

# Package: idopNetwork (via r-universe)

October 29, 2024

**Type** Package

**Title** A Network Tool to Dissect Spatial Community Ecology

**Version** 0.1.2

**Author** Ang Dong

**Maintainer** Ang Dong <fantasys05227@gmail.com>

**Description** Most existing approaches for network reconstruction can only infer an overall network and, also, fail to capture a complete set of network properties. To address these issues, a new model has been developed, which converts static data into their 'dynamic' form. 'idopNetwork' is an 'R' interface to this model, it can inferring informative, dynamic, omnidirectional and personalized networks. For more information on functional clustering part, see Kim et al. (2008) <doi:10.1534/genetics.108.093690>, Wang et al. (2011) <doi:10.1093/bib/bbr032>. For more information on our model, see Chen et al. (2019) <doi:10.1038/s41540-019-0116-1>, and Cao et al. (2022) <doi:10.1080/19490976.2022.2106103>.

**License** GPL (>= 3)

**Imports** grDevices, stats, mvtnorm, orthopolynom, parallel, deSolve, ggplot2, reshape2, glmnet, igraph, scales, patchwork

**Encoding** UTF-8

**LazyData** true

**Depends** R (>= 3.50)

**RoxygenNote** 7.2.1

**Suggests** covr, knitr, rmarkdown

**VignetteBuilder** knitr

**URL** <https://github.com/cxzdsa2332/idopNetwork>

**BugReports** <https://github.com/cxzdsa2332/idopNetwork/issues>

**Repository** <https://cxzdsa2332.r-universe.dev>

**RemoteUrl** <https://github.com/cxzdsa2332/idopnetwork>

**RemoteRef** HEAD

**RemoteSha** a1a00a27890b5c9d09e99140c9284d37c11e2f2f

## Contents

bifun_clu . . . . .	3
bifun_clu_convert . . . . .	4
bifun_clu_parallel . . . . .	4
bifun_clu_plot . . . . .	5
biget_par_int . . . . .	6
bipower_equation_plot . . . . .	6
biqODE_plot_all . . . . .	7
biqODE_plot_base . . . . .	8
biQ_function . . . . .	8
darken . . . . .	9
data_cleaning . . . . .	10
data_match . . . . .	10
fun_clu . . . . .	11
fun_clu_BIC . . . . .	12
fun_clu_convert . . . . .	12
fun_clu_parallel . . . . .	13
fun_clu_plot . . . . .	13
fun_clu_select . . . . .	14
get_biSAD1 . . . . .	14
get_interaction . . . . .	15
get_legendre_matrix . . . . .	16
get_legendre_par . . . . .	16
get_mu . . . . .	17
get_mu2 . . . . .	17
get_par_int . . . . .	18
get_SAD1_covmatrix . . . . .	18
gut_microbe . . . . .	19
legendre_fit . . . . .	19
logsumexp . . . . .	20
mustard_microbe . . . . .	20
network_conversion . . . . .	21
network_maxeffect . . . . .	21
network_plot . . . . .	22
normalization . . . . .	22
power_equation . . . . .	23
power_equation_all . . . . .	23
power_equation_base . . . . .	24
power_equation_fit . . . . .	24
power_equation_plot . . . . .	25
qdODEmod . . . . .	25
qdODEplot_convert . . . . .	26
qdODE_all . . . . .	26

qdODE_fit . . . . .	27
qdODE_ls . . . . .	28
qdODE_parallel . . . . .	28
qdODE_plot_all . . . . .	29
qdODE_plot_base . . . . .	29
Q_function . . . . .	30

## Index 31

bifun\_clu *main function for bifunctional clustering*

### Description

main function for bifunctional clustering

### Usage

```
bifun_clu(
  data1,
  data2,
  k,
  Time1 = NULL,
  Time2 = NULL,
  trans = log10,
  inv.cov = NULL,
  initial.pars = NULL,
  iter.max = 100,
  parscale = 0.001
)
```

