# EXERCISES (v) - Maths for Biology

Computational Methods in Ecology and Evolution
Imperial College London
Silwood Park

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Instructions for the final report. Deadline - one week before the exam.

The report will consist on a single tar file containing a pdf file with the exercises and different folders (one for each script you made) and one folder containing any source data needed to run the scripts (called data_sources or similar). The folders should be identified with any logic label such as Exercise4_Integrals (as usual, please avoid any blank or weird character in the names of files and folders). The script can be made in any language as soon as it can be run straight in a Linux environment. As the scripts are easy, I recommend you to use an interpreted language like R or Python (and not a compiled one like C, in which case please talk to me first). In every folder, you will provide whatever code is needed to run the script and a Readme file with instructions to run it. Your scripts should be set in such a way that no movement of data between folders is needed to run them (i.e. your scripts will look for the data in the folder data_folders). In general, try to consider any good programming practice as those suggested for the mini project

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# Exercises linear algebra

Unless otherwise is stated, all vectors and matrices are given in the standard basis.

## Basic Operations

**Exercise 1. Systems of equations [EXM] SON LOS MISMOS QUE DI EN CLASE, CAMBIAR**
Solve the following systems of equations:

1.

$$\begin{aligned} x + 2y - 3z &= 1 \\ 2x + 5y - 8z &= 4 \\ 3x + 8y - 13z &= 7 \end{aligned}$$

2.

$$\begin{aligned} 2x + y - 2z &= 10 \\ 3x + 2y + 2z &= 1 \\ 5x + 4y + 3z &= 4 \end{aligned}$$

3.

$$\begin{aligned} x + 2y - 3z &= -1 \\ 3x - y - 2z &= 7 \\ 5x + 3y - 4z &= 2 \end{aligned}$$

Clue: Each of the systems corresponds to one of the situations described by this THEOREM: Any system of linear equations has either i) a unique solution, ii) no solution, iii) infinity solutions.

**Exercise 2. Distributive law of vectors** Consider the following vectors $a$, $b$, $c$ and the scalar $k$:

$$a = (1, 2, 3)$$
$$b = (4, 0, 1)$$
$$c = (3, 2, 2)$$

$$k = 2$$

and demonstrate that:

1. $a(b + c)^t = ab^t + ac^t$ (where the superscript $t$ stands for the transpose).
2. $(a + b)c^t = a^t c + b^t c$
3. $a(kb^t) = (ka)b^t + k(ab^t)$

**Exercise 3. Matrix basics (i)** Consider the following matrices $A$, $B$, $C$, and the scalar $k$:

$$A = \begin{pmatrix} 1 & 2 & 3 \\ 4 & 5 & 6 \end{pmatrix}; \quad B = \begin{pmatrix} 0 & 1 & 1 \\ 5 & 1 & 3 \end{pmatrix}; \quad C = \begin{pmatrix} 1 & 3 & 4 \\ 9 & 6 & 9 \end{pmatrix};$$

$$k = 3$$

and test if the following expressions hold:

1. $C = A + B = B + A$
2. $C^t = A^t + B^t = B^t + A^t$
3. $A + (B + C) = A + B + C = (A + B) + C$
4. $A(kB^t) = (kA)B^t$
5. $AB^t = BA^t$

**Exercise 4. Matrix basics (ii)** Consider the following matrix $B$ and the vectors $a$ and $b$:

$$a = (1, 1, 2); \quad B = \begin{pmatrix} 1 & 2 & 3 \\ 0 & 1 & 2 \\ 3 & 0 & 1 \end{pmatrix}; \quad c^t = \begin{pmatrix} 2 \\ 1 \\ 3 \end{pmatrix};$$

And compute:

1. $D = aB$
2. $E = aBc^t$
3. $F = aBa^t$

**Exercise 5. Matrix basics (iii)** Consider the following matrices:

$$A = \begin{pmatrix} -1 & 3 & 2 \\ 2 & 0 & 1 \end{pmatrix}; \quad B = \begin{pmatrix} 2 & 3 \\ 1 & 4 \\ 1 & 2 \end{pmatrix} \quad ;$$

And compute:

1. $C = AB$
2. $D = BA$

**Exercise 6. Matrix basics (iv)** Consider the following matrices:

$$A = \begin{pmatrix} 1 & 4 & 1 \\ 2 & 5 & 1 \\ 3 & 6 & 2 \end{pmatrix}; \quad D_1 = \begin{pmatrix} 3 & 0 & 0 \\ 0 & 2 & 0 \\ 0 & 0 & 1 \end{pmatrix}; \quad D_2 = \begin{pmatrix} 2 & 0 & 0 \\ 0 & 2 & 0 \\ 0 & 0 & 2 \end{pmatrix}; \; M = \begin{pmatrix} -1 & 0 & 0 \\ 0 & -1 & 0 \\ 0 & 0 & 1 \end{pmatrix}; \; I = \begin{pmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{pmatrix}$$

And compute:

1. $C = D_1 A$
2. $D = AD_1$
3. $E = D_2 A D_1$
4. $F = D_1^2$
5. $G = AF$
6. $H = IA = AI$

**Exercise 7. The contact overlap and the designability [DLV]** Reproduce the Table 1 and the Figure 6 of the Snake Puzzle paper (Nido *et al.* in the folder Readings/Teaching in Blackboard), providing the scripts.

**Exercise 8. The nestedness [DLV]** Mutualistic networks of plants and pollinators or plants and seed dispersers are networks in which it is represented the interaction between plants and animals. Plants and animals are the nodes of the network and the links represent a mutualistic interaction, namely that an animal pollinates one plant (and viceversa). This kind of networks are called bipartite, because there are two pools of nodes (animals and plants) and the interactions occur only between members of the different pools (i.e. there are no mutualistic links animals-animals nor plants-plants, although there are competitive interactions *within* pools). In its simplest form –when we just see if there is an interaction and not how strong it is– these networks are represented with binary matrices $A_{ik}^{(P)}$ of size $M \times N$, where the superscript indicates that plants occupy the $M$ rows and the animals the $N$ columns, and where the elements are 0 and 1, being $A_{ik}^{(P)} = 1$ if plant $i$ is pollinated by animal $k$ and $A_{ik}^{(P)} = 0$ otherwise. The matrix of animals $A_{ik}^{(A)}$ is the transposed matrix of the matrix of plants, i.e. $A_{ik}^{(A)} = (A_{ik}^{(P)})^t$ (APG: It was written a "prime" mark instead a t, the meaning was the same), the and the other way around. For simplicity of the exposition, in the following we will consider most of the times only the matrix of plants (and you should perform the exercise for measures of plants), although we should keep in mind that some of the measures proposed (like the nestedness) might be different for animals, even if they would be computed in a completely symmetric way just considering the matrix of animals.

It was observed (see for instance Ref. [1]) that these matrices have a non-random pattern that it is called nestedness. In Fig. 1 you can see an illustration of a perfectly nested matrix. The most intriguing feature of these matrices, is that specialist species (that only pollinate or are pollinated by a single species) tend to interact with a generalist species. There are different hypothesis explaining this result and criticisms (overall if we think the oversimplified representation of reality of these matrices). But it is interesting to imagine what would happen in an assembly process in which a new specialist species arrives to an environment with this structured network, and it tries to coexist with the other species. Because, according with the nestedness pattern, this new species

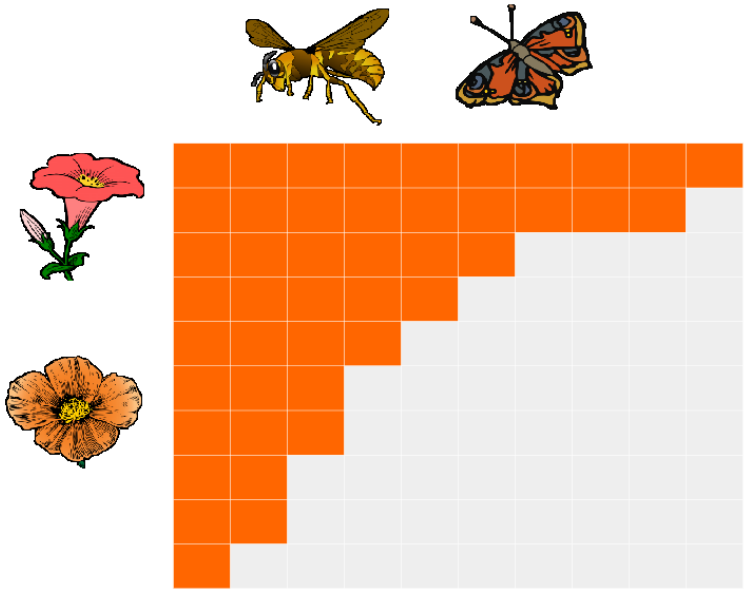

Figure 1: Illustration of a completely nested matrix.

will tend to interact with the most connected species, and we may find this counter intuitive given that we could expect that it is with this species where it would support most competition, as it is the most connected.

