

# Package ‘RPA’

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**biocViews** GeneExpression, Microarray, Preprocessing, QualityControl

**Description** Probabilistic analysis of probe reliability and  
differential gene expression on short oligonucleotide  
arrays.

**License** BSD\_2\_clause + file LICENSE

**URL** <https://github.com/antagomir/RPA>

**BugReports** <https://github.com/antagomir/RPA>

**VignetteBuilder** knitr

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RPA-package

*RPA: probabilistic analysis of probe reliability and gene expression*


---

### Description

Brief summary of the RPA package

## Details

Package: RPA  
Type: Package  
Version: See sessionInfo() or DESCRIPTION file  
Date: 2008-2016  
License: FreeBSD  
LazyLoad: yes

## Author(s)

Leo Lahti <leo.lahti@iki.fi>

## References

See citation("RPA")

## Examples

#

---

calculate.rpa	<i>RPA with HITChip</i>
---------------	-------------------------

---

## Description

Fit RPA for HITChip.

## Usage

```
calculate.rpa(level, phylo, oligo.data)
```

## Arguments

level	level
phylo	phylo
oligo.data	oligo.data

## Value

RPA preprocessed data

## Author(s)

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

## References

See citation("microbiome")

```
collect.hyperparameters  
    collect.hyperparameters
```

---

### **Description**

Collect probe-level parameters during online-learning from the batch files.

### **Usage**

```
collect.hyperparameters(  
  batches,  
  unique.run.identifier,  
  save.batches.dir,  
  save.batches,  
  verbose = TRUE  
)
```

### **Arguments**

batches	batch list
unique.run.identifier	Batch file identifier string
save.batches.dir	Batch file directory
save.batches	Logical. Determines whether batches are available.
verbose	verbose

### **Author(s)**

Leo Lahti <leo.lahti@iki.fi>

### **References**

See citation("RPA")

### **Examples**

```
# hpe <- collect.hyperparameters(batches, unique.run.identifier, save.batches.dir, save.batches)
```

---

d.update.fast	<i>Fast d update</i>
---------------	----------------------

---

**Description**

Computes weighted average over the probes, weighted by their inverse probe-specific variances.

**Usage**

```
d.update.fast(St, s2)
```

**Arguments**

St	probes x samples data matrix
s2	variances for the probes

**Details**

Returns summarized probeset-level weighted average

**Author(s)**

Leo Lahti <leo.lahti@iki.fi>

**References**

See citation("RPA")

**Examples**

```
#
```

---

estimate.affinities	<i>estimate.affinities</i>
---------------------	----------------------------

---

**Description**

Probe affinity estimation. Estimates probe-specific affinity parameters.

**Usage**

```
estimate.affinities(dat, a)
```

**Arguments**

dat	Input data set: probes x samples.
a	Estimated expression signal from RPA model.

## Details

To estimate means in the original data domain let us assume that each probe-level observation  $x$  is of the following form:  $x = d + v + \text{noise}$ , where  $x$  and  $d$  are vectors over samples,  $v$  is a scalar (vector with identical elements) noise is Gaussian with zero mean and probe-specific variance parameters  $\tau^2$ . Then the parameter  $\mu$  will indicate how much probe-level observation deviates from the estimated signal shape  $d$ . This deviation is further decomposed as  $\mu = \mu.\text{real} + \mu.\text{probe}$ , where  $\mu.\text{real}$  describes the 'real' signal level, common for all probes  $\mu.\text{probe}$  describes probe affinity effect. Let us now assume that  $\mu.\text{probe} \sim N(0, \sigma.\text{probe})$ . This encodes the assumption that in general the affinity effect of each probe tends to be close to zero. Then we just calculate ML estimates of  $\mu.\text{real}$  and  $\mu.\text{probe}$  based on particular assumptions. Note that this part of the algorithm has not been defined in full probabilistic terms yet, just calculating the point estimates. Note that while  $\tau^2$  in RPA measures stochastic noise, and NOT the affinity effect, we use it here as a heuristic solution to weigh the probes according to how much they contribute to the overall signal shape. Intuitively, probes that have little effect on the signal shape (i.e. are very noisy and likely to be contaminated by many unrelated signals) should also contribute less to the absolute signal estimate. If no other prior information is available, using stochastic parameters  $\tau^2$  to determine probe weights is likely to work better than simple averaging of the probes without weights. Also in this case the probe affinities sum close to zero but there is some flexibility, and more noisy probes can be downweighted.

## Value

A vector with probe-specific affinities.

## Author(s)

Leo Lahti <leo.lahti@iki.fi>

## References

See citation("RPA")

## See Also

rpa.fit

## Examples

```
# mu <- estimate.affinities(dat, a)
```

---

estimate.hyperparameters

*estimate.hyperparameters*

---

## Description

Hyperparameter estimation.

**Usage**

```
estimate.hyperparameters(
  sets = NULL,
  probe.parameters = list(alpha = 2, beta = 1),
  batches,
  cdf = NULL,
  bg.method = "rma",
  epsilon = 0.01,
  load.batches = FALSE,
  save.hyperparameter.batches = FALSE,
  mc.cores = 1,
  verbose = TRUE,
  normalization.method = "quantiles",
  save.batches.dir = ".",
  unique.run.identifier = NULL,
  set.inds = set.inds
)
```

**Arguments**

sets	Probesets to handle. All probesets by default.
probe.parameters	User-defined priors. May also include quantile.basis
batches	Data batches for online learning
cdf	CDF probeset definition file
bg.method	Background correction method
epsilon	Convergence parameter
load.batches	Logical. Load preprocessed data whose identifiers are picked from names(batches). Assuming that the same batch list (batches) was used to create the files in on-line.quantiles function.
save.hyperparameter.batches	Save hyperparameters for each batch into files using the identifiers with batch name with -hyper.RData suffix.
mc.cores	Number of cores for parallel computation
verbose	Print progress information
normalization.method	Normalization method
save.batches.dir	Specify the output directory for temporary batch saves.
unique.run.identifier	Define identifier for this run for naming the temporary batch files. By default, a random id is generated.
set.inds	Probeset indices

**Value**

alpha: Hyperparameter alpha (same for all probesets); betas: Hyperparameter beta (probe-specific); variances: Probe-specific variances (beta/alpha)

**Author(s)**

Leo Lahti <leo.lahti@iki.fi>

**References**

See citation("RPA")

**Examples**

```
#
```

---

```
frpa
```

```
frpa
```

---

**Description**

Frozen-RPA preprocessing using precalculated probe parameters.

