

# Package ‘VERSO’

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**Title** Viral Evolution ReconStructiOn (VERSO)

**Depends** R (>= 4.1.0)

**Imports** utils, data.tree, ape, parallel, Rfast, stats

**Suggests** BiocGenerics, BiocStyle, testthat, knitr

**Name** VERSO: an R package for the inference of viral evolution models

**Description** Mutations that rapidly accumulate in viral genomes during a pandemic can be used to track the evolution of the virus and, accordingly, unravel the viral infection network.

To this extent, sequencing samples of the virus can be employed to estimate models from genomic epidemiology and may

serve, for instance, to estimate the proportion of undetected infected people by uncovering cryptic transmissions, as

well as to predict likely trends in the number of infected, hospitalized, dead and recovered people.

VERSO is an algorithmic framework that processes variants profiles from viral samples to produce phylogenetic

models of viral evolution. The approach solves a Boolean Matrix Factorization problem with phylogenetic constraints,

by maximizing a log-likelihood function. VERSO includes two separate and subsequent steps; in this package we provide

an R implementation of VERSO STEP 1.

**Encoding** UTF-8

**License** file LICENSE

**URL** <https://github.com/BIMIB-DISCo/VERSO>

**BugReports** <https://github.com/BIMIB-DISCo/VERSO>

**biocViews** BiomedicalInformatics, Sequencing, SomaticMutation

**RoxygenNote** 7.3.2

**VignetteBuilder** knitr

**git\_url** <https://git.bioconductor.org/packages/VERSO>

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inference	<i>Results obtained running VERSO on the provided input dataset.</i>
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### Description

Results obtained running VERSO on the provided input dataset.

### Usage

data(inference)

### Format

results obtained running VERSO on the provided input dataset

### Value

results obtained running VERSO on the provided input dataset

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variants	<i>Mutation data obtained by variant calling from raw data of a selected set of SARS-CoV-2 samples available from NCBI BioProject PRJNA610428.</i>
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### Description

The dataset includes variants for a selected set of 15 SARS-CoV-2 samples obtained by variant calling from raw data available from NCBI BioProject PRJNA610428.

### Usage

data(variants)

**Format**

SARS-CoV-2 variants

**Value**

SARS-CoV-2 variants

**Source**

NCBI BioProject PRJNA610428

VERSO

*VERSO*

**Description**

Perform the inference of the maximum log-likelihood *VERSO* phylogenetic tree.

**Usage**

```
VERSO(
  D,
  alpha = NULL,
  beta = NULL,
  initialization = NULL,
  random_tree = FALSE,
  keep_equivalent = TRUE,
  check_indistinguishable = TRUE,
  marginalize = FALSE,
  num_rs = 10,
  num_iter = 10000,
  n_try_bs = 1000,
  num_processes = Inf,
  verbose = TRUE,
  log_file = ""
)
```

**Arguments**

- D                    Input data for the inference reporting presence (as 1), absence (as 0) or missing information (as NA) for a set of variants.
- alpha                False positive error rate provided as a vector; if a vector of alpha (and beta) is provided, the inference is performed for multiple values and the solution at maximum-likelihood is returned.
- beta                 False negative error rate provided as a vector; if a vector of beta (and alpha) is provided, the inference is performed for multiple values and the solution at maximum-likelihood is returned.
- initialization      Binary matrix representing a perfect phylogeny tree; genotypes are rows and mutations are columns. This parameter overrides "random\_tree".

<code>random_tree</code>	Boolean. Shall I start MCMC search from a random tree? If FALSE (default) and initialization is NULL, search is started from a TRaIT tree (BMC Bioinformatics . 2019 Apr 25;20(1):210. doi: 10.1186/s12859-019-2795-4).
<code>keep_equivalent</code>	Boolean. Shall I return results (B and C) at equivalent likelihood with the best returned solution?
<code>check_indistinguishable</code>	Boolean. Shall I remove any indistinguishable variant from input data prior inference?
<code>marginalize</code>	Boolean. Shall I marginalize C when computing likelihood?
<code>num_rs</code>	Number of restarts during MCMC inference.
<code>num_iter</code>	Maximum number of MCMC steps to be performed during the inference.
<code>n_try_bs</code>	Number of steps without changes in likelihood of best solution after which to stop the MCMC.
<code>num_processes</code>	Number of processes to be used during parallel execution. To execute in single process mode, this parameter needs to be set to either 1, NA or NULL.
<code>verbose</code>	Boolean. Shall I print to screen information messages during the execution?
<code>log_file</code>	log file where to print outputs when using parallel. If parallel execution is disabled, this parameter is ignored.

### Value

A list of 9 elements: B, C, `phylogenetic_tree`, `corrected_genotypes`, `genotypes_prevalence`, `genotypes_summary`, `log_likelihood` and `error_rates`. Here, B returns the maximum likelihood variants tree (inner nodes of the phylogenetic tree), C the attachment of patients to genotypes and `phylogenetic_tree` VERSO phylogenetic tree, including both variants tree and patients attachments to variants; `corrected_genotypes` is the corrected genotypes, which corrects D given VERSO phylogenetic tree, `genotypes_prevalence` the number of patients and observed prevalence of each genotype and `genotypes_summary` provide a summary of association of mutations to genotypes. In `equivalent_solutions`, solutions (B and C) with likelihood equivalent to the best solution are returned. Finally `log_likelihood` and `error_rates` return the likelihood of the inferred phylogenetic model and best values of alpha and beta as estimated by VERSO.

### Examples

```
data(variants)
set.seed(12345)
inference = VERSO(D = variants,
  alpha = c(0.01,0.05),
  beta = c(0.01,0.05),
  check_indistinguishable = TRUE,
  num_rs = 5,
  num_iter = 100,
  n_try_bs = 50,
  num_processes = 1,
  verbose = FALSE)
```



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