

## **Molecular mimicry: statistical analysis and evolutive implications**

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The hypothesis of the existence of generally spread out evolutive convergence processes, guided by the phenomenon of "molecular mimicry" between viruses and their hosts, has been put forward by many authors [1].

We present here a thorough statistical investigation aimed at testing the experimental basis of this conjecture. To this end we have adapted to this problem a previously developed code [2], designed to select "biologically homologous" pairs of short sequences of amino-acids (peptides) belonging to non-homologous proteins, with the idea of comparing the actual number of homologous peptide pairs found by the searching algorithm among different classes of proteins with the number expected from purely statistical considerations.

Although the data we have collected do not yield a clearcut answer to the question concerning the existence of possible evolutive convergence processes, in analyzing murine-virus proteins versus murine proteins, we have found [3] that most of the homologous peptide pairs selected by our algorithm happen to belong to a class of proteins, called "transforming proteins" [4], that are known to be associated with various types of murine cancers. Unfortunately we cannot offer any satisfactory biological explanation for such an unexpected but very suggestive result.

### References

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