

# Package ‘RNAdecay’

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**Title** Maximum Likelihood Decay Modeling of RNA Degradation Data

**Version** 1.27.0

**Description** RNA degradation is monitored through measurement of RNA abundance after inhibiting RNA synthesis. This package has functions and example scripts to facilitate (1) data normalization, (2) data modeling using constant decay rate or time-dependent decay rate models, (3) the evaluation of treatment or genotype effects, and (4) plotting of the data and models. Data Normalization: functions and scripts make easy the normalization to the initial (T0) RNA abundance, as well as a method to correct for artificial inflation of Reads per Million (RPM) abundance in global assessments as the total size of the RNA pool decreases. Modeling: Normalized data is then modeled using maximum likelihood to fit parameters. For making treatment or genotype comparisons (up to four), the modeling step models all possible treatment effects on each gene by repeating the modeling with constraints on the model parameters (i.e., the decay rate of treatments A and B are modeled once with them being equal and again allowing them to both vary independently). Model Selection: The AICc value is calculated for each model, and the model with the lowest AICc is chosen. Modeling results of selected models are then compiled into a single data frame. Graphical Plotting: functions are provided to easily visualize decay data model, or half-life distributions using ggplot2 package functions.

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**Author** Reed Sorenson [aut, cre],  
 Katrina Johnson [aut],  
 Frederick Adler [aut],  
 Leslie Sieburth [aut]

**Maintainer** Reed Sorenson <reedssorenson@gmail.com>

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aic

*Akaike information criterion (with correction)*

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### Description

Calculates AIC or AICc.

**Usage**

```
aic(maxLLik, p)
```

```
aicc(maxLLik, p, n)
```

**Arguments**

maxLLik	maximum log likelihood value identified upon model convergence
p	number of parameters in the model
n	is the total number of observations of a single gene (e.g., 8 time points X 4 replicates X 4 treatments/genotypes = 128)

**Value**

returns the AIC or AICc values

**Examples**

```
aicc(100,5,15)
```

---

a_high	<i>calculates bounds for modeled parameters</i>
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**Description**

Calculates maximum and minimum bounds for parameter alpha based on experimental time points ( $t_0, t_1, t_2, t_3, \dots, t_{\max}$ ). If RNA level is too low at  $t_1$ , then the decay has happened before our observations began - there is an upper bound to the decay rate we can detect (*a\_high*). If RNA level is too high at  $t_{\max}$ , then relatively little decay has happened and we can not distinguish the decay rate and the decay of the decay rate - there is a lower bound to the base decay rate of the decaying decay model (*a\_low*).

**Usage**

```
a_high(t_min)
```

```
a_low(t_max)
```

```
b_low(t_max)
```

**Arguments**

t_min	time of first experiental time point after inhibition of transcription (not T0)
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t_max	time of last experimental time point
-------	--------------------------------------

**Details**

Similarly, limits on beta are required to prevent precude ranges in which the decay rate and decaing decay are indistinguishable. See vignette "RNAdecay\_workflow" for more information.

**Value**

returns the lowest/highest parameter values to be used as bounds on modeled parameters

**Examples**

```
a_high(7.5)
a_low(480)
b_low(480)
```

---

cols	<i>Indexes column names of a data.frame matching multiple patterns (i.e., multigrep)</i>
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---

**Description**

Identifies dataframe column names that have all of the pattern arguments .

**Usage**

```
cols(patterns, df, w = NA, x = NA, y = NA, z = NA)
```

**Arguments**

patterns	character vector or vector of regular expressions passed to grep pattern argument
df	a dataframe with column names to index
w, x, y, z	(for backwards compatibility) separate arguments for patterns, if used patterns argument will be ignored

**Details**

Be aware that column data labels that are part of another data label are not advisable (e.g. mut1, mut2, mut1.mut2; cols(df,'mut1') will return indices for both 'mut1' and 'mut1.mut2' labeled columns

**Value**

returns a vector of integer indices of the column names of df that match to all of patterns

