 \end{pmatrix} \right) + JV(\hat{\theta}).J'$$

where $H_{uu}$ denotes random effect block of the full joint Hessian of $\text{obj.env.f}$ and $J$ denotes the Jacobian of $\left( \frac{\partial u}{\partial \theta} \right)$ wrt. $\theta$. Here, the first term represents the expected conditional variance given the parameters and the second term represents the variance of the conditional mean wrt. the parameters.

Now the delta method can be applied on a general non-linear function $\phi(u, \theta)$ of random effects $u$ and parameters $\theta$:

$$V(\phi(\hat{u}, \hat{\theta})) \approx \nabla \phi V(\hat{u}, \hat{\theta}) \nabla \phi'$$

The full joint covariance is not returned by default, because it may require large amounts of memory. It may be obtained by specifying getJointPrecision=TRUE, in which case $V(\hat{u}, \hat{\theta})^{-1}$ will be part of the output. This matrix must be manually inverted using solve(jointPrecision) in order to get the joint covariance matrix. Note, that the parameter order will follow the original order (i.e. obj.env.par).

Using $\phi(\hat{u}, \hat{\theta})$ as estimator of $\phi(u, \theta)$ may result in substantial bias. This may be the case if either $\phi$ is non-linear or if the distribution of $u$ given $x$ (data) is sufficiently non-symmetric. A generic correction is enabled with bias.correct=TRUE. It is based on the identity

$$E_{\theta}[\phi(u, \theta)|x] = \partial_{\varepsilon} \left( \log \int \exp(-f(u, \theta) + \varepsilon \phi(u, \theta)) \, du \right)_{\varepsilon=0}$$

stating that the conditional expectation can be written as a marginal likelihood gradient wrt. a nuisance parameter $\varepsilon$. The marginal likelihood is replaced by its Laplace approximation.

If bias.correct.control$sd=TRUE the variance of the estimator is calculated using

$$V_{\theta}[\phi(u, \theta)|x] = \partial_{\varepsilon}^2 \left( \log \int \exp(-f(u, \theta) + \varepsilon \phi(u, \theta)) \, du \right)_{\varepsilon=0}$$

A further correction is added to this variance to account for the effect of replacing $\theta$ by the MLE $\hat{\theta}$ (unless ignore.param.uncertainty=TRUE).

Bias correction can be be performed in chunks in order to reduce memory usage or in order to only bias correct a subset of variables. First option is to pass a list of indices as bias.correct.control$split.
E.g. a list `list(1:2,3:4)` calculates the first four ADREPORTed variables in two chunks. The internal function `obj$env$ADreportIndex()` gives an overview of the possible indices of ADREPORTed variables.

Second option is to pass the number of chunks as `bias.correct.control$nsplit` in which case all ADREPORTed variables are bias corrected in the specified number of chunks. Also note that `skip.delta.method` may be necessary when bias correcting a large number of variables.

### Value

Object of class `sdreport`

### See Also

`summary.sdreport`, `print.sdreport`, `as.list.sdreport`

### Examples

```r
## Not run:
runExample("linreg_parallel", thisR = TRUE) ## Non-random effect example
dsreport(obj)
## End(Not run)

runExample("simple", thisR = TRUE) ## Random effect example
rep <- sdreport(obj)
summary(rep, "random") ## Only random effects
summary(rep, "fixed", p.value = TRUE) ## Only non-random effects
summary(rep, "report") ## Only report

## Bias correction
rep <- sdreport(obj, bias.correct = TRUE)
summary(rep, "report") ## Include bias correction
```

### Description

Summarize output from `checkConsistency`.

### Usage

```r
## S3 method for class 'checkConsistency'
summary(object, na.rm = FALSE, ...)
```

### Arguments

- **object**: Output from `checkConsistency`.
- **na.rm**: Logical; Remove failed simulations?
- **...**: Not used.
Value

List of diagnostics

---

`summary.sdreport` summary tables of model parameters

Description

Extract parameters, random effects and reported variables along with uncertainties and optionally Chi-square statistics. Bias corrected quantities are added as additional columns if available.

