

# Resource Summary Report

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## MSM

RRID:SCR\_015500

Type: Tool

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### Proper Citation

MSM (RRID:SCR\_015500)

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### Resource Information

**URL:** <https://cran.r-project.org/web/packages/msm/index.html>

**Proper Citation:** MSM (RRID:SCR\_015500)

**Description:** Source code for fitting continuous-time Markov and hidden Markov multi-state models to longitudinal data. It was originally designed for processes observed at arbitrary times in continuous time but some other observation schemes are supported. Both Markov transition rates and the hidden Markov output process can be modelled in terms of covariates, which may be constant or piecewise-constant in time.

**Synonyms:** Multi-State Markov and Hidden Markov Models in Continuous Time (MSM), Multi-State Markov and Hidden Markov Models in Continuous Time

**Resource Type:** source code, software resource

**Defining Citation:** [DOI:10.18637/jss.v038.i08](https://doi.org/10.18637/jss.v038.i08)

**Keywords:** markov, continuous time markov, hidden markov multi state model

**Availability:** Available for download

**Resource Name:** MSM

**Resource ID:** SCR\_015500

**Alternate URLs:** <https://www.jstatsoft.org/article/view/v038i08>

**Record Creation Time:** 20220129T080326+0000

**Record Last Update:** 20260817T040540+0000

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### Ratings and Alerts

No rating or validation information has been found for MSM.

No alerts have been found for MSM.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [NIF](#) .

Lees JA, et al. (2017) Genome-wide identification of lineage and locus specific variation associated with pneumococcal carriage duration. eLife, 6.