

# Package ‘scorematchingad’

May 21, 2024

**Title** Score Matching Estimation by Automatic Differentiation

**Version** 0.0.60

**Description** Hyvärinen's score matching (Hyvärinen, 2005) <<https://jmlr.org/papers/v6/hyvarinen05a.html>> is a useful estimation technique when the normalising constant for a probability distribution is difficult to compute. This package implements score matching estimators using automatic differentiation in the 'CppAD' library <<https://github.com/coin-or/CppAD>> and is designed for quickly implementing score matching estimators for new models. Also available is general robustification (Windham, 1995) <<https://www.jstor.org/stable/2346159>>. Already in the package are estimators for directional distributions (Mardia, Kent and Laha, 2016) <[doi:10.48550/arXiv.1604.08470](https://doi.org/10.48550/arXiv.1604.08470)> and the flexible Polynomially-Tilted Pairwise Interaction model for compositional data. The latter estimators perform well when there are zeros in the compositions (Scealy and Wood, 2023) <[doi:10.1080/01621459.2021.2016422](https://doi.org/10.1080/01621459.2021.2016422)>, even many zeros (Scealy, Hingee, Kent, and Wood, 2024) <[doi:10.1007/s11222-024-10412-w](https://doi.org/10.1007/s11222-024-10412-w)>.

**License** GPL (>= 3)

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.3.1

**Suggests** testthat, ks, movMF, cubature, simdd, numDeriv

**Enhances** RcppEigen (>= 0.3.3.7), RcppXPTrUtils

**Depends** R (>= 3.5.0)

**Imports** MCMCpack, optimx, FixedPoint, Rdpack, Rcpp (>= 1.0.9),  
methods, stats, R6, utils, rlang, ellipsis

**RdMacros** Rdpack

**LinkingTo** Rcpp (>= 1.0.9), RcppEigen (>= 0.3.3.7)

**Config/testthat/edition** 3

**NeedsCompilation** yes

**Author** Kassel Liam Hingee [aut, cre] (<<https://orcid.org/0000-0001-9894-2407>>),  
Janice Scealy [aut] (<<https://orcid.org/0000-0002-9718-869X>>),  
Bradley M. Bell [cph]

**Maintainer** Kassel Liam Hingee <kassel.hingee@anu.edu.au>

**Repository** CRAN

**Date/Publication** 2024-05-21 14:50:03 UTC

## R topics documented:

scorematchingad-package . . . . .	2
ADFun . . . . .	5
Bingham . . . . .	7
buildsmdtape . . . . .	8
cppad_closed . . . . .	12
cppad_search . . . . .	14
customll . . . . .	15
dppi . . . . .	17
evalll . . . . .	18
evaltape . . . . .	19
FB . . . . .	20
microbiome . . . . .	21
moretapebuilders . . . . .	23
ppi . . . . .	25
ppi_cW . . . . .	29
ppi_mmmm . . . . .	30
ppi_param_tools . . . . .	31
ppi_robust . . . . .	33
quadrattape_parts . . . . .	35
rppi . . . . .	36
rsymmetricmatrix . . . . .	38
scorematchingtheory . . . . .	39
smvalues . . . . .	41
testquadratic . . . . .	43
vMF . . . . .	44
vMF_robust . . . . .	46
Windham . . . . .	46
Windham_populationinverse . . . . .	48
<b>Index</b>	<b>50</b>

---

scorematchingad-package

*scorematchingad: Score Matching Estimation by Automatic Differentiation*

---

## Description

Hyvärinen's score matching (Hyvärinen, 2005) <https://jmlr.org/papers/v6/hyvarinen05a.html> is a useful estimation technique when the normalising constant for a probability distribution is difficult to compute. This package implements score matching estimators using automatic differentiation in the 'CppAD' library <https://github.com/coin-or/CppAD> and is designed for quickly implementing score matching estimators for new models. Also available is general robustification (Windham, 1995) <https://www.jstor.org/stable/2346159>. Already in the package are estimators for directional distributions (Mardia, Kent and Laha, 2016) [doi:10.48550/arXiv.1604.08470](https://doi.org/10.48550/arXiv.1604.08470) and the flexible Polynomially-Tilted Pairwise Interaction model for compositional data. The latter estimators perform well when there are zeros in the compositions (Scealy and Wood, 2023) [doi:10.1080/01621459.2021.2016422](https://doi.org/10.1080/01621459.2021.2016422), even many zeros (Scealy, Hingee, Kent, and Wood, 2024) [doi:10.1007/s1122202410412w](https://doi.org/10.1007/s1122202410412w).

## Details

This package's main features are

- A general capacity to implement score matching estimators that use algorithmic differentiation to avoid tedious manual algebra. The package uses CppAD and Eigen to differentiate model densities and compute the score matching discrepancy function (see [scorematchingtheory](#)). The score matching discrepancy is usually minimised by solving a quadratic equation, but a method for solving numerically (through `optimx::Rcgmin()`) is also included. On Linux platforms using the gcc compiler new models can be fitted with the help of `customll()`, in a similar fashion to models in the TMB package. New manifolds or new transforms require small alterations to the source code of this package.
- Score matching estimators for the Polynomially-Tilted Pairwise Interaction (PPI) model (Scealy and Wood 2023; Scealy et al. 2024). See function `ppi()`.
- Score matching and hybrid score matching estimators for von Mises Fisher, Bingham and Fisher-Bingham directional distributions (Mardia et al. 2016). See `vmf()`, `Bingham()` and `FB()`.
- Implementation of a modification of Windham's robustifying method (Windham 1995) for many exponential family distributions. See `Windham()`. For some models the density approaches infinity at some locations, creating difficulties for the weights in Windham's original method (Scealy et al. 2024).

## Acknowledgements

Colleagues Andrew T. A. Wood and John T. Kent played important roles in developing the statistical ideas and theory for score matching estimation for the PPI model (Scealy et al. 2024).

We developed this package on Ngunnawal and Ngambri Country. We thank the Country for its influence.

## Author(s)

**Maintainer:** Kassel Liam Hingee <kassel.hingee@anu.edu.au> ([ORCID](#))

Authors:

- Janice Scealy ([ORCID](#))

Other contributors:

- Bradley M. Bell [copyright holder]

## References

- Amaral GJA, Dryden IL, Wood ATA (2007). “Pivotal Bootstrap Methods for k-Sample Problems in Directional Statistics and Shape Analysis.” *Journal of the American Statistical Association*, **102**(478), 695–707. 27639898, <http://www.jstor.org/stable/27639898>.
- Bell B (2023). “CppAD: A Package for Differentiation of C++ Algorithms.” <https://github.com/coin-or/CppAD>.
- Hyvärinen A (2005). “Estimation of Non-Normalized Statistical Models by Score Matching.” *Journal of Machine Learning Research*, **6**(24), 695–709. <https://jmlr.org/papers/v6/hyvarinen05a.html>.
- Hyvärinen A (2007). “Some extensions of score matching.” *Computational Statistics & Data Analysis*, **51**(5), 2499–2512. doi:10.1016/j.csda.2006.09.003.
- Liu S, Kanamori T, Williams DJ (2019). “Estimating Density Models with Truncation Boundaries using Score Matching.” doi:10.48550/arXiv.1910.03834.
- Mardia K (2018). “A New Estimation Methodology for Standard Directional Distributions.” In *2018 21st International Conference on Information Fusion (FUSION)*, 724–729. doi:10.23919/ICIF.2018.8455640.
- Mardia KV, Jupp PE (2000). *Directional Statistics*, Probability and Statistics. Wiley, Great Britain. ISBN 0-471-95333-4.
- Mardia KV, Kent JT, Laha AK (2016). “Score matching estimators for directional distributions.” doi:10.48550/arXiv.1604.08470.
- Martin I, Uh H, Supali T, Mitreva M, Houwing-Duistermaat JJ (2019). “The mixed model for the analysis of a repeated-measurement multivariate count data.” *Statistics in Medicine*, **38**(12), 2248–2268. doi:10.1002/sim.8101.
- Scealy JL, Hingee KL, Kent JT, Wood ATA (2024). “Robust score matching for compositional data.” *Statistics and Computing*, **34**, 93. doi:10.1007/s1122202410412w.
- Scealy JL, Wood ATA (2023). “Score matching for compositional distributions.” *Journal of the American Statistical Association*, **118**(543), 1811–1823. doi:10.1080/01621459.2021.2016422.
- Windham MP (1995). “Robustifying Model Fitting.” *Journal of the Royal Statistical Society. Series B (Methodological)*, **57**(3), 599–609. 2346159, <http://www.jstor.org/stable/2346159>.
- Wiria AE, Prasetyani MA, Hamid F, Wammes LJ, Lell B, Ariawan I, Uh HW, Wibowo H, Djuardi Y, Wahyuni S, Sutanto I, May L, Luty AJ, Verweij JJ, Sartono E, Yazdanbakhsh M, Supali T (2010). “Does treatment of intestinal helminth infections influence malaria?” *BMC Infectious Diseases*, **10**,

77. doi:10.1186/147123341077.

Yu S, Drton M, Shojaie A (2019). “Generalized Score Matching for Non-Negative Data.” *Journal of Machine Learning Research*, **20**(76), 1–70. <https://jmlr.org/papers/v20/18-278.html>.

Yu S, Drton M, Shojaie A (2020). “Generalized Score Matching for General Domains.” doi:10.48550/arXiv.2009.11428.

---

ADFun

*A Class for Storing a CppAD Tape (ADFun) Object*

---

## Description

*This is a low level object useful for implementing score matching estimators.* An R6 class for storing a ‘pointer’ to a CppAD tape in C++ (also called an ADFun) and associated information. Currently tools for modifying this information are not available in this package, however tools for creating new ADFun objects from an existing ADFun are available. Typically an ADFun object will be created by `buildsmdtape()`.

## Introduction to CppAD Tapes

This package uses version 2022000.2 of the algorithmic differentiation library CppAD (Bell 2023) to build score matching estimators. Full help for CppAD can be found at <https://cppad.readthedocs.io/>.

Differentiation proceeds by *taping* the basic (*atomic*) operations performed on the independent variables and dynamic parameters. The atomic operations include multiplication, division, addition, sine, cosine, exponential and many more. Example values for the variables and parameters are used to conduct this taping, so care must be taken with any conditional (e.g. if-then) operations, and CppAD has **special tools for this**. The result of taping is an ADFun object, often called a *tape*. This ADFun object can be evaluated, differentiated, used for further taping (see `base2ad`), solving differential equations and more. The differentiation is with respect to the independent variables, however the dynamic parameters can be altered which allows for creating a new ADFun object where the dynamic parameters become independent variables (see `tapeSwap()`). For the purposes of score matching, there are also *fixed* parameters, which are the elements of the model’s parameter vector that are given and not estimated.

## Warning: multiple CPU

Each time a tape is evaluated the corresponding C++ object is altered. Parallel use of the same ADFun object thus requires care and is not tested. For now I recommend creating a new ADFun object for each CPU.

## Active bindings

`ptr` A Rcpp external pointer to a CppAD ADFun object.

`xtape` The (numeric) vector of independent variable values used for taping.

`dyntaxe` The (numeric) vector of dynamic parameters used for taping.

`usertheta` A (numeric) vector of NA values and fixed values specifying the parameters of taped function that were considered dynamic parameters or fixed parameters respectively.

`name` An easy to read name for the taped function

## Methods

### Public methods:

- [ADFun\\$new\(\)](#)

**Method** `new()`: Create a new ADFun object from an external pointer to a CppAD ADFun object.

*Usage:*

```
ADFun$new(
  ptr,
  name = NULL,
  xtape = vector("numeric"),
  dyntape = vector("numeric"),
  usertheta = rep(NA_real_, length(dyntape))
)
```

*Arguments:*

`ptr` A Rcpp external pointer to a CppAD ADFun object.

`name` An easy to read name for the taped function

`xtape` The (numeric) vector of independent variables used for taping.

`dyntape` The (numeric) vector of dynamic parameters used for taping.

`usertheta` A (numeric) vector of NA values and fixed values specifying the inputs of the taped function that were considered independent variables or dynamic parameters respectively.

## Examples

```
tapes <- buildsmdtape(
  "sim", "sqrt", "sph",
  ll = "ppi",
  ytape = rep(1/3, 3),
  usertheta = ppi_paramvec(p=3),
  bdryw = "minsq",
  acut = 0.01,
  verbose = FALSE)
tapes$smdtape$xtape
tapes$smdtape$dyntape
tapes$smdtape$name
tapes$smdtape$ptr
```

**Description**

Score matching estimators for the Bingham distribution's parameter matrix. Two methods are available: a full score matching method that estimates the parameter matrix directly and a hybrid method by Mardia et al. (2016) that uses score matching to estimate just the eigenvalues of the parameter matrix.

