Signal transduction pathways recover a crucial role in cellular processes: they represent a connection between environmental conditions and cellular reactions. There are many pathways and they all are related to create a network. But how can every protein find the right way more fast than possible? How can it find the right down-streaming kinase in the cellular sea and not another very similar kinase?

Every signal transduction pathway can be seen as two distincted processes: the signal must reach every kinase and then it must travel through the enzyme until its active site: quantum walks could be the answer to both the questions.

Every signal transduction pathway is composed by one receptor and some kinases that bring the environmental signal to the nucleus. Usually, when the ligand binds the receptor, it activates a kinase by phosphorylation, the signal travel through the kinase and then the kinase activates the next one in the chain.

Electronic energy transfer involving oscillatory populations of donors and acceptors was first discussed more than 70 years ago\(^1\). Quantum coherence in photosynthetic complexes have been predicted\(^2,3\) and indirectly observed\(^4\). Recently, direct evidence of long-lived coherence has been experimentally demonstrated for the dynamics of the Fenna-Matthews-Olson (FMO) protein complex\(^5\).

Mohseni et al.\(^6\) developed a theoretical framework for studying the role of quantum interference effects in energy transfer dynamics of molecular arrays. However, the relevance of quantum dynamical processes to the exciton transfer efficiency is to a large extent unknown.

Quantum mechanics can explain the extreme efficiency, in that it allows the complexes to sample vast areas of space to find the most efficient path.

Many articles\(^7,8,9,10\) report electron transfer examples in polypeptides, but always refered to metalloproteins. However if we align the sequences of different kinases, we find that the most conserved residues are in the middle of loops and turns, as shown in figure 1\(^11\).
Moreover, considering kinases alignments at http://kinase.com/human/kinome/phylogeny.html positive and negative amino acids have an high frequency: 1/3 respect to 1/4 as a mean.

The large majority of protein kinases is activated by the phosphorylation of a polypeptide region (activation loop) that lies outside the active-site cleft. Analysis of the X-ray crystallographic structures of the insulin receptor with the activation loop in the phosphorylated and dephosphorylated forms offers a testable model for the mechanism of activity regulation by the loop\textsuperscript{13}.

In conclusion, these data indicate that inside the kinases the signal jumps (being an electron?) from a loop to another until it reaches the active site where phosphorylation takes place.

Figure 2 (14) represents the positive residues (in blue) that can reveal the path from the site of interaction with the previous enzyme, where phosphorylation takes place to the active site.
Every signal transduction pathway can be seen as two distincted processes: the signal travel through the kinase until its active site and then it must reach the next kinase. Random walks (r.w.) allow to estimate the position of a particle after a time interval described by a probability distribution according to the nature of the process. Our goal is to check if a r.w. based model is useful to describe kinases’ dynamics or if to consider quantum walks (q.w.). It is possible to calculate the time required to transport the signal to the nucleus, but this estimation do not take into consideration the probability of two kinases to match, equal to the probability of extracting two pre-established numbers over $15 \times 10^8$. This calculation shows that we have to take into account q.w. instead of r.w.

In conclusion, quantum mechanics could lead to better understand signal transduction pathways involved in cancer and memory mechanisms and open the way for other quantum mechanical effects on biological systems.

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