### Arguments

data1	matrix or data for cluster
data2	matrix or data for cluster
k	vector for the cluster number
Time1	vector for the time point
Time2	vector for the time point
trans	indicate log/log2/log10 transform dataset
inv.cov	matrix for directly solve cov matrix, default not given(currently not available)
initial.pars	vector for manual give initial parameters, default not given
iter.max	scales control iteration for EM algorithm
parscale	scales control parameters scales for cov pars

### Value

the initial parameters for functional clustering

bifun\_clu\_convert      *convert result of bifunctional clustering result*

---

**Description**

convert result of bifunctional clustering result

**Usage**

```
bifun_clu_convert(result, best.k)
```

**Arguments**

result	list directly from bifun_clu_parallel function
best.k	scale of BIC-determined cluster number

**Value**

list contain module data and fitted data

---

bifun\_clu\_parallel      *parallel version for functional clustering*

---

**Description**

parallel version for functional clustering

**Usage**

```
bifun_clu_parallel(  
  data1,  
  data2,  
  Time1 = NULL,  
  Time2 = NULL,  
  trans = log10,  
  start,  
  end,  
  iter.max = 100,  
  thread = 2  
)
```

**Arguments**

data1	data for cluster
data2	data for cluster
Time1	vector for the time point
Time2	vector for the time point
trans	indicate log/log2/log10 transform dataset
start	vector for the minimum cluster number
end	vector for the maximum cluster number
iter.max	scales control iteration for EM algorithm
thread	scales for how many thread used

**Value**

the initial parameters for functional clustering

---

bifun_clu_plot	<i>bifunctional clustering plot</i>
----------------	-------------------------------------

---

**Description**

bifunctional clustering plot

**Usage**

```
bifun_clu_plot(
  result,
  best.k,
  label = 10,
  degree = 1/4,
  show.legend = FALSE,
  color1 = "#38E54D",
  color2 = "#FF8787"
)
```

**Arguments**

result	list directly from bifun_clu_parallel function
best.k	scale of BIC-determined cluster number
label	relabel x and y label due to log-transform, set 10 as default
degree	scalar control transparency degree
show.legend	show legend or not
color1	Hex Color Codes for first data
color2	Hex Color Codes for second data

**Value**

functional clustering plot

---

biget\_par\_int                    *acquire initial parameters for functional clustering*

---

**Description**

acquire initial parameters for functional clustering

**Usage**

```
biget_par_int(X, k, times1, times2, n1, n2)
```

**Arguments**

X	matrix for cluster
k	vector for the cluster number
times1	vector for the x values or time points
times2	vector for the x values or time points
n1	scalar for number of column contain first trait/location etc
n2	scalar for number of column contain second trait/location etc

**Value**

the initial parameters for functional clustering

---

bipower\_equation\_plot   *plot power equation fitting results for bi-variate model*

---

**Description**

plot power equation fitting results for bi-variate model

**Usage**

```
bipower_equation_plot(
  result,
  label = 10,
  n = 9,
  show.legend = FALSE,
  color1 = "#38E54D",
  color2 = "#FF8787"
)
```

**Arguments**

result	list object returned from data_match
label	relabel x and y label due to log-transform, set 10 as default
n	scales for how many subplots needed
show.legend	show legend or not
color1	Hex Color Codes for first data
color2	Hex Color Codes for second data

**Value**

plot show power curve fitting result

---

biqdODE\_plot\_all      *plot all decompose plot for two data*

---

**Description**

plot all decompose plot for two data

**Usage**

```
biqdODE_plot_all(
  result1,
  result2,
  label = 10,
  show.legend = FALSE,
  remove.label = TRUE,
  nrow = NULL,
  ncol = NULL
)
```

**Arguments**

result1	list of qdODE all for first data
result2	list of qdODE all for second data
label	relabel x and y label due to log-transform, set 10 as default
show.legend	to show legend
remove.label	to remove x and y label
nrow	scalar for subplot row number
ncol	scalar for subplot column number