**Usage**

```
Bingham(Y, A = NULL, w = rep(1, nrow(Y)), method = "Mardia")
```

**Arguments**

Y	A matrix of multivariate observations in Cartesian coordinates. Each row is a multivariate measurement (i.e. each row corresponds to an individual).
A	For full score matching only: if supplied, then NA elements of A are estimated and the other elements are fixed. For identifiability the final element of <code>diag(A)</code> must be NA.
w	An optional vector of weights for each measurement in Y
method	Either "Mardia" or "hybrid" for the hybrid score matching estimator from Mardia et al. (2016) or "smfull" for the full score matching estimator.

**Details**

The Bingham distribution has a density proportional to

$$\exp(z^T A z),$$

where  $A$  is a symmetric matrix and the trace (sum of the diagonals) of  $A$  is zero for identifiability (p181, Mardia and Jupp 2000).

The full score matching method estimates all elements of  $A$  directly except the final element of the diagonal, which is calculated from the sum of the other diagonal elements to ensure that the trace of  $A$  is zero.

The method by Mardia et al. (2016) first calculates the maximum-likelihood estimate of the eigenvectors  $G$  of  $A$ . The observations  $Y$  are then standardised to  $YG$ . This standardisation corresponds to diagonalising  $A$  where the eigenvalues of  $A$  become the diagonal elements of the new  $A$ . The diagonal elements of the new  $A$  are then estimated using score matching, with the final diagonal element calculated from the sum of the other elements. See Mardia et al. (2016) for details.

**Value**

A list of `est`, `SE` and `info`.

- `est` contains the estimated matrix  $A$  and a vector form, `paramvec`, of  $A$  (ordered according to `c(diag(A)[1:(p-1)], A[upper.tri(A)])`). For the Mardia method, the estimated eigenvalues of  $A$  (named `evals`) and eigenvectors of  $A$  (named `G`) are also returned.
- `SE` contains estimates of the standard errors if computed. See `cppad_closed()`.
- `info` contains a variety of information about the model fitting procedure and results.

**References**

Mardia KV, Jupp PE (2000). *Directional Statistics*, Probability and Statistics. Wiley, Great Britain. ISBN 0-471-95333-4.

Mardia KV, Kent JT, Laha AK (2016). "Score matching estimators for directional distributions." [doi:10.48550/arXiv.1604.08470](https://doi.org/10.48550/arXiv.1604.08470).

**See Also**

Other directional model estimators: `FB()`, `VMF()`, `VMF_robust()`

**Examples**

```
p <- 4
A <- rsymmetricmatrix(p)
A[p,p] <- -sum(diag(A)[1:(p-1)]) #to satisfy the trace = 0 constraint
if (requireNamespace("simdd")){
  Y <- simdd::rBingham(100, A)
  Bingham(Y, method = "Mardia")
}
```

---

buildsmdtape

*Build CppAD Tapes for Score Matching*

---

**Description**

For a parametric model family, the function `buildsmdtape()` generates CppAD tapes (called ADFuns) for the improper log-likelihood (without normalising constant) of the family and the score matching discrepancy function  $A(z) + B(z) + C(z)$  (defined in [scorematchingtheory](#)). Three steps are performed by `buildsmdtape()`: first an object that specifies the manifold and any transformation to another manifold is created; then a tape of the log-likelihood (without normalising constant) is created; finally a tape of  $A(z) + B(z) + C(z)$  is created.



**Usage**

```

buildsmdtape(
  start,
  tran = "identity",
  end = start,
  ll,
  ytape,
  usertheta,
  bdryw = "ones",
  acut = 1,
  thetatape_creator = function(n) {
    seq(length.out = n)
  },
  verbose = FALSE
)

```

**Arguments**

start	The starting manifold. Used for checking that tran and man match.
tran	The name of a transformation. Available transformations are <ul style="list-style-type: none"> <li>• “sqrt”</li> <li>• “alr”</li> <li>• “clr”</li> <li>• “none” or ‘identity’</li> </ul>
end	The name of the manifold that tran maps start to. Available manifolds are: <ul style="list-style-type: none"> <li>• “sph” unit sphere</li> <li>• “Hn111” hyperplane normal to the vector 1, 1, 1, 1, ...</li> <li>• “sim” simplex</li> <li>• “Euc” Euclidean space</li> </ul>
ll	The name of an inbuilt improper log-likelihood function to tape (which also specifies the parametric model family). On Linux operating systems a custom log-likelihood function created by <code>customll()</code> can also be used; the ll should operate on the untransformed (i.e. starting) manifold.
ytape	An example measurement value to use for creating the tapes. In the natural (i.e. start) manifold of the log-likelihood function. Please ensure that ytape is the interior of the manifold and non-zero.
usertheta	A vector of parameter elements for the likelihood function. NA elements will become <i>dynamic parameters</i> . Other elements will be fixed at the provided value. The length of usertheta must be the correct length for the log-likelihood - <b>no checking is conducted</b> .
bdryw	The name of the boundary weight function. "ones" for manifolds without boundary. For the simplex and positive orthant of the sphere, "prodsq" and "minsq" are possible - see <code>ppi()</code> for more information on these.
acut	A parameter passed to the boundary weight function bdryw. Ignored for bdryw = "ones".

thetatape_creator	A function that accepts an integer $n$ , and returns a vector of $n$ length. The function is used to fill in the NA elements of <code>usertheta</code> when building the tapes. Please ensure that the values filled by <code>thetatape_creator</code> lead to plausible parameter vectors for the chosen log-likelihood.
verbose	If TRUE more details are printed when taping. These details are for debugging and will likely be comprehensible only to users familiar with the source code of this package.

## Details

The improper log-likelihood (without normalising constant) must be implemented in C++ and is selected by name. Similarly the transforms of the manifold must be implemented in C++ and selected by name.

When using, CppAD one first creates *tapes* of functions. These tapes can then be used for evaluating the function and its derivatives, and generating further tapes through argument swapping, differentiation and composition. The taping relies on specifying typical argument values for the functions (see **Introduction to CppAD Tapes** below). Tapes can have both *independent* variables and *dynamic* parameters. The differentiation with CppAD occurs with respect to the independent variables. Tapes of tapes are possible, including tapes that swap the independent and dynamic variables - this is how this package differentiates with respect to a dynamic variables (see `tapeSwap()`).

To build a tape for the score matching discrepancy function, the package first tapes the map from a point  $z$  on the end manifold to the value of the improper log-likelihood, where the independent variable is the  $z$ , the dynamic parameter is a vector of the parameters to estimate, and the remaining model parameters are fixed and not estimated. This tape is then used to generate a tape for the score matching discrepancy function where the parameters to estimate are the independent variable.

Only some combinations of `start`, `tran` and `end` are available because `tran` must map between `start` and `end`. These combinations of `start-tran-end` are currently available:

- `sim-sqrt-sph`
- `sim-identity-sim`
- `sim-alr-Euc`
- `sim-clr-Hn11`
- `sph-identity-sph`
- `Euc-identity-Euc`

Currently available improper log-likelihood functions are:

- `dirichlet`
- `ppi`
- `vMF`
- `Bingham`
- `FB`

**Value**

A list of:

- an `ADFun` object containing a tape of an improper likelihood with  $z$  on the end manifold as the independent variable
- an `ADFun` object containing a tape of the score matching discrepancy function with the non-fixed parameters as the independent variable, and the measurements on the end manifold as the dynamic parameter.
- some information about the tapes

**Introduction to CppAD Tapes**

This package uses version 2022000.2 of the algorithmic differentiation library CppAD (Bell 2023) to build score matching estimators. Full help for CppAD can be found at <https://cppad.readthedocs.io/>.

Differentiation proceeds by *taping* the basic (*atomic*) operations performed on the independent variables and dynamic parameters. The atomic operations include multiplication, division, addition, sine, cosine, exponential and many more. Example values for the variables and parameters are used to conduct this taping, so care must be taken with any conditional (e.g. if-then) operations, and CppAD has **special tools for this**. The result of taping is an `ADFun` object, often called a *tape*. This `ADFun` object can be evaluated, differentiated, used for further taping (see `base2ad`), solving differential equations and more. The differentiation is with respect to the independent variables, however the dynamic parameters can be altered which allows for creating a new `ADFun` object where the dynamic parameters become independent variables (see `tapeSwap()`). For the purposes of score matching, there are also *fixed* parameters, which are the elements of the model's parameter vector that are given and not estimated.

**Warning: multiple CPU**

Each time a tape is evaluated the corresponding C++ object is altered. Parallel use of the same `ADFun` object thus requires care and is not tested. For now I recommend creating a new `ADFun` object for each CPU.

**Warning**

There is no checking of the inputs `ytape` and `usertheta`.

**References**

Bell B (2023). "CppAD: A Package for Differentiation of C++ Algorithms." <https://github.com/coin-or/CppAD>.

**See Also**

Other tape builders: [moretapebuilders](#)

## Examples

```

p <- 3
u <- rep(1/sqrt(p), p)
ltheta <- p #length of VMF parameter vector
intheta <- rep(NA, length.out = ltheta)
tapes <- buildsmdtape("sph", "identity", "sph", "VMF",
  ytape = u,
  usertheta = intheta,
  "ones", verbose = FALSE
)
evaltape(tapes$lltape, u, runif(n = ltheta))
evaltape(tapes$smdtape, runif(n = ltheta), u)

u <- rep(1/3, 3)
tapes <- buildsmdtape("sim", "sqrt", "sph", "ppi",
  ytape = u,
  usertheta = ppi_paramvec(p = 3),
  bdryw = "minsq", acut = 0.01,
  verbose = FALSE
)
evaltape(tapes$lltape, u, rppi_egmodel(1)$theta)
evaltape(tapes$smdtape, rppi_egmodel(1)$theta, u)

```

---

cppad\_closed

*Score Matching Estimator for Quadratic-Form Score Matching Discrepancies*


---

## Description

For a tape (i.e. an ADFun object) of a quadratic-form score matching discrepancy function, calculates the vector of parameters such that the gradient of the score matching discrepancy is zero. Also estimates standard errors and covariance. Many score matching estimators have an objective function that has a quadratic form (see [scorematchingtheory](#)).

## Usage

```

cppad_closed(
  smdtape,
  Y,
  Yapproxcentres = NA * Y,
  w = rep(1, nrow(Y)),
  approxorder = 10
)

```

## Arguments

smdtape      A CppAD tape of a score matching discrepancy function that has *quadratic form*. Test for quadratic form using [testquadratic\(\)](#). The smdtape's independent

	variables are assumed to be the model parameters to fit and the smdtape's dynamic parameter is a (multivariate) measurement.
Y	A matrix of multivariate observations. Each row is an observation.
Yapproxcentres	A matrix of Taylor approximation centres for rows of Y that require approximation. NA for rows that do not require approximation.
w	Weights for each observation.
approxorder	The order of Taylor approximation to use.

## Details

When the score matching discrepancy function is of quadratic form, then the gradient of the score matching discrepancy is zero at  $H^{-1}b$ , where  $H$  is the average of the Hessian of the score matching discrepancy function evaluated at each measurement and  $b$  is the average of the gradient offset (see [quadrattape\\_parts\(\)](#)) evaluated at each measurement. Both the Hessian and the gradient offset are constant with respect to the model parameters for quadratic-form score matching discrepancy functions.

Standard errors use the Godambe information matrix (aka sandwich method) and are only computed when the weights are constant. The estimate of the negative of the sensitivity matrix  $-G$  is the average of the Hessian of smdtape evaluated at each observation in Y. The estimate of the variability matrix  $J$  is the sample covariance (denominator of  $n - 1$ ) of the gradient of smdtape evaluated at each of the observations in Y for the estimated  $\theta$ . The estimated variance of the estimator is then as  $G^{-1}JG^{-1}/n$ , where  $n$  is the number of observations.

Taylor approximation is available because boundary weight functions and transformations of the measure in Hyvärinen divergence can remove singularities in the model log-likelihood, however evaluation at these singularities may still involve computing intermediate values that are unbounded. If the singularity is ultimately removed, then Taylor approximation from a nearby location will give a very accurate evaluation at the removed singularity.

## See Also

Other generic score matching tools: [Windham\(\)](#), [cppad\\_search\(\)](#)

## Examples

```
smdtape <- buildsmdtape("sim", "sqrt", "sph", "ppi",
  ytape = rep(1/3, 3),
  usertheta = ppi_paramvec(p = 3),
  bdryw = "minsq", acut = 0.01,
  verbose = FALSE
)$smdtape
Y <- rppi_egmodel(100)
cppad_closed(smdtape, Y$sample)
```

---

cppad_search	<i>Iterative Score Matching Estimator Using Conjugate-Gradient Descent</i>
--------------	--

---

### Description

Uses conjugate gradient descent to search for a vector of parameters such that gradient of the score matching discrepancy is within tolerance of zero. Also estimates standard errors and covariance.

