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Math 2270

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Biochemical Pathways as Linear Systems

Introduction:

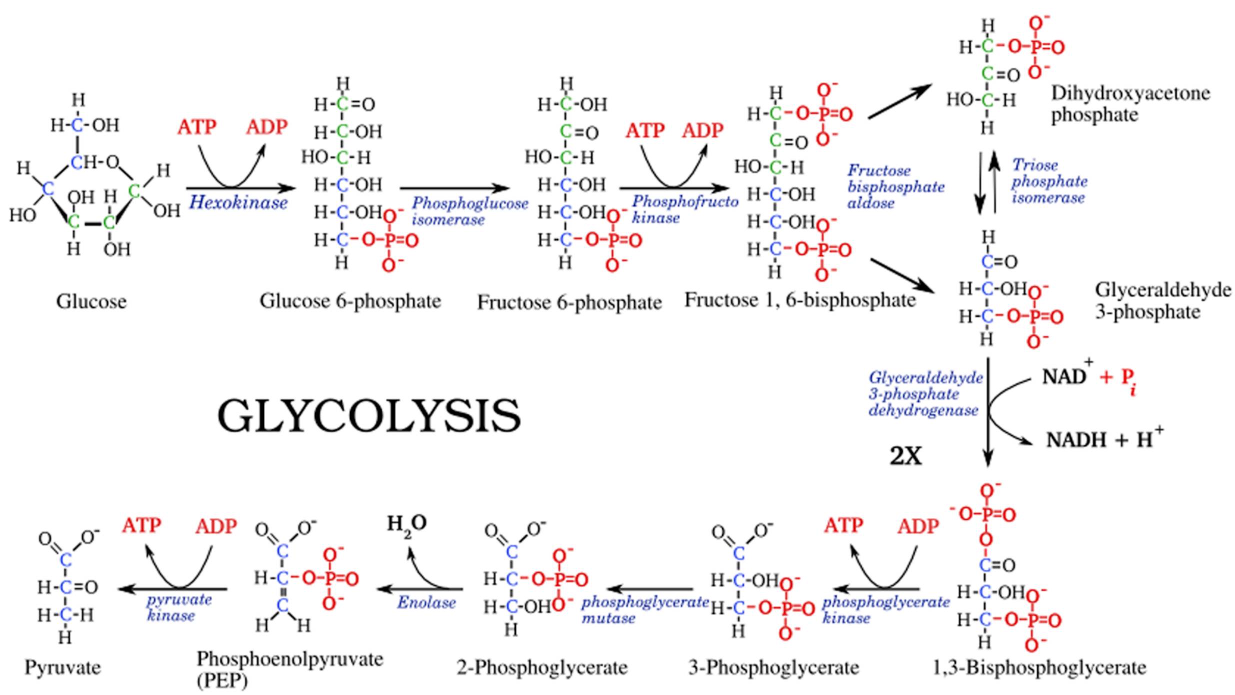
The human body is an extremely complex system, especially when you look at it from a chemical standpoint. When you zoom in past the ordered structures of organs and organ systems you are confronted with what could be described as chaos. You have thousands of reactions happening constantly within each cell, of which there are trillions, in your body. Every time you make the slightest movement, smell something, see something, or even just simply sit still, your body is working at dizzying rates to keep you alive and able to function. One of the most basic reactions, and the one I will be examining, is cellular metabolism. Cellular metabolism is the process of taking glucose, the preferred source for fuel in the body, and converting it to carbon dioxide, water and, most importantly, Adenosine Triphosphate (ATP). Just about anyone who has taken an introductory course to biology knows the net reaction and overall process for this mechanism, but it is actually much more complex than many people realize. The amazing thing about biochemistry, however, is that it can be easily modeled in a linear system. Using systems of linear equations we can create stoichiometric matrices based on the individual chemical equations and use these matrices to determine the overall net reaction involved in this chemical pathway. The use of computing software, such as Maple or Matlab, has greatly reduced the tedium and time required to model this pathway.