**Examples**

```
cols(df=data.frame(xyz=1:5,zay=6:10,ybz=11:15,tuv=16:20),patterns = c('y', 'z')) ## returns 1 2 3
cols(df=data.frame(xyz=1:5,zay=6:10,ybz=11:15,tuv=16:20), w = 'y', x = 'z') ## returns 1 2 3
```

---

comb_cv	<i>combined adjusted coefficient of variation</i>
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**Description**

Calculates the sum of the column standard deviation divided by the sum of the column mean and a small value to avoid dividing by 0 (eps)

**Usage**

```
comb_cv(X, eps = 1e-04)
```

**Arguments**

X	data.frame or matrix of numeric data
eps	small value to add to the mean to avoid dividing by 0; defaults to 1e-4

**Value**

returns the sum of the coefficients of variation for all columns of X

**Examples**

```
comb_cv( data.frame( test1=rep(0,5), test2=c(0.2,0.3,0.35,0.27,0.21) ) )
```

---

constraint_fun_list_maker	<i>constraint function list maker</i>
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**Description**

Individual double exponential models are all nested within model number 1 in which alpha and beta parameters vary independently for each treatment. Models that assume no difference in parameters between specific treatments manifest as constraints in the modeling. These constraints are coded as functions that are passed to the optimization process. Each model has a distinct constraint function.

**Usage**

```
constraint_fun_list_maker(mods, groups)
```

**Arguments**

mods	data.frame specifying alpha and beta group pairs for each model
groups	grouping matrix for alphas or betas

**Value**

Returns a list of constraint functions to be passed to the optimization function.

**Examples**

```
constraint_fun_list_maker(mods = data.frame(a = c(1,1,1,2,2,2), b = c(1,2,3,1,2,3),
  row.names = paste0('mod',1:6)),
  groups = data.frame(treat1 = c(1,1,NA), treat2 = c(2,1,NA)))
```

---

const_decay	<i>exponential decay functions</i>
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---

**Description**

Constant decay rate function (const\_decay(), case when betas=0)  $e^{-a*t}$ ; decaying decay rate function (decaying\_decay())  $e^{-(a/b)*(1-e^{-b*t})}$ . Functions are normalized so at  $t=0$  the function is 1.

**Usage**

```
const_decay(t, a)
decaying_decay(t, par)
```

**Arguments**

t	time (in minutes)
a	alpha (in per time, thus in per minute when time is in minutes)
par	vector of length 2 containing alpha (par[1]) and beta (par[2]) values; alpha=initial decay rate, beta=decay of decay rate (both in per time, thus in per minute when time is in minutes)

**Value**

returns abundance after time  $t$  at alpha initial decay rate and beta decay of decay rate relative to an initial abundance of 1

**Examples**

```
const_decay(10, log(2)/10) ## returns 0.5
decaying_decay(10, c(log(2)/10, 0.01)) ##returns 0.5170495
```

---

decay_data	<i>Normalized RNA abundance RNA decay timecourse</i>
------------	--

---

### Description

A long form dataset of RNA abundance of 118 genes in four Arabidopsis thaliana genotypes (WT, sov, vcs, vcs sov). Four biological replicates were collected 0, 7.5, 15, 30, 60, 120, 240, 480 min after blocking transcription. RNA was extracted, subjected to ribodepletion, and sequenced by RNA-seq (Illumina 50 nt single end reads). RPM values were normalized to mean T0 abundance and corrected by a decay factor.

### Usage

```
decay_data
```

### Format

a data frame with 5 columns and 15104 rows.

**geneID** gene identifier; AGI

**treatment** Arabidopsis genotype

**t.decay** time of decay, in minutes

**rep** replicate number

**value** RPM value normalized to the replicate samples' mean T0 abundance and decay factor corrected

### Source

Sorenson et al. (2017) Submitted; <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE86361>

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decay_plot	<i>decay_plot() function</i>
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### Description

Plots RNA decay data and/or decay models using the ggplot2 package.