### Usage

```
cppad_search(
  smdtape,
  theta,
  Y,
  Yapproxcentres = NA * Y,
  w = rep(1, nrow(Y)),
  approxorder = 10,
  control = list(tol = 1e-15, checkgrad = TRUE)
)
```

### Arguments

smdtape	A CppAD tape of a score matching discrepancy function that has <i>quadratic form</i> . Test for quadratic form using <a href="#">testquadratic()</a> . The smdtape's independent variables are assumed to be the model parameters to fit and the smdtape's dynamic parameter is a (multivariate) measurement.
theta	The starting parameter set
Y	A matrix of multivariate observations. Each row is an observation.
Yapproxcentres	A matrix of Taylor approximation centres for rows of Y that require approximation. NA for rows that do not require approximation.
w	Weights for each observation.
approxorder	The order of Taylor approximation to use.
control	Control parameters passed to <a href="#">optimx::Rcgmin()</a>

### Details

The score matching discrepancy function and gradient of the score matching function are passed to [optimx::Rcgmin\(\)](#). The call to [optimx::Rcgmin\(\)](#) uses the *sum* of observations (as opposed to the mean) to reduce floating point inaccuracies. This has implications for the meaning of the control parameters passed to [Rcgmin\(\)](#) (e.g. `tol`). The results are converted into averages so the use of sums can be ignored when not setting control parameters, or studying the behaviour of [Rcgmin\(\)](#).

Standard errors use the Godambe information matrix (aka sandwich method) and are only computed when the weights are constant. The estimate of the sensitivity matrix  $G$  is the negative of the average over the Hessian of `smdtape` evaluated at each observation in `Y`. The estimate of the variability

matrix  $J$  is then the sample covariance (denominator of  $n - 1$ ) of the gradient of `smdtape` evaluated at each of the observations in  $Y$  for the estimated  $\theta$ . The variance of the estimator is then estimated as  $G^{-1}JG^{-1}/n$ , where  $n$  is the number of observations.

Taylor approximation is available because boundary weight functions and transformations of the measure in Hyvärinen divergence can remove singularities in the model log-likelihood, however evaluation at these singularities may still involve computing intermediate values that are unbounded. If the singularity is ultimately removed, then Taylor approximation from a nearby location will give a very accurate evaluation at the removed singularity.

### Warning

There appears to be floating point issues with evaluation of the gradient leading to slow or no convergence in many situations. Tweaking the convergence tolerance `tol` may be appropriate. If the closed form solution exists please use `cppad_closed()` instead.

### See Also

Other generic score matching tools: [Windham\(\)](#), [cppad\\_closed\(\)](#)

### Examples

```
smdtape <- buildsmdtape("sim", "sqrt", "sph", "ppi",
  ytape = rep(1/3, 3),
  usertheta = ppi_paramvec(p = 3),
  bdryw = "minsq", acut = 0.01,
  verbose = FALSE
)$smdtape
Y <- rppi_egmodel(100)
cppad_search(smdtape, 0.9 * Y$theta, Y$sample)
sum((smvalues_wsum(smdtape, Y$sample, Y$theta)$grad/nrow(Y$sample))^2)
```

---

customll

*Compile a custom log-likelihood function.*

---

### Description

Supply C++ code to specify a custom log-likelihood, much like `TMB::compile()` is passed C++ code that formulate models. For score matching the normalising constant of the log-likelihood can be omitted. Taping of the function currently only works with the `gcc` compiler, typically on Linux; taping works if `customll_test()` returns `TRUE`. Packages `RcppEigen` and `RcppXPtrUtils` must be installed.

### Usage

```
customll(
  code,
  rebuild = FALSE,
  includes = character(),
```

```

    cacheDir = getOption("rcpp.cache.dir", tempdir()),
    showOutput = verbose,
    verbose = getOption("verbose")
)

customll_test()

```

## Arguments

code	C++ code for a log-likelihood function (with normalising constant omitted if desired). See details for more.
rebuild	passed to <code>Rcpp::cppFunction()</code> .
includes	passed to <code>Rcpp::cppFunction()</code> . For internal use.
cacheDir	passed to <code>Rcpp::cppFunction()</code> .
showOutput	passed to <code>Rcpp::cppFunction()</code> .
verbose	passed to <code>Rcpp::cppFunction()</code> .

## Details

The function uses `RcppXPtUtils::cppXPt()` and `Rcpp::cppFunction()`. It is good practice to check the returned object using `evalll()`. The first compilation in a session can be very slow.

## Value

`customll()` returns an `adloglikelihood` object (which is just an `externalptr` with attributes) for the compiled log-likelihood function. The returned object has an attribute `fname`.

`customll_test()` returns `TRUE` if taping works in your R session. Otherwise it will return `FALSE` and generate warnings.

## Code Argument

code must be C++ that uses only CppAD and Eigen, which makes it very similar to the requirements of the input to `TMB::compile()` (which also uses CppAD and Eigen).

The start of code should always be `"a1type fname(const veca1 &x, const veca1 &theta){"` where `fname` is your chosen name of the log-likelihood function, `x` represents a point in the data space and `theta` is a vector of parameters for the log-likelihood. This specifies that the function will have two vector arguments (of type `veca1`) and will return a single numeric value (`a1type`).

The type `a1type` is a double with special ability for being taped by CppAD. The `veca1` type is a vector of `a1type` elements, with the vector wrapping supplied by the Eigen C++ package (that is an Eigen matrix with 1 column and dynamic number of rows).

The body of the function must use operations from Eigen and/or CppAD, prefixed by `Eigen::` and `CppAD::` respectively. There are no easy instructions for writing these as it is genuine C++ code, which can be very opaque to those unfamiliar with C++. See the [Eigen documentation](#) for quick reference to available operations from Eigen. Limited operations are available directly from CppAD without Eigen: [unary operations](#) and [binary operations](#). For the purposes of score matching the operations should all be smooth to create a smooth log-likelihood and the normalising constant may be omitted.



**Examples**

```
## Not run: customll_test()

myll <- customll("atype dirichlet(const veca1 &u, const veca1 &beta) {
  size_t d = u.size();
  atype y(0.); // initialize summation at 0
  for(size_t i = 0; i < d; i++)
  {   y   += beta[i] * log(u[i]);
  }
  return y;
}")
evalll(myll, rep(1/3, 3), rep(-0.5, 3))

tapes <- buildsmdtape("sim", "identity", "sim",
  myll, rep(1/3, 3), rep(NA, 3),
  bdryw="minsq", acut = 0.01)
evaltape(tapes$l1tape, rep(1/3, 3), rep(-0.5, 3))
## End(Not run)
```

dppi

*Improper Log-Density of the PPI Model***Description**

Compute the **natural logarithm** of the improper density for the PPI model for the given matrix of measurements  $Y$ . Rows with negative values or with a sum that differs from 1 by more than  $1E-15$  are assigned a value of  $-\text{Inf}$ .

**Usage**

```
dppi(Y, ..., paramvec = NULL)
```

**Arguments**

$Y$	A matrix of measurements in the simplex. Each row is a multivariate measurement.
$\dots$	Arguments passed on to <a href="#">ppi_paramvec</a>
$A_L$	Either NULL, a $p-1 \times p-1$ symmetric matrix, a number, or "diag". If NULL then all $A_L$ elements will be set to NA. If a single number, then $A_L$ will be fixed as a matrix of the given value. If "diag" then the non-diagonal elements of $A_L$ will be fixed to 0, and the diagonal will be NA.
$b_L$	Either NULL, a number, or a vector of length $p-1$ . If NULL, then all elements of $b_L$ will be set to NA. If a single number, then $b_L$ will be fixed at the supplied value.
$\beta$	Either NULL, a number, or a vector of length $p$ . If NULL then all elements of $\beta$ will be set to NA. If a single number then the $\beta$ elements will be fixed at the given number.

	betaL	Either NULL, a number, or a vector of length p-1. If NULL then the 1...(p-1)th $\beta$ elements will be set to NA. If a single number then the 1...(p-1)th $\beta$ elements will be fixed at the given number.
	betap	Either NULL or a number. If NULL then the pth element of $\beta$ will be set to NA, and <code>ppi()</code> will estimate it. If a number, then the pth element of $\beta$ will be fixed at the given value.
	p	The number of components. If NULL then p will be inferred from other inputs.
	Astar	The $A^*$ matrix (a p by p symmetric matrix)
paramvec		The PPI parameter vector, created easily using <code>ppi_paramvec()</code> and also returned by <code>ppi()</code> . Use paramvec instead of . . . .

### Details

The value calculated by `dppi` is

$$z_L^T A_L z_L + b_L^T z_L + \beta^T \log(z),$$

where  $z$  is the multivariate observation (i.e. a row of  $Y$ ), and  $z_L$  omits the final element of  $z$ .

### See Also

Other PPI model tools: `ppi()`, `ppi_param_tools`, `ppi_robust()`, `rppi()`

### Examples

```
m <- rppi_egmodel(10)
dppi(m$sample, paramvec = m$theta)
```

---

evalll

*Evaluate a custom log-likelihood function*

---

### Description

Evaluates a custom log-likelihood function from `customll()` without taping. This is useful to check that the custom log-likelihood is behaving. To check a tape of the custom log-likelihood use `buildsmdtape()` then `evaltape()`.

### Usage

```
evalll(ll, u, theta)
```

### Arguments

ll	A compiled log-likelihood function created by <code>customll()</code> .
u	A vector of measurements for an individual
theta	A vector of parameters

### Value

The value of the log-likelihood at  $u$  with parameters  $\theta$ .

evaltape

*Evaluate a CppAD Tape Many Times***Description**

Evaluates a tape exactly or approximately for an array of provided variable values and dynamic parameter values. The function `evaltape_wsum()` computes the column-wise weighted sum of the result.

**Usage**

```
evaltape(tape, xmat, pmat, xcentres = NA * xmat, approxorder = 10)
```

```
evaltape_wsum(
  tape,
  xmat,
  pmat,
  w = NULL,
  xcentres = NA * xmat,
  approxorder = 10
)
```

**Arguments**

tape	An <a href="#">ADFun</a> object (i.e. a tape of a function).
xmat	A matrix of (multivariate) independent variables where each represents a single independent variable vector. Or a single independent variable vector that is used for all rows of pmat.
pmat	A matrix of dynamic parameters where each row specifies a new set of values for the dynamic parameters of tape. Or a single vector of dynamic parameters to use for all rows of xmat.
xcentres	A matrix of approximation for Taylor approximation centres for xmat. Use values of NA for rows that do not require Taylor approximation.
approxorder	Order of Taylor approximation
w	Weights to apply to each row of xmat for computing the weighted sum. If NULL then each row is given a weight of 1.

**Details**

Approximation is via Taylor approximation of the independent variable around the approximation centre provided in `xcentres`.

**Value**

A matrix, each row corresponding to the evaluation of the same row in `xmat`, `pmat` and `xcentres`.

**See Also**

Other tape evaluators: [quadratictape\\_parts\(\)](#), [smvalues\(\)](#), [testquadratic\(\)](#)

**Examples**

```
u <- rep(1/3, 3)
tapes <- buildsmdtape("sim", "sqrt", "sph", "ppi",
  ytape = u,
  usertheta = ppi_paramvec(p = 3),
  bdryw = "minsq", acut = 0.01,
  verbose = FALSE
)
evaltape(tapes$lltape, u, rppi_egmodel(1)$theta)
evaltape(tapes$smdtape, rppi_egmodel(1)$theta, u)
evaltape(tapes$lltape, rbind(c(0, 0, 1), c(0,0,1)),
  rppi_egmodel(1)$theta,
  xcentres = rbind(c(0.0005, 0.0005, 0.999), NA))
```

---

 FB

---

*Estimate the Fisher-Bingham Distribution*


---

**Description**

Estimates parameters for the Fisher-Bingham distribution using score-matching.

**Usage**

```
FB(Y, km = NULL, A = NULL)
```

**Arguments**

Y	A matrix of multivariate observations in Cartesian coordinates. Each row is a multivariate measurement (i.e. each row corresponds to an individual).
km	Optional. A vector of the same length as the dimension, representing the parameter vector for the von Mises-Fisher component (i.e. the $\kappa\mu$ see <a href="#">vmf()</a> ). If supplied, the non-NA elements are fixed.
A	Optional. The Bingham matrix. If supplied the non-NA elements of the Bingham matrix are fixed. The final element of the diagonal of A must be NA as the software calculates this value to ensure the trace of the Bingham matrix is zero.

**Details**

The density of the Fisher-Bingham distribution is proportional to

$$\exp(z^T A z + \kappa \mu^T z),$$

where  $A$  is a matrix as in the Bingham distribution, and  $\kappa$  and  $\mu$  are the concentration and mean direction, respectively, as in the von Mises-Fisher distribution.

**Warning: Slow Convergence with Sample Size**

Score matching estimates of all elements of  $A$  and  $\kappa\mu$  converge slowly with sample size. Even with a million simulated measurements, the gradient of the score matching discrepancy at the true parameters can have size (L2 Euclidean norm) more than 0.001, which is substantially non-zero.