Irrespective of the process explaining this pattern, what is clear is that it is non-random. Similar to the exercise we made with the three bits system, we would like to identify the constraints acting on the system. In particular, we would like to know the significance of this particular pattern, and which could be its origin if we impose simple constraints in our matrix. Let's understand first what is understood as nestedness.

We start calling the degree of a species to the number of interactions that the species have. For instance, for a plant species $i$ we will have that its degree is $n_i = \sum_k A_{ik}^{(P)}$ (see Ref. [2] in Supplementary Material). A similar definition would apply for animals $m_k = \sum_i A_{ik}^{(P)}$.

Next we define the overlap between two species of plants $i$ and $j$ as the number of insects that pollinate both plants:

$$n_{ij}^{(P)} = \sum_k A_{ik}^{(P)} A_{jk}^{(P)}.$$

Note that, for a matrix as the one we have seen in the Figure, this quantity is maximized. If we sum for every pair of plants and we normalize it, we will find the definition of nestedness:

$$\eta^{(P)} = \frac{\sum_{i<j} n_{ij}^{(P)}}{\sum_{i<j} \min(n_i^{(P)}, n_j^{(P)})}.$$

To understand what $i < j$ means in the summatory, start counting for $i = 1$ (and then $j$ will run from 2 to $M$) then $i$ will be 2 (and $j$ will run from 3 to $M$) etc. And follow how the indexes run looking at a simple matrix.

As we are talking about how many animals every pair is sharing, we are computing here a normalized average of the amount of overlap between plant species. A completely nested pattern will take a value equal to one, and the value of a random matrix will depend on the model we use to generate the randomization (and it is of course not zero, because it is very unlikely that there is no overlap at all). Things like the size of the matrix or the number of observations will influence the expected value. Thinking in ecological terms, we could expect that if more overlap exist between species, more competition there is, although there are good reasons to think that it is rather the opposite! (see again Ref. [2]).

For real matrices, a significantly high nestedness has been reported in the literature. To test if this pattern is significant in real matrices we should think in null models. For instance, how likely it is to get a highly nested matrix if you generate a random matrix containing some constraints? The most basic constraint one can think for a matrix is, apart from its size ($M$ and $N$), the number of ones it contains, what is called the connectance. For instance, in the trivial case of a matrix fully connected, the nestedness would be one (although this is unrealistic unless there are very few species involved). But would this be the case, we would not be able to say if it is significant or not, because any random matrix with the same connectance would be exactly the same!

To generate random matrices $G_{ik}$ which conserve the connectance we can use the equation:

$$G_{ik} = \frac{n_i + m_k}{N + M}$$

You should just compute these values and create the matrix $G_{ik}$ (of course of size $M \times N$) that will be a kind of "generator" of random matrices. To generate the random matrices (that we will call $R_{ik}$), imagine that one specific value of the matrix $G_{ik}$ is 0.3 for the cell $i = 1$ and $k = 2$, ($G_{12}$). This would mean that you have 0.3 chances of having an observation in the cell $R_{12}$ of a random matrix. Then, you just need to randomly draw a value $r$ with your computer between 0 and 1 and, if $r \leq G_{12}$ you will generate an observation ($R_{12} = 1$) and if $r > G_{12}$ we make $R_{12} = 0$. If you repeat this procedure for every cell you will generate a random matrix with almost the same connectance. It might not be exactly the same, but the average of the connectance of all the random matrices generated will tend to the observed connectance, and more you generate closer it will go the average of the whole set of randomizations to this value, being in this way more difficult to reject the null model.