Usage

```r
## S3 method for class 'sdreport'
summary(object, select = c("all", "fixed", "random", "report"), p.value = FALSE, ...)
```

Arguments

- `object` Output from `sdreport`
- `select` Parameter classes to select. Can be any subset of "fixed" (\(\hat{\theta}\)), "random" (\(\hat{u}\)) or "report" (\(\phi(\hat{u}, \hat{\theta})\)) using notation as `sdreport`.
- `p.value` Add column with approximate p-values
- `...` Not used

Value

- `matrix`

---

`template` Create cpp template to get started.

Description

Create a cpp template to get started.

Usage

```r
template(file = NULL)
```

Arguments

- `file` Optional name of cpp file.
Details

This function generates a C++ template with a header and include statement. Here is a brief overview of the C++ syntax used to code the objective function. For a full reference see the Doxygen documentation (more information at the package URL).

Macros to read data and declare parameters:

<table>
<thead>
<tr>
<th>Template Syntax</th>
<th>C++ type</th>
<th>R type</th>
</tr>
</thead>
<tbody>
<tr>
<td>DATA_VECTOR(name)</td>
<td>vector&lt;Type&gt;</td>
<td>vector</td>
</tr>
<tr>
<td>DATA_MATRIX(name)</td>
<td>matrix&lt;Type&gt;</td>
<td>matrix</td>
</tr>
<tr>
<td>DATA_SCALAR(name)</td>
<td>Type</td>
<td>numeric(1)</td>
</tr>
<tr>
<td>DATA_INTEGER(name)</td>
<td>int</td>
<td>integer(1)</td>
</tr>
<tr>
<td>DATA_FACTOR(name)</td>
<td>vector&lt;int&gt;</td>
<td>factor</td>
</tr>
<tr>
<td>DATA_IVECTOR(name)</td>
<td>vector&lt;int&gt;</td>
<td>integer</td>
</tr>
<tr>
<td>DATA_SPARSE_MATRIX(name)</td>
<td>Eigen::SparseMatrix&lt;Type&gt;</td>
<td>dgTMatrix</td>
</tr>
<tr>
<td>DATA_ARRAY(name)</td>
<td>array&lt;Type&gt;</td>
<td>array</td>
</tr>
<tr>
<td>PARAMETER_MATRIX(name)</td>
<td>matrix&lt;Type&gt;</td>
<td>matrix</td>
</tr>
<tr>
<td>PARAMETER_VECTOR(name)</td>
<td>vector&lt;Type&gt;</td>
<td>vector</td>
</tr>
<tr>
<td>PARAMETER_ARRAY(name)</td>
<td>array&lt;Type&gt;</td>
<td>array</td>
</tr>
<tr>
<td>PARAMETER(name)</td>
<td>Type</td>
<td>numeric(1)</td>
</tr>
</tbody>
</table>

Basic calculations:

<table>
<thead>
<tr>
<th>Template Syntax</th>
<th>Explanation</th>
</tr>
</thead>
<tbody>
<tr>
<td>REPORT(x)</td>
<td>Report x back to R</td>
</tr>
<tr>
<td>ADREPORT(x)</td>
<td>Report x back to R with derivatives</td>
</tr>
<tr>
<td>vector&lt;Type&gt; v(n1);</td>
<td>R equivalent of v=numeric(n1)</td>
</tr>
<tr>
<td>matrix&lt;Type&gt; m(n1,n2);</td>
<td>R equivalent of m=matrix(0,n1,n2)</td>
</tr>
<tr>
<td>array&lt;Type&gt; a(n1,n2,n3);</td>
<td>R equivalent of a=matrix(0,c(n1,n2,n3))</td>
</tr>
<tr>
<td>v+v,v-v,v*v,v/v</td>
<td>Pointwise binary operations</td>
</tr>
<tr>
<td>m*v</td>
<td>Matrix-vector multiply</td>
</tr>
<tr>
<td>a.col(i)</td>
<td>R equivalent of a[i]</td>
</tr>
<tr>
<td>a.col(i),col(j)</td>
<td>R equivalent of a[i,j,i]</td>
</tr>
<tr>
<td>a(i,j,k)</td>
<td>R equivalent of a[i,j,k]</td>
</tr>
<tr>
<td>exp(v)</td>
<td>Pointwise math</td>
</tr>
<tr>
<td>m(i,j)</td>
<td>R equivalent of m[i,j]</td>
</tr>
<tr>
<td>v.sum()</td>
<td>R equivalent of sum(v)</td>
</tr>
<tr>
<td>m.transpose()</td>
<td>R equivalent of t(m)</td>
</tr>
</tbody>
</table>

Some distributions are available as C++ templates with syntax close to R’s distributions:

<table>
<thead>
<tr>
<th>Function header</th>
<th>Distribution</th>
</tr>
</thead>
<tbody>
<tr>
<td>dbinom2(x, mu, var, int give_log=0)</td>
<td>Negative binomial with mean and variance</td>
</tr>
<tr>
<td>dpois(x, lambda, int give_log=0)</td>
<td>Poisson distribution as in R</td>
</tr>
<tr>
<td>dlgamma(y, shape, scale, int give_log=0)</td>
<td>log-gamma distribution</td>
</tr>
<tr>
<td>dnorm(x, mean, sd, int give_log=0)</td>
<td>Normal distribution as in R</td>
</tr>
</tbody>
</table>
Examples

template()
tmbroot

Value
data.frame with parameter and function values.

See Also
plot.tmbprofile, confint.tmbprofile

Examples

## Not run:
runExample("simple", thisR=TRUE)
## Parameter names for this model:
## beta  beta  logsdv  logsd0

## Profile wrt. sigma0:
prof <- tmbprofile(obj, "logsd0")
plot(prof)
confint(prof)

## Profile the difference between the beta parameters (name is optional):
prof2 <- tmbprofile(obj, name="beta1 - beta2", lincomb = c(1,-1,0,0))
plot(prof2)
confint(prof2)

## End(Not run)

---

tmbroot  
Compute likelihood profile confidence intervals of a TMB object by root-finding

Description
Compute likelihood profile confidence intervals of a TMB object by root-finding in contrast to tmbprofile, which tries to compute somewhat equally spaced values along the likelihood profile (which is useful for visualizing the shape of the likelihood surface), and then (via confint.tmbprofile) extracting a critical value by linear interpolation,

Usage
tmbroot(obj, name, target = 0.5 * qchisq(0.95, df = 1), lincomb,
        parm.range = c(NA, NA), sd.range = 7, trace = FALSE,
        continuation = FALSE)

Arguments

- **obj**: Object from MakeADFun that has been optimized.
- **name**: Name or index of a parameter to profile.
target  desired deviation from minimum log-likelihood. Default is set to retrieve the 95th percentile.

lincomb  Optional linear combination of parameters to profile. By default a unit vector corresponding to name.

parm.range  lower and upper limits; if NA, a value will be guessed based on the parameter value and sd.range.

sd.range  in the absence of explicit parm.range values, the range chosen will be the parameter value plus or minus sd.range. May be specified as a two-element vector for different ranges below and above the parameter value.

trace  report information?

continuation  use continuation method, i.e. set starting parameters for non-focal parameters to solutions from previous fits?

Value

a two-element numeric vector containing the lower and upper limits (or NA if the target is not achieved in the range), with an attribute giving the total number of function iterations used.

Examples

```r
## Not run:
runExample("simple",thisR=TRUE)
logsd0.ci <- tmbroot(obj,"logsd0")

## End(Not run)
```
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