---

biqdODE\_plot\_base      *plot single decompose plot for two data*

---

### Description

plot single decompose plot for two data

### Usage

```
biqdODE_plot_base(
  result1,
  result2,
  label = 10,
  show.legend = FALSE,
  remove.label = FALSE
)
```

### Arguments

result1	list of qdODE all for first data
result2	list of qdODE all for second data
label	relabel x and y label due to log-transform, set 10 as default
show.legend	to show legend
remove.label	to remove x and y label

---

biQ\_function      *Q-function to replace log-likelihood function*

---

### Description

Q-function to replace log-likelihood function

### Usage

```
biQ_function(par, prob_log, omega_log, X, k, n1, n2, times1, times2)
```

### Arguments

par	numeric vector for parameters need to be estimated
prob_log	mixture component weights(log)
omega_log	latent variables(log)
X	matrix for cluster
k	vector for the cluster number



n1                scalar for number of column contain first trait/location etc  
n2                scalar for number of column contain second trait/location etc  
times1           vector for the x values or time points  
times2           vector for the x values or time points

**Value**

the Loglikelihood value

---

darken	<i>make color more dark</i>
--------	-----------------------------

---

**Description**

make color more dark

**Usage**

```
darken(color, factor = 1.2)
```

**Arguments**

color            hex color code  
factor           scalar for darken level

**Value**

darkened hex color code

**Examples**

```
darken("#FF0000")
```

---

data_cleaning	<i>remove observation with too many 0 values</i>
---------------	--

---

**Description**

remove observation with too many 0 values

**Usage**

```
data_cleaning(data, x = round(ncol(data) * 0.3))
```

**Arguments**

data	dataframe of imported dataset, must have first column as ID
x	scales indicate how many 0 to remove

**Value**

a dataframe without too many 0 observations

**Examples**

```
data_cleaning(matrix(c(c(0,1,1,0,0,1,1), c(2,1,0,3,5,2,2), c(1,1,3,2,4,5,1)), 3, 7), 2)
```

---

data_match	<i>match power_equation fit result for bi-variate model</i>
------------	---

---

**Description**

match power\_equation fit result for bi-variate model

**Usage**

```
data_match(result1, result2)
```

**Arguments**

result1	list object from power_equation fit
result2	list object from power_equation fit

**Value**

a id match list for input dataset

---

fun_clu	<i>main function for functional clustering</i>
---------	--

---

### Description

main function for functional clustering

### Usage

```
fun_clu(  
  data,  
  k,  
  Time = NULL,  
  trans = log10,  
  inv.cov = NULL,  
  initial.pars = NULL,  
  iter.max = 100,  
  parscale = 0.1  
)
```

### Arguments

data	matrix or data for cluster
k	vector for the cluster number
Time	vector for the time point
trans	indicate log/log2/log10 transform dataset
inv.cov	matrix for directly solve cov matrix, default not given(currently not available)
initial.pars	vector for manual give initial parameters, default not given
iter.max	scales control iteration for EM algorithm
parscale	scales control parameters scales for cov pars

### Value

the initial parameters for functional clustering

---

fun_clu_BIC	<i>plot BIC results for functional clustering</i>
-------------	---

---

**Description**

plot BIC results for functional clustering

**Usage**

```
fun_clu_BIC(result, crit = "BIC", title = NULL)
```

**Arguments**

result	list directly from fun_clu_parallel function
crit	either BIC or AIC for module selection
title	title for the plot

**Value**

the BIC plot

---

fun_clu_convert	<i>convert result of functional clustering result</i>
-----------------	---

---

**Description**

convert result of functional clustering result

**Usage**

```
fun_clu_convert(result, best.k)
```

**Arguments**

result	list directly from fun_clu_parallel function
best.k	scale of BIC-determined cluster number

**Value**

list contain module data and fitted data

---

fun\_clu\_parallel      *parallel version for functional clustering*

---

**Description**

parallel version for functional clustering

**Usage**

```
fun_clu_parallel(  
  data,  
  Time = NULL,  
  trans = log10,  
  start,  
  end,  
  iter.max = 100,  
  thread = 2  
)
```