**Usage**

```
frpa(
  abatch = NULL,
  probe.parameters = NULL,
  verbose = FALSE,
  cdf = NULL,
  cel.files = NULL,
  cel.path = NULL,
  mc.cores = 1,
  summarize.with.affinities = FALSE
)
```

**Arguments**

abatch	An AffyBatch object.
probe.parameters	A list with tau2 (probe variance), quantile.basis (basis for quantile normalization in log2 domain), and optionally affinity (probe affinities). The probe.parameters\$tau2 and probe.parameters\$affinity are lists, each element corresponding to a probe-set and containing a parameter vector over the probes. The quantile.basis is a vector over the probes, the probes need to be listed in the same order as in tau2 and affinity. probe.parameters can be optionally provided as a data frame.
verbose	Print progress information during computation.
cdf	Specify an alternative CDF environment. Default: none.
cel.files	List of CEL files to preprocess.
cel.path	Path to CEL file directory.
mc.cores	Number of cores for parallelized processing.
summarize.with.affinities	Use affinity estimates in probe summarization step. Default: FALSE.



**Details**

fRPA function to preprocess Affymetrix CEL files with RPA using precalculated (frozen) probe parameters.

**Value**

Preprocessed expression matrix in expressionSet format

**Author(s)**

Leo Lahti <leo.lahti@iki.fi>

**References**

See citation("RPA")

**See Also**

rpa, AffyBatch, ExpressionSet

**Examples**

```
# eset <- frpa(abatch, probe.parameters)
```

---

get.batches

*get.batches Split data into batches*

---

**Description**

get.batches Split data into batches

**Usage**

```
get.batches(items, batch.size = NULL, shuffle = FALSE)
```

**Arguments**

items	A vector of items to be splitted into batches.
batch.size	Batch size. The last batch may contain less elements than the other batches which have batch.size elements each.
shuffle	Split the elements randomly in the batches.

**Value**

A list. Each element corresponds to one batch and contains a vector listing the elements in that batch.

**Author(s)**

Leo Lahti <leo.lahti@iki.fi>

**References**

See citation("RPA")

**Examples**

```
#
```

---

```
get.probe.matrix      get.probe.matrix
```

---

**Description**

Get probe matrix.

**Usage**

```
get.probe.matrix(  
  cels,  
  cdf = NULL,  
  quantile.basis,  
  bg.method = "rma",  
  normalization.method = "quantiles",  
  batch = NULL,  
  verbose = TRUE  
)
```

**Arguments**

<code>cels</code>	List of CEL files to preprocess
<code>cdf</code>	Specify an alternative CDF environment
<code>quantile.basis</code>	Pre-calculated basis for quantile normalization in log2 domain
<code>bg.method</code>	Specify background correction method. See <code>bgcorrect.methods()</code> for options.
<code>normalization.method</code>	normalization method
<code>batch</code>	batch
<code>verbose</code>	Print progress information during computation

**Details**

Returns background-corrected, quantile normalized log2 probes x samples matrix

**Author(s)**

Leo Lahti <leo.lahti@iki.fi>

**References**

See citation("RPA")

**Examples**

```
#
```

---

get.probe.parameters    *get.probe.parameters*

---

### Description

Get probe-level hyperparameter from batch files

### Usage

```
get.probe.parameters(  
  affinities,  
  unique.run.identifier,  
  save.batches.dir = ".",  
  mode = "list"  
)
```

### Arguments

affinities	probe affinities
unique.run.identifier	Batch file identifier string
save.batches.dir	Batch file directory
mode	"list" or "table"

### Author(s)

Leo Lahti <leo.lahti@iki.fi>

### References

See citation("RPA")

### Examples

```
# df <- get.probe.parameters(unique.run.identifier, save.batches.dir = ".", mode = "list")
```

---

get.probeset                    *Get probeset*

---

### Description

Get probeset matrix.

### Usage

```
get.probeset(name, level, taxonomy, probedata, log10 = TRUE)
```

**Arguments**

name	name
level	taxonomic level
taxonomy	taxonomy
probedata	oligos vs. samples preprocessed data matrix; absolute scale
log10	Logical. Logarithmize the data TRUE/FALSE

**Value**

probeset data matrix

**Author(s)**

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

**References**

See citation('microbiome')

**Examples**

```
#taxonomy <- GetPhylogeny('HITChip', 'filtered')
#data.dir <- system.file("extdata", package = "microbiome")
#probedata <- read_hitchip(data.dir, "rpa")$probedata
#ps <- get.probeset('Akkermansia', 'L2', taxonomy, probedata)
```

---

hyperparameter.update *hyperparameter.update*

---

**Description**

Update hyperparameters Update shape (alpha) and scale (beta) parameters of the inverse gamma distribution.

**Usage**

```
hyperparameter.update(dat, alpha, beta, th = 0.01)
```

**Arguments**

dat	A probes x samples matrix (probeset).
alpha	Shape parameter of inverse gamma density for the probe variances.
beta	Scale parameter of inverse gamma density for the probe variances.
th	Convergence threshold.

**Details**

Shape update:  $\alpha \leftarrow \alpha + T/2$ ; Scale update:  $\beta \leftarrow \alpha * s2$  where  $s2$  is the updated variance for each probe (the mode of variances is given by  $\beta/\alpha$ ). The variances ( $s2$ ) are updated by EM type algorithm, see `s2.update`.

