

# Package ‘phenopath’

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**Type** Package

**Title** Genomic trajectories with heterogeneous genetic and environmental backgrounds

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**Description** PhenoPath infers genomic trajectories (pseudotimes) in the presence of heterogeneous genetic and environmental backgrounds and tests for interactions between them.

**License** Apache License (== 2.0)

**Imports** Rcpp (>= 0.12.8), SummarizedExperiment, methods, stats, dplyr, tibble, ggplot2, tidyr

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**biocViews** ImmunoOncology, RNASeq, GeneExpression, Bayesian, SingleCell, PrincipalComponent

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|      |                         |
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| clvm | <i>Fit a CLVM Model</i> |
|------|-------------------------|

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## Description

Fit a covariate latent variable model using coordinate ascent variational inference.

## Usage

```
clvm(y, x, maxiter = 10000, elbo_tol = 1e-05, thin = 1, verbose = TRUE,
     z_init = 1, tau_q = 1, tau_mu = 1, tau_c = 1, a = 2, b = 2,
     tau_alpha = 1, a_beta = 10, b_beta = 1, q = rep(0, nrow(y)),
     model_mu = FALSE, scale_y = TRUE)
```

## Arguments

|           |  |
|-----------|--|
| y         | A N-by-G (dynamic) input matrix  |
| x         | A N-by-P (static) input matrix   |
| maxiter   | Maximum number of CAVI iterations  |
| elbo_tol  | The (percent) change in the ELBO below which it is considered converged  |
| thin      | The number of iterations to wait each time before re-calculating the elbo  |
| verbose   | Print convergence messages   |
| z_init    | The initialisation of the latent trajectory. Should be one of <ol style="list-style-type: none"> <li>1. A positive integer describing which principal component of the data should be used for initialisation (default 1), <i>or</i></li> <li>2. A numeric vector of length number of samples to be used directly for initialisation, <i>or</i></li> <li>3. The text character "random", for random initialisation from a standard normal distribution.</li> </ol> |
| tau_q     | Hyperparameter tau_q   |
| tau_mu    | Hyperparameter tau_mu  |
| tau_c     | Hyperparameter tau_c   |
| a         | Hyperparameter a   |
| b         | Hyperparameter b   |
| tau_alpha | Hyperparameter tau_alpha   |
| a_beta    | Hyperparameter a_beta  |
| b_beta    | Hyperparameter b_beta  |
| q         | Priors on the latent variables   |
| model_mu  | Logical - should a gene-specific intercept term be modelled?   |
| scale_y   | Logical - should the expression matrix be centre scaled?   |

**Value**

A list whose entries correspond to the converged values of the variational parameters along with the ELBO.

**Examples**

```
sim <- simulate_phenopath()
fit <- clvm(sim$y, matrix(sim$x))
```

---

|              |                                     |
|--------------|-------------------------------------|
| interactions | <i>Tidy summary of interactions</i> |
|--------------|-------------------------------------|

---

**Description**

Computes a tidy data frame of the interaction effects, pathway scores, and significance for each gene and covariate interaction.

**Usage**

```
interactions(phenopath_fit, n = 3)
```

**Arguments**

`phenopath_fit` An object returned by a call to `phenopath`

`n` The number of standard deviations away from 0 the posterior of the interaction effect sizes should be to be designated as significant

**Value**

A data frame with the following columns:

- `feature` The feature (usually gene)
- `covariate` The covariate, specified from the order originally supplied to the call to `phenopath`
- `interaction_effect_size` The effect size of the interaction (*beta* from the statistical model)
- `significant` Boolean for whether the interaction effect is significantly different from 0
- `chi` The precision of the ARD prior on *beta*
- `pathway_loading` The pathway loading *lambda*, showing the overall effect for each gene marginalised over the covariate

**Examples**

```
sim <- simulate_phenopath()
fit <- phenopath(sim$y, sim$x, elbo_tol = 1e-2)
interactions(fit)
```

interaction\_effects     *Get the interaction effect sizes*

---

**Description**

Get the interaction effect sizes

**Usage**

```
interaction_effects(phenopath_fit)
```

**Arguments**

phenopath\_fit     An object of class phenopath\_fit

**Value**

TODO

**Examples**

```
sim <- simulate_phenopath()
fit <- phenopath(sim$y, sim$x, elbo_tol = 1e-2)
beta <- interaction_effects(fit)
```