**Arguments**

data	data for cluster
Time	vector for the time point
trans	indicate log/log2/log10 transform dataset
start	vector for the minimum cluster number
end	vector for the maximum cluster number
iter.max	scales control iteration for EM algorithm
thread	scales for how many threads used

**Value**

the initial parameters for functional clustering

---

fun\_clu\_plot      *functional clustering plot*

---

**Description**

functional clustering plot

**Usage**

```
fun_clu_plot(result, best.k, label = 10, degree = 1)
```

**Arguments**

result	list directly from fun_clu_parallel function
best.k	scalar of BIC-determined cluster number
label	relabel x and y label due to log-transform, set 10 as default
degree	scalar control transparency degree

**Value**

functional clustering plot

---

fun_clu_select	<i>select result of functional clustering result</i>
----------------	--

---

**Description**

select result of functional clustering result

**Usage**

```
fun_clu_select(result_fit, result_funclu, i)
```

**Arguments**

result_fit	list directly from power_equation_fit
result_funclu	list from fun_clu_convert
i	scale of which cluster selected

**Value**

list contain microbe data and fitted data

---

get_biSAD1	<i>generate biSAD1 covariance matrix</i>
------------	--

---

**Description**

generate biSAD1 covariance matrix

**Usage**

```
get_biSAD1(par, n1, n2)
```

**Arguments**

- par                vector with four number, first two for ck and the rest for stress
- n1                scalar indicate length of time1
- n2                scalar indicate length of time2

**Value**

biSAD1 covariance matrix

**Examples**

```
get_biSAD1(par=c(2,0.5,2,0.1),n1=4, n2 = 5)
```

---

get\_interaction                *Lasso-based variable selection*

---

**Description**

Lasso-based variable selection

**Usage**

```
get_interaction(data, col, reduction = FALSE)
```

**Arguments**

- data                data of clustered results, do not contain cluster column
- col                scalar of which row number selected
- reduction                use  $n/\log(n)$  dimension reduction

**Value**

list contain relationship of each row

get\_legendre\_matrix    *generate legendre matrix*

---

**Description**

generate legendre matrix

**Usage**

```
get_legendre_matrix(x, legendre_order)
```

**Arguments**

x                    vector equal to the x value for legendre polynomials(in this case times)  
legendre\_order    the order of legendre polynomials

**Value**

the polynomials value of each order

**Examples**

```
get_legendre_matrix(1:14,4)
```

---

get\_legendre\_par        *use legendre polynomials to fit a given data*

---

**Description**

use legendre polynomials to fit a given data

**Usage**

```
get_legendre_par(y, legendre_order, x)
```

**Arguments**

y                    vector equal to the y observed data(in this case generic effect)  
legendre\_order    scalar of legendre polynomials  
x                    vector equal to the x value for legendre polynomials(in this case times)

**Value**

the polynomials coefficients

**Examples**

```
get_legendre_par(14:1,4,1:14)
```



---

get_mu	<i>curve fit with modified logistic function</i>
--------	--

---

**Description**

curve fit with modified logistic function

**Usage**

```
get_mu(mu_par, times)
```

**Arguments**

mu_par	vector with five number
times	vector of time point

**Value**

numeric vector with the same length to times

**Examples**

```
get_mu(mu_par = 1:5, times = 1:14)
```

---

get_mu2	<i>generate mean vectors with ck and stress condition</i>
---------	---

---

**Description**

generate mean vectors with ck and stress condition

**Usage**

```
get_mu2(par, times)
```

**Arguments**

par	vector with ten number, first five for ck and the rest for stress
times	vector of time point

**Value**

numeric vector with the double length to times

**Examples**

```
get_mu2(par = 1:10, times = 1:14)
```

---

get_par_int	<i>acquire initial parameters for functional clustering</i>
-------------	---