**Value**

A list with elements alpha, beta (corresponding to the shape and scale parameters of inverse gamma distribution, respectively).

**Author(s)**

Leo Lahti <leo.lahti@iki.fi>

**References**

See citation("RPA")

**See Also**

s2.update, rpa.online

**Examples**

```
#
## Generate and fit toydata, learn hyperparameters
#set.seed(11122)
#P <- 11 # number of probes
#N <- 5000 # number of arrays
#real <- sample.probeset(P = P, n = N, shape = 3, scale = 1, mu.real = 4)
#dat <- real$dat # probes x samples#
#
## Set priors
#alpha <- 1e-2
#beta <- rep(1e-2, P)
## Operate in batches
#step <- 1000
#for (ni in seq(1, N, step)) {
#  batch <- ni:(ni+step-1)
#  hp <- hyperparameter.update(dat[,batch], alpha, beta, th = 1e-2)
#  alpha <- hp$alpha
#  beta <- hp$beta
#}
## Final variance estimate
#s2 <- beta/alpha
#
## Compare real and estimated variances
#plot(sqrt(real$tau2), sqrt(s2), main = cor(sqrt(real$tau2), sqrt(s2))); abline(0,1)
```

---

levelmap

*Map taxonomic levels*

---

**Description**

Map taxa between hierarchy levels.

**Usage**

```
levelmap(taxa = NULL, from, to, tax.table)
```

**Arguments**

taxa	taxa to convert; if NULL then considering all taxa in the tax.table
from	convert from taxonomic level
to	convert to taxonomic level
tax.table	tax.table

**Value**

mappings

**Author(s)**

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

**References**

See citation('microbiome')

---

`n.phylotypes.per.oligo`

*n.phylotypes.per.oligo*

---

**Description**

Check number of matching phylotypes for each probe

**Usage**

```
n.phylotypes.per.oligo(taxonomy, level)
```

**Arguments**

taxonomy	oligo - phylotype matching data.frame
level	phylotype level

**Value**

number of matching phylotypes for each probe

**Author(s)**

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

**References**

See citation("microbiome")

---

online.quantile	<i>online.quantile</i> Quantile normalization tools for online preprocessing. Estimate quantiles for quantile normalization based on subset of the data (random, or specified by the user).
-----------------	---

---

## Description

online.quantile Quantile normalization tools for online preprocessing. Estimate quantiles for quantile normalization based on subset of the data (random, or specified by the user).

## Usage

```
online.quantile(abatch, n)
```

## Arguments

abatch	AffyBatch
n	Numeric: number of random samples to use to define quantile basis. Vector: specify samples to be used in quantile basis calculation.

## Details

"online.quantile": Ordinary quantile normalization is exhaustively memory-consuming in large data sets. Then the quantiles can be calculated based on subset of the data to allow efficient normalization. This function can also be used to investigate effect of subset size to convergence of the quantile estimates;"qnorm.basis.online": sweeps through the data in batches to calculate the basis for quantile normalization (average over sorted profiles).

## Value

"online.quantile": AffyBatch; "qnorm.basis.online": a vector containing the basis for quantile normalization.

## Author(s)

Leo Lahti <leo.lahti@iki.fi>

## References

See citation("RPA")

## Examples

```
#
```

---

```
probe.parameters.tolist
      probe.parameters.tolist
```

---

**Description**

Convert probe parameter table into a list format

**Usage**

```
probe.parameters.tolist(probe.parameters)
```

**Arguments**

```
probe.parameters
      A data.frame with alpha, betas, tau2, affinities, quantile.basis
```

**Author(s)**

```
Leo Lahti <leo.lahti@iki.fi>
```

**References**

See citation("RPA")

**Examples**

```
# df <- probe.parameters.tolist(probe.parameters.table)
```

---

```
probe.performance      Probe performance
```

---

**Description**

Provide a table of probe-level parameter estimates (affinity and stochastic noise) for RPA output.

**Usage**

```
probe.performance(probe.parameters, abatch, sets = NULL)
```

**Arguments**

```
probe.parameters
      List with affinities and variances for the probesets

abatch
      Affybatch used in the analysis

sets
      Specify the probesets to include in the output. Default: All probesets
```

**Value**

Data frame of probe-level parameter estimates



**Author(s)**

Leo Lahti <leo.lahti@iki.fi>

**References**

See citation("RPA")

---

probeplot	<i>probeplot Plot RPA results and probe-level data for a specified probeset.</i>
-----------	--

---

**Description**

probeplot Plot RPA results and probe-level data for a specified probeset.

**Usage**

```
probeplot(
  dat,
  highlight.probes = NULL,
  pcol = "darkgrey",
  hcol = "red",
  cex.lab = 1.5,
  cex.axis = 1,
  cex.main = 1,
  cex.names = 1,
  main = "",
  ...
)
```

**Arguments**

- dat Background-corrected and normalized data: probes x samples.
- highlight.probes Optionally highlight some of the probes (with dashed line)
- pcol Color for probe signal visualization.
- hcol Color for probe highlight
- cex.lab Label size adjustment parameters.
- cex.axis Axis size adjustment parameters.
- cex.main Title size adjustment parameters.
- cex.names Names size adjustment parameters.
- main Title text.
- ... Other parameters to pass for plot function.

**Details**

Plots the preprocessed probe-level observations, estimated probeset-level signal, and probe-specific variances. It is also possible to highlight individual probes and external summary measures.

**Value**

Used for its side-effects. Returns probes x samples matrix of probe-level data plotted on the image.

**Author(s)**

Leo Lahti <leo.lahti@iki.fi>

**References**

See citation("RPA")

**Examples**

```
#
```

---

probetable

*probetable*

---

**Description**

Convert probe-level hyperparameter lists into a table format.

**Usage**

```
probetable(probe.parameters)
```

**Arguments**

```
probe.parameters
```

A list with alpha, betas, variances and affinities

**Author(s)**

Leo Lahti <leo.lahti@iki.fi>

**References**

See citation("RPA")

**Examples**

```
# df <- probetable(probe.parameters)
```

---

retrieve.probesets	<i>Retrieve probesets</i>
--------------------	---------------------------

---

**Description**

List probes for each probeset in taxonomic data.