**Usage**

```
decay_plot(
  geneID,
  xlim = c(0, 500),
  ylim = c(0, 1.25),
  xticks = NA,
  yticks = 0:5/4,
  alphaSZ = 8,
  what = c("Desc", "models", "reps", "meanSE", "alphas&betas"),
  DATA,
  treatments = NA,
  colors = NA,
  mod.results = NA,
  gdesc = NA,
  desc.width = 55
)
```

**Arguments**

geneID	single gene ID from data set (e.g. "AT1G00100") for which to plot data/model
xlim, ylim	vector of length 2 defining the limits of the plot (zooms in on data)
xticks, yticks	vectors specifying tick marks for the x and y axes
alphaSZ	text size of alpha and beta parameter labels if plotted
what	character vector specifying what to plot; any or all (default) of "Desc", "models", "reps", "meanSE", "alphas&betas" "Desc" - plots gene descriptions behind data "models" - plots the selected fit model "reps" - plots individual replicate data as distinct shapes "meanSE" - plots the replicate means and standard errors "alphas&betas" - plots the values of the alphas and betas for each model below the model at the greatest x position
DATA	(required) normalized abundance decay data with column names: "geneID", "treatment", "t.decay", "rep", "value"
treatments	what treatments/genotypes to plot from the supplied data
colors	vector of R recognized colors (e.g. "red", "darkblue")
mod.results	(optional; required for plotting models) data.frame of the model results as output from the modeling (e.g. "alphas+betas+mods+grps+patterns+relABs.txt")
gdesc	(optional; required for plotting gene descriptions) gene descriptions (geneID-named vector of gene descriptions geneID must match those of data)
desc.width	width of gene descriptions (in number of characters) before word wrap

**Value**

returns a ggplot to be used with print; could also be modified using the syntax of ggplot2 e.g. '+geom\_XXXX(...)'



**Examples**

```
p<-decay_plot("Gene_BooFu",
  mod.results = data.frame(alpha_WT = 0.0830195, beta_WT = 0.04998945,
    model = 1, alpha_grp = 1, beta_grp = 1, alpha_subgroup = 1.1,
    row.names = "Gene_BooFu"),
  what = c("meanSE", "alphas&betas", "models"),
  treatments = "WT",
  colors = "black",
  DATA = data.frame(geneID=rep("Gene_BooFu",15),
    treatment=rep("WT",15),
    t.decay=rep(c(0,7.5,15,30,60),3),
    rep=paste0("rep",c(rep(1,5),rep(2,5),rep(3,5))),
    value= c(0.9173587, 0.4798672, 0.3327807, 0.1990708, 0.1656554,
      0.9407511, 0.7062988, 0.3450886, 0.3176824, 0.2749946,
      1.1026497, 0.6156978, 0.4563346, 0.2865779, 0.1680075)),
  xlim = c(0, 65),
  alphaSZ = 10)
print(p)
```

---

fit\_var

*sigma<sup>2</sup> estimation*


---

**Description**

Calculates the variance ( $\sigma^2$ ) estimate from the sum of the squared errors from the fit model.

**Usage**

```
fit_var(sse, n)
```

**Arguments**

sse	is the minimum SSE (sum of the squared errors) from the slsqp() fitting
n	is the total number of observations of a single gene (e.g., 8 time points X 4 replicates X 4 treatments/genotypes = 128)

**Value**

returns the sigma squared estimate

**Examples**

```
fit_var(1,128)
```

---

 groupings

*Combinatorial groups matrix generator*


---

### Description

Generates a combinatorial grouping matrix based on the decaydata data.frame.

### Usage

```
groupings(decaydata)
```

### Arguments

decaydata      a data.frame with column names: 'geneID', 'treatment', 't.decay', 'rep', 'value' with classes factor, factor, numeric, factor, numeric

### Details

The resulting matrix of indices is used to constrain treatment alphas or treatment betas in combination. For example, in one model, treatment alphas might be allowed to vary independently (gp1), but the beta models might be constrained to be equal for some treatments indicated by having the same index number (other gp).

### Value

returns a matrix of equivalence group indices based on the number of levels in the 'treatment' column (max of 4).

