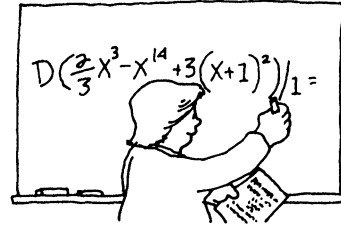


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A Classroom Capsule is a short article that contains a new insight on a topic taught in the earlier years of undergraduate mathematics. Please submit manuscripts prepared according to the guidelines on the inside front cover to Tom Farmer.

## Collapsed Matrices with (Almost) the Same Eigenstuff

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How can we collapse an  $n \times n$  matrix to a smaller  $m \times m$  matrix while maintaining the same dominant eigenvalue and a meaningful associated eigenvector? Such an algorithm would be useful for reducing the size of some matrices used in modeling so as to produce more workable classroom examples.

**Example.** The dominant eigenvalue and its associated eigenvector for the matrix

$$A = \begin{bmatrix} 0 & 0 & 37 & 64 & 82 \\ .06 & 0 & 0 & 0 & 0 \\ 0 & .34 & 0 & 0 & 0 \\ 0 & 0 & .16 & 0 & 0 \\ 0 & 0 & 0 & .08 & 0 \end{bmatrix}$$

are  $\mu \approx 0.9954$  and  $e_1 \approx (.9221, .0556, .0190, .0031, .0002)^T$ .  $A$  is the annual transition matrix for a Leslie matrix model [5] of the population of female brook trout in Hunt Creek, Michigan, with five age groups [2]. Each entry in the first row of  $A$  gives the number of female fingerlings expected from each member of one age group. The entries in the subdiagonal give the fraction of each age group that is expected to survive for one year. So, given an initial population vector  $\mathbf{v}$ ,  $A^n \mathbf{v}$  shows the expected populations in each age group after  $n$  years. The entries in the eigenvector represent the long-run fraction of the population in each age group. The dominant eigenvalue represents the eventual annual growth rate of the population.

We show how to collapse  $A$  to

$$B = \begin{bmatrix} 0 & 11.5691 & 82 \\ 0.06 & 0.2826 & 0 \\ 0 & 0.0031 & 0 \end{bmatrix},$$

whose dominant eigenvalue and associated eigenvector are  $\mu \approx 0.9954$  and  $e_2 \approx (.9221, .0776, .0002)^T$ . This matrix is the result of combining the middle three age groups into one, assuming that the distribution of ages in the combined group is the same as what is expected in the long run, as represented by the eigenvector for  $A$ .

**Defining the algorithm.** The Leslie population model provides us with clues for defining the steps of the algorithm. Suppose we choose to merge age groups  $i$  and  $i + 1$ . Given an  $n \times n$  matrix  $L$  with real dominant eigenvalue  $\mu$  and associated real eigenvector  $\mathbf{x} = (x_1, x_2, \dots, x_i, x_{i+1}, \dots, x_n)^T$ , we wish to construct an  $(n - 1) \times (n - 1)$  collapsed matrix  $C$  with the same dominant eigenvalue  $\mu$  but associated eigenvector  $\mathbf{y} = (x_1, x_2, \dots, x_i + x_{i+1}, \dots, x_n)^T$ . This preserves the interpretation of  $\mathbf{y}$  as giving the population proportions in Leslie models or the long-run proportions of categories in a Markov process [6].

To construct the collapsed matrix  $C$  we first merge rows  $i$  and  $i + 1$  and then columns  $i$  and  $i + 1$ . We note that the entry in  $\mathbf{y}$  corresponding to the merged group is  $x_i + x_{i+1}$ , the sum of the entries from groups  $i$  and  $i + 1$ . Replacing rows  $i$  and  $i + 1$  in  $A$  by the sums of the entries in rows  $i$  and  $i + 1$  results in a matrix which when multiplied on the right by  $\mathbf{x}$  gives such a vector  $\mathbf{y}$ .

The procedure for merging the columns of the partially collapsed matrix can be motivated by the population model. To determine the entries in column  $i$  of the new collapsed matrix we need to know the proportion of the new merged group that will survive for one year. But a collapsed vector will report only the total number in the merged group and not the numbers that came from the original groups  $i$  and  $i + 1$ . We know what fraction of the original group  $i$  survives to join  $i + 1$  and we know what fraction of the original group  $i + 1$  survives to join  $i + 2$ . But, without knowing the breakdown of the merged group, we cannot use this information. So what we do is act as if the distribution of ages in the merged group agrees with the long run proportions that appear in the eigenvector  $\mathbf{x}$ . Thus, we define weights  $r_i = x_i / (x_i + x_{i+1})$  and  $r_{i+1} = x_{i+1} / (x_i + x_{i+1})$ , which are the proportions of the merged age group that we expect in the long run to be from the original age group  $i$  and age group  $i + 1$ . Then the fraction in the combined group advancing in the long run to age group  $j$  in one year would be  $A_{j,i}r_i + A_{j,i+1}r_{i+1}$  because  $r_i$  is the fraction of the combined group that we assume is from age group  $i$  and  $A_{j,i}$  represents the fraction of age group  $i$  that advances to age group  $j$ . Therefore, column  $i$  in collapsed matrix  $C$  is made of entries which are the weighted averages, using weights  $r_i$  and  $r_{i+1}$ , of columns  $i$  and  $i + 1$  of the partially collapsed matrix.