**Usage**

```
retrieve.probesets(tax.table, level = "species", name = NULL)
```

**Arguments**

tax.table	data.frame with oligo - phylotype mapping info
level	phylotype level for probesets
name	specify phylotypes to check (optional)

**Value**

A list. Probes for each phylotype.

**Author(s)**

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

**References**

See citation('microbiome')

**Examples**

```
#tax.table <- GetPhylogeny('HITChip')  
#sets <- retrieve.probesets(tax.table, 'species', 'Weissella confusa')
```

---

rpa	<i>rpa</i>
-----	------------

---

**Description**

Wrapper for RPA preprocessing.

**Usage**

```
rpa(
  abatch = NULL,
  verbose = FALSE,
  bg.method = "rma",
  normalization.method = "quantiles.robust",
  cdf = NULL,
  cel.files = NULL,
  cel.path = NULL,
  probe.parameters = NULL,
  mc.cores = 1,
  summarize.with.affinities = FALSE
)
```

**Arguments**

<code>abatch</code>	An AffyBatch object.
<code>verbose</code>	Print progress information during computation.
<code>bg.method</code>	Specify background correction method. Default: "rma". See <code>bgcorrect.methods()</code> for other options.
<code>normalization.method</code>	Specify quantile normalization method. Default: "pmonly". See <code>normalize.methods(Dilution)</code> for other options.
<code>cdf</code>	Specify an alternative CDF environment. Default: none.
<code>cel.files</code>	List of CEL files to preprocess.
<code>cel.path</code>	Path to CEL file directory.
<code>probe.parameters</code>	A list, each element corresponding to a probe set. Each probeset element has the following optional elements: <code>mu</code> (affinity), <code>tau2</code> (variance), <code>alpha</code> (shape prior), <code>beta</code> (scale prior). Each of these elements contains a vector over the probeset probes, specifying the probe parameters according to the RPA model. If variance is given, it overrides the priors. Can be also used to set user-specified priors for the model parameters. Not used <code>tau2.method = "var"</code> . The prior parameters <code>alpha</code> and <code>beta</code> are prior parameters for inverse Gamma distribution of probe-specific variances. Noninformative prior is obtained with <code>alpha, beta -&gt; 0</code> . Not used with <code>tau2.method 'var'</code> . Scalar <code>alpha</code> and <code>beta</code> specify an identical inverse Gamma prior for all probes, which regularizes the solution. Can be also specified as lists, each element corresponding to one probeset. May also include <code>quantile.basis</code>
<code>mc.cores</code>	Number of cores for parallelized processing.
<code>summarize.with.affinities</code>	Use affinity estimates in probe summarization step. Default: FALSE.

**Details**

RPA preprocessing function. Gives an estimate of the probeset-level mean parameter `d` of the RPA model, and returns these in an `expressionSet` object. The choices `tau2.method = "robust"` and `d.method = "fast"` are recommended. With small sample size and informative prior, `d.method = "basic"` may be preferable. For very large expression data collections, see `rpa.online` function.

**Value**

Preprocessed expression matrix in expressionSet format

**Author(s)**

Leo Lahti <leo.lahti@iki.fi>

**References**

See citation("RPA")

**See Also**

rpa.online, AffyBatch, ExpressionSet, estimate.affinities, rpa.fit

**Examples**

```
# eset <- rpa(abatch)
```

---

rpa.complete

*Complete RPA preprocessing*

---

**Description**

RPA preprocessing, also returns probe parameters.

**Usage**

```
rpa.complete(  
  abatch = NULL,  
  sets = NULL,  
  epsilon = 0.01,  
  tau2.method = "robust",  
  d.method = "fast",  
  verbose = FALSE,  
  bg.method = "rma",  
  normalization.method = "quantiles.robust",  
  cdf = NULL,  
  cel.files = NULL,  
  cel.path = NULL,  
  probe.parameters = list(),  
  mc.cores = 1,  
  summarize.with.affinities = FALSE  
)
```

**Arguments**

abatch	An AffyBatch object.
sets	Probesets for which RPA will be computed.
epsilon	Convergence tolerance. The iteration is deemed converged when the change in all parameters is < epsilon.
tau2.method	Optimization method for tau2 (probe-specific variances). This parameter is denoted by tau^2 in the vignette and manuscript "robust": (default) update tau2 by posterior mean, regularized by informative priors that are identical for all probes (user-specified by setting scalar values for alpha, beta). This regularizes the solution, and avoids overfitting where a single probe obtains infinite reliability. This is a potential problem in the other tau2 update methods with non-informative variance priors. The default values alpha = 2; beta = 1 are used if alpha and beta are not specified. "mode": update tau2 with posterior mean "mean": update tau2 with posterior mean "var": update tau2 with variance around d. Applies the fact that tau2 cost function converges to variance with large sample sizes.
d.method	Method to optimize d. "fast": (default) weighted mean over the probes, weighted by probe variances. The solution converges to this with large sample size. "basic": optimization scheme to find a mode used in Lahti et al. TCBB/IEEE; relatively slow; this is the preferred method with small sample sizes.
verbose	Print progress information during computation.
bg.method	Specify background correction method. Default: "rma". See bgcorrect.methods() for other options.
normalization.method	Specify quantile normalization method. Default: "pmonly". See normalize.methods(Dilution) for other options.
cdf	Specify an alternative CDF environment. Default: none.
cel.files	List of CEL files to preprocess.
cel.path	Path to CEL file directory.
probe.parameters	A list, each element corresponding to a probe set. Each probeset element has the following optional elements: affinity (affinity), tau2 (variance), alpha (shape prior), betas (scale prior). Each of these elements contains a vector over the probeset probes, specifying the probe parameters according to the RPA model. If variance is given, it overrides the priors. Can be also used to set user-specified priors for the model parameters. Not used tau2.method = "var". The prior parameters alpha and beta are prior parameters for inverse Gamma distribution of probe-specific variances. Noninformative prior is obtained with alpha, beta -> 0. Not used with tau2.method 'var'. Scalar alpha and beta specify an identical inverse Gamma prior for all probes, which regularizes the solution. Can be also specified as lists, each element corresponding to one probeset. Can also include quantile.basis
mc.cores	Number of cores for parallelized processing.
summarize.with.affinities	Use affinity estimates in probe summarization step. Default: FALSE.