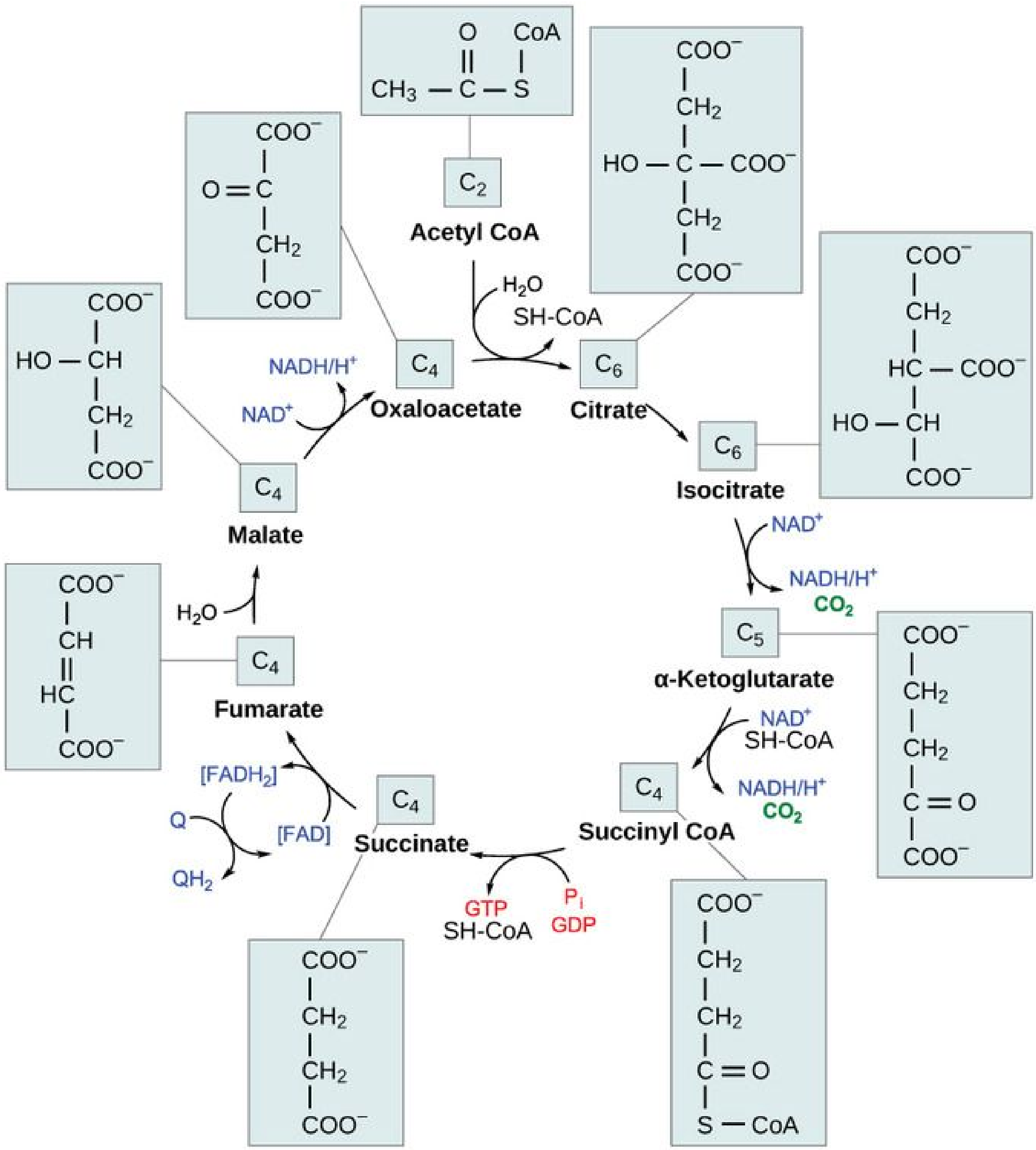
Chemical Reactions of Metabolism:

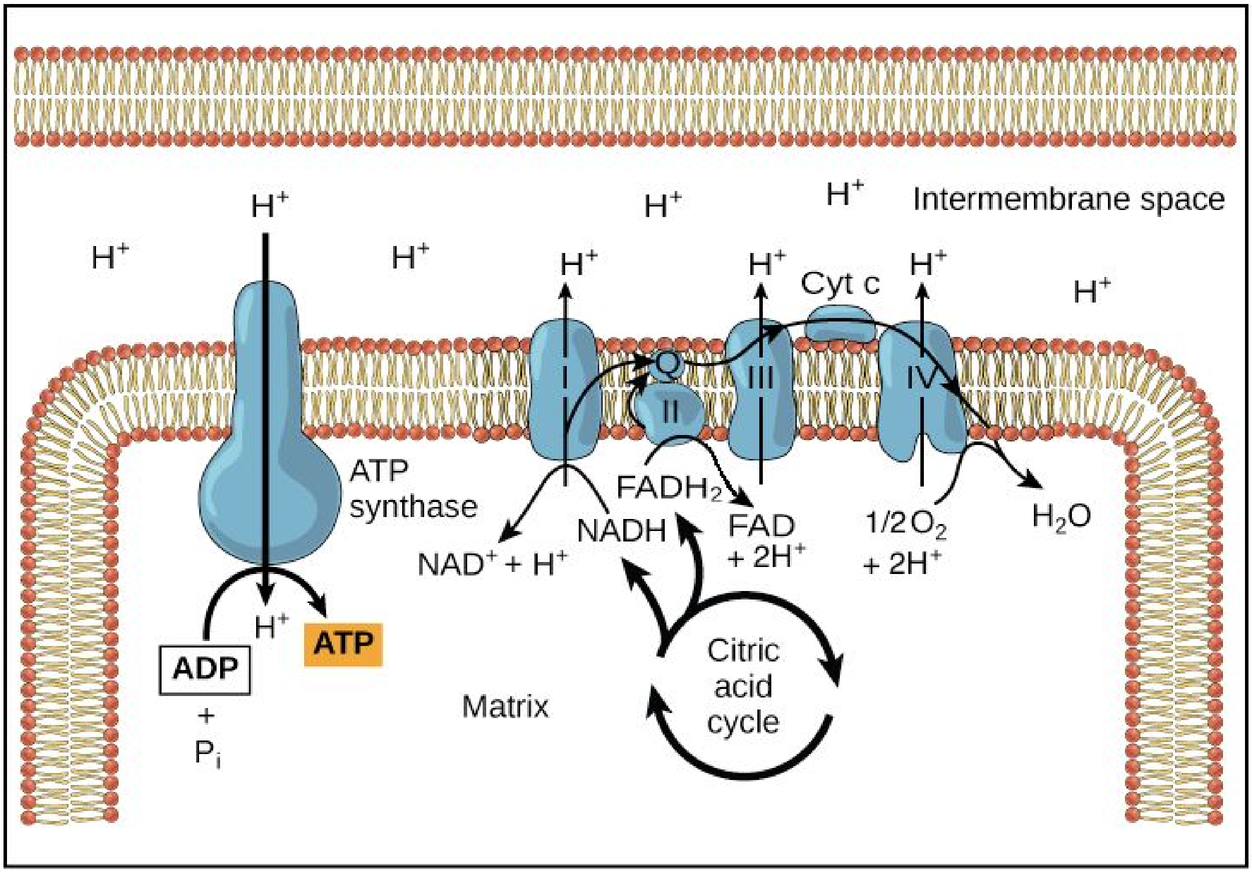
I will briefly explain the chemical pathway of the conversion of Glucose to ATP. There are approximately 21 reactions involved in this chemical pathway:

1. glucose + ATP = glucose 6-phosphate + ADP
2. glucose 6-phosphate = fructose 6-phosphate
3. fructose 6-phosphate + ATP = fructose 1,6-bisphosphate+ ADP
4. fructose 1,6-bisphosphate = glycerone phosphate + glyceraldehyde 3-phosphate
5. glycerone phosphate = glyceraldehyde 3-phosphate
6. glyceraldehyde 3-phosphate + Pi + NAD^+ = 3-phospho-D-glyceroyl phosphate + NADH
7. 3-phospho-o-glyceroy1 phosphate+ ADP= 3-phospho-D-glycerate + ATP
8. 3-phospho-D-glycerate = 2-phospho-D-glycerate
9. 2-phosphoglycerate = phosphoenolpyruvate +H2O
10. phosphoenolpyruvate + ADP = pyruvate+ ATP
11. pyruvate + CoA + NAD^+ = acetyl-CoA + CO2 + NADH
12. acetyl-CoA + oxaloacetate + H20 = citrate + CoA
13. citrate = cis-aconitate+ H2O
14. cis-aconitate+ H20 = isocitrate
15. isocitrate + NAD^+ =2-oxoglutarate + CO2 + NADH
16. 2-oxoglutarate + NAD^+ + CoA = succinyl-CoA+ CO2+ NADH
17. succinyl-CoA + Pi + ADP = succinate + ATP + CoA
18. succinate + NAD^+ = fumarate + NADH
19. fumarate + H2O = (S)-malate
20. (S)-malate + NAD^+ = oxaloacetate + NADH
21. NADH + 1/2O2 + 3Pi + 3ADP = NAD^+ + 4H20 + 3ATP