### Examples

```
groupings(data.frame(geneID=paste0('gene', 1:4), treatment=as.factor(paste0('treat', 1:4)),
  t.decay=0:3, rep=rep('rep1'), value=c(1, 0.5, 0.25, 0.12)))
```

---

 group\_map

*model color map*


---

### Description

group\_map makes a color map of alpha and beta equivalence groups by model. Similar colors in a row indicate constrained parameter equivalence between treatments. Gray indicates values of 0.

### Usage

```
group_map(decaydata, path, nEquivGrp = nEquivGrp, groups = groups, mods = mods)
```

**Arguments**

decaydata	5 column data.frame with colnames "geneID", "treatment", "t.decay", "rep", "value"
path	write path and file name, must end in ".pdf"
nEquivGrp	number of equivalence groups based on number of treatments
groups	equivalence group matrix
mods	alpha beta equivalence group usage index (matrix)

**Value**

creates a model colormap and writes it to a pdf file named path

**Examples**

```
group_map(decaydata=data.frame(geneID=paste0("gene", 1:4),
                              treatment=as.factor(rep(paste0("treat", 1:2), 2)),
                              t.decay=0:3,
                              rep=rep("rep1"),
                              value=c(1,0.5,0.25,0.12)),
          path=paste0(tempdir(), "/parameter equivalence colormap.pdf"),
          nEquivGrp = 2,
          groups = t(matrix(c(1,2,1,1,NA,NA), nrow=2,
                            dimnames=list(c("treat1", "treat2"), c("grp1", "grp2", "grp3")))),
          mods = t(matrix(c(1,1,1,2,1,3,2,1,2,2,2,3), nrow=2,
                          dimnames=list(c("a", "b"), paste0("mod", 1:6)))))
```

hl\_plot

*hl\_plot() function***Description**

Plots RNA half-life distribution with select half-lives of select RNAs as large arrows colored by treatment using the ggplot2 package.

**Usage**

```
hl_plot(
  geneID,
  gene_symbol = "",
  df_decay_rates,
  hl_dist_treatment,
  hl_treatment,
  arrow_colors = NA,
  arrow_lab_loc = c("key"),
  x_limits = log(2)/c(0.25, 0.00045),
  x_breaks = c(5, 1:12 * 10, 180, 240, 300, 360, 420, 480, 720, 1080, 1440),
  x_tick_labels = c("5", "10", "", "30", "", "", "60", "", "", "", "", "", "2h", "",
                    "4h", "", "", "", "8h", "12h", "", "24h")
)
```

**Arguments**

geneID	single gene ID from data set (e.g. "AT3G14100") for which to plot data/model
gene_symbol	(optional) pasted to gene ID in plot label (e.g., "AT3G14100/UBP1C")
df_decay_rates	data.frame of modeling results with decay rate columns labeled as alpha_<treatment>
hl_dist_treatment	name of the treatment for which the background distribution will be plotted
hl_treatment	names of the treatments for which arrows indicating half-life will be plotted
arrow_colors	(optional) character vector of R colors; named with corresponding treatments
arrow_lab_loc	label arrows on plot ("plot") or in a key ("key")
x_limits	x-axis (half-life) limits in min; default is log(2)/c(0.25,4.5e-4)
x_breaks	x-axis (half-life) breaks/tick marks in min defaults to c(5,1:12*10,180,240,300,360,420,480,720,1080,1440)
x_tick_labels	x-axis (half-life) break labels, defaults to c("5", "10", "", "30", "", "", "60", "", "", "", "", "2h", "", "4h", "", "", "", "")

**Value**

returns a ggplot to be used with print; could also be modified using the syntax of ggplot2 e.g. ' +geom\_XXXX(...)'