**Details**

RPA preprocessing function. Gives an estimate of the probeset-level mean parameter  $d$  of the RPA model, and returns these in an expressionSet object. The choices `tau2.method = "robust"` and `d.method = "fast"` are recommended. With small sample size and informative prior, `d.method = "basic"` may be preferable. For very large expression data collections, see `rpa.online` function.

**Value**

List with preprocessed expression matrix, corresponding probe parameters, AffyBatch and CDF

**Author(s)**

Leo Lahti <leo.lahti@iki.fi>

**References**

See `citation("RPA")`

**Examples**

```
# eset <- rpa(abatch)
```

---

rpa.fit

*RPA fit*

---

**Description**

Fit the RPA model.

**Usage**

```
rpa.fit(
  dat,
  epsilon = 0.01,
  alpha = NULL,
  beta = NULL,
  tau2.method = "robust",
  d.method = "fast",
  summarize.with.affinities = FALSE
)
```

**Arguments**

<code>dat</code>	Original data: probes x samples.
<code>epsilon</code>	Convergence tolerance. The iteration is deemed converged when the change in all parameters is < epsilon.
<code>alpha</code>	alpha prior for inverse Gamma distribution of probe-specific variances. Non-informative prior is obtained with <code>alpha, beta -&gt; 0</code> . Not used with <code>tau2.method 'var'</code> . Scalar alpha and beta are specify equal inverse Gamma prior for all probes to regularize the solution. The defaults depend on the method.

beta	beta prior for inverse Gamma distribution of probe-specific variances. Noninformative prior is obtained with alpha, beta -> 0. Not used with tau2.method 'var'. Scalar alpha and beta are specify equal inverse Gamma prior for all probes to regularize the solution. The defaults depend on the method.
tau2.method	Optimization method for tau2 (probe-specific variances); "robust": (default) update tau2 by posterior mean, regularized by informative priors that are identical for all probes (user-specified by setting scalar values for alpha, beta). This regularizes the solution, and avoids overfitting where a single probe obtains infinite reliability. This is a potential problem in the other tau2 update methods with non-informative variance priors. The default values alpha = 2; beta = 1 are used if alpha and beta are not specified. "mode": update tau2 with posterior mean "mean": update tau2 with posterior mean "var": update tau2 with variance around d. Applies the fact that tau2 cost function converges to variance with large sample sizes.
d.method	Method used to optimize d. Options: "fast": (default) weighted mean over the probes, weighted by probe variances. The solution converges to this with large sample size. "basic": optimization scheme to find a mode used in Lahti et al. TCBB/IEEE; relatively slow; preferred with small sample size.
summarize.with.affinities	Use affinity estimates in probe summarization step. Default: FALSE.

## Details

Fits the RPA model, including estimation of probe-specific affinity parameters. First learns a point estimate for the RPA model in terms of differential expression values w.r.t. reference sample. After this, probe affinities are estimated by comparing original data and differential expression shape, and setting prior assumptions concerning probe affinities.

## Value

mu: Fitted signal in original data:  $\mu_{\text{real}} + d$ ; mu.real: Shifting parameter of the reference sample;  
tau2: Probe-specific stochastic noise; affinity: Probe-specific affinities; data: Probeset data matrix;  
alpha, beta: prior parameters

## Author(s)

Leo Lahti <leo.lahti@iki.fi>

## References

See citation("RPA")

## See Also

rpa, estimate.affinities

## Examples

```
# res <- rpa.fit(dat, epsilon, alpha, beta, tau2.method, d.method, affinity.method)
```



---

RPA.iteration	<i>RPA iteration</i>
---------------	----------------------

---

### Description

Estimating model parameters d and tau2.

### Usage

```
RPA.iteration(
  S,
  epsilon = 0.001,
  alpha = NULL,
  beta = NULL,
  tau2.method = "fast",
  d.method = "fast",
  maxloop = 1e+06
)
```

### Arguments

S	Matrix of probe-level observations for a single probeset: samples x probes.
epsilon	Convergence tolerance. The iteration is deemed converged when the change in all parameters is < epsilon.
alpha	alpha prior for inverse Gamma distribution of probe-specific variances. Non-informative prior is obtained with alpha, beta -> 0. Not used with tau2.method 'var'. Scalar alpha and beta are specify equal inverse Gamma prior for all probes to regularize the solution. The defaults depend on the method.
beta	beta prior for inverse Gamma distribution of probe-specific variances. Noninformative prior is obtained with alpha, beta -> 0. Not used with tau2.method 'var'. Scalar alpha and beta are specify equal inverse Gamma prior for all probes to regularize the solution. The defaults depend on the method.
tau2.method	Optimization method for tau2 (probe-specific variances). "robust": (default) update tau2 by posterior mean, regularized by informative priors that are identical for all probes (user-specified by setting scalar values for alpha, beta). This regularizes the solution, and avoids overfitting where a single probe obtains infinite reliability. This is a potential problem in the other tau2 update methods with non-informative variance priors. The default values alpha = 2; beta = 1 are used if alpha and beta are not specified. "mode": update tau2 with posterior mean "mean": update tau2 with posterior mean "var": update tau2 with variance around d. Applies the fact that tau2 cost function converges to variance with large sample sizes.
d.method	Method to optimize d. "fast": (default) weighted mean over the probes, weighted by probe variances The solution converges to this with large sample size. "basic": optimization scheme to find a mode used in Lahti et al. TCBB/IEEE; relatively slow; this is the preferred method with small sample sizes.
maxloop	Maximum number of iterations in the estimation process.

