

Smoothing discrete data (I)

– using the `smooth.discrete()` function in the `mhsmm` package

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1 Introduction

The `smooth.discrete()` function provides a simple smoothing of a time series of discrete values measured at equidistant times. Under the hood of `smooth.discrete()` is a hidden Markov model.

More details – and an additional example – is provided in the vignette “Smoothing discrete data (II)”

2 Using `smooth.discrete()`

For example consider the data:

```
> y1 <- c(1,1,1,1,2,1,1,NA,1,1,2,1,1,1,2,1,1,1,1,2,2,2,2,1,2,2,2,1,2,2,2,1,1,1,1,1,1,1,1,2,2,2,1,1)
```

Calling `smooth.discrete()` on these data gives

```
> obj <- smooth.discrete(y1)

A 'smoothDiscrete' object
List of 4
 $ s      : num [1:45] 1 1 1 1 1 1 1 1 1 1 1 ...
 $ model  :List of 9
 ..- attr(*, "class")= chr "hmm"
 $ data   :List of 3
 $ initial:List of 3
 - attr(*, "class")= chr "smoothDiscrete"
NULL
```

The `s` slot of the object contains the smoothed values. We illustrate the results in Figure 1.

```
> plot(y1, ylim=c(0.8,2))
> addStates(obj$s)
```

The smoothed sequence of states is by default the jointly most likely sequence of states as obtained by the Viterbi algorithm.

A smooth of a new time series is produced as

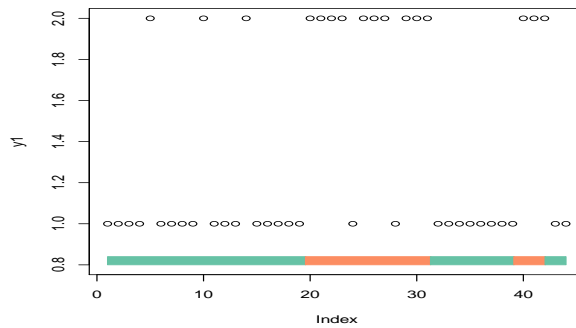


Figure 1: Observed and smoothed discrete time series.

```
> y2 <- c(1,1,1,1,2,2,2,1,1,2,1,1,1,2,1,1,1,1,2,2,2,NA,1,1,1,2,2,1,2,2,2)
> predict(obj,x=y2)

$s
[1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 2 2 2 2 2 2 2 2 2 2 2 2

$x
[1] 1 1 1 1 2 2 2 1 1 2 1 1 1 2 1 1 1 1 2 2 2 NA 1 1
[26] 1 2 2 1 2 2 2

$N
[1] 32

$loglik
[1] -24.53755

attr("class")
[1] "hsmm.data"
```

Here the smoothed values are in the `s` slot. Again, the sequence is by default the jointly most likely sequence of states.

The estimated parameters are:

```
> summary(obj)

init:
 1 0

transition:
      [,1] [,2]
[1,] 0.920 0.080
[2,] 0.136 0.864

emission:
$pmf
      [,1]      [,2]
[1,] 0.7925235 0.2147958
[2,] 0.3418576 0.6443388
```

3 The arguments to `smooth.discrete()`

The arguments of `smooth.discrete()` are

```
> args(smooth.discrete)
```

```
function (y, init = NULL, trans = NULL, parms.emission = 0.5,
  method = "viterbi", details = 0, ...)
  NULL
```

- **init** is a vector of initial probabilities for the Markov chain. If **init=NULL** then the initial distribution is taken to be the relative frequencies in data, that is

```
> table(y1)/sum(table(y1))
```

```
y1
      1      2
0.6363636 0.3636364
```

- **trans** is the transition matrix for the Markov chain. If **trans=NULL** then the transition matrix is derived from data as:

```
> ttt<-table(y1[-length(y1)],y1[-1])
> ttt
```

```
      1  2
1 19  7
2  7  9
```

```
> sweep(ttt, 1, rowSums(ttt), "/")
```

```
      1      2
1 0.7307692 0.2692308
2 0.4375000 0.5625000
```

If **trans** is a vector (of numbers smaller than 1) then these are taken to be the diagonal of the transition matrix and the off-diagonal elements are then, within each row, taken to be identical so that the rows sum to 1. Elements of **trans** are recycled so as to make the dimensions match. Under the hood, the matrix is created as, for example:

```
> createTransition(c(0.8,0.9),2)
```

```
      [,1] [,2]
[1,]  0.8  0.2
[2,]  0.1  0.9
```

- **parms.emission** is a matrix describing the conditional probabilities of the observed states given the latent states. If **parms.emission** is a vector then the matrix is created following the same scheme as for the transition matrix described above.
- The **method** argument is either "viterbi" (which produces the jointly most likely sequence of states). The alternative method is **smoothed** which produces the individually most likely states.
- The dotted arguments are passed on the the **hmmfit** function. For example, one may specify **lock.transition=TRUE** in which case the transition matrix is not estimated from data.