**Examples**

```
p <- hl_plot(
  geneID = rownames(RNAdecay::results)[4],
  df_decay_rates = RNAdecay::results,
  hl_treatment = c("WT", "sov", "vcs", "vcs.sov"),
  hl_dist_treatment = "WT",
  arrow_colors = c(WT = "#88CCEE", sov = "#CC6677", vcs = "#117733", vcs.sov = "#882255"),
  arrow_lab_loc = "key",
  gene_symbol = ""
)

print(p)

p <- hl_plot(
  geneID = rownames(RNAdecay::results)[4],
  gene_symbol = "",
  df_decay_rates = RNAdecay::results,
  hl_dist_treatment = "WT",
  hl_treatment = c("WT", "sov", "vcs", "vcs.sov"),
  arrow_colors = c(WT = "#88CCEE", sov = "#CC6677", vcs = "#117733", vcs.sov = "#882255"),
  arrow_lab_loc = "plot"
)

print(p)
```

---

log_lik	<i>log likelihood</i>
---------	-----------------------

---

**Description**

Calculates the log likelihood value from the sum of the squared errors, sigma2, and the total number of data points.

**Usage**

```
log_lik(x, y, n)
```

**Arguments**

x	is the minimum SSE from the slsqp() fitting
y	is sigma2 cooresponding to the minimum SSE
n	is the total number of observations of a single gene (e.g., 8 time points X 4 replicates X 4 treatments/genotypes = 128)

**Value**

returns Log Likelihood

**Examples**

```
log_lik(1,1/128,128)
```

---

models	<i>Example double exponential decay modeling results</i>
--------	--

---

**Description**

Example results from maximum likelihood modeling of double exponential RNA decay of 118 genes.

**Usage**

```
models
```

**Format**

a list of data frames, each with 240 rows (1/model) with 22 columns and 240 rows.

**geneID** gene identifier

**mod** model names as factors

**alpha\_XXX** decay rate estimate of genotype XXX, in per time ( $\text{min}^{-1}$ )

**beta\_XXX** decay of decay rate estimate of genotype XXX, in per time ( $\text{min}^{-1}$ )

**sigma2** variance estimate

**logLik** maximum log likelihood

**nPar** number of parameters in the given model

**nStarts** number of parameter starting value sets (of 50) that converged on a maximum likelihood peak

**J** number of parameter starting value sets that converged on the highest - within  $1e-4$  - maximum likelihood of all parameter starting value sets

**range.LL** range of maximum likelihoods values reached by algorithm convergence from all parameter starting value sets

**nUnique.LL** number of unique maximum likelihoods values reached by algorithm convergence from all parameter starting value sets

**C.alpha** sum of all coefficients of variation for each column of alpha estimates

**C.beta** sum of all coefficients of variation for each column of beta estimates

**C.tot** C.alpha+C.beta

**AICc** calculated from the single highest maximum likelihood of all parameter starting value sets

**AICc\_est** calculated from the log likelihood value computed by using the mean of each parameter from all optimizations that converged on the highest maximum likelihood of all starting parameter value sets

**Source**

Sorenson et al. (2017) Submitted; <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE86361>

## Description

The `mod_optimization` function finds the estimates of model parameters by maximum likelihood, for a single gene on a specified list of models, and saves a tab delimited text file of the results named, '[geneID]\_results.txt'. The function does the following for each gene: (1) it calculates log likelihood for each point in a 2 dimensional grid of evenly spaced alpha and beta values within the alpha and beta bounds specified using the null model (in which all treatment alphas are equivalent and all betas are equivalent). (2) it calculates log likelihood for each point in a 1 dimensional range of evenly spaced alpha values within the alpha bounds using the single exponential null model (in which all treatment alphas are equivalent). (3) For each of the grid points with the highest log likelihood from steps (1) and (2) 25 starting parameter value sets that are normally distributed around these points are generated. (4) Parameter values are optimized for maximum likelihood using each of these 50 starting parameter sets using pre-compiled C++ functions loaded from dynamically linked libraries stored in the package on all models specified in the `models` argument. (5) evaluates parameter estimates of all 50 optimizations based on the reported maximum likelihood upon convergence. Only parameter estimates that converged on the same and highest maximum likelihood are returned. (6) returns the optimized parameter estimates, with model selection statistics.