**See Also**

Other directional model estimators: [Bingham\(\)](#), [VMF\(\)](#), [VMF\\_robust\(\)](#)

**Examples**

```
p <- 3
A <- rsymmetricmatrix(p, -10, 10)
A[p,p] <- -sum(diag(A)[1:(p-1)]) #to satisfy the trace = 0 constraint
m <- runif(p, -10, 10)
m <- m / sqrt(sum(m^2))
if (requireNamespace("simdd")){
  Y <- simdd::rFisherBingham(1000, 2 * m, A)
  FB(Y)
}
```

---

microbiome

*16s Microbiome Data for Soil-Transmitted Helminths*


---

**Description**

The microbiome data contains paired DNA samples from before treatment and 21 months after treatment for helminth infections (Martin et al. 2019). This data was analysed by Martin et al. (2019) and a further subset was studied by Scealy and Wood (2023). The data are from a study into the effect of helminth infections on the course of malaria infections (ImmunoSPIN-Malaria) in the Nangapanda subdistrict, Indonesia (Wiria et al. 2010). As part of the study, some participants were given 400mg of albendazole every three months for 1.5 years, remaining participants were given a placebo (Wiria et al. 2010).

**Usage**

```
microbiome
```

**Format**

A dataframe with 300 rows (two rows per individual) and 31 columns:

**IndividualID** An integer uniquely specifying the individual.

**Year** The collection year for the sample. 2008 for before treatment. 2010 for after treatment.

**Sex** 1 if female, 0 otherwise.

**Treatment** TRUE if individual given 400mg of albendazole every three months for 1.5 years, FALSE otherwise.

**Age** Age at first sample.

**ct\_Al** A Helminth measurement: The qPCR cycle threshold (CT) for *Ascaris lumbricoides* (large roundworm). *Ascaris lumbricoides* can be considered present if the value is 30 or less.

**ct\_Na** A Helminth measurement: The qPCR cycle threshold (CT) for *Necator americanus* (a hookworm). *Necator americanus* can be considered present if the value is 30 or less.

**ct\_Ad** A Helminth measurement: The qPCR cycle threshold (CT) for *Ancylostoma duodenale* (a hookworm). *Ancylostoma duodenale* can be considered present if the value is 30 or less.

**micr\_Tt** A Helminth measurement: The presence of *Trichuris trichiura* as determined by microscopy. A value of TRUE means *Trichuris trichiura* was detected.

**Helminth** A Helminth measurement: If any of the above helminths were detected then TRUE, otherwise FALSE.

**Remaining columns** Count prevalence of 18 bacterial phyla and 2 unclassified columns.

## Details

The measurements in the data come from stool samples before and after treatment. Gut microbiome prevalence was measured using 16s rRNA 454 sequencing (Martin et al. 2019). Helminth infections were detected by PCR or microscopy (Martin et al. 2019).

The subset studied by Scealy and Wood (2023) contained only the measurements from before treatment, and only those individuals with a helminth infection. These measurements can be obtained by running

```
microbiome[microbiome$Year == 2008 & microbiome$Helminth, ]
```

Two further individuals (IndividualID of 2079 and 2280) were deemed outliers by Scealy and Wood (2023).

## Modifications from the Source

The microbiome data was created from the file `S1_Table.xlsx` hosted on [Nematode.net](https://www.nematode.net) using the below code.

```
microbiome <- readxl::read_excel("S1_Table.xlsx",
  range = "A3:AE303") #avoids the genus data, keeping - only phyla
metacolnames <- readxl::read_excel("S1_Table.xlsx",
  range = "A2:J2",
  col_names = FALSE)
colnames(microbiome)[1:ncol(metacolnames)] <- metacolnames[1, ]
colnames(microbiome)[2] <- "Year"
microbiome[, 11] <- (microbiome$ct_Al <= 30) | (microbiome$ct_Na <= 30) |
  (microbiome$ct_Ad <= 30) | (microbiome$ct_St <= 30) |
  (microbiome$micr_Tt == 1)
colnames(microbiome)[11] <- "Helminth"
microbiome <- microbiome |>
  dplyr::mutate(across(c(1,2,3,12:31), as.integer)) |>
  dplyr::mutate(micr_Tt = as.logical(micr_Tt),
    Treatment = as.logical(Treatment)) |>
  dplyr::rename(IndividualID = `Individual ID`)
microbiome <- as.data.frame(microbiome)
```

## Source

[S1\\_Table.xlsx](#) from <http://nematode.net>. [S1\\_Table.xlsx](#) was created by Dr. Bruce A Rosa for Martin et al. (2019). Permission to share this data was obtained from Dr. Bruce Rosa and Dr. Ivonne Martin.

## References

Martin I, Uh H, Supali T, Mitreva M, Houwing-Duistermaat JJ (2019). “The mixed model for the analysis of a repeated-measurement multivariate count data.” *Statistics in Medicine*, **38**(12), 2248–2268. doi:10.1002/sim.8101.

Scealy JL, Wood ATA (2023). “Score matching for compositional distributions.” *Journal of the American Statistical Association*, **118**(543), 1811–1823. doi:10.1080/01621459.2021.2016422.

Wiria AE, Prasetyani MA, Hamid F, Wammes LJ, Lell B, Ariawan I, Uh HW, Wibowo H, Djuardi Y, Wahyuni S, Sutanto I, May L, Luty AJ, Verweij JJ, Sartono E, Yazdanbakhsh M, Supali T (2010). “Does treatment of intestinal helminth infections influence malaria?” *BMC Infectious Diseases*, **10**, 77. doi:10.1186/147123341077.

---

moretapebuilders

*Build New Tapes from Existing Tapes*

---

## Description

Build new tapes (i.e [ADFun](#) objects) from existing tapes, including differentiation, swapping independent variables and dynamic parameters, and Jacobian determinants.

## Usage

```
tapeJacobian(tape)
```

```
tapeHessian(tape)
```

```
tapeGradOffset(tape)
```

```
tapeLogJacDet(tape)
```

```
tapeSwap(tape)
```

## Arguments

tape            An [ADFun](#) object.

## Details

The information in the fields `xtape` and `dyntape` of `tape` are used to perform the taping.

### **tapeJacobian:**

The returned vector is ordered with the range elements iterating fastest, then the domain elements. See <https://cppad.readthedocs.io/latest/Jacobian.html>.

### **tapeHessian:**

Suppose the function represented by `tape` maps from  $d$ -dimensional space to 1-dimensional space, then the first  $d$  elements of the vector is the gradient of the partial derivative with respect to the first dimension of the function's domain. The next  $d$  elements of the vector is the gradient of the partial derivative of the second dimension of the function's domain. The Hessian as a matrix, can be obtained by using `matrix()` with `ncol = d`.

### **tapeGradOffset:**

A quadratic function can be written as

$$f(x; \theta) = \frac{1}{2}x^T W(\theta)x + b(\theta)^T x + c,$$

where the vector  $x$  is the independent variable of `tape` and the vector  $\theta$  is the dynamic parameter vector of `tape`. The gradient of  $f(x; \theta)$  with respect to  $x$  is

$$\Delta f(x; \theta) = \frac{1}{2}(W(\theta) + W(\theta)^T)x + b(\theta).$$

The Hessian is

$$Hf(x; \theta) = \frac{1}{2}(W(\theta) + W(\theta)^T),$$

which does not depend on  $x$ , so the gradient of the function can be rewritten as

$$\Delta f(x; \theta) = Hf(x; \theta)x + b(\theta)^T.$$

The `tape` calculates  $b(\theta)$  as

$$b(\theta) = \Delta f(x; \theta) - Hf(x; \theta)x,$$

which does not depend on  $x$ .

## Value

An `ADFun` object.

## Functions

- `tapeJacobian()`: Tape the Jacobian of a `tape`. The resulting `tape` returns the Jacobian as a vector.
- `tapeHessian()`: Tape the Hessian of a `tape`. The resulting `tape` returns the Jacobian as a vector (see <https://cppad.readthedocs.io/latest/Hessian.html>).
- `tapeGradOffset()`: A quadratic function can be written as

$$f(x; \theta) = \frac{1}{2}x^T W(\theta)x + b(\theta)^T x + c.$$

The function `tapeGradOffset` creates a `tape` of  $b(\theta)$  where  $\theta$  is the independent variable.



- `tapeLogJacDet()`: Creates a tape of the log of the Jacobian determinant of a function taped in tape. The dimensions of the domain (length of independent variable) and range (length of output variable) of tape must be equal for computation of the determinant.
- `tapeSwap()`: Convert an `ADFun` so that the independent variables become dynamic parameters and the dynamic parameters become independent variables.

### See Also

[ADFun](#)

Other tape builders: [buildsmdtape\(\)](#)

### Examples

```
tapes <- buildsmdtape("sph", "identity", "sph", "vMF",
  ytape = rep(1, 3)/sqrt(3),
  usertheta = rep(NA, 3)
)
tapeJacobian(tapes$smdtape)
tapeHessian(tapes$smdtape)
tapeLogJacDet(tapeJacobian(tapes$smdtape))
tapeSwap(tapes$smdtape)
```

### Description

Estimates the parameters of the Polynomially-Tilted Pairwise Interaction (PPI) model (Scealy and Wood 2023) for compositional data. By default `ppi()` uses [cppad\\_closed\(\)](#) to find estimate. For many situations a hard-coded implementation of the score matching estimator is also available.

For a given parameter vector `evalparam`, `ppi_smvalues()` computes the score matching discrepancy, the gradient and the Hessian of the score matching discrepancy (see [smvalues\(\)](#)) and the gradient offset of the score matching discrepancy (see [quadratictape\\_parts\(\)](#) and [tapeGradOffset\(\)](#)).

### Usage

```
ppi(
  Y,
  paramvec = NULL,
  trans,
  method = "closed",
  w = rep(1, nrow(Y)),
  constrainbeta = FALSE,
  bdryw = "ones",
  acut = NULL,
  bdrythreshold = 1e-10,
  shiftsize = bdrythreshold,
```

```

    approxorder = 10,
    control = list(tol = 1e-15, checkgrad = TRUE),
    paramvec_start = NULL
)

ppi_smvalues(
  Y,
  paramvec = NULL,
  evalparam,
  trans,
  method = "closed",
  w = rep(1, nrow(Y)),
  bdryw = "ones",
  acut = NULL,
  bdrythreshold = 1e-10,
  shiftsize = bdrythreshold,
  approxorder = 10,
  average = TRUE
)

```

### Arguments

Y	A matrix of measurements. Each row is a compositional measurement (i.e. each row sums to 1 and has non-negative elements).
paramvec	Optionally a vector of the PPI models parameters. NA-valued elements of this vector are estimated and non-NA values are fixed. Generate paramvec easily using <code>ppi_paramvec()</code> . If NULL then all elements of $A_L$ , $b_L$ and $\beta$ are estimated.
trans	The name of the transformation of the manifold in Hyvärinen divergence (See <a href="#">scorematchingtheory</a> ): "clr" (centred log ratio), "alr" (additive log ratio), "sqrt" or "none".
method	"closed" uses CppAD to solve in closed form the a quadratic score matching discrepancy using <code>cppad_closed()</code> . "hardcoded" uses hardcoded implementations. "iterative" uses <code>cppad_search()</code> (which uses CppAD and <code>optimx::Rcgmin()</code> ) to iteratively find the minimum of the weighted Hyvärinen divergence.
w	Weights for each observation, if different observations have different importance. Used by <code>Windham()</code> and <code>ppi_robust()</code> for robust estimation.
constrainbeta	If TRUE, elements of $\beta$ that are less than -1 are converted to $-1 + 1E-7$ .
bdryw	The boundary weight function for down weighting measurements as they approach the manifold boundary. Either "ones", "minsq" or "prodsq". See details.
acut	The threshold $a_c$ in bdryw to avoid over-weighting measurements interior to the simplex
bdrythreshold	iterative or closed methods only. For measurements within bdrythreshold of the simplex boundary a Taylor approximation is applied by shifting the measurement shiftsize towards the center of the simplex.
shiftsize	iterative or closed methods only. For measurements within bdrythreshold of the simplex boundary a Taylor approximation is applied by shifting the measurement shiftsize towards the center of the simplex.

approxorder	iterative or closed methods only. Order of the Taylor approximation for measurements on the boundary of the simplex.
control	iterative only. Passed to <code>optimx::Rcgmin()</code> to control the iterative solver.
paramvec_start	iterative method only. The starting guess for Rcgmin. Generate paramvec_start easily using <code>ppi_paramvec()</code> .
evalparam	The parameter set to evaluate the score matching values. This is different to paramvec, which specifies which parameters to estimate. All elements of evalparam must be non-NA, and any parameters fixed by paramvec must have the same value in evalparam.
average	If TRUE return the (weighted average) of the measurements, otherwise return the values for each measurement.

