

Introduction to Linear Algebra

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The notes deliver a brief introduction to linear algebra (Boas 3.1). Without losing too much generality, linear algebra is all about *matrix*. It is quite interesting that matrices play an important role in many physical phenomena. For instance, consider two simple harmonic oscillators,

$$m\ddot{x}_1 = -k_1x_1, \quad m\ddot{x}_2 = -k_2x_2.$$

For simplicity, I have assumed that the masses for the oscillators are the same. It is obvious that the (angular) frequencies are different, $\omega_i = \sqrt{k_i/m}$ with $i = 1, 2$. However, if we couple the oscillators in series (Fig. 12.1 in Boas), their motions are coupled together,

$$\begin{aligned} m\ddot{x}_1 &= -k_1x_1 + k_{12}(x_2 - x_1), \\ m\ddot{x}_2 &= -k_2x_2 - k_{12}(x_2 - x_1), \end{aligned} \tag{1}$$

where k_{12} denotes the spring constant connecting two oscillators together. It is quite interesting that the coupled differential equations can be cast into matrix form,

$$m \begin{pmatrix} \ddot{x}_1 \\ \ddot{x}_2 \end{pmatrix} = - \begin{pmatrix} k_1 + k_{12} & -k_{12} \\ -k_{12} & k_2 + k_{12} \end{pmatrix} \begin{pmatrix} x_1 \\ x_2 \end{pmatrix}. \tag{2}$$

What are the angular frequencies when $k_{12} \neq 0$? The answer apparently is embedded in the 2×2 matrix K . We will learn how to find out the frequencies for the coupled oscillators later.

• Quasi-species equations

Let turn to another interesting question which seems totally unrelated to the coupled oscillators. One of the challenging problems in the origin of life is how a stable sequence outcompetes others in presence of mutations. Back in 1971, Eigen proposed a charming idea to explain the occurrence for the very first sequence – be it RNA or DNA. In the dense chemical soup, each sequence X_i evolves with the fitness f_i ,

$$\frac{dX_i}{dt} = f_i X_i. \tag{3}$$

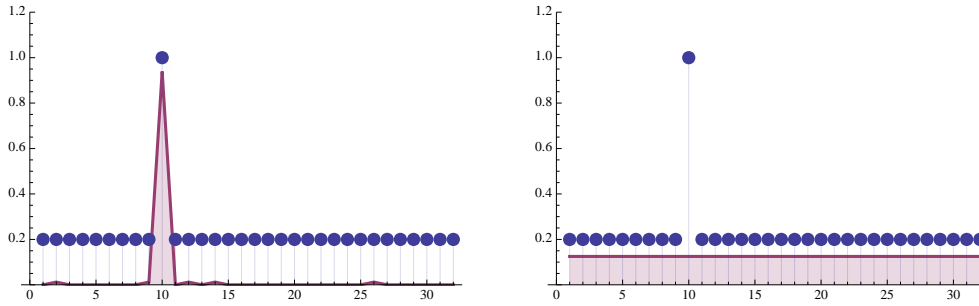


Figure 1: For the single-peak fitness landscape, there exists a mutation threshold u_c . For $u < u_c$, frequency profile is localized near the fitness peak. On the other hand, for $u > u_c$, an extended state (not necessarily uniform) emerges and the notion of quasi-species no longer exists.

The above equations are not coupled and thus can be solved easily. It is straightforward to convince yourself that Darwinism reigns, i.e. the sequence with maximal fitness survives.

However, all sequences suffers from mutations. The mutation matrix q_{ij} denotes the probability for mutations from the j -th sequence to the i -th sequence, satisfying the sum rule $\sum_i q_{ji} = 1$. To make the story simple, let's assume the dominant processes are point mutations so that the mutation matrix takes the simple form

$$q_{ji} = u^{d_{ji}}(1 - u)^{L - d_{ji}}, \quad (4)$$

where u is the probability for point mutation and d_{ji} is the distance between two sequences (minimal number of point mutations to bring one sequence into another). Since $d_{ji} = d_{ij}$, the mutation matrix is also symmetric $q_{ji} = q_{ij}$.

To describe the evolution of different sequences, the evolutionary equations are coupled by mutations,

$$\frac{dX_i}{dt} = \sum_j q_{ij} f_j X_j = \sum_j F_{ij} X_j. \quad (5)$$

It is quite interesting that the evolution of the sequences is now described by the fitness matrix F_{ij} . Note that the fitness matrix is diagonal in the absence of mutations and the evolution is sort of boring. In the presence of mutations, evolutions of different sequences are coupled and exhibit interesting complexity. I shall give you some numerical demo in class.