---

interaction\_sds     *Get the interaction standard deviations*

---

**Description**

Get the interaction standard deviations

**Usage**

```
interaction_sds(phenopath_fit)
```

**Arguments**

phenopath\_fit     An object of class phenopath\_fit

**Value**

TODO

**Examples**

```
sim <- simulate_phenopath()
fit <- phenopath(sim$y, sim$x, elbo_tol = 1e-2)
beta_sd <- interaction_sds(fit)
```

phenopath

*PhenoPath - genomic trajectories with heterogeneous backgrounds***Description**

PhenoPath learns genomic trajectories in the presence of heterogeneous environmental and genetic backgrounds. It takes input gene expression measurements that are modelled by a single unobserved factor (the "trajectory"). The regulation of genes along the trajectory is perturbed by an additional set of covariates (such as genetic or environmental status) allowing for the identification of covariate-trajectory interactions. The model is fitted using mean-field co-ordinate ascent variational inference.

**Usage**

```
phenopath(exprs_obj, x, sce_assay = "exprs", elbo_tol = 1e-05, z_init = 1,
          ...)
```

**Arguments**

|           |  |
|-----------|--|
| exprs_obj | Input gene expression, either <ol style="list-style-type: none"> <li>1. An <a href="#">SummarizedExperiment</a> object, <i>or</i></li> <li>2. A cell-by-gene matrix of normalised expression values in log form.</li> </ol>  |
| x         | The covariate vector, either <ol style="list-style-type: none"> <li>1. The name of a column of <code>colData(exprs_obj)</code> if <code>exprs_obj</code> is an <code>SummarizedExperiment</code>, <i>or</i></li> <li>2. A numeric or factor vector of length equal to the number of cells, <i>or</i></li> <li>3. A formula from which to build a model matrix from <code>colData(exprs_obj)</code>, if <code>exprs_obj</code> is a <a href="#">SummarizedExperiment</a></li> </ol> |
| sce_assay | The assay from <code>exprs_obj</code> to use as expression if <code>exprs_obj</code> is a <code>SummarizedExperiment</code>  |
| elbo_tol  | The relative pct change in the ELBO below which is considered converged. See convergence section in details below.   |
| z_init    | The initialisation of the latent trajectory. Should be one of <ol style="list-style-type: none"> <li>1. A positive integer describing which principal component of the data should be used for initialisation (default 1), <i>or</i></li> <li>2. A numeric vector of length number of samples to be used directly for initialisation, <i>or</i></li> <li>3. The text character "random", for random initialisation from a standard normal distribution.</li> </ol>                 |
| ...       | Additional arguments to be passed to <code>clvm</code> . See description below for more details or call <code>?clvm</code> .   |

**Details****Input expression**

If an `SummarizedExperiment` is provided, `assay(exprs_obj, sce_assay)` is used. This is assumed to be in a form that is suitably normalised and approximately normal, such as the log of TPM values (plus a suitable offset) or similar.

**Encoding covariates**

See the vignette.

**Convergence of variational inference**

It is strongly recommended to call `plot_elbo(phenopath_fit)` after the fitting procedure to ensure the ELBO has approximately converged (though convergence metrics are printed during the fitting process). For a good introduction to variational inference see Blei, D.M., Kucukelbir, A. & McAuliffe, J.D., 2017. Variational Inference: A Review for Statisticians. Journal of the American Statistical Association.

**Additional arguments**

Additional arguments to `clvm` are passed via `...`. For full documentation, call `?clvm`. Some notable options:

- `thin` - The ELBO is expensive to compute for larger datasets. The model will compute the ELBO and compare convergence every `thin` iterations.
- `q` and `tau_q` - Priors (such as capture times) for the latent space. Note that `model_mu` should be true if `q` is non-zero.
- `scale_y` By default the input expression is centre-scaled for each gene. If `scale_y` is FALSE this does not happen - but note that `model_mu` should be TRUE in such a case.

**Value**

An S3 structure with the following entries:

- `m_z` The converged mean estimates of the trajectory
- `s_z` The converged standard deviation estimates of `z`
- `m_beta` A P-by-G matrix of interaction coefficients
- `s_beta` A P-by-G matrix of interaction standard deviations

**See Also**

[clvm](#) for the underlying CAVI function, [trajectory](#) to extract the latent trajectory, [interaction\\_effects](#) for the interaction effect sizes, [significant\\_interactions](#) for the results of Bayesian significance testing.