If you compute now $\eta^{(P)}$ for every random matrix, you will see if the value observed in the real matrix is significant or not. Consider that you generate 1000 random matrices and you compute the nestedness for all of them, obtaining a vector $\{\eta_1^{(P)}, ..., \eta_{1000}^{(P)}\}$ that you have sorted in such a way that $\eta_i^{(P)} < \eta_j^{(P)}$ if $i < j$. If it happens that the nestedness of the observed matrix is:

- $\eta_{obs}^{(P)} > \eta_{1000}^{(P)}$ then you have 1/1000 confidence that the observed value is significant, and then you can say that it is significant with a p-value $p = 0.001$.
- $\eta_{501}^{(P)} > \eta_{obs}^{(P)} > \eta_{500}^{(P)}$ then you have 1/500 confidence that the observed value is significant, and then you can say that it is significant with a p-value $p = 0.005$.
- And it will be the same for any other confidence interval. Then, the position of the value of nestedness for the observed matrix will give you the p-value of the observation.

Therefore, you will be able to generate a null model and test its significance with this method. But someone may say that conserving only the connectance is not very relevant, and that the fact that a given species is generalist or specialist is a particular feature of every species and, thus, you should conserve not only the connectance but the number of observations that every species has, namely the values $n_i$ and $m_k$. Fair enough, as our hypothesis is that the nestedness may be a consequence of ecological interactions, we should neglect any pattern that could be due to individual effects and not to interaction effects. We can generate a null model that conserve on average (again, not for a particular matrix but for the average of all matrices) not only the connectance but the number of observations of every species. This is achieved with the model:

$$\tilde{G}_{ik} = \frac{p_i q_k}{2}.$$

where $p_i = n_i/M$ and $q_k = m_k/N$. Therefore, $p_i$ ($q_k$) codify the fraction of ones observed in the row $i$ (column $k$). The procedure to obtain the significance would be the same than above. The exercise consists in the following. Go to the website "www.web-of-life.es" and look for pollinator networks (seed dispersers would be ok as well). Select a network of your choice (not very small, at least 80 species for instance). Build for this network the two generator models $G_{ik}$ and $\tilde{G}_{ik}$ and create one thousand matrices for each model. Compute the nestedness of plants for the observed matrix and for the random matrices generated, and report the p-values you obtain for each model and the scripts (please refer clearly the matrix you used). Try to interact with your mates to select different matrices, in this way you can explore how general are your results.

## Basic Properties

**Exercise 1. Trace [EXM]** Consider the following THEOREM: Let's assume that $A = (a_{ij})$ and $B = (b_{ij})$ are squared matrices and $k$ a scalar. Then:

1. $\text{tr}(A + B) = \text{tr}(A) + \text{tr}(B)$.
2. $\text{tr}(kA) = k\text{tr}(A)$
3. $\text{tr}(AB) = \text{tr}(BA)$

In this problem I just want you to get used on mathematical notation, and I ask you to demonstrate that this theorem is true. I show you how the first point is demonstrated. Let me call $A + B = C$. The idea when we demonstrate properties of matrices is that we change the notation to an explicit representation in which we "see" what happens with the cells values, we operate on cells values (which are scalars and we know well how to operate with them) and then we come back to matrix notation:

$$\text{tr}(A + B) = \text{tr}(C) = \sum_{k=1}^{n} c_{kk} = \sum_{k=1}^{n} (a_{kk} + b_{kk}) = \sum_{k=1}^{n} a_{kk} + \sum_{k=1}^{n} b_{kk} = \text{tr}(A) + \text{tr}(B).$$

Now you should demonstrate points 2 and 3 proceeding similarly.

**Exercise 2. More complex expressions with matrices [EXM]** We can use equations in more complex expressions. Consider for example the function $g(x) = x^2 - x - 8$, where $x$ is a square matrix. It may sound weird, because we have the number 8 and we haven't talked about the sum of a matrix and scalar. Therefore, if we see this kind of expression we should consider that the independent term is a number multiplying an identity matrix with the same size than $x$. Taking this into account, demonstrate that $A = \begin{pmatrix} 1 & 3 \\ 4 & -3 \end{pmatrix}$ is a root of $g(x)$, i.e. show that $g(A)$ is equal to the null matrix.

**Exercise 3. Determinants (i)** Consider a generic matrix $B$ obtained after applying elemental operations on the matrix:

$$A = \begin{pmatrix} 1 & 2 & -4 \\ -1 & -1 & 5 \\ 2 & 7 & -3 \end{pmatrix}$$

and check if the following theorem holds. Note that I am not asking you to proof the theorem, because to proof the theorem I would ask you to demonstrate that it holds for *any* operation, and I just ask you to check if for *one* operation of your choice it is true:

THEOREM:

- If you interchange two rows or columns in $A$, then $|B| = -|A|$. (Obtain the matrix $B$ doing the operation mentioned and test the statement.)
- If you multiply any row or column by a scalar $k$,then $|B| = k|A|$.
- If you sum a multiple of a row or column to another row (column) (e.g. $R_2 = R_2 + kR_1$, where $R_i$ is the row $i$ and $k$ is an integer), then $|B| = |A|$.