Reactions 1-10 are the steps in of glycolysis, which happens in the cytosol of a cell. And reactions 11-21 are known as the Citric Acid Cycle or the Kreb's Cycle. Glycolysis, in actuality, produces 2 pyruvate per glucose for entry into the citric acid cycle. This means that every step of the Citric Acid Cycle happens twice, yielding 6 CO2 as byproducts, fully accounting for every carbon in glucose. This can also be seen in the final step, where ½ of an O2 molecule would be produced. Because you cannot create half a molecule, this reaction happens twice, consuming one full molecule of O2. For future clarity, Pi is inorganic phosphate which, when bound to another molecule, is a source of a high energy bond, which, when broken, can be a source of the energy required for the formation of new bonds between substrates; ADP is Adenosine Diphosphate, which is ATP with one phosphate group removed as Pi. The matrices we will produce will be absent of any H+ or metal ion quantities because they are often at pre-specified concentrations at points in the body and their overall quantities will not change. Finally, below you will see a graphical representation of glycolysis, the citric acid cycle and the oxidative phosphorylation. Below that we can finally move past the chemistry portion and explore the mathematics behind metabolism!




Acetyl CoA
Citrate
Isocitrate
α-Ketoglutarate
Succinyl CoA
Succinate
Fumarate
Malate
Oxaloacetate
C2
C6
C6
C5
C4
C4
C4
C4
C4
H2O
SH-CoA
NAD+
NADH/H+
CO2
NAD+
SH-CoA
NADH/H+
CO2
Pi
GDP
GTP
SH-CoA
[FAD]
[FADH2]
Q
QH2
H2O
NAD+
NADH/H+



You will notice the presence of FADH2 which did not appear in the above reactions. This is because FADH2 acts as an electron carrier for NADH generated in glycolysis, which happens in the cytosol of a cell. Because NADH cannot pass through membranes, a process known as the glycerol phosphate shuttle utilizes FADH2 to help move electrons from NADH outside the mitochondrial matrix to NADH inside the mitochondrial matrix.

Mathematics Behind Metabolism:

The calculation of a biochemical pathway through linear algebra is done with a stoichiometric number matrix. This is a matrix which gives the stoichiometric number for the various molecules encountered in an independent reaction. In these matrices, the number of rows is determined by the number of substrates encountered in a pathway, and the number of columns is determined by the number of reactions involved in an overall pathway. In each individual reaction, the reactants will be given a (-) in front of their stoichiometric number because they are being consumed, while the products will have a (+) stoichiometric number. This matrix can then be multiplied by a column vector, which is called the pathway vector. The pathway vector will have a row for each reaction (or column) of the number matrix. For a given set of reactions a solution will not always exist. The solution will only exist when the final column of the number matrix is a linear combination of the columns of the number matrix.

$$\begin{bmatrix} \nu_{11} & \nu_{12} & \dots & \nu_{1R} \\ \nu_{21} & \nu_{22} & \dots & \nu_{2R} \\ \dots & \dots & \dots & \dots \\ \dots & \dots & \dots & \dots \\ \nu_{N1} & \nu_{N2} & \dots & \nu_{NR} \end{bmatrix} \begin{bmatrix} s_1 \\ s_2 \\ \dots \\ s_R \end{bmatrix} = \begin{bmatrix} \nu_{net1} \\ \nu_{net2} \\ \dots \\ \dots \\ \nu_{netN} \end{bmatrix}$$

$$S_1 \begin{bmatrix} v_{11} \\ v_{21} \\ \dots \\ v_{N1} \end{bmatrix} + S_2 \begin{bmatrix} v_{12} \\ v_{22} \\ \dots \\ v_{N2} \end{bmatrix} + \dots + S_R \begin{bmatrix} v_{1R} \\ v_{2R} \\ \dots \\ v_{NR} \end{bmatrix} = \begin{bmatrix} v_{net1} \\ v_{net2} \\ \dots \\ v_{netN} \end{bmatrix}$$

