INTRODUCTION

The One Day Symposium on Numerical Cladistics was held at the American Museum of Natural History (New York) on May 22, 1998, organized by Ward Wheeler, Dan Janies, and Gonzalo Giribet. The symposium was organized with the intention of bringing together a series of speakers to present the newest algorithmic developments happening in the field of cladistics and systematics in general. Invited speakers were Jim Carpenter (American Museum of Natural History), Steve Farris (Naturhistoriska riksmuseet), Pablo Goloboff (Instituto Miguel Lillo; Pablo could not attend and his contribution was read by Inés Horovitz), Atte Moilanen (University of Helsinki), Kevin Nixon (Cornell University), Mark Siddall (then at the University of Michigan), and Ward Wheeler (American Museum of Natural History). A synopsis of their talks was previously published in Cladistics (Horovitz, 1999).

Many new ideas were presented at the symposium, some of which have been already published (Farris et al., 1996; Wheeler, 1999; Nixon, 1999; Moilanen, 1999). These ideas led to the most impressive algorithmic shortcuts ever implemented in a tree search computer program (Goloboff, 1999; Goloboff et al., 2000; Wheeler and Gladstein, 2000). However, many of the ideas or revisionary talks presented have not yet been published and are compiled in this special issue of Cladistics. In this issue, Goloboff and Farris present their talk on quick consensus estimation, a method implemented in their upcoming parsimony analysis software TNT. Moilanen gives a discussion on global optimization and local searches and reviews his method of evolutionary optimization as well as the computer program Parsigal. Nixon, Carpenter, and Borgardt present an alternative format for data management in systematic studies based on a “fileless” design such as Structured Query Language. Siddall discusses and evaluates several forms of randomization in systematics and gives an interpretation of what randomization means and does not mean in the context of evaluating hypotheses. Wheeler presents a discussion of homology in sequence data and how homology is seen in multiple sequence alignments, optimization alignment, and fixed-states alignment.

The issue is complemented with two essays related to the use of POY (Wheeler and Gladstein, 2000) that were not presented at the symposium, but that in a certain mode complement the talk by Wheeler. Janies and Wheeler evaluate the efficiency of parallelism during tree search using optimization alignment, and Giribet compares optimization alignment and fixed states within and among methods, according to gap cost, fragment size, tree length, character congruence, topological congruence, primary homology statements, and computation time.

We hope that these discussions give the reader a wide vision of the newest breakthroughs in numerical cladistics.

REFERENCES

Introduction


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