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Another view of sequence evolution

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We describe another view of sequence evolution, that allows to change one alignment column by introducing extra mutations on the tree. The mathematical description of this model leads to analytical formulas for the posterior probability of the number of substitutions that occurred for an alignment site on a phylogenetic tree. Moreover, the model allows to compute the number of extra mutations required to fit an alignment to a tree. We will give a few illustrative examples and discuss the impact of our analysis on phylogenetic inferences.

Klaere S, Gesell T, von Haeseler A (2008) The impact of single substitutions on multiple sequence alignments. *Phil. Trans. R. Soc. Lond. B*, 363, 4041-4047

Short CV

Arndt von Haeseler was appointed scientific director of the Center for Integrative Bioinformatics Vienna (CIBIV) in September 2005 and professor for bioinformatics. He studied biology and mathematics and received his PhD in Mathematics at the University of Bielefeld.

Then he did his post-doc at the University of Southern California (Los Angeles). Subsequently he was an assistant professor at the University of Munich, an associate professor at the Max Planck Institute for evolutionary Anthropology, and full professor for Bioinformatics at the University of Düsseldorf.

His research interests are: phylogenetic tree reconstruction, modelling evolution, and population genetics, algorithms for bioinformatics, biodiversity.