## Details

Finds point estimates of the model parameters  $d$  (estimated true signal underlying probe-level observations), and  $\tau^2$  (probe-specific variances). Assuming data set  $S$  with  $P$  observations of signal  $d$  with Gaussian noise that is specific for each observation (specified by a vector  $\tau^2$  of length  $P$ ), this method gives a point estimate of  $d$  and  $\tau^2$ . Probe-level variance priors  $\alpha$ ,  $\beta$  can be used with  $\tau^2$ .methods 'robust', 'mode', and 'mean'. The  $d$ .method = "fast" is the recommended method for point computing point estimates with large samples size.

## Value

A list with the following elements:  $d$ : A vector. Estimated 'true' signal underlying the noisy probe-level observations.;  $\tau^2$ : A vector. Estimated variances for each measurement (or probe).

## Author(s)

Leo Lahti <leo.lahti@iki.fi>

## References

See citation("RPA")

## Examples

```
#
```

---

rpa.online

*rpa.online*

---

## Description

RPA-online for preprocessing very large expression data sets.

## Usage

```
rpa.online(  
  cel.path = NULL,  
  cel.files = NULL,  
  sets = NULL,  
  cdf = NULL,  
  bg.method = "rma",  
  probe.parameters = list(alpha = 1, beta = 1),  
  epsilon = 0.01,  
  mc.cores = 1,  
  verbose = TRUE,  
  shuffle = TRUE,  
  batch.size = 100,  
  batches = NULL,  
  save.batches.dir = ".",  
  keep.batch.files = FALSE,  
  unique.run.identifier = paste("RPA-run-id-", rnorm(1), sep = ""),  
  rseed = 23,
```

```

    speedup = TRUE,
    summarize.with.affinities = FALSE
  )

```

### Arguments

<code>cel.path</code>	Path to CEL file directory
<code>cel.files</code>	List of CEL files to preprocess
<code>sets</code>	Probesets for which RPA will be computed
<code>cdf</code>	Specify an alternative CDF environment
<code>bg.method</code>	Specify background correction method. See <code>bgcorrect.methods()</code> for options.
<code>probe.parameters</code>	Can be used to set user-specified priors for the model parameters alpha, beta. Not used <code>tau2.method = "var"</code> . The prior parameters alpha and beta are prior parameters for inverse Gamma distribution of probe-specific variances. Noninformative prior is obtained with alpha, beta $\rightarrow 0$ . Not used with <code>tau2.method 'var'</code> . Scalar alpha and beta specify an identical inverse Gamma prior for all probes, which regularizes the solution. Can be also specified as lists, each element corresponding to one probeset. May also include <code>quantile.basis</code> , which should be provided at log2 domain.
<code>epsilon</code>	Convergence tolerance. The iteration is deemed converged when the change in all parameters is $< \epsilon$ .
<code>mc.cores</code>	Number of cores for parallel computation
<code>verbose</code>	Print progress information during computation
<code>shuffle</code>	Form random batches
<code>batch.size</code>	Batch size for online mode ( <code>rpa.online</code> ); the complete list of CEL files will be preprocessed in batches with this size using Bayesian online-updates for probe-specific parameters.
<code>batches</code>	User-defined CEL file batches
<code>save.batches.dir</code>	Output directory for temporary batch saves.
<code>keep.batch.files</code>	Logical. Keep (TRUE) or remove (FALSE) the batch files after preprocessing.
<code>unique.run.identifier</code>	Define identifier for this run for naming the temporary batch files. By default, a random id is generated.
<code>rseed</code>	Random seed.
<code>speedup</code>	Speed up computations with approximations.
<code>summarize.with.affinities</code>	Use affinity estimates in probe summarization step. Default: FALSE.

### Details

`rpa.online` is used to preprocess very large expression data collections based on a Bayesian hyperparameter update procedure. Returns an `expressionSet` object preprocessed with RPA. Gives an estimate of the probeset-level mean parameter  $d$  of the RPA model, and returns these in an `expressionSet` object. The CEL files are handled in batches to obtain Bayesian updates for probe-specific hyperpriors; after sweeping through the database in batches the results are combined. The online mode is useful for preprocessing very large expression data sets where ordinary preprocessing algorithms fail, without compromises in modelling stage.

**Value**

List with two elements: an instance of the 'expressionSet' class and probe parameters. For probe.parameters contents, see the probe.parameters input argument.

**Author(s)**

Leo Lahti <leo.lahti@iki.fi>

**References**

See citation("RPA")

**See Also**

rpa, AffyBatch, ExpressionSet

**Examples**

```
# eset <- rpa.online(CEL.file.path)
```

---

rpa.plot

*rpa.plot*

---

**Description**

Plot RPA results and probe-level data for a specified probeset.

**Usage**

```
rpa.plot(  
  x,  
  set,  
  highlight.probes = NULL,  
  pcol = "darkgrey",  
  mucol = "black",  
  ecol = "red",  
  external.signal = NULL,  
  main = NULL,  
  plots = "all",  
  ...  
)
```

**Arguments**

x	Output from rpa.complete function
set	probeset
highlight.probes	mark probes for highlight
pcol	probe color
mucol	probeset signal color

```

ecol          external signal color
external.signal
              external signal to be plotted on top
main          title
plots        plot type
...          other arguments to be passed

```

### Details

Plots the preprocessed probe-level observations, estimated probeset-level signal, and probe-specific variances. It is also possible to highlight individual probes and external summary measures.

### Value

Used for its side-effects. Returns probes x samples matrix of probe-level data plotted on the image.

### Author(s)

Leo Lahti <leo.lahti@iki.fi>

### References

See citation("RPA")

### Examples

```
#
```

---

RPA.preprocess	<i>RPA preprocessing</i>
----------------	--------------------------

---

### Description

Preprocess AffyBatch object for RPA.