---

**Description**

acquire initial parameters for functional clustering

**Usage**

```
get_par_int(X, k, times)
```

**Arguments**

X	matrix for cluster
k	vector for the cluster number
times	vector for the x values or time points

**Value**

the initial parameters for functional clustering

---

get_SAD1_covmatrix	<i>generate standard SAD1 covariance matrix</i>
--------------------	---

---

**Description**

generate standard SAD1 covariance matrix

**Usage**

```
get_SAD1_covmatrix(par, n)
```

**Arguments**

par	vector with two number for SAD1 covariance matrix
n	scalar indicate length of time d

**Value**

SAD1 covariance matrix

**Examples**

```
get_SAD1_covmatrix(par = c(2,0.5), n = 14)
```

---

gut_microbe	<i>gut_microbe OTU data (species level)</i>
-------------	---

---

**Description**

The original nucleotide sequences of this study were deposited to the NCBI Sequence Read Archive under accession number SRP128619.

**Usage**

```
data(gut_microbe)
```

**Format**

A data frame with 65 rows and 21 column, contain first column as microbe ID:

---

legendre_fit	<i>generate curve based on legendre polynomials</i>
--------------	---

---

**Description**

generate curve based on legendre polynomials

**Usage**

```
legendre_fit(par, x)
```

**Arguments**

par	vector of legendre polynomials coefficients
x	vector equal to the x value for legendre polynomials(in this case times)

**Value**

the polynomials value

**Examples**

```
legendre_fit(rep(1,5),1:14)
```

---

logsumexp	<i>calculate log-sum-exp values</i>
-----------	-------------------------------------

---

**Description**

calculate log-sum-exp values

**Usage**

```
logsumexp(v)
```

**Arguments**

v                    numeric vector

**Value**

log-sum-exp values

**Examples**

```
logsumexp(c(100, 1000, 10000))
```

---

mustard_microbe	<i>mustard microbe OTU data</i>
-----------------	---------------------------------

---

**Description**

Wagner, M. R. et al. Host genotype and age shape the leaf and root microbiomes of a wild perennial plant. *Nat. Commun.* 7:12151 doi: 10.1038/ncomms12151 (2016) This dataset is a subset of otuTable97, we select location = JAM, keep samples with both root and leaf data, and then run data\_cleaning first (set x = 50) to reduce size of this data. Moreover, sample 8\_1382 is removed for the outlier reason.

**Usage**

```
data(mustard_microbe)
```

**Format**

A data frame with 1557 rows and 176 column, contain first column as OTU ID:

---

network_conversion	<i>convert ODE results(ODE_solving2) to basic network plot table</i>
--------------------	--

---

**Description**

convert ODE results(ODE\_solving2) to basic network plot table

**Usage**

```
network_conversion(result)
```

**Arguments**

result            list result from qsODE\_parallel

**Value**

a list with basic information to plot network

---

network_maxeffect	<i>convert ODE results(ODE_solving2) to basic network plot table</i>
-------------------	--

---

**Description**

convert ODE results(ODE\_solving2) to basic network plot table

**Usage**

```
network_maxeffect(result)
```

**Arguments**

result            list result from qsODE\_parallel

**Value**

a list with basic information to plot network

---

network_plot	<i>generate network plot</i>
--------------	------------------------------

---

**Description**

generate network plot

**Usage**

```
network_plot(result, title = NULL, maxeffect = NULL, type = NULL)
```

**Arguments**

result	list result from network_conversion
title	text for plot title
maxeffect	control edge size when compare networks
type	select module effect or microbe effect

**Value**

network plot

---

normalization	<i>min-max normalization</i>
---------------	------------------------------

---

**Description**

min-max normalization

**Usage**

```
normalization(x, z = 0.2)
```

**Arguments**

x	numeric vector
z	scalar add minimum value to avoid 0

**Value**

normalized vector

**Examples**

```
normalization(runif(100,min = -100, max = 100))
```

---

power\_equation      *use power equation parameters to generate y values*

---

**Description**

use power equation parameters to generate y values

**Usage**

```
power_equation(x, power_par)
```

**Arguments**

x                      vector for x values  
power\_par              matrix contain parameters for power equation