## Usage

```
mod_optimization(
  gene,
  data,
  alpha_bounds,
  beta_bounds,
  models,
  group,
  mod,
  file_only = TRUE,
  path = "modeling_results"
)
```

## Arguments

<code>gene</code>	geneID from data to be modeled
<code>data</code>	decay data data.frame with columns named 'geneID', 'treatment', 't.decay', 'rep', 'value.'
<code>alpha_bounds</code>	vector of length 2 with lower and upper bounds for alpha
<code>beta_bounds</code>	vector of length 2 with lower and upper bounds for beta
<code>models</code>	vector specifying which models to run optimization on (e.g., c('mod1', 'mod239'))
<code>group</code>	grouping matrix for alphas or betas
<code>mod</code>	data.frame specifying alpha and beta group pairs for each model
<code>file_only</code>	logical; should output only be written to file (TRUE) or also return a data.frame of the results (FALSE)
<code>path</code>	specify folder for output to be written

**Value**

returns (if `file_only = FALSE`) and writes to `path` a data frame of model optimization results for models one row for each for gene using values for it found in `data`, the columns of the data frame are: `geneID`, `mod` (model), model estimates [`alpha_treatment1`, ..., `alpha_treatmentn`, `beta_treatment1`, ..., `beta_treatmentn`, `sigma2`], `logLik` (maximum log likelihood), `nPar` (number of parameters in the model), `nStarts` (number of parameter starting value sets (of 50) that converged on a maximum likelihood peak), `J` (number of parameter starting value sets that converged on the highest - within  $1e-4$  - maximum likelihood of all parameter starting value sets), `range.LL` (range of maximum likelihoods values reached by algorithm convergence from all parameter starting value sets), `nUnique.LL` (number of unique maximum likelihoods values reached by algorithm convergence from all parameter starting value sets), `C.alpha` (sum of all coefficients of variation for each column of alpha estimates), `C.beta` (sum of all coefficients of variation for each column of beta estimates), `C.tot` (`C.alpha+C.beta`), `AICc` (calculated from the single highest maximum likelihood of all parameter starting value sets), `AICc_est` (calculated from the log likelihood value computed by using the mean of each parameter from all optimizations that converged on the highest maximum likelihood of all starting parameter value sets.)

**Examples**

```
mod_optimization(gene = 'Gene_BooFu',
  data = data.frame(geneID=rep('Gene_BooFu',30),
    treatment=c(rep('WT',15),rep('mut',15)),
    t.decay=rep(c(0,7.5,15,30,60),6),
    rep=rep(paste0('rep',c(rep(1,5),rep(2,5),rep(3,5))),2),
    value= c(0.9173587, 0.4798672, 0.3327807, 0.1990708, 0.1656554,
      0.9407511, 0.7062988, 0.3450886, 0.3176824, 0.2749946,
      1.1026497, 0.6156978, 0.4563346, 0.2865779, 0.1680075,
      0.8679866, 0.6798788, 0.2683555, 0.5120951, 0.2593122,
      1.1348219, 0.8535835, 0.6423996, 0.5308946, 0.4592902,
      1.1104068, 0.5966838, 0.3949790, 0.3742632, 0.2613560)),
  alpha_bounds = c(1e-4,0.75),
  beta_bounds = c(1e-3,0.075),
  models = 'mod1',
  group = t(matrix(c(1,2,1,1,NA,NA),nrow=2,
    dimnames=list(c('treat1','treat2'),c('mod1','mod2','mod3')))),
  mod = as.data.frame(t(matrix(c(1,1,1,2,1,3,2,1,2,2,2,3),nrow=2,
    dimnames=list(c('a','b'),paste0('mod',1:6))))),
  file_only = FALSE,
  path = paste0(tempdir(),"/modeling results"))
```

---

n\_par

*number of Parameters function*


---

**Description**

Calculates number of parameters for a specified model given the model parameter constraints.



**Usage**

```
n_par(model, mod, group)
```

**Arguments**

model	model name (e.g. 'mod1')
mod	two column data.frame with combination of alpha and beta grouping numbers in each model with rownames 'modX'
group	matrix of all treatment alpha or beta equivalence groups

**Value**

returns the integer value of number of parameters in model

**Examples**

```
n_par('mod1', data.frame('a'=1:5, 'b'=rep(2,5), row.names=paste0('mod', 1:5)),
      t(matrix(c(1,2,3,4,1,2,2,2,1,1,2,2,1,1,1,2,1,2,1,2,1,2,2,1), nrow=4)))
```

---

plain_theme	<i>a custom ggplot2 theme</i>
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---

**Description**

A custom ggplot2 theme generating function for ggplot2 plots; can be further manipulated using standard ggplot2 syntax.