### Usage

```

RPA.preprocess(
  abatch,
  bg.method = "rma",
  normalization.method = "quantiles.robust",
  cdf = NULL,
  cel.files = NULL,
  cel.path = NULL,
  quantile.basis = NULL
)

```

**Arguments**

<code>abatch</code>	An AffyBatch object.
<code>bg.method</code>	Specify background correction method. See <code>bgcorrect.methods(abatch)</code> for options.
<code>normalization.method</code>	Specify normalization method. See <code>normalize.methods(abatch)</code> for options. For memory-efficient online version, use "quantiles.online".
<code>cdf</code>	The CDF environment used in the analysis.
<code>cel.files</code>	List of CEL files to preprocess.
<code>cel.path</code>	Path to CEL file directory.
<code>quantile.basis</code>	Optional. Basis for quantile normalization. NOTE: required in original, not log2 scale!

**Details**

Background correction, quantile normalization and log2-transformation for probe-level raw data in `abatch`. Then probe-level differential expression is computed between the specified 'reference' array (`cind`) and the other arrays. Probe-specific variance estimates are robust against the choice of reference array.

**Value**

`fcmat`: Probes x arrays preprocessed differential expression matrix. `cind`: Specifies which array in `abatch` was selected as a reference in calculating probe-level differential expression. `cdf`: The CDF environment used in the analysis. `set.inds`: Indices for probes in each probeset, corresponding to the rows of `fcmat`.

**Author(s)**

Leo Lahti <leo.lahti@iki.fi>

**References**

See `citation("RPA")`

**Examples**

```
#
```

---

<code>rpa.summarize</code>	<i>rpa.summarize</i>
----------------------------	----------------------

---

**Description**

RPA summarization.

**Usage**

```
rpa.summarize(dat, affinities, variances, summarize.with.affinities = FALSE)
```

**Arguments**

`dat` Original data: probes x samples.  
`affinities` Probe affinities  
`variances` Probe variances  
`summarize.with.affinities` Use affinity estimates in probe summarization step. Default: FALSE.

**Details**

Summarizes the probes in a probe set according to the RPA model based on the given affinity and variance parameters.

**Value**

A vector. Probeset-level summary signal.

**Author(s)**

Leo Lahti <leo.lahti@iki.fi>

**References**

See citation("RPA")

**See Also**

`rpa`

**Examples**

```
# res <- rpa.summarize(dat, affinities, variances, summarize.with.affinities = FALSE)
```

---

`rpaplot` *rpaplot Plot RPA results and probe-level data for a specified probeset.*

---

**Description**

`rpaplot` Plot RPA results and probe-level data for a specified probeset.

**Usage**

```
rpaplot(  
  dat,  
  mu = NULL,  
  tau2 = NULL,  
  affinity = NULL,  
  highlight.probes = NULL,  
  pcol = "darkgrey",  
  mucol = "black",  
  ecol = "red",  
  cex.lab = 1.5,
```

```

    cex.axis = 1,
    cex.main = 1,
    cex.names = 1,
    external.signal = NULL,
    main = "",
    plots = "all",
    ...
)

```

### Arguments

<code>dat</code>	Background-corrected and normalized data: probes x samples.
<code>mu</code>	probeset signal
<code>tau2</code>	probe variances
<code>affinity</code>	probe affinities
<code>highlight.probes</code>	Optionally highlight some of the probes (with dashed line)
<code>pcol</code>	Color for probe signal visualization.
<code>mucol</code>	Color for summary estimate.
<code>ecol</code>	Color for external signal.
<code>cex.lab</code>	Label size adjustment parameters.
<code>cex.axis</code>	Axis size adjustment parameters.
<code>cex.main</code>	Title size adjustment parameters.
<code>cex.names</code>	Names size adjustment parameters.
<code>external.signal</code>	Plot external signal on the probeset. For instance, an alternative summary estimate from another preprocessing methods
<code>main</code>	Title text.
<code>plots</code>	"all": plot data and summary, noise and affinity; "data": plot data and summary
<code>...</code>	Other parameters to pass for plot function.

### Details

Plots the preprocessed probe-level observations, estimated probeset-level signal, and probe-specific variances. It is also possible to highlight individual probes and external summary measures.

### Value

Used for its side-effects. Returns probes x samples matrix of probe-level data plotted on the image.

### Author(s)

Leo Lahti <leo.lahti@iki.fi>

### References

See citation("RPA")

### Examples

```
#
```



---

sample.probeset	<i>sample.probeset</i>
-----------------	------------------------

---

## Description

Toydata generator for probeset data.

## Usage

```
sample.probeset(P = 10, n = 20, shape = 1, scale = 1, mu.real = 2)
```

## Arguments

P	Number of probes.
n	Number of samples.
shape	Shape parameter of the inverse Gamma function used to generate the probe-specific variances.
scale	Scale parameters of the inverse Gamma function used to generate the probe-specific variances.
mu.real	Absolute signal level of the probeset.

## Details

Generate random probeset with varying probe-specific affinities and variances. The toy data generator follows distributional assumptions of the RPA model and allows quantitative estimation of model accuracy with different options, noise levels and sample sizes. Probeset-level summary estimate is obtained as  $\mu.\text{real} + d$ .

## Value

A list with the following elements:

dat	Probeset data: probes x samples
tau2	Probe variances.
affinity	Probe affinities.
d	Probeset signal shape.
mu.real	Probeset signal level.
mu	Probeset-level total signal.

## Author(s)

Leo Lahti <leo.lahti@iki.fi>

## References

See citation("RPA")

## Examples

```
# real <- sample.probeset(P = 10, n = 20, shape = 1, scale = 1, mu.real = 2)
```

summarize.batch      *summarize.batch*

---

## Description

Summarize batch.