**Value**

y values for given power equation parameters

**Examples**

```
power_equation(c(1,2,3,5,7), matrix(c(2,1,1,2),2,2))
```

---

power\_equation\_all      *use power equation to fit observed values*

---

**Description**

use power equation to fit observed values

**Usage**

```
power_equation_all(x, y, maxit = 100)
```

**Arguments**

x                      vector for x values  
y                        vector for y values  
maxit                  numeric value for maximum initial pars try

**Value**

nls model

**Examples**

```
power_equation_all(c(1,2,3,5,7), c(5,10,15,17,20))
```

---

power\_equation\_base    *use power equation to fit observed values*

---

**Description**

use power equation to fit observed values

**Usage**

```
power_equation_base(x, y)
```

**Arguments**

x	vector for x values
y	vector for y values

**Value**

nls model

**Examples**

```
power_equation_base(c(1,2,3,5,7), c(5,10,15,17,20))
```

---

power\_equation\_fit    *use power equation to fit given dataset*

---

**Description**

use power equation to fit given dataset

**Usage**

```
power_equation_fit(data, n = 30, trans = log10, thread = 2)
```

**Arguments**

data	cleaned dataframe
n	scales for how many interpolation needed
trans	indicate log/log2/log10 transform dataset
thread	scales for how many thread used

**Value**

list contain power equation parameters and fitted data



---

power\_equation\_plot     *plot power equation fitting results*

---

**Description**

plot power equation fitting results

**Usage**

```
power_equation_plot(result, label = 10, n = 9)
```

**Arguments**

result	list object returned from power_equation_fit
label	relabel x and y label due to log-transform, set 10 as default
n	scales for how many subplots needed

**Value**

plot show power curve fitting result

---

qdODEmod     *quasi-dynamic lotka volterra model*

---

**Description**

quasi-dynamic lotka volterra model

**Usage**

```
qdODEmod(Time, State, Pars, power_par)
```

**Arguments**

Time	vector of time point
State	vector of ODE initial state
Pars	vector for unknown ODE parameters
power_par	matrix of power equation parameters for dependent effect

**Value**

list used in ode function

---

qdODEplot_convert	<i>convert qdODE results to plot data</i>
-------------------	---

---

**Description**

convert qdODE results to plot data

**Usage**

```
qdODEplot_convert(result)
```

**Arguments**

result	list of qdODE all
--------	-------------------

---

qdODE_all	<i>wrapper for qdODE model</i>
-----------	--------------------------------

---

**Description**

wrapper for qdODE model

**Usage**

```
qdODE_all(
  result,
  relationship,
  i,
  init_pars = 1,
  LOP_order = 6,
  method = "ls",
  new_time = NULL,
  n_expand = 100,
  maxit = 1000
)
```

**Arguments**

result	result from power_equation_fit
relationship	list contain variable selection results
i	scalar for which id used for qdODE solving, must <= nrow
init_pars	scalar for initial parameters
LOP_order	scalar of LOP order
method	scalar of qdODE solving methodm, cuurent only support least square

new_time	vector produce new defined time point
n_expand	scalar for how many interpolation needed
maxit	scalar of Optim iteration setting

**Value**

list contain variable selection results and LOP parameters for every row

---

qdODE_fit	<i>legendre polynomials fit to qdODE model</i>
-----------	--

---

**Description**

legendre polynomials fit to qdODE model

**Usage**

```
qdODE_fit(
  pars,
  data,
  Time,
  power_par,
  LOP_order = 6,
  new_time = NULL,
  n_expand = 100
)
```

**Arguments**

pars	vector of qdODE parameters
data	dataframe of observed data
Time	vector of time point
power_par	matrix of power equation parameters for dependent effect
LOP_order	scalar of LOP order
new_time	vector produce new defined time point
n_expand	scalar for how many interpolation needed