**Examples**

```
sim <- simulate_phenopath() # returns a list with gene expression in y and covariates in x
fit <- phenopath(sim$y, sim$x, elbo_tol = 1e-2)

# Extract the trajectory
z <- trajectory(fit)
```

---

|           |                       |
|-----------|-----------------------|
| plot_elbo | <i>Plots the ELBO</i> |
|-----------|-----------------------|

---

**Description**

Plots the evidence lower bound (ELBO) as a function of iterations

**Usage**

```
plot_elbo(fit)
```

**Arguments**

fit                    An object returned by a call to phenopath

**Value**

A ggplot2 object of the ELBO against the number of iterations

**Examples**

```
sim <- simulate_phenopath()
fit <- phenopath(sim$y, sim$x)
plot_elbo(fit)
```

---

|                     |                              |
|---------------------|------------------------------|
| print.phenopath_fit | <i>Print a PhenoPath fit</i> |
|---------------------|------------------------------|

---

**Description**

Print a PhenoPath fit

**Usage**

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

**Arguments**

x                    A phenopath\_fit returned by a call to phenopath  
...                    Additional arguments

**Value**

A string representation of a phenopath\_fit object.

**Examples**

```
sim <- simulate_phenopath()
fit <- phenopath(sim$y, sim$x, elbo_tol = 1e-2)
print(fit)
```

---

significant\_interactions

*Significance testing for interaction features*

---

### Description

Given the results of `clvm`, decide which features show significant interactions between the latent trajectory and covariates. Significant features are designated as those where the variational mean of the interaction coefficient falls outside the  $n\sigma$  interval of 0.

### Usage

```
significant_interactions(phenopath_fit, n = 3)
```

### Arguments

`phenopath_fit` The results of a call to `clvm`

`n` The number of standard deviations away from 0 the posterior estimate of beta should be to be designated significant.

### Value

A logical vector describing whether each feature passes the significance test.

### Examples

```
sim <- simulate_phenopath()
fit <- phenopath(sim$y, sim$x, elbo_tol = 1e-2)
signints <- significant_interactions(fit)
```

---

simulate\_phenopath     *Simulate from phenopath model*

---

### Description

Simulate synthetic data from the phenopath model, where each gene is sampled from one of four types (see details).

### Usage

```
simulate_phenopath(N = 100, G = 40, G_de = NULL, G_pst = NULL,
  G_pst_beta = NULL, G_de_pst_beta = NULL)
```



**Arguments**

|               |  |
|---------------|--|
| N             | Number of samples to simulate  |
| G             | Number of genes to simulate. Should be divisible by 4  |
| G_de          | Number of genes to simulate from the <i>differential expression</i> regime                             |
| G_pst         | Number of genes to simulate from the <i>pseudotime</i> regime  |
| G_pst_beta    | Number of genes to simulate from the <i>pseudotime + beta interactions</i> regime                      |
| G_de_pst_beta | Number of genes to simulate from the <i>differential expression + pseudotime + interactions</i> regime |

**Details**

Will simulate data for a number of genes corresponding to one of four regimes:

1. de ('differential expression'), where the gene has no association to the latent trajectory and exhibits differential expression only
2. pst ('pseudotime'), the gene shows pseudotemporal regulation but no differential regulation
3. pst\_beta ('pseudotime + beta interactions'), the gene shows pseudotemporal regulation that is modulated by covariate interactions
4. de\_pst\_beta ('differential expression + pseudotime + interactions'), all of the above

**Value**

A list with four entries:

- parameters A tibble with an entry for each gene and a column for each parameter value and simulation regime (see details).
- y The N-by-G simulated gene expression matrix.
- x The N-length vector of covariates.
- z The N-length vector of pseudotimes.

**Examples**

```
sim <- simulate_phenopath()
```

---

|            |  |
|------------|--|
| trajectory | <i>Get the latent PhenoPath trajectory</i> |
|------------|--|

---

**Description**

Get the latent PhenoPath trajectory

**Usage**

```
trajectory(phenopath_fit)
```

**Arguments**

phenopath\_fit An object of class phenopath\_fit

**Value**

A vector of latent trajectory (pseudotime) values

**Examples**

```
sim <- simulate_phenopath()
fit <- phenopath(sim$y, sim$x, elbo_tol = 1e-2)
z <- trajectory(fit)
```

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