

Estimation of Transition Matrices

Based on Craig and Sendi (2002)

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Transition probability matrix

A Markov model with M states will have the transition matrix

$$P = \begin{bmatrix} p_{1,1} & p_{1,2} & \cdots & p_{1,M} \\ p_{2,1} & p_{2,2} & \cdots & p_{2,M} \\ \vdots & \vdots & \ddots & \vdots \\ p_{M,1} & p_{M,2} & \cdots & p_{M,M} \end{bmatrix},$$

where $p_{i,j}$ is the transition probability from state i to state j in period T .

Transition count matrix

The transition count matrix represents the observed transitions in period T and is expressed as

$$N = \begin{bmatrix} n_{1,1} & n_{1,2} & \cdots & n_{1,M} \\ n_{2,1} & n_{2,2} & \cdots & n_{2,M} \\ \vdots & \vdots & \ddots & \vdots \\ n_{M,1} & n_{M,2} & \cdots & n_{M,M} \end{bmatrix},$$

where $n_{i,j}$ is the number of occurrences between state i and state j in period T .

Estimation of P from longitudinal cohort data

The maximum likelihood estimation (MLE) of P is simply the row proportions of N

$$\hat{P} = \{\hat{\mathbf{p}}\} \text{ where } \hat{p}_{i,j} = \frac{n_{i,j}}{\sum_{m=1}^M n_{i,m}}$$

Estimate of P for a different time scale

- ▶ If the observation periods of the longitudinal cohort study are carried out every t_0 , then the MLE estimate of its corresponding transition probability matrix is \hat{P}_{t_0} .
- ▶ You are interested in a transition matrix for a different time scale (e.g., monthly or biannual)
- ▶ If t_0 is the original time scale and t_f the desired time scale, by the invariance property, the MLE of P_{t_f} associated with a cycle length of t_f is simply

$$\hat{P}_{t_f} = \hat{P}_{t_0}^{(t_f/t_0)}$$

- ▶ For example, to obtain a one-year transition matrix from a one-month transition matrix we just simply raise the one-month transition matrix to the twelfth power

$$\hat{P}_{yr} = \hat{P}_{mo}^{(12)}$$

Potential issues

- ▶ It is relatively easy to go from a shorter time scale to a longer time scale if the latter is a multiple of the former (i.e., (t_f/t_0) is a positive integer)
- ▶ In our monthly to annual scale example we just simply multiply \hat{P}_{mo} 12 times!

$$\hat{P}_{yr} = \hat{P}_{mo} \cdots \hat{P}_{mo}$$

- ▶ If this is not the case, we need to do eigenvalues-eigenvectors (spectral) decomposition.

Spectral decomposition

- ▶ If P is our $M \times M$ transition probability matrix, then its spectral decomposition is defined by

$$P = VDV^{-1}, \text{ where } D = \begin{bmatrix} \lambda_1 & 0 & \cdots & 0 \\ 0 & \lambda_2 & \ddots & \vdots \\ \vdots & \ddots & \ddots & 0 \\ 0 & \cdots & 0 & \lambda_M \end{bmatrix},$$

and λ_i is the i th eigenvalue and its associated eigenvector is the i th column of V .

Spectral decomposition (Cinlar 1975)

- ▶ If we want a transition matrix P_t in a time scale that is t times the original scale (where t could be an integer or not), then it follows that

$$P_t = VD^tV^{-1}, \text{ where } D^t = \begin{bmatrix} \lambda_1^t & 0 & \cdots & 0 \\ 0 & \lambda_2^t & \ddots & \vdots \\ \vdots & \ddots & \ddots & 0 \\ 0 & \cdots & 0 & \lambda_M^t \end{bmatrix},$$

- ▶ The eigenvalues are raised to the power t but the eigenvectors do not change.

Example in R

Install `markovchain` package to obtain example data

```
install.packages(markovchain)
```

Load package and example data `craigsendi` from Craig and Sendi (2002). These data comes from the Swiss HIV cohort study and describes the progression of HIV-infected subjects in terms of their observed six-month CD4-cell count transitions

```
require(markovchain)  
data(craigsendi)  
N<-craigsendi
```

Example

Display the 6-month transition count matrix N

N

##		0-49	50-74	75-UP
## 0-49		682	33	25
## 50-74		154	64	47
## 75-UP		19	19	43

Example

Initialize a 3×3 matrix

```
P <- matrix(nrow = 3, ncol = 3, 0)
colnames(P) <- rownames(P) <- colnames(N)
P
```

##	0-49	50-74	75-UP
## 0-49	0	0	0
## 50-74	0	0	0
## 75-UP	0	0	0

Example

Compute the MLE of the 6-month transition probability matrix P from transition count matrix N .

```
for (i in 1:3) P[i, ] <- N[i, ] / sum(N[i, ])  
P
```

```
##           0-49    50-74    75-UP  
## 0-49    0.9216 0.04459 0.03378  
## 50-74 0.5811 0.24151 0.17736  
## 75-UP 0.2346 0.23457 0.53086
```

Example

Compute one-month transition probability matrix P_1 from the 6-month transition matrix P using the eigen vectors and eigen values decomposition

```
eig <- eigen(P)
eig
```

```
## $values
## [1] 1.0000 0.5702 0.1238
##
## $vectors
##      [,1]      [,2]      [,3]
## [1,] 0.5774  0.1276  0.02818
## [2,] 0.5774 -0.2867 -0.87302
## [3,] 0.5774 -0.9495  0.48688
```

Example

- ▶ Create diagonal matrix D with eigen values

```
D <- diag(eig$values)
```

- ▶ Create matrix V with eigen vectors

```
V <- eig$vectors
```

Example

- Show that both matrices can recreate P

```
V %*% D %*% solve(V)
```

```
##           [,1]      [,2]      [,3]
## [1,] 0.9216 0.04459 0.03378
## [2,] 0.5811 0.24151 0.17736
## [3,] 0.2346 0.23457 0.53086
```

and they do!

- Take the sixth root of each of the diagonal's element of matrix D

```
d <- D^(1/6)
```

Example

Generate the one-month transition matrix

```
P1 <- V %*% d %*% solve(V)
P1
```

```
##           [,1]      [,2]      [,3]
## [1,] 0.9819 0.01220 0.005901
## [2,] 0.1766 0.75170 0.071719
## [3,] 0.0177 0.09929 0.883011
```


References

Cinlar, Erhan. 1975. *Introduction to Stochastic Processes*. Prentice-Hall, Inc.

Craig, Bruce A, and Peter P Sendi. 2002. "Estimation of the Transition Matrix of a Discrete-Time Markov Chain." *Health Economics* 42 (11): 33–42.