## Details

Estimation may be performed via transformation of the measure in Hyvärinen divergence from Euclidean space to the simplex (inverse of the additive log ratio transform), from a hyperplane to the simplex (inverse of the centred log ratio transform), from the positive quadrant of the sphere to the simplex (inverse of the square root transform), or without any transformation. In the latter two situations there is a boundary and *weighted Hyvärinen divergence* (Equation 7, Scealy and Wood 2023) is used. Properties of the estimator using the square root transform were studied by Scealy and Wood (2023). Properties of the estimator using the additive log ratio transform were studied by Scealy et al. (2024).

There are three boundary weight functions available:

- The function "ones" applies no weights and should be used whenever the manifold does not have a boundary.
- The function "minsq" is the minima-based boundary weight function for the PPI model (Equation 12, Scealy and Wood 2023)

$$\tilde{h}(z)^2 = \min(z_1^2, z_2^2, \dots, z_p^2, a_c^2).$$

where  $z$  is a point in the positive orthant of the  $p$ -dimensional unit sphere and  $z_j$  is the  $j$ th component of  $z$ .

- The function "prodsq" is the product-based (Equation 9, Scealy and Wood 2023)

$$\tilde{h}(z)^2 = \min\left(\prod_{j=1}^p z_j^2, a_c^2\right).$$

where  $z$  is a point in the positive orthant of the  $p$ -dimensional unit sphere and  $z_j$  is the  $j$ th component of  $z$ .

Scealy and Wood (Theorem 1, Scealy and Wood 2023) prove that minimising the weighted Hyvärinen Divergence is equivalent to minimising  $\psi(f, f_0)$  (See [scorematchingtheory](#)) when the boundary weight function is smooth or for the functions "minsq" and "prodsq" above when the manifold is the simplex or positive orthant of a sphere.

Hard-coded estimators are available for the following situations:

- Square root transformation ("sqrt") with the "minsq" boundary weight function:

- full parameter vector (paramvec not provided)
- paramvec fixes only the final element of  $\beta$
- paramvec fixes all elements of  $\beta$
- paramvec fixes  $b_L = 0$  and provides fixed values of  $\beta$
- paramvec fixes  $A_L = 0$  and  $b_L = 0$ , leaving  $\beta$  to be fitted.
- Square root transformation ("sqrt") with the "prodsq" boundary weight function:
  - paramvec fixes all elements of  $\beta$
  - paramvec fixes  $b_L = 0$  and provides fixed values of  $\beta$
  - paramvec fixes  $A_L = 0$  and  $b_L = 0$ , leaving  $\beta$  to be fitted.
- The additive log ratio transformation ("alr") using the final component on the denominator, with  $b_L = 0$  and fixed final component of  $\beta$ .

## Value

ppi() returns: A list of est, SE and info.

- est contains the estimates in vector form, paramvec, and as  $A_L$ ,  $b_L$  and  $\beta$ .
- SE contains estimates of the standard errors if computed. See [cppad\\_closed\(\)](#).
- info contains a variety of information about the model fitting procedure and results.

ppi\_smvalues() returns a list of

- obj the score matching discrepancy value
- grad the gradient of the score matching discrepancy
- hess the Hessian of the score matching discrepancy
- offset gradient offset (see [quadratictape\\_parts\(\)](#))

## PPI Model

The PPI model density is proportional to

$$\exp(z_L^T A_L z_L + b_L^T z_L) \prod_{i=1}^p z_i^{\beta_i},$$

where  $p$  is the dimension of a compositional measurement  $z$ , and  $z_L$  is  $z$  without the final ( $p$ th) component.  $A_L$  is a  $(p-1) \times (p-1)$  symmetric matrix that controls the covariance between components.  $b_L$  is a  $(p-1)$  vector that controls the location within the simplex. The  $i$ th component  $\beta_i$  of  $\beta$  controls the concentration of density when  $z_i$  is close to zero: when  $\beta_i \geq 0$  there is no concentration and  $\beta_i$  is hard to identify; when  $\beta_i < 0$  then the probability density of the PPI model increases unboundedly as  $z_i$  approaches zero, with the increasing occurring more rapidly and sharply the closer  $\beta_i$  is to  $-1$ .

## References

Scealy JL, Hingee KL, Kent JT, Wood ATA (2024). "Robust score matching for compositional data." *Statistics and Computing*, **34**, 93. [doi:10.1007/s1122202410412w](https://doi.org/10.1007/s1122202410412w).

Scealy JL, Wood ATA (2023). "Score matching for compositional distributions." *Journal of the American Statistical Association*, **118**(543), 1811–1823. [doi:10.1080/01621459.2021.2016422](https://doi.org/10.1080/01621459.2021.2016422).

**See Also**

Other PPI model tools: [dppi\(\)](#), [ppi\\_param\\_tools](#), [ppi\\_robust\(\)](#), [rppi\(\)](#)

**Examples**

```
model <- rppi_egmodel(100)
estalr <- ppi(model$sample,
              paramvec = ppi_paramvec(betap = -0.5, p = ncol(model$sample)),
              trans = "alr")
estsqrt <- ppi(model$sample,
               trans = "sqrt",
               bdryw = "minsq", acut = 0.1)
```

ppi\_cW

*Quickly Generate a Vector of Windham Exponents for the PPI Model***Description**

These functions help to quickly generate a set of Windham exponents for use in [ppi\\_robust\(\)](#) or [Windham\(\)](#). Rows and columns of  $A_L$  and  $b_L$  corresponding to components with strong concentrations of probability mass near zero have non-zero constant tuning exponent, and all other elements have a tuning constant of zero. All elements of  $\beta$  have a tuning exponent of zero.

The function `ppi_cW_auto()` automatically detects concentrations near zero by fitting a PPI distribution with  $A_L = 0$  and  $b_L = 0$  (i.e. a Dirichlet distribution) with the centred log-ratio transformation of the manifold.

**Usage**

```
ppi_cW(cW, ...)
```

```
ppi_cW_auto(cW, Y)
```

**Arguments**

cW	The value of the non-zero Windham tuning exponents.
...	Values of TRUE or FALSE in the same order of the components specifying that a component has probability mass concentrated near zero.
Y	A matrix of observations

**Details**

The Windham robustifying method involves weighting observations by a function of the proposed model density (Windham 1995). Sealy et al. (2024) found that only some of the tuning constants should be non-zero: the tuning exponents corresponding to  $\beta$  should be zero to avoid infinite weights; and to improve efficiency any rows or columns of  $A_L$  corresponding to components without concentrations of probability mass (i.e. outliers can't exist) should have exponents of zero. Sealy et al. (2024) set the remaining tuning exponents to a constant.

**Value**

A vector of the same length as the parameter vector of the PPI model. Elements of  $A_L$  will have a value of  $cW$  if both their row and column component has probability mass concentrated near zero. Similarly, elements of  $b_L$  will have a value of  $cW$  if their row corresponds to a component that has a probability mass concentrated near zero. All other elements are zero.

**References**

Scealy JL, Hingee KL, Kent JT, Wood ATA (2024). “Robust score matching for compositional data.” *Statistics and Computing*, **34**, 93. doi:10.1007/s1122202410412w.

Windham MP (1995). “Robustifying Model Fitting.” *Journal of the Royal Statistical Society. Series B (Methodological)*, **57**(3), 599–609. 2346159, <http://www.jstor.org/stable/2346159>.

**Examples**

```
Y <- rppi_egmodel(100)$sample
ppi_cW_auto(0.01, Y)
ppi_cW(0.01, TRUE, TRUE, FALSE)
```

---

ppi_mmmm	<i>A PPI Score-Matching Marginal Moment Matching Estimator (dimension=3 only)</i>
----------	---

---

**Description**

Computes a marginal moment matching estimator (Section 6.2, Scealy and Wood 2023), which assumes  $\beta$  is a known vector with the same value in each element, and  $b_L = 0$ . Only  $A_L$  is estimated.

**Usage**

```
ppi_mmmm(Y, ni, beta0, w = rep(1, nrow(Y)))
```

**Arguments**

Y	Count data, each row is a multivariate observation.
ni	The total for each sample (sum across rows)
beta0	$\beta = \beta_0$ is the same for each component.
w	Weights for each observation. Useful for weighted estimation in <a href="#">Windham()</a> .

**Details**

$\beta = \beta_0$  is fixed and not estimated.  $b_L$  is fixed at zero. See (Section 6.2 and A.8 of Scealy and Wood 2023). The boundary weight function in the score matching discrepancy is the unthresholded product weight function

$$h(z)^2 = \min \left( \prod_{j=1}^p z_j^2, a_c^2 \right).$$

**Value**

A vector of estimates for  $A_L$  entries (diagonal and off diagonal).

**References**

Scealy JL, Wood ATA (2023). “Score matching for compositional distributions.” *Journal of the American Statistical Association*, **118**(543), 1811–1823. doi:10.1080/01621459.2021.2016422.

---

 ppi\_param\_tools

*PPI Parameter Tools*


---

**Description**

The default parameterisation of the PPI model is a symmetric covariance-like matrix  $A_L$ , a location-like vector  $b_L$  and a set of Dirichlet exponents  $\beta$ . For  $p$  components,  $A_L$  has  $p-1$  rows,  $b_L$  is a vector with  $p-1$  elements and  $\beta$  is a vector with  $p$  elements. For score matching estimation this form of the parameters must be converted into a single parameter vector using `ppi_paramvec()`. `ppi_paramvec()` also includes easy methods to set parameters to NA for estimation with `ppi()` (in `ppi()` the NA-valued elements are estimated and all other elements are fixed). The reverse of `ppi_paramvec()` is `ppi_parammats()`. An alternative parametrisation of the PPI model uses a single  $p$  by  $p$  matrix  $A^*$  instead of  $A_L$  and  $b_L$ , and for identifiability  $A^*$  is such that  $1^T A^* 1 = 0$  where  $1 = (1, 1, \dots, 1)$  and  $0 = (0, 0, \dots, 0)$  (Scealy and Wood 2023). Convert between parametrisations using `ppi_toAstar()` and `ppi_fromAstar()`.

**Usage**

```
ppi_paramvec(
  p = NULL,
  AL = NULL,
  bL = NULL,
  Astar = NULL,
  beta = NULL,
  betaL = NULL,
  betap = NULL
)

ppi_parammats(paramvec)

ppi_toAstar(AL, bL)

ppi_fromAstar(Astar)
```

**Arguments**

`p` The number of components. If NULL then `p` will be inferred from other inputs.

AL	Either NULL, a $p-1 \times p-1$ symmetric matrix, a number, or "diag". If NULL then all $A_L$ elements will be set to NA. If a single number, then $A_L$ will be fixed as a matrix of the given value. If "diag" then the non-diagonal elements of $A_L$ will be fixed to 0, and the diagonal will be NA.
bL	Either NULL, a number, or a vector of length $p-1$ . If NULL, then all elements of $b_L$ will be set to NA. If a single number, then $b_L$ will be fixed at the supplied value.
Astar	The $A^*$ matrix (a $p$ by $p$ symmetric matrix)
beta	Either NULL, a number, or a vector of length $p$ . If NULL then all elements of $\beta$ will be set to NA. If a single number then the $\beta$ elements will be fixed at the given number.
betaL	Either NULL, a number, or a vector of length $p-1$ . If NULL then the 1...(p-1)th $\beta$ elements will be set to NA. If a single number then the 1...(p-1)th $\beta$ elements will be fixed at the given number.
betap	Either NULL or a number. If NULL then the $p$ th element of $\beta$ will be set to NA, and <code>ppi()</code> will estimate it. If a number, then the $p$ th element of $\beta$ will be fixed at the given value.
paramvec	A PPI parameter vector, typically created by <code>ppi_paramvec()</code> or as an output of <code>ppi()</code> .

## Details

`ppi_paramvec()` returns a vector starting with the diagonal elements of  $A_L$ , then the off-diagonal elements extracted by `upper.tri()` (which extracts elements of  $A_L$  along each row, left to right, then top to bottom), then  $b_L$ , then  $\beta$ .

The Astar parametrisation rewrites the PPI density as proportional to

$$\exp(z^T A^* z) \prod_{i=1}^p z_i^{\beta_i},$$

where  $A^*$  (Astar) is a  $p$  by  $p$  matrix. Because  $z$  lies in the simplex (in particular  $\sum z_i = 1$ ), the density is the same regardless of the value of  $1^T A^* 1 = \text{sum}(A^*)$ , where  $1$  is the vector of ones. Thus  $A_L$  and  $b_L$  specify  $A^*$  up to an additive factor. In the conversion `ppi_toAstar()`,  $A^*$  is returned such that  $1^T A^* 1 = 0$ . NULL values or NA elements are not allowed for `ppi_toAstar()` and `ppi_fromAstar()`.

## Value

`ppi_paramvec()`: a vector of length  $p + (p-1)(2 + (p-1)/2)$ .

`ppi_parammats()`: A named list of  $A_L$ ,  $b_L$ , and  $\beta$ .

`ppi_toAstar()`: The matrix  $A^*$ .

`ppi_fromAstar()`: A list of the matrix  $A_L$ , the vector  $b_L$  and a discarded constant.



