



## Structural evolution of G-protein-coupled receptors: a sequence space approach

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Résumé en anglais	<p>Class A G-protein-coupled receptors (GPCRs) provide a fascinating example of evolutionary success. In this review, we discuss how metric multidimensional scaling (MDS), a multivariate analysis method, complements traditional tree-based phylogenetic methods and helps decipher the mechanisms that drove the evolution of class A GPCRs. MDS provides low-dimensional representations of a distance matrix. Applied to a multiple sequence alignment, MDS represents the sequences in a Euclidean space as points whose interdistances are as close as possible to the distances in the alignment (the so-called sequence space). We detail how to perform the MDS analysis of a multiple sequence alignment and how to analyze and interpret the resulting sequence space. We also show that the projection of supplementary data (a property of the MDS method) can be used to straightforwardly monitor the evolutionary drift of specific subfamilies. The sequence space of class A GPCRs reveals the key role of mutations at the level of the TM2 and TM5 proline residues in the evolution of class A GPCRs.</p>
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### Liens

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