

# Package ‘**VERSO**’

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**Version** 1.0.0

**Date** 2020-10-22

**Title** Viral Evolution ReconStructiOn (VERSO)

**Depends** R (>= 4.0.0)

**Imports** 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

**LazyData** TRUE

**License** file LICENSE

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

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

**biocViews** BiomedicalInformatics, Sequencing, SomaticMutation

**RoxygenNote** 7.1.1

**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,
  check_indistinguishable = TRUE,
  num_rs = 10,
  num_iter = 10000,
  n_try_bs = 1000,
  num_processes = Inf,
  verbose = TRUE
)
```

**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.
check_indistinguishable	Boolean. Shall I remove any indistinguishable variant from input data prior inference?
num_rs	Number of restarts during MCMC inference.
num_iter	Maximum number of MCMC steps to be performed during the inference.
n_try_bs	Number of steps without changes in likelihood of best solution after which to stop the MCMC.
num_processes	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.
verbose	Boolean. Shall I print to screen information messages during the execution?

**Value**

A list of 8 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; 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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```
write.newick.tree      write.newick.tree
```

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**Description**

Write a phylogenetic tree as inferred by VERSO to a newick format file.

**Usage**

```
write.newick.tree(phylogenetic_tree, phylogeny_file = "phylogenetic_tree.new")
```

**Arguments**

```
phylogenetic_tree
    Inference results by VERSO.
phylogeny_file  File where to save the phylogenetic tree in newick format.
```

**Value**

A phylogenetic tree as inferred by VERSO in newick format.

**Examples**

```
data(inference)
write.newick.tree(phylogenetic_tree = inference,
                  phylogeny_file = "inference_tree.new")
```

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