Routine libraries for pattern recognition in quasispecies

E.A. Marucci[1], G.F.D. Zafalon[1], A.C.G. Jardim[2], L.H.T. Yamasaki[2], C. Bittar[2], P. Rahal[2] and J.M. Machado[1]

[1]Laboratório de Bioinformática, Universidade Estadual Paulista,
São José do Rio Preto, SP, Brasil
[2]Laboratório de Estudos Genômicos, Universidade Estadual Paulista,
São José do Rio Preto, SP, Brasil

Corresponding author: G.F.D. Zafalon
E-mail: zafalon@gmail.com

ABSTRACT. The results obtained through biological research usually need to be analyzed using computational tools, since manual analysis becomes unfeasible due to the complexity and size of these results. For instance, the study of quasispecies frequently demands the analysis of several, very lengthy sequences of nucleotides and amino acids. Therefore, bioinformatics tools for the study of quasispecies are constantly being developed due to different problems found by biologists. In the present study, we address the development of a software tool for the evaluation of population diversity in

quasispecies. Special attention is paid to the localization of genome regions prone to changes, as well as of possible hot spots.

Key words: Bioinformatics; Quasispecies; Pattern recognition; Genetic variability