## PPI Model

The PPI model density is proportional to

$$\exp(z_L^T A_L z_L + b_L^T z_L) \prod_{i=1}^p z_i^{\beta_i},$$

where  $p$  is the dimension of a compositional measurement  $z$ , and  $z_L$  is  $z$  without the final ( $p$ th) component.  $A_L$  is a  $(p-1) \times (p-1)$  symmetric matrix that controls the covariance between components.  $b_L$  is a  $(p-1)$  vector that controls the location within the simplex. The  $i$ th component  $\beta_i$  of  $\beta$  controls the concentration of density when  $z_i$  is close to zero: when  $\beta_i \geq 0$  there is no concentration and  $\beta_i$  is hard to identify; when  $\beta_i < 0$  then the probability density of the PPI model increases unboundedly as  $z_i$  approaches zero, with the increasing occurring more rapidly and sharply the closer  $\beta_i$  is to  $-1$ .

## See Also

Other PPI model tools: [dppi\(\)](#), [ppi\(\)](#), [ppi\\_robust\(\)](#), [rppi\(\)](#)

## Examples

```
ppi_paramvec(AL = "diag", bL = 0, betap = -0.5, p = 3)
vec <- ppi_paramvec(AL = rsymmetricmatrix(2), beta = c(-0.8, -0.7, 0))
ppi_parammats(vec)
Astar <- rWishart(1, 6, diag(3))[, , 1]
ppi_fromAstar(Astar)
ppi_toAstar(ppi_fromAstar(Astar)$AL, ppi_fromAstar(Astar)$bL)
```

---

ppi\_robust

*Robustly Estimate Parameters of the PPI Distribution*

---

## Description

`ppi_robust()` uses [Windham\(\)](#) and [ppi\(\)](#) to estimate a PPI distribution robustly. There are many arguments to the [ppi\(\)](#) function and we highly recommend testing your arguments on [ppi\(\)](#) first before running `ppi_robust()`.

`ppi_robust_alrgengamma()` performs the Windham robustification algorithm exactly as described in Scaely et al. (2024) for score matching via log-ratio transform of the PPI model with  $b_L = 0$ . This function calls the more general [Windham\(\)](#) and [ppi\(\)](#).

## Usage

```
ppi_robust(Y, cW, ...)

ppi_robust_alrgengamma(
  Y,
  cW,
  ...,
  fpcontrol = list(Method = "Simple", ConvergenceMetricThreshold = 1e-10)
)
```

**Arguments**

Y	A matrix of measurements. Each row is a measurement, each component is a dimension of the measurement.
cW	A vector of robustness tuning constants. Easy to build using <code>ppi_cw()</code> and <code>ppi_cw_auto()</code> . See <code>Windham()</code> for more details on cW.
...	Passed to <code>Windham()</code> and on to <code>ppi()</code> .
fpcontrol	A named list of control arguments to pass to <code>FixedPoint::FixedPoint()</code> for the fixed point iteration.

**Details**

`ppi_robust_alrgengamma()`: must fit a PPI model via additive-log ratio transform of the simplex with  $b_L = 0$  fixed and the final element of  $\beta$  fixed. The default convergence metric and threshold are different to the default for `ppi_robust()` to match the implementation in (Scealy et al. 2024): convergence is measured by the change in the first element of  $\beta$ , and convergence is reached when the change is smaller than  $1E-6$ . Override this behaviour by specifying the elements `ConvergenceMetric` and `ConvergenceMetricThreshold` in a list passed as `fpcontrol`. `Windham()` is called with `alternative_populationinverse = TRUE`.

**Value**

A list:

- `est` The estimated parameters in vector form (`paramvec`) and as `AL`, `BL` and `beta`.
- `SE` "Not calculated." Returned for consistency with other estimators.
- `info` Information returned in the `optim` slot of `Windham()`. Includes the final weights in `finalweights`.

**References**

Scealy JL, Hingee KL, Kent JT, Wood ATA (2024). "Robust score matching for compositional data." *Statistics and Computing*, **34**, 93. doi:10.1007/s1122202410412w.

**See Also**

Other PPI model tools: `dppi()`, `ppi()`, `ppi_param_tools`, `rppi()`

Other Windham robustness functions: `Windham()`, `vMF_robust()`

**Examples**

```
model <- rppi_egmodel(100)
estsqrt <- ppi_robust(model$sample,
  cw = ppi_cw_auto(0.01, model$sample),
  trans = "sqrt", bdryw = "minsq", acut = 0.1)
model <- rppi_egmodel(100)
ppi_robust_alrgengamma(model$sample,
  cw = ppi_cw_auto(0.01, model$sample),
  paramvec = ppi_paramvec(betap = -0.5, p = ncol(model$sample)))
```

---

quadrattape\_parts     *Evaluate the Hessian and Gradient Offset of a Taped Quadratic Function*

---

### Description

When the score matching discrepancy function is quadratic then the gradient of the score matching discrepancy function can be written using the Hessian and an offset term. This can be useful for solving for the situation when the gradient is zero. The Hessian and offset term are computed using CppAD tapes. Taylor approximation can be used for locations at removed singularities (i.e. where intermediate values are unbounded). `quadrattape_parts()` will error if `testquadratic(tape)` returns FALSE.

### Usage

```
quadrattape_parts(tape, tmat, tcentres = NA * tmat, approxorder = 10)
```

### Arguments

tape	A tape of a quadratic function where the independent and dynamic parameters correspond to the $x$ and $t$ in the details section, respectively. For score matching tape should be a tape of the score matching discrepancy function $A(z) + B(z) + C(z)$ in <a href="#">scorematchingtheory</a> with $z$ the <i>dynamic parameters</i> and the model parameters the <i>independent variable</i> (which is the usual for the return of <code>buildsmdtape()</code> ).
tmat	A matrix of vectors corresponding to values of $t$ (see details). Each row corresponds to a vector. For score matching, these vectors are measurements.
tcentres	A matrix of Taylor approximation centres for rows of tmat that require approximation. NA for rows that do not require approximation.
approxorder	The order of the Taylor approximation to use.

### Details

A quadratic function can be written

$$f(x; t) = \frac{1}{2}x^T W(t)x + b(t)^T x + c,$$

where  $t$  is considered a vector that is constant with respect to the differentiation. The Hessian of the function is with respect to  $x$  is

$$Hf(x; t) = \frac{1}{2}(W(t) + W(t)^T).$$

The gradient of the function with respect to  $x$  can then be written

$$\Delta f(x; t) = Hf(x; t)x + b(t)^T x,$$

where the Hessian and offset  $b(t)$  depend only on  $t$ .

The functions here evaluate the Hessian and offset  $b(t)$  for many values of  $t$ . Tapes of the Hessian and gradient offset are created using `tapeHessian()` and `tapeGradOffset()` respectively. These tapes are then evaluated for every row of `tmat`. When the corresponding `tcentres` row is not NA, then approximate (but very accurate) results are calculated using Taylor approximation around the location given by the row of `tcentres`.

For score matching  $x$  is the set of model parameters and the vector  $t$  is a (multivariate) measurement.

### Value

A list of

- offset Array of offsets  $b(t)$ , each row corresponding to a row in `tmat`
- Hessian Array of vectorised  $Hf(x; t)$  (see `tapeHessian()`), each row corresponding to a row in `tmat`. For each row, obtain the Hessian in matrix format by using `matrix(ncol = length(tape$xtape))`.

### See Also

Other tape evaluators: `evaltape()`, `smvalues()`, `testquadratic()`

### Examples

```
u <- rep(1/3, 3)
smdtape <- buildsmdtape("sim", "sqrt", "sph", "ppi",
  ytape = u,
  usertheta = ppi_paramvec(p = 3),
  bdryw = "minsq", acut = 0.01,
  verbose = FALSE
)$smdtape
quadrattape_parts(smdtape,
  tmat = rbind(u, c(1/4, 1/4, 1/2)))
```

---

rppi

*Simulate from a PPI Model*

---

### Description

Given parameters of the PPI model, generates independent samples.

### Usage

```
rppi(n, ..., paramvec = NULL, maxden = 4, maxmemorysize = 1e+05)
rppi_egmodel(n, maxden = 4)
```

**Arguments**

n	Number of samples to generate
...	Arguments passed on to <code>ppi_paramvec</code>
AL	Either NULL, a p-1 x p-1 symmetric matrix, a number, or "diag". If NULL then all $A_L$ elements will be set to NA. If a single number, then $A_L$ will be fixed as a matrix of the given value. If "diag" then the non-diagonal elements of $A_L$ will be fixed to 0, and the diagonal will be NA.
bL	Either NULL, a number, or a vector of length p-1. If NULL, then all elements of $b_L$ will be set to NA. If a single number, then $b_L$ will be fixed at the supplied value.
beta	Either NULL, a number, or a vector of length p. If NULL then all elements of $\beta$ will be set to NA. If a single number then the $\beta$ elements will be fixed at the given number.
betaL	Either NULL, a number, or a vector of length p-1. If NULL then the 1...(p-1)th $\beta$ elements will be set to NA. If a single number then the 1...(p-1)th $\beta$ elements will be fixed at the given number.
betap	Either NULL or a number. If NULL then the pth element of $\beta$ will be set to NA, and <code>ppi()</code> will estimate it. If a number, then the pth element of $\beta$ will be fixed at the given value.
p	The number of components. If NULL then p will be inferred from other inputs.
Astar	The $A^*$ matrix (a p by p symmetric matrix)
paramvec	The PPI parameter vector, created easily using <code>ppi_paramvec()</code> and also returned by <code>ppi()</code> . Use paramvec instead of ...
maxden	This is the constant $\log(C)$ in (Appendix A.1.3 Scely and Wood 2023).
maxmemorysize	Advanced use. The maximum size, in bytes, for matrices containing simulated Dirichlet samples. The default of 1E5 corresponds to 100 mega bytes.

**Details**

We recommend running `rppi()` a number of times to ensure the choice of `maxden` is good. `rppi()` will error when `maxden` is too low.

The simulation uses a rejection-sampling algorithm with Dirichlet proposal (Appendix A.1.3 Scely and Wood 2023). Initially  $n$  Dirichlet proposals are generated. After rejection there are fewer samples remaining, say  $n^*$ . The ratio  $n^*/n$  is used to guess the number of new Dirichlet proposals to generate until  $n$  samples of the PPI model are reached.

Advanced use: The number of Dirichlet proposals created at a time is limited such that the matrices storing the Dirichlet proposals are always smaller than `maxmemorysize` bytes (give or take a few bytes for wrapping). Larger `maxmemorysize` leads to faster simulation so long as `maxmemorysize` bytes are reliably contiguously available in RAM.

**Value**

A matrix with  $n$  rows and  $p$  columns. Each row is an independent draw from the specified PPI distribution.

`rppi_egmodel` returns a list:

- sample A matrix of the simulated samples (n rows)
- p The number of components of the model
- theta The PPI parameter vector
- AL The  $A_L$  parameter matrix
- bL The  $b_L$  parameter vector
- beta The  $\beta$  parameter vector

### Functions

- `rppi_egmodel()`: Simulates the 3-component PPI model from (Section 2.3, Scaely and Wood 2023) and returns both simulations and model parameters.

### References

Scaely JL, Wood ATA (2023). “Score matching for compositional distributions.” *Journal of the American Statistical Association*, **118**(543), 1811–1823. doi:10.1080/01621459.2021.2016422.

### See Also

Other PPI model tools: `dppi()`, `pipi()`, `pipi_param_tools`, `pipi_robust()`

### Examples

```
beta0=c(-0.8, -0.8, -0.5)
AL = diag(nrow = 2)
bL = c(2, 3)
samp <- rppi(100,beta=beta0,AL=AL,bL=bL)
rppi_egmodel(1000)
```

---

rsymmetricmatrix

*Quickly Generate a Symmetric Matrix for Testing and Examples*

---

### Description

A simple function for generating a symmetric matrix for use in examples. The diagonal, and upper-triangular elements of the matrix are simulated independently from a uniform distribution. The lower-triangle of the output matrix is copied from the upper-triangle. These matrices **do not** represent the full range of possible symmetric matrices.

### Usage

```
rsymmetricmatrix(p, min = 0, max = 1)
```

### Arguments

p	The desired dimension of the matrix
min	The minimum of the uniform distribution.
max	The maximum of the uniform distribution

**Value**

A  $p \times p$  symmetric matrix.

**Examples**

```
rsymmetricmatrix(5)
```

---

scorematchingtheory    *Introduction to Score Matching*

---

**Description**

This package includes score matching estimators for particular distributions and a general capacity to implement additional score matching estimators. Score matching is a popular estimation technique when normalising constants for the proposed model are difficult to calculate or compute. Score matching was first developed by Hyvärinen (2005) and was further developed for subsets of Euclidean space (Hyvärinen 2007; Yu et al. 2019; Yu et al. 2020; Liu et al. 2019), Riemannian manifolds (Mardia et al. 2016; Mardia 2018), and Riemannian manifolds with boundary (Scealy and Wood 2023). In this help entry we briefly describe score matching estimation.