**Usage**

```
plain_theme(bigFont = 30, smFont = 0.85, x.ang = 0, leg.pos = c(0.85, 0.85))
```

**Arguments**

bigFont	larger font size of axis labels in points (used for plot title, axis titles, facet titles)
smFont	fractional multiplier of bigFont (used for axis text)
x.ang	x-axis label angle
leg.pos	legend position on plot as relative coordinates c(x,y) (i.e., range is [0,1]) or 'right', 'left', 'above', 'below'

**Value**

returns a ggplot2 theme of class "theme" "gg"

**Examples**

```
plain_theme(10)
```

---

results

*Example double exponential decay modeling results*

---

### Description

Example results from maximum likelihood modeling of double exponential RNA decay of 118 genes. Results include parameter estimates, selected model, and alpha and beta groupings.

### Usage

results

### Format

a data frame with 18 columns and 118 rows.

**alpha\_XXX** decay rate estimate of genotype XXX, in per time ( $\text{min}^{-1}$ )

**beta\_XXX** decay of decay rate estimate of genotype XXX, in per time ( $\text{min}^{-1}$ )

**sigma2** variance estimate

**model** selected model number

**alpha\_grp** model alpha grouping number

**beta\_grp** model beta grouping number

**alpha\_subgroup** model alpha subgroup number

**alphaPattern** model alpha subgroup pattern; i.e. order of genotypes of increasing decay rate

**betaPattern** model beta subgroup pattern; i.e. order of genotypes of increasing decay of decay rate

**rA\_XXX** relative alpha value of genotype XXX compared to WT

**nEqMods** number of models that were not different than the selected model based on a AICc difference  $< 2$

**nEqAgp** number of alpha groups represented in nEqMods

### Source

Sorenson et al. (2017) Submitted; <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE86361>

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RPMs

*RNA abundance reads per million over RNA decay timecourse*

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### Description

A dataset of RNA abundance of 118 genes in four *Arabidopsis thaliana* genotypes (WT, sov, vcs, vcs sov). Four biological replicates were collected 0, 7.5, 15, 30, 60, 120, 240, 480 min after blocking transcription. RNA was extracted, subjected to ribodepletion, and sequenced by RNA-seq (Illumina 50 nt single end reads).

### Usage

RPMs

### Format

a data frame with 118 rows and 128 columns; data are all RNA abundance values presented as reads per million. Column names indicate genotype, time point, and replicate number separated by underscores.

### Source

Sorenson et al. (2017) Submitted; <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE86361>

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sse\_null\_decaying\_decay

*sum of the squared errors for null models*

---

### Description

For a model that uses a constant decay rate or a decaying decay rate, calculates the sum of the squared errors (differences between the supplied data points and the modeled values based on alpha and/or beta values). For these models all treatments are assumed to have the same a (alpha) and/or b (beta).

### Usage

sse\_null\_decaying\_decay(a, b, m, t)

sse\_null\_const\_decay(a, m, t)

**Arguments**

a	alpha value
b	beta value
m	mRNA abundance values
t	time points of m

**Value**

Returns the sum of the squared errors

**Examples**

```
sse_null_decaying_decay(a=0.05, b = 0.001,  
  m = c(1,1,1,0.99,0.5,0.5,0.5,0.49,0.25,0.25,0.25,0.24,0.12,0.125,0.125,0.126),  
  t = rep(c(0,10,20,30),each = 4))  
sse_null_const_decay(a=0.05,  
  m = c(1,1,1,0.99,0.5,0.5,0.5,0.49,0.25,0.25,0.25,0.24,0.12,0.125,0.125,0.126),  
  t = rep(c(0,10,20,30),each = 4))
```

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