**Exercise 4. Determinants (ii) [DLV]** When we have a square matrix of dimension $n > 3$ we said that it is not so easy to compute the determinant, and that we should compute it using its minors. If the matrix is very large it might be a mess, so ideally we would like to perform operations in the matrix until we get just a single minor of size $n = 3$. In addition, it is useful to keep in mind the following

THEOREM: Let's consider $A$ a square matrix

- If $A$ has any rows (or column) filled of zeros, then $|A| = 0$.

- If $A$ has two rows (or columns) that are equal, then $|A| = 0$.
- If $A$ is triangular, what means that $A$ has only zeros above or below the diagonal then $|A|$ is equal to the product of the diagonal elements only. For instance, for the identity matrix $I$ the determinant will be $|I| = 1$.

Let's see an example. Compute the determinant of the matrix

$$A = \begin{pmatrix} 5 & 4 & 2 & 1 \\ 2 & 3 & 1 & -2 \\ -5 & -7 & -3 & 9 \\ 1 & -2 & -1 & 4 \end{pmatrix}$$

I can consider the third result shown in the theorem of Exercise 3, and do the following elemental operations. I will get the row number two $R_2$ and I will use it to modify the other rows as follows: $R_1 \to R_1 - 2R_2$ (I subtract two times the second row to the first one). Then, $R_3 \to R_3 + 3R_2$ and $R_4 \to R_4 + R_2$. Note that we always used the second row, that we will call the "pivot" row (or column). With these operations I obtain the matrix:

$$A' = \begin{pmatrix} 1 & -2 & 0 & 5 \\ 2 & 3 & 1 & -2 \\ 1 & 2 & 0 & 3 \\ 3 & 1 & 0 & 2 \end{pmatrix}$$

And I know by means of the theorem of Exercise 3 that $|A'| = |A|$. If you realize, the third column has all the elements zero except the element $a'_{23} = 1$. Therefore, to compute the determinant, if I consider that column, there is only one minor "surviving" (because all the others would be multiplied by zero). Then, computing the determinant of $A'$ is equivalent to compute the determinant of the matrix:

$$A'' = \begin{pmatrix} 1 & -2 & 5 \\ 1 & 2 & 3 \\ 3 & 1 & 2 \end{pmatrix}.$$

You can easily proof that $|A''| = 38$. Now you should follow the same reasoning to compute the determinant of the scary matrix:

$$B = \begin{pmatrix} 6 & 2 & 1 & 0 & 5 \\ 2 & 1 & 1 & -2 & 1 \\ 1 & 1 & 2 & -2 & 3 \\ 3 & 0 & 2 & 3 & -1 \\ -1 & -1 & -3 & 4 & 2 \end{pmatrix}$$

Clue: The second row seems to be a good pivot candidate again.

**Exercise 5. Inverse of a matrix** Look for the inverse of the matrices:

$$A = \begin{pmatrix} 3 & 5 \\ 2 & 3 \end{pmatrix}; \; B = \begin{pmatrix} 1 & 2 & -4 \\ -1 & -1 & 5 \\ 2 & 7 & -3 \end{pmatrix}$$

and remember this THEOREM: If $A$ is a square matrix, it is equivalent to say:

- $A$ has an inverse ($A^{-1}$).
- $AX = 0$ has only the trivial solution.
- The determinant of is different from zero: $|A| \neq 0$.

## Some Geometry

**Exercise 1. Geometry** Given the vectors $a = (1, 2)$ and $b = (0, 2)$ calculate:

- The length of the vectors.
- Their scalar product.
- The projection of $a$ on $b$.
- The angle between both vectors.

**Exercise 2. Gram-Schmidt orthonormalization [EXM]**

Consider the basis given by the vectors $a_1 = (2, 1, 2)$, $a_2 = (3, -1, 5)$ and $a_3 = (0, 1, -1)$ and transform it into an orthonormal basis using the Gram-Schmidt procedure.

