

dsmmR: Estimation and Simulation of Drifting

- ² Semi-Markov Models
- ³ Vlad Stefan Barbu ¹, Ioannis Mavrogiannis¹, and Nicolas Vergne¹
- 4 1 Univ Rouen Normandie, CNRS, LMRS UMR 6085, F-76000 Rouen, France ¶ Corresponding author

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Software

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Summary

Markov models are a common approach in the researcher's toolbox in order to deal with the modeling of many real-life phenomenons presented as a sequence under discrete time. However, this imposes the assumption that the sequence under inspection is homogeneous with respect to time and furthermore that the sojourn times follow the Geometric distribution. This is not always true in practice when modeling, for example, DNA sequences.

Drifting semi-Markov models (DSMM) formulate the combination of semi-Markov models, which allow arbitrary distributions for the sojourn times, together with drifting Markov models, which describe the non-homogeneity of a sequence through a smooth, known shape that is gradually evolving, expressed through a linear (polynomial) function. As a result, DSMM are best suited to capture the non-homogeneity that occurs from the intrinsic evolution of the system or from the interactions between the system and the environment. For a detailed introduction to semi-Markov models see (Barbu & Limnios, 2009). Drifting Markov models were first introduced in (Vergne, 2008).

dsmmR is an R package which allows the user to perform parametric and non-parametric estimation and simulation of drifting semi-Markov processes. The user can also define their own parametric and non-parametric DSMM specifications, allowing for a necessary degree of freedom when dealing with a research question. Furthermore, three different types of DSMM are considered. These three models differ in the way they characterize the drifting semi-Markov kernel. Specifically, the first model allows both the transition matrix and the sojourn time distribution to vary (i.e. to "drift"), the second model allows only the transition matrix to drift while the third model allows only the sojourn time distribution to drift.

The main functions of dsmmR are the following:

- fit_dsmm(): estimates a DSMM given a sequence.
- parametric dsmm(): defines a parametric DSMM.
- nonparametric_dsmm(): defines a non-parametric DSMM.
- simulate(): simulates a sequence.
 - get_kernel(): returns the drifting semi-Markov kernel.

The estimation of the DSMM kernel is parametric or non-parametric and can be defined through the function fit_dsmm(), which returns an object of the S3 class (fit_dsmm_parametric, dsmm) or (fit_dsmm_nonparametric, dsmm). In the parametric estimation case, several discrete sojourn time distributions are considered for the sojourn times: Uniform, Geometric, Poisson, Discrete Weibull (of type 1) and Negative Binomial. The parametric DSMM specification can be defined through the function parametric_dsmm(), which returns an object of the S3 class (dsmm_parametric, dsmm). In the parametric definition case, we have the same discrete sojourn time distributions. The non-parametric DSMM specification can be defined through the function nonparametric_dsmm(), which returns an object of the S3 class (dsmm_nonparametric, dsmm).



- The dsmm class acts like a wrapper class, enabling the handling of all three models and parametric or non-parametric cases for any degree when it comes to the following actions:
- Simulating a sequence of states under a drifting semi-Markov kernel through the S3 method simulate.dsmm().
 - Calculating the drifting semi-Markov kernel through the generic function get_kernel().

Statement of need

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Drifting semi-Markov processes represent a versatile tool that can be applied in many fields of science like reliability, survival analysis, bioinformatics, engineering, finance and more. The present R package consists of a novel approach to tackle gradually evolving non-homogeneity in a polynomial way and also allows for arbitrary sojourn time distributions. Instead, existing R packages deal with semi-Markov models, hidden semi-Markov models and drifting Markov models.

For semi-Markov models we have the R package SemiMarkov (Król & Saint-Pierre, 2015) 55 that performs maximum likelihood estimation for parametric continuous-time semi-Markov processes, where the distribution can be chosen between Exponential, Weibull or exponentiated Weibull. That package computes associated hazard rates; covariates can also be taken into account through the Cox proportional hazard model. The R package smmR (Barbu, Lecocq, et 59 al., 2021) deals with discrete-time multi-state semi-Markov models, performing parametric and non-parametric estimation and simulation, with k-th order Markov chains also considered. For 61 the parametric estimation the following sojourn times were considered: Uniform, Geometric, Poisson, Discrete Weibull and Negative Binomial. One or more sample paths were considered, with or without censoring at the beginning or the end of the sample paths. Few R packages are also dedicated to hidden semi-Markov models, implementing estimation and prediction methods. Among them, we can cite the HMM R package (Himmelmann, 2022), the HiddenMarkov R package (Harte, 2021) and the mhsmm R package (O'Connell & Højsgaard, 2011).

Furthermore, for drifting Markov models the R package drimmR (Barbu, Lothode, et al., 2021) was developed, performing non-parametric estimation and simulation, also allowing for the exact computation of the associated reliability measures and for several frameworks with regards to how many samples were used, considering if they were complete or incomplete and if they were of the same length. In this package, a linear (polynomial) function was used to capture the non-homogeneity.

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