**Score Matching in General**

In the most general form (Riemannian manifolds with boundary) score matching minimises the weighted Hyvärinen divergence (Equation 7, Scealy and Wood 2023)

$$\phi(f, f_0) = \frac{1}{2} \int_M f_0(z) h(z)^2 \left\| P(z) \left( \nabla_z \log(f) - \nabla_z \log(f_0) \right) \right\|^2 dM(z),$$

where

- $M$  is the manifold, isometrically embedded in Euclidean space, and  $dM(z)$  is the unnormalised uniform measure on  $M$ .
- $P(z)$  is the matrix that projects points onto the tangent space of the manifold at  $z$ , which is closely related to the Riemannian metric of  $M$ .
- $f_0$  is the density of the data-generating process, defined with respect to  $dM(z)$ .
- $f$  is the density of a posited model, again defined with respect to  $dM(z)$ .
- $h(z)$  is a function, termed the *boundary weight function*, that is zero on the boundary of  $M$  and smooth (Section 3.2, Scealy and Wood 2023) or potentially piecewise smooth.
- $\nabla_z$  is the Euclidean gradient operator that differentiates with respect to  $z$ .
- $\|\cdot\|$  is the Euclidean norm.

Note that, because  $P(z)$  is the projection matrix,  $\left\| P(z) \left( \nabla_z \log(f) - \nabla_z \log(f_0) \right) \right\|^2$  is the natural inner product of the gradient of the log ratio of  $f$  and  $f_0$ .

When the density functions  $f$  and  $f_0$  are smooth and positive inside  $M$ , and the boundary weight function is smooth or of particular forms for specific manifolds (Section 3.2, Scealy and Wood

2023), then minimising the weighted Hyvärinen divergence  $\phi(f, f_0)$  is equivalent to minimising the score matching discrepancy (Theorem 1, Scealy and Wood 2023)

$$\psi(f, f_0) = \int f_0(z)(A(z) + B(z) + C(z))dM(z),$$

where

$$A(z) = \frac{1}{2}h(z)^2 (\nabla_z \log(f))^T P(z) (\nabla_z \log(f)),$$

$$B(z) = h(z)^2 \Delta_z \log(f),$$

$$C(z) = (\nabla_z h(z)^2)^T P(z) (\nabla_z \log(f)),$$

and  $\Delta$  is the Laplacian operator. We term

$$A(z) + B(z) + C(z)$$

the *score matching discrepancy function*.

We suspect that (Theorem 1, Scealy and Wood 2023) holds more generally for nearly all realistic continuous and piecewise-smooth boundary weight functions, although no proof exists to our knowledge.

When  $n$  independent observations from  $f_0$  are available, the integration in  $\psi(f, f_0)$  can be approximated by an average over the observations,

$$\psi(f, f_0) \approx \hat{\psi}(f, f_0) = \frac{1}{n} \sum_{i=1}^n A(z_i) + B(z_i) + C(z_i).$$

If we parameterise a family of models  $f_\theta$  according to a vector of parameters  $\theta$ , then the *score matching estimate* is the  $\theta$  that minimises  $\hat{\psi}(f_\theta, f_0)$ . In general, the score matching estimate must be found via numerical optimisation techniques, such as in the function `cppad_search()`. However, when the family of models is a canonical exponential family then often  $\hat{\psi}(f_\theta, f_0)$  and the score matching discrepancy function is a quadratic function of  $\theta$  (Mardia 2018) and the minimum has a closed-form solution found by `cppad_closed()`.

Note that when  $M$  has a few or more dimensions, the calculations of  $A(z)$ ,  $B(z)$  and  $C(z)$  can become cumbersome. This package uses CppAD to automatically compute  $A(z)$ ,  $B(z)$  and  $C(z)$ , and the quadratic simplification if it exists.

## Transformations

Hyvärinen divergence  $\phi(f, f_0)$  is sensitive to transformations of the measure  $dM(z)$ , including transforming the manifold. That is, transforming the manifold  $M$  changes the divergence between distributions and changes the minimum of  $\hat{\psi}(f_\theta, f_0)$ . The transformation changes measure  $dM(z)$ , the divergence and the estimator but does *not* transform the data.

For example, many different transformations of the simplex (i.e. compositional data) are possible (Appendix A.3, Scealy et al. 2024). Hyvärinen divergences that use the sphere, obtained from the simplex by a square root, have different behaviour to Hyvärinen divergence using Euclidean space obtained from the simplex using logarithms (Scealy et al. 2024). The estimator for the latter does not apply logarithms to the observations, in fact the estimator involves only polynomials of the observed compositions (Scealy et al. 2024).



The variety of estimator behaviour available through different transformations was a major motivator for this package as each transformation has different  $A(z)$ ,  $B(z)$  and  $C(z)$ , and without automatic differentiation, implementation of the score matching estimator in each case would require a huge programming effort.

## References

- Hyvärinen A (2005). “Estimation of Non-Normalized Statistical Models by Score Matching.” *Journal of Machine Learning Research*, **6**(24), 695–709. <https://jmlr.org/papers/v6/hyvarinen05a.html>.
- Hyvärinen A (2007). “Some extensions of score matching.” *Computational Statistics & Data Analysis*, **51**(5), 2499–2512. doi:10.1016/j.csda.2006.09.003.
- Liu S, Kanamori T, Williams DJ (2019). “Estimating Density Models with Truncation Boundaries using Score Matching.” doi:10.48550/arXiv.1910.03834.
- Mardia K (2018). “A New Estimation Methodology for Standard Directional Distributions.” In *2018 21st International Conference on Information Fusion (FUSION)*, 724–729. doi:10.23919/ICIF.2018.8455640.
- Mardia KV, Kent JT, Laha AK (2016). “Score matching estimators for directional distributions.” doi:10.48550/arXiv.1604.08470.
- Scealy JL, Hingee KL, Kent JT, Wood ATA (2024). “Robust score matching for compositional data.” *Statistics and Computing*, **34**, 93. doi:10.1007/s1122202410412w.
- Scealy JL, Wood ATA (2023). “Score matching for compositional distributions.” *Journal of the American Statistical Association*, **118**(543), 1811–1823. doi:10.1080/01621459.2021.2016422.
- Yu S, Drton M, Shojaie A (2019). “Generalized Score Matching for Non-Negative Data.” *Journal of Machine Learning Research*, **20**(76), 1–70. <https://jmlr.org/papers/v20/18-278.html>.
- Yu S, Drton M, Shojaie A (2020). “Generalized Score Matching for General Domains.” doi:10.48550/arXiv.2009.11428.

---

smvalues

*Compute Score Matching Discrepancy Value, Gradient, and Hessian*

---

## Description

Computes a range of relevant information for investigating score matching estimators.

## Usage

```
smvalues(smdtape, xmat, pmat, xcentres = NA * xmat, approxorder = 10)
```

```
smvalues_wsum(
  tape,
  xmat,
  pmat,
  w = NULL,
  xcentres = NA * xmat,
  approxorder = 10
)
```

### Arguments

smdtape	A taped score matching discrepancy. Most easily created by <a href="#">buildsmdtape()</a> .
xmat	A matrix of (multivariate) independent variables where each represents a single independent variable vector. Or a single independent variable vector that is used for all rows of pmat.
pmat	A matrix of dynamic parameters where each row specifies a new set of values for the dynamic parameters of tape. Or a single vector of dynamic parameters to use for all rows of xmat.
xcentres	A matrix of approximation for Taylor approximation centres for xmat. Use values of NA for rows that do not require Taylor approximation.
approxorder	Order of Taylor approximation
tape	An <a href="#">ADFun</a> object (i.e. a tape of a function).
w	Weights to apply to each row of xmat for computing the weighted sum. If NULL then each row is given a weight of 1.

### Details

Computes the score matching discrepancy function from [scorematchingtheory](#) or weighted sum of the score matching discrepancy function. The gradient and Hessian are returned as arrays of row-vectors with each row corresponding to a row in xmat and pmat. Convert a Hessian row-vector to a matrix using `matrix(ncol = length(smdtape$tape))`.

### Value

A list of

- obj the score matching discrepancy values
- grad the gradient of the score matching discrepancy
- hess the Hessian of the score matching discrepancy

### See Also

Other tape evaluators: [evaltape\(\)](#), [quadratictape\\_parts\(\)](#), [testquadratic\(\)](#)

**Examples**

```

m <- rppi_egmodel(100)
smdtape <- buildsmdtape("sim", "sqrt", "sph", "ppi",
  ytape = rep(1/m$p, m$p),
  usertheta = ppi_paramvec(beta = m$beta),
  bdryw = "minsq", acut = 0.01)$smdtape
smvalues(smdtape, xmat = m$sample, pmat = m$theta[1:5])
smvalues_wsum(smdtape, m$sample, m$theta[1:5])$grad/nrow(m$sample)

```

---

testquadratic	<i>Test Whether a CppAD Tape is a Quadratic Function</i>
---------------	--

---

**Description**

Uses the **CppAD parameter property** and derivatives (via `tapeJacobian()`) to test whether the tape is quadratic.

**Usage**

```
testquadratic(tape, xmat = NULL, dynparammat = NULL, verbose = FALSE)
```

**Arguments**

tape	An ADFun object.
xmat	If non-NULL and dynparammat non-NULL then the third-order derivatives at independent variable values of the rows of xmat and dynamic parameters from the rows of dynparammat are tested.
dynparammat	If non-NULL and xmat non-NULL then the third-order derivatives at independent variable values of the rows of xmat and dynamic parameters from the rows of dynparammat are tested.
verbose	If TRUE information about the failed tests is printed.

**Details**

Uses the xtape and dyntape values stored in tape to create new tapes. A tape of the Hessian is obtained by applying `tapeJacobian()` twice, and then uses a **CppAD property** to test whether the Hessian is constant. A function of quadratic form should have constant Hessian.

If xmat and dynparammat are non-NULL then `testquadratic()` also checks the Jacobian of the Hessian at xmat and dynparammat values. For quadratic form functions the Jacobian of the Hessian should be zero.

**Value**

TRUE or FALSE

**See Also**

Other tape evaluators: [evaltape\(\)](#), [quadrattape\\_parts\(\)](#), [smvalues\(\)](#)

**Examples**

```
tapes <- buildsmdtape(
  "sim", "sqrt", "sph",
  ll = "ppi",
  ytape = c(0.2, 0.3, 0.5),
  usertheta = ppi_paramvec(p = 3),
  bdryw = "minsq",
  acut = 0.1,
  verbose = FALSE)

testquadratic(tapes$smdtape)
```

vMF

*Score Matching Estimator for the von-Mises Fisher Distribution***Description**

In general the normalising constant in von Mises Fisher distributions is hard to compute, so Mardia et al. (2016) suggested a hybrid method that uses maximum likelihood to estimate the mean direction and score matching for the concentration. We can also estimate all parameters using score matching (`smfull` method), although this estimator is likely to be less efficient than the hybrid estimator. On the circle the hybrid estimators were often nearly as efficient as maximum likelihood estimators (Mardia et al. 2016). For maximum likelihood estimators of the von Mises Fisher distribution, which all use approximations of the normalising constant, consider `movMF::movMF()`.

**Usage**

```
vMF(Y, paramvec = NULL, method = "Mardia", w = rep(1, nrow(Y)))
```

**Arguments**

<code>Y</code>	A matrix of multivariate observations in Cartesian coordinates. Each row is a multivariate measurement (i.e. each row corresponds to an individual).
<code>paramvec</code>	<code>smfull</code> method only: Optional. A vector of same length as the dimension, representing the elements of the $\kappa\mu$ vector.
<code>method</code>	Either "Mardia" or "hybrid" for the hybrid score matching estimator from Mardia et al. (2016) or "smfull" for the full score matching estimator.
<code>w</code>	An optional vector of weights for each measurement in <code>Y</code>

**Details**

The full score matching estimator (`method = "smfull"`) estimates  $\kappa\mu$ . The hybrid estimator (`method = "Mardia"`) estimates  $\kappa$  and  $\mu$  separately. Both use [cppad\\_closed\(\)](#) for score matching estimation.

**Value**

A list of est, SE and info.

- est contains the estimates in vector form, paramvec, and with user friendly names k and m.
- SE contains estimates of the standard errors if computed. See `cppad_closed()`.
- info contains a variety of information about the model fitting procedure and results.

**von Mises Fisher Model**

The von Mises Fisher density is proportional to

$$\exp(\kappa \mu^T z),$$

where  $z$  is on a unit sphere,  $\kappa$  is termed the *concentration*, and  $\mu$  is the *mean direction unit vector*. The effect of the  $\mu$  and  $\kappa$  can be decoupled in a sense (p169, Mardia and Jupp 2000), allowing for estimating  $\mu$  and  $\kappa$  separately.