**Exercise 3. Rotations [DLV]** We will now discuss another measure widely used in protein structure comparison, the Root Mean Square Deviation

$$\text{RMSD} = \min_R \sqrt{\frac{1}{n} \sum_i \left| \vec{r}_i^{(x)} - R\vec{r}_{a(i)}^{(y)} \right|^2}$$

where $\vec{r}_i^{(x)}$ indicates the coordinates of atom $i$ in structure $x$, $|\cdot|^2$ is the Euclidean distance, $R$ denotes a rotation matrix that has to be optimized to find the optimal superimposition, and both $\vec{r}_i^{(x)}$ and $\vec{r}_i^{(y)}$ are translated in such a way that their centers of mass stay at the origin. The above formula for the RMSD helps to avoid the confusion between alignment$a(i)$ and superposition $R$.

Instead of comparing interatomic distances between pairs of atoms as the Contact Overlap does, the RMSD compares the distances of individual aligned atoms after optimal superimposition, which is apparently simpler. However, this simplification is obtained at the price to determine the optimal rotation matrix $R$ that minimizes the RMSD. This minimization can be performed analytically through the classical algorithm by Kabsch based on Singular Value Decomposition. Nevertheless, the optimal superimposition is strongly influenced by the aligned atom $i$ that is farther away in the two structures. This determines a trade-off between alignment length and RMSD, since we can decide not to align residues that are too distant, obtaining shorter alignments with smaller RMSD. In this sense, the measure of the RMSD is not uniquely determined unless the alignment is trivial. In fact, there is no structure alignment method based on the minimization of the RMSD.

In this exercise, you will consider a single coordinate in the 3D Euclidean space given by the vector $a$=(1,2,5) and another coordinate given by $b = (-2, -1, 1)$ in the standard basis. You already know how to perform rotations over any vector $v$ in two dimensions, you just need to perform the operation $v' = Rv^t$ where $R$ is the 2D rotation matrix. In three dimensions, the rotation matrix is a little bit more complex, but there are simple expressions if you rotate just around one axes. The following matrices

$$R_x(\theta) = \begin{pmatrix} 1 & 0 & 0 \\ 0 & \cos\theta & -\sin\theta \\ 0 & \sin\theta & \cos\theta \end{pmatrix}$$

$$R_y(\theta) = \begin{pmatrix} \cos\theta & 0 & \sin\theta \\ 0 & 1 & 0 \\ -\sin\theta & 0 & \cos\theta \end{pmatrix}$$

$$R_z(\theta) = \begin{pmatrix} \cos\theta & -\sin\theta & 0 \\ \sin\theta & \cos\theta & 0 \\ 0 & 0 & 1 \end{pmatrix}$$

will allow you to rotate a vector an angle $\theta$ around the axes $\overline{OX}$, $\overline{OY}$ and $\overline{OZ}$ respectively. Now, you should do a script that performs the following operations. It takes the vector $a$ and one of the axes, let say $\overline{OX}$, and rotates

the vector for different values between 0 and $2\pi$, i.e. you compute $a_x(\theta) = R_x(\theta)a^t$ (remember that $t$ stands for transposition). For the vectors obtained at each of these values ($a_x(\theta)$), it computes the euclidean distance with respect to the other vector $b$. You should then return the vector $a_x^{min}$ having the minimum euclidean distance with $b$, their angle $\theta_x^{min}$, and the value of the distance.

Once you determined the vector $a_x^{min}$ you will rotate it now around other axes $\overline{OY}$, proceeding similarly until you get another vector $a_y^{min}$ (which is therefore the vector with minimum distance with $b$ obtained rotating $a_x^{min}$ around $\overline{OY}$). Again, you record the final values obtained $a_y^{min}$, $\theta_y^{min}$ and the euclidean distance. Finally, you repeat the exercise rotating the vector $a$ in the opposite order, i.e. first around $\overline{OY}$ and then around $\overline{OX}$. Compare both results.

