

Structured models

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Structured models. linear only. (Unrealistic but very useful for understanding short-term growth/growth when rare ...)

e.g. *Leslie matrix* model: $\mathbf{A}=0$ except for first row (fecundities, ≥ 0) and first subdiagonal (survival, $0 < a_{i+1,i} \leq 1$). *Lefkovich* model: the same except that more column entries can be non-zero (columns add to ≤ 1).

Irreducible non-negative matrix: For every ij there exists k such that $(\mathbf{A}^k)_{ij}$ is not zero. (There are no “dead-end”, or absorbing stages. At some point, individuals in any stage will have ‘offspring’ in any other stage.)

Primitive matrix: There exists k such that for *all* ij , $(\mathbf{A}^k)_{ij}$ is positive. (Equivalently: the greatest divisor of all loop lengths is 1. We cannot have multiple cycles running in parallel.)

Perron-Frobenius theorem: for a non-negative, irreducible, primitive matrix, there is a single positive largest root; its associated eigenvector is the only positive (all-equal-sign) eigenvector. (If the matrix is not primitive then the largest root may be repeated — i.e. out-of-phase cohorts.)

If the max. modulus of the eigenvalues $\max |\lambda|$ (also called *spectral radius*) > 1 , then the population grows geometrically in the long-term; the associated eigenvalue is called the *stable age (stage) distribution*. (Transients may

be different; e.g. start with no adults.) (Note eigenvectors can be scaled any way you like: $\sum e_i = 1$ is convenient for interpretation, Python scales so that $\sum e_i^2 = 1$.)

1 Markov models

Special case of structured models: columns of transition matrix sum to 1 ($\sum_i \mathbf{M}_{ij} = 1$). $\mathbf{M} - \mathbf{I}$ is **not** invertible. Dominant eigenvalue is 1; its associated eigenvector e_1 (scaled to sum to 1) is the equilibrium state of the system. (Any multiple of e_1 is also technically an equilibrium, but we restrict starting values $p(0)$ to sum to 1.)

An **absorbing state** is a state with only inflows, no outflows; if state j is absorbing, $\mathbf{M}_{jj} = 1$, $\mathbf{M}_{ij} = 0$ for all $i \neq j$. If the Markov model has absorbing states, we can compute useful stuff by ordering the state vector/transition matrix so that the absorbing states are the *last* elements; if there are a non-absorbing and b absorbing states, denote the top left $a \times a$ matrix as \mathbf{A} and the bottom left $b \times a$ matrix as \mathbf{B} . Then $\mathbf{F} = (\mathbf{I} - \mathbf{A})^{-1}$ ($a \times a$) represents the number of expected time steps spent in each state i before absorption, if starting in state j (the column sums represent the total number of time steps before absorption if starting in state j). \mathbf{BF} ($b \times a$) gives the probability of absorption in state i if starting in state j .