**References**

Mardia KV, Jupp PE (2000). *Directional Statistics*, Probability and Statistics. Wiley, Great Britain. ISBN 0-471-95333-4.

Mardia KV, Kent JT, Laha AK (2016). "Score matching estimators for directional distributions." [doi:10.48550/arXiv.1604.08470](https://doi.org/10.48550/arXiv.1604.08470).

**See Also**

Other directional model estimators: `Bingham()`, `FB()`, `vMF_robust()`

**Examples**

```
if (requireNamespace("movMF")){
  Y <- movMF::rmovMF(1000, 100 * c(1, 1) / sqrt(2))
  movMF::movMF(Y, 1) #maximum likelihood estimate
} else {
  Y <- matrix(rnorm(1000 * 2, sd = 0.01), ncol = 2)
  Y <- Y / sqrt(rowSums(Y^2))
}
vMF(Y, method = "smfull")
vMF(Y, method = "Mardia")
vMF(Y, method = "hybrid")
```

---

vMF_robust	<i>Robust Fitting of von Mises Fisher</i>
------------	---

---

**Description**

Robust estimation for von Mises Fisher distribution using [Windham\(\)](#).

**Usage**

```
vMF_robust(Y, cW, ...)
```

**Arguments**

Y	A matrix of observations in Cartesian coordinates.
cW	Tuning constants for each parameter in the vMF parameter vector. If a single number then the constant is the same for each element of the parameter vector.
...	Passed to <a href="#">Windham()</a> and then passed onto <a href="#">vMF()</a> .

**See Also**

Other directional model estimators: [Bingham\(\)](#), [FB\(\)](#), [vMF\(\)](#)  
 Other Windham robustness functions: [Windham\(\)](#), [ppi\\_robust\(\)](#)

**Examples**

```
if (requireNamespace("movMF")){
  Y <- movMF::rmovMF(1000, 100 * c(1, 1) / sqrt(2))
} else {
  Y <- matrix(rnorm(1000 * 2, sd = 0.01), ncol = 2)
  Y <- Y / sqrt(rowSums(Y^2))
}
vMF_robust(Y, cW = c(0.01, 0.01), method = "smfull")
vMF_robust(Y, cW = c(0.01, 0.01), method = "Mardia")
```

---

Windham	<i>Windham Robustification of Point Estimators for Exponential Family Distributions</i>
---------	---

---

**Description**

Performs a generalisation of Windham's robustifying method (Windham 1995) for exponential models with natural parameters that are a linear function of the parameters for estimation. Estimators must solve estimating equations of the form

$$\sum_{i=1}^n U(z_i; \theta) = 0.$$

The estimate is found iteratively through a fixed point method as suggested by Windham (1995).

**Usage**

```
Windham(
  Y,
  estimator,
  ldenfun,
  cW,
  ...,
  fpcontrol = list(Method = "Simple", ConvergenceMetricThreshold = 1e-10),
  paramvec_start = NULL,
  alternative_populationinverse = FALSE
)
```

**Arguments**

Y	A matrix of measurements. Each row is a measurement, each component is a dimension of the measurement.
estimator	A function that estimates parameters from weighted observations. It must have arguments Y that is a matrix of measurements and w that are weights associated with each row of Y. If it accepts arguments paramvec or paramvec_start then these will be used to specify fixed elements of the parameter vector and the starting guess of the parameter vector, respectively. The estimated parameter vector, including any fixed elements, must be the returned object, or the first element of a returned list, or as the paramvec slot within the est slot of the returned object.
ldenfun	A function that returns a vector of values proportional to the log-density for a matrix of observations Y and parameter vector theta.
cW	A vector of robustness tuning constants. When computing the weight for an observation the parameter vector is multiplied element-wise with cW. For the PPI model, generate cW easily using <code>ppi_cw()</code> and <code>ppi_cw_auto()</code> .
...	Arguments passed to estimator.
fpcontrol	A named list of control arguments to pass to <code>FixedPoint::FixedPoint()</code> for the fixed point iteration.
paramvec_start	Initially used to check the function estimator. If estimator accepts a paramvec_start, then the current estimate of the parameter vector is passed as paramvec_start to estimator in each iteration.
alternative_populationinverse	The default is to use <code>Windham_populationinverse()</code> . If TRUE an alternative implementation in <code>Windham_populationinverse_alternative()</code> is used. So far we have not seen any difference between the results.

**Details**

For any family of models with density  $f(z; \theta)$ , Windham's method finds the parameter set  $\hat{\theta}$  such that the estimator applied to observations weighted by  $f(z; \hat{\theta})^c$  returns an estimate that matches the theoretical effect of weighting the full population of the model. When  $f$  is proportional to  $\exp(\eta(\theta) \cdot T(z))$  and  $\eta(\theta)$  is linear, these weights are equivalent to  $f(z; c\hat{\theta})$  and the theoretical effect of the weighting on the full population is to scale the parameter vector  $\theta$  by  $1 + c$ .

The function `Windham()` assumes that  $f$  is proportional to  $\exp(\eta(\theta) \cdot T(z))$  and  $\eta(\theta)$  is linear. It allows a generalisation where  $c$  is a vector so the weight for an observation  $z$  is

$$f(z; c \circ \theta),$$

where  $\theta$  is the parameter vector,  $c$  is a vector of tuning constants, and  $\circ$  is the element-wise product (Hadamard product).

The solution is found iteratively (Windham 1995). Given a parameter set  $\theta_n$ , `Windham()` first computes weights  $f(z; c \circ \theta_n)$  for each observation  $z$ . Then, a new parameter set  $\hat{\theta}_{n+1}$  is estimated by estimator with the computed weights. This new parameter set is element-wise-multiplied by the (element-wise) reciprocal of  $1 + c$  to obtain an adjusted parameter set  $\theta_{n+1}$ . The estimate returned by `Windham()` is the parameter set  $\hat{\theta}$  such that  $\theta_n \approx \theta_{n+1}$ .

### Value

A list:

- `paramvec` the estimated parameter vector
- `optim` information about the fixed point iterations and optimisation process. Including a slot `finalweights` for the weights in the final iteration.

### See Also

Other generic score matching tools: [cppad\\_closed\(\)](#), [cppad\\_search\(\)](#)

Other Windham robustness functions: [ppi\\_robust\(\)](#), [vmf\\_robust\(\)](#)

### Examples

```
if (requireNamespace("movMF")){
  Y <- movMF::rmovMF(1000, 100 * c(1, 1) / sqrt(2))
} else {
  Y <- matrix(rnorm(1000 * 2, sd = 0.01), ncol = 2)
  Y <- Y / sqrt(rowSums(Y^2))
}
Windham(Y = Y,
  estimator = vmf,
  ldenfun = function(Y, theta){ #here theta is km
    return(drop(Y %*% theta))
  },
  cW = c(0.01, 0.01),
  method = "Mardia")
```

---

Windham\_populationinverse

*Inverse Transform for the Population Parameters Under Windham Weights*

---



**Description**

Returns the matrix which reverses the effect of weights on a population for certain models.

**Usage**

```
Windham_populationinverse(cW)
```

```
Windham_populationinverse_alternative(newtheta, previoustheta, cW, cWav)
```

**Arguments**

cW	A vector of tuning constants for the Windham robustification method performed by <code>Windham()</code> .
newtheta	The parameter vector most recently estimated
previoustheta	The parameter vector estimated in the previous step
cWav	The value of the non-zero elements of cW. That is cW have elements that are zero or equal to cWav.

**Details**

In the Windham robustification method (`Windham()`) the effect of weighting a population plays a central role. When the the model density is proportional to  $\exp(\eta(\theta) \cdot T(u))$ , where  $T(u)$  is a vector of sufficient statistics for a measurement  $u$ , and  $\eta$  is a *linear* function, Then weights proportional to  $\exp(\eta(c \circ \theta) \cdot t(u))$ , where  $c$  is a vector of tuning constants and  $\circ$  is the Hadamard (element-wise) product, have a very simple effect on the population parameter vector  $\theta$ : the weighted population follows a density of the same form, but with a parameter vector of  $(1 + c) \circ \theta$ . The inverse of this change to the parameter vector is then a matrix multiplication by a diagonal matrix with elements  $1/(1 + c_i)$ , with  $c_i$  denoting the elements of  $c$ .

**Value**

A diagonal matrix with the same number of columns as cW.

**Functions**

- `Windham_populationinverse()`: The matrix with diagonal elements  $1/(1 + c_i)$
- `Windham_populationinverse_alternative()`: The transform implemented as described by Scaely et al. (2024). It is mathematically equivalent to multiplication by the result of `Windham_populationinverse()` in the situation in Scaely et al. (2024).

# Index

- \* **PPI model tools**
    - dppi, 17
    - ppi, 25
    - ppi\_param\_tools, 31
    - ppi\_robust, 33
    - rpqi, 36
  - \* **Windham robustness functions**
    - ppi\_robust, 33
    - vmf\_robust, 46
    - Windham, 46
  - \* **datasets**
    - microbiome, 21
  - \* **directional model estimators**
    - Bingham, 7
    - FB, 20
    - vmf, 44
    - vmf\_robust, 46
  - \* **generic score matching tools**
    - cppad\_closed, 12
    - cppad\_search, 14
    - Windham, 46
  - \* **tape builders**
    - buildsmdtape, 8
    - moretapebuilders, 23
  - \* **tape evaluators**
    - evaltape, 19
    - quadratictape\_parts, 35
    - smvalues, 41
    - testquadratic, 43
- ADFun, 5, 11, 19, 23–25, 42
- Bingham, 7, 21, 45, 46
- Bingham(), 3
- buildsmdtape, 8, 25
- buildsmdtape(), 5, 18, 35, 42
- cppad\_closed, 12, 15, 48
- cppad\_closed(), 8, 25, 26, 28, 44, 45
- cppad\_search, 13, 14, 48
- cppad\_search(), 26
- customll, 15
- customll(), 3, 9, 18
- customll\_test(customll), 15
- dppi, 17, 29, 33, 34, 38
- evalll, 18
- evalll(), 16
- evaltape, 19, 36, 42, 44
- evaltape(), 18
- evaltape\_wsum(evaltape), 19
- FB, 8, 20, 45, 46
- FB(), 3
- FixedPoint::FixedPoint(), 34, 47
- matrix(), 24
- microbiome, 21
- moretapebuilders, 11, 23
- movMF::movMF(), 44
- optimx::Rcgmin(), 3, 14, 26, 27
- ppi, 18, 25, 33, 34, 38
- ppi(), 3, 9, 18, 31–34, 37
- ppi\_cw, 29
- ppi\_cw(), 34, 47
- ppi\_cw\_auto(ppi\_cw), 29
- ppi\_cw\_auto(), 34, 47
- ppi\_fromAstar(ppi\_param\_tools), 31
- ppi\_mmmm, 30
- ppi\_param\_tools, 18, 29, 31, 34, 38
- ppi\_parammats(ppi\_param\_tools), 31
- ppi\_paramvec, 17, 37
- ppi\_paramvec(ppi\_param\_tools), 31
- ppi\_paramvec(), 18, 26, 27, 32, 37
- ppi\_robust, 18, 29, 33, 33, 38, 46, 48
- ppi\_robust(), 26, 29, 34
- ppi\_robust\_alrgengamma(ppi\_robust), 33
- ppi\_smvalues(ppi), 25

ppi\_toAstar (ppi\_param\_tools), 31

quadratictape\_parts, 20, 35, 42, 44  
quadratictape\_parts(), 13, 25, 28

Rcpp::cppFunction(), 16  
RcppXPtrUtils::cppXPtr(), 16  
rppi, 18, 29, 33, 34, 36  
rppi\_egmodel (rppi), 36  
rsymmetricmatrix, 38

scorematchingad  
    (scorematchingad-package), 2  
scorematchingad-package, 2  
scorematchingtheory, 3, 8, 12, 26, 27, 35,  
    39, 42  
smvalues, 20, 36, 41, 44  
smvalues(), 25  
smvalues\_wsum (smvalues), 41

tapeGradOffset (moretapebuilders), 23  
tapeGradOffset(), 25, 36  
tapeHessian (moretapebuilders), 23  
tapeHessian(), 36  
tapeJacobian (moretapebuilders), 23  
tapeJacobian(), 43  
tapeLogJacDet (moretapebuilders), 23  
tapeSwap (moretapebuilders), 23  
tapeSwap(), 5, 10, 11  
testquadratic, 20, 36, 42, 43  
testquadratic(), 12, 14

upper.tri(), 32

vMF, 8, 21, 44, 46  
vMF(), 3, 20, 46  
vMF\_robust, 8, 21, 34, 45, 46, 48

Windham, 13, 15, 34, 46, 46  
Windham(), 3, 26, 29, 30, 33, 34, 46, 49  
Windham\_populationinverse, 48  
Windham\_populationinverse(), 47  
Windham\_populationinverse\_alternative  
    (Windham\_populationinverse), 48  
Windham\_populationinverse\_alternative(),  
    47