Mutation matrix in the reduced sequence space

```

Clear[prob, L, q]
L = 32;
prob[i_, j_] :=
  Binomial[L, Abs[i - j]] * u^Abs[i - j] * (1 - u)^(L - Abs[i - j]) /; Abs[i - j] ≥ i && i ≤ (L + 1) / 2
prob[i_, j_] := 1 / 2 * Binomial[L, Abs[i - j]] * u^Abs[i - j] * (1 - u)^(L - Abs[i - j]) /;
  0 < Abs[i - j] < i && i ≤ (L + 1) / 2
prob[i_, j_] := Binomial[L, Abs[i - j]] * u^Abs[i - j] * (1 - u)^(L - Abs[i - j]) /;
  Abs[i - j] > L - i && i > (L + 1) / 2
prob[i_, j_] := 1 / 2 * Binomial[L, Abs[i - j]] * u^Abs[i - j] * (1 - u)^(L - Abs[i - j]) /;
  0 < Abs[i - j] ≤ L - i && i > (L + 1) / 2

prob[i_, j_] := 1 - ∑_{k=1}^{i-1} prob[i, k] - ∑_{k=i+1}^L prob[i, k] /; i == j

q = Table[prob[i, j], {i, 1, L}, {j, 1, L}];

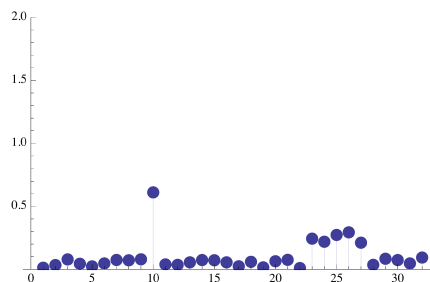
```

For single-peak fitness landscape, set **peak1=0.6** and **peak2=0**.
 To reveal the competition between the single peak and the mesa, set **peak1=0.6** and **peak2=0.2**.

```

Clear[peak1, peak2];
Clear[ini, f];
Clear[fit];
peak1 = 0.6;
peak2 = 0.2;
ini = Table[KroneckerDelta[i, L], {i, 1, L}];
SeedRandom[12345];
f =
  Table[N[RandomReal[{0, 0.1}] + peak1 * KroneckerDelta[i, 10] + peak2 * KroneckerDelta[i, 23] +
    peak2 * KroneckerDelta[i, 24] + peak2 * KroneckerDelta[i, 25] +
    peak2 * KroneckerDelta[i, 26] + peak2 * KroneckerDelta[i, 27]], {i, 1, L}]
ListPlot[f, Filling -> Axis, PlotStyle -> {PointSize[0.03], Thick}, PlotRange -> {0, 2}]
{0.0121246, 0.0329922, 0.0782753, 0.0430168, 0.0223586, 0.0463053, 0.0738017, 0.0707618,
0.0790911, 0.610571, 0.038044, 0.0349269, 0.0545578, 0.0730743, 0.0714425, 0.0546648,
0.0233454, 0.0590656, 0.0145935, 0.0632964, 0.0746537, 0.00945845, 0.242613, 0.218646,
0.2721, 0.292917, 0.210553, 0.0345443, 0.0835872, 0.073089, 0.0458819, 0.0932325}

```



Choose the probability of point mutation $u=0.01$ to see the emergence of the quasi-species.

Choose $u=0.04$ for transition from QS1 to QS2.

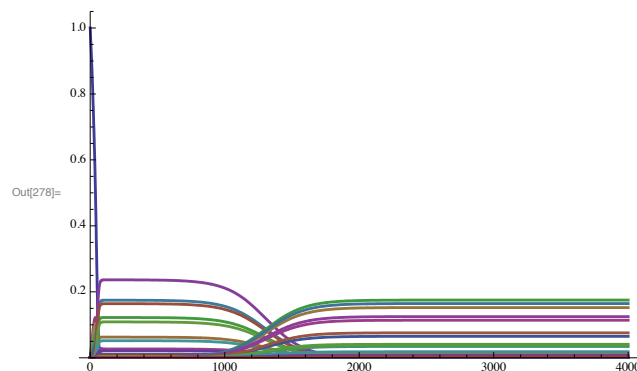
Choose $u=0.2$ and the QS disappears.

```

In[267]:= Clear[eqns];
Clear[x];
Clear[u, tspan, variables, sol, freq]

ini = Table[KroneckerDelta[i, 1], {i, 1, L}];
u = 0.04;
tspan = 4000;
eqns = {};
For[i = 1, i <= L, i++,
  eq[i] = {x[i]'[t] = Sum[x[j][t] * f[[j]] * q[[j, i]], {j, 1, L} -
    Sum[f[[j]] * x[j][t], {j, 1, L}] * x[i][t], x[i][0] = ini[[i]]};
  eqns = Join[eqns, eq[i]]
]
variables = Table[x[i], {i, 1, L}];
sol = NDSolve[eqns, variables, {t, 0, tspan}];
freq = Table[x[i][t] /. sol, {i, 1, L}];
Plot[freq, {t, 0, tspan}, PlotRange -> {0, 1.05}, PlotStyle -> {Thick}

```



Set `initime` and `evoltime` for the animation of the evolution.

```
evol[t_] := Table[x[i][t] /. sol[[1]], {i, 1, L}];
initime = 0;
evoltime = 1600;
evolution = Animate[ListPlot[{f, evol[t]},
  Joined -> {False, True}, Filling -> Axis,
  PlotStyle -> {PointSize[0.03], Thick}, PlotRange -> {0, 1.2}
], {t, initime, initime + evoltime}, AnimationRunning -> True,
  AnimationRepetitions -> 2, AppearanceElements -> "ResetButton"]
```