The trick with this system is that it is easy to calculate the net energy production when you can multiply a number matrix by a pathway vector, but what if you don't know the pathway vector? This seems like the kind of roadblock that could stop an aspiring mathematician right in their tracks. Luckily, there is a workaround. We can create a stoichiometric number matrix without any of the reactions involving energetic molecules, namely Pi, ADP, ATP, NADH, NAD^+. We can then simplify these reactions down to their lowest stoichiometric number, which can provide a pathway vector for the abbreviated matrix. This will not balance any energetic molecules, but it will allow us to balance the carbon, oxygen and sulfur used. This will generate pathway vectors which we can then use to calculate a net energy output for the metabolism depending on starting substrates.

Attached will be the Maple file with the matrices used in the following calculations. The dimensions of the unabbreviated matrix will be 30x21. There are 30 total molecular species and 21 reactions used in the pathway. The abbreviated number matrix will be 25x21. The energetic molecules listed above have been removed from the reactions with some waters added to help balance charges. To save on space, and because this is a lesson mostly on math and not the biochemistry possibilities, I will only include 3 of the possible pathways. One starting from glucose, one starting from a phosphorylated version of glucose, and one coming from an already partially oxidized species stemming from glucose. The columns of the unabbreviated matrix will go in the following order of molecular species, while the abbreviated matrix will simply follow in the same order with the energetic molecules removed:

1. Glucose
2. Pi
3. ADP
4. NAD^+
5. Pyruvate
6. ATP
7. NADH
8. H2O
9. CoA
10. Acetyl-CoA
11. CO2
12. O2
13. Glucose 6-phosphate
14. Fructose 6-phosphate
15. Fructose 1,6-bisphosphate
16. Glycerone phosphate
17. Glyceraldehyde 3-phosphate
18. 3-phospho-D-glycerol phosphate
19. 3-phospho-D-glycerate
20. 2-phospho-D-glycerate
21. Phosphoenolpyruvate
22. Oxaloacetate
23. Citrate
24. Cis-aconitate
25. Isocitrate
26. 2-oxoglutarate
27. Succinyl-CoA
28. Succinate
29. Fumarate
30. Malate

We can take the abbreviated number matrix and the 3 simplified net reactions and relate these to each other with the matrix equation: Ax=b. In this example, A is the number matrix, b is the matrix made up of vector representations of the simplified net reactions, and x, which is typically a column vector, will be the reaction pathway we wish to solve for.

The abbreviated number matrix will be denoted by matrix A:

$$A := \begin{bmatrix}
-1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & -1 & 0 & 0 & 1 & 0 & 0 & -1 & 1 & -1 & 0 & 0 & -1 & 0 & -1 & 0 & 1 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -1 & 1 & 0 & 0 & 0 & -1 & 1 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 1 & 1 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -\frac{1}{2} \\
1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 1 & 1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & -1 & 0
\end{bmatrix}$$

We will denote the abbreviated net reactions by the matrix B:

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

By using the LinearSolve tool in Maple, we can determine the Matrix, C, of pathway vectors that can relate A to B:

$$C := \begin{bmatrix} 1 & 0 & 0 \\ 1 & 0 & 0 \\ 1 & 0 & 0 \\ 1 & 1 & 0 \\ 1 & 1 & 0 \\ 2 & 2 & 0 \\ 2 & 2 & 0 \\ 2 & 2 & 0 \\ 2 & 2 & 0 \\ 2 & 2 & 2 \\ 2 & 2 & 2 \\ 2 & 2 & 2 \\ 2 & 2 & 2 \\ 2 & 2 & 2 \\ 2 & 2 & 2 \\ 2 & 2 & 2 \\ 2 & 2 & 2 \\ 2 & 2 & 2 \\ 2 & 2 & 2 \\ 2 & 2 & 2 \\ 12 & 12 & 10 \end{bmatrix}$$

One observation that in hindsight seems obvious is the fact that the first 20 rows of matrix C correspond to how many times substrate passes through each enzyme that catalyzes that step. This makes perfect sense when you think about what exactly a pathway vector represents. The pathway vectors represent how many times each of the 20 reactions of glycolysis and the citric acid cycle occur per one starting material. The final row represents the ATP generated through oxidative phosphorylation, or the electron transport chain, which is itself dependent on the quantities of byproducts from the first 20 reactions.