## Usage

```
summarize.batch(  
  q,  
  set.inds,  
  probe.parameters = list(),  
  epsilon,  
  verbose = FALSE,  
  mc.cores = 1,  
  summarize.with.affinities = FALSE  
)
```

## Arguments

q	Background corrected, quantile-normalized, log2 probes x samples matrix
set.inds	Indices for each probeset, corresponding to q matrix
probe.parameters	A list, each element corresponding to a probe set. Each probeset element has the following elements: affinity, variance and optionally alpha and beta priors. Each of these elements contains a vector over the probeset probes, specifying the probe parameters according to the RPA model. If variances are given, that overrides the priors.
epsilon	Convergence tolerance. The iteration is deemed converged when the change in all parameters is < epsilon.
verbose	Print progress information during computation.
mc.cores	Number of cores for parallel processing
summarize.with.affinities	Use affinity estimates in probe summarization step. Default: FALSE.

## Author(s)

Leo Lahti <leo.lahti@iki.fi>

## References

See citation("RPA")

## Examples

#

---

summarize.batches      *summarize.batches*


---

## Description

Summarize batches.

## Usage

```
summarize.batches(
  sets = NULL,
  probe.parameters = list(),
  batches,
  load.batches = FALSE,
  mc.cores = 1,
  cdf = NULL,
  bg.method = "rma",
  normalization.method = "quantiles",
  verbose = TRUE,
  save.batches.dir = ".",
  unique.run.identifier = NULL,
  save.batches = FALSE,
  set.inds,
  speedup = FALSE,
  summarize.with.affinities = FALSE
)
```

## Arguments

sets	Probesets to summarize
probe.parameters	Optional probe parameters, including priors.
batches	Data batches for online learning
load.batches	Logical. Load precalculated data for the batches.
mc.cores	Number of cores for parallel computation
cdf	CDF for alternative probeset definitions
bg.method	Background correction method
normalization.method	Normalization method
verbose	Print progress information
save.batches.dir	Specify the output directory for temporary batch saves.
unique.run.identifier	Define identifier for this run for naming the temporary batch files. By default, a random id is generated.
save.batches	Save batches?
set.inds	Probeset indices
speedup	Speed up calculations with approximations.
summarize.with.affinities	Use affinity estimates in probe summarization step. Default: FALSE.

**Details**

Sweeps through the batches. Summarizes the probesets within each batch based on the precalculated model parameter point estimates.

**Value**

Expression matrix: probesets x samples.

**Author(s)**

Leo Lahti <leo.lahti@iki.fi>

**References**

See citation("RPA")

**Examples**

```
#
```

---

summarize.rpa	<i>RPA summarization</i>
---------------	--------------------------

---

**Description**

Probeset summarization with RPA for taxonomic data.

**Usage**

```
summarize.rpa(
  taxonomy,
  level,
  probedata,
  verbose = TRUE,
  probe.parameters = NULL
)
```

**Arguments**

taxonomy	oligo - phylotype matching data.frame
level	taxonomic level for the summarization.
probedata	preprocessed probes x samples data matrix in absolute domain
verbose	print intermediate messages
probe.parameters	Optional. If probe.parameters are given, the summarization is based on these and model parameters are not estimated. A list. One element for each probeset with the following probe vectors: affinities, variances

**Value**

List with two elements: abundance.table (summarized data matrix in absolute scale) and probe.parameters (RPA probe level parameter estimates)

**Author(s)**

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

**References**

See citation("microbiome")

---

summarize.sum

*Sum-based probe summarization*

---

**Description**

Probeset summarization with the standard sum method.

**Usage**

```
summarize.sum(  
  taxonomy,  
  level,  
  probedata,  
  verbose = TRUE,  
  downweight.ambiguous.probes = TRUE  
)
```

**Arguments**

taxonomy	oligo - phylotype matching data.frame
level	taxonomic level for the summarization.
probedata	preprocessed probes x samples data matrix in absolute domain
verbose	print intermediate messages
downweight.ambiguous.probes	Downweight probes with multiple targets

**Value**

List with two elements: abundance.table (summarized data matrix in absolute scale) and probe.parameters used in the calculations

**Author(s)**

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

**References**

See citation("microbiome")

---

summarize\_probedata     *Summarize probedata*

---

## Description

Summarize phylogenetic microarray probe-level data from given input folder.

## Usage

```
summarize_probedata(  
  data.dir = NULL,  
  probedata = NULL,  
  taxonomy = NULL,  
  level,  
  method,  
  probe.parameters = NULL  
)
```

## Arguments

data.dir	Data folder.
probedata	probe-level data matrix in absolute domain
taxonomy	probe taxonomy
level	Summarization level
method	Summarization method
probe.parameters	Precalculater probe parameters. Optional.

## Value

data matrix (taxa x samples)

## Author(s)

Contact: Leo Lahti <microbiome-admin@googlegroups.com>

## References

See citation('microbiome')

## Examples

```
## Not run:  
#library(microbiome)  
#data.directory <- system.file("extdata", package = "microbiome")  
# Read oligo-level data (here: simulated example data)  
#probedata <- read_hitchip(data.directory, method = "frpa")$probedata  
# Read phylogeny map  
# NOTE: use phylogeny.filtered for species/L1/L2 summarization  
# Load taxonomy from output directory  
#taxonomy <- GetPhylogeny("HITChip", "filtered")
```

```
# Summarize oligos into higher level phylotypes
#dat <- summarize_probedata(
#      probedata = probedata,
#      taxonomy = taxonomy,
#      method = "rpa",
#      level = "species")
#
## End(Not run)
```

---

updating.hyperparameters

*updating hyperparameters*

---

## Description

Hyperparameter update.

## Usage

```
updating.hyperparameters(
  q,
  set.inds,
  verbose,
  mc.cores = 1,
  alpha,
  betas,
  epsilon
)
```

## Arguments

q	probes x samples matrix
set.inds	Probe set indices
verbose	Print progress information
mc.cores	Number of cores for parallel computation
alpha	alpha hyperparameter
betas	beta hyperparameters
epsilon	Convergence parameter

## Value

List with the following elements: alpha, betas, s2s (variances)

## Author(s)

Leo Lahti <leo.lahti@iki.fi>

## References

See citation("RPA")

**Examples**

#



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