**Exercise 4. Other geometric operations** If you plot the following four points in the plane, you will see that they represent a square:

$$P = (1, 1); \quad Q = (1, -1); \quad R = (-1, 1); \quad S = (-1, -1);$$

Now consider the following matrices:

$$A = \begin{pmatrix} 1 & 1 \\ 0 & 1 \end{pmatrix}$$

$$B = \begin{pmatrix} 2 & 0 \\ 0 & 2 \end{pmatrix}$$

$$C = \begin{pmatrix} 2 & 0 \\ 0 & 1 \end{pmatrix}$$

$$D = \begin{pmatrix} -1 & 0 \\ 0 & 1 \end{pmatrix}$$

$$E = \begin{pmatrix} 0 & 1 \\ 1 & 0 \end{pmatrix}$$

and apply each of these matrices to all four vectors and, for each matrix, plot the four new points it generates. You can do this transformations with the computer if you want, but you should keep in mind that to observe the effects it is necessary that you are able to distinguish which is each point before and after the transformation, i.e. you should keep the points labeled at all times. Then, determine which matrix performs one of the following operations: i) a reflection, ii) a central dilation, iii) a stretch, iv) a shear and v) a permutation. Take into account the meaning of the matrices having only diagonal elements, and now think that any of these matrices represent a contact matrix, where a contact represents the interaction between two species, and the vectors over which you apply the matrix are the abundances of two species. If you diagonalize the interaction matrix you will obtain a a matrix like $B$, $C$ and $D$ (unless you get complex eigenvalues...). Imagine that you apply each of these matrices to the vector of abundances, and then again the same matrix to the resultant vector, and again, and again... and go to the bar to think in the population dynamics it generates.

## Basis and diagonalization

**Exercise 1. Cayley-Hamilton [EXM]** In a previous exercise, we observed that the matrix $A = \begin{pmatrix} 1 & 3 \\ 4 & -3 \end{pmatrix}$ was a root of $g(x)$. Now, the Cayley-Hamilton THEOREM states that every matrix is a root of its own characteristic polynomial. Demonstrate that this is true with this matrix as well.

**Exercise 2. Basis [EXM]** Determine if the following vectors constitute a basis in $\mathbb{R}^3$:

$$a = (1, 1, 1); \; b = (1, 2, 3); \; c = (2, -1, 1)$$

**Exercise 3. Subspaces [EXM]** Two subespaces of $\mathbb{R}^3$ that we will call $U$ and $W$ are described by the following vectors:

$$u_1 = (1, 1, -1);\ u_2 = (2, 3, -1);\ u_3 = (3, 1, -5);$$

$$w_1 = (1, -1, -3);\ w_2 = (3, -2, -8);\ w_3 = (2, 1, -3).$$

You should represent each subespace with a matrix and, reducing each matrix to its row canonical form, show that $U = W$.

**Exercise 4. Changing the basis [EXM]** Consider the following basis in $\mathbb{R}^3$:

$$S = \{u_1 = (1, 2, 0), u_2 = (2, 3, 1), u_3 = (0, 2, 3)\}$$

You should look for:

- The matrix $P$ that changes the basis from the standard basis $E = \{e_1, e_2, e_3\}$ to the basis of $S$.
- Take a generic vector $(a, b, c)$ and write it in the basis of $S$.
- ~~Then obtain~~ Which is the matrix $Q$ that allows you to change back the coordinates ~~of a vector~~ of the basis $S$ to $E$? ~~(i.e. $P^{-1} = Q$).~~
- Bring the coordinates of generic vector you obtained in the basis $S$ back to the basis $E$ ~~using $Q$.~~

**Exercise 4. Diagonalization (i) [EXM]** Diagonalize the following matrix $A$, and find the matrix $P$ such that $D = P^{-1}AP$, being $D$ the diagonal matrix. Once you obtain $D$ and $P$, demonstrate that $A = PDP^{-1}$. Finally, find the value of $A^5$.

$$A = \begin{pmatrix} 4 & 2 \\ 3 & -1 \end{pmatrix}$$

**Exercise 5. Diagonalization (ii) [EXM]** Diagonalize the following matrix $A$, and find the matrix $P$ such that $D = P^{-1}AP$, being $D$ the diagonal matrix. Once you obtain $D$ and $P$, demonstrate that $A = PDP^{-1}$. Finally, find the value of $A^5$.

$$A = \begin{pmatrix} 2 & 2 \\ 1 & 3 \end{pmatrix}$$

**Exercise 6. Diagonalization (iii) [EXM]** Look for the eigenvalues of the following matrix $B$, and then look for a set of eigenvectors linearly independent. Is it $B$ diagonalizable?

$$B = \begin{pmatrix} -3 & 1 & -1 \\ -7 & 5 & -1 \\ -6 & 6 & -2 \end{pmatrix}$$

# References


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