**Value**

list contain legendre polynomials parameters, qdODE values and LOP fitted values

---

qdODE\_ls                      *least-square fit for qdODE model*

---

**Description**

least-square fit for qdODE model

**Usage**

```
qdODE_ls(pars, data, Time, power_par)
```

**Arguments**

pars	vector for unknown ODE parameters
data	data contain independent effect as first row and dependent effect
Time	vector of time point
power_par	matrix of power equation parameters for dependent effect

**Value**

mean-square error

---

qdODE\_parallel                      *wrapper for qdODE\_all in parallel version*

---

**Description**

wrapper for qdODE\_all in parallel version

**Usage**

```
qdODE_parallel(result, reduction = FALSE, thread = 2, maxit = 1000)
```

**Arguments**

result	result from power_equation_fit
reduction	use n/log(n) dimension reduction
thread	scales for how many threads used
maxit	scalar of Optim iteration setting

**Value**

list contain variable selection results and LOP parameters for every row

---

qdODE\_plot\_all      *plot all decompose plot*

---

**Description**

plot all decompose plot

**Usage**

```
qdODE_plot_all(
  result,
  label = 10,
  show.legend = TRUE,
  nrow = NULL,
  ncol = NULL
)
```

**Arguments**

result	list of qdODE parallel
label	relabel x and y label due to log-transform, set 10 as default
show.legend	to show legend
nrow	scalar for subplot row number
ncol	scalar for subplot column number

**Value**

all effect curve decompose plot

---

qdODE\_plot\_base      *plot single decompose plot*

---

**Description**

plot single decompose plot

**Usage**

```
qdODE_plot_base(result, label = 10, show.legend = TRUE)
```

**Arguments**

result	list of qdODE all
label	relabel x and y label due to log-transform, set 10 as default
show.legend	to show legend

---

Q_function	<i>Q-function to replace log-likelihood function</i>
------------	--

---

**Description**

Q-function to replace log-likelihood function

**Usage**

```
Q_function(par, prob_log, omega_log, X, k, times)
```

**Arguments**

par	numeric vector for parameters need to be estimated
prob_log	mixture component weights(log)
omega_log	latent variables(log)
X	matrix for cluster
k	vector for the cluster number
times	vector for the x values or time points

**Value**

the Loglikelihood value

# Index

## \* datasets

gut\_microbe, 19  
mustard\_microbe, 20

bifun\_clu, 3  
bifun\_clu\_convert, 4  
bifun\_clu\_parallel, 4  
bifun\_clu\_plot, 5  
biget\_par\_int, 6  
bipower\_equation\_plot, 6  
biQ\_function, 8  
biqdODE\_plot\_all, 7  
biqdODE\_plot\_base, 8

darken, 9  
data\_cleaning, 10  
data\_match, 10

fun\_clu, 11  
fun\_clu\_BIC, 12  
fun\_clu\_convert, 12  
fun\_clu\_parallel, 13  
fun\_clu\_plot, 13  
fun\_clu\_select, 14

get\_biSAD1, 14  
get\_interaction, 15  
get\_legendre\_matrix, 16  
get\_legendre\_par, 16  
get\_mu, 17  
get\_mu2, 17  
get\_par\_int, 18  
get\_SAD1\_covmatrix, 18  
gut\_microbe, 19

legendre\_fit, 19  
logsumexp, 20

mustard\_microbe, 20

network\_conversion, 21

network\_maxeffect, 21  
network\_plot, 22  
normalization, 22

power\_equation, 23  
power\_equation\_all, 23  
power\_equation\_base, 24  
power\_equation\_fit, 24  
power\_equation\_plot, 25

Q\_function, 30  
qdODE\_all, 26  
qdODE\_fit, 27  
qdODE\_ls, 28  
qdODE\_parallel, 28  
qdODE\_plot\_all, 29  
qdODE\_plot\_base, 29  
qdODEmod, 25  
qdODEplot\_convert, 26