This pathway matrix balances the reaction with regards to the “non energetic” atoms such as carbon, oxygen, and phosphates when they are attached. Because the energetic molecules are attached to these reactions, we can then add them back into the number matrix and determine their output. The unabbreviated number matrix is represented by matrix A1:

$$A1 := \begin{bmatrix}
-1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -1 & 0 & 0 & 0 & -3 \\
1 & 0 & 1 & 0 & 0 & 0 & -1 & 0 & 0 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & -1 & 0 & 0 & 0 & -3 \\
0 & 0 & 0 & 0 & 0 & -1 & 0 & 0 & 0 & 0 & -1 & 0 & 0 & 0 & -1 & -1 & 0 & -1 & 0 & -1 & 1 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
-1 & 0 & -1 & 0 & 0 & 0 & 1 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 3 \\
0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 1 & 1 & 0 & 1 & 0 & 1 & -1 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & -1 & 1 & -1 & 0 & 0 & 0 & 0 & -1 & 0 & 4 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -1 & 1 & 0 & 0 & 0 & -1 & 1 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 1 & 1 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -\frac{1}{2} \\
1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & -1 & 0
\end{bmatrix}$$

We can then use matrix multiplication to observe the overall net reactions of glycolysis:

$$AI \cdot C = \begin{bmatrix} -1 & 0 & 0 \\ -40 & -40 & -32 \\ -40 & -42 & -34 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \\ 40 & 42 & 34 \\ 0 & 0 & 0 \\ 46 & 46 & 36 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \\ 6 & 6 & 6 \\ -6 & -6 & -5 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \\ 0 & -1 & 0 \\ 0 & 0 & 0 \\ -1 & -1 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & -2 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

We can now compare the values in row 6 to compare the ATP generated per 1 molecule of starting material. You will notice that no NADH shows up even though it is typically considered an “energetic” molecule when balancing energy expenditure. This is because NADH is used in oxidative phosphorylation to help establish the proton gradient which in turn generates the ATP. So NADH’s energy comes not from itself, but from its potential as a reducing agent for the electron transport chain.

The results on the energy output make sense as well. The results in column 1 are the results when the starting material is glucose. This is the compound the body uses so we can use this as a base line. You will notice the results from column 2 have a higher energy output than glucose. This is because the starting compound used in this pathway was Fructose 1,6-bisphosphate, which is a glucose derivative that has been phosphorylated. Because the starting material has already been phosphorylated, the energy input to phosphorylate it has been negated, increasing the net energy output. From the other side, the energy output from column 3 is lower than that of glucose. This is because that starting material, Phosphoenolpyruvate, is a derivative of glucose which has already been partially oxidized so it cannot be oxidized to the same extent of glucose.

Conclusion:

Using the example of metabolism, which is fairly complex but by no means the most complex chemical reaction the body undergoes, we can see that as long as certain aspects of a chemical pathway are known that we can model it in a linear system. Once we have a linear representation of it, we can then use simple matrix properties to solve for any unknown or desired quantities.

References:

Alberty, R.a. "Calculation of Biochemical Net Reactions and Pathways by Using Matrix Operations." *Biophysical Journal* 71.1 (1996): 507-15. Web.

Akinola, R. O., S. Y. Kutchin, I. A. Nyam, and O. Adeyanju. "Using Row Reduced Echelon Form in Balancing Chemical Equations." *Advances in Linear Algebra & Matrix Theory*06.04 (2016): 146-57. Web.

Rhodes, Carl Douglas, Kirsten Fertuck, P. David Josephy, Roger E. Koeppe, and Jeremy M. Berg. *Biochemistry, Eighth Edition*. New York: W.H. Freeman and, a Macmillan Education, 2015. Print.

Lay, David C., Steven R. Lay, and Judi J. McDonald. *Linear Algebra and Its Applications*. Boston: Pearson, 2016. Print.

"Oxidative Phosphorylation." *Khan Academy*. N.p., n.d. Web. 18 Apr. 2018.

"Glycolysis." *Khan Academy*. N.p., n.d. Web. 18 Apr. 2018.

"The Citric Acid Cycle." *Khan Academy*. N.p., n.d. Web. 18 Apr. 2018.