To complete the collapsing process as described in the algorithm we must know the eigenvector  $\mathbf{x}$ , but knowledge of the eigenvalue  $\mu$  is not necessary. To obtain  $\mathbf{x}$  in the case of a population model it is possible for the long run proportion of each age group to be estimated through field sampling of a stable population [4] in an undisturbed ecosystem.

**Matrix characterization.** Let  $I_k$  represent the  $k \times k$  identity matrix and let

$P = \begin{bmatrix} I_{i-1} & 0 & 0 & 0 \\ 0 & 1 & 1 & 0 \\ 0 & 0 & 0 & I_{n-i-1} \end{bmatrix}$ . The first step of the algorithm is to left-multiply  $L$  by  $P$

which has the effect of replacing row  $i$  and  $i + 1$  with their sum. Note also that  $P\mathbf{x} = \mathbf{y}$ .

Next we right-multiply  $PL$  by  $Q = \begin{bmatrix} I_{i-1} & 0 & 0 \\ 0 & r_i & 0 \\ 0 & r_{i+1} & 0 \\ 0 & 0 & I_{n-i-1} \end{bmatrix}$ , where  $r_i = x_i / (x_i + x_{i+1})$

and  $r_{i+1} = x_{i+1} / (x_i + x_{i+1})$ . This has the effect of replacing columns  $i$  and  $i + 1$  of  $PL$  with a single column containing the weighted averages of the entries in each row. Also,  $Q\mathbf{y} = \mathbf{x}$  since  $r_i(x_i + x_{i+1}) = x_i$  and  $r_{i+1}(x_i + x_{i+1}) = x_{i+1}$ .

Therefore, given  $n \times n$  matrix  $L$  with real eigenvalue  $\mu$  and associated real eigenvector  $\mathbf{x}$ , the algorithm constructs a collapsed  $(n - 1) \times (n - 1)$  matrix  $C = PLQ$  such that

$$C\mathbf{y} = PLQ\mathbf{y} = PL\mathbf{x} = P\mu\mathbf{x} = \mu P\mathbf{x} = \mu\mathbf{y}.$$

Thus matrix  $C$  has eigenvalue  $\mu$  and associated eigenvector  $\mathbf{y}$ , as desired.

**Generalizations.** It is a good exercise to verify that the collapsing algorithm can be modified to reduce the size of matrix  $L$  by more than one row and column at a time. Several rows can be summed to create the replacement row and several columns replaced by the weighted average of the appropriate eigenvector entries. This saves time reducing the size of large matrices such as the  $15 \times 15$  population transition matrix for spotted owls in [3] or the  $26 \times 26$  matrix for the Yellowstone grizzly bear population given in [1].

For example, matrix  $A$  was collapsed to form  $B$  by summing the second, third and fourth rows and then combining the second, third and fourth columns using weights  $r_2 = .0556 / (.0556 + .0190 + .00305) = .7160$ ,  $r_3 = .0190 / (.0556 + .0190 + .00305) = .2447$ , and  $r_4 = .00305 / (.0556 + .0190 + .00305) = .0393$ . Thus,  $B = PAQ$  where

$$P = \begin{bmatrix} 1 & 0 & 0 & 0 & 0 \\ 0 & 1 & 1 & 1 & 0 \\ 0 & 0 & 0 & 0 & 1 \end{bmatrix} \quad \text{and} \quad Q = \begin{bmatrix} 1 & 0 & 0 \\ 0 & .7160 & 0 \\ 0 & .2447 & 0 \\ 0 & .0393 & 0 \\ 0 & 0 & 1 \end{bmatrix}.$$

Note that the algorithm does not depend upon using the dominant eigenvalue and its associated eigenvector. Any real eigenvector can be chosen and any set of entries of that eigenvector combined as long as they do not sum to zero, so that the weights are defined. The collapsing algorithm preserves the eigenvalue associated with the chosen eigenvector but, in general, alters the other eigenvalues.

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